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	279798 23 h-index	552781 26 g-index
36 all docs	36 docs citations	36 times ranked	40233 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	27.8	13,998
2	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
3	The complete sequence of a human genome. Science, 2022, 376, 44-53.	12.6	1,222
4	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
5	SpeedSeq: ultra-fast personal genome analysis and interpretation. Nature Methods, 2015, 12, 966-968.	19.0	515
6	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	17.5	435
7	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. Nature Biotechnology, 2020, 38, 1044-1053.	17.5	344
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. Science, 2013, 342, 1235587.	12.6	341
9	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. PLoS Genetics, 2011, 7, e1002236.	3.5	278
10	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. Nature Genetics, 2016, 48, 593-599.	21.4	273
11	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	5.5	264
12	MOSAIK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. PLoS ONE, 2014, 9, e90581.	2.5	249
13	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
14	SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications. PLoS ONE, 2013, 8, e82138.	2.5	175
15	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	8.8	150
16	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
17	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
18	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	4.1	59

#	Article	IF	Citations
19	Genomic diversity and novel genome-wide association with fruit morphology in Capsicum, from 746k polymorphic sites. Scientific Reports, 2019, 9, 10067.	3.3	53
20	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	1.6	46
21	Removing reference bias and improving indel calling in ancient DNA data analysis by mapping to a sequence variation graph. Genome Biology, 2020, 21, 250.	8.8	44
22	ODGI: understanding pangenome graphs. Bioinformatics, 2022, 38, 3319-3326.	4.1	44
23	A graph extension of the positional Burrowsâ€“Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	1.2	33
24	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	4.1	18
25	The distribution and mutagenesis of short coding INDELs from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	2.8	9
26	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	3.2	5