

# Nicholas A Bokulich

## 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.

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	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment.. <i>PLoS Computational Biology</i> , <b>2022</b> , 18, e1009876	5	0
49	RESCRIPT: Reproducible sequence taxonomy reference database management. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009581	5	30
48	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> , <b>2021</b> , 5, nzab027	0.4	4
47	Sources and Assembly of Microbial Communities in Vineyards as a Functional Component of Winegrowing. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 673810	5.7	13
46	Beating Naive Bayes at Taxonomic Classification of 16S rRNA Gene Sequences. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 644487	5.7	2
45	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1009056	5	0
44	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> , <b>2021</b> , 9,	3.7	4
43	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. <i>Microbiology Spectrum</i> , <b>2021</b> , 9, e0013821	8.9	3
42	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> , <b>2020</b> , 70, e100	24.2	63
41	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , <b>2020</b> , 13, 1984-1999	4.8	9
40	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , <b>2020</b> , 9, 657	3.6	7
39	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 4048-4062	6.8	15
38	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. <i>Cancer Medicine</i> , <b>2020</b> , 9, 797-806	4.8	19
37	A total crapshoot? Evaluating bioinformatic decisions in animal diet metabarcoding analyses. <i>Ecology and Evolution</i> , <b>2020</b> , 10, 9721-9739	2.8	10
36	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , <b>2019</b> , 8, 617-628	4.8	33
35	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , <b>2019</b> , 4,	5	11
34	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 852-857	44.5	4050

33	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , <b>2019</b> , 10, 4643	17.4	22
32	Learning representations of microbe-metabolite interactions. <i>Nature Methods</i> , <b>2019</b> , 16, 1306-1314	21.6	79
31	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , <b>2018</b> , 6, 90	16.6	1227
30	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , <b>2018</b> , 3,	5.2	56
29	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science <b>2018</b> ,		78
28	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , <b>2018</b> , 3,	7.6	104
27	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> , <b>2018</b> , 16, 244	8.5	44
26	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , <b>2017</b> , 551, 457-463	50.4	1076
25	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , <b>2016</b> , 1,	7.6	55
24	Antibiotics, birth mode, and diet shape microbiome maturation during early life. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 343ra82	17.5	680
23	Associations among Wine Grape Microbiome, Metabolome, and Fermentation Behavior Suggest Microbial Contribution to Regional Wine Characteristics. <i>MBio</i> , <b>2016</b> , 7,	7.8	205
22	A new perspective on microbial landscapes within food production. <i>Current Opinion in Biotechnology</i> , <b>2016</b> , 37, 182-189	11.4	73
21	Partial restoration of the microbiota of cesarean-born infants via vaginal microbial transfer. <i>Nature Medicine</i> , <b>2016</b> , 22, 250-3	50.5	536
20	The soil microbiome influences grapevine-associated microbiota. <i>MBio</i> , <b>2015</b> , 6,	7.8	465
19	Mapping microbial ecosystems and spoilage-gene flow in breweries highlights patterns of contamination and resistance. <i>ELife</i> , <b>2015</b> , 4,	8.9	47
18	Microbial biogeography of the transnational fermented milk matsoni. <i>Food Microbiology</i> , <b>2015</b> , 50, 12-9 6		35
17	A bitter aftertaste: unintended effects of artificial sweeteners on the gut microbiome. <i>Cell Metabolism</i> , <b>2014</b> , 20, 701-703	24.6	17
16	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> , <b>2014</b> , 111, E139-48	11.5	557

15	Indigenous bacteria and fungi drive traditional kimoto sake fermentations. <i>Applied and Environmental Microbiology</i> , <b>2014</b> , 80, 5522-9	4.8	59
14	The microbiology of malting and brewing. <i>Microbiology and Molecular Biology Reviews</i> , <b>2013</b> , 77, 157-72	13.2	169
13	Improved selection of internal transcribed spacer-specific primers enables quantitative, ultra-high-throughput profiling of fungal communities. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 2519-26	4.8	292
12	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , <b>2013</b> , 10, 57-9	21.6	2167
11	Facility-specific "house" microbiome drives microbial landscapes of artisan cheesemaking plants. <i>Applied and Environmental Microbiology</i> , <b>2013</b> , 79, 5214-23	4.8	170
10	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 9, 657	3.6	1
9	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
8	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
7	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
6	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		2
5	A standardized, extensible framework for optimizing classification improves marker-gene taxonomic assignments		8
4	Species abundance information improves sequence taxonomy classification accuracy		2
3	RESCRIPt: Reproducible sequence taxonomy reference database management for the masses		24
2	q2-longitudinal: a QIIME 2 plugin for longitudinal and paired-sample analyses of microbiome data		8
1	Lack of Evidence that Ursodeoxycholic Acid Effects on the Gut Microbiome Influence Colorectal Adenoma Risk		1