

Xi Chen

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

2,735
citations

361296

20
h-index

477173

29
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all docs

36
docs citations

36
times ranked

5680
citing authors

#	ARTICLE	IF	CITATIONS
1	Reinvestigation of Classic T Cell Subsets and Identification of Novel Cell Subpopulations by Single-Cell RNA Sequencing. <i>Journal of Immunology</i> , 2022, 208, 396-406.	0.4	34
2	Progressive chromatin silencing of ABA biosynthesis genes permits seed germination in Arabidopsis. <i>Plant Cell</i> , 2022, 34, 2871-2891.	3.1	14
3	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. <i>Nature Protocols</i> , 2021, 16, 4084-4107.	5.5	40
4	Quantitative control of noise in mammalian gene expression by dynamic histone regulation. <i>ELife</i> , 2021, 10, .	2.8	3
5	A Modified SMART-Seq Method for Single-Cell Transcriptomic Analysis of Embryoid Body Differentiation. <i>Methods in Molecular Biology</i> , 2021, , 233-259.	0.4	2
6	dbInDel: a database of enhancer-associated insertion and deletion variants by analysis of H3K27ac CHIP-Seq. <i>Bioinformatics</i> , 2020, 36, 1649-1651.	1.8	3
7	Transporting ESCs in FBS at ambient temperature. <i>Stem Cell Research</i> , 2020, 49, 102009.	0.3	4
8	Transcriptome dynamics of CD4+ T cells during malaria maps gradual transit from effector to memory. <i>Nature Immunology</i> , 2020, 21, 1597-1610.	7.0	43
9	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 2020, 11, 3588.	5.8	54
10	Mammalian SWI/SNF Chromatin Remodeling Complexes in Embryonic Stem Cells: Regulating the Balance Between Pluripotency and Differentiation. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 626383.	1.8	13
11	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	2.9	186
12	Genome-wide Interrogation of Protein-DNA Interactions in Mammalian Cells Using ChIPmentation. <i>STAR Protocols</i> , 2020, 1, 100187.	0.5	3
13	Genome-wide CRISPR Screens in T Helper Cells Reveal Pervasive Crosstalk between Activation and Differentiation. <i>Cell</i> , 2019, 176, 882-896.e18.	13.5	135
14	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019, 50, 493-504.e7.	6.6	352
15	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019, 21, 687-699.	4.6	261
16	The BAF and PRC2 Complex Subunits Dpf2 and Eed Antagonistically Converge on Tbx3 to Control ESC Differentiation. <i>Cell Stem Cell</i> , 2019, 24, 138-152.e8.	5.2	30
17	Single cell RNA-seq and ATAC-seq analysis of cardiac progenitor cell transition states and lineage settlement. <i>Nature Communications</i> , 2018, 9, 4877.	5.8	174
18	Genome-wide analyses reveal the IRE1a-XBP1 pathway promotes T helper cell differentiation by resolving secretory stress and accelerating proliferation. <i>Genome Medicine</i> , 2018, 10, 76.	3.6	67

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19	A rapid and robust method for single cell chromatin accessibility profiling. Nature Communications, 2018, 9, 5345.	5.8	188
20	Gene expression variability across cells and species shapes innate immunity. Nature, 2018, 563, 197-202.	13.7	165
21	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
22	Establishment of mouse expanded potential stem cells. Nature, 2017, 550, 393-397.	13.7	223
23	Single-cell RNA-seq identifies a PD-1hi ILC progenitor and defines its development pathway. Nature, 2016, 539, 102-106.	13.7	257
24	Genetics and immunity in the era of single-cell genomics. Human Molecular Genetics, 2016, 25, R141-R148.	1.4	19
25	Single-cell analysis at the threshold. Nature Biotechnology, 2016, 34, 1111-1118.	9.4	64
26	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
27	Deregulation of the FOXM1 target gene network and its coregulatory partners in oesophageal adenocarcinoma. Molecular Cancer, 2015, 14, 69.	7.9	30
28	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
29	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