Benjamin J Callahan

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6583634/publications.pdf

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31 papers	37,117 citations	489802 18 h-index	651938 25 g-index
37 all docs	37 docs citations	37 times ranked	36218 citing authors

#	ARTICLE	IF	CITATIONS
1	Ultra-accurate microbial amplicon sequencing with synthetic long reads. Microbiome, 2021, 9, 130.	4.9	53
2	Perspectives and Benefits of High-Throughput Long-Read Sequencing in Microbial Ecology. Applied and Environmental Microbiology, 2021, 87, e0062621.	1.4	80
3	Understanding and interpreting community sequencing measurements of the vaginal microbiome. BJOG: an International Journal of Obstetrics and Gynaecology, 2020, 127, 139-146.	1.1	18
4	Clostridioides difficile carriage in animals and the associated changes in the host fecal microbiota. Anaerobe, 2020, 66, 102279.	1.0	8
5	The role of the microbiome in host evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190588.	1.8	32
6	Pathogen resistance may be the principal evolutionary advantage provided by the microbiome. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190592.	1.8	62
7	Evaluation of fecal Lactobacillus populations in dogs with idiopathic epilepsy: a pilot study. Animal Microbiome, 2020, 2, .	1.5	13
8	Multiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. Bioinformatics, 2019, 35, 95-103.	1.8	162
9	Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 2019, 37, 852-857.	9.4	11,167
10	High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution. Nucleic Acids Research, 2019, 47, e103-e103.	6.5	349
11	Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal Escherichia coli, and the microbiome of steers. PLoS ONE, 2019, 14, e0223378.	1.1	21
12	Consistent and correctable bias in metagenomic sequencing experiments. ELife, 2019, 8, .	2.8	263
13	Title is missing!. , 2019, 14, e0223378.		0
14	Title is missing!. , 2019, 14, e0223378.		0
15	Title is missing!. , 2019, 14, e0223378.		0
16	Title is missing!. , 2019, 14, e0223378.		0
17	Title is missing!. , 2019, 14, e0223378.		0
18	Title is missing!. , 2019, 14, e0223378.		0

#	ARTICLE	IF	CITATIONS
19	Simple statistical identification and removal of contaminant sequences in marker-gene and metagenomics data. Microbiome, 2018, 6, 226.	4.9	1,729
20	Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in Steers. Frontiers in Microbiology, 2018, 9, 2190.	1.5	14
21	In Nature, There Is Only Diversity. MBio, 2018, 9, .	1.8	11
22	Replication and refinement of a vaginal microbial signature of preterm birth in two racially distinct cohorts of US women. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 9966-9971.	3.3	297
23	Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. ISME Journal, 2017, 11, 2639-2643.	4.4	2,357
24	DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 2016, 13, 581-583.	9.0	18,691
25	1,2-Dichloroethane Exposure Alters the Population Structure, Metabolism, and Kinetics of a Trichloroethene-Dechlorinating <i>Dehalococcoides mccartyi</i> Consortium. Environmental Science & Technology, 2016, 50, 12187-12196.	4.6	16
26	Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. Nature Communications, 2016, 7, 10516.	5.8	196
27	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.	3.3	876
28	Rapid evolution of adaptive niche construction in experimental microbial populations. Evolution; International Journal of Organic Evolution, 2014, 68, 3307-3316.	1.1	41
29	The length scale of selection in protein evolution. Fly, 2012, 6, 16-20.	0.9	0
30	Denoising PCR-amplified metagenome data. BMC Bioinformatics, 2012, 13, 283.	1.2	85
31	Correlated Evolution of Nearby Residues in Drosophilid Proteins. PLoS Genetics, 2011, 7, e1001315.	1.5	48