Noah Alexander

List of Publications by Year in descending order

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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	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
2	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
3	A crowdsourced set of curated structural variants for the human genome. PLoS Computational Biology, 2020, 16, e1007933.	3.2	6
4	A crowdsourced set of curated structural variants for the human genome., 2020, 16, e1007933.		0
5	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		O
6	A crowdsourced set of curated structural variants for the human genome., 2020, 16, e1007933.		0
7	A crowdsourced set of curated structural variants for the human genome. , 2020, 16, e1007933.		O
8	Rapid antigen diversification through mitotic recombination in the human malaria parasite Plasmodium falciparum. PLoS Biology, 2019, 17, e3000271.	5 . 6	44
9	Single-molecule sequencing detection of N6-methyladenine in microbial reference materials. Nature Communications, 2019, 10, 579.	12.8	131
10	Chromosome End Repair and Genome Stability in Plasmodium falciparum. MBio, 2017, 8, .	4.1	27
11	Nanopore DNA Sequencing and Genome Assembly on the International Space Station. Scientific Reports, 2017, 7, 18022.	3.3	264
12	Precision Metagenomics: Rapid Metagenomic Analyses for Infectious Disease Diagnostics and Public Health Surveillance. Journal of Biomolecular Techniques, 2017, 28, 40-45.	1.5	47
13	Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. Genome Biology, 2017, 18, 182.	8.8	260
14	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
15	Nanopore sequencing in microgravity. Npj Microgravity, 2016, 2, 16035.	3.7	76
16	Extensive sequencing of seven human genomes to characterize benchmark reference materials. Scientific Data, 2016, 3, 160025.	5. 3	575
17	Genome Sequence and Analysis of <i>Escherichia coli < /i>MRE600, a Colicinogenic, Nonmotile Strain that Lacks RNase I and the Type I Methyltransferase, EcoKI. Genome Biology and Evolution, 2016, 8, 742-752.</i>	2,5	35
18	Modern Methods for Delineating Metagenomic Complexity. Cell Systems, 2015, 1, 6-7.	6.2	20

#	Article	IF	CITATIONS
19	Geospatial Resolution of Human and Bacterial Diversity with City-Scale Metagenomics. Cell Systems, 2015, 1, 72-87.	6.2	241