

# Mark J P Chaisson

## List of Publications by Year in descending order

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Version: 2024-02-01

18  
papers

6,819  
citations

471509

17  
h-index

794594

19  
g-index

21  
all docs

21  
docs citations

21  
times ranked

10040  
citing authors

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