Fernando J Calero-Nieto

List of Publications by Year
in descending order

39 papers	3,705 citations	279798 23 h-index	302126 39 g-index
45 all docs	45 docs citations	45 times ranked	7528 citing authors

#	Article	IF	Citations
1	A single-cell molecular map of mouse gastrulation and early organogenesis. Nature, 2019, 566, 490-495.	27.8	658
2	Functionally Distinct Subsets of Lineage-Biased Multipotent Progenitors Control Blood Production in Normal and Regenerative Conditions. Cell Stem Cell, 2015, 17, 35-46.	11.1	494
3	Single-cell multi-omics analysis of the immune response in COVID-19. Nature Medicine, 2021, 27, 904-916.	30.7	452
4	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	11.1	376
5	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.	10.3	257
6	Local and systemic responses to SARS-CoV-2 infection in children and adults. Nature, 2022, 602, 321-327.	27.8	179
7	Myeloid progenitor cluster formation drives emergency and leukaemic myelopoiesis. Nature, 2017, 544, 53-58.	27.8	155
8	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. Nature Cell Biology, 2018, 20, 127-134.	10.3	112
9	The transcriptional program controlled by the stem cell leukemia gene Scl/Tal1 during early embryonic hematopoietic development. Blood, 2009, 113, 5456-5465.	1.4	107
10	Role of the Transcriptional Activator XlnR of Fusarium oxysporum in Regulation of Xylanase Genes and Virulence. Molecular Plant-Microbe Interactions, 2007, 20, 977-985.	2.6	73
11	BET protein inhibition shows efficacy against JAK2V617F-driven neoplasms. Leukemia, 2014, 28, 88-97.	7.2	70
12	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. Genome Research, 2017, 27, 1795-1806.	5.5	70
13	Single-cell RNA-sequencing reveals a distinct population of proglucagon-expressing cells specific to the mouse upper small intestine. Molecular Metabolism, 2017, 6, 1296-1303.	6.5	68
14	Single-cell chromatin accessibility maps reveal regulatory programs driving early mouse organogenesis. Nature Cell Biology, 2020, 22, 487-497.	10.3	62
15	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. EMBO Journal, 2014, 33, 1212-26.	7.8	61
16	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. ELife, 2016, 5, e11469.	6.0	61
17	Integrated genome-scale analysis of the transcriptional regulatory landscape in a blood stem/progenitor cell model. Blood, 2016, 127, e12-e23.	1.4	49
18	The human GFI136N variant induces epigenetic changes at the Hoxa9 locus and accelerates K-RAS driven myeloproliferative disorder in mice. Blood, 2012, 120, 4006-4017.	1.4	40

#	ARTICLE	IF	CITATIONS
19	Notch ligand Dll4 impairs cell recruitment to aortic clusters and limits blood stem cell generation. EMBO Journal, 2020, 39, e104270.	7.8	40
20	Transcriptional regulation of haematopoietic transcription factors. Stem Cell Research and Therapy, 2011, 2, 6.	5.5	36
21	Runx1 binds as a dimeric complex to overlapping Runx1 sites within a palindromic element in the human GM-CSF enhancer. Nucleic Acids Research, 2010, 38, 6124-6134.	14.5	35
22	A Conserved Insulator That Recruits CTCF and Cohesin Exists between the Closely Related but Divergently Regulated Interleukin-3 and Granulocyte-Macrophage Colony-Stimulating Factor Genes. Molecular and Cellular Biology, 2009, 29, 1682-1693.	2.3	28
23	Transcription-dependent silencing of inducible convergent transgenes in transgenic mice. Epigenetics and Chromatin, 2010, 3, 3.	3.9	27
24	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. Stem Cell Reports, 2019, 13, 515-529.	4.8	27
25	Single-cell transcriptome analysis of CAR T-cell products reveals subpopulations, stimulation, and exhaustion signatures. OncoImmunology, 2021, 10, 1866287.	4.6	21
26	Genome-scale definition of the transcriptional programme associated with compromised PU.1 activity in acute myeloid leukaemia. Leukemia, 2016, 30, 14-23.	7.2	18
27	CHD7 and Runx1 interaction provides a braking mechanism for hematopoietic differentiation. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23626-23635.	7.1	18
28	Transcriptional regulation of Elf-1 : locus-wide analysis reveals four distinct promoters, a tissue-specific enhancer, control by PU.1 and the importance of Elf-1 downregulation for erythroid maturation. Nucleic Acids Research, 2010, 38, 6363-6374.	14.5	15
29	Enhanced hemato-endothelial specification during human embryonic differentiation through developmental cooperation between *AF4-MLL* and *MLL-AF4* fusions. Haematologica, 2019, 104, 1189-1201.	3.5	15
30	HOX-mediated LMO2 expression in embryonic mesoderm is recapitulated in acute leukaemias. Oncogene, 2013, 32, 5471-5480.	5.9	13
31	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. Nature Communications, 2020, 11, 1407.	12.8	13
32	Bivalent promoter marks and a latent enhancer may prime the leukaemia oncogene LMO1 for ectopic expression in T-cell leukaemia. Leukemia, 2013, 27, 1348-1357.	7.2	11
33	Regulatory elements mediating expression of xylanase genes in Fusarium oxysporum. Fungal Genetics and Biology, 2008, 45, 28-34.	2.1	8
34	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. IScience, 2022, 25, 103971.	4.1	7
35	Integration of Elf-4 into Stem/Progenitor and Erythroid Regulatory Networks through Locus-Wide Chromatin Studies Coupled with *In Vivo* Functional Validation. Molecular and Cellular Biology, 2012, 32, 763-773.	2.3	5
36	Single-Cell Analysis of Hematopoietic Stem Cells. Methods in Molecular Biology, 2021, 2308, 301-337.	0.9	3

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37	Shared transcription factors contribute to distinct cell fates. Transcription, 2014, 5, e978173.	3.1	1
38	The LMO2 -25 Region Harbours GATA2-Dependent Myeloid Enhancer and RUNX-Dependent T-Lymphoid Repressor Activity. PLoS ONE, 2015, 10, e0131577.	2.5	1
39	Single Cell RNA-Seq Characterises Pre-Leukemic Transformation Driven By CEBPA N321D in the Hoxb8-FL Cell Line. Blood, 2018, 132, 3887-3887.	1.4	0