

Qiyun Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

58
papers

20,354
citations

136885

32
h-index

138417

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. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
3	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
4	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020, 579, 567-574.	13.7	691
5	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
6	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, 2500.	5.8	368
7	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	1.7	293
8	FXR Regulates Intestinal Cancer Stem Cell Proliferation. <i>Cell</i> , 2019, 176, 1098-1112.e18.	13.5	291
9	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
10	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	9.0	198
11	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	5.8	197
12	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. <i>Nature</i> , 2022, 602, 647-653.	13.7	179
13	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort. <i>Nature Genetics</i> , 2022, 54, 134-142.	9.4	164
14	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	1.7	123
15	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. <i>BMC Genomics</i> , 2014, 15, 717.	1.2	122
16	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity. <i>Nature Microbiology</i> , 2022, 7, 262-276.	5.9	110
17	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018, 9, 2832.	5.8	108
18	Origin of microbial biomineralization and magnetotaxis during the Archean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 2171-2176.	3.3	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.	0.1	88
20	Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 129-139.	1.2	85
21	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020, 5, 108-115.	5.9	83
22	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	3.9	73
23	<i>Bartonella</i> spp. in Fruit Bats and Blood-Feeding Ectoparasites in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003532.	1.3	71
24	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science & Technology</i> , 2021, 55, 4899-4913.	4.6	71
25	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	5.9	68
26	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	9.0	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.	3.1	60
28	Insight into the function and evolution of the Woodá€“Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	4.4	55
29	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	3.8	47
30	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020, 8, 152.	4.9	44
31	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020, 36, 4088-4090.	1.8	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, .	1.7	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.	6.5	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.	1.5	37
35	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	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.	7.2	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.	1.7	35
38	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, 3669.	1.6	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.	4.9	30
40	Compositional and genetic alterations in Gravesâ€™ disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	4.4	30
41	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	1.7	28
42	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
43	Fast and accurate distanceâ€based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	2.2	25
44	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	9.4	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.	1.1	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.	1.2	23
47	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelersâ€™ diarrhea. <i>Microbiome</i> , 2018, 6, 201.	4.9	20
48	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
49	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
50	The origin of Chinese domestic horses revealed with novel mtDNA variants. <i>Animal Science Journal</i> , 2017, 88, 19-26.	0.6	13
51	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	2.7	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.	2.3	10
53	Microbiome and metabolome profiles of high screen time in a cohort of healthy college students. <i>Scientific Reports</i> , 2022, 12, 3452.	1.6	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.	3.3	3
56	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. MSystems, 2022, 7, e0137821.	1.7	3
57	Abstract 3054: Pan-cancer characterization of the tumor mycobiome and its clinical effects. Cancer Research, 2022, 82, 3054-3054.	0.4	1
58	RNA: An Expanding View of Function and Evolution. Evolutionary Bioinformatics, 2015, 11s1, EBO.S38105.	0.6	0