

Chun-Hsi Huang

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4054814/publications.pdf>

Version: 2024-02-01

33
papers

235
citations

1478505

6
h-index

1199594

12
g-index

33
all docs

33
docs citations

33
times ranked

517
citing authors

#	ARTICLE	IF	CITATIONS
1	A Bisection Reinforcement Learning Approach to 3-D Indoor Localization. IEEE Internet of Things Journal, 2021, 8, 6519-6535.	8.7	17
2	Nongreedy Unbalanced Huffman Tree Compressor for Single and Multifasta Files. Journal of Computational Biology, 2020, 27, 868-876.	1.6	9
3	Neuroimaging Subjective Labeling Dichotomization and Class Imbalance Alleviation. , 2019, , .		0
4	LFastQC: A lossless non-reference-based FASTQ compressor. PLoS ONE, 2019, 14, e0224806.	2.5	11
5	Performance evaluation for MOTIFSIM. Biological Procedures Online, 2018, 20, 23.	2.9	0
6	A Locality-Aware, Energy-Efficient Cache Design for Large-Scale Multi-Core Systems. , 2018, , .		0
7	A QoS Framework for SDN-Based Networks. , 2018, , .		12
8	MODSIDE: a motif discovery pipeline and similarity detector. BMC Genomics, 2018, 19, 755.	2.8	1
9	Top-Down Indoor Localization with Wi-Fi Fingerprints Using Deep Q-Network. , 2018, , .		12
10	MOTIFSIM 2.1: An Enhanced Software Platform for Detecting Similarity in Multiple DNA Motif Data Sets. Journal of Computational Biology, 2017, 24, 895-905.	1.6	2
11	Toward a Better Compression for DNA Sequences Using Huffman Encoding. Journal of Computational Biology, 2017, 24, 280-288.	1.6	18
12	Cloud-based MOTIFSIM: Detecting Similarity in Large DNA Motif Data Sets. Journal of Computational Biology, 2017, 24, 450-459.	1.6	2
13	Software-defined extreme scale networks for bigdata applications. , 2017, , .		8
14	Speedup higher-order masking of AES using normal basis and SIMD. , 2016, , .		2
15	On SDN-based extreme-scale networks. , 2016, , .		5
16	ET-Motif: Solving the Exact (l, d)-Planted Motif Problem Using Error Tree Structure. Journal of Computational Biology, 2016, 23, 615-623.	1.6	2
17	An efficient high-order masking of AES using SIMD. , 2015, , .		4
18	Cross-Disciplinary Detection and Analysis of Network Motifs. Bioinformatics and Biology Insights, 2015, 9, BBI.S23619.	2.0	16

#	ARTICLE	IF	CITATIONS
19	MOTIFSIM: A web tool for detecting similarity in multiple DNA motif datasets. <i>BioTechniques</i> , 2015, 59, 26-33.	1.8	3
20	Accelerating higher-order masking of AES using composite field and SIMD. , 2015, , .		2
21	LASAGNA-Search 2.0: integrated transcription factor binding site search and visualization in a browser. <i>Bioinformatics</i> , 2014, 30, 1923-1925.	4.1	58
22	Gene Expression and Gene Ontology Enrichment Analysis for H3K4me3 and H3K4me1 in Mouse Liver and Mouse Embryonic Stem Cell Using CHIP-Seq and RNA-Seq. <i>Gene Regulation and Systems Biology</i> , 2014, 8, GRSB.S13612.	2.3	3
23	Biological data classifications with LDA and SPRT. , 2010, , .		2
24	Finding Hamiltonian paths in tournaments on clusters. <i>Cluster Computing</i> , 2006, 9, 345-353.	5.0	0
25	Clustering of Gene Expression Data: Performance and Similarity Analysis. , 2006, , .		2
26	BioGrid- bridging life science and information technology. , 2005, , .		0
27	HealthGrid " Bridging Life Science and Information Technology. <i>Journal of Clinical Monitoring and Computing</i> , 2005, 19, 259-262.	1.6	9
28	EXACT ALGORITHMS FOR PLANTED MOTIF CHALLENGE PROBLEMS. , 2005, , .		26
29	Distributed Path-Based Inference in Semantic Networks. <i>Journal of Supercomputing</i> , 2004, 29, 211-227.	3.6	4
30	Distributed path-based inference in semantic networks. , 2004, , .		0
31	Parallel pattern identification in biological sequences on clusters. <i>IEEE Transactions on Nanobioscience</i> , 2003, 2, 29-34.	3.3	3
32	Parallel pattern identification in biological sequences on clusters. , 0, , .		1
33	TROJAN: a scalable distributed semantic network system. , 0, , .		1