

Shoba Ranganathan

List of Publications by Year in descending order

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207
papers

7,738
citations

57758

44
h-index

64796

79
g-index

223
all docs

223
docs citations

223
times ranked

11096
citing authors

#	ARTICLE	IF	CITATIONS
1	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
2	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	21.4	383
3	Establishing bioinformatics research in the Asia Pacific. <i>BMC Bioinformatics</i> , 2006, 7, 1.	2.6	356
4	<i>Ascaris suum</i> draft genome. <i>Nature</i> , 2011, 479, 529-533.	27.8	246
5	An Integrated Transcriptomics and Proteomics Analysis of the Secretome of the Helminth Pathogen <i>Fasciola hepatica</i> . <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1891-1907.	3.8	244
6	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , 2006, 8, 6-21.	6.5	235
7	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	21.4	166
8	A common site within factor H SCR α ,7 responsible for binding heparin, C α -reactive protein and streptococcal M protein. <i>European Journal of Immunology</i> , 2003, 33, 962-969.	2.9	151
9	In silico grouping of peptide/HLA class I complexes using structural interaction characteristics. <i>Bioinformatics</i> , 2007, 23, 177-183.	4.1	133
10	β -Hefutoxin1, a Novel Toxin from the Scorpion <i>Heterometrus fulvipes</i> with Unique Structure and Function. <i>Journal of Biological Chemistry</i> , 2002, 277, 30040-30047.	3.4	130
11	Correlations between the solvent hydrogen bond acceptor parameter β and the calculated molecular electrostatic potential. <i>Journal of Organic Chemistry</i> , 1991, 56, 3734-3737.	3.2	122
12	The whey acidic protein family: a new signature motif and three-dimensional structure by comparative modeling. <i>Journal of Molecular Graphics and Modelling</i> , 1999, 17, 106-113.	2.4	121
13	Functional and Structural Studies of Wild Type SOX9 and Mutations Causing Campomelic Dysplasia. <i>Journal of Biological Chemistry</i> , 1999, 274, 24023-24030.	3.4	101
14	Methods and protocols for prediction of immunogenic epitopes. <i>Briefings in Bioinformatics</i> , 2006, 8, 96-108.	6.5	91
15	Radial behavior of the average local ionization energies of atoms. <i>Journal of Chemical Physics</i> , 1991, 95, 6699-6704.	3.0	88
16	Modeling the bound conformation of <i>Pemphigus vulgaris</i> -associated peptides to MHC Class II DR and DQ alleles. <i>Immunome Research</i> , 2006, 2, 1.	0.1	88
17	Accelerating the search for the missing proteins in the human proteome. <i>Nature Communications</i> , 2017, 8, 14271.	12.8	86
18	Functional and Structural Implications of the Complement Factor H Y402H Polymorphism Associated with Age-Related Macular Degeneration. , 2008, 49, 1763.		85

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19	Modeling the structure of bound peptide ligands to major histocompatibility complex. <i>Protein Science</i> , 2004, 13, 2523-2532.	7.6	84
20	Prediction of desmoglein-3 peptides reveals multiple shared T-cell epitopes in HLA DR4- and DR6-associated <i>Pemphigus vulgaris</i> . <i>BMC Bioinformatics</i> , 2006, 7, S7.	2.6	81
21	An ethnobotanical study of medicinal plants used by the Yaegl Aboriginal community in northern New South Wales, Australia. <i>Journal of Ethnopharmacology</i> , 2012, 139, 244-255.	4.1	80
22	SPdb—a signal peptide database. <i>BMC Bioinformatics</i> , 2005, 6, 249.	2.6	78
23	OMIA (Online Mendelian Inheritance in Animals): an enhanced platform and integration into the Entrez search interface at NCBI. <i>Nucleic Acids Research</i> , 2006, 34, D599-D601.	14.5	73
24	Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e130.	3.0	72
25	The Gene for a Novel Member of the Whey Acidic Protein Family Encodes Three Four-disulfide Core Domains and Is Asynchronously Expressed during Lactation. <i>Journal of Biological Chemistry</i> , 2000, 275, 23074-23081.	3.4	71
26	CASVM: web server for SVM-based prediction of caspase substrates cleavage sites. <i>Bioinformatics</i> , 2007, 23, 3241-3243.	4.1	71
27	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e684.	3.0	66
28	Flanking signal and mature peptide residues influence signal peptide cleavage. <i>BMC Bioinformatics</i> , 2008, 9, S15.	2.6	62
29	Physicochemical property space distribution among human metabolites, drugs and toxins. <i>BMC Bioinformatics</i> , 2009, 10, S10.	2.6	62
30	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , 2010, 38, e171-e171.	14.5	62
31	Hybrid Quantum and Molecular Mechanical (QM/MM) Studies on the Pyruvate to L-Lactate Interconversion in L-Lactate Dehydrogenase. <i>Journal of Physical Chemistry B</i> , 1997, 101, 5614-5618.	2.6	60
32	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , 2007, 35, W143-W147.	14.5	60
33	Bioinformatics Education—Perspectives and Challenges. <i>PLoS Computational Biology</i> , 2005, 1, e52.	3.2	59
34	A comprehensive assessment of N-terminal signal peptides prediction methods. <i>BMC Bioinformatics</i> , 2009, 10, S2.	2.6	58
35	Complement factor H: sequence analysis of 221 kb of human genomic DNA containing the entire fH, fHR-1 and fHR-3 genes. <i>Molecular Immunology</i> , 2000, 37, 41-52.	2.2	56
36	Secretome: clues into pathogen infection and clinical applications. <i>Genome Medicine</i> , 2009, 1, 113.	8.2	56

