

# Shoba Ranganathan

## List of Publications by Citations

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190  
papers

6,118  
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40  
h-index

72  
g-index

223  
ext. papers

6,820  
ext. citations

6.7  
avg, IF

5.49  
L-index

#	Paper	IF	Citations
190	The genome sequence of taurine cattle: a window to ruminant biology and evolution. <i>Science</i> , <b>2009</b> , 324, 522-8	33.3	863
189	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , <b>2012</b> , 44, 221-5	36.3	325
188	<i>Ascaris suum</i> draft genome. <i>Nature</i> , <b>2011</b> , 479, 529-33	50.4	217
187	An integrated transcriptomics and proteomics analysis of the secretome of the helminth pathogen <i>Fasciola hepatica</i> : proteins associated with invasion and infection of the mammalian host. <i>Molecular and Cellular Proteomics</i> , <b>2009</b> , 8, 1891-907	7.6	203
186	A hitchhiker's guide to expressed sequence tag (EST) analysis. <i>Briefings in Bioinformatics</i> , <b>2007</b> , 8, 6-21	13.4	200
185	A common site within factor H SCR 7 responsible for binding heparin, C-reactive protein and streptococcal M protein. <i>European Journal of Immunology</i> , <b>2003</b> , 33, 962-9	6.1	143
184	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , <b>2014</b> , 46, 261-269	36.3	139
183	In silico grouping of peptide/HLA class I complexes using structural interaction characteristics. <i>Bioinformatics</i> , <b>2007</b> , 23, 177-83	7.2	123
182	Establishing bioinformatics research in the Asia Pacific. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 1	3.6	114
181	kappa-Hefutoxin1, a novel toxin from the scorpion <i>Heterometrus fulvipes</i> with unique structure and function. Importance of the functional diad in potassium channel selectivity. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 30040-7	5.4	114
180	The whey acidic protein family: a new signature motif and three-dimensional structure by comparative modeling. <i>Journal of Molecular Graphics and Modelling</i> , <b>1999</b> , 17, 106-13, 134-6	2.8	111
179	Correlations between the solvent hydrogen bond acceptor parameter .beta. and the calculated molecular electrostatic potential. <i>Journal of Organic Chemistry</i> , <b>1991</b> , 56, 3734-3737	4.2	106
178	Functional and structural studies of wild type SOX9 and mutations causing campomelic dysplasia. <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 24023-30	5.4	85
177	Methods and protocols for prediction of immunogenic epitopes. <i>Briefings in Bioinformatics</i> , <b>2007</b> , 8, 96-108	13.4	83
176	Radial behavior of the average local ionization energies of atoms. <i>Journal of Chemical Physics</i> , <b>1991</b> , 95, 6699-6704	3.9	82
175	Accelerating the search for the missing proteins in the human proteome. <i>Nature Communications</i> , <b>2017</b> , 8, 14271	17.4	73
174	Modeling the bound conformation of <i>Pemphigus vulgaris</i> -associated peptides to MHC Class II DR and DQ alleles. <i>Immunome Research</i> , <b>2006</b> , 2, 1		71

173	SPdb--a signal peptide database. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 249	3.6	71
172	Functional and structural implications of the complement factor H Y402H polymorphism associated with age-related macular degeneration. <i>Investigative Ophthalmology and Visual Science</i> , <b>2008</b> , 49, 1763-70		70
171	Modeling the structure of bound peptide ligands to major histocompatibility complex. <i>Protein Science</i> , <b>2004</b> , 13, 2523-32	6.3	70
170	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> , <b>2000</b> , 275, 23074-81	5.4	67
169	Massively parallel sequencing and analysis of the <i>Necator americanus</i> transcriptome. <i>PLoS Neglected Tropical Diseases</i> , <b>2010</b> , 4, e684	4.8	66
168	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> , <b>2008</b> , 2, e130	4.8	66
167	CASVM: web server for SVM-based prediction of caspase substrates cleavage sites. <i>Bioinformatics</i> , <b>2007</b> , 23, 3241-3	7.2	61
166	A practical, bioinformatic workflow system for large data sets generated by next-generation sequencing. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e171	20.1	60
165	OMIA (Online Mendelian Inheritance in Animals): an enhanced platform and integration into the Entrez search interface at NCBI. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D599-601	20.1	59
164	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, W143-7	20.1	56
163	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> , <b>1997</b> , 101, 5614-5618	3.4	53
162	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> , <b>2000</b> , 37, 41-52	4.3	52
161	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 3415-31	5.6	50
160	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> , <b>2010</b> , 10, 1199-207	4.5	50
159	SVM-based prediction of caspase substrate cleavage sites. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 5, S14	3.6	48
158	Bond-order-bond-energy correlations. <i>Chemical Physics Letters</i> , <b>1986</b> , 124, 527-530	2.5	46
157	Computational evaluation and comparison of some nitramine properties. <i>Journal of the American Chemical Society</i> , <b>1988</b> , 110, 3425-3430	16.4	46
156	A comprehensive assessment of N-terminal signal peptides prediction methods. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 15, S2	3.6	45

