Kun Qu

List of Publications by Year
in descending order

55 papers	7,819 citations	136885 32 h-index	149623 56 g-index
60 all docs	60 docs citations	60 times ranked	14262 citing authors

#	Article	IF	Citations
1	Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions. Molecular Cell, 2011, 44, 667-678.	4.5	1,104
2	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. Cell Stem Cell, 2014, 15, 707-719.	5.2	990
3	Control of somatic tissue differentiation by the long non-coding RNA TINCR. Nature, 2013, 493, 231-235.	13.7	810
4	Hierarchical Mechanisms for Direct Reprogramming of Fibroblasts to Neurons. Cell, 2013, 155, 621-635.	13.5	531
5	Landscape and variation of RNA secondary structure across the human transcriptome. Nature, 2014, 505, 706-709.	13.7	519
6	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. Cell, 2021, 184, 1895-1913.e19.	13.5	512
7	Structure and Thermodynamics of N^6-Methyladenosine in RNA: A Spring-Loaded Base Modification. Journal of the American Chemical Society, 2015, 137, 2107-2115.	6.6	331
8	Human CD96 Correlates to Natural Killer Cell Exhaustion and Predicts the Prognosis of Human Hepatocellular Carcinoma. Hepatology, 2019, 70, 168-183.	3.6	209
9	Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human β Cell Function. Cell Metabolism, 2016, 23, 909-920.	7.2	205
10	An inducible long noncoding RNA amplifies DNA damage signaling. Nature Genetics, 2016, 48, 1370-1376.	9.4	195
11	Single-cell analysis of two severe COVID-19 patients reveals a monocyte-associated and tocilizumab-responding cytokine storm. Nature Communications, 2020, 11, 3924.	5.8	180
12	A LncRNA-MAF:MAFB Transcription Factor Network Regulates Epidermal Differentiation. Developmental Cell, 2015, 32, 693-706.	3.1	172
13	Revealing long noncoding RNA architecture and functions using domain-specific chromatin isolation by RNA purification. Nature Biotechnology, 2014, 32, 933-940.	9.4	161
14	Single-cell profiling of the human decidual immune microenvironment in patients with recurrent pregnancy loss. Cell Discovery, 2021, 7, 1.	3.1	152
15	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. Cancer Cell, 2017, 32, 27-41.e4.	7.7	136
16	A novel ATAC-seq approach reveals lineage-specific reinforcement of the open chromatin landscape via cooperation between BAF and p63. Genome Biology, 2015, 16, 284.	3.8	135
17	Benchmarking spatial and single-cell transcriptomics integration methods for transcript distribution prediction and cell type deconvolution. Nature Methods, 2022, 19, 662-670.	9.0	130
18	Individuality and Variation of Personal Regulomes in Primary Human T Cells. Cell Systems, 2015, 1, 51-61.	2.9	128

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19	The DNA Methylcytosine Dioxygenase Tet2 Sustains Immunosuppressive Function of Tumor-Infiltrating Myeloid Cells to Promote Melanoma Progression. Immunity, 2017, 47, 284-297.e5.	6.6	115
20	Liver-Resident NK Cells Control Antiviral Activity of Hepatic T Cells via the PD-1-PD-L1 Axis. Immunity, 2019, 50, 403-417.e4.	6.6	114
21	Dissecting noncoding and pathogen RNAâ€"protein interactomes. Rna, 2015, 21, 135-143.	1.6	71
22	Accumulation of Tumor-Infiltrating CD49a+ NK Cells Correlates with Poor Prognosis for Human Hepatocellular Carcinoma. Cancer Immunology Research, 2019, 7, 1535-1546.	1.6	66
23	CALML5 is a ZNF750- and TINCR-induced protein that binds stratifin to regulate epidermal differentiation. Genes and Development, 2015, 29, 2225-2230.	2.7	61
24	A genome-wide long noncoding RNA CRISPRi screen identifies *PRANCR* as a novel regulator of epidermal homeostasis. Genome Research, 2020, 30, 22-34.	2.4	59
25	The novel lncRNA lnc-NR2F1 is pro-neurogenic and mutated in human neurodevelopmental disorders. ELife, 2019, 8, .	2.8	59
26	An Integrated Cell Purification and Genomics Strategy Reveals Multiple Regulators of Pancreas Development. PLoS Genetics, 2014, 10, e1004645.	1.5	49
27	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. Developmental Cell, 2017, 43, 227-239.e5.	3.1	48
28	Chromatin accessibility analysis reveals regulatory dynamics of developing human retina and hiPSC-derived retinal organoids. Science Advances, 2020, 6, eaay5247.	4.7	47
29	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. Nature Methods, 2016, 13, 245-247.	9.0	44
30	Detecting riboSNitches with RNA folding algorithms: a genome-wide benchmark. Nucleic Acids Research, 2015, 43, 1859-1868.	6.5	43
31	Systematic Characterization of Long Noncoding RNAs Reveals the Contrasting Coordination of *Cis* - and *Trans* -Molecular Regulation in Human Fetal and Adult Hearts. Circulation: Cardiovascular Genetics, 2016, 9, 110-118.	5.1	42
32	Menin enhances c-Myc-mediated transcription to promote cancer progression. Nature Communications, 2017, 8, 15278.	5.8	41
33	Myc-mediated SDHA acetylation triggers epigenetic regulation of gene expression and tumorigenesis. Nature Metabolism, 2020, 2, 256-269.	5.1	33
34	Reduced CD160 Expression Contributes to Impaired NK-cell Function and Poor Clinical Outcomes in Patients with HCC. Cancer Research, 2018, 78, 6581-6593.	0.4	32
35	Induction of Viable but Nonculturable State in Rhodococcus and Transcriptome Analysis Using RNA-seq. PLoS ONE, 2016, 11, e0147593.	1.1	31
36	Single-cell analysis of COVID-19, sepsis, and HIV infection reveals hyperinflammatory and immunosuppressive signatures in monocytes. Cell Reports, 2021, 37, 109793.	2.9	29

