Erik P Garrison

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9010635/publications.pdf

Version: 2024-02-01

26 papers	22,488 citations	279701 23 h-index	552653 26 g-index
36 all docs	36 docs citations	36 times ranked	40233 citing authors

#	Article	IF	Citations
1	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
2	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	13.7	192
3	ODGI: understanding pangenome graphs. Bioinformatics, 2022, 38, 3319-3326.	1.8	44
4	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	1.8	18
5	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
6	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5
7	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	6.0	132
8	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	1.8	59
9	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. Genome Biology, 2020, 21, 250.	3.8	44
10	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	9.4	344
11	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	2.5	148
12	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	3.8	150
13	Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. Scientific Reports, 2019, 9, 10067.	1.6	53
14	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	0.8	46
15	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	9.4	435
16	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	2.4	264
17	A graph extension of the positional Burrowsâ€“Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	0.3	33
18	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	9.4	273

#	Article	IF	Citations
19	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	1.2	9
20	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
21	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
22	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	9.0	515
23	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	1.1	249
24	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	6.0	341
25	SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications. PLoS ONE, 2013, 8, e82138.	1.1	175
26	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	1.5	278