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37	First transcriptomic analysis of the economically important parasitic nematode, <i>Trichostrongylus colubriformis</i> , using a next-generation sequencing approach. <i>Infection, Genetics and Evolution</i> , 2010, 10, 1199-1207.	2.3	55
38	Mass spectrometry-based protein identification in proteomics—a review. <i>Briefings in Bioinformatics</i> , 2021, 22, 1620-1638.	6.5	55
39	Bond-order-bond-energy correlations. <i>Chemical Physics Letters</i> , 1986, 124, 527-530.	2.6	54
40	SVM-based prediction of caspase substrate cleavage sites. <i>BMC Bioinformatics</i> , 2006, 7, S14.	2.6	53
41	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015, 14, 3415-3431.	3.7	53
42	Multiple ligand binding sites on domain seven of human complement factor H. <i>International Immunopharmacology</i> , 2001, 1, 433-443.	3.8	50
43	Clinically Relevant Post-Translational Modification Analyses—Maturing Workflows and Bioinformatics Tools. <i>International Journal of Molecular Sciences</i> , 2019, 20, 16.	4.1	50
44	Computational evaluation and comparison of some nitramine properties. <i>Journal of the American Chemical Society</i> , 1988, 110, 3425-3430.	13.7	49
45	SCORPION2: A database for structure-function analysis of scorpion toxins. <i>Toxicon</i> , 2006, 47, 356-363.	1.6	48
46	A proposed minimum skill set for university graduates to meet the informatics needs and challenges of the "-omics" era. <i>BMC Genomics</i> , 2009, 10, S36.	2.8	45
47	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). <i>PLoS Neglected Tropical Diseases</i> , 2008, 2, e301.	3.0	44
48	The gramicidin A channel: comparison of the energy profiles of Na ⁺ , K ⁺ and Cs ⁺ . <i>FEBS Letters</i> , 1984, 173, 301-306.	2.8	42
49	Prediction of HLA-DQ3.2 ² Ligands: evidence of multiple registers in class II binding peptides. <i>Bioinformatics</i> , 2006, 22, 1232-1238.	4.1	42
50	Gender-enriched transcripts in <i>Haemonchus contortus</i> —predicted functions and genetic interactions based on comparative analyses with <i>Caenorhabditis elegans</i> . <i>International Journal for Parasitology</i> , 2008, 38, 65-83.	3.1	40
51	Applications of machine learning in GPCR bioactive ligand discovery. <i>Current Opinion in Structural Biology</i> , 2019, 55, 66-76.	5.7	39
52	Helminth secretome database (HSD): a collection of helminth excretory/secretory proteins predicted from expressed sequence tags (ESTs). <i>BMC Genomics</i> , 2012, 13, S8.	2.8	38
53	Transcriptome analysis reveals pathogenicity and evolutionary history of the pathogenic oomycete <i>Pythium insidiosum</i> . <i>Fungal Biology</i> , 2014, 118, 640-653.	2.5	38
54	pDOCK: a new technique for rapid and accurate docking of peptide ligands to Major Histocompatibility Complexes. <i>Immunome Research</i> , 2010, 6, S2.	0.1	37

