## Catherine A Lozupone

List of Publications by Year in descending order

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Version: 2024-02-01

67 papers

87,984 citations

70961 41 h-index 65 g-index

78 all docs 78 docs citations

78 times ranked 77164 citing authors

#	Article	IF	CITATIONS
1	QIIME allows analysis of high-throughput community sequencing data. Nature Methods, 2010, 7, 335-336.	9.0	31,818
2	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
3	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.	3.3	7,425
4	UniFrac: a New Phylogenetic Method for Comparing Microbial Communities. Applied and Environmental Microbiology, 2005, 71, 8228-8235.	1.4	7,007
5	Human gut microbiome viewed across age and geography. Nature, 2012, 486, 222-227.	13.7	6,247
6	Obesity alters gut microbial ecology. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 11070-11075.	3.3	5,247
7	Diversity, stability and resilience of the human gut microbiota. Nature, 2012, 489, 220-230.	13.7	4,114
8	Quantitative and Qualitative $\hat{l}^2$ Diversity Measures Lead to Different Insights into Factors That Structure Microbial Communities. Applied and Environmental Microbiology, 2007, 73, 1576-1585.	1.4	2,418
9	UniFrac: an effective distance metric for microbial community comparison. ISME Journal, 2011, 5, 169-172.	4.4	2,280
10	Global patterns in bacterial diversity. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11436-11440.	3.3	1,461
11	Normalization and microbial differential abundance strategies depend upon data characteristics. Microbiome, 2017, 5, 27.	4.9	1,434
12	UniFracan online tool for comparing microbial community diversity in a phylogenetic context. BMC Bioinformatics, 2006, 7, 371.	1.2	1,321
13	Muc5b is required for airway defence. Nature, 2014, 505, 412-416.	13.7	617
14	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. ISME Journal, 2016, 10, 1669-1681.	4.4	593
15	Alterations in the Gut Microbiota Associated with HIV-1 Infection. Cell Host and Microbe, 2013, 14, 329-339.	5.1	387
16	The Macaque Gut Microbiome in Health, Lentiviral Infection, and Chronic Enterocolitis. PLoS Pathogens, 2008, 4, e20.	2.1	371
17	Global patterns in the biogeography of bacterial taxa. Environmental Microbiology, 2011, 13, 135-144.	1.8	362
18	Meta-analyses of studies of the human microbiota. Genome Research, 2013, 23, 1704-1714.	2.4	352

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19	Low diversity gut microbiota dysbiosis: drivers, functional implications and recovery. Current Opinion in Microbiology, 2018, 44, 34-40.	2.3	262
20	Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. Anaerobe, 2018, 49, 121-131.	1.0	249
21	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
22	Gut microbiota phenotypes of obesity. Npj Biofilms and Microbiomes, 2019, 5, 18.	2.9	144
23	HIV-induced alteration in gut microbiota. Gut Microbes, 2014, 5, 562-570.	4.3	131
24	The environment, epigenome, and asthma. Journal of Allergy and Clinical Immunology, 2017, 140, 14-23.	1.5	125
25	Pre-pregnancy weight, gestational weight gain, and the gut microbiota of mothers and their infants. Microbiome, 2017, 5, 113.	4.9	123
26	Gut Microbiota in the First 2 Years of Life and the Association with Body Mass Index at Age 12 in a Norwegian Birth Cohort. MBio, 2018, 9, .	1.8	121
27	The convergence of carbohydrate active gene repertoires in human gut microbes. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 15076-15081.	3.3	120
28	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
29	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men. Microbiome, 2018, 6, 198.	4.9	111
30	Diverse Intestinal Bacteria Contain Putative Zwitterionic Capsular Polysaccharides with Anti-inflammatory Properties. Cell Host and Microbe, 2016, 20, 535-547.	5.1	108
31	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
32	Subversion of Systemic Glucose Metabolism as a Mechanism to Support the Growth of Leukemia Cells. Cancer Cell, 2018, 34, 659-673.e6.	7.7	90
33	Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. Nucleic Acids Research, 2010, 38, 3869-3879.	6.5	85
34	Selection of the simplest RNA that binds isoleucine. Rna, 2003, 9, 1315-1322.	1.6	83
35	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. EBioMedicine, 2018, 30, 192-202.	2.7	78
36	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. MSystems, 2017, 2, .	1.7	75

