

Shian Su

List of Publications by Year in descending order

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Version: 2024-02-01

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