Kun Zhang

List of Publications by Year in Descending Order

120 papers	15,823 citations	55 h-index	125 g-index
132 ext. papers	19,362 ext. citations	18.4 avg, IF	6.3 L-index

#	Paper	IF	Citations
120	Temporal analyses of postnatal liver development and maturation by single-cell transcriptomics.. *Developmental Cell*, **2022**, 57, 398-414.e5	10.2	1
119	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases.. *Science*, **2022**, 375, 522-528	33.3	1
118	TET1s deficiency exacerbates oscillatory shear flow-induced atherosclerosis.. *International Journal of Biological Sciences*, **2022**, 18, 2163-2180	11.2	2
117	Comparative cellular analysis of motor cortex in human, marmoset and mouse. *Nature*, **2021**, 598, 111-119	50.4	31
116	A multimodal cell census and atlas of the mammalian primary motor cortex. *Nature*, **2021**, 598, 86-102	50.4	44
115	Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). *Nature Protocols*, **2021**, 16, 4992-5029	18.8	2
114	A multimodal and integrated approach to interrogate human kidney biopsies with rigor and reproducibility: guidelines from the Kidney Precision Medicine Project. *Physiological Genomics*, **2021**, 53, 1-11	3.6	21
113	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. *Molecular Cancer Research*, **2021**, 19, 451-464	6.6	1
112	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. *IScience*, **2021**, 24, 103149	6.1	0
111	Defining the Teratoma as a Model for Multi-lineage Human Development. *Cell*, **2020**, 183, 1402-1419.e18	36.2	12
110	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. *Genome Research*, **2020**, 30, 602-610	9.7	8
109	Tools for the analysis of high-dimensional single-cell RNA sequencing data. *Nature Reviews Nephrology*, **2020**, 16, 408-421	14.9	29
108	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. *Translational Psychiatry*, **2020**, 10, 4	8.6	30
107	The role of the NMD factor UPF3B in olfactory sensory neurons. *ELife*, **2020**, 9,	8.9	9
106	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. *Nature Communications*, **2020**, 11, 3475	17.4	135
105	Precise in vivo genome editing via single homology arm donor mediated intron-targeting gene integration for genetic disease correction. *Cell Research*, **2019**, 29, 804-819	24.7	26
104	A comparative study of the genetic components of three subcategories of autism spectrum disorder. *Molecular Psychiatry*, **2019**, 24, 1720-1731	15.1	18

103	A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. *Nature Communications*, **2019**, 10, 2832	17.4	100
102	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. *IScience*, **2019**, 20, 402-414	6.1	6
101	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. *Blood Advances*, **2019**, 3, 2845-2858	7.8	21
100	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. *Nature Biotechnology*, **2019**, 37, 1452-1457	44.5	227
99	Fever Promotes T Lymphocyte Trafficking via a Thermal Sensory Pathway Involving Heat Shock Protein 90 and 4 Integrins. *Immunity*, **2019**, 50, 137-151.e6	32.3	38
98	Epigenetically Silenced Candidate Tumor Suppressor Genes in Prostate Cancer: Identified by Modeling Methylation Stratification and Applied to Progression Prediction. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 198-207	4	3
97	VarCards: an integrated genetic and clinical database for coding variants in the human genome. *Nucleic Acids Research*, **2018**, 46, D1039-D1048	20.1	86
96	Gel-seq: A Method for Simultaneous Sequencing Library Preparation of DNA and RNA Using Hydrogel Matrices. *Journal of Visualized Experiments*, **2018**,	1.6	1
95	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. *Nature Neuroscience*, **2018**, 21, 432-439	25.5	172
94	Reply to TDNA methylation haplotypes as cancer markersT *Nature Genetics*, **2018**, 50, 1063-1066	36.3	0
93	Performance evaluation of pathogenicity-computation methods for missense variants. *Nucleic Acids Research*, **2018**, 46, 7793-7804	20.1	100
92	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. *Cell Reports*, **2018**, 24, 2029-2041	10.6	37
91	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. *Theranostics*, **2018**, 8, 4345-4358	12.1	41
90	DNA Methylation Identifies Genetically and Prognostically Distinct Subtypes of MDS. *Blood*, **2018**, 132, 106-106	2.2	
89	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. *Nature Biotechnology*, **2018**, 36, 70-80	44.5	433
88	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. *Methods in Molecular Biology*, **2018**, 1708, 365-382	1.4	1
87	Mapping Cellular Reprogramming via Pooled Overexpression Screens with Paired Fitness and Single-Cell RNA-Sequencing Readout. *Cell Systems*, **2018**, 7, 548-555.e8	10.6	15
86	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. *Cell Systems*, **2018**, 7, 656-666.e4	10.6	30

