Cheng Li

List of Publications by Year
in descending order

58 papers	9,984 citations	185998 28 h-index	161609 54 g-index
65 all docs	65 docs citations	65 times ranked	14051 citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Derivation of Pluripotent Stem Cells with In Vivo Embryonic and Extraembryonic Potency. Cell, 2017, 169, 243-257.e25.	13.5	382
3	Single-cell transcriptome profiling reveals neutrophil heterogeneity in homeostasis and infection. Nature Immunology, 2020, 21, 1119-1133.	7.0	380
4	Elimination of senescent cells by β-galactosidase-targeted prodrug attenuates inflammation and restores physical function in aged mice. Cell Research, 2020, 30, 574-589.	5.7	187
5	Chemical reprogramming of human somatic cells to pluripotent stem cells. Nature, 2022, 605, 325-331.	13.7	144
6	Single-Cell RNA-Seq Reveals Dynamic Early Embryonic-like Programs during Chemical Reprogramming. Cell Stem Cell, 2018, 23, 31-45.e7.	5.2	122
7	3D genome of multiple myeloma reveals spatial genome disorganization associated with copy number variations. Nature Communications, 2017, 8, 1937.	5.8	99
8	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
9	Cell-Cycle-Targeting MicroRNAs as Therapeutic Tools against Refractory Cancers. Cancer Cell, 2017, 31, 576-590.e8.	7.7	84
10	Nuclear actin regulates inducible transcription by enhancing RNA polymerase II clustering. Science Advances, 2020, 6, eaay6515.	4.7	81
11	Cdk1 Controls Global Epigenetic Landscape in Embryonic Stem Cells. Molecular Cell, 2020, 78, 459-476.e13.	4.5	76
12	3D Genome of macaque fetal brain reveals evolutionary innovations during primate corticogenesis. Cell, 2021, 184, 723-740.e21.	13.5	76
13	Phase separation of OCT4 controls TAD reorganization to promote cell fate transitions. Cell Stem Cell, 2021, 28, 1868-1883.e11.	5.2	66
14	Single-Cell Transcriptomics Reveals Chemotaxis-Mediated Intraorgan Crosstalk During Cardiogenesis. Circulation Research, 2019, 125, 398-410.	2.0	61
15	Branched-Chain Amino Acid Metabolic Reprogramming Orchestrates Drug Resistance to EGFR Tyrosine Kinase Inhibitors. Cell Reports, 2019, 28, 512-525.e6.	2.9	59
16	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. PLoS Computational Biology, 2020, 16, e1007287.	1.5	56
17	Human pluripotent stem-cell-derived islets ameliorate diabetes in non-human primates. Nature Medicine, 2022, 28, 272-282.	15.2	55
18	Establishment of intestinal organoid cultures modeling injury-associated epithelial regeneration. Cell Research, 2021, 31, 259-271.	5.7	54

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19	Identification of HSC/MPP expansion units in fetal liver by single-cell spatiotemporal transcriptomics. Cell Research, 2022, 32, 38-53.	5.7	48
20	OCEAN-C: mapping hubs of open chromatin interactions across the genome reveals gene regulatory networks. Genome Biology, 2018, 19, 54.	3.8	47
21	Derivation of totipotent-like stem cells with blastocyst-like structure forming potential. Cell Research, 2022, 32, 513-529.	5.7	47
22	In vivo chemical reprogramming of astrocytes into neurons. Cell Discovery, 2021, 7, 12.	3.1	46
23	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
24	Genome and epigenome analysis of monozygotic twins discordant for congenital heart disease. BMC Genomics, 2018, 19, 428.	1.2	43
25	tagHi-C Reveals 3D Chromatin Architecture Dynamics during Mouse Hematopoiesis. Cell Reports, 2020, 32, 108206.	2.9	43
26	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
27	3D genome and its disorganization in diseases. Cell Biology and Toxicology, 2018, 34, 351-365.	2.4	41
28	Overcoming resistance to immune checkpoint therapy in PTEN-null prostate cancer by intermittent anti-PI3Kα/β/δ treatment. Nature Communications, 2022, 13, 182.	5.8	40
29	Senescence-activated enhancer landscape orchestrates the senescence-associated secretory phenotype in murine fibroblasts. Nucleic Acids Research, 2020, 48, 10909-10923.	6.5	35
30	3Disease Browser: A Web server for integrating 3D genome and disease-associated chromosome rearrangement data. Scientific Reports, 2016, 6, 34651.	1.6	32
31	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
32	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
33	rRNA biogenesis regulates mouse 2C-like state by 3D structure reorganization of peri-nucleolar heterochromatin. Nature Communications, 2021, 12, 6365.	5.8	24
34	Synthetic immunology: T-cell engineering and adoptive immunotherapy. Synthetic and Systems Biotechnology, 2018, 3, 179-185.	1.8	23
35	Generation of human hepatocytes from extended pluripotent stem cells. Cell Research, 2020, 30, 810-813.	5.7	22
36	Genetic variant repressing ADH1A expression confers susceptibility to esophageal squamous-cell carcinoma. Cancer Letters, 2018, 421, 43-50.	3.2	16

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37	Chemically defined and xeno-free culture condition for human extended pluripotent stem cells. Nature Communications, 2021, 12, 3017.	5.8	16
38	Exogenous artificial DNA forms chromatin structure with active transcription in yeast. Science China Life Sciences, 2021, , 1.	2.3	15
39	In vivo miRNA knockout screening identifies miR-190b as a novel tumor suppressor. PLoS Genetics, 2020, 16, e1009168.	1.5	14
40	iSeq: Web-Based RNA-seq Data Analysis and Visualization. Methods in Molecular Biology, 2018, 1754, 167-181.	0.4	13
41	The exon junction complex regulates the splicing of cell polarity gene dlg1 to control Wingless signaling in development. ELife, 2016, 5, .	2.8	12
42	The effects of MicroRNA deregulation on pre-RNA processing network in multiple myeloma. Leukemia, 2020, 34, 167-179.	3.3	11
43	Architectural proteins for the formation and maintenance of the 3D genome. Science China Life Sciences, 2020, 63, 795-810.	2.3	11
44	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
45	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
46	Identification of cell cycle-targeting microRNAs through genome-wide screens. Cell Cycle, 2017, 16, 2241-2248.	1.3	7
47	Multiomics Analysis Identifies SOCS1 as Restraining T Cell Activation and Preventing Graft–Versus–Host Disease. Advanced Science, 2022, 9, e2200978.	5.6	7
48	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
49	Spatial density of open chromatin: an effective metric for the functional characterization of topologically associated domains. Briefings in Bioinformatics, 2021, 22, .	3.2	5
50	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
51	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
52	A graphical article-level metric for intuitive comparison of large-scale literatures. Scientometrics, 2016, 106, 41-50.	1.6	2
53	Mixed secondary chromatin structure revealed by modeling radiation-induced DNA fragment length distribution. Science China Life Sciences, 2020, 63, 825-834.	2.3	2
54	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

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55	DeepHiC: A generative adversarial network for enhancing Hi-C data resolution. , 2020, 16, e1007287.		0
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