

Nicholas A Bokulich

List of Publications by Citations

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Version: 2024-04-28

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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.

50
papers

12,843
citations

28
h-index

57
g-index

57
ext. papers

20,831
ext. citations

11.5
avg, IF

6.24
L-index

#	Paper	IF	Citations
50	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
49	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013 , 10, 57-9	21.6	2167
48	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018 , 6, 90	16.6	1227
47	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
46	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <i>Science Translational Medicine</i> , 2016 , 8, 343ra82	17.5	680
45	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, E139-48	11.5	557
44	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , 2016 , 22, 250-3	50.5	536
43	The soil microbiome influences grapevine-associated microbiota. <i>MBio</i> , 2015 , 6,	7.8	465
42	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, 2519-26	4.8	292
41	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. <i>MBio</i> , 2016 , 7,	7.8	205
40	Facility-specific "house" microbiome drives microbial landscapes of artisan cheesemaking plants. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5214-23	4.8	170
39	The microbiology of malting and brewing. <i>Microbiology and Molecular Biology Reviews</i> , 2013 , 77, 157-72	13.2	169
38	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
37	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018 , 3,	7.6	104
36	Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , 2019 , 16, 1306-1314	21.6	79
35	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
34	A new perspective on microbial landscapes within food production. <i>Current Opinion in Biotechnology</i> , 2016 , 37, 182-189	11.4	73

33	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
32	Indigenous bacteria and fungi drive traditional kimoto sake fermentations. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5522-9	4.8	59
31	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018 , 3,	5.2	56
30	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016 , 1,	7.6	55
29	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. <i>ELife</i> , 2015 , 4,	8.9	47
28	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, 244	8.5	44
27	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
26	Microbial biogeography of the transnational fermented milk matsoni. <i>Food Microbiology</i> , 2015 , 50, 12-9	6	35
25	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , 2019 , 8, 617-628	4.8	33
24	RESCRIPt: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , 2021 , 17, e1009581	5	30
23	RESCRIPt: Reproducible sequence taxonomy reference database management for the masses		24
22	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019 , 10, 4643	17.4	22
21	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. <i>Cancer Medicine</i> , 2020 , 9, 797-806	4.8	19
20	A bitter aftertaste: unintended effects of artificial sweeteners on the gut microbiome. <i>Cell Metabolism</i> , 2014 , 20, 701-703	24.6	17
19	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 4048-4062	6.8	15
18	Sources and Assembly of Microbial Communities in Vineyards as a Functional Component of Winegrowing. <i>Frontiers in Microbiology</i> , 2021 , 12, 673810	5.7	13
17	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , 2019 , 4,	5	11
16	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , 2020 , 10, 9721-9739	2.8	10

15	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , 2020 , 13, 1984-1999	4.8	9
14	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		8
13	q2-longitudinal: a QIIME 2 plugin for longitudinal and paired-sample analyses of microbiome data		8
12	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020 , 9, 657	3.6	7
11	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	0.4	4
10	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,	3.7	4
9	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. <i>Microbiology Spectrum</i> , 2021 , 9, e0013821	8.9	3
8	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
7	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
6	Species abundance information improves sequence taxonomy classification accuracy		2
5	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. <i>Frontiers in Microbiology</i> , 2021 , 12, 644487	5.7	2
4	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 9, 657	3.6	1
3	Lack of Evidence that Ursodeoxycholic Acid Effects on the Gut Microbiome Influence Colorectal Adenoma Risk		1
2	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021 , 17, e1009056	5	0
1	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009876	5	0