

# Jordan M Eizenga

## List of Publications by Year in descending order

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Version: 2024-02-01

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	A complete pedigree-based graph workflow for rare candidate variant analysis. <i>Genome Research</i> , 2022, , .	5.5	1
2	Efficient dynamic variation graphs. <i>Bioinformatics</i> , 2021, 36, 5139-5144.	4.1	18
3	Walk-Preserving Transformation of Overlapped Sequence Graphs into Blunt Sequence Graphs with GetBlunted. <i>Lecture Notes in Computer Science</i> , 2021, , 169-177.	1.3	6
4	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , 2021, 18, 1322-1332.	19.0	139
5	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	12.6	132
6	Distance indexing and seed clustering in sequence graphs. <i>Bioinformatics</i> , 2020, 36, i146-i153.	4.1	10
7	Pangenome Graphs. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 139-162.	6.2	148
8	Bayesian Framework for Detecting Gene Expression Outliers in Individual Samples. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 160-170.	2.1	4
9	Genotyping structural variants in pangenome graphs using the vg toolkit. <i>Genome Biology</i> , 2020, 21, 35.	8.8	150
10	Conserved novel ORFs in the mitochondrial genome of the ctenophore <i>Beroë forskalii</i> . <i>PeerJ</i> , 2020, 8, e8356.	2.0	16
11	Aerosol Microbiome over the Mediterranean Sea Diversity and Abundance. <i>Atmosphere</i> , 2019, 10, 440.	2.3	22
12	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	1.6	5
13	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	1.6	14
14	Superbubbles, Ultrabubbles, and Cacti. <i>Journal of Computational Biology</i> , 2018, 25, 649-663.	1.6	46
15	A Flow Procedure for Linearization of Genome Sequence Graphs. <i>Journal of Computational Biology</i> , 2018, 25, 664-676.	1.6	3
16	Variation graph toolkit improves read mapping by representing genetic variation in the reference. <i>Nature Biotechnology</i> , 2018, 36, 875-879.	17.5	435
17	Mapping DNA methylation with high-throughput nanopore sequencing. <i>Nature Methods</i> , 2017, 14, 411-413.	19.0	390
18	A phylogenetic approach for haplotype analysis of sequence data from complex mitochondrial mixtures. <i>Forensic Science International: Genetics</i> , 2017, 30, 93-105.	3.1	39

#	ARTICLE	IF	CITATIONS
19	Genome graphs and the evolution of genome inference. <i>Genome Research</i> , 2017, 27, 665-676.	5.5	264
20	Modelling haplotypes with respect to reference cohort variation graphs. <i>Bioinformatics</i> , 2017, 33, i118-i123.	4.1	12
21	Describing the Local Structure of Sequence Graphs. <i>Lecture Notes in Computer Science</i> , 2017, , 24-46.	1.3	2