Jordan M Eizenga

List of Publications by Year
in descending order

21 papers	2,021 citations	759233 12 h-index	713466 21 g-index
36 all docs	36 docs citations	36 times ranked	2563 citing authors

#	Article	IF	Citations
1	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	17.5	435
2	Mapping DNA methylation with high-throughput nanopore sequencing. Nature Methods, 2017, 14, 411-413.	19.0	390
3	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	5.5	264
4	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	8.8	150
5	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
6	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. Nature Methods, 2021, 18, 1322-1332.	19.0	139
7	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
8	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	1.6	46
9	A phylogenetic approach for haplotype analysis of sequence data from complex mitochondrial mixtures. Forensic Science International: Genetics, 2017, 30, 93-105.	3.1	39
10	Aerosol Microbiome over the Mediterranean Sea Diversity and Abundance. Atmosphere, 2019, 10, 440.	2.3	22
11	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	4.1	18
12	Conserved novel ORFs in the mitochondrial genome of the ctenophore Beroe forskalii. PeerJ, 2020, 8, e8356.	2.0	16
13	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
14	Modelling haplotypes with respect to reference cohort variation graphs. Bioinformatics, 2017, 33, i118-i123.	4.1	12
15	Distance indexing and seed clustering in sequence graphs. Bioinformatics, 2020, 36, i146-i153.	4.1	10
16	Walk-Preserving Transformation of Overlapped Sequence Graphs into Blunt Sequence Graphs with GetBlunted. Lecture Notes in Computer Science, 2021, , 169-177.	1.3	6
17	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
18	Bayesian Framework for Detecting Gene Expression Outliers in Individual Samples. JCO Clinical Cancer Informatics, 2020, 4, 160-170.	2.1	4

#	Article	IF	Citations
19	A Flow Procedure for Linearization of Genome Sequence Graphs. Journal of Computational Biology, 2018, 25, 664-676.	1.6	3
20	Describing the Local Structure of Sequence Graphs. Lecture Notes in Computer Science, 2017, , 24-46.	1.3	2
21	A complete pedigree-based graph workflow for rare candidate variant analysis. Genome Research, 2022, , .	5.5	1