

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	Determination of Effect Sizes for Power Analysis for Microbiome Studies Using Large Microbiome Databases. <i>Genes</i> , 2023, 14, 1239.	2.4	4
2	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
3	Testing GitHub projects on custom resources using unprivileged Kubernetes runners. , 2023, , .		1
4	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
5	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
6	Applications and Comparison of Dimensionality Reduction Methods for Microbiome Data. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.2	16
7	Swapping Metagenomics Preprocessing Pipeline Components Offers Speed and Sensitivity Increases. <i>MSystems</i> , 2022, 7, e0137821.	4.1	6
8	Phylogeny-Aware Analysis of Metagenome Community Ecology Based on Matched Reference Genomes while Bypassing Taxonomy. <i>MSystems</i> , 2022, 7, e0016722.	4.1	52
9	Compositionally Aware Phylogenetic Beta-Diversity Measures Better Resolve Microbiomes Associated with Phenotype. <i>MSystems</i> , 2022, 7, e0005022.	4.1	7
10	Optimizing UniFrac with OpenACC Yields Greater Than One Thousand Times Speed Increase. <i>MSystems</i> , 2022, 7, .	4.1	2
11	Enhancing untargeted metabolomics using metadata-based source annotation. <i>Nature Biotechnology</i> , 2022, 40, 1774-1779.	21.0	33
12	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. <i>Nature</i> , 2022, 609, 101-108.	36.3	268
13	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
14	Standardized multi-omics of Earth's microbiomes reveals microbial and metabolite diversity. <i>Nature Microbiology</i> , 2022, 7, 2128-2150.	13.0	64
15	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.	1.4	124
16	Chemically informed analyses of metabolomics mass spectrometry data with Qemistree. <i>Nature Chemical Biology</i> , 2021, 17, 146-151.	8.1	80
17	High-accuracy long-read amplicon sequences using unique molecular identifiers with Nanopore or PacBio sequencing. <i>Nature Methods</i> , 2021, 18, 165-169.	19.6	233
18	Context-aware dimensionality reduction deconvolutes gut microbial community dynamics. <i>Nature Biotechnology</i> , 2021, 39, 165-168.	21.0	67

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19	Reply to: Examining microbial metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 40-41.	19.6	8
20	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
21	Evaluation of the Effect of Storage Methods on Fecal, Saliva, and Skin Microbiome Composition. <i>MSystems</i> , 2021, 6, .	4.1	34
22	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
23	EMPress Enables Tree-Guided, Interactive, and Exploratory Analyses of Multi-omic Data Sets. <i>MSystems</i> , 2021, 6, .	4.1	38
24	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
25	Accelerating Key Bioinformatics Tasks 100-fold by Improving Memory Access. , 2021, , .		0
26	Nutritional Interventions and the Gut Microbiome in Children. <i>Annual Review of Nutrition</i> , 2021, 41, 479-510.	10.4	20
27	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.	4.1	108
28	Naturalization of the microbiota developmental trajectory of Cesarean-born neonates after vaginal seeding. <i>Med</i> , 2021, 2, 951-964.e5.	4.4	44
29	Efficient computation of Faith's phylogenetic diversity with applications in characterizing microbiomes. <i>Genome Research</i> , 2021, 31, 2131-2137.	5.6	17
30	The Fecal Microbiome and Metabolome of Pitt Hopkins Syndrome, a Severe Autism Spectrum Disorder. <i>MSystems</i> , 2021, 6, e0100621.	4.1	8
31	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
32	Effects of the microalgae <i>Chlamydomonas</i> on gastrointestinal health. <i>Journal of Functional Foods</i> , 2020, 65, 103738.	3.5	73
33	The emergence of microbiome centres. <i>Nature Microbiology</i> , 2020, 5, 2-3.	13.0	13
34	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
35	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
36	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

