Nathan D Olson

List of Publications by Year
in descending order

28 papers	4,629 citations	361413 20 h-index	434195 31 g-index
47 all docs	47 docs citations	47 times ranked	5341 citing authors

#	Article	IF	Citations
1	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
2	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. Nature Biotechnology, 2019, 37, 1155-1162.	17.5	1,010
3	An open resource for accurately benchmarking small variant and reference calls. Nature Biotechnology, 2019, 37, 561-566.	17.5	277
4	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
5	Nitrogen fixation and nitrogen transformations in marine symbioses. Trends in Microbiology, 2010, 18, 455-463.	7.7	183
6	Performing Skin Microbiome Research: A Method to the Madness. Journal of Investigative Dermatology, 2017, 137, 561-568.	0.7	164
7	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. Frontiers in Genetics, 2015, 6, 235.	2.3	160
8	A complete reference genome improves analysis of human genetic variation. Science, 2022, 376, eabl3533.	12.6	144
9	Diazotrophic bacteria associated with Hawaiian Montipora corals: Diversity and abundance in correlation with symbiotic dinoflagellates. Journal of Experimental Marine Biology and Ecology, 2009, 371, 140-146.	1.5	139
10	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. Briefings in Bioinformatics, 2019, 20, 1140-1150.	6.5	113
11	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	17.5	90
12	DNA extract characterization process for microbial detection methods development and validation. BMC Research Notes, 2012, 5, 668.	1.4	79
13	Antibiotic Concentrations Decrease during Wastewater Treatment but Persist at Low Levels in Reclaimed Water. International Journal of Environmental Research and Public Health, 2017, 14, 668.	2.6	78
14	Benchmarking challenging small variants with linked and long reads. Cell Genomics, 2022, 2, 100128.	6.5	77
15	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. Cell Genomics, 2022, 2, 100129.	6.5	72
16	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. Science of the Total Environment, 2018, 639, 1126-1137.	8.0	43
17	Assembly and annotation of an Ashkenazi human reference genome. Genome Biology, 2020, 21, 129.	8.8	42
18	The genotype€phenotype landscape of an allosteric protein. Molecular Systems Biology, 2021, 17, e10179.	7.2	40

#	ARTICLE	IF	CITATIONS
19	Diazotrophic diversity in the Caribbean coral, Montastraea cavernosa. Archives of Microbiology, 2013, 195, 853-859.	2.2	31
20	Impact of Processing Method on Recovery of Bacteria from Wipes Used in Biological Surface Sampling. Applied and Environmental Microbiology, 2012, 78, 5872-5881.	3.1	30
21	High-coverage, long-read sequencing of Han Chinese trio reference samples. Scientific Data, 2019, 6, 91.	5.3	13
22	Challenging a bioinformatic tool's ability to detect microbial contaminants using *in silico* whole genome sequencing data. PeerJ, 2017, 5, e3729.	2.0	8
23	PEPR: pipelines for evaluating prokaryotic references. Analytical and Bioanalytical Chemistry, 2016, 408, 2975-2983.	3.7	5
24	*metagenomeFeatures*: an R package for working with 16S rRNA reference databases and marker-gene survey feature data. Bioinformatics, 2019, 35, 3870-3872.	4.1	4
25	Report from the Standards for Pathogen Identification via Next-Generation Sequencing (SPIN) Workshop. Standards in Genomic Sciences, 2015, 10, .	1.5	3
26	International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. Biomolecular Detection and Quantification, 2015, 3, 17-24.	7.0	3
27	Evaluation of microbial qPCR workflows using engineered Saccharomyces cerevisiae. Biomolecular Detection and Quantification, 2016, 7, 27-33.	7.0	3
28	A framework for assessing 16S rRNA marker-gene survey data analysis methods using mixtures.. Microbiome, 2020, 8, 35.	11.1	2