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37	Fecal Bacterial Communities in treated HIV infected individuals on two antiretroviral regimens. Scientific Reports, 2017, 7, 43741.	1.6	67
38	Microbiome and metabolome data integration provides insight into health and disease. Translational Research, 2017, 189, 51-64.	2.2	58
39	Gut microbiota from high-risk men who have sex with men drive immune activation in gnotobiotic mice and in vitro HIV infection. PLoS Pathogens, 2019, 15, e1007611.	2.1	55
40	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
41	Gut microbiota in adolescents and the association with fatty liver: the EPOCH study. Pediatric Research, 2018, 84, 219-227.	1.1	42
42	The Gut Microbiome in Autism: Study-Site Effects and Longitudinal Analysis of Behavior Change. MSystems, 2021, 6, .	1.7	28
43	Functional Microbiomics in Liver Transplantation: Identifying Novel Targets for Improving Allograft Outcomes. Transplantation, 2019, 103, 668-678.	0.5	25
44	Striking a Balance with Help from our Little Friends - How the Gut Microbiota Contributes to Immune Homeostasis. Yale Journal of Biology and Medicine, 2016, 89, 389-395.	0.2	24
45	Prevalence and Source of Fecal and Oral Bacteria on Infant, Child, and Adult Hands. MSystems, 2018, 3,	1.7	23
46	The unifrac significance test is sensitive to tree topology. BMC Bioinformatics, 2015, 16, 211.	1.2	22
47	A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. ISME Journal, 2020, 14, 1359-1368.	4.4	21
48	Unraveling Interactions between the Microbiome and the Host Immune System To Decipher Mechanisms of Disease. MSystems, $2018, 3, \ldots$	1.7	19
49	Can gut microbiota of men who have sex with men influence HIV transmission?. Gut Microbes, 2020, 11, 610-619.	4.3	18
50	Towards large-cohort comparative studies to define the factors influencing the gut microbial community structure of ASD patients. Microbial Ecology in Health and Disease, 2015, 26, 26555.	3.8	16
51	Alteration of the gut fecal microbiome in children living with HIV on antiretroviral therapy in Yaounde, Cameroon. Scientific Reports, 2021, 11, 7666.	1.6	15
52	Multiple-Ascending-Dose Phase 1 Clinical Study of the Safety, Tolerability, and Pharmacokinetics of CRS3123, a Narrow-Spectrum Agent with Minimal Disruption of Normal Gut Microbiota. Antimicrobial Agents and Chemotherapy, 2019, 64, .	1.4	13
53	Intestinal Parasites Infections among HIV Infected Children Under Antiretrovirals Treatment in Yaounde, Cameroon. Journal of Tropical Pediatrics, 2020, 66, 178-186.	0.7	9
54	Blood type and the microbiome- untangling a complex relationship with lessons from pathogens. Current Opinion in Microbiology, 2020, 56, 59-66.	2.3	9

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55	Multiomic Predictors of Shortâ€Term Weight Loss and Clinical Outcomes During a Behavioralâ€Based Weight Loss Intervention. Obesity, 2021, 29, 859-869.	1.5	9
56	Visualizing microbiome–immune system interplay. Immunotherapy, 2019, 11, 63-67.	1.0	8
57	Intestinal microbial communities and <i>Holdemanella</i> isolated from HIV+/â^ men who have sex with men increase frequencies of lamina propria CCR5 <sup>+</sup> CD4 <sup>+</sup> T cells. Gut Microbes, 2021, 13, 1997292.	4.3	8
58	The HIV-Associated Enteric Microbiome Has Gone Viral. Cell Host and Microbe, 2016, 19, 270-272.	5.1	7
59	Systems Analysis of Gut Microbiome Influence on Metabolic Disease in HIV-Positive and High-Risk Populations. MSystems, 2021, 6, .	1.7	7
60	VOLARE: visual analysis of disease-associated microbiome-immune system interplay. BMC Bioinformatics, 2019, 20, 432.	1.2	6
61	Dietary fat promotes antibiotic-induced Clostridioides difficile mortality in mice. Npj Biofilms and Microbiomes, 2022, $8,15.$	2.9	6
62	CANTARE: finding and visualizing network-based multi-omic predictive models. BMC Bioinformatics, 2021, 22, 80.	1.2	4
63	Disruption of Genes Encoding Putative Zwitterionic Capsular Polysaccharides of Diverse Intestinal Bacteroides Reduces the Induction of Host Anti-Inflammatory Factors. Microbial Ecology, 2023, 85, 1620-1629.	1.4	4
64	Microbial Biodiversity: Straight from the Dolphin'sÂMouth. Current Biology, 2017, 27, R1307-R1309.	1.8	0
65	Reply to Moossavi and Azad, "Quantifying and Interpreting the Association between Early-Life Gut Microbiota Composition and Childhood Obesity― MBio, 2019, 10, .	1.8	0
66	What The HIVâ€Associated Gut Microbiome May Tell As about The Role of The Adaptive Immune System in Matching Our Gut Microbes to Our Diet. FASEB Journal, 2015, 29, 105.2.	0.2	0
67	A Summary of the Sixth International Workshop on Microbiome in HIV Pathogenesis, Prevention, and Treatment. AIDS Research and Human Retroviruses, 2022, 38, 173-180.	0.5	O