

# Xi Chen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8448941/publications.pdf>

Version: 2024-02-01

29  
papers

2,735  
citations

361296

20  
h-index

477173

29  
g-index

36  
all docs

36  
docs citations

36  
times ranked

5680  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cell Transcriptomics of Regulatory T Cells Reveals Trajectories of Tissue Adaptation. <i>Immunity</i> , 2019, 50, 493-504.e7.	6.6	352
2	Establishment of porcine and human expanded potential stem cells. <i>Nature Cell Biology</i> , 2019, 21, 687-699.	4.6	261
3	Single-cell RNA-seq identifies a PD-1hi ILC progenitor and defines its development pathway. <i>Nature</i> , 2016, 539, 102-106.	13.7	257
4	Establishment of mouse expanded potential stem cells. <i>Nature</i> , 2017, 550, 393-397.	13.7	223
5	A rapid and robust method for single cell chromatin accessibility profiling. <i>Nature Communications</i> , 2018, 9, 5345.	5.8	188
6	Single-Cell RNA Sequencing Reveals a Dynamic Stromal Niche That Supports Tumor Growth. <i>Cell Reports</i> , 2020, 31, 107628.	2.9	186
7	The Forkhead Transcription Factor FOXM1 Controls Cell Cycle-Dependent Gene Expression through an Atypical Chromatin Binding Mechanism. <i>Molecular and Cellular Biology</i> , 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. <i>Nature Communications</i> , 2018, 9, 4877.	5.8	174
9	Gene expression variability across cells and species shapes innate immunity. <i>Nature</i> , 2018, 563, 197-202.	13.7	165
10	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
11	From Tissues to Cell Types and Back: Single-Cell Gene Expression Analysis of Tissue Architecture. <i>Annual Review of Biomedical Data Science</i> , 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. <i>Genome Medicine</i> , 2018, 10, 76.	3.6	67
13	Single-cell analysis at the threshold. <i>Nature Biotechnology</i> , 2016, 34, 1111-1118.	9.4	64
14	Tumors induce de novo steroid biosynthesis in T cells to evade immunity. <i>Nature Communications</i> , 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. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4854-63.	3.3	46
16	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
17	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
18	Genome-wide binding studies reveal DNA binding specificity mechanisms and functional interplay amongst Forkhead transcription factors. <i>Nucleic Acids Research</i> , 2016, 44, 1566-1578.	6.5	35

#	ARTICLE	IF	CITATIONS
19	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
20	Deregulation of the FOXM1 target gene network and its coregulatory partners in oesophageal adenocarcinoma. <i>Molecular Cancer</i> , 2015, 14, 69.	7.9	30
21	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
22	Genetics and immunity in the era of single-cell genomics. <i>Human Molecular Genetics</i> , 2016, 25, R141-R148.	1.4	19
23	Progressive chromatin silencing of ABA biosynthesis genes permits seed germination in Arabidopsis. <i>Plant Cell</i> , 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. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 626383.	1.8	13
25	Transporting ESCs in FBS at ambient temperature. <i>Stem Cell Research</i> , 2020, 49, 102009.	0.3	4
26	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
27	Quantitative control of noise in mammalian gene expression by dynamic histone regulation. <i>ELife</i> , 2021, 10, .	2.8	3
28	Genome-wide Interrogation of Protein-DNA Interactions in Mammalian Cells Using CHIPmentation. <i>STAR Protocols</i> , 2020, 1, 100187.	0.5	3
29	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