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55	MPID: MHC-Peptide Interaction Database for sequence-structure-function information on peptides binding to MHC molecules. <i>Bioinformatics</i> , 2003, 19, 309-310.	4.1	35
56	Ecological niche modeling of customary medicinal plant species used by Australian Aborigines to identify species-rich and culturally valuable areas for conservation. <i>Ecological Modelling</i> , 2011, 222, 3437-3443.	2.5	35
57	Predicted structure of the extracellular region of ligand-gated ion channel receptors shows SH2-like and SH3-like domains forming the ligand-binding site. <i>Protein Science</i> , 1997, 6, 983-998.	7.6	33
58	Linking structural features of protein complexes and biological function. <i>Protein Science</i> , 2015, 24, 1486-1494.	7.6	33
59	A novel multiplexed immunoassay identifies CEA, IL-8 and prolactin as prospective markers for Dukes™ stages A-D colorectal cancers. <i>Clinical Proteomics</i> , 2015, 12, 10.	2.1	33
60	MGAlignIt: a web service for the alignment of mRNA/EST and genomic sequences. <i>Nucleic Acids Research</i> , 2003, 31, 3533-3536.	14.5	32
61	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. <i>Standards in Genomic Sciences</i> , 2010, 3, 259-266.	1.5	32
62	Structural diversity of biologically interesting datasets: a scaffold analysis approach. <i>Journal of Cheminformatics</i> , 2011, 3, 30.	6.1	32
63	In silico secretome analysis approach for next generation sequencing transcriptomic data. <i>BMC Genomics</i> , 2011, 12, S14.	2.8	32
64	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
65	DEDB: a database of <i>Drosophila melanogaster</i> exons in splicing graph form. <i>BMC Bioinformatics</i> , 2004, 5, 189.	2.6	31
66	Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. <i>BMC Genomics</i> , 2009, 10, S11.	2.8	31
67	Deep insights into <i>Dictyocaulus viviparus</i> transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , 2011, 29, 261-271.	11.7	31
68	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. <i>Scientific Reports</i> , 2018, 8, 17923.	3.3	31
69	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
70	Advanced in silico analysis of expressed sequence tag (EST) data for parasitic nematodes of major socio-economic importance " Fundamental insights toward biotechnological outcomes. <i>Biotechnology Advances</i> , 2009, 27, 439-448.	11.7	29
71	Advancing standards for bioinformatics activities: persistence, reproducibility, disambiguation and Minimum Information About a Bioinformatics investigation (MIABI). <i>BMC Genomics</i> , 2010, 11, S27.	2.8	29
72	The Transcriptome Analysis of <i>Strongyloides stercoralis</i> L3i Larvae Reveals Targets for Intervention in a Neglected Disease. <i>PLoS Neglected Tropical Diseases</i> , 2012, 6, e1513.	3.0	29

