Paul J Mcmurdie

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1858789/publications.pdf

Version: 2024-02-01

25 papers 41,254 citations

361413 20 h-index 677142 22 g-index

26 all docs

26 docs citations

26 times ranked 39219 citing authors

#	Article	IF	Citations
1	Increased circulating butyrate and ursodeoxycholate during probiotic intervention in humans with type 2 diabetes. BMC Microbiology, 2022, 22, 19.	3.3	14
2	Butyrate-producing human gut symbiont, <i>Clostridium butyricum</i> , and its role in health and disease. Gut Microbes, 2021, 13, 1-28.	9.8	157
3	Improvements to postprandial glucose control in subjects with type 2 diabetes: a multicenter, double blind, randomized placebo-controlled trial of a novel probiotic formulation. BMJ Open Diabetes Research and Care, 2020, 8, e001319.	2.8	79
4	Colonic microbiota is associated with inflammation and host epigenomic alterations in inflammatory bowel disease. Nature Communications, 2020, 11, 1512.	12.8	167
5	758-P: Medical Food (MF) with Butyrate Producing (BP)+Mucin Regulating (MR) Microbes Improves Glucose Control (GC) in T2D. Diabetes, 2019, 68, 758-P.	0.6	0
6	Leveraging sequence-based faecal microbial community survey data to identify a composite biomarker for colorectal cancer. Gut, 2018, 67, 882-891.	12.1	159
7	Normalization of Microbiome Profiling Data. Methods in Molecular Biology, 2018, 1849, 143-168.	0.9	10
8	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. ISME Journal, 2017, 11, 2639-2643.	9.8	2,357
9	Bioconductor Workflow for Microbiome Data Analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	664
10	DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 2016, 13, 581-583.	19.0	18,691
11	Bioconductor workflow for microbiome data analysis: from raw reads to community analyses. F1000Research, 2016, 5, 1492.	1.6	466
12	Shiny-phyloseq: Web application for interactive microbiome analysis with provenance tracking. Bioinformatics, 2015, 31, 282-283.	4.1	131
13	Temporal and spatial variation of the human microbiota during pregnancy. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11060-11065.	7.1	876
14	Waste Not, Want Not: Why Rarefying Microbiome Data Is Inadmissible. PLoS Computational Biology, 2014, 10, e1003531.	3.2	2,343
15	Advancing Our Understanding of the Human Microbiome Using QIIME. Methods in Enzymology, 2013, 531, 371-444.	1.0	553
16	phyloseq: An R Package for Reproducible Interactive Analysis and Graphics of Microbiome Census Data. PLoS ONE, 2013, 8, e61217.	2. 5	13,960
17	Hydrogen production in photosynthetic microbial mats in the Elkhorn Slough estuary, Monterey Bay. ISME Journal, 2012, 6, 863-874.	9.8	48
18	Phyloseq: a bioconductor package for handling and analysis of high-throughput phylogenetic sequence data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 235-46.	0.7	84

#	Article	IF	CITATION
19	Comparisons of distance methods for combining covariates and abundances in microbiome studies. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 213-24.	0.7	24
20	PHYLOSEQ: A BIOCONDUCTOR PACKAGE FOR HANDLING AND ANALYSIS OF HIGH-THROUGHPUT PHYLOGENETIC SEQUENCE DATA. , $2011,$, .		45
21	COMPARISONS OF DISTANCE METHODS FOR COMBINING COVARIATES AND ABUNDANCES IN MICROBIOME STUDIES. , $2011, \dots$		29
22	Site-Specific Mobilization of Vinyl Chloride Respiration Islands by a Mechanism Common in Dehalococcoides. BMC Genomics, 2011, 12, 287.	2.8	55
23	Localized Plasticity in the Streamlined Genomes of Vinyl Chloride Respiring Dehalococcoides. PLoS Genetics, 2009, 5, e1000714.	3.5	162
24	Monitoring Abundance and Expression of " <i>Dehalococcoides</i> ―Species Chloroethene-Reductive Dehalogenases in a Tetrachloroethene-Dechlorinating Flow Column. Applied and Environmental Microbiology, 2008, 74, 5695-5703.	3.1	133
25	Unusual Codon Bias in Vinyl Chloride Reductase Genes of Dehalococcoides Species. Applied and Environmental Microbiology, 2007, 73, 2744-2747.	3.1	25