

Feng Luo

List of Publications by Year in descending order

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39
papers

1,863
citations

471509

17
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g-index

42
all docs

42
docs citations

42
times ranked

2896
citing authors

#	ARTICLE	IF	CITATIONS
1	Dual-Level Knowledge Distillation via Knowledge Alignment and Correlation. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 2425-2435.	11.3	3
2	SACall: A Neural Network Basecaller for Oxford Nanopore Sequencing Data Based on Self-Attention Mechanism. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 614-623.	3.0	14
3	BlockPolish: accurate polishing of long-read assembly via block divide-and-conquer. Briefings in Bioinformatics, 2022, 23, .	6.5	2
4	CatCharger: Deploying In-Motion Wireless Chargers in a Metropolitan Road Network via Categorization and Clustering of Vehicle Traffic. IEEE Internet of Things Journal, 2022, 9, 9525-9541.	8.7	2
5	Predicting the formation of fractionally doped perovskite oxides by a function-confined machine learning method. Communications Materials, 2022, 3, .	6.9	7
6	A Gene Rank Based Approach for Single Cell Similarity Assessment and Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 431-442.	3.0	12
7	Efficient assembly of nanopore reads via highly accurate and intact error correction. Nature Communications, 2021, 12, 60.	12.8	166
8	A Chi-MIC Based Adaptive Multi-Branch Decision Tree. IEEE Access, 2021, 9, 78962-78972.	4.2	9
9	NeuralPolish: a novel Nanopore polishing method based on alignment matrix construction and orthogonal Bi-GRU Networks. Bioinformatics, 2021, 37, 3120-3127.	4.1	13
10	Genome-wide detection of cytosine methylations in plant from Nanopore data using deep learning. Nature Communications, 2021, 12, 5976.	12.8	47
11	Improving de novo Assembly Based on Read Classification. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 177-188.	3.0	19
12	MultiMotifMaker: A Multi-Thread Tool for Identifying DNA Methylation Motifs from Pacbio Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 220-225.	3.0	12
13	Integrated Genome-Scale Analysis Identifies Novel Genes and Networks Underlying Senescence in Maize. Plant Cell, 2019, 31, 1968-1989.	6.6	63
14	EPGA-SC : A framework for de novo assembly of single-cell sequencing reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 18, 1-1.	3.0	3
15	DeepSignal: detecting DNA methylation state from Nanopore sequencing reads using deep-learning. Bioinformatics, 2019, 35, 4586-4595.	4.1	158
16	A Novel Method to Efficiently Highlight Nonlinearly Expressed Genes. Frontiers in Genetics, 2019, 10, 1410.	2.3	3
17	Prediction of lncRNA“disease associations based on inductive matrix completion. Bioinformatics, 2018, 34, 3357-3364.	4.1	227
18	BioRank: A Similarity Assessment Method for Single Cell Clustering. , 2018, , .		1

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19	N6-Methyladenine DNA modification in <i>Xanthomonas oryzae</i> pv. <i>oryzicola</i> genome. <i>Scientific Reports</i> , 2018, 8, 16272.	3.3	18
20	A Rare De Novo RAI1 Gene Mutation Affecting BDNF-Enhancer-Driven Transcription Activity Associated with Autism and Atypical Smith-Magenis Syndrome Presentation. <i>Biology</i> , 2018, 7, 31.	2.8	14
21	MECAT: fast mapping, error correction, and de novo assembly for single-molecule sequencing reads. <i>Nature Methods</i> , 2017, 14, 1072-1074.	19.0	357
22	Dynamic Management of In-Memory Storage for Efficiently Integrating Compute-and Data-Intensive Computing on HPC Systems. , 2017, , .		1
23	Accelerating big data analytics on HPC clusters using two-level storage. <i>Parallel Computing</i> , 2017, 61, 18-34.	2.1	19
24	Identifying and sequencing a <i>Mycobacterium</i> sp. strain F4 as a potential bioremediation agent for quinclorac. <i>PLoS ONE</i> , 2017, 12, e0185721.	2.5	6
25	A New Algorithm to Optimize Maximal Information Coefficient. <i>PLoS ONE</i> , 2016, 11, e0157567.	2.5	20
26	Association analyses of large-scale glycan microarray data reveal novel host-specific substructures in influenza A virus binding glycans. <i>Scientific Reports</i> , 2015, 5, 15778.	3.3	18
27	Genome-Wide Comparative Analysis Reveals Similar Types of NBS Genes in Hybrid <i>Citrus sinensis</i> Genome and Original <i>Citrus clementine</i> Genome and Provides New Insights into Non-TIR NBS Genes. <i>PLoS ONE</i> , 2015, 10, e0121893.	2.5	9
28	Predicting protein phosphorylation from gene expression: top methods from the IMPROVER Species Translation Challenge. <i>Bioinformatics</i> , 2015, 31, 462-470.	4.1	14
29	Isolation, Identification and Characteristics of an Endophytic Quinclorac Degrading Bacterium <i>Bacillus megaterium</i> Q3. <i>PLoS ONE</i> , 2014, 9, e108012.	2.5	26
30	A quantitative structure-activity relationship (QSAR) study on glycan array data to determine the specificities of glycan-binding proteins. <i>Glycobiology</i> , 2012, 22, 552-560.	2.5	22
31	Predicting synthetic lethal genetic interactions in <i>Saccharomyces cerevisiae</i> using short polypeptide clusters. <i>Proteome Science</i> , 2012, 10, S4.	1.7	3
32	Understanding and predicting synthetic lethal genetic interactions in <i>Saccharomyces cerevisiae</i> using domain genetic interactions. <i>BMC Systems Biology</i> , 2011, 5, 73.	3.0	12
33	Identifying differentially expressed genes in cancer patients using a non-parameter Ising model. <i>Proteomics</i> , 2011, 11, 3845-3852.	2.2	6
34	Core and periphery structures in protein interaction networks. <i>BMC Bioinformatics</i> , 2009, 10, S8.	2.6	36
35	Modular organization of protein interaction networks. <i>Bioinformatics</i> , 2007, 23, 207-214.	4.1	151
36	Constructing gene co-expression networks and predicting functions of unknown genes by random matrix theory. <i>BMC Bioinformatics</i> , 2007, 8, 299.	2.6	221

#	ARTICLE	IF	CITATIONS
37	Exploring Local Community Structures in Large Networks. , 2006, , .		63
38	Detecting Functional Modules from Protein Interaction Networks. , 2006, , .		1
39	Application of random matrix theory to microarray data for discovering functional gene modules. Physical Review E, 2006, 73, 031924.	2.1	63