

# Kun Qu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Genome-wide CRISPR screen identifies synthetic lethality between DOCK1 inhibition and metformin in liver cancer. <i>Protein and Cell</i> , 2022, 13, 825-841.	4.8	15
2	Ly49E separates liver ILC1s into embryo-derived and postnatal subsets with different functions. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	25
3	Single-cell transcriptomics reveal a unique memory-like NK cell subset that accumulates with ageing and correlates with disease severity in COVID-19. <i>Genome Medicine</i> , 2022, 14, 46.	3.6	19
4	Benchmarking spatial and single-cell transcriptomics integration methods for transcript distribution prediction and cell type deconvolution. <i>Nature Methods</i> , 2022, 19, 662-670.	9.0	130
5	A transcriptome atlas and interactive analysis platform for autoimmune disease. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	2
6	Single-cell profiling of the human decidual immune microenvironment in patients with recurrent pregnancy loss. <i>Cell Discovery</i> , 2021, 7, 1.	3.1	152
7	Development of double-positive thymocytes at single-cell resolution. <i>Genome Medicine</i> , 2021, 13, 49.	3.6	17
8	Single-cell data clustering based on sparse optimization and low-rank matrix factorization. <i>G3: Genes, Genomes, Genetics</i> , 2021, 11, .	0.8	1
9	WEDGE: imputation of gene expression values from single-cell RNA-seq datasets using biased matrix decomposition. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	17
10	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19.	13.5	512
11	Chromatin accessibility landscapes of immune cells in rheumatoid arthritis nominate monocytes in disease pathogenesis. <i>BMC Biology</i> , 2021, 19, 79.	1.7	5
12	Single-cell analysis of COVID-19, sepsis, and HIV infection reveals hyperinflammatory and immunosuppressive signatures in monocytes. <i>Cell Reports</i> , 2021, 37, 109793.	2.9	29
13	Single-Cell RNA Sequencing Reveals the Heterogeneity of Infiltrating Immune Cell Profiles in the Hepatic Cystic Echinococcosis Microenvironment. <i>Infection and Immunity</i> , 2021, 89, e0029721.	1.0	7
14	Chromatin accessibility analysis identifies the transcription factor ETV5 as a suppressor of adipose tissue macrophage activation in obesity. <i>Cell Death and Disease</i> , 2021, 12, 1023.	2.7	5
15	A genome-wide long noncoding RNA CRISPRi screen identifies <i>PRANCR</i> as a novel regulator of epidermal homeostasis. <i>Genome Research</i> , 2020, 30, 22-34.	2.4	59
16	Chromatin accessibility landscapes of skin cells in systemic sclerosis nominate dendritic cells in disease pathogenesis. <i>Nature Communications</i> , 2020, 11, 5843.	5.8	22
17	Single-cell analysis of two severe COVID-19 patients reveals a monocyte-associated and tocilizumab-responding cytokine storm. <i>Nature Communications</i> , 2020, 11, 3924.	5.8	180
18	APEC: an accession-based method for single-cell chromatin accessibility analysis. <i>Genome Biology</i> , 2020, 21, 116.	3.8	12

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19	Myc-mediated SDHA acetylation triggers epigenetic regulation of gene expression and tumorigenesis. <i>Nature Metabolism</i> , 2020, 2, 256-269.	5.1	33
20	SMAtool reveals sequences and structural principles of protein-RNA interaction. <i>Biochemical and Biophysical Research Communications</i> , 2020, 525, 53-56.	1.0	1
21	Chromatin accessibility analysis reveals regulatory dynamics of developing human retina and hiPSC-derived retinal organoids. <i>Science Advances</i> , 2020, 6, eaay5247.	4.7	47
22	Landscape and Dynamics of the Transcriptional Regulatory Network During Natural Killer Cell Differentiation. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 501-515.	3.0	16
23	ATAC-pipe: general analysis of genome-wide chromatin accessibility. <i>Briefings in Bioinformatics</i> , 2019, 20, 1934-1943.	3.2	25
24	Accumulation of Tumor-Infiltrating CD49a+ NK Cells Correlates with Poor Prognosis for Human Hepatocellular Carcinoma. <i>Cancer Immunology Research</i> , 2019, 7, 1535-1546.	1.6	66
25	Liver-Resident NK Cells Control Antiviral Activity of Hepatic T Cells via the PD-1-PD-L1 Axis. <i>Immunity</i> , 2019, 50, 403-417.e4.	6.6	114
26	PIRCh-seq: functional classification of non-coding RNAs associated with distinct histone modifications. <i>Genome Biology</i> , 2019, 20, 292.	3.8	20
27	Molecular Dynamics Simulations of Noble Gas Fractionation during Diffusion through Silica Nanopores. <i>ACS Earth and Space Chemistry</i> , 2019, 3, 62-69.	1.2	1
28	Human CD96 Correlates to Natural Killer Cell Exhaustion and Predicts the Prognosis of Human Hepatocellular Carcinoma. <i>Hepatology</i> , 2019, 70, 168-183.	3.6	209
29	The novel lncRNA lnc-NR2F1 is pro-neurogenic and mutated in human neurodevelopmental disorders. <i>ELife</i> , 2019, 8, .	2.8	59
30	Reduced CD160 Expression Contributes to Impaired NK-cell Function and Poor Clinical Outcomes in Patients with HCC. <i>Cancer Research</i> , 2018, 78, 6581-6593.	0.4	32
31	Chromatin Accessibility Landscape of Cutaneous T Cell Lymphoma and Dynamic Response to HDAC Inhibitors. <i>Cancer Cell</i> , 2017, 32, 27-41.e4.	7.7	136
32	CSNK1a1 Regulates PRMT1 to Maintain the Progenitor State in Self-Renewing Somatic Tissue. <i>Developmental Cell</i> , 2017, 43, 227-239.e5.	3.1	48
33	The DNA Methylcytosine Dioxygenase Tet2 Sustains Immunosuppressive Function of Tumor-Infiltrating Myeloid Cells to Promote Melanoma Progression. <i>Immunity</i> , 2017, 47, 284-297.e5.	6.6	115
34	Menin enhances c-Myc-mediated transcription to promote cancer progression. <i>Nature Communications</i> , 2017, 8, 15278.	5.8	41
35	Age-Dependent Pancreatic Gene Regulation Reveals Mechanisms Governing Human $\beta$ Cell Function. <i>Cell Metabolism</i> , 2016, 23, 909-920.	7.2	205
36	An inducible long noncoding RNA amplifies DNA damage signaling. <i>Nature Genetics</i> , 2016, 48, 1370-1376.	9.4	195

