

J Gregory Caporaso

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment.. <i>PLoS Computational Biology</i> , 2022 , 18, e1009876	5	0
84	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021 , 17, e1009056	5	0
83	Leptospira in river and soil in a highly endemic area of Ecuador. <i>BMC Microbiology</i> , 2021 , 21, 17	4.5	5
82	Designing Inclusive HPV Cancer Vaccines and Increasing Uptake among Native Americans-A Cultural Perspective Review. <i>Current Oncology</i> , 2021 , 28, 3705-3716	2.8	2
81	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. <i>Microbiology Spectrum</i> , 2021 , 9, e0013821	8.9	3
80	Impact of Different Exercise Modalities on the Human Gut Microbiome. <i>Sports</i> , 2021 , 9,	3	15
79	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020 , 11,	7.8	18
78	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020 , 6, 192-204	12.5	79
77	QIIME 2 Enables Comprehensive End-to-End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020 , 70, e100	24.2	63
76	Microbiotyping the Sinonasal Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020 , 10, 137	5.9	8
75	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , 2020 , 13, 1984-1999	4.8	9
74	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020 , 9, 657	3.6	7
73	Oral microbial community composition is associated with pancreatic cancer: A case-control study in Iran. <i>Cancer Medicine</i> , 2020 , 9, 797-806	4.8	19
72	Association of Body Mass Index with Fecal Microbial Diversity and Metabolites in the Northern Finland Birth Cohort. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 2289-2299	4	6
71	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , 2019 , 8, 617-628	4.8	33
70	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , 2019 , 4,	5	11
69	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of <i>Clostridioides (Clostridium) difficile</i> , despite cellular susceptibility to its toxins. <i>Anaerobe</i> , 2019 , 58, 53-72 ⁸	2.8	13

68	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. <i>Scientific Reports</i> , 2019 , 9, 5821	4.9	240
67	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
66	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019 , 10, 4643	17.4	22
65	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018 , 24, 392-400	50.5	823
64	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018 , 6, 90	16.6	1227
63	An Introduction to Applied Bioinformatics: a free, open, and interactive text. <i>The Journal of Open Source Education</i> , 2018 , 1,	1.2	9
62	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018 , 3,	5.2	56
61	QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 2018 ,		78
60	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018 , 3,	7.6	104
59	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018 , 15, 796-798	21.6	231
58	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018 , 15, 962-968	21.6	608
57	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017 , 5, 10	16.6	595
56	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017 , 2,	7.6	80
55	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017 , 2,	7.6	35
54	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016 , 1,	7.6	55
53	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016 , 1,	7.6	84
52	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016 , 5, 27	7.6	16
51	Ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016 , 4, 11	16.6	30

50	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016 , 1,	7.6	120
49	qual-id: Globally Unique, Correctable, and Human-Friendly Sample Identifiers for Comparative Omics Studies. <i>MSystems</i> , 2016 , 1,	7.6	4
48	Accurate Estimation of Fungal Diversity and Abundance through Improved Lineage-Specific Primers Optimized for Illumina Amplicon Sequencing. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 7217-7226	4.8	180
47	Quantitative microbial ecology through stable isotope probing. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 7570-81	4.8	143
46	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. <i>Springer Protocols</i> , 2015 , 89-113	0.3	1
45	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <i>Microbiome</i> , 2015 , 3, 20	16.6	88
44	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. <i>Environmental Microbiology</i> , 2015 , 17, 4078-88	5.2	88
43	Gut microbial and short-chain fatty acid profiles in adults with chronic constipation before and after treatment with lubiprostone. <i>Anaerobe</i> , 2015 , 33, 33-41	2.8	37
42	Conducting a microbiome study. <i>Cell</i> , 2014 , 158, 250-262	56.2	428
41	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014 , 5, 4500	17.4	330
40	Advancing the microbiome research community. <i>Cell</i> , 2014 , 159, 227-30	56.2	50
39	The personal human oral microbiome obscures the effects of treatment on periodontal disease. <i>PLoS ONE</i> , 2014 , 9, e86708	3.7	66
38	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014 , 2, e545	3.1	395
37	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014 , 15, 531	18.3	255
36	A hybrid DNA extraction method for the qualitative and quantitative assessment of bacterial communities from poultry production samples. <i>Journal of Visualized Experiments</i> , 2014 ,	1.6	16
35	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013 , 31, 814-21	44.5	5270
34	Advancing our understanding of the human microbiome using QIIME. <i>Methods in Enzymology</i> , 2013 , 531, 371-444	1.7	373
33	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013 , 10, 57-9	21.6	2167

32	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013 , 2, e004589	58.9	616
31	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, 21390-5	11.5	956
30	The Western English Channel contains a persistent microbial seed bank. <i>ISME Journal</i> , 2012 , 6, 1089-93	11.9	140
29	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012 , 27, 233-43	10.9	322
28	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012 , 1, 7	7.6	484
27	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012 , 6, 1621-4	11.9	5059
26	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012 , 486, 222-7	50.4	4616
25	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. <i>ISME Journal</i> , 2012 , 6, 1273-6	11.9	79
24	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 Suppl 1, 4516-22	11.5	4742
23	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011 , 12, R50	18.3	723
22	Host-associated and free-living phage communities differ profoundly in phylogenetic composition. <i>PLoS ONE</i> , 2011 , 6, e16900	3.7	21
21	PrimerProspector: de novo design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011 , 27, 1159-61	7.2	273
20	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
19	PyNAST: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010 , 26, 266-7	7.2	2728
18	Detecting coevolution without phylogenetic trees? Tree-ignorant metrics of coevolution perform as well as tree-aware metrics. <i>BMC Evolutionary Biology</i> , 2008 , 8, 327	3	24
17	Intrinsic evaluation of text mining tools may not predict performance on realistic tasks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008 , 640-51	1.3	20
16	Rapid pattern development for concept recognition systems: application to point mutations. <i>Journal of Bioinformatics and Computational Biology</i> , 2007 , 5, 1233-59	1	7
15	MutationFinder: a high-performance system for extracting point mutation mentions from text. <i>Bioinformatics</i> , 2007 , 23, 1862-5	7.2	106

14 PyCogent: a toolkit for making sense from sequence. *Genome Biology*, **2007**, 8, R171 18.3 151

13 INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS **2007**, 4

12 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

11 Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. *F1000Research*, **9**, 657 3.6 1

10 QIIME 2: Reproducible, interactive, scalable, and extensible microbiome data science 36

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5 q2-longitudinal: a QIIME 2 plugin for longitudinal and paired-sample analyses of microbiome data 8

4 Lack of Evidence that Ursodeoxycholic Acid Effects on the Gut Microbiome Influence Colorectal Adenoma Risk 1

3 q2-sample-classifier: machine-learning tools for microbiome classification and regression 4

2 The international sinonasal microbiome study (ISMS): a multi-centre, multi-national collaboration characterising the microbial ecology of the sinonasal cavity 2

1 Microbiotyping the sinonasal microbiome 1