Wenfei Jin

List of Publications by Year
in descending order

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	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. American Journal of Human Genetics, 2009, 85, 762-774.	6.2	338
2	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. Molecular Biology and Evolution, 2011, 28, 1003-1011.	8.9	311
3	Genome-wide detection of DNase I hypersensitive sites in single cells and FFPE tissue samples. Nature, 2015, 528, 142-146.	27.8	303
4	CTCF-Mediated Enhancer-Promoter Interaction Is a Critical Regulator of Cell-to-Cell Variation of Gene Expression. Molecular Cell, 2017, 67, 1049-1058.e6.	9.7	219
5	Transformation of Accessible Chromatin and 3D Nucleome Underlies Lineage Commitment of Early T Cells. Immunity, 2018, 48, 227-242.e8.	14.3	188
6	Principles of nucleosome organization revealed by single-cell micrococcal nuclease sequencing. Nature, 2018, 562, 281-285.	27.8	135
7	Genome-wide incorporation dynamics reveal distinct categories of turnover for the histone variant H3.3. Genome Biology, 2013, 14, R121.	9.6	123
8	Genome-wide detection of natural selection in African Americans pre- and post-admixture. Genome Research, 2012, 22, 519-527.	5.5	89
9	Y Chromosomes of 40% Chinese Descend from Three Neolithic Super-Grandfathers. PLoS ONE, 2014, 9, e105691.	2.5	82
10	Trac-looping measures genome structure and chromatin accessibility. Nature Methods, 2018, 15, 741-747.	19.0	74
11	Focal adhesion protein Kindlin-2 regulates bone homeostasis in mice. Bone Research, 2020, 8, 2.	11.4	50
12	Visualization of Single Cell RNA-Seq Data Using t-SNE in R. Methods in Molecular Biology, 2020, 2117, 159-167.	0.9	46
13	A Map of Copy Number Variations in Chinese Populations. PLoS ONE, 2011, 6, e27341.	2.5	44
14	A plate-based single-cell ATAC-seq workflow for fast and robust profiling of chromatin accessibility. Nature Protocols, 2021, 16, 4084-4107.	12.0	40
15	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.	2.8	39
16	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. American Journal of Human Genetics, 2012, 91, 849-862.	6.2	36
17	A systematic characterization of genes underlying both complex and Mendelian diseases. Human Molecular Genetics, 2012, 21, 1611-1624.	2.9	35
18	Haplotype-Sharing Analysis Showing Uyghurs Are Unlikely Genetic Donors. Molecular Biology and Evolution, 2009, 26, 2197-2206.	8.9	34

#	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.	0.8	34
20	Kindlin-2 regulates skeletal homeostasis by modulating PTH1R in mice. Signal Transduction and Targeted Therapy, 2020, 5, 297.	17.1	31
21	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.	2.8	30
22	Integrated decoding hematopoiesis and leukemogenesis using single-cell sequencing and its medical implication. Cell Discovery, 2021, 7, 2.	6.7	30
23	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. European Journal of Human Genetics, 2015, 23, 536-542.	2.8	22
24	Evaluating information content of SNPs for sample-tagging in re-sequencing projects. Scientific Reports, 2015, 5, 10247.	3.3	21
25	A topology-preserving dimensionality reduction method for single-cell RNA-seq data using graph autoencoder. Scientific Reports, 2021, 11, 20028.	3.3	21
26	Diploid genome architecture revealed by multi-omic data of hybrid mice. Genome Research, 2020, 30, 1097-1106.	5.5	18
27	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.	0.8	17
28	Single-Cell Transcriptome Analysis Reveals Six Subpopulations Reflecting Distinct Cellular Fates in Senescent Mouse Embryonic Fibroblasts. Frontiers in Genetics, 2020, 11, 867.	2.3	16
29	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. The HUGO Journal, 2014, 8, 5.	4.1	14
30	Genome-wide identification of histone H2A and histone variant H2A.Z-interacting proteins by bPPI-seq. Cell Research, 2017, 27, 1258-1274.	12.0	14
31	Exploring the changing landscape of cell-to-cell variation after CTCF knockdown via single cell RNA-seq. BMC Genomics, 2019, 20, 1015.	2.8	13
32	Cross-Tissue Characterization of Heterogeneities of Mesenchymal Stem Cells and Their Differentiation Potentials. Frontiers in Cell and Developmental Biology, 2021, 9, 781021.	3.7	13
33	H4K20me3 methyltransferase SUV420H2 shapes the chromatin landscape of pluripotent embryonic stem cells. Development (Cambridge), 2020, 147, .	2.5	11
34	The MicroRNA *miR-22* Represses Th17 Cell Pathogenicity by Targeting PTEN-Regulated Pathways. ImmunoHorizons, 2020, 4, 308-318.	1.8	6
35	A Comprehensive Characterization of Monoallelic Expression During Hematopoiesis and Leukemogenesis via Single-Cell RNA-Sequencing. Frontiers in Cell and Developmental Biology, 2021, 9, 702897.	3.7	5
36	Association of Two Variants in SMAD7 with the Risk of Congenital Heart Disease in the Han Chinese Population. PLoS ONE, 2013, 8, e72423.	2.5	4

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37	Kssd: sequence dimensionality reduction by k-mer substring space sampling enables real-time large-scale datasets analysis. Genome Biology, 2021, 22, 84.	8.8	4
38	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.	3.7	3
39	Complex Selective Forces Shaping the Genes Underlying Human Diseases. Springer Theses, 2015, , 73-92.	0.1	0
40	Genome-Wide Search for Signatures of Natural Selection in African Americans. Springer Theses, 2015, , 53-71.	0.1	0
41	Distribution of Length of Ancestral Chromosomal Segments in Admixed Genomes. Springer Theses, 2015, , 23-33.	0.1	0
42	Exploring Population Admixture Dynamics via Distribution of LACS. Springer Theses, 2015, , 35-51.	0.1	0
43	Three-Dimensional Chromatin Architecture Landscape of Aging and Alzheimer's Disease. SSRN Electronic Journal, 0, , .	0.4	0