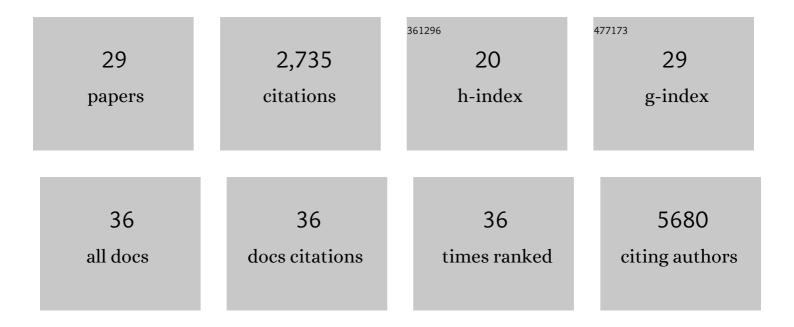


List of Publications by Year in descending order

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Version: 2024-02-01



#	Article	IF	CITATIONS
1	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. Immunity, 2019, 50, 493-504.e7.	6.6	352
2	Establishment of porcine and human expanded potential stem cells. Nature Cell Biology, 2019, 21, 687-699.	4.6	261
3	Single-cell RNA-seq identifies a PD-1hi ILC progenitor and defines its development pathway. Nature, 2016, 539, 102-106.	13.7	257
4	Establishment of mouse expanded potential stem cells. Nature, 2017, 550, 393-397.	13.7	223
5	A rapid and robust method for single cell chromatin accessibility profiling. Nature Communications, 2018, 9, 5345.	5.8	188
6	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. Cell Reports, 2020, 31, 107628.	2.9	186
7	The Forkhead Transcription Factor FOXM1 Controls Cell Cycle-Dependent Gene Expression through an Atypical Chromatin Binding Mechanism. Molecular and Cellular Biology, 2013, 33, 227-236.	1.1	185
8	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. Nature Communications, 2018, 9, 4877.	5.8	174
9	Gene expression variability across cells and species shapes innate immunity. Nature, 2018, 563, 197-202.	13.7	165
10	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. Cell, 2019, 176, 882-896.e18.	13.5	135
11	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. Annual Review of Biomedical Data Science, 2018, 1, 29-51.	2.8	91
12	Genome-wide analyses reveal the IRE1a-XBP1 pathway promotes T helper cell differentiation by resolving secretory stress and accelerating proliferation. Genome Medicine, 2018, 10, 76.	3.6	67
13	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	9.4	64
14	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. Nature Communications, 2020, 11, 3588.	5.8	54
15	Screen for multi-SUMO–binding proteins reveals a multi-SIM–binding mechanism for recruitment of the transcriptional regulator ZMYM2 to chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4854-63.	3.3	46
16	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. Nature Immunology, 2020, 21, 1597-1610.	7.0	43
17	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. Nature Protocols, 2021, 16, 4084-4107.	5.5	40
18	Genome-wide binding studies reveal DNA binding specificity mechanisms and functional interplay amongst Forkhead transcription factors. Nucleic Acids Research, 2016, 44, 1566-1578.	6.5	35

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#	Article	IF	CITATIONS
19	Reinvestigation of Classic T Cell Subsets and Identification of Novel Cell Subpopulations by Single-Cell RNA Sequencing. Journal of Immunology, 2022, 208, 396-406.	0.4	34
20	Deregulation of the FOXM1 target gene network and its coregulatory partners in oesophageal adenocarcinoma. Molecular Cancer, 2015, 14, 69.	7.9	30
21	The BAF and PRC2 Complex Subunits Dpf2 and Eed Antagonistically Converge on Tbx3 to Control ESC Differentiation. Cell Stem Cell, 2019, 24, 138-152.e8.	5.2	30
22	Genetics and immunity in the era of single-cell genomics. Human Molecular Genetics, 2016, 25, R141-R148.	1.4	19
23	Progressive chromatin silencing of ABA biosynthesis genes permits seed germination in Arabidopsis. Plant Cell, 2022, 34, 2871-2891.	3.1	14
24	Mammalian SWI/SNF Chromatin Remodeling Complexes in Embryonic Stem Cells: Regulating the Balance Between Pluripotency and Differentiation. Frontiers in Cell and Developmental Biology, 2020, 8, 626383.	1.8	13
25	Transporting ESCs in FBS at ambient temperature. Stem Cell Research, 2020, 49, 102009.	0.3	4
26	dbInDel: a database of enhancer-associated insertion and deletion variants by analysis of H3K27ac ChIP-Seq. Bioinformatics, 2020, 36, 1649-1651.	1.8	3
27	Quantitative control of noise in mammalian gene expression by dynamic histone regulation. ELife, 2021, 10, .	2.8	3
28	Genome-wide Interrogation of Protein-DNA Interactions in Mammalian Cells Using ChIPmentation. STAR Protocols, 2020, 1, 100187.	0.5	3
29	A Modified SMART-Seq Method for Single-Cell Transcriptomic Analysis of Embryoid Body Differentiation. Methods in Molecular Biology, 2021, , 233-259.	0.4	2