Ana Cvejic

List of Publications by Year in descending order

34 papers	4,116 citations	279798 23 h-index	395702 33 g-index
42 all docs	42 docs citations	42 times ranked	9905 citing authors

#	Article	IF	Citations
1	Integrative Single-Cell RNA-Seq and ATAC-Seq Analysis of Human Developmental Hematopoiesis. Cell Stem Cell, 2021, 28, 472-487.e7.	11.1	184
2	Lineage tracing of human development through somatic mutations. Nature, 2021, 595, 85-90.	27.8	79
3	Analysis of single-cell RNA sequencing data based on autoencoders. BMC Bioinformatics, 2021, 22, 309.	2.6	15
4	Single-Cell Transcriptomic Analysis of Hematopoietic Cells. Methods in Molecular Biology, 2021, 2185, 135-158.	0.9	1
5	Unsupervised generative and graph representation learning for modelling cell differentiation. Scientific Reports, 2020, 10, 9790.	3.3	11
6	Analysis of endothelial-to-haematopoietic transition at the single cell level identifies cell cycle regulation as a driver of differentiation. Genome Biology, 2020, 21, 157.	8.8	35
7	A cellular census of human lungs identifies novel cell states in health and in asthma. Nature Medicine, 2019, 25, 1153-1163.	30.7	631
8	Application of single-cell RNA sequencing methodologies in understanding haematopoiesis and immunology. Essays in Biochemistry, 2019, 63, 217-225.	4.7	16
9	Dissecting human disease with single-cell omics: application in model systems and in the clinic. DMM Disease Models and Mechanisms, 2018, 11, .	2.4	39
10	Single-cell transcriptional analysis reveals ILC-like cells in zebrafish. Science Immunology, 2018, 3, .	11.9	103
11	Single-cell biology: resolving biological complexity, one cell at a time. Development (Cambridge), 2018, 145, .	2.5	7
12	Single-cell transcriptome analysis of fish immune cells provides insight into the evolution of vertebrate immune cell types. Genome Research, 2017, 27, 451-461.	5.5	126
13	Power analysis of single-cell RNA-sequencing experiments. Nature Methods, 2017, 14, 381-387.	19.0	496
14	Loss of the homologous recombination gene rad51 leads to Fanconi anemia-like symptoms in zebrafish. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E4452-E4461.	7.1	30
15	Single-cell RNA-sequencing uncovers transcriptional states and fate decisions in haematopoiesis. Nature Communications, 2017, 8, 2045.	12.8	147
16	CD4-Transgenic Zebrafish Reveal Tissue-Resident Th2- and Regulatory T Cellâ€“like Populations and Diverse Mononuclear Phagocytes. Journal of Immunology, 2016, 197, 3520-3530.	0.8	113
17	Single-Cell RNA-Sequencing Reveals a Continuous Spectrum of Differentiation in Hematopoietic Cells. Cell Reports, 2016, 14, 966-977.	6.4	164
18	Mechanisms of fate decision and lineage commitment during haematopoiesis. Immunology and Cell Biology, 2016, 94, 230-235.	2.3	18

#	Article	IF	Citations
19	The Ribosome Biogenesis Protein Nol9 Is Essential for Definitive Hematopoiesis and Pancreas Morphogenesis in Zebrafish. PLoS Genetics, 2015, 11, e1005677.	3.5	23
20	A Loss of Function Screen of Identified Genome-Wide Association Study Loci Reveals New Genes Controlling Hematopoiesis. PLoS Genetics, 2014, 10, e1004450.	3.5	39
21	From genome-wide association study hits to new insights into experimental hematology. Experimental Hematology, 2014, 42, 630-636.	0.4	1
22	Transcriptional diversity during lineage commitment of human blood progenitors. Science, 2014, 345, 1251033.	12.6	253
23	SMIM1 underlies the Vel blood group and influences red blood cell traits. Nature Genetics, 2013, 45, 542-545.	21.4	96
24	Compound inheritance of a low-frequency regulatory SNP and a rare null mutation in exon-junction complex subunit RBM8A causes TAR syndrome. Nature Genetics, 2012, 44, 435-439.	21.4	355
25	Image-based characterization of thrombus formation in time-lapse DIC microscopy. Medical Image Analysis, 2012, 16, 915-931.	11.6	6
26	The role of meis1 in primitive and definitive hematopoiesis during zebrafish development. Haematologica, 2011, 96, 190-198.	3.5	33
27	Exome sequencing identifies NBEAL2 as the causative gene for gray platelet syndrome. Nature Genetics, 2011, 43, 735-737.	21.4	245
28	New gene functions in megakaryopoiesis and platelet formation. Nature, 2011, 480, 201-208.	27.8	401
29	Genome-wide Analysis of Simultaneous GATA1/2, RUNX1, FLI1, and SCL Binding in Megakaryocytes Identifies Hematopoietic Regulators. Developmental Cell, 2011, 20, 597-609.	7.0	255
30	Silencing of RhoA nucleotide exchange factor, ARHGEF3, reveals its unexpected role in iron uptake. Blood, 2011, 118, 4967-4976.	1.4	34
31	Joint Thrombus and Vessel Segmentation Using Dynamic Texture Likelihoods and Shape Prior. Lecture Notes in Computer Science, 2011, 14, 579-586.	1.3	2
32	Thrombus segmentation by texture dynamics from microscopic image sequences. , 2010, , .		3
33	Functional genomics in zebrafish permits rapid characterization of novel platelet membrane proteins. Blood, 2009, 113, 4754-4762.	1.4	69
34	Analysis of WASp function during the wound inflammatory response â€“ live-imaging studies in zebrafish larvae. Journal of Cell Science, 2008, 121, 3196-3206.	2.0	73