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37	Integrative genomic analysis by interoperation of bioinformatics tools in GenomeSpace. <i>Nature Methods</i> , 2016, 13, 245-247.	9.0	44
38	Systematic Characterization of Long Noncoding RNAs Reveals the Contrasting Coordination of <i>Cis</i> - and <i>Trans</i> -Molecular Regulation in Human Fetal and Adult Hearts. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 110-118.	5.1	42
39	Genome-Wide Probing of RNA Structures In Vitro Using Nucleases and Deep Sequencing. <i>Methods in Molecular Biology</i> , 2016, 1361, 141-160.	0.4	4
40	Induction of Viable but Nonculturable State in <i>Rhodococcus</i> and Transcriptome Analysis Using RNA-seq. <i>PLoS ONE</i> , 2016, 11, e0147593.	1.1	31
41	Novel Gene Expression Profile of Women with Intrinsic Skin Youthfulness by Whole Transcriptome Sequencing. <i>PLoS ONE</i> , 2016, 11, e0165913.	1.1	11
42	A novel ATAC-seq approach reveals lineage-specific reinforcement of the open chromatin landscape via cooperation between BAF and p63. <i>Genome Biology</i> , 2015, 16, 284.	3.8	135
43	CALML5 is a ZNF750- and TINCR-induced protein that binds stratifin to regulate epidermal differentiation. <i>Genes and Development</i> , 2015, 29, 2225-2230.	2.7	61
44	Dissecting noncoding and pathogen RNA-protein interactomes. <i>Rna</i> , 2015, 21, 135-143.	1.6	71
45	Structure and Thermodynamics of N <sup>6</sup> -Methyladenosine in RNA: A Spring-Loaded Base Modification. <i>Journal of the American Chemical Society</i> , 2015, 137, 2107-2115.	6.6	331
46	Detecting riboSNitches with RNA folding algorithms: a genome-wide benchmark. <i>Nucleic Acids Research</i> , 2015, 43, 1859-1868.	6.5	43
47	A LncRNA-MAF:MAFB Transcription Factor Network Regulates Epidermal Differentiation. <i>Developmental Cell</i> , 2015, 32, 693-706.	3.1	172
48	Individuality and Variation of Personal Regulomes in Primary Human T Cells. <i>Cell Systems</i> , 2015, 1, 51-61.	2.9	128
49	An Integrated Cell Purification and Genomics Strategy Reveals Multiple Regulators of Pancreas Development. <i>PLoS Genetics</i> , 2014, 10, e1004645.	1.5	49
50	Landscape and variation of RNA secondary structure across the human transcriptome. <i>Nature</i> , 2014, 505, 706-709.	13.7	519
51	m6A RNA Modification Controls Cell Fate Transition in Mammalian Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2014, 15, 707-719.	5.2	990
52	Revealing long noncoding RNA architecture and functions using domain-specific chromatin isolation by RNA purification. <i>Nature Biotechnology</i> , 2014, 32, 933-940.	9.4	161
53	Hierarchical Mechanisms for Direct Reprogramming of Fibroblasts to Neurons. <i>Cell</i> , 2013, 155, 621-635.	13.5	531
54	Control of somatic tissue differentiation by the long non-coding RNA TINCR. <i>Nature</i> , 2013, 493, 231-235.	13.7	810

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55	Genomic Maps of Long Noncoding RNA Occupancy Reveal Principles of RNA-Chromatin Interactions. <i>Molecular Cell</i> , 2011, 44, 667-678.	4.5	1,104