

Nicholas D Youngblut

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

930
citations

623574

14
h-index

752573

20
g-index

34
all docs

34
docs citations

34
times ranked

1243
citing authors

#	ARTICLE	IF	CITATIONS
1	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. <i>Nature Communications</i> , 2019, 10, 2200.	5.8	317
2	Syntrophy via Interspecies H ₂ Transfer between <i>Christensenella</i> and <i>Methanobrevibacter</i> Underlies Their Global Cooccurrence in the Human Gut. <i>MBio</i> , 2020, 11, .	1.8	73
3	Soil characteristics and land-use drive bacterial community assembly patterns. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	1.3	58
4	Plant Phylogeny and Life History Shape Rhizosphere Bacterial Microbiome of Summer Annuals in an Agricultural Field. <i>Frontiers in Microbiology</i> , 2017, 8, 2414.	1.5	56
5	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. <i>MSystems</i> , 2020, 5, .	1.7	47
6	SIPSim: A Modeling Toolkit to Predict Accuracy and Aid Design of DNA-SIP Experiments. <i>Frontiers in Microbiology</i> , 2018, 9, 570.	1.5	37
7	HTSSIP: An R package for analysis of high throughput sequencing data from nucleic acid stable isotope probing (SIP) experiments. <i>PLoS ONE</i> , 2018, 13, e0189616.	1.1	37
8	Vertebrate host phylogeny influences gut archaeal diversity. <i>Nature Microbiology</i> , 2021, 6, 1443-1454.	5.9	34
9	Multisubstrate DNA stable isotope probing reveals guild structure of bacteria that mediate soil carbon cycling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	33
10	Intra-genomic variation in ¹³ C content and its implications for ¹³ C stable isotope probing. <i>Environmental Microbiology Reports</i> , 2014, 6, 767-775.	1.0	31
11	Struo: a pipeline for building custom databases for common metagenome profilers. <i>Bioinformatics</i> , 2020, 36, 2314-2315.	1.8	30
12	DeepMAseD: evaluating the quality of metagenomic assemblies. <i>Bioinformatics</i> , 2020, 36, 3011-3017.	1.8	27
13	Differentiation and Structure in <i>Sulfolobus islandicus</i> Rod-Shaped Virus Populations. <i>Viruses</i> , 2017, 9, 120.	1.5	26
14	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. <i>PeerJ</i> , 2021, 9, e12198.	0.9	24
15	Free-Living, Psychrotrophic Bacteria of the Genus <i>Psychrobacter</i> Are Descendants of Pathobionts. <i>MSystems</i> , 2021, 6, .	1.7	23
16	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. <i>MSystems</i> , 2021, 6, .	1.7	21
17	Strain-Level Analysis of <i>Bifidobacterium</i> spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. <i>MSystems</i> , 2020, 5, .	1.7	12
18	Reclassification of <i>Catabacter hongkongensis</i> as <i>Christensenella hongkongensis</i> comb. nov. based on whole genome analysis. <i>International Journal of Systematic and Evolutionary Microbiology</i> , 2021, 71, .	0.8	11

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19	Data Analysis for DNA Stable Isotope Probing Experiments Using Multiple Window High-Resolution SIP. <i>Methods in Molecular Biology</i> , 2019, 2046, 109-128.	0.4	8
20	Incorporating genome-based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes. <i>Environmental Microbiology</i> , 2022, 24, 3966-3984.	1.8	2