

Shoba Ranganathan

List of Publications by Year in descending order

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Version: 2024-02-01

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	Leveraging homologies for cross-species plasma proteomics in ungulates using data-independent acquisition. <i>Journal of Proteomics</i> , 2022, 250, 104384.	2.4	7
2	Proliferation and Apoptosis Pathways and Factors in Oral Squamous Cell Carcinoma. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1562.	4.1	23
3	A Bioinformatics Approach to Mine the Microbial Proteomic Profile of COVID-19 Mass Spectrometry Data. <i>Applied Microbiology</i> , 2022, 2, 150-164.	1.6	3
4	Editorial: Bioinformatics and the Translation of Data-Driven Discoveries. <i>Frontiers in Genetics</i> , 2022, 13, .	2.3	1
5	Mass spectrometryâ€‘based protein identification in proteomicsâ€‘a review. <i>Briefings in Bioinformatics</i> , 2021, 22, 1620-1638.	6.5	55
6	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
7	Bacterial Antigens Reduced the Inhibition Effect of Capsaicin on Cal 27 Oral Cancer Cell Proliferation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8686.	4.1	8
8	Machine Learning Assisted Approach for Finding Novel High Activity Agonists of Human Ectopic Olfactory Receptors. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11546.	4.1	10
9	ML218 HCl Is More Efficient Than Capsaicin in Inhibiting Bacterial Antigen-Induced Cal 27 Oral Cancer Cell Proliferation. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12559.	4.1	3
10	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. <i>Scientific Reports</i> , 2020, 10, 19430.	3.3	18
11	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
12	iSwathX 2.0 for Processing DDA Spectral Libraries for DIA Data Analysis. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e101.	25.8	3
13	iSwathX: an interactive web-based application for extension of DIA peptide reference libraries. <i>Bioinformatics</i> , 2019, 35, 538-539.	4.1	12
14	Identification of Proteins From Proteomic Analysis. , 2019, , 855-870.		1
15	Protocol for Protein Structure Modelling. , 2019, , 252-272.		12
16	Structure-Based Drug Design Workflow. , 2019, , 273-282.		4
17	Quantification of Proteins From Proteomic Analysis. , 2019, , 871-890.		1
18	Editorial overview: Theory and simulation: demystifying GPCRs â€‘ structure, function and drug design. <i>Current Opinion in Structural Biology</i> , 2019, 55, vi-viii.	5.7	0

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19	Structural bioinformatics analysis of variants on GPCR function. <i>Current Opinion in Structural Biology</i> , 2019, 55, 161-177.	5.7	6
20	Bioinformatics approaches for improving seminal plasma proteome analysis. <i>Theriogenology</i> , 2019, 137, 43-49.	2.1	2
21	Applications of machine learning in GPCR bioactive ligand discovery. <i>Current Opinion in Structural Biology</i> , 2019, 55, 66-76.	5.7	39
22	APBioNet's annual International Conference on Bioinformatics (InCoB) returns to India in 2018. <i>BMC Genomics</i> , 2019, 19, 266.	2.8	1
23	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
24	Prediction of novel mouse ATLR9 agonists using a random forest approach. <i>BMC Molecular and Cell Biology</i> , 2019, 20, 56.	2.0	5
25	Clinically Relevant Post-Translational Modification Analyses—Maturing Workflows and Bioinformatics Tools. <i>International Journal of Molecular Sciences</i> , 2019, 20, 16.	4.1	50
26	Looking for Missing Proteins. , 2019, , .		2
27	Molecular Dynamics Pinpoint the Global Fluorine Effect in Balanoid Binding to PKC μ and PKA. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 511-519.	5.4	7
28	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. <i>Scientific Reports</i> , 2018, 8, 17923.	3.3	31
29	Imaginative Order from Reasonable Chaos: Conformation-Driven Activity and Reactivity in Exploring Protein—Ligand Interactions. <i>Australian Journal of Chemistry</i> , 2018, 71, 917.	0.9	0
30	Role of solvent accessibility for aggregation-prone patches in protein folding. <i>Scientific Reports</i> , 2018, 8, 12896.	3.3	10
31	Clinically-actionable colorectal cancer plasma and tissue proteomic biosignatures. <i>Pathology</i> , 2018, 50, S3.	0.6	0
32	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. <i>BMC Genomics</i> , 2018, 19, 88.	2.8	8
33	A bioinformatics potpourri. <i>BMC Genomics</i> , 2018, 19, 920.	2.8	1
34	Accelerating the search for the missing proteins in the human proteome. <i>Nature Communications</i> , 2017, 8, 14271.	12.8	86
35	Divergent response of homologous ATP sites to stereospecific ligand fluorination for selectivity enhancement. <i>Organic and Biomolecular Chemistry</i> , 2017, 15, 1570-1574.	2.8	12
36	De Novo Peptide Sequencing: Deep Mining of High-Resolution Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2017, 1549, 119-134.	0.9	10

