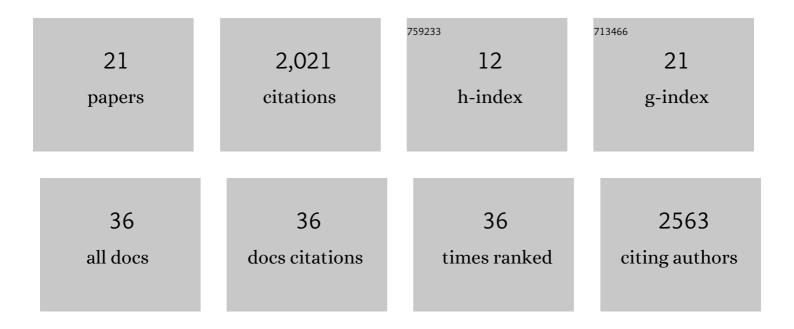
## Jordan M Eizenga

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1602915/publications.pdf Version: 2024-02-01



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

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