155	SCORPION2: a database for structure-function analysis of scorpion toxins. <i>Toxicon</i> , <b>2006</b> , 47, 356-63	2.8	45
154	Physiochemical property space distribution among human metabolites, drugs and toxins. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 15, S10	3.6	43
153	Bioinformatics education--perspectives and challenges. <i>PLoS Computational Biology</i> , <b>2005</b> , 1, e52	5	43
152	Flanking signal and mature peptide residues influence signal peptide cleavage. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 12, S15	3.6	42
151	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> , <b>2008</b> , 2, e301	4.8	40
150	Secretome: clues into pathogen infection and clinical applications. <i>Genome Medicine</i> , <b>2009</b> , 1, 113	14.4	39
149	An ethnobotanical study of medicinal plants used by the Yaegl Aboriginal community in northern New South Wales, Australia. <i>Journal of Ethnopharmacology</i> , <b>2012</b> , 139, 244-55	5	38
148	Prediction of HLA-DQ3.2beta ligands: evidence of multiple registers in class II binding peptides. <i>Bioinformatics</i> , <b>2006</b> , 22, 1232-8	7.2	38
147	Multiple ligand binding sites on domain seven of human complement factor H. <i>International Immunopharmacology</i> , <b>2001</b> , 1, 433-43	5.8	38
146	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> , <b>2008</b> , 38, 65-83	4.3	36
145	The gramicidin A channel: comparison of the energy profiles of Na <sup>+</sup> , K <sup>+</sup> and Cs <sup>+</sup> . Influence of the flexibility of the ethanolamine end chain on the profiles. <i>FEBS Letters</i> , <b>1984</b> , 173, 301-6	3.8	35
144	A proposed minimum skill set for university graduates to meet the informatics needs and challenges of the "-omics" era. <i>BMC Genomics</i> , <b>2009</b> , 10 Suppl 3, S36	4.5	32
143	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> , <b>1997</b> , 6, 983-98	6.3	32
142	MPID: MHC-Peptide Interaction Database for sequence-structure-function information on peptides binding to MHC molecules. <i>Bioinformatics</i> , <b>2003</b> , 19, 309-10	7.2	31
141	Helminth secretome database (HSD): a collection of helminth excretory/secretory proteins predicted from expressed sequence tags (ESTs). <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S8	4.5	29
140	Linking structural features of protein complexes and biological function. <i>Protein Science</i> , <b>2015</b> , 24, 1486-94	6.4	28
139	A novel multiplexed immunoassay identifies CEA, IL-8 and prolactin as prospective markers for DukesPstages A-D colorectal cancers. <i>Clinical Proteomics</i> , <b>2015</b> , 12, 10	5	28
138	Structural diversity of biologically interesting datasets: a scaffold analysis approach. <i>Journal of Cheminformatics</i> , <b>2011</b> , 3, 30	8.6	28