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37	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
38	Human Prestin: A Candidate PE1 Protein Lacking Stringent Mass Spectrometric Evidence?. <i>Journal of Proteome Research</i> , 2017, 16, 4531-4535.	3.7	6
39	Prediction of interface residue based on the features of residue interaction network. <i>Journal of Theoretical Biology</i> , 2017, 432, 49-54.	1.7	14
40	Exploration of charge states of balanol analogues acting as ATP-competitive inhibitors in kinases. <i>BMC Bioinformatics</i> , 2017, 18, 572.	2.6	10
41	Bioinformatics and systems biology research update from the 15th International Conference on Bioinformatics (InCoB2016). <i>BMC Bioinformatics</i> , 2016, 17, 524.	2.6	3
42	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016, 15, 339-359.	3.7	26
43	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. <i>BMC Bioinformatics</i> , 2015, 16, 11.	2.6	1
44	Discrete structural features among interface residue-level classes. <i>BMC Bioinformatics</i> , 2015, 16, S8.	2.6	11
45	Linking structural features of protein complexes and biological function. <i>Protein Science</i> , 2015, 24, 1486-1494.	7.6	33
46	Coherence analysis discriminates between retroviral integration patterns in CD34+ cells transduced under differing clinical trial conditions. <i>Molecular Therapy - Methods and Clinical Development</i> , 2015, 2, 15015.	4.1	1
47	A novel multiplexed immunoassay identifies CEA, IL-8 and prolactin as prospective markers for Dukesâ€™ stages A-D colorectal cancers. <i>Clinical Proteomics</i> , 2015, 12, 10.	2.1	33
48	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
49	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
50	InCoB2014: mining biological data from genomics for transforming industry and health. <i>BMC Genomics</i> , 2014, 15, 11.	2.8	3
51	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
52	Genome of the human hookworm <i>Necator americanus</i> . <i>Nature Genetics</i> , 2014, 46, 261-269.	21.4	166
53	A site for direct integrin Î±vÎ²6-Î±PAR interaction from structural modelling and docking. <i>Journal of Structural Biology</i> , 2014, 185, 327-335.	2.8	13
54	Protannotator: A Semiautomated Pipeline for Chromosome-Wise Functional Annotation of the âœMissingâœ Human Proteome. <i>Journal of Proteome Research</i> , 2014, 13, 76-83.	3.7	13

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55	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
56	InCoB2014: bioinformatics to tackle the data to knowledge challenge. <i>BMC Bioinformatics</i> , 2014, 15, 11.	2.6	0
57	InCoB2014: Systems Biology update from the Asia-Pacific. <i>BMC Systems Biology</i> , 2014, 8, 11.	3.0	4
58	Structure-Based Clustering of Major Histocompatibility Complex (MHC) Proteins for Broad-Based T-Cell Vaccine Design. <i>Methods in Molecular Biology</i> , 2014, 1184, 503-511.	0.9	1
59	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
60	Simple re-instantiation of small databases using cloud computing. <i>BMC Genomics</i> , 2013, 14, S13.	2.8	10
61	InCoB2013 introduces Systems Biology as a major conference theme. <i>BMC Systems Biology</i> , 2013, 7, S1.	3.0	6
62	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
63	Functional Annotation of the Human Chromosome 7 α -Missing Proteins: A Bioinformatics Approach. <i>Journal of Proteome Research</i> , 2013, 12, 2504-2510.	3.7	17
64	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
65	Vaccine adjuvant informatics. , 2013, , 123-130.		1
66	Database design. , 2013, , 47-57.		0
67	Infectious disease informatics. , 2013, , 99-110.		0
68	APBioNetâ€”Transforming Bioinformatics in the Asia-Pacific Region. <i>PLoS Computational Biology</i> , 2013, 9, e1003317.	3.2	7
69	Computational T cell vaccine design. , 2013, , 59-86.		2
70	Scientific publications and databases. , 2013, , 21-46.		2
71	Adaptive Immune System. , 2013, , 10-11.		2
72	Computer-aided vaccine design. , 2013, , .		3

