Benjamin Langmead

List of Publications by Year
in descending order

58	90,285	159525	161767
papers	citations	30 h-index	54 g-index

91	91	91	123636
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Fast gapped-read alignment with Bowtie 2. Nature Methods, 2012, 9, 357-359.	9.0	42,357
2	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. Genome Biology, 2009, 10, R25.	13.9	19,212
3	HISAT: a fast spliced aligner with low memory requirements. Nature Methods, 2015, 12, 357-360.	9.0	16,262
4	Improved metagenomic analysis with Kraken 2. Genome Biology, 2019, 20, 257.	3.8	2,909
5	Tackling the widespread and critical impact of batch effects in high-throughput data. Nature Reviews Genetics, 2010, 11, 733-739.	7.7	1,641
6	Aligning Short Sequencing Reads with Bowtie. Current Protocols in Bioinformatics, 2010, 32, Unit 11.7.	25.8	1,027
7	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	9.4	968
8	Ballgown bridges the gap between transcriptome assembly and expression analysis. Nature Biotechnology, 2015, 33, 243-246.	9.4	716
9	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. Genome Biology, 2012, 13, R83.	13.9	650
10	Scaling read aligners to hundreds of threads on general-purpose processors. Bioinformatics, 2019, 35, 421-432.	1.8	467
11	Searching for SNPs with cloud computing. Genome Biology, 2009, 10, R134.	13.9	437
12	Reproducible RNA-seq analysis using recount2. Nature Biotechnology, 2017, 35, 319-321.	9.4	395
13	Reversible switching between epigenetic states in honeybee behavioral subcastes. Nature Neuroscience, 2012, 15, 1371-1373.	7.1	305
14	Cloud-scale RNA-sequencing differential expression analysis with Myrna. Genome Biology, 2010, 11, R83.	13.9	268
15	Polyester: simulating RNA-seq datasets with differential transcript expression. Bioinformatics, 2015, 31, 2778-2784.	1.8	250
16	Cloud computing and the DNA data race. Nature Biotechnology, 2010, 28, 691-693.	9.4	242
17	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	3.2	207
18	Cloud computing for genomic data analysis and collaboration. Nature Reviews Genetics, 2018, 19, 208-219.	7.7	205

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19	Lighter: fast and memory-efficient sequencing error correction without counting. Genome Biology, 2014, 15, 509.	3.8	201
20	ReCount: A multi-experiment resource of analysis-ready RNA-seq gene count datasets. BMC Bioinformatics, 2011, 12, 449.	1.2	144
21	Large-scale hypomethylated blocks associated with Epstein-Barr virusâ€“induced B-cell immortalization. Genome Research, 2014, 24, 177-184.	2.4	130
22	recount3: summaries and queries for large-scale RNA-seq expression and splicing. Genome Biology, 2021, 22, 323.	3.8	103
23	Human splicing diversity and the extent of unannotated splice junctions across human RNA-seq samples on the Sequence Read Archive. Genome Biology, 2016, 17, 266.	3.8	94
24	Alignment of Next-Generation Sequencing Reads. Annual Review of Genomics and Human Genetics, 2015, 16, 133-151.	2.5	91
25	The DNA data deluge. IEEE Spectrum, 2013, 50, 28-33.	0.5	67
26	Dashing: fast and accurate genomic distances with HyperLogLog. Genome Biology, 2019, 20, 265.	3.8	64
27	FORGe: prioritizing variants for graph genomes. Genome Biology, 2018, 19, 220.	3.8	59
28	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. Bioinformatics, 2017, 33, 4033-4040.	1.8	57
29	Flexible expressed region analysis for RNA-seq with<tt>derfinder</tt>. Nucleic Acids Research, 2017, 45, e9-e9.	6.5	54
30	ASCOT identifies key regulators of neuronal subtype-specific splicing. Nature Communications, 2020, 11, 137.	5.8	50
31	Reference flow: reducing reference bias using multiple population genomes. Genome Biology, 2021, 22, 8.	3.8	44
32	Snaptron: querying splicing patterns across tens of thousands of RNA-seq samples. Bioinformatics, 2018, 34, 114-116.	1.8	39
33	Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. Journal of Computational Biology, 2020, 27, 500-513.	0.8	35
34	Recounting the FANTOM CAGE-Associated Transcriptome. Genome Research, 2020, 30, 1073-1081.	2.4	35
35	Prefix-free parsing for building big BWTs. Algorithms for Molecular Biology, 2019, 14, 13.	0.3	33
36	Arioc: high-throughput read alignment with GPU-accelerated exploration of the seed-and-extend search space. PeerJ, 2015, 3, e808.	0.9	33

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37	Genotyping in the Cloud with Crossbow. Current Protocols in Bioinformatics, 2012, 39, Unit15.3.	25.8	30
38	How bioinformatics and open data can boost basic science in countries and universities with limited resources. Nature Biotechnology, 2019, 37, 324-326.	9.4	25
39	MONI: A Pangenomic Index for Finding Maximal Exact Matches. Journal of Computational Biology, 2022, 29, 169-187.	0.8	23
40	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. Nucleic Acids Research, 2019, 47, e117-e117.	6.5	22
41	Megadepth: efficient coverage quantification for BigWigs and BAMs. Bioinformatics, 2021, 37, 3014-3016.	1.8	18
42	Vargas: heuristic-free alignment for assessing linear and graph read aligners. Bioinformatics, 2020, 36, 3712-3718.	1.8	17
43	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. Proteomics, 2019, 19, e1800315.	1.3	16
44	Pan-genomic matching statistics for targeted nanopore sequencing. IScience, 2021, 24, 102696.	1.9	15
45	A tandem simulation framework for predicting mapping quality. Genome Biology, 2017, 18, 152.	3.8	14
46	PHONI: Streamed Matching Statistics with Multi-Genome References. , 2021, 2021, 193-202.		10
47	Widespread splicing of repetitive element loci into coding regions of gene transcripts. Human Molecular Genetics, 2016, 25, ddw321.	1.4	8
48	LevioSAM: fast lift-over of variant-aware reference alignments. Bioinformatics, 2021, 37, 4243-4245.	1.8	7
49	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. IScience, 2019, 18, 1-10.	1.9	6
50	Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. Lecture Notes in Computer Science, 2019, , 158-173.	1.0	6
51	Matching Reads to Many Genomes with the r-Index. Journal of Computational Biology, 2020, 27, 514-518.	0.8	6
52	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. Bioinformatics, 2016, 32, 2551-2553.	1.8	5
53	Boiler: lossy compression of RNA-seq alignments using coverage vectors. Nucleic Acids Research, 2016, 44, e133-e133.	6.5	4
54	Fast and memory-efficient scRNA-seq k -means clustering with various distances. , 2021, 2021, .		4

#	Article	IF	Citations
55	Finding Maximal Exact Matches Using the r-Index. Journal of Computational Biology, 2022, 29, 188-194.	0.8	4
56	Two-stage linked component analysis for joint decomposition of multiple biologically related data sets. Biostatistics, 2022, 23, 1200-1217.	0.9	3
57	Practical software for big genomics data. , 2013, , .		2
58	Measurement, Summary, and Methodological Variation in RNA-sequencing. , 2014, , 115-128.		0