85	Identification of methylation haplotype blocks aids in deconvolution of heterogeneous tissue samples and tumor tissue-of-origin mapping from plasma DNA. *Nature Genetics*, **2017**, 49, 635-642	36.3	237
84	Vitamin D-related genes are subjected to significant de novo mutation burdens in autism spectrum disorder. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2017**, 174, 568-577	3.5	15
83	Gel-seq: whole-genome and transcriptome sequencing by simultaneous low-input DNA and RNA library preparation using semi-permeable hydrogel barriers. *Lab on A Chip*, **2017**, 17, 2619-2630	7.2	2
82	High-resolution RNA allelotyping along the inactive X chromosome: evidence of RNA polymerase III in regulating chromatin configuration. *Scientific Reports*, **2017**, 7, 45460	4.9	6
81	Ultraaccurate genome sequencing and haplotyping of single human cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 12512-12517	11.5	27
80	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. *Molecular Psychiatry*, **2017**, 22, 1282-1290	15.1	53
79	A comparative strategy for single-nucleus and single-cell transcriptomes confirms accuracy in predicted cell-type expression from nuclear RNA. *Scientific Reports*, **2017**, 7, 6031	4.9	115
78	In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. *Nature*, **2016**, 540, 144-149	50.4	645
77	The Action of Discoidin Domain Receptor 2 in Basal Tumor Cells and Stromal Cancer-Associated Fibroblasts Is Critical for Breast Cancer Metastasis. *Cell Reports*, **2016**, 15, 2510-23	10.6	64
76	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. *Nature Biotechnology*, **2016**, 34, 726-37	44.5	204
75	Neuronal subtypes and diversity revealed by single-nucleus RNA sequencing of the human brain. *Science*, **2016**, 352, 1586-90	33.3	531
74	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. *Nature Methods*, **2016**, 13, 241-4	21.6	257
73	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. *Journal of Genetics and Genomics*, **2016**, 43, 587-592	4	35
72	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. *Genome Biology*, **2016**, 17, 20	18.3	40
71	Mechanical signals regulate and activate SNAIL1 protein to control the fibrogenic response of cancer-associated fibroblasts. *Journal of Cell Science*, **2016**, 129, 1989-2002	5.3	41
70	AJUBA LIM Proteins Limit Hippo Activity in Proliferating Cells by Sequestering the Hippo Core Kinase Complex in the Cytosol. *Molecular and Cellular Biology*, **2016**, 36, 2526-42	4.8	39
69	The lncRNA DEANR1 facilitates human endoderm differentiation by activating FOXA2 expression. *Cell Reports*, **2015**, 11, 137-48	10.6	102
68	Humanized Mice Reveal Differential Immunogenicity of Cells Derived from Autologous Induced Pluripotent Stem Cells. *Cell Stem Cell*, **2015**, 17, 353-9	18	167

