Haoyu Cheng

List of Publications by Year
in descending order

13 papers	**3,637** citations	1051969 **10** h-index	1336881 **12** g-index
18 all docs	**18** docs citations	**18** times ranked	**2049** citing authors

#	Article	IF	Citations
1	Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. Nature Methods, 2021, 18, 170-175.	9.0	1,675
2	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
3	Haplotype-resolved assembly of diploid genomes without parental data. Nature Biotechnology, 2022, 40, 1332-1335.	9.4	139
4	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	9.4	109
5	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
6	Metagenome assembly of high-fidelity long reads with hifiasm-meta. Nature Methods, 2022, 19, 671-674.	9.0	56
7	Real-time mapping of nanopore raw signals. Bioinformatics, 2021, 37, i477-i483.	1.8	41
8	Fast alignment and preprocessing of chromatin profiles with Chromap. Nature Communications, 2021, 12, 6566.	5.8	39
9	BitMapper: an efficient all-mapper based on bit-vector computing. BMC Bioinformatics, 2015, 16, 192.	1.2	26
10	LVMapper: A Large-Variance Clone Detector Using Sequencing Alignment Approach. IEEE Access, 2020, 8, 27986-27997.	2.6	14
11	FMtree: a fast locating algorithm of FM-indexes for genomic data. Bioinformatics, 2018, 34, 416-424.	1.8	7
12	BitMapper2: A GPU-Accelerated All-Mapper Based on the Sparseq-Gram Index. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 886-897.	1.9	7
13	An Efficient Filtration Method Based on Variable-Length Seeds for Sequence Alignment. Communications in Computer and Information Science, 2017, , 214-223.	0.4	0