

Nathan D Olson

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8418954/publications.pdf>

Version: 2024-02-01

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	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	17.5	90
2	A complete reference genome improves analysis of human genetic variation. <i>Science</i> , 2022, 376, eabl3533.	12.6	144
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
4	PrecisionFDA Truth Challenge V2: Calling variants from short and long reads in difficult-to-map regions. <i>Cell Genomics</i> , 2022, 2, 100129.	6.5	72
5	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	6.5	77
6	The genotype-phenotype landscape of an allosteric protein. <i>Molecular Systems Biology</i> , 2021, 17, e10179.	7.2	40
7	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020, 38, 1347-1355.	17.5	233
8	Assembly and annotation of an Ashkenazi human reference genome. <i>Genome Biology</i> , 2020, 21, 129.	8.8	42
9	A framework for assessing 16S rRNA marker-gene survey data analysis methods using mixtures. <i>Microbiome</i> , 2020, 8, 35.	11.1	2
10	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	17.5	1,010
11	High-coverage, long-read sequencing of Han Chinese trio reference samples. <i>Scientific Data</i> , 2019, 6, 91.	5.3	13
12	<i>metagenomeFeatures</i> : an R package for working with 16S rRNA reference databases and marker-gene survey feature data. <i>Bioinformatics</i> , 2019, 35, 3870-3872.	4.1	4
13	An open resource for accurately benchmarking small variant and reference calls. <i>Nature Biotechnology</i> , 2019, 37, 561-566.	17.5	277
14	Metagenomic assembly through the lens of validation: recent advances in assessing and improving the quality of genomes assembled from metagenomes. <i>Briefings in Bioinformatics</i> , 2019, 20, 1140-1150.	6.5	113
15	Conventional wastewater treatment and reuse site practices modify bacterial community structure but do not eliminate some opportunistic pathogens in reclaimed water. <i>Science of the Total Environment</i> , 2018, 639, 1126-1137.	8.0	43
16	Performing Skin Microbiome Research: A Method to the Madness. <i>Journal of Investigative Dermatology</i> , 2017, 137, 561-568.	0.7	164
17	Antibiotic Concentrations Decrease during Wastewater Treatment but Persist at Low Levels in Reclaimed Water. <i>International Journal of Environmental Research and Public Health</i> , 2017, 14, 668.	2.6	78
18	Challenging a bioinformatic tool's ability to detect microbial contaminants using <i>in silico</i> whole genome sequencing data. <i>PeerJ</i> , 2017, 5, e3729.	2.0	8

#	ARTICLE	IF	CITATIONS
19	PEPR: pipelines for evaluating prokaryotic references. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 2975-2983.	3.7	5
20	Evaluation of microbial qPCR workflows using engineered <i>Saccharomyces cerevisiae</i> . <i>Biomolecular Detection and Quantification</i> , 2016, 7, 27-33.	7.0	3
21	Report from the Standards for Pathogen Identification via Next-Generation Sequencing (SPIN) Workshop. <i>Standards in Genomic Sciences</i> , 2015, 10, .	1.5	3
22	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015, 6, 235.	2.3	160
23	International interlaboratory study comparing single organism 16S rRNA gene sequencing data: Beyond consensus sequence comparisons. <i>Biomolecular Detection and Quantification</i> , 2015, 3, 17-24.	7.0	3
24	Diazotrophic diversity in the Caribbean coral, <i>Montastraea cavernosa</i> . <i>Archives of Microbiology</i> , 2013, 195, 853-859.	2.2	31
25	Impact of Processing Method on Recovery of Bacteria from Wipes Used in Biological Surface Sampling. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5872-5881.	3.1	30
26	DNA extract characterization process for microbial detection methods development and validation. <i>BMC Research Notes</i> , 2012, 5, 668.	1.4	79
27	Nitrogen fixation and nitrogen transformations in marine symbioses. <i>Trends in Microbiology</i> , 2010, 18, 455-463.	7.7	183
28	Diazotrophic bacteria associated with Hawaiian <i>Montipora</i> corals: Diversity and abundance in correlation with symbiotic dinoflagellates. <i>Journal of Experimental Marine Biology and Ecology</i> , 2009, 371, 140-146.	1.5	139