

Benjamin J Callahan

List of Publications by Year in descending order

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

Version: 2024-02-01

31
papers

37,117
citations

430442

18
h-index

580395

25
g-index

37
all docs

37
docs citations

37
times ranked

33348
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Ultra-accurate microbial amplicon sequencing with synthetic long reads. <i>Microbiome</i> , 2021, 9, 130. | 4.9 | 53 |
| 2 | Perspectives and Benefits of High-Throughput Long-Read Sequencing in Microbial Ecology. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0062621. | 1.4 | 80 |
| 3 | Understanding and interpreting community sequencing measurements of the vaginal microbiome. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2020, 127, 139-146. | 1.1 | 18 |
| 4 | <i>Clostridioides difficile</i> carriage in animals and the associated changes in the host fecal microbiota. <i>Anaerobe</i> , 2020, 66, 102279. | 1.0 | 8 |
| 5 | The role of the microbiome in host evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190588. | 1.8 | 32 |
| 6 | Pathogen resistance may be the principal evolutionary advantage provided by the microbiome. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020, 375, 20190592. | 1.8 | 62 |
| 7 | Evaluation of fecal <i>Lactobacillus</i> populations in dogs with idiopathic epilepsy: a pilot study. <i>Animal Microbiome</i> , 2020, 2, . | 1.5 | 13 |
| 8 | Multimiomics modeling of the immunome, transcriptome, microbiome, proteome and metabolome adaptations during human pregnancy. <i>Bioinformatics</i> , 2019, 35, 95-103. | 1.8 | 162 |
| 9 | Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. <i>Nature Biotechnology</i> , 2019, 37, 852-857. | 9.4 | 11,167 |
| 10 | High-throughput amplicon sequencing of the full-length 16S rRNA gene with single-nucleotide resolution. <i>Nucleic Acids Research</i> , 2019, 47, e103-e103. | 6.5 | 349 |
| 11 | Ceftiofur formulation differentially affects the intestinal drug concentration, resistance of fecal <i>Escherichia coli</i> , and the microbiome of steers. <i>PLoS ONE</i> , 2019, 14, e0223378. | 1.1 | 21 |
| 12 | Consistent and correctable bias in metagenomic sequencing experiments. <i>ELife</i> , 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. <i>Microbiome</i> , 2018, 6, 226. | 4.9 | 1,729 |
| 20 | Dosing Regimen of Enrofloxacin Impacts Intestinal Pharmacokinetics and the Fecal Microbiota in Steers. <i>Frontiers in Microbiology</i> , 2018, 9, 2190. | 1.5 | 14 |
| 21 | In Nature, There Is Only Diversity. <i>MBio</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9966-9971. | 3.3 | 297 |
| 23 | Exact sequence variants should replace operational taxonomic units in marker-gene data analysis. <i>ISME Journal</i> , 2017, 11, 2639-2643. | 4.4 | 2,357 |
| 24 | DADA2: High-resolution sample inference from Illumina amplicon data. <i>Nature Methods</i> , 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. <i>Environmental Science & Technology</i> , 2016, 50, 12187-12196. | 4.6 | 16 |
| 26 | Marine mammals harbor unique microbiotas shaped by and yet distinct from the sea. <i>Nature Communications</i> , 2016, 7, 10516. | 5.8 | 196 |
| 27 | Temporal and spatial variation of the human microbiota during pregnancy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 11060-11065. | 3.3 | 876 |
| 28 | Rapid evolution of adaptive niche construction in experimental microbial populations. <i>Evolution; International Journal of Organic Evolution</i> , 2014, 68, 3307-3316. | 1.1 | 41 |
| 29 | The length scale of selection in protein evolution. <i>Fly</i> , 2012, 6, 16-20. | 0.9 | 0 |
| 30 | Denosing PCR-amplified metagenome data. <i>BMC Bioinformatics</i> , 2012, 13, 283. | 1.2 | 85 |
| 31 | Correlated Evolution of Nearby Residues in Drosophilid Proteins. <i>PLoS Genetics</i> , 2011, 7, e1001315. | 1.5 | 48 |