

# Qiyun Zhu

## List of PR Articles by Year in descending order

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55

PR articles

8,615

PR citations

75308

36

PR h-index

132421

54

g-index

60

documents

26384

doc citations

79788

38

h-index

36002

citing authors

#	ARTICLE	IF	PR CITATIONS
1	A conserved interdomain microbial network underpins cadaver decomposition despite environmental variables. <i>Nature Microbiology</i> , 2024, 9, 595-613.	16.5	56
2	An evolutionary optimum amid moderate heritability in prokaryotic cell size. <i>Cell Reports</i> , 2024, 43, 114268.	6.4	7
3	DEPP: Deep Learning Enables Extending Species Trees using Single Genes. <i>Systematic Biology</i> , 2023, 72, 17-34.	5.1	27
4	Greengenes2 unifies microbial data in a single reference tree. <i>Nature Biotechnology</i> , 2023, 42, 715-718.	32.2	421
5	Generation of accurate, expandable phylogenomic trees with uDance. <i>Nature Biotechnology</i> , 2023, 42, 768-777.	32.2	17
6	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2022, 22, 1213-1227.	4.8	37
7	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.	16.5	307
8	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.	26.1	461
9	A gut-derived metabolite alters brain activity and anxiety behaviour in mice. <i>Nature</i> , 2022, 602, 647-653.	38.7	393
10	Microbiome and metabolome profiles of high screen time in a cohort of healthy college students. <i>Scientific Reports</i> , 2022, 12, .	3.5	19
11	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.	26.2	73
12	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, .	4.5	103
13	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022, 14, 35-53.	5.7	20
14	Abstract 3054: Pan-cancer characterization of the tumor mycobiome and its clinical effects. <i>Cancer Research</i> , 2022, 82, 3054-3054.	0.6	1
15	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	32.2	65
16	Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. <i>Nature Microbiology</i> , 2022, 7, 2128-2150.	16.5	153
17	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	25.9	361
18	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	5.3	31

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19	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science &amp; Technology</i> , 2021, 55, 4899-4913.	11.1	114
20	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	4.5	52
21	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021, 18, 618-626.	25.9	116
22	Insight into the function and evolution of the Woodâ€™Ljungdahl pathway in <i>Actinobacteria</i> . <i>ISME Journal</i> , 2021, 15, 3005-3018.	9.1	118
23	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, .	11.5	59
24	Compositional and genetic alterations in Gravesâ€™ disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021, 15, 3399-3411.	9.1	57
25	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	4.6	40
26	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020, 8, .	11.5	69
27	SHOGLIN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020, 36, 4088-4090.	4.8	65
28	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020, 11, .	13.9	704
29	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2020, 17, 146-151.	12.0	103
30	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, .	8.2	72
31	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	4.5	33
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, .	4.5	53
33	FXR Regulates Intestinal Cancer Stem Cell Proliferation. <i>Cell</i> , 2019, 176, 1098-1112.e18.	34.1	401
34	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, .	13.9	329
35	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018, 8, .	3.5	43
36	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018, 3, .	4.5	142

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37	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018, 6, .	11.5	24
38	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018, 3, .	4.5	415
39	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, .	3.9	44
40	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, .	4.2	33
41	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	4.5	789
42	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	85.9	1,555
43	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	16.5	91
44	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	7.0	30
45	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018, 9, .	13.9	144
46	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.	0.3	113
47	The origin of Chinese domestic horses revealed with novel mtDNA variants. <i>Animal Science Journal</i> , 2017, 88, 19-26.	1.1	19
48	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.	7.6	125
49	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	38.7	2,576
50	Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. <i>Molecular Phylogenetics and Evolution</i> , 2015, 90, 129-139.	2.9	113
51	<i>Bartonella</i> spp. in Fruit Bats and Blood-Feeding Ectoparasites in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2015, 9, e0003532.	3.1	83
52	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.	2.4	26
53	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. <i>BMC Genomics</i> , 2014, 15, 717.	3.3	165
54	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. <i>Nucleic Acids Research</i> , 2011, 39, 9463-9472.	15.7	46

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55	Motif-Blind, Genome-Wide Discovery of cis-Regulatory Modules in Drosophila and Mouse. <i>Developmental Cell</i> , 2009, 17, 568-579.	7.8	67