

Daniel McDonald

List of Publications by Year in descending order

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Version: 2024-02-01

73
papers

72,997
citations

61945

43
h-index

82499

72
g-index

95
all docs

95
docs citations

95
times ranked

67129
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
3	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
4	An improved Greengenes taxonomy with explicit ranks for ecological and evolutionary analyses of bacteria and archaea. <i>ISME Journal</i> , 2012, 6, 610-618.	4.4	4,581
5	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	5.1	2,582
6	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	13.7	1,942
7	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	1.7	1,339
8	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	13.6	1,138
9	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	13.7	929
10	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	5.9	830
11	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	3.3	671
12	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018, 24, 1532-1535.	15.2	629
13	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	1.7	604
14	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	5.9	590
15	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
16	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	1.7	376
17	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	1.7	284
18	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016, 1, .	1.3	283

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19	The Microbiome and Human Biology. Annual Review of Genomics and Human Genetics, 2017, 18, 65-86.	2.5	266
20	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. MSystems, 2019, 4, .	1.7	214
21	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
22	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. Nature, 2022, 609, 101-108.	13.7	200
23	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	9.0	198
24	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	5.8	197
25	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. Clinical Gastroenterology and Hepatology, 2019, 17, 218-230.	2.4	187
26	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome, 2019, 7, 50.	4.9	158
27	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. Schizophrenia Research, 2019, 204, 23-29.	1.1	157
28	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. MSystems, 2017, 2, .	1.7	116
29	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. Gastroenterology, 2021, 160, 183-192.e3.	0.6	113
30	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	1.7	101
31	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. MSystems, 2018, 3, .	1.7	96
32	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	5.1	95
33	Gut microbiome composition in the Hispanic Community Health Study/Study of Latinos is shaped by geographic relocation, environmental factors, and obesity. Genome Biology, 2019, 20, 219.	3.8	94
34	Rapid, Large-Scale Wastewater Surveillance and Automated Reporting System Enable Early Detection of Nearly 85% of COVID-19 Cases on a University Campus. MSystems, 2021, 6, e0079321.	1.7	94
35	Species abundance information improves sequence taxonomy classification accuracy. Nature Communications, 2019, 10, 4643.	5.8	86
36	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. MSystems, 2020, 5, .	1.7	81

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37	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	3.9	73
38	Striped UniFrac: enabling microbiome analysis at unprecedented scale. <i>Nature Methods</i> , 2018, 15, 847-848.	9.0	71
39	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	5.9	68
40	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , 2020, 65, 103738.	1.6	66
41	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	9.4	61
42	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. <i>Genome Biology</i> , 2019, 20, 201.	3.8	57
43	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.	0.5	42
44	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.	4.9	40
45	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	4.9	37
46	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	2.2	37
47	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	1.7	36
48	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	1.7	35
49	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	1.7	35
50	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	1.8	28
51	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	1.7	28
52	A posteriori dietary patterns better explain variations of the gut microbiome than individual markers in the American Gut Project. <i>American Journal of Clinical Nutrition</i> , 2022, 115, 432-443.	2.2	28
53	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	2.3	27
54	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	9.4	25

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55	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	1.7	22
56	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020, 5, .	1.3	20
57	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , 2021, 41, 479-510.	4.3	18
58	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , 2021, 22, 336.	3.8	18
59	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	1.7	16
60	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	2.4	16
61	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020, 5, 2-3.	5.9	13
62	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.	4.9	13
63	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	1.0	10
64	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	1.7	9
65	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , 2021, 6, e0100621.	1.7	8
66	Reply to: Examining microbeâ€“metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	9.0	6
67	Impact of Vaginal Estrogen on the Urobiome in Postmenopausal Women With Recurrent Urinary Tract Infection. <i>Female Pelvic Medicine and Reconstructive Surgery</i> , 2022, 28, 20-26.	0.6	5
68	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	1.7	4
69	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. <i>MSystems</i> , 2022, 7, e0137821.	1.7	3
70	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	1.7	2
71	Reduced Independence in Daily Living Is Associated with the Gut Microbiome in People with HIV and HCV. <i>MSystems</i> , 2020, 5, .	1.7	1
72	Reply to Sun et al., â€œIdentifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracyâ€•. <i>MBio</i> , 2019, 10, .	1.8	0

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73	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0