Shian Su

List of Publications by Year
in descending order

17 papers	3,769 citations	759233 12 h-index	1058476 14 g-index
28 all docs	28 docs citations	28 times ranked	6973 citing authors

#	Article	IF	Citations
1	The long and the short of it: unlocking nanopore long-read RNA sequencing data with short-read differential expression analysis tools. NAR Genomics and Bioinformatics, 2021, 3, lqab028.	3.2	26
2	Clonal multi-omics reveals Bcor as a negative regulator of emergency dendritic cell development. Immunity, 2021, 54, 1338-1351.e9.	14.3	25
3	NanoMethViz: An R/Bioconductor package for visualizing long-read methylation data. PLoS Computational Biology, 2021, 17, e1009524.	3.2	11
4	Dashboard-style interactive plots for RNA-seq analysis are R Markdown ready with *Glimma* 2.0. NAR Genomics and Bioinformatics, 2021, 3, lqab116.	3.2	2
5	Covering all your bases: incorporating intron signal from RNA-seq data. NAR Genomics and Bioinformatics, 2020, 2, lqaa073.	3.2	37
6	Opportunities and challenges in long-read sequencing data analysis. Genome Biology, 2020, 21, 30.	8.8	1,536
7	Benchmarking single cell RNA-sequencing analysis pipelines using mixture control experiments. Nature Methods, 2019, 16, 479-487.	19.0	259
8	BiocPkgTools: Toolkit for mining the Bioconductor package ecosystem. F1000Research, 2019, 8, 752.	1.6	0
9	scPipe: A flexible R/Bioconductor preprocessing pipeline for single-cell RNA-sequencing data. PLoS Computational Biology, 2018, 14, e1006361.	3.2	97
10	Glimma: interactive graphics for gene expression analysis. Bioinformatics, 2017, 33, 2050-2052.	4.1	128
11	Deciphering the Innate Lymphoid Cell Transcriptional Program. Cell Reports, 2016, 17, 436-447.	6.4	131
12	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	1.6	368
13	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 2016, 5, 1408.	1.6	394
14	Why weight? Modelling sample and observational level variability improves power in RNA-seq analyses. Nucleic Acids Research, 2015, 43, e97-e97.	14.5	430
15	edgeR: a versatile tool for the analysis of shRNA-seq and CRISPR-Cas9 genetic screens. F1000Research, 2014, 3, 95.	1.6	80
16	RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR. F1000Research, 0, 5, 1408.	1.6	149
17	shRNA-seq data analysis with edgeR. F1000Research, 0, 3, 95.	1.6	43