

Nicola K Wilson

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

3,643
citations

361413

20
h-index

454955

30
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docs citations

32
times ranked

7374
citing authors

#	ARTICLE	IF	CITATIONS
1	Unique molecular and functional features of extramedullary hematopoietic stem and progenitor cell reservoirs in humans. <i>Blood</i> , 2022, 139, 3387-3401.	1.4	26
2	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. <i>Science</i> , 2022, 25, 103971.	4.1	7
3	Single-cell transcriptomics reveals the identity and regulators of human mast cell progenitors. <i>Blood Advances</i> , 2022, 6, 4439-4449.	5.2	10
4	STAT1 is essential for HSC function and maintains MHCIIhi stem cells that resist myeloablation and neoplastic expansion. <i>Blood</i> , 2022, 140, 1592-1606.	1.4	15
5	Single-cell molecular profiling provides a high-resolution map of basophil and mast cell development. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 1731-1742.	5.7	42
6	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021, 27, 904-916.	30.7	452
7	Blood and immune development in human fetal bone marrow and Down syndrome. <i>Nature</i> , 2021, 598, 327-331.	27.8	73
8	Gata3 targets Runx1 in the embryonic haematopoietic stem cell niche. <i>IUBMB Life</i> , 2020, 72, 45-52.	3.4	14
9	Manipulating niche composition limits damage to haematopoietic stem cells during Plasmodium infection. <i>Nature Cell Biology</i> , 2020, 22, 1399-1410.	10.3	26
10	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23626-23635.	7.1	18
11	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. <i>Blood</i> , 2019, 134, 2195-2208.	1.4	39
12	Nasal unsedated seated percutaneous endoscopic gastrostomy (nuPEG): a safe and effective technique for percutaneous endoscopic gastrostomy placement in high-risk candidates. <i>Frontline Gastroenterology</i> , 2018, 9, 105-109.	1.8	6
13	A single-cell hematopoietic landscape resolves 8 lineage trajectories and defects in Kit mutant mice. <i>Blood</i> , 2018, 131, e1-e11.	1.4	158
14	Single-Cell Sequencing in Normal and Malignant Hematopoiesis. <i>HemaSphere</i> , 2018, 2, e34.	2.7	13
15	Single-cell approaches identify the molecular network driving malignant hematopoietic stem cell self-renewal. <i>Blood</i> , 2018, 132, 791-803.	1.4	24
16	Reconstructing blood stem cell regulatory network models from single-cell molecular profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 5822-5829.	7.1	89
17	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , 2016, 535, 289-293.	27.8	261
18	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. <i>Blood</i> , 2016, 127, e12-e23.	1.4	49

#	ARTICLE	IF	CITATIONS
19	A single-cell resolution map of mouse hematopoietic stem and progenitor cell differentiation. <i>Blood</i> , 2016, 128, e20-e31.	1.4	608
20	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. <i>ELife</i> , 2016, 5, e11469.	6.0	61
21	Index sorting resolves heterogeneous murine hematopoietic stem cell populations. <i>Experimental Hematology</i> , 2015, 43, 803-811.	0.4	44
22	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. <i>Cell Stem Cell</i> , 2015, 16, 712-724.	11.1	376
23	CODEX: a next-generation sequencing experiment database for the haematopoietic and embryonic stem cell communities. <i>Nucleic Acids Research</i> , 2015, 43, D1117-D1123.	14.5	112
24	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. <i>EMBO Journal</i> , 2014, 33, 1212-26.	7.8	61
25	Transcriptional regulation of haematopoietic transcription factors. <i>Stem Cell Research and Therapy</i> , 2011, 2, 6.	5.5	36
26	Deciphering transcriptional control mechanisms in hematopoiesis – The impact of high-throughput sequencing technologies. <i>Experimental Hematology</i> , 2011, 39, 961-968.	0.4	8
27	Cf1 Expression Is Controlled by Five Distinct Regulatory Regions Spread over 100 Kilobases, with Scl/Tal1, Gata2, PU.1, Erg, Meis1, and Runx1 Acting as Upstream Regulators in Early Hematopoietic Cells. <i>Molecular and Cellular Biology</i> , 2010, 30, 3853-3863.	2.3	61
28	Combinatorial Transcriptional Control In Blood Stem/Progenitor Cells: Genome-wide Analysis of Ten Major Transcriptional Regulators. <i>Cell Stem Cell</i> , 2010, 7, 532-544.	11.1	623
29	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. <i>Blood</i> , 2009, 113, 5456-5465.	1.4	107
30	Gata2, Fli1, and Scl form a recursively wired gene-regulatory circuit during early hematopoietic development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 17692-17697.	7.1	208
31	p57Kip2 regulates embryonic blood stem cells by controlling sympathoadrenal progenitor expansion. <i>Blood</i> , 0, , .	1.4	3