J Gregory Caporaso

List of Publications by Citations

85 papers	**62,985** citations	**46** h-index	**106** g-index
106 ext. papers	**85,610** ext. citations	**11.6** avg, IF	**7.22** L-index

#	Paper	IF	Citations
85	QIIME allows analysis of high-throughput community sequencing data. *Nature Methods*, **2010**, 7, 335-6	21.6	22879
84	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. *Nature Biotechnology*, **2013**, 31, 814-21	44.5	5270
83	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. *ISME Journal*, **2012**, 6, 1621-4	11.9	5059
82	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108 Suppl 1, 4516-22	11.5	4742
81	Human gut microbiome viewed across age and geography. *Nature*, **2012**, 486, 222-7	50.4	4616
80	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. *Nature Biotechnology*, **2019**, 37, 852-857	44.5	4050
79	PyNAST: a flexible tool for aligning sequences to a template alignment. *Bioinformatics*, **2010**, 26, 266-7	7.2	2728
78	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. *Nature Methods*, **2013**, 10, 57-9	21.6	2167
77	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. *Microbiome*, **2018**, 6, 90	16.6	1227
76	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 21390-5	11.5	956
75	Current understanding of the human microbiome. *Nature Medicine*, **2018**, 24, 392-400	50.5	823
74	Moving pictures of the human microbiome. *Genome Biology*, **2011**, 12, R50	18.3	723
73	Cohabiting family members share microbiota with one another and with their dogs. *ELife*, **2013**, 2, e00458	8.9	616
72	Species-level functional profiling of metagenomes and metatranscriptomes. *Nature Methods*, **2018**, 15, 962-968	21.6	608
71	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. *Microbiome*, **2017**, 5, 10	16.6	595
70	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. *GigaScience*, **2012**, 1, 7	7.6	484
69	Conducting a microbiome study. *Cell*, **2014**, 158, 250-262	56.2	428

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68	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. *PeerJ*, **2014**, 2, e545	3.1	395
67	Advancing our understanding of the human microbiome using QIIME. *Methods in Enzymology*, **2013**, 531, 371-444	1.7	373
66	Individual diet has sex-dependent effects on vertebrate gut microbiota. *Nature Communications*, **2014**, 5, 4500	17.4	330
65	Sequencing our way towards understanding global eukaryotic biodiversity. *Trends in Ecology and Evolution*, **2012**, 27, 233-43	10.9	322
64	PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. *Bioinformatics*, **2011**, 27, 1159-61	7.2	273
63	Temporal variability is a personalized feature of the human microbiome. *Genome Biology*, **2014**, 15, 531	18.3	255
62	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. *Scientific Reports*, **2019**, 9, 5821	4.9	240
61	Qiita: rapid, web-enabled microbiome meta-analysis. *Nature Methods*, **2018**, 15, 796-798	21.6	231
60	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	4.8	180
59	PyCogent: a toolkit for making sense from sequence. *Genome Biology*, **2007**, 8, R171	18.3	151
58	Quantitative microbial ecology through stable isotope probing. *Applied and Environmental Microbiology*, **2015**, 81, 7570-81	4.8	143
57	The Western English Channel contains a persistent microbial seed bank. *ISME Journal*, **2012**, 6, 1089-93	11.9	140
56	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		138
55	Open-Source Sequence Clustering Methods Improve the State Of the Art. *MSystems*, **2016**, 1,	7.6	120
54	MutationFinder: a high-performance system for extracting point mutation mentions from text. *Bioinformatics*, **2007**, 23, 1862-5	7.2	106
53	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. *MSystems*, **2018**, 3,	7.6	104
52	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. *Microbiome*, **2015**, 3, 20	16.6	88
51	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. *Environmental Microbiology*, **2015**, 17, 4078-88	5.2	88