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73	Protein-Protein Interactions and Prediction: A Comprehensive Overview. <i>Protein and Peptide Letters</i> , 2013, 21, 779-789.	0.9	19
74	TR Recognition of MHC-Peptide Complexes. , 2013, , 2212-2218.		0
75	B Cell-mediated Immune Response. , 2013, , 67-67.		0
76	T Cell Activation. , 2013, , 2115-2115.		0
77	PMHC Epitope. , 2013, , 1718-1719.		0
78	PMHC Imprint. , 2013, , 1719-1719.		0
79	Structural Immunoinformatics. , 2013, , 2022-2023.		0
80	T Cell Signaling. , 2013, , 2119-2119.		0
81	TR Germline Bias. , 2013, , 2212-2212.		0
82	T Cell Epitopes. , 2013, , 2118-2119.		0
83	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
84	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
85	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
86	Whole-genome sequence of <i>Schistosoma haematobium</i> . <i>Nature Genetics</i> , 2012, 44, 221-225.	21.4	383
87	TranSeqAnnotator: large-scale analysis of transcriptomic data. <i>BMC Bioinformatics</i> , 2012, 13, S24.	2.6	6
88	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
89	Bioinformatics meets parasitology. <i>Parasite Immunology</i> , 2012, 34, 265-275.	1.5	23
90	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

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91	Deep insights into Dictyocaulus viviparus transcriptomes provides unique prospects for new drug targets and disease intervention. Biotechnology Advances, 2011, 29, 261-271.	11.7	31
92	Ascaris suum draft genome. Nature, 2011, 479, 529-533.	27.8	246
93	Structural diversity of biologically interesting datasets: a scaffold analysis approach. Journal of Cheminformatics, 2011, 3, 30.	6.1	32
94	Towards big data science in the decade ahead from ten years of InCoB and the 1st ISCB-Asia Joint Conference. BMC Bioinformatics, 2011, 12, S1.	2.6	20
95	In silico approach to screen compounds active against parasitic nematodes of major socio-economic importance. BMC Bioinformatics, 2011, 12, S25.	2.6	9
96	In silico secretome analysis approach for next generation sequencing transcriptomic data. BMC Genomics, 2011, 12, S14.	2.8	32
97	A comparative structural bioinformatics analysis of inherited mutations in Î²-D-Mannosidase across multiple species reveals a genotype-phenotype correlation. BMC Genomics, 2011, 12, S22.	2.8	15
98	Molecular similarity and diversity approaches in chemoinformatics. Drug Development Research, 2011, 72, 74-84.	2.9	9
99	MPID-T2: a database for sequenceâ€“structureâ€“function analyses of pMHC and TR/pMHC structures. Bioinformatics, 2011, 27, 1192-1193.	4.1	18
100	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
101	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
102	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
103	Meeting Report from the Second â€œMinimum Information for Biological and Biomedical Investigationsâ€• (MIBBI) workshop. Standards in Genomic Sciences, 2010, 3, 259-266.	1.5	32
104	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. BMC Bioinformatics, 2010, 11, S1.	2.6	3
105	Network analysis of human protein location. BMC Bioinformatics, 2010, 11, S9.	2.6	12
106	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
107	Advancing standards for bioinformatics activities: persistence, reproducibility, disambiguation and Minimum Information About a Bioinformatics investigation (MIABI). BMC Genomics, 2010, 11, S27.	2.8	29
108	First transcriptomic analysis of the economically important parasitic nematode, Trichostrongylus colubriformis, using a next-generation sequencing approach. Infection, Genetics and Evolution, 2010, 10, 1199-1207.	2.3	55

