

Rob Patro

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1659334/publications.pdf>

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	Salmon provides fast and bias-aware quantification of transcript expression. <i>Nature Methods</i> , 2017, 14, 417-419.	9.0	7,460
2	TransRate: reference-free quality assessment of de novo transcriptome assemblies. <i>Genome Research</i> , 2016, 26, 1134-1144.	2.4	650
3	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. <i>Nature Biotechnology</i> , 2014, 32, 462-464.	9.4	594
4	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. <i>Genome Biology</i> , 2019, 20, 65.	3.8	195
5	Identification of alternative topological domains in chromatin. <i>Algorithms for Molecular Biology</i> , 2014, 9, 14.	0.3	192
6	Global network alignment using multiscale spectral signatures. <i>Bioinformatics</i> , 2012, 28, 3105-3114.	1.8	175
7	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. <i>PLoS Computational Biology</i> , 2020, 16, e1007664.	1.5	165
8	RNA Sequencing Data: Hitchhiker's Guide to Expression Analysis. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 139-173.	2.8	101
9	RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. <i>Bioinformatics</i> , 2016, 32, i192-i200.	1.8	99
10	A General-Purpose Counting Filter. , 2017, , .		96
11	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020, 21, 239.	3.8	96
12	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	0.8	87
13	Mantis: A Fast, Small, and Exact Large-Scale Sequence-Search Index. <i>Cell Systems</i> , 2018, 7, 201-207.e4.	2.9	79
14	A space and time-efficient index for the compacted colored de Bruijn graph. <i>Bioinformatics</i> , 2018, 34, i169-i177.	1.8	63
15	Swimming downstream: statistical analysis of differential transcript usage following Salmon quantification. <i>F1000Research</i> , 2018, 7, 952.	0.8	63
16	Squeakr: an exact and approximate k -mer counting system. <i>Bioinformatics</i> , 2018, 34, 568-575.	1.8	60
17	Nonparametric expression analysis using inferential replicate counts. <i>Nucleic Acids Research</i> , 2019, 47, e105-e105.	6.5	54
18	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

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19	Reference-based compression of short-read sequences using path encoding. <i>Bioinformatics</i> , 2015, 31, 1920-1928.	1.8	46
20	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. <i>PLoS Computational Biology</i> , 2021, 17, e1008585.	1.5	46
21	Sketching and Sublinear Data Structures in Genomics. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 93-118.	2.8	37
22	Data-dependent bucketing improves reference-free compression of sequencing reads. <i>Bioinformatics</i> , 2015, 31, 2770-2777.	1.8	36
23	deBGR: an efficient and near-exact representation of the weighted de Bruijn graph. <i>Bioinformatics</i> , 2017, 33, i133-i141.	1.8	31
24	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. <i>Nature Methods</i> , 2022, 19, 316-322.	9.0	31
25	Cuttlefish: fast, parallel and low-memory compaction of de Bruijn graphs from large-scale genome collections. <i>Bioinformatics</i> , 2021, 37, i177-i186.	1.8	25
26	Improved data-driven likelihood factorizations for transcript abundance estimation. <i>Bioinformatics</i> , 2017, 33, i142-i151.	1.8	23
27	Rich Chromatin Structure Prediction from Hi-C Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1448-1458.	1.9	22
28	An Efficient, Scalable, and Exact Representation of High-Dimensional Color Information Enabled Using de Bruijn Graph Search. <i>Journal of Computational Biology</i> , 2020, 27, 485-499.	0.8	22
29	Topological properties of chromosome conformation graphs reflect spatial proximities within chromatin. , 2013, , .		21
30	Predicting protein interactions via parsimonious network history inference. <i>Bioinformatics</i> , 2013, 29, i237-i246.	1.8	21
31	PuffAligner: a fast, efficient and accurate aligner based on the Pufferfish index. <i>Bioinformatics</i> , 2021, 37, 4048-4055.	1.8	19
32	A junction coverage compatibility score to quantify the reliability of transcript abundance estimates and annotation catalogs. <i>Life Science Alliance</i> , 2019, 2, e201800175.	1.3	19
33	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. <i>Bioinformatics</i> , 2019, 35, i136-i144.	1.8	17
34	Parsimonious reconstruction of network evolution. <i>Algorithms for Molecular Biology</i> , 2012, 7, 25.	0.3	13
35	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. <i>Bioinformatics</i> , 2020, 36, i292-i299.	1.8	13
36	Grouper: graph-based clustering and annotation for improved <i>de novo</i> transcriptome analysis. <i>Bioinformatics</i> , 2018, 34, 3265-3272.	1.8	12

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37	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. <i>Bioinformatics</i> , 2020, 36, i102-i110.	1.8	11
38	An Efficient, Scalable and Exact Representation of High-Dimensional Color Information Enabled via de Bruijn Graph Search. <i>Lecture Notes in Computer Science</i> , 2019, , 1-18.	1.0	9
39	Airpart: interpretable statistical models for analyzing allelic imbalance in single-cell datasets. <i>Bioinformatics</i> , 2022, 38, 2773-2780.	1.8	6
40	Towards Selective-Alignment. , 2018, , .		5
41	Quark enables semi-reference-based compression of RNA-seq data. <i>Bioinformatics</i> , 2017, 33, 3380-3386.	1.8	4
42	Compression of quantification uncertainty for scRNA-seq counts. <i>Bioinformatics</i> , 2021, 37, 1699-1707.	1.8	4
43	An incrementally updatable and scalable system for large-scale sequence search using the Bentleyâ€Saxe transformation. <i>Bioinformatics</i> , 2022, 38, 3155-3163.	1.8	4
44	AGAMEMNON: an Accurate metaGenomics And MEtatranscriptoMics quaNtificatiON analysis suite. <i>Genome Biology</i> , 2022, 23, 39.	3.8	3
45	Algorithms meet sequencing technologies â€“ 10th edition of the RECOMB-Seq workshop. <i>IScience</i> , 2021, 24, 101956.	1.9	0
46	Perplexity: evaluating transcript abundance estimation in the absence of ground truth. <i>Algorithms for Molecular Biology</i> , 2022, 17, 6.	0.3	0
47	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
48	Tximeta: Reference sequence checksums for provenance identification in RNA-seq. , 2020, 16, e1007664.		0
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