

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Multi-omics analyses of the ulcerative colitis gut microbiome link <i>Bacteroides vulgatus</i> proteases with disease severity.. <i>Nature Microbiology</i> , 2022 ,	26.6	13
70	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	36.3	18
69	A gut-derived metabolite alters brain activity and anxiety behaviour in mice.. <i>Nature</i> , 2022 ,	50.4	25
68	Microbiome and metabolome profiles of high screen time in a cohort of healthy college students.. <i>Scientific Reports</i> , 2022 , 12, 3452	4.9	0
67	Early prediction of incident liver disease using conventional risk factors and gut-microbiome-augmented gradient boosting.. <i>Cell Metabolism</i> , 2022 ,	24.6	2
66	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases.. <i>MSystems</i> , 2022 , e0137821	7.6	0
65	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , 2022 , e0016722	7.6	3
64	The Host-Microbiome Response to Hyperbaric Oxygen Therapy in Ulcerative Colitis Patients.. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2022 ,	7.9	2
63	Fast and accurate distance-based phylogenetic placement using divide and conquer. <i>Molecular Ecology Resources</i> , 2021 ,	8.4	3
62	Exploring the Composition and Functions of Plastic Microbiome Using Whole-Genome Sequencing. <i>Environmental Science & Technology</i> , 2021 , 55, 4899-4913	10.3	20
61	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021 , 6,	7.6	14
60	Challenges in benchmarking metagenomic profilers. <i>Nature Methods</i> , 2021 , 18, 618-626	21.6	15
59	Insight into the function and evolution of the Wood-Ljungdahl pathway in Actinobacteria. <i>ISME Journal</i> , 2021 , 15, 3005-3018	11.9	11
58	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	16.6	5
57	Compositional and genetic alterations in Graves' disease gut microbiome reveal specific diagnostic biomarkers. <i>ISME Journal</i> , 2021 , 15, 3399-3411	11.9	7
56	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021 , 17, 146-151	11.7	29
55	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021 , 18, 165-169	21.6	67

54	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021 , 19,	6	6
53	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021 , 31, 2131-2137	9.7	3
52	SHOGUN: a modular, accurate and scalable framework for microbiome quantification. <i>Bioinformatics</i> , 2020 , 36, 4088-4090	7.2	13
51	Precise phylogenetic analysis of microbial isolates and genomes from metagenomes using PhyloPhlAn 3.0. <i>Nature Communications</i> , 2020 , 11, 2500	17.4	99
50	Microbiome analyses of blood and tissues suggest cancer diagnostic approach. <i>Nature</i> , 2020 , 579, 567-574	56.4	244
49	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	24.2	63
48	Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity 2020 ,		14
47	Home chemical and microbial transitions across urbanization. <i>Nature Microbiology</i> , 2020 , 5, 108-115	26.6	43
46	Expanding magnetic organelle biogenesis in the domain Bacteria. <i>Microbiome</i> , 2020 , 8, 152	16.6	18
45	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019 , 4,	7.6	20
44	Evaluating Metagenomic Prediction of the Metaproteome in a 4.5-Year Study of a Patient with Crohn's Disease. <i>MSystems</i> , 2019 , 4,	7.6	24
43	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
42	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019 , 20, 226	18.3	24
41	FXR Regulates Intestinal Cancer Stem Cell Proliferation. <i>Cell</i> , 2019 , 176, 1098-1112.e18	56.2	151
40	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019 , 10, 5477	17.4	89
39	Creating a 3D microbial and chemical snapshot of a human habitat. <i>Scientific Reports</i> , 2018 , 8, 3669	4.9	23
38	KatharoSeq Enables High-Throughput Microbiome Analysis from Low-Biomass Samples. <i>MSystems</i> , 2018 , 3,	7.6	74
37	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018 , 44, 61-69	7.9	18

36	Genomic inference of the metabolism and evolution of the archaeal phylum Aigarchaeota. <i>Nature Communications</i> , 2018 , 9, 2832	17.4	50
35	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	6	54
34	Visualization-assisted binning of metagenome assemblies reveals potential new pathogenic profiles in idiopathic travelers' diarrhea. <i>Microbiome</i> , 2018 , 6, 201	16.6	10
33	Evaluating the Information Content of Shallow Shotgun Metagenomics. <i>MSystems</i> , 2018 , 3,	7.6	175
32	Metagenomics-Based, Strain-Level Analysis of From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018 , 9, 2559	5.7	24
31	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 ³⁻⁴	13	
30	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
29	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422	22.2	668
28	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018 , 3, 652-661	26.6	43
27	The origin of Chinese domestic horses revealed with novel mtDNA variants. <i>Animal Science Journal</i> , 2017 , 88, 19-26	1.8	9
26	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	11.5	66
25	Reply to Wang and Chen: An ancient origin of magnetotactic bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E5019-E5020	11.5	1
24	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
23	On the probability of dinosaur fleas. <i>BMC Evolutionary Biology</i> , 2016 , 16, 9	3	6
22	Fleas (Siphonaptera) are Cretaceous, and evolved with Theria. <i>Molecular Phylogenetics and Evolution</i> , 2015 , 90, 129-39	4.1	66
21	Bartonella spp. in fruit bats and blood-feeding Ectoparasites in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2015 , 9, e0003532	4.8	52
20	RNA: An Expanding View of Function and Evolution. <i>Evolutionary Bioinformatics</i> , 2015 , 11, 77-9	1.9	
19	HGTector: an automated method facilitating genome-wide discovery of putative horizontal gene transfers. <i>BMC Genomics</i> , 2014 , 15, 717	4.5	62

18	Horizontal transfers and gene losses in the phospholipid pathway of bartonella reveal clues about early ecological niches. <i>Genome Biology and Evolution</i> , 2014 , 6, 2156-69	3.9	14
17	Improved accuracy of supervised CRM discovery with interpolated Markov models and cross-species comparison. <i>Nucleic Acids Research</i> , 2011 , 39, 9463-72	20.1	27
16	Motif-blind, genome-wide discovery of cis-regulatory modules in Drosophila and mouse. <i>Developmental Cell</i> , 2009 , 17, 568-79	10.2	51
15	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
14	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
13	Expanding magnetic organelle biogenesis in the domain Bacteria		1
12	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
11	Early prediction of liver disease using conventional risk factors and gut microbiome-augmented gradient boosting		10
10	Reference data based insights expand understanding of human metabolomes		4
9	Combined effects of host genetics and diet on human gut microbiota and incident disease in a single population cohort		4
8	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		5
7	American Gut: an Open Platform for Citizen-Science Microbiome Research		11
6	Evaluating the information content of shallow shotgun metagenomics		3
5	Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing		24
4	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7
3	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
2	APPLES-2: Faster and More Accurate Distance-based Phylogenetic Placement using Divide and Conquer		1
1	DEPP: Deep Learning Enables Extending Species Trees using Single Genes		9

