Mark J P Chaisson

List of Publications by Year
in descending order

18	6,819	471509 17	794594 19
papers	citations	h-index	g-index

21	21	21	10040
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
2	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	27.8	1,139
3	Resolving the complexity of the human genome using single-molecule sequencing. Nature, 2015, 517, 608-611.	27.8	714
4	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
5	Long-read sequence assembly of the gorilla genome. Science, 2016, 352, aae0344.	12.6	368
6	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
7	Discovery and genotyping of structural variation from long-read haploid genome sequence data. Genome Research, 2017, 27, 677-685.	5.5	323
8	High-resolution comparative analysis of great ape genomes. Science, 2018, 360, .	12.6	304
9	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
10	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
11	Long-read sequence and assembly of segmental duplications. Nature Methods, 2019, 16, 88-94.	19.0	139
12	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	17.5	127
13	Human-specific tandem repeat expansion and differential gene expression during primate evolution. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23243-23253.	7.1	82
14	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	6.2	72
15	lra: A long read aligner for sequences and contigs. PLoS Computational Biology, 2021, 17, e1009078.	3.2	59
16	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	5.5	32
17	Profiling variable-number tandem repeat variation across populations using repeat-pangenome graphs. Nature Communications, 2021, 12, 4250.	12.8	27
18	TT-Mars: structural variants assessment based on haplotype-resolved assemblies. Genome Biology, 2022, 23, 110.	8.8	9