

Tin Wee Tan

List of Publications by Year in descending order

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66
papers

2,467
citations

186265

28
h-index

223800

46
g-index

70
all docs

70
docs citations

70
times ranked

4014
citing authors

#	ARTICLE	IF	CITATIONS
1	A multi-task CNN learning model for taxonomic assignment of human viruses. BMC Bioinformatics, 2021, 22, 194.	2.6	3
2	Architecture of population-differentiated polymorphisms in the human genome. PLoS ONE, 2019, 14, e0224089.	2.5	4
3	Towards precision medicine: interrogating the human genome to identify drug pathways associated with potentially functional, population-differentiated polymorphisms. Pharmacogenomics Journal, 2019, 19, 516-527.	2.0	32
4	Exploring the transcriptome of non-model oleaginous microalga <i>Dunaliella tertiolecta</i> through high-throughput sequencing and high performance computing. BMC Bioinformatics, 2017, 18, 122.	2.6	17
5	Elevated acetyl-CoA by amino acid recycling fuels microalgal neutral lipid accumulation in exponential growth phase for biofuel production. Plant Biotechnology Journal, 2017, 15, 497-509.	8.3	36
6	Analysis of viral diversity for vaccine target discovery. BMC Medical Genomics, 2017, 10, 78.	1.5	14
7	Development of a clinical decision support system for diabetes care: A pilot study. PLoS ONE, 2017, 12, e0173021.	2.5	39
8	Distinct Host Tropism Protein Signatures to Identify Possible Zoonotic Influenza A Viruses. PLoS ONE, 2016, 11, e0150173.	2.5	14
9	T-Cell Epitope Prediction of Chikungunya Virus. Methods in Molecular Biology, 2016, 1426, 201-207.	0.9	3
10	Coverage analysis in a targeted amplicon-based next-generation sequencing panel for myeloid neoplasms. Journal of Clinical Pathology, 2016, 69, 801-804.	2.0	27
11	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. BMC Bioinformatics, 2015, 16, 11.	2.6	1
12	RNA-Seq transcriptomic analysis with Bag2D software identifies key pathways enhancing lipid yield in a high lipid-producing mutant of the non-model green alga <i>Dunaliella tertiolecta</i> . Biotechnology for Biofuels, 2015, 8, 191.	6.2	20
13	STATdb: A Specialised Resource for the STATome. PLoS ONE, 2014, 9, e104597.	2.5	0
14	Simple re-instantiation of small databases using cloud computing. BMC Genomics, 2013, 14, S13.	2.8	10
15	APBioNet—Transforming Bioinformatics in the Asia-Pacific Region. PLoS Computational Biology, 2013, 9, e1003317.	3.2	7
16	Dissecting the Dynamics of HIV-1 Protein Sequence Diversity. PLoS ONE, 2013, 8, e59994.	2.5	14
17	West Nile Virus T-Cell Ligand Sequences Shared with Other Flaviviruses: a Multitude of Variant Sequences as Potential Altered Peptide Ligands. Journal of Virology, 2012, 86, 7616-7624.	3.4	14
18	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

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19	Towards BioDBcore: a community-defined information specification for biological databases. <i>Nucleic Acids Research</i> , 2011, 39, D7-D10.	14.5	32
20	InCoB2010 - 9th International Conference on Bioinformatics at Tokyo, Japan, September 26-28, 2010. <i>BMC Bioinformatics</i> , 2010, 11, S1.	2.6	3
21	T3SEdb: data warehousing of virulence effectors secreted by the bacterial Type III Secretion System. <i>BMC Bioinformatics</i> , 2010, 11, S4.	2.6	42
22	Challenges of the next decade for the Asia Pacific region: 2010 International Conference in Bioinformatics (InCoB 2010). <i>BMC Genomics</i> , 2010, 11, S1.	2.8	14
23	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
24	Complete-Proteome Mapping of Human Influenza A Adaptive Mutations: Implications for Human Transmissibility of Zoonotic Strains. <i>PLoS ONE</i> , 2010, 5, e9025.	2.5	85
25	Classification of Dengue Fever Patients Based on Gene Expression Data Using Support Vector Machines. <i>PLoS ONE</i> , 2010, 5, e11267.	2.5	36
26	Conservation and Variability of West Nile Virus Proteins. <i>PLoS ONE</i> , 2009, 4, e5352.	2.5	24
27	The implementation of e-learning tools to enhance undergraduate bioinformatics teaching and learning: a case study in the National University of Singapore. <i>BMC Bioinformatics</i> , 2009, 10, S12.	2.6	10
28	A comprehensive assessment of N-terminal signal peptides prediction methods. <i>BMC Bioinformatics</i> , 2009, 10, S2.	2.6	58
29	Extending Asia Pacific bioinformatics into new realms in the "-omics" era. <i>BMC Genomics</i> , 2009, 10, S1.	2.8	13
30	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
31	A multi-factor model for caspase degradome prediction. <i>BMC Genomics</i> , 2009, 10, S6.	2.8	16
32	Bioinformatics research in the Asia Pacific: a 2007 update. <i>BMC Bioinformatics</i> , 2008, 9, S1.	2.6	7
33	Identification of human-to-human transmissibility factors in PB2 proteins of influenza A by large-scale mutual information analysis. <i>BMC Bioinformatics</i> , 2008, 9, S18.	2.6	94
34	Rule-based knowledge aggregation for large-scale protein sequence analysis of influenza A viruses. <i>BMC Bioinformatics</i> , 2008, 9, S7.	2.6	9
35	Structural Immunoinformatics. , 2008, , 51-61.		1
36	Automatic synchronization and distribution of biological databases and software over low-bandwidth networks among developing countries. <i>Bioinformatics</i> , 2008, 24, 299-301.	4.1	9