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109	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
110	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
111	Extracting Biomarker Information Applying Natural Language Processing and Machine Learning. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010, , .	0.0	1
112	Massively Parallel Sequencing and Analysis of the <i>Necator americanus</i> Transcriptome. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e684.	3.0	66
113	Towards a career in bioinformatics. <i>BMC Bioinformatics</i> , 2009, 10, S1.	2.6	9
114	Physicochemical property space distribution among human metabolites, drugs and toxins. <i>BMC Bioinformatics</i> , 2009, 10, S10.	2.6	62
115	A comprehensive assessment of N-terminal signal peptides prediction methods. <i>BMC Bioinformatics</i> , 2009, 10, S2.	2.6	58
116	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
117	Extending Asia Pacific bioinformatics into new realms in the "-omics" era. <i>BMC Genomics</i> , 2009, 10, S1.	2.8	13
118	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
119	A multi-species comparative structural bioinformatics analysis of inherited mutations in Î±-D-Mannosidase reveals strong genotype-phenotype correlation. <i>BMC Genomics</i> , 2009, 10, S33.	2.8	13
120	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
121	A multi-factor model for caspase degradome prediction. <i>BMC Genomics</i> , 2009, 10, S6.	2.8	16
122	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
123	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
124	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
125	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	12.6	1,038
126	Secretome: clues into pathogen infection and clinical applications. <i>Genome Medicine</i> , 2009, 1, 113.	8.2	56

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127	Structural Immunoinformatics: Understanding MHC-Peptide-TR Binding. , 2009, , 77-93.		4
128	Bioinformatics research in the Asia Pacific: a 2007 update. BMC Bioinformatics, 2008, 9, S1.	2.6	7
129	In silico analysis of expressed sequence tags from <i>Trichostrongylus vitrinus</i> (Nematoda): comparison of the automated ESTExplorer workflow platform with conventional database searches. BMC Bioinformatics, 2008, 9, S10.	2.6	17
130	Modeling <i>Escherichia coli</i> signal peptidase complex with bound substrate: determinants in the mature peptide influencing signal peptide cleavage. BMC Bioinformatics, 2008, 9, S15.	2.6	12
131	Tandem duplication, circular permutation, molecular adaptation: how Solanaceae resist pests via inhibitors. BMC Bioinformatics, 2008, 9, S22.	2.6	27
132	Flanking signal and mature peptide residues influence signal peptide cleavage. BMC Bioinformatics, 2008, 9, S15.	2.6	62
133	CMKb: a web-based prototype for integrating Australian Aboriginal customary medicinal plant knowledge. BMC Bioinformatics, 2008, 9, S25.	2.6	19
134	Gender-enriched transcripts in <i>Haemonchus contortus</i> " predicted functions and genetic interactions based on comparative analyses with <i>Caenorhabditis elegans</i> . International Journal for Parasitology, 2008, 38, 65-83.	3.1	40
135	Structural Immunoinformatics. , 2008, , 51-61.		1
136	Functional and Structural Implications of the Complement Factor H Y402H Polymorphism Associated with Age-Related Macular Degeneration. , 2008, 49, 1763.		85
137	Critical technologies for bioinformatics. Briefings in Bioinformatics, 2008, 9, 261-262.	6.5	2
138	Transcriptional Changes in the Hookworm, <i>Ancylostoma caninum</i> , during the Transition from a Free-Living to a Parasitic Larva. PLoS Neglected Tropical Diseases, 2008, 2, e130.	3.0	72
139	Needles in the EST Haystack: Large-Scale Identification and Analysis of Excretory-Secretory (ES) Proteins in Parasitic Nematodes Using Expressed Sequence Tags (ESTs). PLoS Neglected Tropical Diseases, 2008, 2, e301.	3.0	44
140	A WORKFLOW FOR MUTATION EXTRACTION AND STRUCTURE ANNOTATION. Journal of Bioinformatics and Computational Biology, 2007, 05, 1319-1337.	0.8	22
141	CASVM: web server for SVM-based prediction of caspase substrates cleavage sites. Bioinformatics, 2007, 23, 3241-3243.	4.1	71
142	In silico grouping of peptide/HLA class I complexes using structural interaction characteristics. Bioinformatics, 2007, 23, 177-183.	4.1	133
143	ESTExplorer: an expressed sequence tag (EST) assembly and annotation platform. Nucleic Acids Research, 2007, 35, W143-W147.	14.5	60
144	Genomic characterization of <i>Tv-ant-1</i> , a <i>Caenorhabditis elegans</i> tag-61 homologue from the parasitic nematode <i>Trichostrongylus vitrinus</i> . Gene, 2007, 397, 12-25.	2.2	8

