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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	Multi-omics data integration reveals metabolome as the top predictor of the cervicovaginal microenvironment. PLoS Computational Biology, 2022, 18, e1009876.	3.2	21
2	Leptospira in river and soil in a highly endemic area of Ecuador. BMC Microbiology, 2021, 21, 17.	3.3	16
3	Experiences and lessons learned from two virtual, hands-on microbiome bioinformatics workshops. PLoS Computational Biology, 2021, 17, e1009056.	3.2	2
4	Designing Inclusive HPV Cancer Vaccines and Increasing Uptake among Native Americansâ€”A Cultural Perspective Review. Current Oncology, 2021, 28, 3705-3716.	2.2	10
5	Cigarette Smoking and Opium Use in Relation to the Oral Microbiota in Iran. Microbiology Spectrum, 2021, 9, e0013821.	3.0	10
6	Impact of Different Exercise Modalities on the Human Gut Microbiome. Sports, 2021, 9, 14.	1.7	48
7	Oral microbial community composition is associated with pancreatic cancer: A caseâ€”control study in Iran. Cancer Medicine, 2020, 9, 797-806.	2.8	42
8	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
9	An Early Pandemic Analysis of SARS-CoV-2 Population Structure and Dynamics in Arizona. MBio, 2020, 11, .	4.1	29
10	The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204.	7.4	162
11	QIIME 2 Enables Comprehensive Endâ€”toâ€”End Analysis of Diverse Microbiome Data and Comparative Studies with Publicly Available Data. Current Protocols in Bioinformatics, 2020, 70, e100.	25.8	212
12	Microbiotyping the Sinonasal Microbiome. Frontiers in Cellular and Infection Microbiology, 2020, 10, 137.	3.9	21
13	Phylogenetic farming: Can evolutionary history predict crop rotation via the soil microbiome?. Evolutionary Applications, 2020, 13, 1984-1999.	3.1	17
14	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 2020, 9, 657.	1.6	14
15	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	17.5	11,167
16	Species abundance information improves sequence taxonomy classification accuracy. Nature Communications, 2019, 10, 4643.	12.8	86
17	Effects of ursodeoxycholic acid on the gut microbiome and colorectal adenoma development. Cancer Medicine, 2019, 8, 617-628.	2.8	71
18	Rapidly Processed Stool Swabs Approximate Stool Microbiota Profiles. MSphere, 2019, 4, .	2.9	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.	2.1	20
20	Long-term benefit of Microbiota Transfer Therapy on autism symptoms and gut microbiota. <i>Scientific Reports</i> , 2019, 9, 5821.	3.3	414
21	Current understanding of the human microbiome. <i>Nature Medicine</i> , 2018, 24, 392-400.	30.7	1,593
22	q2-longitudinal: Longitudinal and Paired-Sample Analyses of Microbiome Data. <i>MSystems</i> , 2018, 3, .	3.8	210
23	Qiita: rapid, web-enabled microbiome meta-analysis. <i>Nature Methods</i> , 2018, 15, 796-798.	19.0	459
24	Species-level functional profiling of metagenomes and metatranscriptomes. <i>Nature Methods</i> , 2018, 15, 962-968.	19.0	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.	11.1	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.	0.4	16
27	q2-sample-classifier: machine-learning tools for microbiome classification and regression. <i>Journal of Open Source Software</i> , 2018, 3, 934.	4.6	116
28	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
29	Significant Impacts of Increasing Aridity on the Arid Soil Microbiome. <i>MSystems</i> , 2017, 2, .	3.8	141
30	Multi-omics Analysis of Periodontal Pocket Microbial Communities Pre- and Posttreatment. <i>MSystems</i> , 2017, 2, .	3.8	47
31	cual-id: Globally Unique, Correctable, and Human-Friendly Sample Identifiers for Comparative Omics Studies. <i>MSystems</i> , 2016, 1, .	3.8	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.	3.1	321
33	mockrobiota: a Public Resource for Microbiome Bioinformatics Benchmarking. <i>MSystems</i> , 2016, 1, .	3.8	89
34	Geography and Location Are the Primary Drivers of Office Microbiome Composition. <i>MSystems</i> , 2016, 1, .	3.8	110
35	Keemei: cloud-based validation of tabular bioinformatics file formats in Google Sheets. <i>GigaScience</i> , 2016, 5, 27.	6.4	35