137	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> , <b>2009</b> , 27, 439-48	17.8	28
136	pDOCK: a new technique for rapid and accurate docking of peptide ligands to Major Histocompatibility Complexes. <i>Immunome Research</i> , <b>2010</b> , 6 Suppl 1, S2		28
135	MGAlignIt: A web service for the alignment of mRNA/EST and genomic sequences. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3533-6	20.1	28
134	Deep insights into Dictyocaulus viviparus transcriptomes provides unique prospects for new drug targets and disease intervention. <i>Biotechnology Advances</i> , <b>2011</b> , 29, 261-71	17.8	27
133	In silico secretome analysis approach for next generation sequencing transcriptomic data. <i>BMC Genomics</i> , <b>2011</b> , 12 Suppl 3, S14	4.5	27
132	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> , <b>2011</b> , 222, 3437-3443	26	26
131	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. <i>Standards in Genomic Sciences</i> , <b>2010</b> , 3, 259-66		26
130	Tandem duplication, circular permutation, molecular adaptation: how Solanaceae resist pests via inhibitors. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 1, S22	3.6	25
129	The integrin alpha L beta 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> , <b>2004</b> , 279, 54334-9	5.4	25
128	The transcriptome analysis of Strongyloides stercoralis L3i larvae reveals targets for intervention in a neglected disease. <i>PLoS Neglected Tropical Diseases</i> , <b>2012</b> , 6, e1513	4.8	24
127	Delineation of modular proteins: domain boundary prediction from sequence information. <i>Briefings in Bioinformatics</i> , <b>2004</b> , 5, 179-92	13.4	24
126	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. <i>Scientific Reports</i> , <b>2018</b> , 8, 17923	4.9	24
125	Cloning and molecular characterization of the first aquatic hyaluronidase, SFHYA1, from the venom of stonefish (Synanceja horrida). <i>Gene</i> , <b>2005</b> , 346, 71-81	3.8	23
124	DEDB: a database of Drosophila melanogaster exons in splicing graph form. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 189	3.6	23
123	Clinically Relevant Post-Translational Modification Analyses-Maturing Workflows and Bioinformatics Tools. <i>International Journal of Molecular Sciences</i> , <b>2018</b> , 20,	6.3	23
122	The hand, foot and mouth disease virus capsid: sequence analysis and prediction of antigenic sites from homology modelling. <i>Applied Bioinformatics</i> , <b>2002</b> , 1, 43-52		23
121	Transcriptome analysis reveals pathogenicity and evolutionary history of the pathogenic oomycete Pythium insidiosum. <i>Fungal Biology</i> , <b>2014</b> , 118, 640-53	2.8	22
120	Unlocking the puzzling biology of the black Périgord truffle Tuber melanosporum. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 5349-56	5.6	22

119	MPID-T: database for sequence-structure-function information on T-cell receptor/peptide/MHC interactions. <i>Applied Bioinformatics</i> , <b>2006</b> , 5, 111-4		22
118	Applications of machine learning in GPCR bioactive ligand discovery. <i>Current Opinion in Structural Biology</i> , <b>2019</b> , 55, 66-76	8.1	20
117	Prediction of desmoglein-3 peptides reveals multiple shared T-cell epitopes in HLA DR4- and DR6-associated pemphigus vulgaris. <i>BMC Bioinformatics</i> , <b>2006</b> , 7 Suppl 5, S7	3.6	20
116	Genome-wide analysis of alternative splicing in cow: implications in bovine as a model for human diseases. <i>BMC Genomics</i> , <b>2009</b> , 10 Suppl 3, S11	4.5	19
115	Advancing standards for bioinformatics activities: persistence, reproducibility, disambiguation and Minimum Information About a Bioinformatics investigation (MIABi). <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 4, S27	4.5	19
114	A workflow for mutation extraction and structure annotation. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2007</b> , 5, 1319-37	1	19
113	Cracking the nodule worm code advances knowledge of parasite biology and biotechnology to tackle major diseases of livestock. <i>Biotechnology Advances</i> , <b>2015</b> , 33, 980-91	17.8	18
112	Bioinformatics meets parasitology. <i>Parasite Immunology</i> , <b>2012</b> , 34, 265-75	2.2	18
111	Comprehensive splicing graph analysis of alternative splicing patterns in chicken, compared to human and mouse. <i>BMC Genomics</i> , <b>2009</b> , 10 Suppl 1, S5	4.5	18
110	Oesophagostomum dentatum: potential as a model for genomic studies of strongylid nematodes, with biotechnological prospects. <i>Biotechnology Advances</i> , <b>2007</b> , 25, 281-93	17.8	18
109	Ab initio study of the stepwise hydration of NO <sup>+</sup> . <i>Chemical Physics Letters</i> , <b>1984</b> , 107, 107-111	2.5	18
108	Mass spectrometry-based protein identification in proteomics-a review. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1620-1638	13.4	18
107	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 339-59	5.6	17
106	Improved insights into the transcriptomes of the human hookworm <i>Necator americanus</i> --fundamental and biotechnological implications. <i>Biotechnology Advances</i> , <b>2009</b> , 27, 122-32	17.8	17
105	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> , <b>2008</b> , 9 Suppl 1, S10	3.6	17
104	SDPMOD: an automated comparative modeling server for small disulfide-bonded proteins. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W356-9	20.1	17
103	Xpro: database of eukaryotic protein-encoding genes. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D59-63	20.1	17
102	Mechanistic aspects of biological redox reactions involving NADH. Part 5. $\Delta$ M1 transition-state studies for the pyruvate $\rightleftharpoons$ lactate interconversion in L-lactate dehydrogenase. <i>Journal of the Chemical Society, Faraday Transactions</i> , <b>1994</b> , 90, 2047-2056		17

