

Carl Kingsford

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.

56

papers

6,947

citations

21

h-index

60

g-index

60

ext. papers

10,949

ext. citations

9.1

avg, IF

6.64

L-index

#	Paper	IF	Citations
56	Salmon provides fast and bias-aware quantification of transcript expression. <i>Nature Methods</i> , 2017 , 14, 417-419	21.6	3249
55	A fast, lock-free approach for efficient parallel counting of occurrences of k-mers. <i>Bioinformatics</i> , 2011 , 27, 764-70	7.2	1727
54	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014 , 32, 462-4	44.5	422
53	The power of protein interaction networks for associating genes with diseases. <i>Bioinformatics</i> , 2010 , 26, 1057-63	7.2	253
52	What are decision trees?. <i>Nature Biotechnology</i> , 2008 , 26, 1011-3	44.5	207
51	Genome analysis linking recent European and African influenza (H5N1) viruses. <i>Emerging Infectious Diseases</i> , 2007 , 13, 713-8	10.2	164
50	Assembly complexity of prokaryotic genomes using short reads. <i>BMC Bioinformatics</i> , 2010 , 11, 21	3.6	92
49	Fast search of thousands of short-read sequencing experiments. <i>Nature Biotechnology</i> , 2016 , 34, 300-2	44.5	80
48	Salmon provides accurate, fast, and bias-aware transcript expression estimates using dual-phase inference		78
47	Accurate assembly of transcripts through phase-preserving graph decomposition. <i>Nature Biotechnology</i> , 2017 , 35, 1167-1169	44.5	75
46	A Semidefinite Programming Approach to Side Chain Positioning with New Rounding Strategies. <i>INFORMS Journal on Computing</i> , 2004 , 16, 380-392	2.4	66
45	Network archaeology: uncovering ancient networks from present-day interactions. <i>PLoS Computational Biology</i> , 2011 , 7, e1001119	5	50
44	GiRaF: robust, computational identification of influenza reassortments via graph mining. <i>Nucleic Acids Research</i> , 2011 , 39, e34	20.1	44
43	Revealing biological modules via graph summarization. <i>Journal of Computational Biology</i> , 2009 , 16, 253-64	4.7	40
42	Reference-based compression of short-read sequences using path encoding. <i>Bioinformatics</i> , 2015 , 31, 1920-8	7.2	32
41	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020 , 21, 239	18.3	31
40	2009 Swine-origin influenza A (H1N1) resembles previous influenza isolates. <i>PLoS ONE</i> , 2009 , 4, e6402	3.7	28

39	Isoform-level ribosome occupancy estimation guided by transcript abundance with Ribomap. <i>Bioinformatics</i> , 2016 , 32, 1880-2	7.2	26
38	Data-dependent bucketing improves reference-free compression of sequencing reads. <i>Bioinformatics</i> , 2015 , 31, 2770-7	7.2	22
37	Finding biologically accurate clusterings in hierarchical tree decompositions using the variation of information. <i>Journal of Computational Biology</i> , 2010 , 17, 503-16	1.7	22
36	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , 2017 , 13, e1005777	5	22
35	Sketching and Sublinear Data Structures in Genomics. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 93-118	5.6	21
34	Improved Search of Large Transcriptomic Sequencing Databases Using Split Sequence Bloom Trees. <i>Journal of Computational Biology</i> , 2018 , 25, 755-765	1.7	21
33	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2016 , 257-268	0.9	17
32	Predicting protein interactions via parsimonious network history inference. <i>Bioinformatics</i> , 2013 , 29, i237-46	7.2	15
31	Improving Bloom Filter Performance on Sequence Data Using k-mer Bloom Filters. <i>Journal of Computational Biology</i> , 2017 , 24, 547-557	1.7	14
30	Chromosomal dynamics predicted by an elastic network model explains genome-wide accessibility and long-range couplings. <i>Nucleic Acids Research</i> , 2017 , 45, 3663-3673	20.1	13
29	Improved Search of Large Transcriptomic Sequencing Databases Using Split Sequence Bloom Trees. <i>Lecture Notes in Computer Science</i> , 2017 , 257-271	0.9	13
28	Uncovering Genomic Reassortments among Influenza Strains by Enumerating Maximal Bicliques 2008 ,		12
27	Parsimonious reconstruction of network evolution. <i>Algorithms for Molecular Biology</i> , 2012 , 7, 25	1.8	11
26	A unified model explaining the offsets of overlapping and near-overlapping prokaryotic genes. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2091-8	8.3	9
25	Finding Biologically Accurate Clusterings in Hierarchical Tree Decompositions Using the Variation of Information. <i>Lecture Notes in Computer Science</i> , 2009 , 400-417	0.9	8
24	Exploring biological network dynamics with ensembles of graph partitions. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010 , 166-77	1.3	7
23	Alignment and mapping methodology influence transcript abundance estimation		7
22	Exploring Ribosome Positioning on Translating Transcripts with Ribosome Profiling. <i>Methods in Molecular Biology</i> , 2016 , 1358, 71-97	1.4	6

