

# 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

279487

23  
h-index

552369

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. <i>Nature</i> , 2015, 526, 68-74.	13.7	13,998
2	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015, 526, 75-81.	13.7	1,994
3	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	6.0	1,222
4	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	13.7	1,139
5	SpeedSeq: ultra-fast personal genome analysis and interpretation. <i>Nature Methods</i> , 2015, 12, 966-968.	9.0	515
6	Variation graph toolkit improves read mapping by representing genetic variation in the reference. <i>Nature Biotechnology</i> , 2018, 36, 875-879.	9.4	435
7	Nanopore sequencing and the Shasta toolkit enable efficient de novo assembly of eleven human genomes. <i>Nature Biotechnology</i> , 2020, 38, 1044-1053.	9.4	344
8	Integrative Annotation of Variants from 1092 Humans: Application to Cancer Genomics. <i>Science</i> , 2013, 342, 1235587.	6.0	341
9	A Comprehensive Map of Mobile Element Insertion Polymorphisms in Humans. <i>PLoS Genetics</i> , 2011, 7, e1002236.	1.5	278
10	Punctuated bursts in human male demography inferred from 1,244 worldwide Y-chromosome sequences. <i>Nature Genetics</i> , 2016, 48, 593-599.	9.4	273
11	Genome graphs and the evolution of genome inference. <i>Genome Research</i> , 2017, 27, 665-676.	2.4	264
12	MOSAİK: A Hash-Based Algorithm for Accurate Next-Generation Sequencing Short-Read Mapping. <i>PLoS ONE</i> , 2014, 9, e90581.	1.1	249
13	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	13.7	192
14	SSW Library: An SIMD Smith-Waterman C/C++ Library for Use in Genomic Applications. <i>PLoS ONE</i> , 2013, 8, e82138.	1.1	175
15	Genotyping structural variants in pangenome graphs using the vg toolkit. <i>Genome Biology</i> , 2020, 21, 35.	3.8	150
16	Pangenome Graphs. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 139-162.	2.5	148
17	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	6.0	132
18	Haplotype-aware graph indexes. <i>Bioinformatics</i> , 2020, 36, 400-407.	1.8	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.	1.6	53
20	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	0.8	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.	3.8	44
22	ODGI: understanding pangenome graphs. Bioinformatics, 2022, 38, 3319-3326.	1.8	44
23	A graph extension of the positional Burrows-Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	0.3	33
24	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	1.8	18
25	The distribution and mutagenesis of short coding INDELS from 1,128 whole exomes. BMC Genomics, 2015, 16, 143.	1.2	9
26	GRAFIMO: Variant and haplotype aware motif scanning on pangenome graphs. PLoS Computational Biology, 2021, 17, e1009444.	1.5	5