

Kieran R Campbell

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

3,027
citations

686830

13
h-index

996533

15
g-index

21
all docs

21
docs citations

21
times ranked

6133
citing authors

#	ARTICLE	IF	CITATIONS
1	Scater: pre-processing, quality control, normalization and visualization of single-cell RNA-seq data in R. <i>Bioinformatics</i> , 2017, 33, 1179-1186.	1.8	1,283
2	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	3.8	742
3	Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. <i>Nature Methods</i> , 2019, 16, 1007-1015.	9.0	241
4	Dissociation of solid tumor tissues with cold active protease for single-cell RNA-seq minimizes conserved collagenase-associated stress responses. <i>Genome Biology</i> , 2019, 20, 210.	3.8	171
5	Single-Cell Sequencing of iPSC-Dopamine Neurons Reconstructs Disease Progression and Identifies HDAC4 as a Regulator of Parkinson Cell Phenotypes. <i>Cell Stem Cell</i> , 2019, 24, 93-106.e6.	5.2	123
6	clonealign: statistical integration of independent single-cell RNA and DNA sequencing data from human cancers. <i>Genome Biology</i> , 2019, 20, 54.	3.8	92
7	Uncovering pseudotemporal trajectories with covariates from single cell and bulk expression data. <i>Nature Communications</i> , 2018, 9, 2442.	5.8	80
8	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. <i>Nature</i> , 2021, 595, 585-590.	13.7	71
9	Order Under Uncertainty: Robust Differential Expression Analysis Using Probabilistic Models for Pseudotime Inference. <i>PLoS Computational Biology</i> , 2016, 12, e1005212.	1.5	59
10	A descriptive marker gene approach to single-cell pseudotime inference. <i>Bioinformatics</i> , 2019, 35, 28-35.	1.8	35
11	Single cell transcriptomes of normal endometrial derived organoids uncover novel cell type markers and cryptic differentiation of primary tumours. <i>Journal of Pathology</i> , 2020, 252, 201-214.	2.1	31
12	Automated assignment of cell identity from single-cell multiplexed imaging and proteomic data. <i>Cell Systems</i> , 2021, 12, 1173-1186.e5.	2.9	29
13	Probabilistic modeling of bifurcations in single-cell gene expression data using a Bayesian mixture of factor analyzers. <i>Wellcome Open Research</i> , 2017, 2, 19.	0.9	21
14	Modelling hereditary diffuse gastric cancer initiation using transgenic mouse-derived gastric organoids and single-cell sequencing. <i>Journal of Pathology</i> , 2021, 254, 254-264.	2.1	11
15	Computational modelling in single-cell cancer genomics: methods and future directions. <i>Physical Biology</i> , 2020, 17, 061001.	0.8	2