

# Wenfei Jin

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

2,535  
citations

361413  
20  
h-index

276875  
41  
g-index

63  
all docs

63  
docs citations

63  
times ranked

4229  
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.	0.8	34
2	Integrated decoding hematopoiesis and leukemogenesis using single-cell sequencing and its medical implication. <i>Cell Discovery</i> , 2021, 7, 2.	6.7	30
3	Kssd: sequence dimensionality reduction by k-mer substring space sampling enables real-time large-scale datasets analysis. <i>Genome Biology</i> , 2021, 22, 84.	8.8	4
4	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. <i>Nature Protocols</i> , 2021, 16, 4084-4107.	12.0	40
5	The Tyrosine Kinase-Driven Networks of Novel Long Non-coding RNAs and Their Molecular Targets in Myeloproliferative Neoplasms. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 643043.	3.7	3
6	A topology-preserving dimensionality reduction method for single-cell RNA-seq data using graph autoencoder. <i>Scientific Reports</i> , 2021, 11, 20028.	3.3	21
7	A Comprehensive Characterization of Monoallelic Expression During Hematopoiesis and Leukemogenesis via Single-Cell RNA-Sequencing. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 702897.	3.7	5
8	Cross-Tissue Characterization of Heterogeneities of Mesenchymal Stem Cells and Their Differentiation Potentials. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 781021.	3.7	13
9	Diploid genome architecture revealed by multi-omic data of hybrid mice. <i>Genome Research</i> , 2020, 30, 1097-1106.	5.5	18
10	Single-Cell Transcriptome Analysis Reveals Six Subpopulations Reflecting Distinct Cellular Fates in Senescent Mouse Embryonic Fibroblasts. <i>Frontiers in Genetics</i> , 2020, 11, 867.	2.3	16
11	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. <i>Development (Cambridge)</i> , 2020, 147, .	2.5	11
12	Inhibition of Glycolysis in Pathogenic TH17 Cells through Targeting a miR-21â€Peli1â€c-Rel Pathway Prevents Autoimmunity. <i>Journal of Immunology</i> , 2020, 204, 3160-3170.	0.8	17
13	Visualization of Single Cell RNA-Seq Data Using t-SNE in R. <i>Methods in Molecular Biology</i> , 2020, 2117, 159-167.	0.9	46
14	Kindlin-2 regulates skeletal homeostasis by modulating PTH1R in mice. <i>Signal Transduction and Targeted Therapy</i> , 2020, 5, 297.	17.1	31
15	Focal adhesion protein Kindlin-2 regulates bone homeostasis in mice. <i>Bone Research</i> , 2020, 8, 2.	11.4	50
16	The MicroRNA <i>miR-22</i> Represses Th17 Cell Pathogenicity by Targeting PTEN-Regulated Pathways. <i>ImmunoHorizons</i> , 2020, 4, 308-318.	1.8	6
17	Exploring the changing landscape of cell-to-cell variation after CTCF knockdown via single cell RNA-seq. <i>BMC Genomics</i> , 2019, 20, 1015.	2.8	13
18	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. <i>Immunity</i> , 2018, 48, 227-242.e8.	14.3	188

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19	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. <i>Nature</i> , 2018, 562, 281-285.	27.8	135
20	Trac-looping measures genome structure and chromatin accessibility. <i>Nature Methods</i> , 2018, 15, 741-747.	19.0	74
21	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. <i>Molecular Cell</i> , 2017, 67, 1049-1058.e6.	9.7	219
22	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. <i>Cell Research</i> , 2017, 27, 1258-1274.	12.0	14
23	Evaluating information content of SNPs for sample-tagging in re-sequencing projects. <i>Scientific Reports</i> , 2015, 5, 10247.	3.3	21
24	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. <i>European Journal of Human Genetics</i> , 2015, 23, 536-542.	2.8	22
25	Complex Selective Forces Shaping the Genes Underlying Human Diseases. <i>Springer Theses</i> , 2015, , 73-92.	0.1	0
26	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. <i>Nature</i> , 2015, 528, 142-146.	27.8	303
27	Genome-Wide Search for Signatures of Natural Selection in African Americans. <i>Springer Theses</i> , 2015, , 53-71.	0.1	0
28	Distribution of Length of Ancestral Chromosomal Segments in Admixed Genomes. <i>Springer Theses</i> , 2015, , 23-33.	0.1	0
29	Exploring Population Admixture Dynamics via Distribution of LACS. <i>Springer Theses</i> , 2015, , 35-51.	0.1	0
30	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. <i>The HUGO Journal</i> , 2014, 8, 5.	4.1	14
31	Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. <i>European Journal of Human Genetics</i> , 2014, 22, 930-937.	2.8	30
32	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. <i>European Journal of Human Genetics</i> , 2014, 22, 248-253.	2.8	39
33	Y Chromosomes of 40% Chinese Descend from Three Neolithic Super-Grandfathers. <i>PLoS ONE</i> , 2014, 9, e105691.	2.5	82
34	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. <i>Genome Biology</i> , 2013, 14, R121.	9.6	123
35	Association of Two Variants in SMAD7 with the Risk of Congenital Heart Disease in the Han Chinese Population. <i>PLoS ONE</i> , 2013, 8, e72423.	2.5	4
36	Genome-wide detection of natural selection in African Americans pre- and post-admixture. <i>Genome Research</i> , 2012, 22, 519-527.	5.5	89

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37	A systematic characterization of genes underlying both complex and Mendelian diseases. <i>Human Molecular Genetics</i> , 2012, 21, 1611-1624.	2.9	35
38	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. <i>American Journal of Human Genetics</i> , 2012, 91, 849-862.	6.2	36
39	A Map of Copy Number Variations in Chinese Populations. <i>PLoS ONE</i> , 2011, 6, e27341.	2.5	44
40	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. <i>Molecular Biology and Evolution</i> , 2011, 28, 1003-1011.	8.9	311
41	Haplotype-Sharing Analysis Showing Uyghurs Are Unlikely Genetic Donors. <i>Molecular Biology and Evolution</i> , 2009, 26, 2197-2206.	8.9	34
42	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. <i>American Journal of Human Genetics</i> , 2009, 85, 762-774.	6.2	338
43	Three-Dimensional Chromatin Architecture Landscape of Aging and Alzheimer's Disease. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0