Cheng Li

List of Publications by Year in descending order

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58 papers	9,984 citations	186209 28 h-index	161767 54 g-index
65 all docs	65 docs citations	65 times ranked	14051 citing authors

#	Article	IF	Citations
1	Nuclear peripheral chromatin-lamin B1 interaction is required for global integrity of chromatin architecture and dynamics in human cells. Protein and Cell, 2022, 13, 258-280.	4.8	43
2	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. Cell Research, 2022, 32, 38-53.	5.7	48
3	Overcoming resistance to immune checkpoint therapy in PTEN-null prostate cancer by intermittent anti-PI3KÎ±/Î²/Î´ treatment. Nature Communications, 2022, 13, 182.	5.8	40
4	Human pluripotent stem-cell-derived islets ameliorate diabetes in non-human primates. Nature Medicine, 2022, 28, 272-282.	15.2	55
5	Chemical reprogramming of human somatic cells to pluripotent stem cells. Nature, 2022, 605, 325-331.	13.7	144
6	Derivation of totipotent-like stem cells with blastocyst-like structure forming potential. Cell Research, 2022, 32, 513-529.	5.7	47
7	Multiomics Analysis Identifies SOCS1 as Restraining T Cell Activation and Preventing Graftâ€Versusâ€Host Disease. Advanced Science, 2022, 9, e2200978.	5.6	7
8	Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. Briefings in Bioinformatics, 2021, 22, .	3.2	5
9	3D Genome of macaque fetal brain reveals evolutionary innovations during primate corticogenesis. Cell, 2021, 184, 723-740.e21.	13.5	76
10	In vivo chemical reprogramming of astrocytes into neurons. Cell Discovery, 2021, 7, 12.	3.1	46
11	Chemically defined and xeno-free culture condition for human extended pluripotent stem cells. Nature Communications, 2021, 12, 3017.	5.8	16
12	Phase separation of OCT4 controls TAD reorganization to promote cell fate transitions. Cell Stem Cell, 2021, 28, 1868-1883.e11.	5.2	66
13	Transcriptionally inactive hepatitis B virus episome DNA preferentially resides in the vicinity of chromosome 19 in 3D host genome upon infection. Cell Reports, 2021, 35, 109288.	2.9	24
14	Integrative Analysis of Genome, 3D Genome, and Transcriptome Alterations of Clinical Lung Cancer Samples. Genomics, Proteomics and Bioinformatics, 2021, 19, 741-753.	3.0	3
15	The hierarchical folding dynamics of topologically associating domains are closely related to transcriptional abnormalities in cancers. Computational and Structural Biotechnology Journal, 2021, 19, 1684-1693.	1.9	8
16	Establishment of intestinal organoid cultures modeling injury-associated epithelial regeneration. Cell Research, 2021, 31, 259-271.	5.7	54
17	Using Open Chromatin Enrichment and Network Hi-C (OCEAN-C) to Identify Open Chromatin Interactions. Methods in Molecular Biology, 2021, 2351, 211-227.	0.4	0
18	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. Nature Communications, 2021, 12, 6365.	5.8	24

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19	Exogenous artificial DNA forms chromatin structure with active transcription in yeast. Science China Life Sciences, 2021, , 1.	2.3	15
20	The effects of MicroRNA deregulation on pre-RNA processing network in multiple myeloma. Leukemia, 2020, 34, 167-179.	3.3	11
21	Hepatic spheroids derived from human induced pluripotent stem cells in bio-artificial liver rescue porcine acute liver failure. Cell Research, 2020, 30, 95-97.	5.7	44
22	tagHi-C Reveals 3D Chromatin Architecture Dynamics during Mouse Hematopoiesis. Cell Reports, 2020, 32, 108206.	2.9	43
23	Senescence-activated enhancer landscape orchestrates the senescence-associated secretory phenotype in murine fibroblasts. Nucleic Acids Research, 2020, 48, 10909-10923.	6.5	35
24	Single-cell transcriptome profiling reveals neutrophil heterogeneity in homeostasis and infection. Nature Immunology, 2020, 21, 1119-1133.	7.0	380
25	Generation of human hepatocytes from extended pluripotent stem cells. Cell Research, 2020, 30, 810-813.	5.7	22
26	Genome-wide analyses of chromatin interactions after the loss of Pol I, Pol II, and Pol III. Genome Biology, 2020, 21, 158.	3.8	89
27	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. PLoS Computational Biology, 2020, 16, e1007287.	1.5	56
28	Architectural proteins for the formation and maintenance of the 3D genome. Science China Life Sciences, 2020, 63, 795-810.	2.3	11
29	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. Molecular Cell, 2020, 78, 459-476.e13.	4.5	76
30	Elimination of senescent cells by Î²-galactosidase-targeted prodrug attenuates inflammation and restores physical function in aged mice. Cell Research, 2020, 30, 574-589.	5.7	187
31	Nuclear actin regulates inducible transcription by enhancing RNA polymerase II clustering. Science Advances, 2020, 6, eaay6515.	4.7	81
32	Mixed secondary chromatin structure revealed by modeling radiation-induced DNA fragment length distribution. Science China Life Sciences, 2020, 63, 825-834.	2.3	2
33	In vivo miRNA knockout screening identifies miR-190b as a novel tumor suppressor. PLoS Genetics, 2020, 16, e1009168.	1.5	14
34	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
35	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
36	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0

