Jason T L Wang

List of Publications by Year
in descending order

31	427	933264	794469
papers	citations	10	19
		h-index	g-index

50	50	50	563
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting Solar Energetic Particles Using SDO/HMI Vector Magnetic Data Products and a Bidirectional LSTM Network. Astrophysical Journal, Supplement Series, 2022, 260, 16.	3.0	6
2	Tracing HÎ± Fibrils through Bayesian Deep Learning. Astrophysical Journal, Supplement Series, 2021, 256, 20.	3.0	11
3	Predicting Coronal Mass Ejections Using SDO/HMI Vector Magnetic Data Products and Recurrent Neural Networks. Astrophysical Journal, 2020, 890, 12.	1.6	20
4	Generative Adversarial Networks for Stochastic Video Prediction With Action Control. IEEE Access, 2020, 8, 63336-63348.	2.6	6
5	Inferring Vector Magnetic Fields from Stokes Profiles of GST/NIRIS Using a Convolutional Neural Network. Astrophysical Journal, 2020, 894, 70.	1.6	19
6	Identifying and Tracking Solar Magnetic Flux Elements with Deep Learning. Astrophysical Journal, Supplement Series, 2020, 250, 5.	3.0	7
7	Generative Adversarial Networks for Video Prediction with Action Control. Lecture Notes in Computer Science, 2020, , 87-105.	1.0	2
8	Predicting Solar Flares Using a Long Short-term Memory Network. Astrophysical Journal, 2019, 877, 121.	1.6	88
9	Clinical intelligence: New machine learning techniques for predicting clinical drug response. Computers in Biology and Medicine, 2019, 107, 302-322.	3.9	22
10	A transfer learning approach via procrustes analysis and mean shift for cancer drug sensitivity prediction. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840014.	0.3	34
11	Discovering frequent induced subgraphs from directed networks. Intelligent Data Analysis, 2018, 22, 1279-1296.	0.4	1
12	Reverse Engineering Gene Regulatory Networks Using Graph Mining. Lecture Notes in Computer Science, 2018, , 335-349.	1.0	3
13	Transfer Learning Approaches to Improve Drug Sensitivity Prediction in Multiple Myeloma Patients. IEEE Access, 2017, 5, 7381-7393.	2.6	46
14	Guest Editorial: Special Section on Biological Data Mining and Its Applications in Healthcare. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 501-502.	1.9	1
15	A Time-Delayed Information-Theoretic Approach to the Reverse Engineering of Gene Regulatory Networks Using Apache Spark. , 2017, , .		1
16	MapReduce Algorithms for Inferring Gene Regulatory Networks from Time-Series Microarray Data Using an Information-Theoretic Approach. BioMed Research International, 2017, 2017, 1-8.	0.9	7
17	Inferring Gene Regulatory Networks by Combining Supervised and Unsupervised Methods. , 2016, , .		10
18	CHSalign: A Web Server That Builds upon Junction-Explorer and RNAJAG for Pairwise Alignment of RNA Secondary Structures with Coaxial Helical Stacking. PLoS ONE, 2016, 11, e0147097.	1.1	9

#	Article	IF	Citations
19	Effective alignment of RNA pseudoknot structures using partition function posterior log-odds scores. BMC Bioinformatics, 2015, 16, 39.	1.2	2
20	Semi-supervised prediction of gene regulatory networks using machine learning algorithms. Journal of Biosciences, 2015, 40, 731-740.	0.5	32
21	Effective Classification of MicroRNA Precursors Using Feature Mining and AdaBoost Algorithms. OMICS A Journal of Integrative Biology, 2013, 17, 486-493.	1.0	10
22	Using folding ensemble and stem probability maximization methods to predict RNA H-type pseudoknots. Tsinghua Science and Technology, 2012, 17, 691-700.	4.1	0
23	A New Approach to the Discovery of RNA Structural Elements in the Human Genome. Science, Engineering, and Biology Informatics, 2011, , 117-132.	0.1	0
24	Constrained RNA Structural Alignment: Algorithms and Application to Motif Detection in the Untranslated Regions of Trypanosoma brucei mRNAs. , 2007, , .		0
25	Fast structural search in phylogenetic databases. Evolutionary Bioinformatics, 2007, 1, 37-46.	0.6	5
26	Kernel design for RNA classification using Support Vector Machines. International Journal of Data Mining and Bioinformatics, 2006, 1, 57.	0.1	30
27	MetricMap: An Embedding Technique for Processing Distance-Based Queries in Metric Spaces. IEEE Transactions on Systems, Man, and Cybernetics, 2005, 35, 973-987.	5.5	30
28	Protein Classification: A Geometric Hashing Approach. , 2003, , 163-181.		0
29	XML QUERY BY EXAMPLE. International Journal of Computational Intelligence and Applications, 2002, 02, 329-337.	0.6	10
30	On Comparing and Visualizing RNA Secondary Structures. , 0, , 233-249.		0
31	Wiley Series on Bioinformatics: Computational Techniques and Engineering. , 0, , 373-373.		0