Wenfei Jin

List of Publications by Year
in descending order

43 papers	2,535 citations	361045 20 h-index	276539 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. Journal of Immunology, 2022, 208, 396-406.	0.4	34
2	Integrated decoding hematopoiesis and leukemogenesis using single-cell sequencing and its medical implication. Cell Discovery, 2021, 7, 2.	3.1	30
3	Kssd: sequence dimensionality reduction by k-mer substring space sampling enables real-time large-scale datasets analysis. Genome Biology, 2021, 22, 84.	3.8	4
4	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
5	The Tyrosine Kinase-Driven Networks of Novel Long Non-coding RNAs and Their Molecular Targets in Myeloproliferative Neoplasms. Frontiers in Cell and Developmental Biology, 2021, 9, 643043.	1.8	3
6	A topology-preserving dimensionality reduction method for single-cell RNA-seq data using graph autoencoder. Scientific Reports, 2021, 11, 20028.	1.6	21
7	A Comprehensive Characterization of Monoallelic Expression During Hematopoiesis and Leukemogenesis via Single-Cell RNA-Sequencing. Frontiers in Cell and Developmental Biology, 2021, 9, 702897.	1.8	5
8	Cross-Tissue Characterization of Heterogeneities of Mesenchymal Stem Cells and Their Differentiation Potentials. Frontiers in Cell and Developmental Biology, 2021, 9, 781021.	1.8	13
9	Diploid genome architecture revealed by multi-omic data of hybrid mice. Genome Research, 2020, 30, 1097-1106.	2.4	18
10	Single-Cell Transcriptome Analysis Reveals Six Subpopulations Reflecting Distinct Cellular Fates in Senescent Mouse Embryonic Fibroblasts. Frontiers in Genetics, 2020, 11, 867.	1.1	16
11	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. Development (Cambridge), 2020, 147, .	1.2	11
12	Inhibition of Glycolysis in Pathogenic TH17 Cells through Targeting a miR-21–Peli1–c-Rel Pathway Prevents Autoimmunity. Journal of Immunology, 2020, 204, 3160-3170.	0.4	17
13	Visualization of Single Cell RNA-Seq Data Using t-SNE in R. Methods in Molecular Biology, 2020, 2117, 159-167.	0.4	46
14	Kindlin-2 regulates skeletal homeostasis by modulating PTH1R in mice. Signal Transduction and Targeted Therapy, 2020, 5, 297.	7.1	31
15	Focal adhesion protein Kindlin-2 regulates bone homeostasis in mice. Bone Research, 2020, 8, 2.	5.4	50
16	The MicroRNA <i>miR-22</i> Represses Th17 Cell Pathogenicity by Targeting PTEN-Regulated Pathways. ImmunoHorizons, 2020, 4, 308-318.	0.8	6
17	Exploring the changing landscape of cell-to-cell variation after CTCF knockdown via single cell RNA-seq. BMC Genomics, 2019, 20, 1015.	1.2	13
18	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. Immunity, 2018, 48, 227-242.e8.	6.6	188

#	ARTICLE	IF	CITATIONS
19	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. Nature, 2018, 562, 281-285.	13.7	135
20	Trac-looping measures genome structure and chromatin accessibility. Nature Methods, 2018, 15, 741-747.	9.0	74
21	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. Molecular Cell, 2017, 67, 1049-1058.e6.	4.5	219
22	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. Cell Research, 2017, 27, 1258-1274.	5.7	14
23	Evaluating information content of SNPs for sample-tagging in re-sequencing projects. Scientific Reports, 2015, 5, 10247.	1.6	21
24	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. European Journal of Human Genetics, 2015, 23, 536-542.	1.4	22
25	Complex Selective Forces Shaping the Genes Underlying Human Diseases. Springer Theses, 2015, , 73-92.	0.0	0
26	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. Nature, 2015, 528, 142-146.	13.7	303
27	Genome-Wide Search for Signatures of Natural Selection in African Americans. Springer Theses, 2015, , 53-71.	0.0	0
28	Distribution of Length of Ancestral Chromosomal Segments in Admixed Genomes. Springer Theses, 2015, , 23-33.	0.0	0
29	Exploring Population Admixture Dynamics via Distribution of LACS. Springer Theses, 2015, , 35-51.	0.0	0
30	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. The HUGO Journal, 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. European Journal of Human Genetics, 2014, 22, 930-937.	1.4	30
32	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. European Journal of Human Genetics, 2014, 22, 248-253.	1.4	39
33	Y Chromosomes of 40% Chinese Descend from Three Neolithic Super-Grandfathers. PLoS ONE, 2014, 9, e105691.	1.1	82
34	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. Genome Biology, 2013, 14, R121.	13.9	123
35	Association of Two Variants in SMAD7 with the Risk of Congenital Heart Disease in the Han Chinese Population. PLoS ONE, 2013, 8, e72423.	1.1	4
36	Genome-wide detection of natural selection in African Americans pre- and post-admixture. Genome Research, 2012, 22, 519-527.	2.4	89

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37	A systematic characterization of genes underlying both complex and Mendelian diseases. Human Molecular Genetics, 2012, 21, 1611-1624.	1.4	35
38	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. American Journal of Human Genetics, 2012, 91, 849-862.	2.6	36
39	A Map of Copy Number Variations in Chinese Populations. PLoS ONE, 2011, 6, e27341.	1.1	44
40	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. Molecular Biology and Evolution, 2011, 28, 1003-1011.	3.5	311
41	Haplotype-Sharing Analysis Showing Uyghurs Are Unlikely Genetic Donors. Molecular Biology and Evolution, 2009, 26, 2197-2206.	3.5	34
42	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. American Journal of Human Genetics, 2009, 85, 762-774.	2.6	338
43	Three-Dimensional Chromatin Architecture Landscape of Aging and Alzheimer's Disease. SSRN Electronic Journal, 0, , .	0.4	0