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145	Intelligent Agent System for Bio-medical Literature Mining. , 2007, , .		0
146	A Practical Guide to Structure-Based Prediction of MHC-Binding Peptides. Methods in Molecular Biology, 2007, 409, 301-308.	0.9	7
147	In silico characterization of immunogenic epitopes presented by HLA-Cw*0401. Immunome Research, 2007, 3, 7.	0.1	13
148	A transcriptomic analysis of the adult stage of the bovine lungworm, Dictyocaulus viviparus. BMC Genomics, 2007, 8, 311.	2.8	17
149	Oesophagostomum dentatum – Potential as a model for genomic studies of strongylid nematodes, with biotechnological prospects. Biotechnology Advances, 2007, 25, 281-293.	11.7	19
150	MPID-T. Applied Bioinformatics, 2006, 5, 111-114.	1.6	25
151	A hitchhiker's guide to expressed sequence tag (EST) analysis. Briefings in Bioinformatics, 2006, 8, 6-21.	6.5	235
152	SCORPION2: A database for structure–function analysis of scorpion toxins. Toxicon, 2006, 47, 356-363.	1.6	48
153	OMIA (Online Mendelian Inheritance in Animals): an enhanced platform and integration into the Entrez search interface at NCBI. Nucleic Acids Research, 2006, 34, D599-D601.	14.5	73
154	Modeling the bound conformation of Pemphigus vulgaris-associated peptides to MHC Class II DR and DQ alleles. Immunome Research, 2006, 2, 1.	0.1	88
155	Deduction of functional peptide motifs in scorpion toxins. Journal of Peptide Science, 2006, 12, 420-427.	1.4	11
156	Establishing bioinformatics research in the Asia Pacific. BMC Bioinformatics, 2006, 7, 1.	2.6	356
157	SVM-based prediction of caspase substrate cleavage sites. BMC Bioinformatics, 2006, 7, S14.	2.6	53
158	Prediction of desmoglein-3 peptides reveals multiple shared T-cell epitopes in HLA DR4- and DR6-associated Pemphigus vulgaris. BMC Bioinformatics, 2006, 7, S7.	2.6	81
159	ASGS: an alternative splicing graph web service. Nucleic Acids Research, 2006, 34, W444-W447.	14.5	14
160	Prediction of HLA-DQ3.2 ² Ligands: evidence of multiple registers in class II binding peptides. Bioinformatics, 2006, 22, 1232-1238.	4.1	42
161	Methods and protocols for prediction of immunogenic epitopes. Briefings in Bioinformatics, 2006, 8, 96-108.	6.5	91
162	Comparative Genomic Analysis of Glycoylation Pathways in Yeast, Plants and Higher eukaryotes. Applied Mycology and Biotechnology, 2006, 6, 227-248.	0.3	2

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163	Accurate prediction of scorpion toxin functional properties from primary structures. <i>Journal of Molecular Graphics and Modelling</i> , 2005, 24, 17-24.	2.4	12
164	SPdb--a signal peptide database. <i>BMC Bioinformatics</i> , 2005, 6, 249.	2.6	78
165	Bioinformatics Education--Perspectives and Challenges. <i>PLoS Computational Biology</i> , 2005, 1, e52.	3.2	59
166	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
167	The Integrin β 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
168	SDPMD: an automated comparative modeling server for small disulfide-bonded proteins. <i>Nucleic Acids Research</i> , 2004, 32, W356-W359.	14.5	18
169	Delineation of modular proteins: Domain boundary prediction from sequence information. <i>Briefings in Bioinformatics</i> , 2004, 5, 179-192.	6.5	26
170	DEDB: a database of <i>Drosophila melanogaster</i> exons in splicing graph form. <i>BMC Bioinformatics</i> , 2004, 5, 189.	2.6	31
171	Xpro: database of eukaryotic protein-encoding genes. <i>Nucleic Acids Research</i> , 2004, 32, 59D-63.	14.5	21
172	Modeling the structure of bound peptide ligands to major histocompatibility complex. <i>Protein Science</i> , 2004, 13, 2523-2532.	7.6	84
173	A common site within factor H SCR ϵ ,7 responsible for binding heparin, C-reactive protein and streptococcal M protein. <i>European Journal of Immunology</i> , 2003, 33, 962-969.	2.9	151
174	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
175	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
176	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
177	XdomView: protein domain and exon position visualization. <i>Bioinformatics</i> , 2003, 19, 159-160.	4.1	9
178	Antisense Suppression of a Cytokinin-binding Protein from <i>Petunia</i> Causes Excessive Branching and Reduces Adventitious Shoot Bud Induction in Vitro. , 2003, , 285-287.		0
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