Benjamin Langmead

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.

69 papers	54,792 citations	28 h-index	91 g-index
91 ext. papers	77,543 ext. citations	14.9 avg, IF	8.69 L-index

#	Paper	IF	Citations
69	Fast gapped-read alignment with Bowtie 2. *Nature Methods*, **2012**, 9, 357-9	21.6	24735
68	Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology*, **2009**, 10, R25	18.3	14770
67	HISAT: a fast spliced aligner with low memory requirements. *Nature Methods*, **2015**, 12, 357-60	21.6	8026
66	Tackling the widespread and critical impact of batch effects in high-throughput data. *Nature Reviews Genetics*, **2010**, 11, 733-9	30.1	1232
65	Improved metagenomic analysis with Kraken 2. *Genome Biology*, **2019**, 20, 257	18.3	903
64	Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75	36.3	825
63	Aligning short sequencing reads with Bowtie. *Current Protocols in Bioinformatics*, **2010**, Chapter 11, Unit 11.7	24.2	705
62	BSmooth: from whole genome bisulfite sequencing reads to differentially methylated regions. *Genome Biology*, **2012**, 13, R83	18.3	445
61	Ballgown bridges the gap between transcriptome assembly and expression analysis. *Nature Biotechnology*, **2015**, 33, 243-6	44.5	413
60	Searching for SNPs with cloud computing. *Genome Biology*, **2009**, 10, R134	18.3	333
59	Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, **2012**, 15, 1371-3	25.5	237
58	Cloud-scale RNA-sequencing differential expression analysis with Myrna. *Genome Biology*, **2010**, 11, R83	18.3	227
57	Reproducible RNA-seq analysis using recount2. *Nature Biotechnology*, **2017**, 35, 319-321	44.5	211
56	Cloud computing and the DNA data race. *Nature Biotechnology*, **2010**, 28, 691-3	44.5	193
55	Scaling read aligners to hundreds of threads on general-purpose processors. *Bioinformatics*, **2019**, 35, 421-432	7.2	172
54	Polyester: simulating RNA-seq datasets with differential transcript expression. *Bioinformatics*, **2015** , 31, 2778-84	7.2	160
53	Lighter: fast and memory-efficient sequencing error correction without counting. *Genome Biology*, **2014**, 15, 509	18.3	139

52	Computational pan-genomics: status, promises and challenges. *Briefings in Bioinformatics*, **2018**, 19, 118-135	13.4	130
51	Cloud computing for genomic data analysis and collaboration. *Nature Reviews Genetics*, **2018**, 19, 208-219	30.1	119
50	ReCount: a multi-experiment resource of analysis-ready RNA-seq gene count datasets. *BMC Bioinformatics*, **2011**, 12, 449	3.6	115
49	Large-scale hypomethylated blocks associated with Epstein-Barr virus-induced B-cell immortalization. *Genome Research*, **2014**, 24, 177-84	9.7	99
48	Alignment of Next-Generation Sequencing Reads. *Annual Review of Genomics and Human Genetics*, **2015**, 16, 133-51	9.7	72
47	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	18.3	65
46	The DNA Data Deluge: Fast, efficient genome sequencing machines are spewing out more data than geneticists can analyze. *IEEE Spectrum*, **2013**, 50, 26-33	1.7	40
45	FORGe: prioritizing variants for graph genomes. *Genome Biology*, **2018**, 19, 220	18.3	38
44	Rail-RNA: scalable analysis of RNA-seq splicing and coverage. *Bioinformatics*, **2017**, 33, 4033-4040	7.2	33
43	Flexible expressed region analysis for RNA-seq with derfinder. *Nucleic Acids Research*, **2017**, 45, e9	20.1	32
42	Improved metagenomic analysis with Kraken 2		30
41	Genotyping in the cloud with Crossbow. *Current Protocols in Bioinformatics*, **2012**, Chapter 15, Unit15.3	24.2	23
40	Arioc: high-throughput read alignment with GPU-accelerated exploration of the seed-and-extend search space. *PeerJ*, **2015**, 3, e808	3.1	20
39	Dashing: fast and accurate genomic distances with HyperLogLog. *Genome Biology*, **2019**, 20, 265	18.3	20
38	Snaptron: querying splicing patterns across tens of thousands of RNA-seq samples. *Bioinformatics*, **2018**, 34, 114-116	7.2	18
37	Prefix-free parsing for building big BWTs. *Algorithms for Molecular Biology*, **2019**, 14, 13	1.8	16
36	ASCOT identifies key regulators of neuronal subtype-specific splicing. *Nature Communications*, **2020**, 11, 137	17.4	16
35	Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. *Journal of Computational Biology*, **2020**, 27, 500-513	1.7	15

