

Catherine A Lozupone

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

70
papers

58,697
citations

39
h-index

78
g-index

78
ext. papers

77,320
ext. citations

10.9
avg, IF

7.4
L-index

#	Paper	IF	Citations
70	QIIME allows analysis of high-throughput community sequencing data. <i>Nature Methods</i> , 2010 , 7, 335-6	21.6	22879
69	UniFrac: a new phylogenetic method for comparing microbial communities. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 8228-35	4.8	5136
68	Global patterns of 16S rRNA diversity at a depth of millions of sequences per sample. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108 Suppl 1, 4516-22	11.5	4742
67	Human gut microbiome viewed across age and geography. <i>Nature</i> , 2012 , 486, 222-7	50.4	4616
66	Obesity alters gut microbial ecology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 11070-5	11.5	4146
65	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019 , 37, 852-857	44.5	4050
64	Diversity, stability and resilience of the human gut microbiota. <i>Nature</i> , 2012 , 489, 220-30	50.4	2919
63	Quantitative and qualitative beta diversity measures lead to different insights into factors that structure microbial communities. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 1576-85	4.8	1607
62	UniFrac: an effective distance metric for microbial community comparison. <i>ISME Journal</i> , 2011 , 5, 169-72	11.9	1474
61	UniFrac--an online tool for comparing microbial community diversity in a phylogenetic context. <i>BMC Bioinformatics</i> , 2006 , 7, 371	3.6	1131
60	Global patterns in bacterial diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 11436-40	11.5	1094
59	Normalization and microbial differential abundance strategies depend upon data characteristics. <i>Microbiome</i> , 2017 , 5, 27	16.6	840
58	Muc5b is required for airway defence. <i>Nature</i> , 2014 , 505, 412-6	50.4	450
57	Correlation detection strategies in microbial data sets vary widely in sensitivity and precision. <i>ISME Journal</i> , 2016 , 10, 1669-81	11.9	365
56	The macaque gut microbiome in health, lentiviral infection, and chronic enterocolitis. <i>PLoS Pathogens</i> , 2008 , 4, e20	7.6	334
55	Meta-analyses of studies of the human microbiota. <i>Genome Research</i> , 2013 , 23, 1704-14	9.7	289
54	Alterations in the gut microbiota associated with HIV-1 infection. <i>Cell Host and Microbe</i> , 2013 , 14, 329-39	23.4	284

53	Global patterns in the biogeography of bacterial taxa. <i>Environmental Microbiology</i> , 2011 , 13, 135-144	5.2	279
52	Differences in fecal microbial metabolites and microbiota of children with autism spectrum disorders. <i>Anaerobe</i> , 2018 , 49, 121-131	2.8	155
51	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, 1110-7	10.2	140
50	Low diversity gut microbiota dysbiosis: drivers, functional implications and recovery. <i>Current Opinion in Microbiology</i> , 2018 , 44, 34-40	7.9	138
49	HIV-induced alteration in gut microbiota: driving factors, consequences, and effects of antiretroviral therapy. <i>Gut Microbes</i> , 2014 , 5, 562-70	8.8	106
48	The convergence of carbohydrate active gene repertoires in human gut microbes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15076-81	11.5	102
47	Identifying genomic and metabolic features that can underlie early successional and opportunistic lifestyles of human gut symbionts. <i>Genome Research</i> , 2012 , 22, 1974-84	9.7	97
46	The environment, epigenome, and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 14-23	11.5	92
45	Pre-pregnancy weight, gestational weight gain, and the gut microbiota of mothers and their infants. <i>Microbiome</i> , 2017 , 5, 113	16.6	81
44	Gut Microbiota in the First 2 Years of Life and the Association with Body Mass Index at Age 12 in a Norwegian Birth Cohort. <i>MBio</i> , 2018 , 9,	7.8	80
43	Ribosomal RNA diversity predicts genome diversity in gut bacteria and their relatives. <i>Nucleic Acids Research</i> , 2010 , 38, 3869-79	20.1	74
42	Diverse Intestinal Bacteria Contain Putative Zwitterionic Capsular Polysaccharides with Anti-inflammatory Properties. <i>Cell Host and Microbe</i> , 2016 , 20, 535-547	23.4	73
41	Selection of the simplest RNA that binds isoleucine. <i>Rna</i> , 2003 , 9, 1315-22	5.8	72
40	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	7.0	
39	An exploration of <i>Prevotella</i> -rich microbiomes in HIV and men who have sex with men. <i>Microbiome</i> , 2018 , 6, 198	16.6	64
38	Gut microbiota phenotypes of obesity. <i>Npj Biofilms and Microbiomes</i> , 2019 , 5, 18	8.2	60
37	Subversion of Systemic Glucose Metabolism as a Mechanism to Support the Growth of Leukemia Cells. <i>Cancer Cell</i> , 2018 , 34, 659-673.e6	24.3	55
36	Fecal Microbiota Composition Drives Immune Activation in HIV-infected Individuals. <i>EBioMedicine</i> , 2018 , 30, 192-202	8.8	53