67	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. *Nature Protocols*, **2015**, 10, 442-58	18.8	280
66	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. *Protein and Cell*, **2014**, 5, 59-68	7.2	21
65	Comparable frequencies of coding mutations and loss of imprinting in human pluripotent cells derived by nuclear transfer and defined factors. *Cell Stem Cell*, **2014**, 15, 634-42	18	93
64	Advances in the profiling of DNA modifications: cytosine methylation and beyond. *Nature Reviews Genetics*, **2014**, 15, 647-61	30.1	183
63	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. *Nature Communications*, **2014**, 5, 4330	17.4	84
62	Distinct chemokine signaling regulates integrin ligand specificity to dictate tissue-specific lymphocyte homing. *Developmental Cell*, **2014**, 30, 61-70	10.2	45
61	Mouse SCNT ESCs have lower somatic mutation load than syngeneic iPSCs. *Stem Cell Reports*, **2014**, 2, 399-405	8	17
60	Characterization of genome-methylome interactions in 22 nuclear pedigrees. *PLoS ONE*, **2014**, 9, e99313	3.7	9
59	Development and bias assessment of a method for targeted metagenomic sequencing of marine cyanobacteria. *Applied and Environmental Microbiology*, **2014**, 80, 1116-25	4.8	11
58	Analysis of protein-coding mutations in hiPSCs and their possible role during somatic cell reprogramming. *Nature Communications*, **2013**, 4, 1382	17.4	51
57	The presenilin-1 E9 mutation results in reduced secretase activity, but not total loss of PS1 function, in isogenic human stem cells. *Cell Reports*, **2013**, 5, 974-85	10.6	133
56	Massively parallel polymerase cloning and genome sequencing of single cells using nanoliter microwells. *Nature Biotechnology*, **2013**, 31, 1126-32	44.5	188
55	On the design of clone-based haplotyping. *Genome Biology*, **2013**, 14, R100	18.3	17
54	Genome-wide analysis reveals TET- and TDG-dependent 5-methylcytosine oxidation dynamics. *Cell*, **2013**, 153, 692-706	56.2	390
53	Microfluidic devices with permeable polymer barriers for capture and transport of biomolecules and cells. *Lab on A Chip*, **2013**, 13, 3389-97	7.2	11
52	The unique disulfide bond-stabilized W1 -1 loop in the propeller domain regulates integrin 7 affinity and signaling. *Journal of Biological Chemistry*, **2013**, 288, 14228-14237	5.4	6
51	Disruption of disulfide restriction at integrin knees induces activation and ligand-independent signaling of *Journal of Cell Science*, **2013**, 126, 5030-41	5.3	6
50	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. *Cell Research*, **2013**, 23, 329-39	24.7	125

49	Chromatin signature of widespread monoallelic expression. *ELife*, **2013**, 2, e01256	8.9	55
48	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. *Protein and Cell*, **2013**, 5, 59	7.2	2
47	Tet1 controls meiosis by regulating meiotic gene expression. *Nature*, **2012**, 492, 443-7	50.4	207
46	Whole-genome sequencing in autism identifies hot spots for de novo germline mutation. *Cell*, **2012**, 151, 1431-42	56.2	392
45	Library-free methylation sequencing with bisulfite padlock probes. *Nature Methods*, **2012**, 9, 270-2	21.6	84
44	Evolutionary history and adaptation from high-coverage whole-genome sequences of diverse African hunter-gatherers. *Cell*, **2012**, 150, 457-69	56.2	226
43	Identification of a specific reprogramming-associated epigenetic signature in human induced pluripotent stem cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 16196-201	11.5	129
42	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. *Cell Research*, **2012**, 22, 168-77	24.7	388
41	The regulation of integrin function by divalent cations. *Cell Adhesion and Migration*, **2012**, 6, 20-9	3.2	126
40	A public resource facilitating clinical use of genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 11920-7	11.5	154
39	Specific sorting of single bacterial cells with microfabricated fluorescence-activated cell sorting and tyramide signal amplification fluorescence in situ hybridization. *Analytical Chemistry*, **2011**, 83, 7269-75	7.8	42
38	Increased methylation variation in epigenetic domains across cancer types. *Nature Genetics*, **2011**, 43, 768-75	36.3	825
37	Genome-wide regulation of 5hmC, 5mC, and gene expression by Tet1 hydroxylase in mouse embryonic stem cells. *Molecular Cell*, **2011**, 42, 451-64	17.6	493
36	Targeted gene correction of laminopathy-associated LMNA mutations in patient-specific iPSCs. *Cell Stem Cell*, **2011**, 8, 688-94	18	188
35	Human oocytes reprogram somatic cells to a pluripotent state. *Nature*, **2011**, 478, 70-5	50.4	169
34	Somatic coding mutations in human induced pluripotent stem cells. *Nature*, **2011**, 471, 63-7	50.4	998
33	Recapitulation of premature ageing with iPSCs from Hutchinson-Gilford progeria syndrome. *Nature* , **2011**, 472, 221-5	50.4	428
32	Mediators and dynamics of DNA methylation. *Wiley Interdisciplinary Reviews: Systems Biology and Medicine*, **2011**, 3, 281-98	6.6	7

