

Daniel McDonald

List of Publications by Year in descending order

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79
papers

77,822
citations

55975

42
h-index

57492

78
g-index

106
all docs

106
docs citations

106
times ranked

67698
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.6	32,880
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	21.0	12,956
3	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	21.0	8,414
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.	10.0	4,726
5	The Treatment-Naive Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.1	2,700
6	A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.	36.3	2,060
7	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. <i>MSystems</i> , 2017, 2, .	4.1	1,441
8	Best practices for analysing microbiomes. <i>Nature Reviews Microbiology</i> , 2018, 16, 410-422.	29.2	1,213
9	Strains, functions and dynamics in the expanded Human Microbiome Project. <i>Nature</i> , 2017, 550, 61-66.	36.3	981
10	Dynamics of the human gut microbiome in inflammatory bowel disease. <i>Nature Microbiology</i> , 2017, 2, 17004.	13.0	878
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.	6.8	688
12	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. <i>Nature Medicine</i> , 2018, 24, 1532-1535.	30.5	677
13	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	13.0	675
14	American Gut: an Open Platform for Citizen Science Microbiome Research. <i>MSystems</i> , 2018, 3, .	4.1	632
15	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	19.6	487
16	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	4.1	407
17	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016, 1, .	3.1	305
18	Balance Trees Reveal Microbial Niche Differentiation. <i>MSystems</i> , 2017, 2, .	4.1	294

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19	The Microbiome and Human Biology. Annual Review of Genomics and Human Genetics, 2017, 18, 65-86.	6.4	273
20	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. Nature, 2022, 609, 101-108.	36.3	268
21	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. MSystems, 2019, 4, .	4.1	237
22	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. Nature Methods, 2021, 18, 165-169.	19.6	233
23	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. Nature Communications, 2019, 10, 5477.	13.2	230
24	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. Clinical Gastroenterology and Hepatology, 2019, 17, 218-230.	4.8	199
25	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. Schizophrenia Research, 2019, 204, 23-29.	2.1	177
26	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. Microbiome, 2019, 7, 50.	11.6	171
27	Fecal Microbiota Transplantation Is Highly Effective in Real-World Practice: Initial Results From the FMT National Registry. Gastroenterology, 2021, 160, 183-192.e3.	1.4	124
28	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. MSystems, 2017, 2, .	4.1	120
29	The impact of skin care products on skin chemistry and microbiome dynamics. BMC Biology, 2019, 17, 47.	3.9	113
30	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.	4.1	108
31	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	11.1	101
32	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. MSystems, 2018, 3, .	4.1	101
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.	9.1	101
34	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. MSystems, 2020, 5, .	4.1	95
35	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. Nature Chemical Biology, 2021, 17, 146-151.	8.1	80
36	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	19.6	76

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37	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , 2020, 65, 103738.	3.5	73
38	Methods for phylogenetic analysis of microbiome data. <i>Nature Microbiology</i> , 2018, 3, 652-661.	13.0	68
39	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	21.0	67
40	Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. <i>Nature Microbiology</i> , 2022, 7, 2128-2150.	13.0	64
41	Convergence of human and Old World monkey gut microbiomes demonstrates the importance of human ecology over phylogeny. <i>Genome Biology</i> , 2019, 20, 201.	9.1	60
42	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	4.1	52
43	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.	11.6	45
44	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	4.4	44
45	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.	1.0	43
46	SARS-CoV-2 detection status associates with bacterial community composition in patients and the hospital environment. <i>Microbiome</i> , 2021, 9, 132.	11.6	41
47	HCMV-encoded US7 and US8 act as antagonists of innate immunity by distinctively targeting TLR-signaling pathways. <i>Nature Communications</i> , 2019, 10, 4670.	13.2	38
48	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	4.1	38
49	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	4.1	36
50	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	4.1	34
51	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	21.0	33
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.	4.7	32
53	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	4.1	31
54	Host biology, ecology and the environment influence microbial biomass and diversity in 101 marine fish species. <i>Nature Communications</i> , 2022, 13, .	13.2	30

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55	Identifying and Predicting Novelty in Microbiome Studies. <i>MBio</i> , 2018, 9, .	4.3	28
56	Are microbiome studies ready for hypothesis-driven research?. <i>Current Opinion in Microbiology</i> , 2018, 44, 61-69.	5.2	27
57	Microbial co-occurrence complicates associations of gut microbiome with US immigration, dietary intake and obesity. <i>Genome Biology</i> , 2021, 22, 336.	9.1	27
58	Structural basis for substrate specificity and regulation of nucleotide sugar transporters in the lipid bilayer. <i>Nature Communications</i> , 2019, 10, 4657.	13.2	24
59	Nutrition and the Gut Microbiota in 10- to 18-Month-Old Children Living in Urban Slums of Mumbai, India. <i>MSphere</i> , 2020, 5, .	3.1	23
60	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , 2021, 41, 479-510.	10.4	20
61	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.	11.6	17
62	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.6	17
63	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	4.1	16
64	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.2	16
65	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020, 5, 2-3.	13.0	13
66	Global branches and local states of the human gut microbiome define associations with environmental and intrinsic factors. <i>Nature Communications</i> , 2023, 14, .	13.2	10
67	Depression in Individuals Coinfected with HIV and HCV Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	4.1	9
68	Reply to: Examining microbeâ€“metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.6	8
69	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , 2021, 6, e0100621.	4.1	8
70	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.	1.2	7
71	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	4.1	7
72	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. <i>MSystems</i> , 2022, 7, e0137821.	4.1	6

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73	Determination of Effect Sizes for Power Analysis for Microbiome Studies Using Large Microbiome Databases. <i>Genes</i> , 2023, 14, 1239.	2.4	4
74	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	4.1	2
75	Reduced Independence in Daily Living Is Associated with the Gut Microbiome in People with HIV and HCV. <i>MSystems</i> , 2020, 5, .	4.1	1
76	Testing GitHub projects on custom resources using unprivileged Kubernetes runners. , 2023, , .		1
77	Improving microbial phylogeny with citizen science within a mass-market video game. <i>Nature Biotechnology</i> , 0, , .	21.0	1
78	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	4.3	0
79	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0