

Rebecca Hannah

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

1,859
citations

567281

15
h-index

888059

17
g-index

19
all docs

19
docs citations

19
times ranked

4514
citing authors

#	ARTICLE	IF	CITATIONS
1	Interactions between lineage-associated transcription factors govern haematopoietic progenitor states. <i>EMBO Journal</i> , 2020, 39, e104983.	7.8	20
2	Lysine acetyltransferase Tip60 is required for hematopoietic stem cell maintenance. <i>Blood</i> , 2020, 136, 1735-1747.	1.4	33
3	Identification of gene specific cis-regulatory elements during differentiation of mouse embryonic stem cells: An integrative approach using high-throughput datasets. <i>PLoS Computational Biology</i> , 2019, 15, e1007337.	3.2	18
4	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
5	The Lysine Acetyltransferase Tip60 Is Required for Hematopoietic Stem Cell Maintenance. <i>Blood</i> , 2018, 132, 2554-2554.	1.4	0
6	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
7	Critical Modulation of Hematopoietic Lineage Fate by Hepatic Leukemia Factor. <i>Cell Reports</i> , 2017, 21, 2251-2263.	6.4	46
8	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
9	Cytokine-induced megakaryocytic differentiation is regulated by genome-wide loss of a <i>STAT</i> transcriptional program. <i>EMBO Journal</i> , 2016, 35, 580-594.	7.8	66
10	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 572-587.	7.0	213
11	The JAK-STAT signaling pathway is differentially activated in CALR-positive compared with JAK2V617F-positive ET patients. <i>Blood</i> , 2015, 125, 1679-1681.	1.4	35
12	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
13	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. <i>EMBO Journal</i> , 2014, 33, 1212-26.	7.8	61
14	Constrained transcription factor spacing is prevalent and important for transcriptional control of mouse blood cells. <i>Nucleic Acids Research</i> , 2014, 42, 13513-13524.	14.5	21
15	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for <i>PU.1</i> during haematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 4018-4030.	2.5	26
16	Large conserved domains of low DNA methylation maintained by Dnmt3a. <i>Nature Genetics</i> , 2014, 46, 17-23.	21.4	276
17	Epigenomic Profiling of Young and Aged HSCs Reveals Concerted Changes during Aging that Reinforce Self-Renewal. <i>Cell Stem Cell</i> , 2014, 14, 673-688.	11.1	524
18	RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis. <i>EMBO Journal</i> , 2012, 31, 4318-4333.	7.8	158

#	ARTICLE	IF	CITATIONS
19	A compendium of genome-wide hematopoietic transcription factor maps supports the identification of gene regulatory control mechanisms. <i>Experimental Hematology</i> , 2011, 39, 531-541.	0.4	43