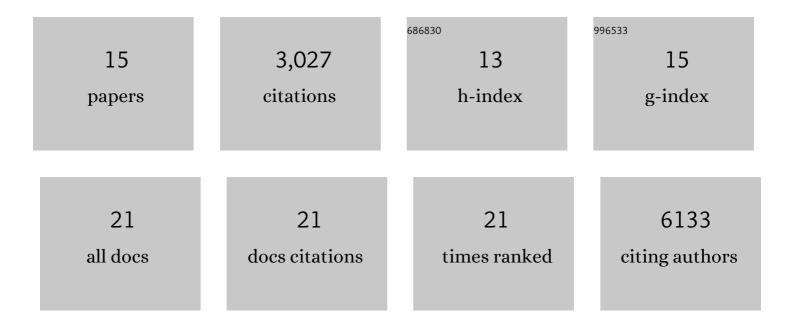
## Kieran R Campbell

List of Publications by Year in descending order

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KIEDAN R CAMPRELL

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