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73	Cloning and molecular characterization of the first aquatic hyaluronidase, SFHYA1, from the venom of stonefish (<i>Synanceja horrida</i>). <i>Gene</i> , 2005, 346, 71-81.	2.2	27
74	Tandem duplication, circular permutation, molecular adaptation: how Solanaceae resist pests via inhibitors. <i>BMC Bioinformatics</i> , 2008, 9, S22.	2.6	27
75	Comprehensive splicing graph analysis of alternative splicing patterns in chicken, compared to human and mouse. <i>BMC Genomics</i> , 2009, 10, S5.	2.8	27
76	Delineation of modular proteins: Domain boundary prediction from sequence information. <i>Briefings in Bioinformatics</i> , 2004, 5, 179-192.	6.5	26
77	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016, 15, 339-359.	3.7	26
78	The hand, foot and mouth disease virus capsid: sequence analysis and prediction of antigenic sites from homology modelling. <i>Applied Bioinformatics</i> , 2002, 1, 43-52.	1.6	26
79	The Integrin α 2 Hybrid Domain Serves as a Link for the Propagation of Activation Signal from Its Stalk Regions to the I-like Domain. <i>Journal of Biological Chemistry</i> , 2004, 279, 54334-54339.	3.4	25
80	MPID-T. <i>Applied Bioinformatics</i> , 2006, 5, 111-114.	1.6	25
81	Unlocking the Puzzling Biology of the Black Périgord Truffle <i>Tuber melanosporum</i> . <i>Journal of Proteome Research</i> , 2013, 12, 5349-5356.	3.7	24
82	Bioinformatics meets parasitology. <i>Parasite Immunology</i> , 2012, 34, 265-275.	1.5	23
83	Proliferation and Apoptosis Pathways and Factors in Oral Squamous Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1562.	4.1	23
84	A WORKFLOW FOR MUTATION EXTRACTION AND STRUCTURE ANNOTATION. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1319-1337.	0.8	22
85	Xpro: database of eukaryotic protein-encoding genes. <i>Nucleic Acids Research</i> , 2004, 32, 59D-63.	14.5	21
86	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , 2015, 33, 980-991.	11.7	21
87	Mechanistic aspects of biological redox reactions involving NADH. Part 5. AM1 transition-state studies for the pyruvate \rightleftharpoons L-lactate interconversion in L-lactate dehydrogenase. <i>Journal of the Chemical Society, Faraday Transactions</i> , 1994, 90, 2047-2056.	1.7	20
88	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. <i>BMC Bioinformatics</i> , 2011, 12, S1.	2.6	20
89	<i>Oesophagostomum dentatum</i> – Potential as a model for genomic studies of strongylid nematodes, with biotechnological prospects. <i>Biotechnology Advances</i> , 2007, 25, 281-293.	11.7	19
90	CMKb: a web-based prototype for integrating Australian Aboriginal customary medicinal plant knowledge. <i>BMC Bioinformatics</i> , 2008, 9, S25.	2.6	19

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91	The transcriptome of <i>Echinostoma caproni</i> adults: Further characterization of the secretome and identification of new potential drug targets. <i>Journal of Proteomics</i> , 2013, 89, 202-214.	2.4	19
92	Protein-Protein Interactions and Prediction: A Comprehensive Overview. <i>Protein and Peptide Letters</i> , 2013, 21, 779-789.	0.9	19
93	Ab initio study of the stepwise hydration of NO ⁺ . <i>Chemical Physics Letters</i> , 1984, 107, 107-111.	2.6	18
94	The S-star trial bioinformatics course: An on-line learning success. <i>Biochemistry and Molecular Biology Education</i> , 2003, 31, 20-23.	1.2	18
95	SDPMOD: an automated comparative modeling server for small disulfide-bonded proteins. <i>Nucleic Acids Research</i> , 2004, 32, W356-W359.	14.5	18
96	MPID-T2: a database for sequence-structure-function analyses of pMHC and TR/pMHC structures. <i>Bioinformatics</i> , 2011, 27, 1192-1193.	4.1	18
97	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. <i>BMC Genomics</i> , 2012, 13, S10.	2.8	18
98	Characterization of the Interaction between Heterodimeric $\alpha_5\beta_1$ Integrin and Urokinase Plasminogen Activator Receptor (uPAR) Using Functional Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 5956-5964.	3.7	18
99	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. <i>Scientific Reports</i> , 2020, 10, 19430.	3.3	18
100	A transcriptomic analysis of the adult stage of the bovine lungworm, <i>Dictyocaulus viviparus</i> . <i>BMC Genomics</i> , 2007, 8, 311.	2.8	17
101	In silico analysis of expressed sequence tags from <i>Trichostrongylus vitrinus</i> (Nematoda): comparison of the automated ESTExplorer workflow platform with conventional database searches. <i>BMC Bioinformatics</i> , 2008, 9, S10.	2.6	17
102	Improved insights into the transcriptomes of the human hookworm <i>Necator americanus</i> - Fundamental and biotechnological implications. <i>Biotechnology Advances</i> , 2009, 27, 122-132.	11.7	17
103	Functional Annotation of the Human Chromosome 7 - Missing Proteins: A Bioinformatics Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2504-2510.	3.7	17
104	A multi-factor model for caspase degradome prediction. <i>BMC Genomics</i> , 2009, 10, S6.	2.8	16
105	The gramicidin A channel: theoretical energy profile computed for single occupancy by a divalent cation, Ca ²⁺ . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1985, 818, 23-30.	2.6	15
106	A comparative structural bioinformatics analysis of inherited mutations in β -D-Mannosidase across multiple species reveals a genotype-phenotype correlation. <i>BMC Genomics</i> , 2011, 12, S22.	2.8	15
107	Identification of ovarian cancer associated genes using an integrated approach in a Boolean framework. <i>BMC Systems Biology</i> , 2013, 7, 12.	3.0	15
108	ASGS: an alternative splicing graph web service. <i>Nucleic Acids Research</i> , 2006, 34, W444-W447.	14.5	14

