

Victoria Moignard

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

1,746
citations

516710

16
h-index

888059

17
g-index

17
all docs

17
docs citations

17
times ranked

3385
citing authors

#	ARTICLE	IF	CITATIONS
1	Decoding the regulatory network of early blood development from single-cell gene expression measurements. <i>Nature Biotechnology</i> , 2015, 33, 269-276.	17.5	352
2	Resolving early mesoderm diversification through single-cell expression profiling. <i>Nature</i> , 2016, 535, 289-293.	27.8	261
3	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
4	Defining the earliest step of cardiovascular lineage segregation by single-cell RNA-seq. <i>Science</i> , 2018, 359, 1177-1181.	12.6	230
5	GFI1 proteins orchestrate the emergence of haematopoietic stem cells through recruitment of LSD1. <i>Nature Cell Biology</i> , 2016, 18, 21-32.	10.3	172
6	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. <i>Nature Communications</i> , 2013, 4, 2924.	12.8	158
7	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. <i>EMBO Journal</i> , 2014, 33, 1212-26.	7.8	61
8	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. <i>ELife</i> , 2016, 5, e11469.	6.0	61
9	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
10	Determining Physical Mechanisms of Gene Expression Regulation from Single Cell Gene Expression Data. <i>PLoS Computational Biology</i> , 2016, 12, e1005072.	3.2	25
11	Transcriptional mechanisms of cell fate decisions revealed by single cell expression profiling. <i>BioEssays</i> , 2014, 36, 419-426.	2.5	24
12	BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	24
13	Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. <i>Bioinformatics</i> , 2014, 30, 1867-1875.	4.1	21
14	Dissecting stem cell differentiation using single cell expression profiling. <i>Current Opinion in Cell Biology</i> , 2016, 43, 78-86.	5.4	20
15	Transcriptional hierarchies regulating early blood cell development. <i>Blood Cells, Molecules, and Diseases</i> , 2013, 51, 239-247.	1.4	18
16	Processing, visualising and reconstructing network models from single-cell data. <i>Immunology and Cell Biology</i> , 2016, 94, 256-265.	2.3	18
17	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