

Rob Patro

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

10,891
citations

331259

21
h-index

288905

40
g-index

76
all docs

76
docs citations

76
times ranked

19674
citing authors

#	ARTICLE	IF	CITATIONS
1	AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. Genome Biology, 2022, 23, 39.	3.8	3
2	An incrementally updatable and scalable system for large-scale sequence search using the Bentleyâ€Saxe transformation. Bioinformatics, 2022, 38, 3155-3163.	1.8	4
3	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. Nature Methods, 2022, 19, 316-322.	9.0	31
4	Perplexity: evaluating transcript abundance estimation in the absence of ground truth. Algorithms for Molecular Biology, 2022, 17, 6.	0.3	0
5	Airpart: interpretable statistical models for analyzing allelic imbalance in single-cell datasets. Bioinformatics, 2022, 38, 2773-2780.	1.8	6
6	PuffAligner: a fast, efficient and accurate aligner based on the Pufferfish index. Bioinformatics, 2021, 37, 4048-4055.	1.8	19
7	Cuttlefish: fast, parallel and low-memory compaction of de Bruijn graphs from large-scale genome collections. Bioinformatics, 2021, 37, i177-i186.	1.8	25
8	Compression of quantification uncertainty for scRNA-seq counts. Bioinformatics, 2021, 37, 1699-1707.	1.8	4
9	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. PLoS Computational Biology, 2021, 17, e1008585.	1.5	46
10	Algorithms meet sequencing technologies â€ 10th edition of the RECOMB-Seq workshop. IScience, 2021, 24, 101956.	1.9	0
11	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	1.8	11
12	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. Bioinformatics, 2020, 36, i292-i299.	1.8	13
13	An Efficient, Scalable, and Exact Representation of High-Dimensional Color Information Enabled Using de Bruijn Graph Search. Journal of Computational Biology, 2020, 27, 485-499.	0.8	22
14	Alignment and mapping methodology influence transcript abundance estimation. Genome Biology, 2020, 21, 239.	3.8	96
15	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. PLoS Computational Biology, 2020, 16, e1007664.	1.5	165
16	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
17	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
18	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0

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19	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
20	Rich Chromatin Structure Prediction from Hi-C Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1448-1458.	1.9	22
21	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	6.5	54
22	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. Bioinformatics, 2019, 35, i136-i144.	1.8	17
23	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. Annual Review of Biomedical Data Science, 2019, 2, 139-173.	2.8	101
24	An Efficient, Scalable and Exact Representation of High-Dimensional Color Information Enabled via de Bruijn Graph Search. Lecture Notes in Computer Science, 2019, , 1-18.	1.0	9
25	Sketching and Sublinear Data Structures in Genomics. Annual Review of Biomedical Data Science, 2019, 2, 93-118.	2.8	37
26	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. Genome Biology, 2019, 20, 65.	3.8	195
27	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. Life Science Alliance, 2019, 2, e201800175.	1.3	19
28	Squeakr: an exact and approximate k -mer counting system. Bioinformatics, 2018, 34, 568-575.	1.8	60
29	Towards Selective-Alignment. , 2018, , .		5
30	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	0.8	87
31	A space and time-efficient index for the compacted colored de Bruijn graph. Bioinformatics, 2018, 34, i169-i177.	1.8	63
32	Mantis: A Fast, Small, and Exact Large-Scale Sequence-Search Index. Cell Systems, 2018, 7, 201-207.e4.	2.9	79
33	Groupier: graph-based clustering and annotation for improved $de\ novo$ transcriptome analysis. Bioinformatics, 2018, 34, 3265-3272.	1.8	12
34	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. F1000Research, 2018, 7, 952.	0.8	63
35	Salmon provides fast and bias-aware quantification of transcript expression. Nature Methods, 2017, 14, 417-419.	9.0	7,460
36	A General-Purpose Counting Filter. , 2017, , .		96

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37	deBGR: an efficient and near-exact representation of the weighted de Bruijn graph. <i>Bioinformatics</i> , 2017, 33, i133-i141.	1.8	31
38	Quark enables semi-reference-based compression of RNA-seq data. <i>Bioinformatics</i> , 2017, 33, 3380-3386.	1.8	4
39	Improved data-driven likelihood factorizations for transcript abundance estimation. <i>Bioinformatics</i> , 2017, 33, i142-i151.	1.8	23
40	TransRate: reference-free quality assessment of de novo transcriptome assemblies. <i>Genome Research</i> , 2016, 26, 1134-1144.	2.4	650
41	RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. <i>Bioinformatics</i> , 2016, 32, i192-i200.	1.8	99
42	At RTD – a comprehensive reference transcript dataset resource for accurate quantification of transcript-specific expression in <i>Arabidopsis thaliana</i> . <i>New Phytologist</i> , 2015, 208, 96-101.	3.5	50
43	Reference-based compression of short-read sequences using path encoding. <i>Bioinformatics</i> , 2015, 31, 1920-1928.	1.8	46
44	Data-dependent bucketing improves reference-free compression of sequencing reads. <i>Bioinformatics</i> , 2015, 31, 2770-2777.	1.8	36
45	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014, 32, 462-464.	9.4	594
46	Identification of alternative topological domains in chromatin. <i>Algorithms for Molecular Biology</i> , 2014, 9, 14.	0.3	192
47	Topological properties of chromosome conformation graphs reflect spatial proximities within chromatin. , 2013, , .		21
48	Predicting protein interactions via parsimonious network history inference. <i>Bioinformatics</i> , 2013, 29, i237-i246.	1.8	21
49	Global network alignment using multiscale spectral signatures. <i>Bioinformatics</i> , 2012, 28, 3105-3114.	1.8	175
50	Parsimonious reconstruction of network evolution. <i>Algorithms for Molecular Biology</i> , 2012, 7, 25.	0.3	13