101	An analysis of the transcriptome of <i>Teladorsagia circumcincta</i> : its biological and biotechnological implications. <i>BMC Genomics</i> , <b>2012</b> , 13 Suppl 7, S10	4.5	16
100	Functional annotation of the human chromosome 7 "missing" proteins: a bioinformatics approach. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 2504-10	5.6	16
99	MPID-T2: a database for sequence-structure-function analyses of pMHC and TR/pMHC structures. <i>Bioinformatics</i> , <b>2011</b> , 27, 1192-3	7.2	16
98	A transcriptomic analysis of the adult stage of the bovine lungworm, <i>Dictyocaulus viviparus</i> . <i>BMC Genomics</i> , <b>2007</b> , 8, 311	4.5	16
97	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> , <b>2014</b> , 13, 5956-64	5.6	15
96	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> , <b>2013</b> , 89, 202-14	3.9	15
95	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 13, S1	3.6	15
94	The S-star trial bioinformatics course: An on-line learning success*. <i>Biochemistry and Molecular Biology Education</i> , <b>2003</b> , 31, 20-23	1.3	15
93	CMKb: a web-based prototype for integrating Australian Aboriginal customary medicinal plant knowledge. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 12, S25	3.6	14
92	Protannotator: a semiautomated pipeline for chromosome-wise functional annotation of the "missing" human proteome. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 76-83	5.6	13
91	In silico characterization of immunogenic epitopes presented by HLA-Cw*0401. <i>Immunome Research</i> , <b>2007</b> , 3, 7		13
90	ASGS: an alternative splicing graph web service. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W444-7	20.1	13
89	A site for direct integrin $\alpha 5 \beta 1$ uPAR interaction from structural modelling and docking. <i>Journal of Structural Biology</i> , <b>2014</b> , 185, 327-35	3.4	12
88	A comparative structural bioinformatics analysis of inherited mutations in ED-Mannosidase across multiple species reveals a genotype-phenotype correlation. <i>BMC Genomics</i> , <b>2011</b> , 12 Suppl 3, S22	4.5	12
87	Accurate prediction of scorpion toxin functional properties from primary structures. <i>Journal of Molecular Graphics and Modelling</i> , <b>2005</b> , 24, 17-24	2.8	12
86	An ab initio study of the binding of N <sub>2</sub> to Na <sup>+</sup> and K <sup>+</sup> . <i>Chemical Physics Letters</i> , <b>1984</b> , 110, 346-350	2.5	12
85	The gramicidin A channel: theoretical energy profile computed for single occupancy by a divalent cation, Ca <sup>2+</sup> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , <b>1985</b> , 818, 23-30	3.8	12
84	Protein-protein interactions and prediction: a comprehensive overview. <i>Protein and Peptide Letters</i> , <b>2014</b> , 21, 779-89	1.9	12