34	Recounting the FANTOM CAGE-Associated Transcriptome. *Genome Research*, **2020**, 30, 1073-1081	9.7	13
33	How bioinformatics and open data can boost basic science in countries and universities with limited resources. *Nature Biotechnology*, **2019**, 37, 324-326	44.5	11
32	A tandem simulation framework for predicting mapping quality. *Genome Biology*, **2017**, 18, 152	18.3	9
31	Dashing: Fast and Accurate Genomic Distances with HyperLogLog		9
30	Integrated Transcriptomic and Proteomic Analysis of Primary Human Umbilical Vein Endothelial Cells. *Proteomics*, **2019**, 19, e1800315	4.8	8
29	Vargas: heuristic-free alignment for assessing linear and graph read aligners. *Bioinformatics*, **2020**, 36, 3712-3718	7.2	8
28	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes. *Nucleic Acids Research*, **2019**, 47, e117	20.1	8
27	Reference flow: reducing reference bias using multiple population genomes. *Genome Biology*, **2021**, 22, 8	18.3	8
26	Flexible expressed region analysis for RNA-seq with derfinder		6
25	Widespread splicing of repetitive element loci into coding regions of gene transcripts. *Human Molecular Genetics*, **2016**, 25, 4962-4982	5.6	6
24	Efficient Construction of a Complete Index for Pan-Genomics Read Alignment. *Lecture Notes in Computer Science*, **2019**, 158-173	0.9	5
23	Matching Reads to Many Genomes with the -Index. *Journal of Computational Biology*, **2020**, 27, 514-518	1.7	5
22	Rail-dbGaP: analyzing dbGaP-protected data in the cloud with Amazon Elastic MapReduce. *Bioinformatics*, **2016**, 32, 2551-3	7.2	5
21	Rail-RNA: Scalable analysis of RNA-seq splicing and coverage		5
20	recount: A large-scale resource of analysis-ready RNA-seq expression data		5
19	MONI: A Pangenomic Index for Finding Maximal Exact Matches.. *Journal of Computational Biology*, **2022**,	1.7	4
18	Reducing reference bias using multiple population reference genomes		4
17	recount3: summaries and queries for large-scale RNA-seq expression and splicing. *Genome Biology*, **2021**, 22, 323	18.3	3

List of Publications

16	HISAT: Hierarchical Indexing for Spliced Alignment of Transcripts		3
15	Megadepth: efficient coverage quantification for BigWigs and BAMs. *Bioinformatics*, **2021**,	7.2	3
14	Faster sequence alignment through GPU-accelerated restriction of the seed-and-extend search space **2014**,		2
13	Prefix-Free Parsing for Building Big BWTs		2
12	Snaptron: querying and visualizing splicing across tens of thousands of RNA-seq samples		2
11	Scaling read aligners to hundreds of threads on general-purpose processors		2
10	LevioSAM: Fast lift-over of variant-aware reference alignments. *Bioinformatics*, **2021**,	7.2	2
9	MONI: A Pangenomics Index for Finding MEMs		2
8	Boiler: lossy compression of RNA-seq alignments using coverage vectors. *Nucleic Acids Research*, **2016**, 44, e133	20.1	2
7	Samovar: Single-Sample Mosaic Single-Nucleotide Variant Calling with Linked Reads. *IScience*, **2019**, 18, 1-10	6.1	1
6	Finding Maximal Exact Matches Using the r-Index.. *Journal of Computational Biology*, **2022**,	1.7	1
5	Megadepth: efficient coverage quantification for BigWigs and BAMs		1
4	Analyzing whole genome bisulfite sequencing data from highly divergent genotypes		1
3	Pan-genomic matching statistics for targeted nanopore sequencing. *IScience*, **2021**, 24, 102696	6.1	1
2	PHONI: Streamed Matching Statistics with Multi-Genome References **2021**, 2021, 193-202		1
1	Measurement, Summary, and Methodological Variation in RNA-sequencing **2014**, 115-128		