

J Gregory Caporaso

List of Publications by Year in descending order

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Version: 2024-02-01

74
papers

98,173
citations

57681

46
h-index

84171

75
g-index

106
all docs

106
docs citations

106
times ranked

83470
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment. <i>PLoS Computational Biology</i> , 2022, 18, e1009876.	1.5	21
2	Leptospira in river and soil in a highly endemic area of Ecuador. <i>BMC Microbiology</i> , 2021, 21, 17.	1.3	16
3	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. <i>PLoS Computational Biology</i> , 2021, 17, e1009056.	1.5	2
4	Designing Inclusive HPV Cancer Vaccines and Increasing Uptake among Native Americansâ€”A Cultural Perspective Review. <i>Current Oncology</i> , 2021, 28, 3705-3716.	0.9	10
5	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. <i>Microbiology Spectrum</i> , 2021, 9, e0013821.	1.2	10
6	Impact of Different Exercise Modalities on the Human Gut Microbiome. <i>Sports</i> , 2021, 9, 14.	0.7	48
7	Oral microbial community composition is associated with pancreatic cancer: A caseâ€control study in Iran. <i>Cancer Medicine</i> , 2020, 9, 797-806.	1.3	42
8	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.	1.1	20
9	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. <i>MBio</i> , 2020, 11, .	1.8	29
10	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. <i>Trends in Cancer</i> , 2020, 6, 192-204.	3.8	162
11	QIIME 2 Enables Comprehensive Endâ€toâ€End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e100.	25.8	212
12	Microbiotyping the Sinonasal Microbiome. <i>Frontiers in Cellular and Infection Microbiology</i> , 2020, 10, 137.	1.8	21
13	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. <i>Evolutionary Applications</i> , 2020, 13, 1984-1999.	1.5	17
14	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 2020, 9, 657.	0.8	14
15	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
16	Species abundance information improves sequence taxonomy classification accuracy. <i>Nature Communications</i> , 2019, 10, 4643.	5.8	86
17	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. <i>Cancer Medicine</i> , 2019, 8, 617-628.	1.3	71
18	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. <i>MSphere</i> , 2019, 4, .	1.3	19

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19	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.	1.0	20
20	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5821.	1.6	414
21	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	15.2	1,593
22	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018, 3, .	1.7	210
23	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	9.0	459
24	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	9.0	1,125
25	Optimizing taxonomic classification of marker-gene amplicon sequences with QIIME 2's q2-feature-classifier plugin. <i>Microbiome</i> , 2018, 6, 90.	4.9	3,159
26	An Introduction to Applied Bioinformatics: a free, open, and interactive text.. <i>The Journal of Open Source Education</i> , 2018, 1, 27.	0.2	16
27	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018, 3, 934.	2.0	116
28	Microbiota Transfer Therapy alters gut ecosystem and improves gastrointestinal and autism symptoms: an open-label study. <i>Microbiome</i> , 2017, 5, 10.	4.9	901
29	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017, 2, .	1.7	141
30	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	1.7	47
31	cual-id: Globally Unique, Correctable, and Human-Friendly Sample Identifiers for Comparative Omics Studies. <i>MSystems</i> , 2016, 1, .	1.7	6
32	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.	1.4	321
33	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	1.7	89
34	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016, 1, .	1.7	110
35	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016, 5, 27.	3.3	35
36	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	4.9	51

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37	Open-Source Sequence Clustering Methods Improve the State Of the Art. <i>MSystems</i> , 2016, 1, .	1.7	155
38	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. <i>Springer Protocols</i> , 2015, , 89-113.	0.1	4
39	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. <i>Microbiome</i> , 2015, 3, 20.	4.9	115
40	Continental-scale variation in seaweed host-associated bacterial communities is a function of host condition, not geography. <i>Environmental Microbiology</i> , 2015, 17, 4078-4088.	1.8	160
41	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.	1.0	49
42	Quantitative Microbial Ecology through Stable Isotope Probing. <i>Applied and Environmental Microbiology</i> , 2015, 81, 7570-7581.	1.4	242
43	The Personal Human Oral Microbiome Obscures the Effects of Treatment on Periodontal Disease. <i>PLoS ONE</i> , 2014, 9, e86708.	1.1	79
44	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. <i>PeerJ</i> , 2014, 2, e545.	0.9	535
45	Temporal variability is a personalized feature of the human microbiome. <i>Genome Biology</i> , 2014, 15, 531.	3.8	355
46	Conducting a Microbiome Study. <i>Cell</i> , 2014, 158, 250-262.	13.5	625
47	Individual diet has sex-dependent effects on vertebrate gut microbiota. <i>Nature Communications</i> , 2014, 5, 4500.	5.8	464
48	Advancing the Microbiome Research Community. <i>Cell</i> , 2014, 159, 227-230.	13.5	64
49	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, , .	0.2	22
50	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. <i>Nature Biotechnology</i> , 2013, 31, 814-821.	9.4	8,049
51	Advancing Our Understanding of the Human Microbiome Using QIIME. <i>Methods in Enzymology</i> , 2013, 531, 371-444.	0.4	553
52	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 57-59.	9.0	3,402
53	Cohabiting family members share microbiota with one another and with their dogs. <i>ELife</i> , 2013, 2, e00458.	2.8	801
54	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.	3.3	1,260

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55	The Western English Channel contains a persistent microbial seed bank. <i>ISME Journal</i> , 2012, 6, 1089-1093.	4.4	170
56	Sequencing our way towards understanding global eukaryotic biodiversity. <i>Trends in Ecology and Evolution</i> , 2012, 27, 233-243.	4.2	395
57	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. <i>GigaScience</i> , 2012, 1, 7.	3.3	671
58	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. <i>ISME Journal</i> , 2012, 6, 1621-1624.	4.4	7,430
59	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012, 486, 222-227.	13.7	6,247
60	Comparison of Illumina paired-end and single-direction sequencing for microbial 16S rRNA gene amplicon surveys. <i>ISME Journal</i> , 2012, 6, 1273-1276.	4.4	102
61	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.	3.3	7,425
62	Moving pictures of the human microbiome. <i>Genome Biology</i> , 2011, 12, R50.	13.9	934
63	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. <i>PLoS ONE</i> , 2011, 6, e16900.	1.1	43
64	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. <i>Bioinformatics</i> , 2011, 27, 1159-1161.	1.8	351
65	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010, 7, 335-336.	9.0	31,818
66	PyNAST: a flexible tool for aligning sequences to a template alignment. <i>Bioinformatics</i> , 2010, 26, 266-267.	1.8	3,400
67	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.	3.2	25
68	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.	0.7	21
69	RAPID PATTERN DEVELOPMENT FOR CONCEPT RECOGNITION SYSTEMS: APPLICATION TO POINT MUTATIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2007, 05, 1233-1259.	0.3	8
70	MutationFinder: a high-performance system for extracting point mutation mentions from text. <i>Bioinformatics</i> , 2007, 23, 1862-1865.	1.8	132
71	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
72	INTRINSIC EVALUATION OF TEXT MINING TOOLS MAY NOT PREDICT PERFORMANCE ON REALISTIC TASKS. , 2007, , .		12

#	ARTICLE	IF	CITATIONS
73	Error Minimization and Coding Triplet/Binding Site Associations Are Independent Features of the Canonical Genetic Code. <i>Journal of Molecular Evolution</i> , 2005, 61, 597-607.	0.8	32
74	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. <i>F1000Research</i> , 0, 9, 657.	0.8	8