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37	Consumption of Fermented Foods Is Associated with Systematic Differences in the Gut Microbiome and Metabolome. <i>MSystems</i> , 2020, 5, .	4.1	95
38	Multiple-Disease Detection and Classification across Cohorts via Microbiome Search. <i>MSystems</i> , 2020, 5, .	4.1	16
39	Reply to Sun et al., "Identifying Composition Novelty in Microbiome Studies: Improvement of Prediction Accuracy". <i>MBio</i> , 2019, 10, .	4.3	0
40	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	21.0	12,956
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	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
43	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
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> , 2019, 20, 219.	9.1	101
45	redbiom: a Rapid Sample Discovery and Feature Characterization System. <i>MSystems</i> , 2019, 4, .	4.1	36
46	The impact of skin care products on skin chemistry and microbiome dynamics. <i>BMC Biology</i> , 2019, 17, 47.	3.9	113
47	Age- and Sex-Dependent Patterns of Gut Microbial Diversity in Human Adults. <i>MSystems</i> , 2019, 4, .	4.1	237
48	Calour: an Interactive, Microbe-Centric Analysis Tool. <i>MSystems</i> , 2019, 4, .	4.1	31
49	Characterization of the total and viable bacterial and fungal communities associated with the International Space Station surfaces. <i>Microbiome</i> , 2019, 7, 50.	11.6	171
50	Phylogenomics of 10,575 genomes reveals evolutionary proximity between domains Bacteria and Archaea. <i>Nature Communications</i> , 2019, 10, 5477.	13.2	230
51	Microbiome 101: Studying, Analyzing, and Interpreting Gut Microbiome Data for Clinicians. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 218-230.	4.8	199
52	GABA-modulating bacteria of the human gut microbiota. <i>Nature Microbiology</i> , 2019, 4, 396-403.	13.0	675
53	Differences in gut microbiome composition between persons with chronic schizophrenia and healthy comparison subjects. <i>Schizophrenia Research</i> , 2019, 204, 23-29.	2.1	177
54	Phylogenetic Placement of Exact Amplicon Sequences Improves Associations with Clinical Information. <i>MSystems</i> , 2018, 3, .	4.1	407

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55	Identifying and Predicting Novelty in Microbiome Studies. MBio, 2018, 9, .	4.3	28
56	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	19.6	487
57	Striped UniFrac: enabling microbiome analysis at unprecedented scale. Nature Methods, 2018, 15, 847-848.	19.6	76
58	American Gut: an Open Platform for Citizen Science Microbiome Research. MSystems, 2018, 3, .	4.1	632
59	Best practices for analysing microbiomes. Nature Reviews Microbiology, 2018, 16, 410-422.	29.2	1,213
60	Methods for phylogenetic analysis of microbiome data. Nature Microbiology, 2018, 3, 652-661.	13.0	68
61	Are microbiome studies ready for hypothesis-driven research?. Current Opinion in Microbiology, 2018, 44, 61-69.	5.2	27
62	Regional variation limits applications of healthy gut microbiome reference ranges and disease models. Nature Medicine, 2018, 24, 1532-1535.	30.5	677
63	Intermittent Hypoxia and Hypercapnia, a Hallmark of Obstructive Sleep Apnea, Alters the Gut Microbiome and Metabolome. MSystems, 2018, 3, .	4.1	101
64	Balance Trees Reveal Microbial Niche Differentiation. MSystems, 2017, 2, .	4.1	294
65	Bringing the Dynamic Microbiome to Life with Animations. Cell Host and Microbe, 2017, 21, 7-10.	11.1	101
66	Deblur Rapidly Resolves Single-Nucleotide Community Sequence Patterns. MSystems, 2017, 2, .	4.1	1,441
67	Dynamics of the human gut microbiome in inflammatory bowel disease. Nature Microbiology, 2017, 2, 17004.	13.0	878
68	The Microbiome and Human Biology. Annual Review of Genomics and Human Genetics, 2017, 18, 65-86.	6.4	273
69	A communal catalogue reveals Earth's multiscale microbial diversity. Nature, 2017, 551, 457-463.	36.3	2,060
70	Correcting for Microbial Blooms in Fecal Samples during Room-Temperature Shipping. MSystems, 2017, 2, .	4.1	120
71	Strains, functions and dynamics in the expanded Human Microbiome Project. Nature, 2017, 550, 61-66.	36.3	981
72	Turning Participatory Microbiome Research into Usable Data: Lessons from the American Gut Project. Journal of Microbiology and Biology Education, 2016, 17, 46-50.	1.0	43

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73	Extreme Dysbiosis of the Microbiome in Critical Illness. <i>MSphere</i> , 2016, 1, .	3.1	305
74	The Treatment-Naïve Microbiome in New-Onset Crohn's Disease. <i>Cell Host and Microbe</i> , 2014, 15, 382-392.	11.1	2,700
75	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	21.0	8,414
76	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
77	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
78	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.6	32,880
79	Improving microbial phylogeny with citizen science within a mass-market video game. <i>Nature Biotechnology</i> , 0, , .	21.0	1