Michael J T Stubbington

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/442369/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	The Human Cell Atlas. ELife, 2017, 6, .	6.0	1,547
2	Single-cell reconstruction of the early maternal–fetal interface in humans. Nature, 2018, 563, 347-353.	27.8	1,547
3	The Human Cell Atlas: from vision to reality. Nature, 2017, 550, 451-453.	27.8	511
4	Single-cell transcriptomics to explore the immune system in health and disease. Science, 2017, 358, 58-63.	12.6	440
5	T cell fate and clonality inference from single-cell transcriptomes. Nature Methods, 2016, 13, 329-332.	19.0	411
6	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	27.8	392
7	Aging increases cell-to-cell transcriptional variability upon immune stimulation. Science, 2017, 355, 1433-1436.	12.6	265
8	Single-cell RNA-seq and computational analysis using temporal mixture modeling resolves T _H 1/T _{FH} fate bifurcation in malaria. Science Immunology, 2017, 2, .	11.9	258
9	Circulating and Tissue-Resident CD4+ T Cells With Reactivity to Intestinal Microbiota Are Abundant in Healthy Individuals and Function Is Altered During Inflammation. Gastroenterology, 2017, 153, 1320-1337.e16.	1.3	246
10	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
11	BraCeR: B-cell-receptor reconstruction and clonality inference from single-cell RNA-seq. Nature Methods, 2018, 15, 563-565.	19.0	84
12	An atlas of mouse CD4+ T cell transcriptomes. Biology Direct, 2015, 10, 14.	4.6	82
13	Two Mutually Exclusive Local Chromatin States Drive Efficient V(D)J Recombination. Cell Reports, 2016, 15, 2475-2487.	6.4	78
14	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	17.5	64
15	Intrinsic transcriptional heterogeneity in B cells controls early class switching to IgE. Journal of Experimental Medicine, 2017, 214, 183-196.	8.5	49
16	The Regulatory T Cell Lineage Factor Foxp3 Regulates Gene Expression through Several Distinct Mechanisms Mostly Independent of Direct DNA Binding. PLoS Genetics, 2015, 11, e1005251.	3.5	35
17	The Human Cell Atlas: Technical approaches and challenges. Briefings in Functional Genomics, 2018, 17, 283-294.	2.7	34
18	Non-coding transcription and large-scale nuclear organisation of immunoglobulin recombination. Current Opinion in Genetics and Development, 2013, 23, 81-88.	3.3	25

#	Article	IF	CITATIONS
19	scHLAcount: allele-specific HLA expression from single-cell gene expression data. Bioinformatics, 2020, 36, 3905-3906.	4.1	18
20	Antigen Receptor Sequence Reconstruction and Clonality Inference from scRNA-Seq Data. Methods in Molecular Biology, 2019, 1935, 223-249.	0.9	8
21	IL-7R signaling activates widespread VH and DH gene usage to drive antibody diversity in bone marrow B cells. Cell Reports, 2021, 36, 109349.	6.4	6
22	Are cells from a snowman realistic? Cryopreserved tissues as a source for single-cell RNA-sequencing experiments. Genome Biology, 2017, 18, 54.	8.8	2