

Daniel McDonald

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.

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	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases.. <i>MSystems</i> , 2022 , e0137821	7.6	0
77	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy.. <i>MSystems</i> , 2022 , e0016722	7.6	3
76	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype.. <i>MSystems</i> , 2022 , e0005022	7.6	0
75	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , 2021 , e0100621	7.6	2
74	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021 , 6,	7.6	6
73	Assessment of the microbiome during bacteriophage therapy in combination with systemic antibiotics to treat a case of staphylococcal device infection. <i>Microbiome</i> , 2021 , 9, 92	16.6	11
72	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021 , 6,	7.6	14
71	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021 , 9, 132	16.6	15
70	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. <i>Gastroenterology</i> , 2021 , 160, 183-192.e3	13.3	48
69	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021 , 17, 146-151	11.7	29
68	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
67	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021 , 39, 165-168	44.5	23
66	Reply to: Examining microbe-metabolite correlations by linear methods. <i>Nature Methods</i> , 2021 , 18, 40-41.e1.6	11.6	2
65	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment. <i>Microbiome</i> , 2021 , 9, 25	16.6	7
64	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , 2021 , 41, 479-510	10	5
63	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> , 2021 , 6, e0079321	7.6	14
62	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding.. <i>Med</i> , 2021 , 2, 951-964.e5	31.7	8

61	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021 , 31, 2131-2137	9.7	3
60	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , 2021 , 22, 336	18.3	4
59	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
58	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020 , 5,	7.6	33
57	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020 , 5,	7.6	12
56	Feasibility of using alternative swabs and storage solutions for paired SARS-CoV-2 detection and microbiome analysis in the hospital environment 2020 ,		3
55	Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity 2020 ,		14
54	Microbial context predicts SARS-CoV-2 prevalence in patients and the hospital built environment 2020 ,		10
53	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , 2020 , 65, 103738	5.1	39
52	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020 , 5, 2-3	26.6	7
51	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020 , 5,	5	9
50	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020 , 5,	7.6	2
49	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019 , 4,	7.6	17
48	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019 , 17, 47	7.3	42
47	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019 , 4,	7.6	110
46	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019 , 4,	7.6	20
45	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. <i>Microbiome</i> , 2019 , 7, 50	16.6	77
44	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050

43	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. <i>Genome Biology</i> , 2019 , 20, 201	18.3	33
42	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019 , 10, 4643	17.4	22
41	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> , 2019 , 20, 219	18.3	41
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	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019 , 17, 218-230	6.9	107
38	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019 , 4, 396-403	26.6	296
37	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. <i>Schizophrenia Research</i> , 2019 , 204, 23-29	3.6	98
36	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018 , 3,	7.6	181
35	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018 , 44, 61-69	7.9	18
34	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018 , 24, 1532-1535	50.5	348
33	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. <i>MSystems</i> , 2018 , 3,	7.6	56
32	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
31	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018 , 9,	7.8	21
30	Qiiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21.6	231
29	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018 , 15, 847-848	11.6	40
28	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018 , 3,	7.6	336
27	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018 , 16, 410-422	22.2	668
26	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018 , 3, 652-661	26.6	43

25	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017 , 2,	7.6	177
24	Bringing the Dynamic Microbiome to Life with Animations. <i>Cell Host and Microbe</i> , 2017 , 21, 7-10	23.4	44
23	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017 , 2,	7.6	763
22	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017 , 2, 17004	26.6	533
21	The Microbiome and Human Biology. <i>Annual Review of Genomics and Human Genetics</i> , 2017 , 18, 65-86	9.7	181
20	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017 , 551, 457-463	50.4	1076
19	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. <i>MSystems</i> , 2017 , 2,	7.6	44
18	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017 , 550, 61-66	50.4	595
17	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016 , 1,	5	190
16	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. <i>Journal of Microbiology and Biology Education</i> , 2016 , 17, 46-50	1.3	28
15	The treatment-naive microbiome in new-onset Crohn's disease. <i>Cell Host and Microbe</i> , 2014 , 15, 382-392	23.4	1836
14	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013 , 31, 814-21	44.5	5270
13	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012 , 1, 7	7.6	484
12	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012 , 6, 610-8	11.9	3287
11	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
10	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
9	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
8	Species abundance information improves sequence taxonomy classification accuracy		2

7	Chemically-informed Analyses of Metabolomics Mass Spectrometry Data with Qemistree	3
6	Reference data based insights expand understanding of human metabolomes	4
5	EMPress enables tree-guided, interactive, and exploratory analyses of multi-omic datasets	5
4	Age and sex-dependent patterns of gut microbial diversity in human adults	1
3	Enabling high-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing	24
2	OGUs enable effective, phylogeny-aware analysis of even shallow metagenome community structures	7
1	Multi-omics profiling of Earth's biomes reveals that microbial and metabolite composition are shaped by the environment	3