

J Gregory Caporaso

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

98,173
citations

50276

46
h-index

74163

75
g-index

106
all docs

106
docs citations

106
times ranked

76934
citing authors

#	ARTICLE	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	19.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	17.5	11,167
3	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	17.5	8,049
4	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012, 6, 1621-1624.	9.8	7,430
5	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4516-4522.	7.1	7,425
6	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	27.8	6,247
7	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	19.0	3,402
8	PyNAST: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010, 26, 266-267.	4.1	3,400
9	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	11.1	3,159
10	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	30.7	1,593
11	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21390-21395.	7.1	1,260
12	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	1,125
13	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	9.6	934
14	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017, 5, 10.	11.1	901
15	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	6.0	801
16	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	6.4	671
17	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	28.9	625
18	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	1.0	553

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19	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	2.0	535
20	Individual diet has sex-dependent effects on vertebrate gut microbiota. Nature Communications, 2014, 5, 4500.	12.8	464
21	Qiita: rapid, web-enabled microbiome meta-analysis. Nature Methods, 2018, 15, 796-798.	19.0	459
22	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. Scientific Reports, 2019, 9, 5821.	3.3	414
23	Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution, 2012, 27, 233-243.	8.7	395
24	Temporal variability is a personalized feature of the human microbiome. Genome Biology, 2014, 15, 531.	8.8	355
25	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. Bioinformatics, 2011, 27, 1159-1161.	4.1	351
26	Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. Applied and Environmental Microbiology, 2016, 82, 7217-7226.	3.1	321
27	Quantitative Microbial Ecology through Stable Isotope Probing. Applied and Environmental Microbiology, 2015, 81, 7570-7581.	3.1	242
28	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
29	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. MSystems, 2018, 3, .	3.8	210
30	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	9.6	170
31	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
32	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204.	7.4	162
33	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. Environmental Microbiology, 2015, 17, 4078-4088.	3.8	160
34	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
35	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. MSystems, 2017, 2, .	3.8	141
36	MutationFinder: a high-performance system for extracting point mutation mentions from text. Bioinformatics, 2007, 23, 1862-1865.	4.1	132

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37	q2-sample-classifier: machine-learning tools for microbiome classification and regression. Journal of Open Source Software, 2018, 3, 934.	4.6	116
38	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. Microbiome, 2015, 3, 20.	11.1	115
39	Geography and Location Are the Primary Drivers of Office Microbiome Composition. MSystems, 2016, 1, .	3.8	110
40	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. ISME Journal, 2012, 6, 1273-1276.	9.8	102
41	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. MSystems, 2016, 1, .	3.8	89
42	Species abundance information improves sequence taxonomy classification accuracy. Nature Communications, 2019, 10, 4643.	12.8	86
43	The Personal Human Oral Microbiome Obscures the Effects of Treatment on Periodontal Disease. PLoS ONE, 2014, 9, e86708.	2.5	79
44	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. Cancer Medicine, 2019, 8, 617-628.	2.8	71
45	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
46	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. Microbiome, 2016, 4, 11.	11.1	51
47	Gut microbial and short-chain fatty acid profiles in adults with chronic constipation before and after treatment with lubiprostone. Anaerobe, 2015, 33, 33-41.	2.1	49
48	Impact of Different Exercise Modalities on the Human Gut Microbiome. Sports, 2021, 9, 14.	1.7	48
49	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. MSystems, 2017, 2, .	3.8	47
50	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. PLoS ONE, 2011, 6, e16900.	2.5	43
51	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. Cancer Medicine, 2020, 9, 797-806.	2.8	42
52	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. GigaScience, 2016, 5, 27.	6.4	35
53	Error Minimization and Coding Triplet/Binding Site Associations Are Independent Features of the Canonical Genetic Code. Journal of Molecular Evolution, 2005, 61, 597-607.	1.8	32
54	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. MBio, 2020, 11, .	4.1	29

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55	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. BMC Evolutionary Biology, 2008, 8, 327.	3.2	25
56	A Hybrid DNA Extraction Method for the Qualitative and Quantitative Assessment of Bacterial Communities from Poultry Production Samples. Journal of Visualized Experiments, 2014, , .	0.3	22
57	Microbiotyping the Sinonasal Microbiome. Frontiers in Cellular and Infection Microbiology, 2020, 10, 137.	3.9	21
58	Intrinsic evaluation of text mining tools may not predict performance on realistic tasks. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 640-51.	0.7	21
59	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment. PLoS Computational Biology, 2022, 18, e1009876.	3.2	21
60	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of Clostridioides (Clostridium) difficile, despite cellular susceptibility to its toxins. Anaerobe, 2019, 58, 53-72.	2.1	20
61	Association of Body Mass Index with Fecal Microbial Diversity and Metabolites in the Northern Finland Birth Cohort. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2289-2299.	2.5	20
62	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. MSphere, 2019, 4, .	2.9	19
63	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. Evolutionary Applications, 2020, 13, 1984-1999.	3.1	17
64	Leptospira in river and soil in a highly endemic area of Ecuador. BMC Microbiology, 2021, 21, 17.	3.3	16
65	An Introduction to Applied Bioinformatics: a free, open, and interactive text.. The Journal of Open Source Education, 2018, 1, 27.	0.4	16
66	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 2020, 9, 657.	1.6	14
67	INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS. , 2007, , .		12
68	Designing Inclusive HPV Cancer Vaccines and Increasing Uptake among Native Americansâ€™A Cultural Perspective Review. Current Oncology, 2021, 28, 3705-3716.	2.2	10
69	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. Microbiology Spectrum, 2021, 9, e0013821.	3.0	10
70	RAPID PATTERN DEVELOPMENT FOR CONCEPT RECOGNITION SYSTEMS: APPLICATION TO POINT MUTATIONS. Journal of Bioinformatics and Computational Biology, 2007, 05, 1233-1259.	0.8	8
71	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 0, 9, 657.	1.6	8
72	cual-id: Globally Unique, Correctable, and Human-Friendly Sample Identifiers for Comparative Omics Studies. MSystems, 2016, 1, .	3.8	6

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73	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. Springer Protocols, 2015, , 89-113.	0.3	4
74	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. PLoS Computational Biology, 2021, 17, e1009056.	3.2	2