

# Haoyu Cheng

## List of Publications by Year in Descending Order

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