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37	ATAC-pipe: general analysis of genome-wide chromatin accessibility. Briefings in Bioinformatics, 2019, 20, 1934-1943.	3.2	25
38	Ly49E separates liver ILC1s into embryo-derived and postnatal subsets with different functions. Journal of Experimental Medicine, 2022, 219, .	4.2	25
39	Chromatin accessibility landscapes of skin cells in systemic sclerosis nominate dendritic cells in disease pathogenesis. Nature Communications, 2020, 11, 5843.	5.8	22
40	PIRCh-seq: functional classification of non-coding RNAs associated with distinct histone modifications. Genome Biology, 2019, 20, 292.	3.8	20
41	Single-cell transcriptomics reveal a unique memory-like NK cell subset that accumulates with ageing and correlates with disease severity in COVID-19. Genome Medicine, 2022, 14, 46.	3.6	19
42	Development of double-positive thymocytes at single-cell resolution. Genome Medicine, 2021, 13, 49.	3.6	17
43	WEDGE: imputation of gene expression values from single-cell RNA-seq datasets using biased matrix decomposition. Briefings in Bioinformatics, 2021, 22, .	3.2	17
44	Landscape and Dynamics of the Transcriptional Regulatory Network During Natural Killer Cell Differentiation. Genomics, Proteomics and Bioinformatics, 2020, 18, 501-515.	3.0	16
45	Genome-wide CRISPR screen identifies synthetic lethality between DOCK1 inhibition and metformin in liver cancer. Protein and Cell, 2022, 13, 825-841.	4.8	15
46	APEC: an accesson-based method for single-cell chromatin accessibility analysis. Genome Biology, 2020, 21, 116.	3.8	12
47	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. PLoS ONE, 2016, 11, e0165913.	1.1	11
48	Single-Cell RNA Sequencing Reveals the Heterogeneity of Infiltrating Immune Cell Profiles in the Hepatic Cystic Echinococcosis Microenvironment. Infection and Immunity, 2021, 89, e0029721.	1.0	7
49	Chromatin accessibility landscapes of immune cells in rheumatoid arthritis nominate monocytes in disease pathogenesis. BMC Biology, 2021, 19, 79.	1.7	5
50	Chromatin accessibility analysis identifies the transcription factor ETV5 as a suppressor of adipose tissue macrophage activation in obesity. Cell Death and Disease, 2021, 12, 1023.	2.7	5
51	Genome-Wide Probing of RNA Structures In Vitro Using Nucleases and Deep Sequencing. Methods in Molecular Biology, 2016, 1361, 141-160.	0.4	4
52	A transcriptome atlas and interactive analysis platform for autoimmune disease. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	1.4	2
53	Molecular Dynamics Simulations of Noble Gas Fractionation during Diffusion through Silica Nanopores. ACS Earth and Space Chemistry, 2019, 3, 62-69.	1.2	1
54	SMAtool reveals sequences and structural principles of protein-RNA interaction. Biochemical and Biophysical Research Communications, 2020, 525, 53-56.	1.0	1

#	Article	IF	Citations
55	Single-cell data clustering based on sparse optimization and low-rank matrix factorization. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	1