31	Genome-wide mapping of the sixth base. *Genome Biology*, **2011**, 12, 116	18.3	
30	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. *Nucleic Acids Research*, **2011**, 39, e127	20.1	54
29	Genetic correction and analysis of induced pluripotent stem cells from a patient with gyrate atrophy. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 6537-42	11.5	136
28	Rapid identification of heterozygous mutations in Drosophila melanogaster using genomic capture sequencing. *Genome Research*, **2010**, 20, 981-8	9.7	21
27	Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome. *Genome Research*, **2010**, 20, 883-9	9.7	273
26	Multiplex padlock targeted sequencing reveals human hypermutable CpG variations. *Genome Research*, **2009**, 19, 1606-15	9.7	59
25	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. *Nature Biotechnology*, **2009**, 27, 353-60	44.5	409
24	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. *Nature Methods*, **2009**, 6, 613-8	21.6	136
23	Optimal timing of inner cell mass isolation increases the efficiency of human embryonic stem cell derivation and allows generation of sibling cell lines. *Cell Stem Cell*, **2009**, 4, 103-6	18	148
22	Genome-wide identification of human RNA editing sites by parallel DNA capturing and sequencing. *Science*, **2009**, 324, 1210-3	33.3	415
21	A robust approach to identifying tissue-specific gene expression regulatory variants using personalized human induced pluripotent stem cells. *PLoS Genetics*, **2009**, 5, e1000718	6	46
20	Multiplex amplification of large sets of human exons. *Nature Methods*, **2007**, 4, 931-6	21.6	357
19	Finding the needles in the metagenome haystack. *Microbial Ecology*, **2007**, 53, 475-85	4.4	60
18	Sequencing genomes from single cells by polymerase cloning. *Nature Biotechnology*, **2006**, 24, 680-6	44.5	353
17	Long-range polony haplotyping of individual human chromosome molecules. *Nature Genetics*, **2006**, 38, 382-7	36.3	80
16	Accurate multiplex polony sequencing of an evolved bacterial genome. *Science*, **2005**, 309, 1728-32	33.3	1011
15	HaploBlockFinder: haplotype block analyses. *Bioinformatics*, **2003**, 19, 1300-1	7.2	108
14	Randomly distributed crossovers may generate block-like patterns of linkage disequilibrium: an act of genetic drift. *Human Genetics*, **2003**, 113, 51-9	6.3	38

13	The effect of single nucleotide polymorphism identification strategies on estimates of linkage disequilibrium. *Molecular Biology and Evolution*, **2003**, 20, 232-42	8.3	59
12	Interrogating a high-density SNP map for signatures of natural selection. *Genome Research*, **2002**, 12, 1805-14	9.7	678
11	Distribution of recombination crossovers and the origin of haplotype blocks: the interplay of population history, recombination, and mutation. *American Journal of Human Genetics*, **2002**, 71, 1227-34	11	351
10	The effect that genotyping errors have on the robustness of common linkage-disequilibrium measures. *American Journal of Human Genetics*, **2001**, 68, 1447-56	11	97
9	Visualizing and interpreting single-cell gene expression datasets with Similarity Weighted Nonnegative Embedding		1
8	Integrative single-cell analysis by transcriptional and epigenetic states in human adult brain		5
7	Single nucleus analysis of the chromatin landscape in mouse forebrain development		2
6	Evolution of cellular diversity in primary motor cortex of human, marmoset monkey, and mouse		33
5	A reference tissue atlas for the human kidney		2
4	A multimodal cell census and atlas of the mammalian primary motor cortex		12
3	Linking transcriptome and chromatin accessibility in nanoliter droplets for single-cell sequencing		3
2	A Multimodal and Integrated Approach to Interrogate Human Kidney Biopsies with Rigor and Reproducibility: The Kidney Precision Medicine Project		1
1	An atlas of healthy and injured cell states and niches in the human kidney		10