

Catherine Lozupone

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10806934/publications.pdf>

Version: 2024-02-01

24
papers

33,103
citations

304368

22
h-index

610482

24
g-index

24
all docs

24
docs citations

24
times ranked

37588
citing authors

#	ARTICLE	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857.	9.4	11,167
2	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. <i>Applied and Environmental Microbiology</i> , 2005, 71, 8228-8235.	1.4	7,007
3	Evolution of Mammals and Their Gut Microbes. <i>Science</i> , 2008, 320, 1647-1651.	6.0	3,171
4	Soil bacterial and fungal communities across a pH gradient in an arable soil. <i>ISME Journal</i> , 2010, 4, 1340-1351.	4.4	3,154
5	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011, 5, 169-172.	4.4	2,280
6	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017, 5, 27.	4.9	1,434
7	UniFrac—an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006, 7, 371.	1.2	1,321
8	Fast UniFrac: facilitating high-throughput phylogenetic analyses of microbial communities including analysis of pyrosequencing and PhyloChip data. <i>ISME Journal</i> , 2010, 4, 17-27.	4.4	1,025
9	Short pyrosequencing reads suffice for accurate microbial community analysis. <i>Nucleic Acids Research</i> , 2007, 35, e120-e120.	6.5	638
10	Metagenomic and Small-Subunit rRNA Analyses Reveal the Genetic Diversity of Bacteria, Archaea, Fungi, and Viruses in Soil. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7059-7066.	1.4	480
11	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. <i>Nature Methods</i> , 2010, 7, 813-819.	9.0	249
12	Widespread Colonization of the Lung by <i>Tropheryma whippelii</i> in HIV Infection. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2013, 187, 1110-1117.	2.5	175
13	PyCogent: a toolkit for making sense from sequence. <i>Genome Biology</i> , 2007, 8, R171.	13.9	170
14	Biogeography and habitat modelling of high-alpine bacteria. <i>Nature Communications</i> , 2010, 1, 53.	5.8	141
15	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , 2012, 22, 1974-1984.	2.4	120
16	Gut bacteria in children with autism spectrum disorders: challenges and promise of studying how a complex community influences a complex disease. <i>Microbial Ecology in Health and Disease</i> , 2015, 26, 26914.	3.8	105
17	Host-bacterial coevolution and the search for new drug targets. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 109-114.	2.8	104
18	The Cladistic Basis for the Phylogenetic Diversity (PD) Measure Links Evolutionary Features to Environmental Gradients and Supports Broad Applications of Microbial Ecology's Phylogenetic Beta Diversity Framework. <i>International Journal of Molecular Sciences</i> , 2009, 10, 4723-4741.	1.8	80

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19	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. <i>MSystems</i> , 2017, 2, .	1.7	75
20	Fecal Bacterial Communities in treated HIV infected individuals on two antiretroviral regimens. <i>Scientific Reports</i> , 2017, 7, 43741.	1.6	67
21	Gut microbiome of mothers delivering prematurely shows reduced diversity and lower relative abundance of <i>Bifidobacterium</i> and <i>Streptococcus</i> . <i>PLoS ONE</i> , 2017, 12, e0184336.	1.1	53
22	Stable tRNA-based phylogenies using only 76 nucleotides. <i>Rna</i> , 2010, 16, 1469-1477.	1.6	36
23	The Gut Microbiome in Autism: Study-Site Effects and Longitudinal Analysis of Behavior Change. <i>MSystems</i> , 2021, 6, .	1.7	28
24	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. <i>Trends in Microbiology</i> , 2011, 19, 472-482.	3.5	23