Haoyu Cheng

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6802277/publications.pdf

Version: 2024-02-01

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	Curated variation benchmarks for challenging medically relevant autosomal genes. Nature Biotechnology, 2022, 40, 672-680.	9.4	90
2	Haplotype-resolved assembly of diploid genomes without parental data. Nature Biotechnology, 2022, 40, 1332-1335.	9.4	139
3	The complete sequence of a human genome. Science, 2022, 376, 44-53.	6.0	1,222
4	Metagenome assembly of high-fidelity long reads with hifiasm-meta. Nature Methods, 2022, 19, 671-674.	9.0	56
5	Chromosome-scale, haplotype-resolved assembly of human genomes. Nature Biotechnology, 2021, 39, 309-312.	9.4	109
6	Haplotype-resolved de novo assembly using phased assembly graphs with hifiasm. Nature Methods, 2021, 18, 170-175.	9.0	1,675
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	LVMapper: A Large-Variance Clone Detector Using Sequencing Alignment Approach. IEEE Access, 2020, 8, 27986-27997.	2.6	14
10	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
11	FMtree: a fast locating algorithm of FM-indexes for genomic data. Bioinformatics, 2018, 34, 416-424.	1.8	7
12	An Efficient Filtration Method Based on Variable-Length Seeds for Sequence Alignment. Communications in Computer and Information Science, 2017, , 214-223.	0.4	0
13	BitMapper: an efficient all-mapper based on bit-vector computing. BMC Bioinformatics, 2015, 16, 192.	1.2	26