

Congmin Zhu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

39
papers

823
citations

13
h-index

28
g-index

49
ext. papers

1,391
ext. citations

9.2
avg, IF

4.02
L-index

#	Paper	IF	Citations
39	Clinically Applicable AI System for Accurate Diagnosis, Quantitative Measurements, and Prognosis of COVID-19 Pneumonia Using Computed Tomography. <i>Cell</i> , 2020 , 181, 1423-1433.e11	56.2	314
38	Reconstructing cell cycle pseudo time-series via single-cell transcriptome data. <i>Nature Communications</i> , 2017 , 8, 22	17.4	67
37	Subgingival microbiome in patients with healthy and ailing dental implants. <i>Scientific Reports</i> , 2015 , 5, 10948	4.9	59
36	Evaluation of different 16S rRNA gene V regions for exploring bacterial diversity in a eutrophic freshwater lake. <i>Science of the Total Environment</i> , 2018 , 618, 1254-1267	10.2	50
35	Genome and epigenome of a novel marine Thaumarchaeota strain suggest viral infection, phosphorothioation DNA modification and multiple restriction systems. <i>Environmental Microbiology</i> , 2017 , 19, 2434-2452	5.2	44
34	Seasonal succession and spatial distribution of bacterial community structure in a eutrophic freshwater Lake, Lake Taihu. <i>Science of the Total Environment</i> , 2019 , 669, 29-40	10.2	39
33	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study. <i>PLoS Medicine</i> , 2020 , 17, e1003188	11.6	31
32	Inference of Environmental Factor-Microbe and Microbe-Microbe Associations from Metagenomic Data Using a Hierarchical Bayesian Statistical Model. <i>Cell Systems</i> , 2017 , 4, 129-137.e5	10.6	26
31	A deep-learning pipeline for the diagnosis and discrimination of viral, non-viral and COVID-19 pneumonia from chest X-ray images. <i>Nature Biomedical Engineering</i> , 2021 , 5, 509-521	19	25
30	Microbial profiles of a drinking water resource based on different 16S rRNA V regions during a heavy cyanobacterial bloom in Lake Taihu, China. <i>Environmental Science and Pollution Research</i> , 2017 , 24, 12796-12808	5.1	22
29	Ambient fine particulate matter and hospital admissions for ischemic and hemorrhagic strokes and transient ischemic attack in 248 Chinese cities. <i>Science of the Total Environment</i> , 2020 , 715, 136896	10.2	19
28	Deep-learning models for the detection and incidence prediction of chronic kidney disease and type 2 diabetes from retinal fundus images. <i>Nature Biomedical Engineering</i> , 2021 , 5, 533-545	19	16
27	Alternate succession of aggregate-forming cyanobacterial genera correlated with their attached bacteria by co-pathways. <i>Science of the Total Environment</i> , 2019 , 688, 867-879	10.2	14
26	Distinct Gut Microbiota Induced by Different Fat-to-Sugar-Ratio High-Energy Diets Share Similar Pro-obesity Genetic and Metabolite Profiles in Prediabetic Mice. <i>MSystems</i> , 2019 , 4,	7.6	11
25	Large-scale 16S gene assembly using metagenomics shotgun sequences. <i>Bioinformatics</i> , 2017 , 33, 1447-1456	14.56	9
24	Simultaneous inference of phenotype-associated genes and relevant tissues from GWAS data via Bayesian integration of multiple tissue-specific gene networks. <i>Journal of Molecular Cell Biology</i> , 2017 , 9, 436-452	6.3	9
23	Prioritization Of Nonsynonymous Single Nucleotide Variants For Exome Sequencing Studies Via Integrative Learning On Multiple Genomic Data. <i>Scientific Reports</i> , 2015 , 5, 14955	4.9	8

22	Leveraging multiple gene networks to prioritize GWAS candidate genes via network representation learning. <i>Methods</i> , 2018 , 145, 41-50	4.6	7
21	Ontology-based venous thromboembolism risk assessment model developing from medical records. <i>BMC Medical Informatics and Decision Making</i> , 2019 , 19, 151	3.6	7
20	Reading the Underlying Information From Massive Metagenomic Sequencing Data. <i>Proceedings of the IEEE</i> , 2016 , 1-15	14.3	7
19	Responses of cyanobacterial aggregate microbial communities to algal blooms. <i>Water Research</i> , 2021 , 196, 117014	12.5	6
18	DACE: a scalable DP-means algorithm for clustering extremely large sequence data. <i>Bioinformatics</i> , 2017 , 33, 834-842	7.2	6
17	Dropout training for SVMs with data augmentation. <i>Frontiers of Computer Science</i> , 2018 , 12, 694-713	2.2	4
16	Effect of k-tuple length on sample-comparison with high-throughput sequencing data. <i>Biochemical and Biophysical Research Communications</i> , 2016 , 469, 1021-7	3.4	4
15	GePMI: A statistical model for personal intestinal microbiome identification. <i>Npj Biofilms and Microbiomes</i> , 2018 , 4, 20	8.2	4
14	Leveraging multiple genomic data to prioritize disease-causing indels from exome sequencing data. <i>Scientific Reports</i> , 2017 , 7, 1804	4.9	3
13	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. <i>BMC Bioinformatics</i> , 2019 , 20, 678	3.6	3
12	Determine independent gut microbiota-diseases association by eliminating the effects of human lifestyle factors.. <i>BMC Microbiology</i> , 2022 , 22, 4	4.5	2
11	scAIDE: clustering of large-scale single-cell RNA-seq data reveals putative and rare cell types. <i>NAR Genomics and Bioinformatics</i> , 2020 , 2, lqaa082	3.7	1
10	DeepTriager: A Neural Attention Model for Emergency Triage with Electronic Health Records 2019 ,		1
9	DCMN: Double Core Memory Network for Patient Outcome Prediction with Multimodal Data 2019 ,		1
8	Ontology-based Venous Thromboembolism Risk Factors Mining and Model Developing from Medical Records 2018 ,		1
7	Determine independent gut microbiota-diseases association by eliminating the effects of human lifestyle factors		1
6	redPATH: Reconstructing the Pseudo Development Time of Cell Lineages in Single-cell RNA-seq Data and Applications in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2021 , 19, 292-305	6.5	0
5	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study 2020 , 17, e1003188		

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