Congmin Zhu

List of Publications by Year in Descending Order

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	Determine independent gut microbiota-diseases association by eliminating the effects of human lifestyle factors.. *BMC Microbiology*, **2022**, 22, 4	4.5	2
38	A deep-learning pipeline for the diagnosis and discrimination of viral, non-viral and COVID-19 pneumonia from chest X-ray images. *Nature Biomedical Engineering*, **2021**, 5, 509-521	19	25
37	Responses of cyanobacterial aggregate microbial communities to algal blooms. *Water Research*, **2021**, 196, 117014	12.5	6
36	Deep-learning models for the detection and incidence prediction of chronic kidney disease and type 2 diabetes from retinal fundus images. *Nature Biomedical Engineering*, **2021**, 5, 533-545	19	16
35	redPATH: Reconstructing the Pseudo Development Time of Cell Lineages in Single-cell RNA-seq Data and Applications in Cancer. *Genomics, Proteomics and Bioinformatics*, **2021**, 19, 292-305	6.5	0
34	scAIDE: clustering of large-scale single-cell RNA-seq data reveals putative and rare cell types. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa082	3.7	1
33	Clinically Applicable AI System for Accurate Diagnosis, Quantitative Measurements, and Prognosis of COVID-19 Pneumonia Using Computed Tomography. *Cell*, **2020**, 181, 1423-1433.e11	56.2	314
32	Ambient fine particulate matter and hospital admissions for ischemic and hemorrhagic strokes and transient ischemic attack in 248 Chinese cities. *Science of the Total Environment*, **2020**, 715, 136896	10.2	19
31	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study. *PLoS Medicine*, **2020**, 17, e1003188	11.6	31
30	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study **2020**, 17, e1003188		
29	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study **2020**, 17, e1003188		
28	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study **2020**, 17, e1003188		
27	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study **2020**, 17, e1003188		
26	Ambient air pollution and cause-specific risk of hospital admission in China: A nationwide time-series study **2020**, 17, e1003188		
25	Seasonal succession and spatial distribution of bacterial community structure in a eutrophic freshwater Lake, Lake Taihu. *Science of the Total Environment*, **2019**, 669, 29-40	10.2	39
24	Alternate succession of aggregate-forming cyanobacterial genera correlated with their attached bacteria by co-pathways. *Science of the Total Environment*, **2019**, 688, 867-879	10.2	14
23	Ontology-based venous thromboembolism risk assessment model developing from medical records. *BMC Medical Informatics and Decision Making*, **2019**, 19, 151	3.6	7

22	Distinct Gut Microbiota Induced by Different Fat-to-Sugar-Ratio High-Energy Diets Share Similar Pro-obesity Genetic and Metabolite Profiles in Prediabetic Mice. *MSystems*, **2019**, 4,	7.6	11
21	DeepTriager: A Neural Attention Model for Emergency Triage with Electronic Health Records **2019**,		1
20	DCMN: Double Core Memory Network for Patient Outcome Prediction with Multimodal Data **2019**,		1
19	DeepShape: estimating isoform-level ribosome abundance and distribution with Ribo-seq data. *BMC Bioinformatics*, **2019**, 20, 678	3.6	3
18	Dropout training for SVMs with data augmentation. *Frontiers of Computer Science*, **2018**, 12, 694-713	2.2	4
17	Evaluation of different 16S rRNA gene V regions for exploring bacterial diversity in a eutrophic freshwater lake. *Science of the Total Environment*, **2018**, 618, 1254-1267	10.2	50
16	Leveraging multiple gene networks to prioritize GWAS candidate genes via network representation learning. *Methods*, **2018**, 145, 41-50	4.6	7
15	Ontology-based Venous Thromboembolism Risk Factors Mining and Model Developing from Medical Records **2018**,		1
14	GePMI: A statistical model for personal intestinal microbiome identification. *Npj Biofilms and Microbiomes*, **2018**, 4, 20	8.2	4
13	Inference of Environmental Factor-Microbe and Microbe-Microbe Associations from Metagenomic Data Using a Hierarchical Bayesian Statistical Model. *Cell Systems*, **2017**, 4, 129-137.e5	10.6	26
12	Genome and epigenome of a novel marine Thaumarchaeota strain suggest viral infection, phosphorothioation DNA modification and multiple restriction systems. *Environmental Microbiology*, **2017**, 19, 2434-2452	5.2	44
11	Reconstructing cell cycle pseudo time-series via single-cell transcriptome data. *Nature Communications*, **2017**, 8, 22	17.4	67
10	Microbial profiles of a drinking water resource based on different 16S rRNA V regions during a heavy cyanobacterial bloom in Lake Taihu, China. *Environmental Science and Pollution Research*, **2017**, 24, 12796-12808	5.1	22
9	Large-scale 16S gene assembly using metagenomics shotgun sequences. *Bioinformatics*, **2017**, 33, 1447-1456	7.3	9
8	Leveraging multiple genomic data to prioritize disease-causing indels from exome sequencing data. *Scientific Reports*, **2017**, 7, 1804	4.9	3
7	Simultaneous inference of phenotype-associated genes and relevant tissues from GWAS data via Bayesian integration of multiple tissue-specific gene networks. *Journal of Molecular Cell Biology*, **2017**, 9, 436-452	6.3	9
6	DACE: a scalable DP-means algorithm for clustering extremely large sequence data. *Bioinformatics*, **2017**, 33, 834-842	7.2	6
5	Effect of k-tuple length on sample-comparison with high-throughput sequencing data. *Biochemical and Biophysical Research Communications*, **2016**, 469, 1021-7	3.4	4

4	Reading the Underlying Information From Massive Metagenomic Sequencing Data. *Proceedings of the IEEE*, **2016**, 1-15	14.3	7
3	Subgingival microbiome in patients with healthy and ailing dental implants. *Scientific Reports*, **2015**, 5, 10948	4.9	59
2	Prioritization Of Nonsynonymous Single Nucleotide Variants For Exome Sequencing Studies Via Integrative Learning On Multiple Genomic Data. *Scientific Reports*, **2015**, 5, 14955	4.9	8
1	Determine independent gut microbiota-diseases association by eliminating the effects of human lifestyle factors		1