35	Microbiome and metabolome data integration provides insight into health and disease. <i>Translational Research</i> , 2017 , 189, 51-64	11	49
34	Perinatal Bisphenol A Exposure Induces Chronic Inflammation in Rabbit Offspring via Modulation of Gut Bacteria and Their Metabolites. <i>MSystems</i> , 2017 , 2,	7.6	48
33	Fecal Bacterial Communities in treated HIV infected individuals on two antiretroviral regimens. <i>Scientific Reports</i> , 2017 , 7, 43741	4.9	45
32	Gut microbiota from high-risk men who have sex with men drive immune activation in gnotobiotic mice and in vitro HIV infection. <i>PLoS Pathogens</i> , 2019 , 15, e1007611	7.6	30
31	Gut microbiome of mothers delivering prematurely shows reduced diversity and lower relative abundance of Bifidobacterium and Streptococcus. <i>PLoS ONE</i> , 2017 , 12, e0184336	3.7	29
30	Gut microbiota in adolescents and the association with fatty liver: the EPOCH study. <i>Pediatric Research</i> , 2018 , 84, 219-227	3.2	23
29	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		23
28	Prevalence and Source of Fecal and Oral Bacteria on Infant, Child, and Adult Hands. <i>MSystems</i> , 2018 , 3,	7.6	16
27	Striking a Balance with Help from our Little Friends - How the Gut Microbiota Contributes to Immune Homeostasis. <i>Yale Journal of Biology and Medicine</i> , 2016 , 89, 389-395	2.4	16
26	The UniFrac significance test is sensitive to tree topology. <i>BMC Bioinformatics</i> , 2015 , 16, 211	3.6	14
25	Unraveling Interactions between the Microbiome and the Host Immune System To Decipher Mechanisms of Disease. <i>MSystems</i> , 2018 , 3,	7.6	13
24	Towards large-cohort comparative studies to define the factors influencing the gut microbial community structure of ASD patients. <i>Microbial Ecology in Health and Disease</i> , 2015 , 26, 26555		13
23	Functional Microbiomics in Liver Transplantation: Identifying Novel Targets for Improving Allograft Outcomes. <i>Transplantation</i> , 2019 , 103, 668-678	1.8	12
22	A phylogenetic model for the recruitment of species into microbial communities and application to studies of the human microbiome. <i>ISME Journal</i> , 2020 , 14, 1359-1368	11.9	12
21	Author response: Cohabiting family members share microbiota with one another and with their dogs 2013 ,		11
20	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. <i>Antimicrobial Agents and Chemotherapy</i> , 2019 , 64,	5.9	8
19	The Gut Microbiome in Autism: Study-Site Effects and Longitudinal Analysis of Behavior Change. <i>MSystems</i> , 2021 , 6,	7.6	7
18	Blood type and the microbiome- untangling a complex relationship with lessons from pathogens. <i>Current Opinion in Microbiology</i> , 2020 , 56, 59-66	7.9	6

17	Effects of library size variance, sparsity, and compositionality on the analysis of microbiome data		5
16	Can gut microbiota of men who have sex with men influence HIV transmission?. <i>Gut Microbes</i> , 2020 , 11, 610-619	8.8	5
15	Alteration of the gut fecal microbiome in children living with HIV on antiretroviral therapy in Yaounde, Cameroon. <i>Scientific Reports</i> , 2021 , 11, 7666	4.9	5
14	Visualizing microbiome-immune system interplay. <i>Immunotherapy</i> , 2019 , 11, 63-67	3.8	4
13	Intestinal Parasites Infections among HIV Infected Children Under Antiretrovirals Treatment in Yaounde, Cameroon. <i>Journal of Tropical Pediatrics</i> , 2020 , 66, 178-186	1.2	4
12	The HIV-Associated Enteric Microbiome Has Gone Viral. <i>Cell Host and Microbe</i> , 2016 , 19, 270-2	23.4	3
11	VOLARE: visual analysis of disease-associated microbiome-immune system interplay. <i>BMC Bioinformatics</i> , 2019 , 20, 432	3.6	3
10	SCNIC: Sparse Correlation Network Investigation for Compositional Data		3
9	Systems Analysis of Gut Microbiome Influence on Metabolic Disease in HIV-Positive and High-Risk Populations. <i>MSystems</i> , 2021 , 6,	7.6	3
8	An exploration of Prevotella-rich microbiomes in HIV and men who have sex with men		2
7	Multiomic Predictors of Short-Term Weight Loss and Clinical Outcomes During a Behavioral-Based Weight Loss Intervention. <i>Obesity</i> , 2021 , 29, 859-869	8	1
6	CANTARE: finding and visualizing network-based multi-omic predictive models. <i>BMC Bioinformatics</i> , 2021 , 22, 80	3.6	1
5	Intestinal microbial communities and isolated from HIV+/- men who have sex with men increase frequencies of lamina propria CCR5 CD4 T cells. <i>Gut Microbes</i> , 2021 , 13, 1997292	8.8	0
4	Dietary fat promotes antibiotic-induced Clostridioides difficile mortality in mice.. <i>Npj Biofilms and Microbiomes</i> , 2022 , 8, 15	8.2	0
3	Microbial Biodiversity: Straight from the Dolphin's Mouth. <i>Current Biology</i> , 2017 , 27, R1307-R1309	6.3	
2	What The HIV-Associated Gut Microbiome May Tell As about The Role of The Adaptive Immune System in Matching Our Gut Microbes to Our Diet. <i>FASEB Journal</i> , 2015 , 29, 105.2	0.9	
1	Reply to Moossavi and Azad, "Quantifying and Interpreting the Association between Early-Life Gut Microbiota Composition and Childhood Obesity". <i>MBio</i> , 2019 , 10,	7.8	