

Iain C Macaulay

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

9,664
citations

87723

38
h-index

161609

54
g-index

71
all docs

71
docs citations

71
times ranked

16449
citing authors

#	ARTICLE	IF	CITATIONS
1	High expression of the MADS-box gene <i>VRT2</i> increases the number of rudimentary basal spikelets in wheat. <i>Plant Physiology</i> , 2022, 189, 1536-1552.	2.3	17
2	Into the multiverse: advances in single-cell multiomic profiling. <i>Trends in Genetics</i> , 2022, 38, 831-843.	2.9	46
3	Meiosis and beyond – understanding the mechanistic and evolutionary processes shaping the germline genome. <i>Biological Reviews</i> , 2021, 96, 822-841.	4.7	25
4	Common clonal origin of conventional T cells and induced regulatory T cells in breast cancer patients. <i>Nature Communications</i> , 2021, 12, 1119.	5.8	26
5	Transcriptional characterization of human megakaryocyte polyploidization and lineage commitment. <i>Journal of Thrombosis and Haemostasis</i> , 2021, 19, 1236-1249.	1.9	15
6	Chemotherapy induces canalization of cell state in childhood B-cell precursor acute lymphoblastic leukemia. <i>Nature Cancer</i> , 2021, 2, 835-852.	5.7	25
7	3098 – SINGLE-CELL ANALYSIS OF ALTERNATIVE SPLICING IN HEMATOPOIETIC STEM AND PROGENITOR CELLS. <i>Experimental Hematology</i> , 2021, 100, S89.	0.2	0
8	Sequencing smart: De novo sequencing and assembly approaches for a non-model mammal. <i>GigaScience</i> , 2020, 9, .	3.3	18
9	Non-neuronal expression of SARS-CoV-2 entry genes in the olfactory system suggests mechanisms underlying COVID-19-associated anosmia. <i>Science Advances</i> , 2020, 6, .	4.7	865
10	A low-cost pipeline for soil microbiome profiling. <i>MicrobiologyOpen</i> , 2020, 9, e1133.	1.2	8
11	Spatially resolved transcriptomics reveals plant host responses to pathogens. <i>Plant Methods</i> , 2019, 15, 114.	1.9	17
12	ROS-mediated PI3K activation drives mitochondrial transfer from stromal cells to hematopoietic stem cells in response to infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24610-24619.	3.3	82
13	Acute myeloid leukemia induces protumoral p16INK4a-driven senescence in the bone marrow microenvironment. <i>Blood</i> , 2019, 133, 446-456.	0.6	67
14	Defining Cell Identity with Single-Cell Omics. <i>Proteomics</i> , 2018, 18, e1700312.	1.3	52
15	Perivascular Niche Cells Sense Thrombocytopenia and Activate Platelet-Biased Hscs in an IL-1 Dependent Manner. <i>Experimental Hematology</i> , 2018, 64, S44.	0.2	2
16	Single-Cell Multiomics: Multiple Measurements from Single Cells. <i>Trends in Genetics</i> , 2017, 33, 155-168.	2.9	392
17	Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types. <i>Genome Research</i> , 2017, 27, 451-461.	2.4	126
18	Power analysis of single-cell RNA-sequencing experiments. <i>Nature Methods</i> , 2017, 14, 381-387.	9.0	496

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19	Genome-wide in vivo screen identifies novel host regulators of metastatic colonization. <i>Nature</i> , 2017, 541, 233-236.	13.7	194
20	Embryonic thymopoiesis is initiated by an immune-restricted lympho-myeloid progenitor, independently of notch signaling. <i>Experimental Hematology</i> , 2017, 53, S113-S114.	0.2	0
21	Single-Cell Landscape of Transcriptional Heterogeneity and Cell Fate Decisions during Mouse Early Gastrulation. <i>Cell Reports</i> , 2017, 20, 1215-1228.	2.9	290
22	Pluripotent state transitions coordinate morphogenesis in mouse and human embryos. <i>Nature</i> , 2017, 552, 239-243.	13.7	193
23	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , 2016, 535, 289-293.	13.7	261
24	Single-cell RNA sequencing reveals molecular and functional platelet bias of aged haematopoietic stem cells. <i>Nature Communications</i> , 2016, 7, 11075.	5.8	238
25	Separation and parallel sequencing of the genomes and transcriptomes of single cells using G&T-seq. <i>Nature Protocols</i> , 2016, 11, 2081-2103.	5.5	142
26	Initial seeding of the embryonic thymus by immune-restricted lympho-myeloid progenitors. <i>Nature Immunology</i> , 2016, 17, 1424-1435.	7.0	49
27	Embryonic thymopoiesis is initiated by an immune-restricted lympho-myeloid progenitor independently of notch signaling. <i>Experimental Hematology</i> , 2016, 44, S65.	0.2	0
28	Dynamic spatio-temporal contribution of single $\hat{2}5t+$ cortical epithelial precursors to the thymus medulla. <i>European Journal of Immunology</i> , 2016, 46, 846-856.	1.6	56
29	Heterogeneity in Oct4 and Sox2 Targets Biases Cell Fate in 4-Cell Mouse Embryos. <i>Cell</i> , 2016, 165, 61-74.	13.5	385
30	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. <i>Cell Reports</i> , 2016, 14, 966-977.	2.9	164
31	Parallel single-cell sequencing links transcriptional and epigenetic heterogeneity. <i>Nature Methods</i> , 2016, 13, 229-232.	9.0	602
32	PDGFR $\hat{1}+$ demarcates the cardiogenic clonogenic Sca1 $\hat{+}$ stem/progenitor cell in adult murine myocardium. <i>Nature Communications</i> , 2015, 6, 6930.	5.8	130
33	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , 2015, 16, 712-724.	5.2	376
34	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , 2015, 33, 269-276.	9.4	352
35	G&T-seq: parallel sequencing of single-cell genomes and transcriptomes. <i>Nature Methods</i> , 2015, 12, 519-522.	9.0	633
36	Integrin Based Isolation Enables Purification of Murine Lineage Committed Cardiomyocytes. <i>PLoS ONE</i> , 2015, 10, e0135880.	1.1	6

