

Yingxin Lin

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4454435/publications.pdf>

Version: 2024-02-01

12
papers

656
citations

1040056

9
h-index

1281871

11
g-index

18
all docs

18
docs citations

18
times ranked

886
citing authors

#	ARTICLE	IF	CITATIONS
1	scJoint integrates atlas-scale single-cell RNA-seq and ATAC-seq data with transfer learning. <i>Nature Biotechnology</i> , 2022, 40, 703-710.	17.5	70
2	Construction of a Human Cell Landscape of COVID-19 Infection at Single-cell Level. , 2021, 12, 705.		7
3	Clonal evolution in liver cancer at single-cell and single-variant resolution. <i>Journal of Hematology and Oncology</i> , 2021, 14, 22.	17.0	25
4	Uncovering cell identity through differential stability with Cepo. <i>Nature Computational Science</i> , 2021, 1, 784-790.	8.0	16
5	Investigating higher-order interactions in single-cell data with scHOT. <i>Nature Methods</i> , 2020, 17, 799-806.	19.0	51
6	CiteFuse enables multi-modal analysis of CITE-seq data. <i>Bioinformatics</i> , 2020, 36, 4137-4143.	4.1	63
7	Mutational and transcriptomic landscapes of a rare human prostate basal cell carcinoma. <i>Prostate</i> , 2020, 80, 508-517.	2.3	12
8	scClassify: sample size estimation and multiscale classification of cells using single and multiple reference. <i>Molecular Systems Biology</i> , 2020, 16, e9389.	7.2	79
9	Impact of similarity metrics on single-cell RNA-seq data clustering. <i>Briefings in Bioinformatics</i> , 2019, 20, 2316-2326.	6.5	107
10	Evaluating stably expressed genes in single cells. <i>GigaScience</i> , 2019, 8, .	6.4	44
11	scMerge leverages factor analysis, stable expression, and pseudoreplication to merge multiple single-cell RNA-seq datasets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9775-9784.	7.1	130
12	scDC: single cell differential composition analysis. <i>BMC Bioinformatics</i> , 2019, 20, 721.	2.6	29