21	Quantifying the benefit offered by transcript assembly with Scallop-LR on single-molecule long reads. <i>Genome Biology</i> , 2019 , 20, 287	18.3	6
20	A cooperative combinatorial Particle Swarm Optimization algorithm for side-chain packing 2009 ,		4
19	Deriving Ranges of Optimal Estimated Transcript Expression Due to Non-identifiability		4
18	A Compact Mathematical Programming Formulation for DNA Motif Finding. <i>Lecture Notes in Computer Science</i> , 2006 , 233-245	0.9	4
17	Extracting between-pathway models from E-MAP interactions using expected graph compression. <i>Journal of Computational Biology</i> , 2011 , 18, 379-90	1.7	3
16	Parsimonious Reconstruction of Network Evolution. <i>Lecture Notes in Computer Science</i> , 2011 , 237-249	0.9	3
15	Detecting anomalies in RNA-seq quantification		2
14	Exact transcript quantification over splice graphs. <i>Algorithms for Molecular Biology</i> , 2021 , 16, 5	1.8	2
13	Improving Bloom Filter Performance on Sequence Data Using (k)-mer Bloom Filters. <i>Lecture Notes in Computer Science</i> , 2016 , 137-151	0.9	2
12	More Accurate Transcript Assembly via Parameter Advising. <i>Journal of Computational Biology</i> , 2020 , 27, 1181-1189	1.7	2
11	Accounting for fragments of unexpected origin improves transcript quantification in RNA-seq simulations focused on increased realism		2
10	A cost-aggregating integer linear program for motif finding. <i>Journal of Discrete Algorithms</i> , 2011 , 9, 326-334		1
9	Particle Swarm Optimization for multimodal combinatorial problems and its application to protein design 2010 ,		1
8	Deriving Ranges of Optimal Estimated Transcript Expression due to Nonidentifiability.. <i>Journal of Computational Biology</i> , 2022 ,	1.7	1
7	Towards building an automated bioinformatician: more accurate transcript assembly via parameter advising		1
6	Scallop enables accurate assembly of transcripts through phasing-preserving graph decomposition		1
5	Identification of Microbiota-Induced Gene Expression Changes in the <i>Drosophila melanogaster</i> Head		1
4	Quantifying the Benefit Offered by Transcript Assembly on Single-Molecule Long Reads		1

3	Extracting Between-Pathway Models from E-MAP Interactions Using Expected Graph Compression. <i>Lecture Notes in Computer Science</i> , 2010 , 248-262	0.9	1
2	Detecting, Categorizing, and Correcting Coverage Anomalies of RNA-Seq Quantification. <i>Cell Systems</i> , 2019 , 9, 589-599.e7	10.6	1
1	Maximum likelihood reconstruction of ancestral networks by integer linear programming. <i>Bioinformatics</i> , 2021 , 37, 1083-1092	7.2	0