36	ghost-tree: creating hybrid-gene phylogenetic trees for diversity analyses. <i>Microbiome</i> , 2016, 4, 11.	11.1	51

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37	Open-Source Sequence Clustering Methods Improve the State Of the Art. MSystems, 2016, 1, .	3.8	155
38	Using QIIME to Evaluate the Microbial Communities Within Hydrocarbon Environments. Springer Protocols, 2015, , 89-113.	0.3	4
39	Stability of operational taxonomic units: an important but neglected property for analyzing microbial diversity. Microbiome, 2015, 3, 20.	11.1	115
40	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
41	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
42	Quantitative Microbial Ecology through Stable Isotope Probing. Applied and Environmental Microbiology, 2015, 81, 7570-7581.	3.1	242
43	The Personal Human Oral Microbiome Obscures the Effects of Treatment on Periodontal Disease. PLoS ONE, 2014, 9, e86708.	2.5	79
44	Subsampled open-reference clustering creates consistent, comprehensive OTU definitions and scales to billions of sequences. PeerJ, 2014, 2, e545.	2.0	535
45	Temporal variability is a personalized feature of the human microbiome. Genome Biology, 2014, 15, 531.	8.8	355
46	Conducting a Microbiome Study. Cell, 2014, 158, 250-262.	28.9	625
47	Individual diet has sex-dependent effects on vertebrate gut microbiota. Nature Communications, 2014, 5, 4500.	12.8	464
48	Advancing the Microbiome Research Community. Cell, 2014, 159, 227-230.	28.9	64
49	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
50	Predictive functional profiling of microbial communities using 16S rRNA marker gene sequences. Nature Biotechnology, 2013, 31, 814-821.	17.5	8,049
51	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
52	Quality-filtering vastly improves diversity estimates from Illumina amplicon sequencing. Nature Methods, 2013, 10, 57-59.	19.0	3,402
53	Cohabiting family members share microbiota with one another and with their dogs. ELife, 2013, 2, e00458.	6.0	801
54	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, 21390-21395.	7.1	1,260

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55	The Western English Channel contains a persistent microbial seed bank. ISME Journal, 2012, 6, 1089-1093.	9.8	170
56	Sequencing our way towards understanding global eukaryotic biodiversity. Trends in Ecology and Evolution, 2012, 27, 233-243.	8.7	395
57	The Biological Observation Matrix (BIOM) format or: how I learned to stop worrying and love the ome-ome. GigaScience, 2012, 1, 7.	6.4	671
58	Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. ISME Journal, 2012, 6, 1621-1624.	9.8	7,430
59	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	27.8	6,247
60	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
61	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, 4516-4522.	7.1	7,425
62	Moving pictures of the human microbiome. Genome Biology, 2011, 12, R50.	9.6	934
63	Host-Associated and Free-Living Phage Communities Differ Profoundly in Phylogenetic Composition. PLoS ONE, 2011, 6, e16900.	2.5	43
64	PrimerProspector: <i>de novo</i> design and taxonomic analysis of barcoded polymerase chain reaction primers. Bioinformatics, 2011, 27, 1159-1161.	4.1	351
65	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	19.0	31,818
66	PyNASt: a flexible tool for aligning sequences to a template alignment. Bioinformatics, 2010, 26, 266-267.	4.1	3,400
67	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
68	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
69	RAPID PATTERN DEVELOPMENT FOR CONCEPT RECOGNITION SYSTEMS: APPLICATION TO POINT MUTATIONS. Journal of Bioinformatics and Computational Biology, 2007, 05, 1233-1259.	0.8	8
70	MutationFinder: a high-performance system for extracting point mutation mentions from text. Bioinformatics, 2007, 23, 1862-1865.	4.1	132
71	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	9.6	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. Journal of Molecular Evolution, 2005, 61, 597-607.	1.8	32
74	Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity. F1000Research, 0, 9, 657.	1.6	8