Nicholas D Youngblut

List of Publications by Year
in descending order

20	930	623574	752573
papers	citations	14	20
		h-index	g-index

34	34	34	1243
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Incorporating genome‐based phylogeny and functional similarity into diversity assessments helps to resolve a global collection of human gut metagenomes. Environmental Microbiology, 2022, 24, 3966-3984.	1.8	2
2	Genomic Insights into Adaptations of Trimethylamine-Utilizing Methanogens to Diverse Habitats, Including the Human Gut. MSystems, 2021, 6, .	1.7	21
3	Reclassification of Catabacter hongkongensis as Christensenella hongkongensis comb. nov. based on whole genome analysis. International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	11
4	Free-Living, Psychrotrophic Bacteria of the Genus *Psychrobacter* Are Descendants of Pathobionts. MSystems, 2021, 6, .	1.7	23
5	Struo2: efficient metagenome profiling database construction for ever-expanding microbial genome datasets. PeerJ, 2021, 9, e12198.	0.9	24
6	Vertebrate host phylogeny influences gut archaeal diversity. Nature Microbiology, 2021, 6, 1443-1454.	5.9	34
7	Multisubstrate DNA stable isotope probing reveals guild structure of bacteria that mediate soil carbon cycling. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	33
8	Soil characteristics and land-use drive bacterial community assembly patterns. FEMS Microbiology Ecology, 2020, 96, .	1.3	58
9	Struo: a pipeline for building custom databases for common metagenome profilers. Bioinformatics, 2020, 36, 2314-2315.	1.8	30
10	Strain-Level Analysis of *Bifidobacterium* spp. from Gut Microbiomes of Adults with Differing Lactase Persistence Genotypes. MSystems, 2020, 5, .	1.7	12
11	Large-Scale Metagenome Assembly Reveals Novel Animal-Associated Microbial Genomes, Biosynthetic Gene Clusters, and Other Genetic Diversity. MSystems, 2020, 5, .	1.7	47
12	DeepMAsED: evaluating the quality of metagenomic assemblies. Bioinformatics, 2020, 36, 3011-3017.	1.8	27
13	Syntrophy via Interspecies H_2 Transfer between *Christensenella* and *Methanobrevibacter* Underlies Their Global Cooccurrence in the Human Gut. MBio, 2020, 11, .	1.8	73
14	Data Analysis for DNA Stable Isotope Probing Experiments Using Multiple Window High-Resolution SIP. Methods in Molecular Biology, 2019, 2046, 109-128.	0.4	8
15	Host diet and evolutionary history explain different aspects of gut microbiome diversity among vertebrate clades. Nature Communications, 2019, 10, 2200.	5.8	317
16	SIPSim: A Modeling Toolkit to Predict Accuracy and Aid Design of DNA-SIP Experiments. Frontiers in Microbiology, 2018, 9, 570.	1.5	37
17	HTSSIP: An R package for analysis of high throughput sequencing data from nucleic acid stable isotope probing (SIP) experiments. PLoS ONE, 2018, 13, e0189616.	1.1	37
18	Plant Phylogeny and Life History Shape Rhizosphere Bacterial Microbiome of Summer Annuals in an Agricultural Field. Frontiers in Microbiology, 2017, 8, 2414.	1.5	56

#	Article	IF	Citations
19	Differentiation and Structure in Sulfolobus islandicus Rod-Shaped Virus Populations. Viruses, 2017, 9, 120.	1.5	26
20	Intra‐genomic variation in <scp>G</scp>‰+‰<scp>C</scp> content and its implications for <scp>DNA</scp> stable isotope probing. Environmental Microbiology Reports, 2014, 6, 767-775.	1.0	31