50	Geography and Location Are the Primary Drivers of Office Microbiome Composition. *MSystems*, **2016**, 1,	7.6	84
49	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. *MSystems*, **2017**, 2,	7.6	80
48	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. *Trends in Cancer*, **2020**, 6, 192-204	12.5	79
47	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. *ISME Journal*, **2012**, 6, 1273-6	11.9	79
46	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science **2018**,		78
45	The personal human oral microbiome obscures the effects of treatment on periodontal disease. *PLoS ONE*, **2014**, 9, e86708	3.7	66
44	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	24.2	63
43	q2-sample-classifier: machine-learning tools for microbiome classification and regression. *Journal of Open Source Software*, **2018**, 3,	5.2	56
42	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. *MSystems*, **2016**, 1,	7.6	55
41	Advancing the microbiome research community. *Cell*, **2014**, 159, 227-30	56.2	50
40	Gut microbial and short-chain fatty acid profiles in adults with chronic constipation before and after treatment with lubiprostone. *Anaerobe*, **2015**, 33, 33-41	2.8	37
39	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science		36
38	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. *MSystems*, **2017**, 2,	7.6	35
37	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. *Cancer Medicine*, **2019**, 8, 617-628	4.8	33
36	Ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. *Microbiome*, **2016**, 4, 11	16.6	30
35	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. *BMC Evolutionary Biology*, **2008**, 8, 327	3	24
34	Error minimization and coding triplet/binding site associations are independent features of the canonical genetic code. *Journal of Molecular Evolution*, **2005**, 61, 597-607	3.1	24
33	Species abundance information improves sequence taxonomy classification accuracy. *Nature Communications*, **2019**, 10, 4643	17.4	22

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32	Host-associated and free-living phage communities differ profoundly in phylogenetic composition. *PLoS ONE*, **2011**, 6, e16900	3.7	21
31	Intrinsic evaluation of text mining tools may not predict performance on realistic tasks. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2008**, 640-51	1.3	20
30	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. *Cancer Medicine*, **2020**, 9, 797-806	4.8	19
29	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. *MBio*, **2020**, 11,	7.8	18
28	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. *GigaScience*, **2016**, 5, 27	7.6	16
27	A hybrid DNA extraction method for the qualitative and quantitative assessment of bacterial communities from poultry production samples. *Journal of Visualized Experiments*, **2014**,	1.6	16
26	Impact of Different Exercise Modalities on the Human Gut Microbiome. *Sports*, **2021**, 9,	3	15
25	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	2.8	13
24	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. *MSphere*, **2019**, 4,	5	11
23	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. *Evolutionary Applications*, **2020**, 13, 1984-1999	4.8	9
22	An Introduction to Applied Bioinformatics: a free, open, and interactive text. *The Journal of Open Source Education*, **2018**, 1,	1.2	9
21	Microbiotyping the Sinonasal Microbiome. *Frontiers in Cellular and Infection Microbiology*, **2020**, 10, 137	5.9	8
20	q2-longitudinal: a QIIME 2 plugin for longitudinal and paired-sample analyses of microbiome data		8
19	Rapid pattern development for concept recognition systems: application to point mutations. *Journal of Bioinformatics and Computational Biology*, **2007**, 5, 1233-59	1	7
18	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. *F1000Research*, **2020**, 9, 657	3.6	7
17	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	4	6
16	Defining the Pandemic at the State Level: Sequence-Based Epidemiology of the SARS-CoV-2 virus by the Arizona COVID-19 Genomics Union (ACGU)		5
15	Leptospira in river and soil in a highly endemic area of Ecuador. *BMC Microbiology*, **2021**, 21, 17	4.5	5

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14	INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS **2007**,		4
13	Optimizing taxonomic classification of marker gene amplicon sequences		4
12	q2-sample-classifier: machine-learning tools for microbiome classification and regression		4
11	cual-id: Globally Unique, Correctable, and Human-Friendly Sample Identifiers for Comparative Omics Studies. *MSystems*, **2016**, 1,	7.6	4
10	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. *Microbiology Spectrum*, **2021**, 9, e0013821	8.9	3
9	Species abundance information improves sequence taxonomy classification accuracy		2
8	The international sinonasal microbiome study (ISMS): a multi-centre, multi-national collaboration characterising the microbial ecology of the sinonasal cavity		2
7	Designing Inclusive HPV Cancer Vaccines and Increasing Uptake among Native Americans-A Cultural Perspective Review. *Current Oncology*, **2021**, 28, 3705-3716	2.8	2
6	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. *Springer Protocols*, **2015**, 89-113	0.3	1
5	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. *F1000Research*,9, 657	3.6	1
4	Lack of Evidence that Ursodeoxycholic Acid's Effects on the Gut Microbiome Influence Colorectal Adenoma Risk		1
3	Microbiotyping the sinonasal microbiome		1
2	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. *PLoS Computational Biology*, **2021**, 17, e1009056	5	0
1	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment.. *PLoS Computational Biology*, **2022**, 18, e1009876	5	0