

# Victoria Moignard

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/42874/publications.pdf>

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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	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
2	BNC1 regulates cell heterogeneity in human pluripotent stem cell derived-epicardium. Development (Cambridge), 2019, 146, .	2.5	24
3	Defining the earliest step of cardiovascular lineage segregation by single-cell RNA-seq. Science, 2018, 359, 1177-1181.	12.6	230
4	Determining Physical Mechanisms of Gene Expression Regulation from Single Cell Gene Expression Data. PLoS Computational Biology, 2016, 12, e1005072.	3.2	25
5	Resolving early mesoderm diversification through single-cell expression profiling. Nature, 2016, 535, 289-293.	27.8	261
6	Dissecting stem cell differentiation using single cell expression profiling. Current Opinion in Cell Biology, 2016, 43, 78-86.	5.4	20
7	Processing, visualising and reconstructing network models from single-cell data. Immunology and Cell Biology, 2016, 94, 256-265.	2.3	18
8	GFI1 proteins orchestrate the emergence of haematopoietic stem cells through recruitment of LSD1. Nature Cell Biology, 2016, 18, 21-32.	10.3	172
9	An experimentally validated network of nine haematopoietic transcription factors reveals mechanisms of cell state stability. ELife, 2016, 5, e11469.	6.0	61
10	Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nature Biotechnology, 2015, 33, 269-276.	17.5	352
11	Key regulators control distinct transcriptional programmes in blood progenitor and mast cells. EMBO Journal, 2014, 33, 1212-26.	7.8	61
12	Single-cell analyses of regulatory network perturbations using enhancer-targeting TALEs suggest novel roles for PU.1 during haematopoietic specification. Development (Cambridge), 2014, 141, 4018-4030.	2.5	26
13	Transcriptional mechanisms of cell fate decisions revealed by single cell expression profiling. BioEssays, 2014, 36, 419-426.	2.5	24
14	Probabilistic PCA of censored data: accounting for uncertainties in the visualization of high-throughput single-cell qPCR data. Bioinformatics, 2014, 30, 1867-1875.	4.1	21
15	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
16	Early dynamic fate changes in haemogenic endothelium characterized at the single-cell level. Nature Communications, 2013, 4, 2924.	12.8	158
17	Transcriptional hierarchies regulating early blood cell development. Blood Cells, Molecules, and Diseases, 2013, 51, 239-247.	1.4	18