Noah Alexander

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10689473/publications.pdf

Version: 2024-02-01

687363 940533 2,028 19 13 16 citations h-index g-index papers 22 22 22 4119 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5.3	575
2	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. Scientific Reports, 2017, 7, 18022.	3.3	264
3	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
4	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	6.2	241
5	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
6	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. Nature Communications, 2019, 10, 579.	12.8	131
7	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	3.7	76
8	Genomic Methods and Microbiological Technologies for Profiling Novel and Extreme Environments for the Extreme Microbiome Project (XMP). Journal of Biomolecular Techniques, 2017, 28, 31-39.	1.5	53
9	Precision Metagenomics: Rapid Metagenomic Analyses for Infectious Disease Diagnostics and Public Health Surveillance. Journal of Biomolecular Techniques, 2017, 28, 40-45.	1.5	47
10	Rapid antigen diversification through mitotic recombination in the human malaria parasite Plasmodium falciparum. PLoS Biology, 2019, 17, e3000271.	5.6	44
11	Genome Sequence and Analysis of <i>Escherichia coli </i> i>MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. Genome Biology and Evolution, 2016, 8, 742-752.	2.5	35
12	Chromosome End Repair and Genome Stability in Plasmodium falciparum. MBio, 2017, 8, .	4.1	27
13	Modern Methods for Delineating Metagenomic Complexity. Cell Systems, 2015, 1, 6-7.	6.2	20
14	RP58 Represses Transcriptional Programs Linked to Nonneuronal Cell Identity and Glioblastoma Subtypes in Developing Neurons. Molecular and Cellular Biology, 2021, 41, e0052620.	2.3	8
15	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
16	A crowdsourced set of curated structural variants for the human genome., 2020, 16, e1007933.		0
17	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		0
18	A crowdsourced set of curated structural variants for the human genome., 2020, 16, e1007933.		O

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19 A crowdsourced set of curated structural variants for the human genome., 2020, 16, e1007933. 0