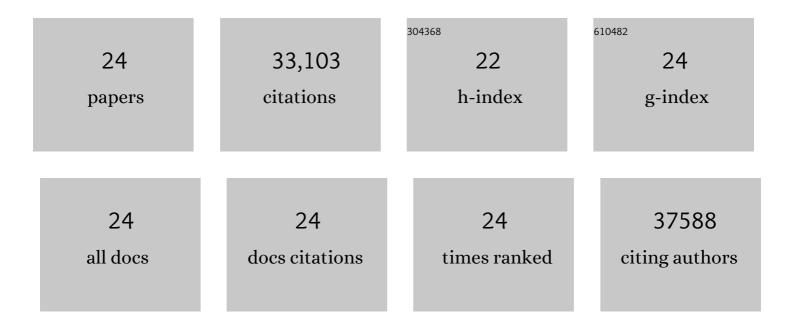
Catherine Lozupone

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10806934/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
2	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. Applied and Environmental Microbiology, 2005, 71, 8228-8235.	1.4	7,007
3	Evolution of Mammals and Their Gut Microbes. Science, 2008, 320, 1647-1651.	6.0	3,171
4	Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME Journal, 2010, 4, 1340-1351.	4.4	3,154
5	UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172.	4.4	2,280
6	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
7	UniFracan online tool for comparing microbial community diversity in a phylogenetic context. BMC Bioinformatics, 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. ISME Journal, 2010, 4, 17-27.	4.4	1,025
9	Short pyrosequencing reads suffice for accurate microbial community analysis. Nucleic Acids Research, 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. Applied and Environmental Microbiology, 2007, 73, 7059-7066.	1.4	480
11	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. Nature Methods, 2010, 7, 813-819.	9.0	249
12	Widespread Colonization of the Lung by <i>Tropheryma whipplei</i> in HIV Infection. American Journal of Respiratory and Critical Care Medicine, 2013, 187, 1110-1117.	2.5	175
13	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	13.9	170
14	Biogeography and habitat modelling of high-alpine bacteria. Nature Communications, 2010, 1, 53.	5.8	141
15	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. Genome Research, 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. Microbial Ecology in Health and Disease, 2015, 26, 26914.	3.8	105
17	Host-bacterial coevolution and the search for new drug targets. Current Opinion in Chemical Biology, 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. International Journal of Molecular Sciences, 2009, 10, 4723-4741.	1.8	80

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