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37	Conservation and Variability of Dengue Virus Proteins: Implications for Vaccine Design. PLoS Neglected Tropical Diseases, 2008, 2, e272.	3.0	79
38	CASVM: web server for SVM-based prediction of caspase substrates cleavage sites. Bioinformatics, 2007, 23, 3241-3243.	4.1	71
39	In silico grouping of peptide/HLA class I complexes using structural interaction characteristics. Bioinformatics, 2007, 23, 177-183.	4.1	133
40	Evolutionarily Conserved Protein Sequences of Influenza A Viruses, Avian and Human, as Vaccine Targets. PLoS ONE, 2007, 2, e1190.	2.5	157
41	In silico characterization of immunogenic epitopes presented by HLA-Cw*0401. Immunome Research, 2007, 3, 7.	0.1	13
42	MPID-T. Applied Bioinformatics, 2006, 5, 111-114.	1.6	25
43	A systematic bioinformatics approach for selection of epitope-based vaccine targets. Cellular Immunology, 2006, 244, 141-147.	3.0	78
44	Establishing bioinformatics research in the Asia Pacific. BMC Bioinformatics, 2006, 7, 1.	2.6	356
45	SVM-based prediction of caspase substrate cleavage sites. BMC Bioinformatics, 2006, 7, S14.	2.6	53
46	Large-scale analysis of antigenic diversity of T-cell epitopes in dengue virus. BMC Bioinformatics, 2006, 7, S4.	2.6	37
47	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
48	ASGS: an alternative splicing graph web service. Nucleic Acids Research, 2006, 34, W444-W447.	14.5	14
49	Prediction of HLA-DQ3.2 [∗] Ligands: evidence of multiple registers in class II binding peptides. Bioinformatics, 2006, 22, 1232-1238.	4.1	42
50	Methods and protocols for prediction of immunogenic epitopes. Briefings in Bioinformatics, 2006, 8, 96-108.	6.5	91
51	PROCESS INTEGRATION FOR BIO-MANUFACTURING GRID. , 2006, , .		0
52	Accurate prediction of scorpion toxin functional properties from primary structures. Journal of Molecular Graphics and Modelling, 2005, 24, 17-24.	2.4	12
53	SPdb--a signal peptide database. BMC Bioinformatics, 2005, 6, 249.	2.6	78
54	Extraction by Example: Induction of Structural Rules for the Analysis of Molecular Sequence Data from Heterogeneous Sources. Lecture Notes in Computer Science, 2005, , 398-405.	1.3	3

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55	BIOLOGICAL DATABASES AND WEB SERVICES: METRICS FOR QUALITY. Series on Advances in Bioinformatics and Computational Biology, 2005, , 771-777.	0.2	0
56	Supporting the curation of biological databases with reusable text mining. Genome Informatics, 2005, 16, 32-44.	0.4	15
57	SDPMOD: an automated comparative modeling server for small disulfide-bonded proteins. Nucleic Acids Research, 2004, 32, W356-W359.	14.5	18
58	DEDB: a database of Drosophila melanogaster exons in splicing graph form. BMC Bioinformatics, 2004, 5, 189.	2.6	31
59	Xpro: database of eukaryotic protein-encoding genes. Nucleic Acids Research, 2004, 32, 59D-63.	14.5	21
60	Modeling the structure of bound peptide ligands to major histocompatibility complex. Protein Science, 2004, 13, 2523-2532.	7.6	84
61	The S-star trial bioinformatics course: An on-line learning success. Biochemistry and Molecular Biology Education, 2003, 31, 20-23.	1.2	18
62	MGAlignIt: a web service for the alignment of mRNA/EST and genomic sequences. Nucleic Acids Research, 2003, 31, 3533-3536.	14.5	32
63	MPID: MHC-Peptide Interaction Database for sequence-structure-function information on peptides binding to MHC molecules. Bioinformatics, 2003, 19, 309-310.	4.1	35
64	XdomView: protein domain and exon position visualization. Bioinformatics, 2003, 19, 159-160.	4.1	9
65	APBioNet: the Asia-Pacific regional consortium for bioinformatics. Applied Bioinformatics, 2002, 1, 101-5.	1.6	7
66	A functional significance for codon third bases. Gene, 2000, 245, 291-298.	2.2	54