

Fernando J Calero-Nieto

List of Publications by Year in descending order

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Version: 2024-02-01

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	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. <i>IScience</i> , 2022, 25, 103971.	4.1	7
2	Local and systemic responses to SARS-CoV-2 infection in children and adults. <i>Nature</i> , 2022, 602, 321-327.	27.8	179
3	Single-cell transcriptome analysis of CAR T-cell products reveals subpopulations, stimulation, and exhaustion signatures. <i>Oncoimmunology</i> , 2021, 10, 1866287.	4.6	21
4	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021, 27, 904-916.	30.7	452
5	Single-Cell Analysis of Hematopoietic Stem Cells. <i>Methods in Molecular Biology</i> , 2021, 2308, 301-337.	0.9	3
6	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
7	Notch ligand Dll4 impairs cell recruitment to aortic clusters and limits blood stem cell generation. <i>EMBO Journal</i> , 2020, 39, e104270.	7.8	40
8	Dissecting the early steps of MLL induced leukaemogenic transformation using a mouse model of AML. <i>Nature Communications</i> , 2020, 11, 1407.	12.8	13
9	Single-cell chromatin accessibility maps reveal regulatory programs driving early mouse organogenesis. <i>Nature Cell Biology</i> , 2020, 22, 487-497.	10.3	62
10	GATA2 Promotes Hematopoietic Development and Represses Cardiac Differentiation of Human Mesoderm. <i>Stem Cell Reports</i> , 2019, 13, 515-529.	4.8	27
11	Enhanced hemato-endothelial specification during human embryonic differentiation through developmental cooperation between <i>AF4-MLL</i> and <i>MLL-AF4</i> fusions. <i>Haematologica</i> , 2019, 104, 1189-1201.	3.5	15
12	A single-cell molecular map of mouse gastrulation and early organogenesis. <i>Nature</i> , 2019, 566, 490-495.	27.8	658
13	Defining murine organogenesis at single-cell resolution reveals a role for the leukotriene pathway in regulating blood progenitor formation. <i>Nature Cell Biology</i> , 2018, 20, 127-134.	10.3	112
14	Single Cell RNA-Seq Characterises Pre-Leukemic Transformation Driven By CEBPA N321D in the Hoxb8-FL Cell Line. <i>Blood</i> , 2018, 132, 3887-3887.	1.4	0
15	Myeloid progenitor cluster formation drives emergency and leukaemic myelopoiesis. <i>Nature</i> , 2017, 544, 53-58.	27.8	155
16	Assessing the reliability of spike-in normalization for analyses of single-cell RNA sequencing data. <i>Genome Research</i> , 2017, 27, 1795-1806.	5.5	70
17	Single-cell RNA-sequencing reveals a distinct population of proglucagon-expressing cells specific to the mouse upper small intestine. <i>Molecular Metabolism</i> , 2017, 6, 1296-1303.	6.5	68
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

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19	Genome-scale definition of the transcriptional programme associated with compromised PU.1 activity in acute myeloid leukaemia. <i>Leukemia</i> , 2016, 30, 14-23.	7.2	18
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	The LMO2 -25 Region Harbours GATA2-Dependent Myeloid Enhancer and RUNX-Dependent T-Lymphoid Repressor Activity. <i>PLoS ONE</i> , 2015, 10, e0131577.	2.5	1
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	Functionally Distinct Subsets of Lineage-Biased Multipotent Progenitors Control Blood Production in Normal and Regenerative Conditions. <i>Cell Stem Cell</i> , 2015, 17, 35-46.	11.1	494
24	Shared transcription factors contribute to distinct cell fates. <i>Transcription</i> , 2014, 5, e978173.	3.1	1
25	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. <i>EMBO Journal</i> , 2014, 33, 1212-26.	7.8	61
26	BET protein inhibition shows efficacy against JAK2V617F-driven neoplasms. <i>Leukemia</i> , 2014, 28, 88-97.	7.2	70
27	Characterization of transcriptional networks in blood stem and progenitor cells using high-throughput single-cell gene expression analysis. <i>Nature Cell Biology</i> , 2013, 15, 363-372.	10.3	257
28	HOX-mediated LMO2 expression in embryonic mesoderm is recapitulated in acute leukaemias. <i>Oncogene</i> , 2013, 32, 5471-5480.	5.9	13
29	Bivalent promoter marks and a latent enhancer may prime the leukaemia oncogene LMO1 for ectopic expression in T-cell leukaemia. <i>Leukemia</i> , 2013, 27, 1348-1357.	7.2	11
30	Integration of Elf-4 into Stem/Progenitor and Erythroid Regulatory Networks through Locus-Wide Chromatin Studies Coupled with <i>In Vivo</i> Functional Validation. <i>Molecular and Cellular Biology</i> , 2012, 32, 763-773.	2.3	5
31	The human GFI136N variant induces epigenetic changes at the Hoxa9 locus and accelerates K-RAS driven myeloproliferative disorder in mice. <i>Blood</i> , 2012, 120, 4006-4017.	1.4	40
32	Transcriptional regulation of haematopoietic transcription factors. <i>Stem Cell Research and Therapy</i> , 2011, 2, 6.	5.5	36
33	Transcription-dependent silencing of inducible convergent transgenes in transgenic mice. <i>Epigenetics and Chromatin</i> , 2010, 3, 3.	3.9	27
34	Runx1 binds as a dimeric complex to overlapping Runx1 sites within a palindromic element in the human GM-CSF enhancer. <i>Nucleic Acids Research</i> , 2010, 38, 6124-6134.	14.5	35
35	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. <i>Nucleic Acids Research</i> , 2010, 38, 6363-6374.	14.5	15
36	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. <i>Molecular and Cellular Biology</i> , 2009, 29, 1682-1693.	2.3	28

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37	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
38	Regulatory elements mediating expression of xylanase genes in <i>Fusarium oxysporum</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 28-34.	2.1	8
39	Role of the Transcriptional Activator XlnR of <i>Fusarium oxysporum</i> in Regulation of Xylanase Genes and Virulence. <i>Molecular Plant-Microbe Interactions</i> , 2007, 20, 977-985.	2.6	73