83	iSwathX: an interactive web-based application for extension of DIA peptide reference libraries. <i>Bioinformatics</i> , <b>2019</b> , 35, 538-539	7.2	11
82	Identification of ovarian cancer associated genes using an integrated approach in a Boolean framework. <i>BMC Systems Biology</i> , <b>2013</b> , 7, 12	3.5	11
81	A multi-factor model for caspase degradome prediction. <i>BMC Genomics</i> , <b>2009</b> , 10 Suppl 3, S6	4.5	10
80	Network analysis of human protein location. <i>BMC Bioinformatics</i> , <b>2010</b> , 11 Suppl 7, S9	3.6	10
79	Discrete structural features among interface residue-level classes. <i>BMC Bioinformatics</i> , <b>2015</b> , 16 Suppl 18, S8	3.6	9
78	Molecular similarity and diversity approaches in chemoinformatics. <i>Drug Development Research</i> , <b>2011</b> , 72, 74-84	5.1	9
77	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 4, S1	4.5	9
76	Modeling Escherichia coli signal peptidase complex with bound substrate: determinants in the mature peptide influencing signal peptide cleavage. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 1, S15	3.6	9
75	Deduction of functional peptide motifs in scorpion toxins. <i>Journal of Peptide Science</i> , <b>2006</b> , 12, 420-7	2.1	9
74	XdomView: protein domain and exon position visualization. <i>Bioinformatics</i> , <b>2003</b> , 19, 159-60	7.2	9
73	Divergent response of homologous ATP sites to stereospecific ligand fluorination for selectivity enhancement. <i>Organic and Biomolecular Chemistry</i> , <b>2017</b> , 15, 1570-1574	3.9	8
72	Prediction of interface residue based on the features of residue interaction network. <i>Journal of Theoretical Biology</i> , <b>2017</b> , 432, 49-54	2.3	8
71	In silico approach to screen compounds active against parasitic nematodes of major socio-economic importance. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 13, S25	3.6	8
70	A multi-species comparative structural bioinformatics analysis of inherited mutations in alpha-D-mannosidase reveals strong genotype-phenotype correlation. <i>BMC Genomics</i> , <b>2009</b> , 10 Suppl 3, S33	4.5	8
69	Genomic characterization of Tv-ant-1, a Caenorhabditis elegans tag-61 homologue from the parasitic nematode Trichostrongylus vitrinus. <i>Gene</i> , <b>2007</b> , 397, 12-25	3.8	8
68	A computational analysis of the electrostatic potentials and relative bond strengths of hydrazine and some of its 1,1-dimethyl derivatives. <i>International Journal of Quantum Chemistry</i> , <b>1990</b> , 37, 611-629	2.1	8
67	Understanding TR binding to pMHC complexes: how does a TR scan many pMHC complexes yet preferentially bind to one. <i>PLoS ONE</i> , <b>2011</b> , 6, e17194	3.7	8
66	De Novo Peptide Sequencing: Deep Mining of High-Resolution Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1549, 119-134	1.4	7



65	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. <i>BMC Genomics</i> , <b>2018</b> , 19, 88	4.5	7
64	Role of solvent accessibility for aggregation-prone patches in protein folding. <i>Scientific Reports</i> , <b>2018</b> , 8, 12896	4.9	7
63	Protocol for Protein Structure Modelling <b>2019</b> , 252-272		6
62	Simple re-instantiation of small databases using cloud computing. <i>BMC Genomics</i> , <b>2013</b> , 14 Suppl 5, S13	4.5	6
61	Molecular modeling on the Web. <i>BioTechniques</i> , <b>2001</b> , 30, 50-2	2.5	6
60	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. <i>Scientific Reports</i> , <b>2020</b> , 10, 19430	4.9	6
59	Exploration of charge states of balanol analogues acting as ATP-competitive inhibitors in kinases. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 572	3.6	5
58	Towards a career in bioinformatics. <i>BMC Bioinformatics</i> , <b>2009</b> , 10 Suppl 15, S1	3.6	5
57	A practical guide to structure-based prediction of MHC-binding peptides. <i>Methods in Molecular Biology</i> , <b>2007</b> , 409, 301-8	1.4	5
56	APBioNet: the Asia-Pacific regional consortium for bioinformatics. <i>Applied Bioinformatics</i> , <b>2002</b> , 1, 101-5		5
55	Human Prestin: A Candidate PE1 Protein Lacking Stringent Mass Spectrometric Evidence?. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 4531-4535	5.6	4
54	TranSeqAnnotator: large-scale analysis of transcriptomic data. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 17, S24	3.6	4
53	Bioinformatics research in the Asia Pacific: a 2007 update. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 1, S1	3.6	4
52	A Systematic Bioinformatics Approach to Identify High Quality Mass Spectrometry Data and Functionally Annotate Proteins and Proteomes. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1549, 163-176	1.4	3
51	Structural bioinformatics analysis of variants on GPCR function. <i>Current Opinion in Structural Biology</i> , <b>2019</b> , 55, 161-177	8.1	3
50	Molecular Dynamics Pinpoint the Global Fluorine Effect in Balanoid Binding to PKC $\beta$ and PKA. <i>Journal of Chemical Information and Modeling</i> , <b>2018</b> , 58, 511-519	6.1	3
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