

Avi Srivastava

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.

26
papers

1,457
citations

11
h-index

33
g-index

33
ext. papers

4,469
ext. citations

14.9
avg, IF

4.9
L-index

#	Paper	IF	Citations
26	Integrated analysis of multimodal single-cell data. <i>Cell</i> , 2021 , 184, 3573-3587.e29	56.2	558
25	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018 , 15, 475-476	21.6	416
24	Integrated analysis of multimodal single-cell data		91
23	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. <i>Genome Biology</i> , 2019 , 20, 65	18.3	84
22	RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. <i>Bioinformatics</i> , 2016 , 32, i192-i200	7.2	71
21	Multimodal single-cell chromatin analysis with Signac		50
20	A space and time-efficient index for the compacted colored de Bruijn graph. <i>Bioinformatics</i> , 2018 , 34, i169-i177	7.2	38
19	Single-cell chromatin state analysis with Signac. <i>Nature Methods</i> , 2021 , 18, 1333-1341	21.6	37
18	Alignment and mapping methodology influence transcript abundance estimation. <i>Genome Biology</i> , 2020 , 21, 239	18.3	31
17	Improved data-driven likelihood factorizations for transcript abundance estimation. <i>Bioinformatics</i> , 2017 , 33, i142-i151	7.2	16
16	Nonparametric expression analysis using inferential replicate counts. <i>Nucleic Acids Research</i> , 2019 , 47, e105	20.1	14
15	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. <i>PLoS Computational Biology</i> , 2021 , 17, e1008585	5	9
14	Texture-based medical image retrieval in compressed domain using compressive sensing. <i>International Journal of Bioinformatics Research and Applications</i> , 2014 , 10, 129-44	0.9	8
13	Alignment and mapping methodology influence transcript abundance estimation		7
12	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. <i>Bioinformatics</i> , 2019 , 35, i136-i144	7.2	6
11	Alevin-fry unlocks rapid, accurate, and memory-frugal quantification of single-cell RNA-seq data		3
10	A like-for-like comparison of lightweight-mapping pipelines for single-cell RNA-seq data pre-processing		3

9	Compression of quantification uncertainty for scRNA-seq counts		2
8	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. <i>Bioinformatics</i> , 2020 , 36, i102-i110	7.2	2
7	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. <i>Bioinformatics</i> , 2020 , 36, i292-i299	7.2	2
6	Accounting for fragments of unexpected origin improves transcript quantification in RNA-seq simulations focused on increased realism		2
5	Compression of quantification uncertainty for scRNA-seq counts. <i>Bioinformatics</i> , 2021 ,	7.2	2
4	GPU parallel implementation of B-spline non-rigid grid registration using free-form deformations. <i>International Journal of Biomedical Engineering and Technology</i> , 2013 , 11, 124	1.3	1
3	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data		1
2	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data		1
1	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data.. <i>Nature Methods</i> , 2022 , 19, 316-322	21.6	1