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109	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). BMC Genomics, 2010, 11, S1.	2.8	14
110	Prediction of interface residue based on the features of residue interaction network. Journal of Theoretical Biology, 2017, 432, 49-54.	1.7	14
111	Understanding TR Binding to pMHC Complexes: How Does a TR Scan Many pMHC Complexes yet Preferentially Bind to One. PLoS ONE, 2011, 6, e17194.	2.5	14
112	In silico characterization of immunogenic epitopes presented by HLA-Cw*0401. Immunome Research, 2007, 3, 7.	0.1	13
113	Extending Asia Pacific bioinformatics into new realms in the "-omics" era. BMC Genomics, 2009, 10, S1.	2.8	13
114	A multi-species comparative structural bioinformatics analysis of inherited mutations in Î±-D-Mannosidase reveals strong genotype-phenotype correlation. BMC Genomics, 2009, 10, S33.	2.8	13
115	A site for direct integrin Î±vÎ²6-Î±PAR interaction from structural modelling and docking. Journal of Structural Biology, 2014, 185, 327-335.	2.8	13
116	Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the Missing Human Proteome. Journal of Proteome Research, 2014, 13, 76-83.	3.7	13
117	An ab initio study of the binding of N2 to Na+ and K+. Chemical Physics Letters, 1984, 110, 346-350.	2.6	12
118	A computational analysis of the electrostatic potentials and relative bond strengths of hydrazine and some of its 1,1-dimethyl derivatives. International Journal of Quantum Chemistry, 1990, 37, 611-629.	2.0	12
119	Accurate prediction of scorpion toxin functional properties from primary structures. Journal of Molecular Graphics and Modelling, 2005, 24, 17-24.	2.4	12
120	Modeling Escherichia coli signal peptidase complex with bound substrate: determinants in the mature peptide influencing signal peptide cleavage. BMC Bioinformatics, 2008, 9, S15.	2.6	12
121	Network analysis of human protein location. BMC Bioinformatics, 2010, 11, S9.	2.6	12
122	Divergent response of homologous ATP sites to stereospecific ligand fluorination for selectivity enhancement. Organic and Biomolecular Chemistry, 2017, 15, 1570-1574.	2.8	12
123	iSwathX: an interactive web-based application for extension of DIA peptide reference libraries. Bioinformatics, 2019, 35, 538-539.	4.1	12
124	Protocol for Protein Structure Modelling. , 2019, , 252-272.		12
125	Deduction of functional peptide motifs in scorpion toxins. Journal of Peptide Science, 2006, 12, 420-427.	1.4	11
126	Discrete structural features among interface residue-level classes. BMC Bioinformatics, 2015, 16, S8.	2.6	11

