Qiyun Zhu

List of Publications by Citations

71 papers	8,408 citations	26 h-index	81 g-index
81 ext. papers	14,739 ext. citations	15.3 avg, IF	5.36 L-index

#	Paper	IF	Citations
71	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
70	A communal catalogue reveals Earth's multiscale microbial diversity. *Nature*, **2017**, 551, 457-463	50.4	1076
69	Best practices for analysing microbiomes. *Nature Reviews Microbiology*, **2018**, 16, 410-422	22.2	668
68	American Gut: an Open Platform for Citizen Science Microbiome Research. *MSystems*, **2018**, 3,	7.6	336
67	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. *Nature*, **2020**, 579, 567-574	50.4	244
66	Evaluating the Information Content of Shallow Shotgun Metagenomics. *MSystems*, **2018**, 3,	7.6	175
65	FXR Regulates Intestinal Cancer Stem Cell Proliferation. *Cell*, **2019**, 176, 1098-1112.e18	56.2	151
64	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
63	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. *Nature Communications*, **2020**, 11, 2500	17.4	99
62	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. *Nature Communications*, **2019**, 10, 5477	17.4	89
61	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. *MSystems*, **2018**, 3,	7.6	74
60	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. *Nature Methods*, **2021**, 18, 165-169	21.6	67
59	Origin of microbial biomineralization and magnetotaxis during the Archean. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 2171-2176	11.5	66
58	Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. *Molecular Phylogenetics and Evolution*, **2015**, 90, 129-39	4.1	66
57	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. *Current Protocols in Bioinformatics*, **2020**, 70, e100	24.2	63
56	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. *BMC Genomics*, **2014**, 15, 717	4.5	62
55	Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. *European Psychiatry*, **2018**, 53, 37-45	6	54

54	Bartonella spp. in fruit bats and blood-feeding Ectoparasites in Madagascar. *PLoS Neglected Tropical Diseases*, **2015**, 9, e0003532	4.8	52
53	Motif-blind, genome-wide discovery of cis-regulatory modules in Drosophila and mouse. *Developmental Cell*, **2009**, 17, 568-79	10.2	51
52	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. *Nature Communications*, **2018**, 9, 2832	17.4	50
51	Home chemical and microbial transitions across urbanization. *Nature Microbiology*, **2020**, 5, 108-115	26.6	43
50	Methods for phylogenetic analysis of microbiome data. *Nature Microbiology*, **2018**, 3, 652-661	26.6	43
49	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
48	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. *Nature Chemical Biology*, **2021**, 17, 146-151	11.7	29
47	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. *Nucleic Acids Research*, **2011**, 39, 9463-72	20.1	27
46	A gut-derived metabolite alters brain activity and anxiety behaviour in mice.. *Nature*, **2022**,	50.4	25
45	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. *MSystems*, **2019**, 4,	7.6	24
44	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. *Genome Biology*, **2019**, 20, 226	18.3	24
43	Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing		24
42	Metagenomics-Based, Strain-Level Analysis of From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. *Frontiers in Microbiology*, **2018**, 9, 2559	5.7	24
41	Creating a 3D microbial and chemical snapshot of a human habitat. *Scientific Reports*, **2018**, 8, 3669	4.9	23
40	Calour: an Interactive, Microbe-Centric Analysis Tool. *MSystems*, **2019**, 4,	7.6	20
39	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. *Environmental Science & Technology*, **2021**, 55, 4899-4913	10.3	20
38	Are microbiome studies ready for hypothesis-driven research?. *Current Opinion in Microbiology*, **2018**, 44, 61-69	7.9	18
37	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort.. *Nature Genetics*, **2022**, 54, 134-142	36.3	18

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36	Expanding magnetic organelle biogenesis in the domain Bacteria. *Microbiome*, **2020**, 8, 152	16.6	18
35	Challenges in benchmarking metagenomic profilers. *Nature Methods*, **2021**, 18, 618-626	21.6	15
34	Horizontal transfers and gene losses in the phospholipid pathway of bartonella reveal clues about early ecological niches. *Genome Biology and Evolution*, **2014**, 6, 2156-69	3.9	14
33	Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity **2020**,		14
32	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. *MSystems*, **2021**, 6,	7.6	14
31	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. *Bioinformatics*, **2020**, 36, 4088-4090	7.2	13
30	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity.. *Nature Microbiology*, **2022**,	26.6	13
29	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (Oreochromis shiranus) and North African catfish (Clarias gariepinus). *MicrobiologyOpen*, **2018**, 7, e00716	3.4	13
28	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
27	Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. *ISME Journal*, **2021**, 15, 3005-3018	11.9	11
26	Early prediction of liver disease using conventional risk factors and gut microbiome-augmented gradient boosting		10
25	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. *Microbiome*, **2018**, 6, 201	16.6	10
24	The origin of Chinese domestic horses revealed with novel mtDNA variants. *Animal Science Journal*, **2017**, 88, 19-26	1.8	9
23	DEPP: Deep Learning Enables Extending Species Trees using Single Genes		9
22	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7
21	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. *ISME Journal*, **2021**, 15, 3399-3411	11.9	7
20	On the probability of dinosaur fleas. *BMC Evolutionary Biology*, **2016**, 16, 9	3	6
19	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. *Marine Drugs*, **2021**, 19,	6	6

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18	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		5
17	Candidate probiotic Lactiplantibacillus plantarum HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. *Microbiome*, **2021**, 9, 151	16.6	5
16	Reference data based insights expand understanding of human metabolomes		4
15	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort		4
14	Fast and accurate distance-based phylogenetic placement using divide and conquer. *Molecular Ecology Resources*, **2021**,	8.4	3
13	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
12	Evaluating the information content of shallow shotgun metagenomics		3
11	Multi-omics profiling of Earth biomes reveals that microbial and metabolite composition are shaped by the environment		3
10	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. *Genome Research*, **2021**, 31, 2131-2137	9.7	3
9	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. *MSystems*, **2022**, e0016722	7.6	3
8	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting.. *Cell Metabolism*, **2022**,	24.6	2
7	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients.. *Cellular and Molecular Gastroenterology and Hepatology*, **2022**,	7.9	2
6	Reply to Wang and Chen: An ancient origin of magnetotactic bacteria. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, E5019-E5020	11.5	1
5	Expanding magnetic organelle biogenesis in the domain Bacteria		1
4	APPLES-2: Faster and More Accurate Distance-based Phylogenetic Placement using Divide and Conquer		1
3	Microbiome and metabolome profiles of high screen time in a cohort of healthy college students.. *Scientific Reports*, **2022**, 12, 3452	4.9	0
2	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases.. *MSystems*, **2022**, e0137821	7.6	0
1	RNA: An Expanding View of Function and Evolution. *Evolutionary Bioinformatics*, **2015**, 11, 77-9	1.9	