Avi Srivastava

List of Publications by Year
in descending order

18 papers	8,324 citations	759233 12 h-index	888059 17 g-index
33 all docs	33 docs citations	33 times ranked	9108 citing authors

#	Article	IF	Citations
1	Integrated analysis of multimodal single-cell data. Cell, 2021, 184, 3573-3587.e29.	28.9	5,912
2	Bioconda: sustainable and comprehensive software distribution for the life sciences. Nature Methods, 2018, 15, 475-476.	19.0	714
3	Single-cell chromatin state analysis with Signac. Nature Methods, 2021, 18, 1333-1341.	19.0	595
4	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. Genome Biology, 2019, 20, 65.	8.8	195
5	RapMap: a rapid, sensitive and accurate tool for mapping RNA-seq reads to transcriptomes. Bioinformatics, 2016, 32, i192-i200.	4.1	99
6	Alignment and mapping methodology influence transcript abundance estimation. Genome Biology, 2020, 21, 239.	8.8	96
7	A space and time-efficient index for the compacted colored de Bruijn graph. Bioinformatics, 2018, 34, i169-i177.	4.1	63
8	Nonparametric expression analysis using inferential replicate counts. Nucleic Acids Research, 2019, 47, e105-e105.	14.5	54
9	Preprocessing choices affect RNA velocity results for droplet scRNA-seq data. PLoS Computational Biology, 2021, 17, e1008585.	3.2	46
10	Characterizing cellular heterogeneity in chromatin state with scCUT&Tag-pro. Nature Biotechnology, 2022, 40, 1220-1230.	17.5	46
11	Alevin-fry unlocks rapid, accurate and memory-frugal quantification of single-cell RNA-seq data. Nature Methods, 2022, 19, 316-322.	19.0	31
12	Improved data-driven likelihood factorizations for transcript abundance estimation. Bioinformatics, 2017, 33, i142-i151.	4.1	23
13	Minnow: a principled framework for rapid simulation of dscRNA-seq data at the read level. Bioinformatics, 2019, 35, i136-i144.	4.1	17
14	A Bayesian framework for inter-cellular information sharing improves dscRNA-seq quantification. Bioinformatics, 2020, 36, i292-i299.	4.1	13
15	Terminus enables the discovery of data-driven, robust transcript groups from RNA-seq data. Bioinformatics, 2020, 36, i102-i110.	4.1	11
16	Texture-based medical image retrieval in compressed domain using compressive sensing. International Journal of Bioinformatics Research and Applications, 2014, 10, 129.	0.2	8
17	Compression of quantification uncertainty for scRNA-seq counts. Bioinformatics, 2021, 37, 1699-1707.	4.1	4
18	GPU parallel implementation of B-spline non-rigid grid registration using free-form deformations. International Journal of Biomedical Engineering and Technology, 2013, 11, 124.	0.2	1