

Qiyun Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

20,354
citations

136950

32
h-index

138484

58
g-index

81
all docs

81
docs citations

81
times ranked

23993
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
2	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	27.8	1,942
3	Best practices for analysing microbiomes. Nature Reviews Microbiology, 2018, 16, 410-422.	28.6	1,138
4	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. Nature, 2020, 579, 567-574.	27.8	691
5	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	3.8	604
6	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. Nature Communications, 2020, 11, 2500.	12.8	368
7	Evaluating the Information Content of Shallow Shotgun Metagenomics. MSystems, 2018, 3, .	3.8	293
8	FXR Regulates Intestinal Cancer Stem Cell Proliferation. Cell, 2019, 176, 1098-1112.e18.	28.9	291
9	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.	25.8	212
10	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	19.0	198
11	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	12.8	197
12	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. Nature, 2022, 602, 647-653.	27.8	179
13	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.	21.4	164
14	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. MSystems, 2018, 3, .	3.8	123
15	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. BMC Genomics, 2014, 15, 717.	2.8	122
16	Multi-omics analyses of the ulcerative colitis gut microbiome link Bacteroides vulgatus proteases with disease severity. Nature Microbiology, 2022, 7, 262-276.	13.3	110
17	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. Nature Communications, 2018, 9, 2832.	12.8	108
18	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.	7.1	98

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19	Gut microbiome and magnetic resonance spectroscopy study of subjects at ultra-high risk for psychosis may support the membrane hypothesis. <i>European Psychiatry</i> , 2018, 53, 37-45.	0.2	88
20	Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 129-139.	2.7	85
21	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020, 5, 108-115.	13.3	83
22	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	8.0	73
23	<i>Bartonella</i> spp. in Fruit Bats and Blood-Feeding Ectoparasites in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003532.	3.0	71
24	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science & Technology</i> , 2021, 55, 4899-4913.	10.0	71
25	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	13.3	68
26	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	19.0	63
27	Motif-Blind, Genome-Wide Discovery of cis-Regulatory Modules in <i>Drosophila</i> and Mouse. <i>Developmental Cell</i> , 2009, 17, 568-579.	7.0	60
28	Insight into the function and evolution of the Wood–Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	9.8	55
29	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	8.8	47
30	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020, 8, 152.	11.1	44
31	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020, 36, 4088-4090.	4.1	42
32	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019, 4, .	3.8	40
33	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. <i>Nucleic Acids Research</i> , 2011, 39, 9463-9472.	14.5	37
34	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	3.5	37
35	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	3.8	36
36	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting. <i>Cell Metabolism</i> , 2022, 34, 719-730.e4.	16.2	35

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37	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	3.8	35
38	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	3.3	34
39	Candidate probiotic <i>Lactiplantibacillus plantarum</i> HNU082 rapidly and convergently evolves within human, mice, and zebrafish gut but differentially influences the resident microbiome. <i>Microbiome</i> , 2021, 9, 151.	11.1	30
40	Compositional and genetic alterations in Graves's disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	9.8	30
41	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	3.8	28
42	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	5.1	27
43	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	4.8	25
44	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	17.5	25
45	Horizontal Transfers and Gene Losses in the Phospholipid Pathway of <i>Bartonella</i> Reveal Clues about Early Ecological Niches. <i>Genome Biology and Evolution</i> , 2014, 6, 2156-2169.	2.5	23
46	Microbial effects of livestock manure fertilization on freshwater aquaculture ponds rearing tilapia (<i>Oreochromis shiranus</i>) and North African catfish (<i>Clarias gariepinus</i>). <i>MicrobiologyOpen</i> , 2018, 7, e00716.	3.0	23
47	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, 201.	11.1	20
48	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	4.6	19
49	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.5	16
50	The origin of Chinese domestic horses revealed with novel mtDNA variants. <i>Animal Science Journal</i> , 2017, 88, 19-26.	1.4	13
51	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	5.6	11
52	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 35-53.	4.5	10
53	Microbiome and metabolome profiles of high screen time in a cohort of healthy college students. <i>Scientific Reports</i> , 2022, 12, 3452.	3.3	8
54	On the probability of dinosaur fleas. <i>BMC Evolutionary Biology</i> , 2016, 16, 9.	3.2	7

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55	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.	7.1	3
56	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. MSystems, 2022, 7, e0137821.	3.8	3
57	Abstract 3054: Pan-cancer characterization of the tumor mycobiome and its clinical effects. Cancer Research, 2022, 82, 3054-3054.	0.9	1
58	RNA: An Expanding View of Function and Evolution. Evolutionary Bioinformatics, 2015, 11s1, EBO.S38105.	1.2	0