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37	Single Cell Genomics: Advances and Future Perspectives. PLoS Genetics, 2014, 10, e1004126.	1.5	337
38	Population and single-cell genomics reveal the <i>Aire</i> dependency, relief from Polycomb silencing, and distribution of self-antigen expression in thymic epithelia. Genome Research, 2014, 24, 1918-1931.	2.4	308
39	Myelodysplastic Syndromes Are Propagated by Rare and Distinct Human Cancer Stem Cells In Vivo. Cancer Cell, 2014, 25, 794-808.	7.7	272
40	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	6.0	253
41	Platelet-biased stem cells reside at the apex of the haematopoietic stem-cell hierarchy. Nature, 2013, 502, 232-236.	13.7	493
42	FLT3-ITDs Instruct a Myeloid Differentiation and Transformation Bias in Lymphomyeloid Multipotent Progenitors. Cell Reports, 2013, 3, 1766-1776.	2.9	40
43	Lymphomyeloid Contribution of an Immune-Restricted Progenitor Emerging Prior to Definitive Hematopoietic Stem Cells. Cell Stem Cell, 2013, 13, 535-548.	5.2	225
44	Establishment of lympho-myeloid restricted progenitors prior to the emergence of definitive hematopoietic stem cells. Experimental Hematology, 2013, 41, S13.	0.2	0
45	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. Nature Cell Biology, 2013, 15, 363-372.	4.6	257
46	Canonical Wnt signaling in megakaryocytes regulates proplatelet formation. Blood, 2013, 121, 188-196.	0.6	42
47	Diverse Genetic Lesions In Myelodysplastic Syndromes Originate Exclusively In Rare MDS Stem Cells. Blood, 2013, 122, 4195-4195.	0.6	0
48	The earliest thymic T cell progenitors sustain B cell and myeloid lineage potential. Nature Immunology, 2012, 13, 412-419.	7.0	132
49	The Earliest Thymic T Cell Progenitors Sustain B Cell and Myeloid Lineage Potentials. Blood, 2011, 118, 2335-2335.	0.6	0
50	The MEIS1 Interactome in Megakaryocytes Reveals a Role in Cell Cycle Regulation,. Blood, 2011, 118, 3380-3380.	0.6	0
51	FLT3-ITDs Introduce a Myeloid Differentiation and Transformation Bias to Multipotent Lympho-Myeloid Progenitors. Blood, 2011, 118, 1380-1380.	0.6	0
52	Transcription profiling in human platelets reveals LRRFIP1 as a novel protein regulating platelet function. Blood, 2010, 116, 4646-4656.	0.6	90
53	Canonical Wnt signaling negatively regulates platelet function. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 19836-19841.	3.3	61
54	Functional genomics in zebrafish permits rapid characterization of novel platelet membrane proteins. Blood, 2009, 113, 4754-4762.	0.6	69

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55	A HaemAtlas: characterizing gene expression in differentiated human blood cells. <i>Blood</i> , 2009, 113, e1-e9.	0.6	215
56	Identification of variation in the platelet transcriptome associated with Glycoprotein 6 haplotype. <i>Platelets</i> , 2008, 19, 258-267.	1.1	9
57	Comparative gene expression profiling of in vitro differentiated megakaryocytes and erythroblasts identifies novel activatory and inhibitory platelet membrane proteins. <i>Blood</i> , 2007, 109, 3260-3269.	0.6	153
58	The novel inhibitory receptor G6B is expressed on the surface of platelets and attenuates platelet function in vitro. <i>Blood</i> , 2007, 109, 4806-4809.	0.6	64
59	Improving the power to detect differentially expressed genes in comparative microarray experiments by including information from self-self hybridizations. <i>Computational Biology and Chemistry</i> , 2007, 31, 178-185.	1.1	1
60	Platelet genomics and proteomics in human health and disease. <i>Journal of Clinical Investigation</i> , 2005, 115, 3370-3377.	3.9	146