

# Daniel McDonald

## List of Publications by Citations

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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.

78  
papers

45,250  
citations

38  
h-index

95  
g-index

95  
ext. papers

62,694  
ext. citations

15.9  
avg, IF

6.67  
L-index

#	Paper	IF	Citations
78	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , <b>2010</b> , 7, 335-6	21.6	22879
77	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 814-21	44.5	5270
76	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 852-857	44.5	4050
75	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , <b>2012</b> , 6, 610-8	11.9	3287
74	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , <b>2014</b> , 15, 382-392	23.4	1836
73	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , <b>2017</b> , 551, 457-463	50.4	1076
72	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , <b>2017</b> , 2,	7.6	763
71	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , <b>2018</b> , 16, 410-422	22.2	668
70	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , <b>2017</b> , 550, 61-66	50.4	595
69	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , <b>2017</b> , 2, 17004	26.6	533
68	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , <b>2012</b> , 1, 7	7.6	484
67	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , <b>2018</b> , 24, 1532-1535	50.5	348
66	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , <b>2018</b> , 3,	7.6	336
65	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , <b>2019</b> , 4, 396-403	26.6	296
64	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , <b>2018</b> , 15, 796-798	21.6	231
63	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , <b>2016</b> , 1,	5	190
62	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , <b>2017</b> , 18, 65-86	9.7	181

61	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , <b>2018</b> , 3,	7.6	181
60	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , <b>2017</b> , 2,	7.6	177
59	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
58	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , <b>2019</b> , 4,	7.6	110
57	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , <b>2019</b> , 17, 218-230	6.9	107
56	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. <i>Schizophrenia Research</i> , <b>2019</b> , 204, 23-29	3.6	98
55	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , <b>2019</b> , 10, 5477	17.4	89
54	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science <b>2018</b> ,		78
53	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. <i>Microbiome</i> , <b>2019</b> , 7, 50	16.6	77
52	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , <b>2021</b> , 18, 165-169	21.6	67
51	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
50	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. <i>MSystems</i> , <b>2018</b> , 3,	7.6	56
49	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. <i>Gastroenterology</i> , <b>2021</b> , 160, 183-192.e3	13.3	48
48	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , <b>2017</b> , 21, 7-10	23.4	44
47	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , <b>2017</b> , 2,	7.6	44
46	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , <b>2018</b> , 3, 652-661	26.6	43
45	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , <b>2019</b> , 17, 47	7.3	42
44	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. <i>Genome Biology</i> , <b>2019</b> , 20, 219	18.3	41

43	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , <b>2018</b> , 15, 847-848.	11.6	40
42	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , <b>2020</b> , 65, 103738	5.1	39
41	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
40	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , <b>2020</b> , 5,	7.6	33
39	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. <i>Genome Biology</i> , <b>2019</b> , 20, 201	18.3	33
38	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 146-151	11.7	29
37	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. <i>Journal of Microbiology and Biology Education</i> , <b>2016</b> , 17, 46-50	1.3	28
36	Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing		24
35	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 165-168	44.5	23
34	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , <b>2019</b> , 10, 4643	17.4	22
33	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , <b>2018</b> , 9,	7.8	21
32	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , <b>2019</b> , 4,	7.6	20
31	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , <b>2018</b> , 44, 61-69	7.9	18
30	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , <b>2019</b> , 4,	7.6	17
29	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , <b>2021</b> , 9, 132	16.6	15
28	Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity <b>2020</b> ,		14
27	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , <b>2021</b> , 6,	7.6	14
26	Rapid, Large-Scale Wastewater Surveillance and Automated Reporting System Enable Early Detection of Nearly 85% of COVID-19 Cases on a University Campus. <i>MSystems</i> , <b>2021</b> , 6, e0079321	7.6	14

25	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , <b>2020</b> , 5,	7.6	12
24	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , <b>2021</b> , 9, 92	16.6	11
23	Microbial context predicts SARS-CoV-2 prevalence in patients and the hospital built environment <b>2020</b> ,		10
22	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , <b>2020</b> , 5,	5	9
21	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding.. <i>Med</i> , <b>2021</b> , 2, 951-964.e5	31.7	8
20	The emergence of microbiome centres. <i>Nature Microbiology</i> , <b>2020</b> , 5, 2-3	26.6	7
19	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures		7
18	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , <b>2021</b> , 9, 25	16.6	7
17	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , <b>2021</b> , 6,	7.6	6
16	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets		5
15	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , <b>2021</b> , 41, 479-510	51.0	5
14	Reference data based insights expand understanding of human metabolomes		4
13	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , <b>2021</b> , 22, 336	18.3	4
12	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree		3
11	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment <b>2020</b> ,		3
10	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment		3
9	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , <b>2021</b> , 31, 2131-2137	9.7	3
8	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , <b>2022</b> , e0016722	7.6	3

7	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , <b>2021</b> , e0100621	7.6	2
6	Species abundance information improves sequence taxonomy classification accuracy		2
5	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , <b>2020</b> , 5,	7.6	2
4	Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , <b>2021</b> , 18, 40-41	7.6	2
3	Age and sex-dependent patterns of gut microbial diversity in human adults		1
2	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases.. <i>MSystems</i> , <b>2022</b> , e0137821	7.6	0
1	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype.. <i>MSystems</i> , <b>2022</b> , e0005022	7.6	0