

Haoyu Cheng

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17
papers

515
citations

7
h-index

18
g-index

18
ext. papers

1,727
ext. citations

18.8
avg, IF

4.84
L-index

#	Paper	IF	Citations
17	Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. <i>Nature Methods</i> , 2021 , 18, 170-175	21.6	242
16	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
15	The complete sequence of a human genome		58
14	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021 , 39, 309-312	44.5	44
13	BitMapper: an efficient all-mapper based on bit-vector computing. <i>BMC Bioinformatics</i> , 2015 , 16, 192	3.6	20
12	Curated variation benchmarks for challenging medically relevant autosomal genes.. <i>Nature Biotechnology</i> , 2022 ,	44.5	12
11	Towards a Comprehensive Variation Benchmark for Challenging Medically-Relevant Autosomal Genes		8
10	BitMapperBS: a fast and accurate read aligner for whole-genome bisulfite sequencing		5
9	Real-time mapping of nanopore raw signals. <i>Bioinformatics</i> , 2021 , 37, i477-i483	7.2	5
8	Automated assembly of high-quality diploid human reference genomes		3
7	Haplotype-resolved assembly of diploid genomes without parental data.. <i>Nature Biotechnology</i> , 2022 ,	44.5	3
6	Metagenome assembly of high-fidelity long reads with hifiasm-meta.. <i>Nature Methods</i> , 2022 ,	21.6	3
5	FMtree: a fast locating algorithm of FM-indexes for genomic data. <i>Bioinformatics</i> , 2018 , 34, 416-424	7.2	2
4	BitMapper2: a GPU-accelerated all-mapper based on the sparse q-gram index. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 ,	3	1
3	Fast alignment and preprocessing of chromatin profiles with Chromap. <i>Nature Communications</i> , 2021 , 12, 6566	17.4	1
2	LVMapper: A Large-Variance Clone Detector Using Sequencing Alignment Approach. <i>IEEE Access</i> , 2020 , 8, 27986-27997	3.5	0
1	An Efficient Filtration Method Based on Variable-Length Seeds for Sequence Alignment. <i>Communications in Computer and Information Science</i> , 2017 , 214-223	0.3	

