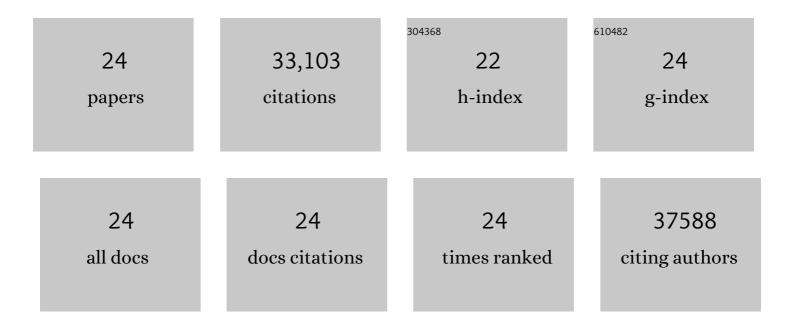
Catherine Lozupone

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The Gut Microbiome in Autism: Study-Site Effects and Longitudinal Analysis of Behavior Change. MSystems, 2021, 6, .	1.7	28
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
3	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
4	Fecal Bacterial Communities in treated HIV infected individuals on two antiretroviral regimens. Scientific Reports, 2017, 7, 43741.	1.6	67
5	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. MSystems, 2017, 2, .	1.7	75
6	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
7	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
8	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
9	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
10	Combined phylogenetic and genomic approaches for the high-throughput study of microbial habitat adaptation. Trends in Microbiology, 2011, 19, 472-482.	3.5	23
11	UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172.	4.4	2,280
12	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
13	Soil bacterial and fungal communities across a pH gradient in an arable soil. ISME Journal, 2010, 4, 1340-1351.	4.4	3,154
14	Microbial community resemblance methods differ in their ability to detect biologically relevant patterns. Nature Methods, 2010, 7, 813-819.	9.0	249
15	Stable tRNA-based phylogenies using only 76 nucleotides. Rna, 2010, 16, 1469-1477.	1.6	36
16	Biogeography and habitat modelling of high-alpine bacteria. Nature Communications, 2010, 1, 53.	5.8	141
17	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
18	Host-bacterial coevolution and the search for new drug targets. Current Opinion in Chemical Biology, 2008, 12, 109-114.	2.8	104

#	Article	IF	CITATIONS
19	Evolution of Mammals and Their Gut Microbes. Science, 2008, 320, 1647-1651.	6.0	3,171
20	Short pyrosequencing reads suffice for accurate microbial community analysis. Nucleic Acids Research, 2007, 35, e120-e120.	6.5	638
21	PyCogent: a toolkit for making sense from sequence. Genome Biology, 2007, 8, R171.	13.9	170
22	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
23	UniFracan online tool for comparing microbial community diversity in a phylogenetic context. BMC Bioinformatics, 2006, 7, 371.	1.2	1,321
24	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. Applied and Environmental Microbiology, 2005, 71, 8228-8235.	1.4	7,007