

Yunpeng Cai

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

700
citations

1040056

9
h-index

1058476

14
g-index

19
all docs

19
docs citations

19
times ranked

1063
citing authors

#	ARTICLE	IF	CITATIONS
1	ESPRIT: estimating species richness using large collections of 16S rRNA pyrosequences. <i>Nucleic Acids Research</i> , 2009, 37, e76-e76.	14.5	232
2	A large-scale benchmark study of existing algorithms for taxonomy-independent microbial community analysis. <i>Briefings in Bioinformatics</i> , 2012, 13, 107-121.	6.5	133
3	ESPRIT-Tree: hierarchical clustering analysis of millions of 16S rRNA pyrosequences in quasilinear computational time. <i>Nucleic Acids Research</i> , 2011, 39, e95-e95.	14.5	131
4	Advanced computational algorithms for microbial community analysis using massive 16S rRNA sequence data. <i>Nucleic Acids Research</i> , 2010, 38, e205-e205.	14.5	43
5	Accurate Prediction of Coronary Heart Disease for Patients With Hypertension From Electronic Health Records With Big Data and Machine-Learning Methods: Model Development and Performance Evaluation. <i>JMIR Medical Informatics</i> , 2020, 8, e17257.	2.6	34
6	Secondary structure information does not improve OTU assignment for partial 16s rRNA sequences. <i>ISME Journal</i> , 2012, 6, 1277-1280.	9.8	24
7	The Relationship between the 24h Blood Pressure Variability and Carotid Intima-Media Thickness: A Compared Study. <i>Computational and Mathematical Methods in Medicine</i> , 2014, 2014, 1-9.	1.3	21
8	CRISPRdigger: detecting CRISPRs with better direct repeat annotations. <i>Scientific Reports</i> , 2016, 6, 32942.	3.3	19
9	ESPRIT-Forest: Parallel clustering of massive amplicon sequence data in subquadratic time. <i>PLoS Computational Biology</i> , 2017, 13, e1005518.	3.2	16
10	Heterogeneous Graph Convolutional Networks and Matrix Completion for miRNA-Disease Association Prediction. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 901.	4.1	10
11	Parallel Hierarchical Clustering in Linearithmic Time for Large-Scale Sequence Analysis. , 2015, , .		8
12	A parallel computational framework for ultra-large-scale sequence clustering analysis. <i>Bioinformatics</i> , 2019, 35, 380-388.	4.1	8
13	Risk Prediction of Renal Failure for Chronic Disease Population Based on Electronic Health Record Big Data. <i>Big Data Research</i> , 2021, 25, 100234.	4.2	7
14	Sparse Weighted Naive Bayes Classifier for Efficient Classification of Categorical Data. , 2018, , .		5
15	Accurate Prediction of Stroke for Hypertensive Patients Based on Medical Big Data and Machine Learning Algorithms: Retrospective Study. <i>JMIR Medical Informatics</i> , 2021, 9, e30277.	2.6	4
16	Estimation of Hypertension Risk from Lifestyle Factors and Health Profile: A Case Study. <i>Scientific World Journal</i> , The, 2014, 2014, 1-10.	2.1	3
17	An efficient automatic electrocardiogram analysis method using smartphones. , 2018, , .		1