

Carl Kingsford

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/11715079/carl-kingsford-publications-by-year.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Deriving Ranges of Optimal Estimated Transcript Expression due to Nonidentifiability.. <i>Journal of Computational Biology</i> , 2022 ,	1.7	1
55	Exact transcript quantification over splice graphs. <i>Algorithms for Molecular Biology</i> , 2021 , 16, 5	1.8	2
54	Maximum likelihood reconstruction of ancestral networks by integer linear programming. <i>Bioinformatics</i> , 2021 , 37, 1083-1092	7.2	0
53	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020 , 21, 239	18.3	31
52	More Accurate Transcript Assembly via Parameter Advising. <i>Journal of Computational Biology</i> , 2020 , 27, 1181-1189	1.7	2
51	Sketching and Sublinear Data Structures in Genomics. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 93-118	5.6	21
50	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
49	Detecting, Categorizing, and Correcting Coverage Anomalies of RNA-Seq Quantification. <i>Cell Systems</i> , 2019 , 9, 589-599.e7	10.6	1
48	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
47	Salmon provides fast and bias-aware quantification of transcript expression. <i>Nature Methods</i> , 2017 , 14, 417-419	21.6	3249
46	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
45	Accurate assembly of transcripts through phase-preserving graph decomposition. <i>Nature Biotechnology</i> , 2017 , 35, 1167-1169	44.5	75
44	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
43	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , 2017 , 13, e1005777	5	22
42	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
41	Exploring Ribosome Positioning on Translating Transcripts with Ribosome Profiling. <i>Methods in Molecular Biology</i> , 2016 , 1358, 71-97	1.4	6
40	Isoform-level ribosome occupancy estimation guided by transcript abundance with Ribomap. <i>Bioinformatics</i> , 2016 , 32, 1880-2	7.2	26

39	Fast search of thousands of short-read sequencing experiments. <i>Nature Biotechnology</i> , 2016 , 34, 300-2	44.5	80
38	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
37	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2016 , 257-268	0.9	17
36	Reference-based compression of short-read sequences using path encoding. <i>Bioinformatics</i> , 2015 , 31, 1920-8	7.2	32
35	Data-dependent bucketing improves reference-free compression of sequencing reads. <i>Bioinformatics</i> , 2015 , 31, 2770-7	7.2	22
34	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014 , 32, 462-4	44.5	422
33	Predicting protein interactions via parsimonious network history inference. <i>Bioinformatics</i> , 2013 , 29, i237-46	7.2	15
32	Parsimonious reconstruction of network evolution. <i>Algorithms for Molecular Biology</i> , 2012 , 7, 25	1.8	11
31	A cost-aggregating integer linear program for motif finding. <i>Journal of Discrete Algorithms</i> , 2011 , 9, 326-334		1
30	A fast, lock-free approach for efficient parallel counting of occurrences of k-mers. <i>Bioinformatics</i> , 2011 , 27, 764-70	7.2	1727
29	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
28	GiRaF: robust, computational identification of influenza reassortments via graph mining. <i>Nucleic Acids Research</i> , 2011 , 39, e34	20.1	44
27	Network archaeology: uncovering ancient networks from present-day interactions. <i>PLoS Computational Biology</i> , 2011 , 7, e1001119	5	50
26	Parsimonious Reconstruction of Network Evolution. <i>Lecture Notes in Computer Science</i> , 2011 , 237-249	0.9	3
25	Particle Swarm Optimization for multimodal combinatorial problems and its application to protein design 2010 ,		1
24	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
23	The power of protein interaction networks for associating genes with diseases. <i>Bioinformatics</i> , 2010 , 26, 1057-63	7.2	253
22	Assembly complexity of prokaryotic genomes using short reads. <i>BMC Bioinformatics</i> , 2010 , 11, 21	3.6	92

21	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
20	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
19	2009 Swine-origin influenza A (H1N1) resembles previous influenza isolates. <i>PLoS ONE</i> , 2009 , 4, e6402	3.7	28
18	A cooperative combinatorial Particle Swarm Optimization algorithm for side-chain packing 2009 ,		4
17	Revealing biological modules via graph summarization. <i>Journal of Computational Biology</i> , 2009 , 16, 253-64	4.7	40
16	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
15	What are decision trees?. <i>Nature Biotechnology</i> , 2008 , 26, 1011-3	44.5	207
14	Uncovering Genomic Reassortments among Influenza Strains by Enumerating Maximal Bicliques 2008 ,		12
13	Genome analysis linking recent European and African influenza (H5N1) viruses. <i>Emerging Infectious Diseases</i> , 2007 , 13, 713-8	10.2	164
12	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
11	A Compact Mathematical Programming Formulation for DNA Motif Finding. <i>Lecture Notes in Computer Science</i> , 2006 , 233-245	0.9	4
10	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
9	Towards building an automated bioinformatician: more accurate transcript assembly via parameter advising		1
8	Deriving Ranges of Optimal Estimated Transcript Expression Due to Non-identifiability		4
7	Salmon provides accurate, fast, and bias-aware transcript expression estimates using dual-phase inference		78
6	Scallop enables accurate assembly of transcripts through phasing-preserving graph decomposition		1
5	Detecting anomalies in RNA-seq quantification		2
4	Identification of Microbiota-Induced Gene Expression Changes in the <i>Drosophila melanogaster</i> Head		1

3	Quantifying the Benefit Offered by Transcript Assembly on Single-Molecule Long Reads	1
2	Alignment and mapping methodology influence transcript abundance estimation	7
1	Accounting for fragments of unexpected origin improves transcript quantification in RNA-seq simulations focused on increased realism	2