

Jason T L Wang

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

427
citations

932766

10
h-index

794141

19
g-index

50
all docs

50
docs citations

50
times ranked

563
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting Solar Flares Using a Long Short-term Memory Network. <i>Astrophysical Journal</i> , 2019, 877, 121.	1.6	88
2	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. <i>IEEE Access</i> , 2017, 5, 7381-7393.	2.6	46
3	A transfer learning approach via procrustes analysis and mean shift for cancer drug sensitivity prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840014.	0.3	34
4	Semi-supervised prediction of gene regulatory networks using machine learning algorithms. <i>Journal of Biosciences</i> , 2015, 40, 731-740.	0.5	32
5	MetricMap: An Embedding Technique for Processing Distance-Based Queries in Metric Spaces. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 2005, 35, 973-987.	5.5	30
6	Kernel design for RNA classification using Support Vector Machines. <i>International Journal of Data Mining and Bioinformatics</i> , 2006, 1, 57.	0.1	30
7	Clinical intelligence: New machine learning techniques for predicting clinical drug response. <i>Computers in Biology and Medicine</i> , 2019, 107, 302-322.	3.9	22
8	Predicting Coronal Mass Ejections Using SDO/HMI Vector Magnetic Data Products and Recurrent Neural Networks. <i>Astrophysical Journal</i> , 2020, 890, 12.	1.6	20
9	Inferring Vector Magnetic Fields from Stokes Profiles of GST/NIRIS Using a Convolutional Neural Network. <i>Astrophysical Journal</i> , 2020, 894, 70.	1.6	19
10	Tracing H α Fibrils through Bayesian Deep Learning. <i>Astrophysical Journal, Supplement Series</i> , 2021, 256, 20.	3.0	11
11	XML QUERY BY EXAMPLE. <i>International Journal of Computational Intelligence and Applications</i> , 2002, 02, 329-337.	0.6	10
12	Effective Classification of MicroRNA Precursors Using Feature Mining and AdaBoost Algorithms. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 486-493.	1.0	10
13	Inferring Gene Regulatory Networks by Combining Supervised and Unsupervised Methods. , 2016, , .		10
14	CHSalign: A Web Server That Builds upon Junction-Explorer and RNAJAG for Pairwise Alignment of RNA Secondary Structures with Coaxial Helical Stacking. <i>PLoS ONE</i> , 2016, 11, e0147097.	1.1	9
15	MapReduce Algorithms for Inferring Gene Regulatory Networks from Time-Series Microarray Data Using an Information-Theoretic Approach. <i>BioMed Research International</i> , 2017, 2017, 1-8.	0.9	7
16	Identifying and Tracking Solar Magnetic Flux Elements with Deep Learning. <i>Astrophysical Journal, Supplement Series</i> , 2020, 250, 5.	3.0	7
17	Generative Adversarial Networks for Stochastic Video Prediction With Action Control. <i>IEEE Access</i> , 2020, 8, 63336-63348.	2.6	6
18	Predicting Solar Energetic Particles Using SDO/HMI Vector Magnetic Data Products and a Bidirectional LSTM Network. <i>Astrophysical Journal, Supplement Series</i> , 2022, 260, 16.	3.0	6

#	ARTICLE	IF	CITATIONS
19	Fast structural search in phylogenetic databases. <i>Evolutionary Bioinformatics</i> , 2007, 1, 37-46.	0.6	5
20	Reverse Engineering Gene Regulatory Networks Using Graph Mining. <i>Lecture Notes in Computer Science</i> , 2018, , 335-349.	1.0	3
21	Effective alignment of RNA pseudoknot structures using partition function posterior log-odds scores. <i>BMC Bioinformatics</i> , 2015, 16, 39.	1.2	2
22	Generative Adversarial Networks for Video Prediction with Action Control. <i>Lecture Notes in Computer Science</i> , 2020, , 87-105.	1.0	2
23	Guest Editorial: Special Section on Biological Data Mining and Its Applications in Healthcare. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 501-502.	1.9	1
24	A Time-Delayed Information-Theoretic Approach to the Reverse Engineering of Gene Regulatory Networks Using Apache Spark. , 2017, , .		1
25	Discovering frequent induced subgraphs from directed networks. <i>Intelligent Data Analysis</i> , 2018, 22, 1279-1296.	0.4	1
26	Constrained RNA Structural Alignment: Algorithms and Application to Motif Detection in the Untranslated Regions of <i>Trypanosoma brucei</i> mRNAs. , 2007, , .		0
27	On Comparing and Visualizing RNA Secondary Structures. , 0, , 233-249.		0
28	Using folding ensemble and stem probability maximization methods to predict RNA H-type pseudoknots. <i>Tsinghua Science and Technology</i> , 2012, 17, 691-700.	4.1	0
29	Protein Classification: A Geometric Hashing Approach. , 2003, , 163-181.		0
30	Wiley Series on Bioinformatics: Computational Techniques and Engineering. , 0, , 373-373.		0
31	A New Approach to the Discovery of RNA Structural Elements in the Human Genome. <i>Science, Engineering, and Biology Informatics</i> , 2011, , 117-132.	0.1	0