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37	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
38	Branched-Chain Amino Acid Metabolic Reprogramming Orchestrates Drug Resistance to EGFR Tyrosine Kinase Inhibitors. Cell Reports, 2019, 28, 512-525.e6.	2.9	59
39	Single-Cell Transcriptomics Reveals Chemotaxis-Mediated Intraorgan Crosstalk During Cardiogenesis. Circulation Research, 2019, 125, 398-410.	2.0	61
40	PCGF6 regulates stem cell pluripotency as a transcription activator via super-enhancer dependent chromatin interactions. Protein and Cell, 2019, 10, 709-725.	4.8	5
41	An enrichment model using regular health examination data for early detection of colorectal cancer. Chinese Journal of Cancer Research: Official Journal of China Anti-Cancer Association, Beijing Institute for Cancer Research, 2019, 31, 686-698.	0.7	5
42	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. Cancer Letters, 2018, 421, 43-50.	3.2	16
43	Traditional herbal medicine-derived sulforaphene promotes mitophagic cell death in lymphoma cells through CRM1-mediated p62/SQSTM1 accumulation and AMPK activation. Chemico-Biological Interactions, 2018, 281, 11-23.	1.7	31
44	OCEAN-C: mapping hubs of open chromatin interactions across the genome reveals gene regulatory networks. Genome Biology, 2018, 19, 54.	3.8	47
45	iSeq: Web-Based RNA-seq Data Analysis and Visualization. Methods in Molecular Biology, 2018, 1754, 167-181.	0.4	13
46	Synthetic immunology: T-cell engineering and adoptive immunotherapy. Synthetic and Systems Biotechnology, 2018, 3, 179-185.	1.8	23
47	3D genome and its disorganization in diseases. Cell Biology and Toxicology, 2018, 34, 351-365.	2.4	41
48	Genome and epigenome analysis of monozygotic twins discordant for congenital heart disease. BMC Genomics, 2018, 19, 428.	1.2	43
49	Single-Cell RNA-Seq Reveals Dynamic Early Embryonic-like Programs during Chemical Reprogramming. Cell Stem Cell, 2018, 23, 31-45.e7.	5.2	122
50	Cell-Cycle-Targeting MicroRNAs as Therapeutic Tools against Refractory Cancers. Cancer Cell, 2017, 31, 576-590.e8.	7.7	84
51	Dynamic chromatin accessibility modeled by Markov process of randomly-moving molecules in the 3D genome. Nucleic Acids Research, 2017, 45, e85-e85.	6.5	7
52	GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. Nucleic Acids Research, 2017, 45, W98-W102.	6.5	7,114
53	Derivation of Pluripotent Stem Cells with InÂVivo Embryonic and Extraembryonic Potency. Cell, 2017, 169, 243-257.e25.	13.5	382
54	3D genome of multiple myeloma reveals spatial genome disorganization associated with copy number variations. Nature Communications, 2017, 8, 1937.	5.8	99

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55	Identification of cell cycle-targeting microRNAs through genome-wide screens. Cell Cycle, 2017, 16, 2241-2248.	1.3	7
56	3Disease Browser: A Web server for integrating 3D genome and disease-associated chromosome rearrangement data. Scientific Reports, 2016, 6, 34651.	1.6	32
57	A graphical article-level metric for intuitive comparison of large-scale literatures. Scientometrics, 2016, 106, 41-50.	1.6	2
58	The exon junction complex regulates the splicing of cell polarity gene dlg1 to control Wingless signaling in development. ELife, 2016, 5, .	2.8	12