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List of PR Articles by Year in descending order

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40

PR articles

16,249

PR citations

162956

27

PR h-index

256151

39

g-index

42

documents

33937

doc citations

174379

28

h-index

39053

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Evaluating stool microbiome integrity after domestic freezer storage using whole-metagenome sequencing, genome assembly, and antimicrobial resistance gene analysis. <i>Microbiology Spectrum</i> , 2025, 13, .	3.7	7
2	Integrating sequence composition information into microbial diversity analyses with k-mer frequency counting. <i>MSystems</i> , 2025, 10, .	4.5	9
3	The future is fermented: Microbial biodiversity of fermented foods is a critical resource for food innovation and human health. <i>Trends in Food Science and Technology</i> , 2024, 150, 104569.	15.3	41
4	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment. <i>PLoS Computational Biology</i> , 2022, 18, e1009876.	3.2	55
5	Lord of the Diptera (and Moths and a Spider): Molecular Diet Analyses and Foraging Ecology of Indiana Bats in Illinois. <i>Frontiers in Ecology and Evolution</i> , 2021, 9, .	2.2	20
6	Effect of Bovine Milk Fat Globule Membrane and Lactoferrin in Infant Formula on Gut Microbiome and Metabolome at 4 Months of Age. <i>Current Developments in Nutrition</i> , 2021, 5, nzab027.	0.2	18
7	Sources and Assembly of Microbial Communities in Vineyards as a Functional Component of Winegrowing. <i>Frontiers in Microbiology</i> , 2021, 12, .	3.9	87
8	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. <i>Frontiers in Microbiology</i> , 2021, 12, .	3.9	33
9	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	3.2	4
10	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. <i>Microbiology Spectrum</i> , 2021, 9, .	3.7	18
11	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021, 17, e1009581.	3.2	774
12	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. <i>Cancer Medicine</i> , 2020, 9, 797-806.	2.7	68
13	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020, 10, 9721-9739.	2.0	58
14	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , 2020, 13, 1984-1999.	3.2	22
15	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 4048-4062.	4.0	77
16	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	0.5	16
17	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	0.5	8
18	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, .	13.9	177

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19	Learning representations of microbial metabolite interactions. <i>Nature Methods</i> , 2019, 16, 1306-1314.	26.1	257
20	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , 2019, 8, 617-628.	2.7	90
21	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , 2019, 4, .	3.1	27
22	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018, 3, .	4.5	292
23	Fecal microbiota and bile acid interactions with systemic and adipose tissue metabolism in diet-induced weight loss of obese postmenopausal women. <i>Journal of Translational Medicine</i> , 2018, 16, .	6.7	98
24	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, .	11.5	5,095
25	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018, 3, 934.	2.1	170
26	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	39.5	2,576
27	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	4.5	102
28	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <i>Science Translational Medicine</i> , 2016, 8, .	13.4	1,291
29	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. <i>MBio</i> , 2016, 7, .	4.5	434
30	A new perspective on microbial landscapes within food production. <i>Current Opinion in Biotechnology</i> , 2016, 37, 182-189.	7.0	127
31	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016, 22, 250-253.	40.4	854
32	Microbial biogeography of the transnational fermented milk matsoni. <i>Food Microbiology</i> , 2015, 50, 12-19.	4.5	53
33	The Soil Microbiome Influences Grapevine-Associated Microbiota. <i>MBio</i> , 2015, 6, .	4.5	941
34	Microbial biogeography of wine grapes is conditioned by cultivar, vintage, and climate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, .	7.8	932
35	Indigenous Bacteria and Fungi Drive Traditional Kimoto Sake Fermentations. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5522-5529.	3.5	110
36	The Microbiology of Malting and Brewing. <i>Microbiology and Molecular Biology Reviews</i> , 2013, 77, 157-172.	7.2	282

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37	Improved Selection of Internal Transcribed Spacer-Specific Primers Enables Quantitative, Ultra-High-Throughput Profiling of Fungal Communities. <i>Applied and Environmental Microbiology</i> , 2013, 79, 2519-2526.	3.5	544
38	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	26.1	4,220
39	Facility-Specific "House" Microbiome Drives Microbial Landscapes of Artisan Cheesemaking Plants. <i>Applied and Environmental Microbiology</i> , 2013, 79, 5214-5223.	3.5	277
40	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. <i>ELife</i> , 0, 4, .	1.6	79