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127	Simple re-instantiation of small databases using cloud computing. BMC Genomics, 2013, 14, S13.	2.8	10
128	De Novo Peptide Sequencing: Deep Mining of High-Resolution Mass Spectrometry Data. Methods in Molecular Biology, 2017, 1549, 119-134.	0.9	10
129	Exploration of charge states of balanol analogues acting as ATP-competitive inhibitors in kinases. BMC Bioinformatics, 2017, 18, 572.	2.6	10
130	Role of solvent accessibility for aggregation-prone patches in protein folding. Scientific Reports, 2018, 8, 12896.	3.3	10
131	Machine Learning Assisted Approach for Finding Novel High Activity Agonists of Human Ectopic Olfactory Receptors. International Journal of Molecular Sciences, 2021, 22, 11546.	4.1	10
132	XdomView: protein domain and exon position visualization. Bioinformatics, 2003, 19, 159-160.	4.1	9
133	Towards a career in bioinformatics. BMC Bioinformatics, 2009, 10, S1.	2.6	9
134	In silico approach to screen compounds active against parasitic nematodes of major socio-economic importance. BMC Bioinformatics, 2011, 12, S25.	2.6	9
135	Molecular similarity and diversity approaches in chemoinformatics. Drug Development Research, 2011, 72, 74-84.	2.9	9
136	Genomic characterization of Tv-ant-1, a Caenorhabditis elegans tag-61 homologue from the parasitic nematode Trichostrongylus vitrinus. Gene, 2007, 397, 12-25.	2.2	8
137	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. BMC Genomics, 2018, 19, 88.	2.8	8
138	Bacterial Antigens Reduced the Inhibition Effect of Capsaicin on Cal 27 Oral Cancer Cell Proliferation. International Journal of Molecular Sciences, 2021, 22, 8686.	4.1	8
139	A Practical Guide to Structure-Based Prediction of MHC-Binding Peptides. Methods in Molecular Biology, 2007, 409, 301-308.	0.9	7
140	Bioinformatics research in the Asia Pacific: a 2007 update. BMC Bioinformatics, 2008, 9, S1.	2.6	7
141	APBioNet—Transforming Bioinformatics in the Asia-Pacific Region. PLoS Computational Biology, 2013, 9, e1003317.	3.2	7
142	Molecular Dynamics Pinpoint the Global Fluorine Effect in Balanoid Binding to PKC μ and PKA. Journal of Chemical Information and Modeling, 2018, 58, 511-519.	5.4	7
143	Leveraging homologies for cross-species plasma proteomics in ungulates using data-independent acquisition. Journal of Proteomics, 2022, 250, 104384.	2.4	7
144	APBioNet: the Asia-Pacific regional consortium for bioinformatics. Applied Bioinformatics, 2002, 1, 101-5.	1.6	7

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145	Molecular Modeling on the Web. <i>BioTechniques</i> , 2001, 30, 50-52.	1.8	6
146	TranSeqAnnotator: large-scale analysis of transcriptomic data. <i>BMC Bioinformatics</i> , 2012, 13, S24.	2.6	6
147	InCoB2013 introduces Systems Biology as a major conference theme. <i>BMC Systems Biology</i> , 2013, 7, S1.	3.0	6
148	Human Prestin: A Candidate PE1 Protein Lacking Stringent Mass Spectrometric Evidence?. <i>Journal of Proteome Research</i> , 2017, 16, 4531-4535.	3.7	6
149	Structural bioinformatics analysis of variants on GPCR function. <i>Current Opinion in Structural Biology</i> , 2019, 55, 161-177.	5.7	6
150	Diverse dynamics features of novel protein kinase C (PKC) isozymes determine the selectivity of a fluorinated balanol analogue for PKC μ . <i>BMC Bioinformatics</i> , 2019, 19, 342.	2.6	6
151	The force field of carbon suboxide. <i>Computational and Theoretical Chemistry</i> , 1982, 90, 219-226.	1.5	5
152	Prediction of novel mouse \hat{A} TLR9 agonists using a random forest approach. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 56.	2.0	5
153	BIO-GATS: A Tool for Automated GPCR Template Selection Through a Biophysical Approach for Homology Modeling. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 617176.	3.5	5
154	InCoB2014: Systems Biology update from the Asia-Pacific. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	4
155	Structure-Based Drug Design Workflow. , 2019, , 273-282.		4
156	A two-stage computational approach to predict novel ligands for a chemosensory receptor. <i>Current Research in Structural Biology</i> , 2020, 2, 213-221.	2.2	4
157	Structural Immunoinformatics: Understanding MHC-Peptide-TR Binding. , 2009, , 77-93.		4
158	The use of CNDO/force and compliance constant methods in evaluating quadratic potential functions of carbonyl and formyl fluorides. <i>Journal of Computational Chemistry</i> , 1983, 4, 175-180.	3.3	3
159	Compliant fields for water, ammonia and methane. <i>Computational and Theoretical Chemistry</i> , 1983, 104, 1-8.	1.5	3
160	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. <i>BMC Bioinformatics</i> , 2010, 11, S1.	2.6	3
161	InCoB2014: mining biological data from genomics for transforming industry and health. <i>BMC Genomics</i> , 2014, 15, 11.	2.8	3
162	Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). <i>BMC Bioinformatics</i> , 2016, 17, 524.	2.6	3

#	ARTICLE	IF	CITATIONS
163	A Systematic Bioinformatics Approach to Identify High Quality Mass Spectrometry Data and Functionally Annotate Proteins and Proteomes. <i>Methods in Molecular Biology</i> , 2017, 1549, 163-176.	0.9	3
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