Kun Zhang

List of Publications by Year
in descending order

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116 papers	21,691 citations	19636 61 h-index	21521 114 g-index
132 all docs	132 docs citations	132 times ranked	33624 citing authors

#	Article	IF	Citations
1	Temporal analyses of postnatal liver development and maturation by single-cell transcriptomics. Developmental Cell, 2022, 57, 398-414.e5.	3.1	30
2	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases. Science, 2022, 375, 522-528.	6.0	31
3	TET1s deficiency exacerbates oscillatory shear flow-induced atherosclerosis. International Journal of Biological Sciences, 2022, 18, 2163-2180.	2.6	13
4	A single-cell regulatory map of postnatal lung alveologenesis in humans and mice. Cell Genomics, 2022, 2, 100108.	3.0	13
5	Dedifferentiationâ€associated inflammatory factors of longâ€term expanded human hepatocytes exacerbate their elimination by macrophages during liver engraftment. Hepatology, 2022, 76, 1690-1705.	3.6	11
6	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	4.7	67
7	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.	1.0	59
8	Rationale and design of the Kidney Precision Medicine Project. Kidney International, 2021, 99, 498-510.	2.6	94
9	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. Molecular Cancer Research, 2021, 19, 451-464.	1.5	3
10	A new approach to decode DNA methylome and genomic variants simultaneously from double strand bisulfite sequencing. Briefings in Bioinformatics, 2021, 22, .	3.2	5
11	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. IScience, 2021, 24, 103149.	1.9	2
12	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	13.7	361
13	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	13.7	316
14	Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). Nature Protocols, 2021, 16, 4992-5029.	5.5	18
15	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. Nature Communications, 2020, 11, 3475.	5.8	341
16	Defining the Teratoma as a Model for Multi-lineage Human Development. Cell, 2020, 183, 1402-1419.e18.	13.5	32
17	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. Genome Research, 2020, 30, 602-610.	2.4	14
18	Tools for the analysis of high-dimensional single-cell RNA sequencing data. Nature Reviews Nephrology, 2020, 16, 408-421.	4.1	80

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19	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. Translational Psychiatry, 2020, 10, 4.	2.4	84
20	The role of the NMD factor UPF3B in olfactory sensory neurons. ELife, 2020, 9, .	2.8	18
21	A comparative study of the genetic components of three subcategories of autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1720-1731.	4.1	22
22	A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. Nature Communications, 2019, 10, 2832.	5.8	206
23	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. IScience, 2019, 20, 402-414.	1.9	11
24	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.	5.7	51
25	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. Blood Advances, 2019, 3, 2845-2858.	2.5	32
26	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 2019, 37, 1452-1457.	9.4	550
27	Fever Promotes T Lymphocyte Trafficking via a Thermal Sensory Pathway Involving Heat Shock Protein 90 and Î±4 Integrins. Immunity, 2019, 50, 137-151.e6.	6.6	69
28	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.	1.1	5
29	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	6.5	148
30	Gel-seq: A Method for Simultaneous Sequencing Library Preparation of DNA and RNA Using Hydrogel Matrices. Journal of Visualized Experiments, 2018, , .	0.2	1
31	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	7.1	290
32	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	9.4	762
33	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. Methods in Molecular Biology, 2018, 1708, 365-382.	0.4	1
34	Mapping Cellular Reprogramming via Pooled Overexpression Screens with Paired Fitness and Single-Cell RNA-Sequencing Readout. Cell Systems, 2018, 7, 548-555.e8.	2.9	35
35	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. Cell Systems, 2018, 7, 656-666.e4.	2.9	63
36	Reply to â€˜DNA methylation haplotypes as cancer markersâ€™. Nature Genetics, 2018, 50, 1063-1066.	9.4	1

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37	Performance evaluation of pathogenicity-computation methods for missense variants. Nucleic Acids Research, 2018, 46, 7793-7804.	6.5	168
38	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. Cell Reports, 2018, 24, 2029-2041.	2.9	64
39	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. Theranostics, 2018, 8, 4345-4358.	4.6	63
40	DNA Methylation Identifies Genetically and Prognostically Distinct Subtypes of MDS. Blood, 2018, 132, 106-106.	0.6	0
41	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.	9.4	384
42	Vitamin Dâ€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.	1.1	20
43	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.	3.1	3
44	High-resolution RNA allelotyping along the inactive X chromosome: evidence of RNA polymerase III in regulating chromatin configuration. Scientific Reports, 2017, 7, 45460.	1.6	10
45	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.	3.3	41
46	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. Molecular Psychiatry, 2017, 22, 1282-1290.	4.1	95
47	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.	1.6	209
48	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. Journal of Genetics and Genomics, 2016, 43, 587-592.	1.7	52
49	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. Genome Biology, 2016, 17, 20.	3.8	55
50	Mechanical signals regulate and activate SNAIL1 protein to control the fibrogenic response of CAFs. Journal of Cell Science, 2016, 129, 1989-2002.	1.2	57
51	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, 2526-2542.	1.1	50
52	In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. Nature, 2016, 540, 144-149.	13.7	906
53	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, 2510-2523.	2.9	85
54	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	9.4	270

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55	Neuronal subtypes and diversity revealed by single-nucleus RNA sequencing of the human brain. Science, 2016, 352, 1586-1590.	6.0	822
56	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. Nature Methods, 2016, 13, 241-244.	9.0	356
57	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. Nature Protocols, 2015, 10, 442-458.	5.5	422
58	The lncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression. Cell Reports, 2015, 11, 137-148.	2.9	127
59	Humanized Mice Reveal Differential Immunogenicity of Cells Derived from Autologous Induced Pluripotent Stem Cells. Cell Stem Cell, 2015, 17, 353-359.	5.2	198
60	Characterization of Genome-Methylome Interactions in 22 Nuclear Pedigrees. PLoS ONE, 2014, 9, e99313.	1.1	15
61	Development and Bias Assessment of a Method for Targeted Metagenomic Sequencing of Marine Cyanobacteria. Applied and Environmental Microbiology, 2014, 80, 1116-1125.	1.4	12
62	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2014, 5, 59-68.	4.8	26
63	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, 634-642.	5.2	113
64	Advances in the profiling of DNA modifications: cytosine methylation and beyond. Nature Reviews Genetics, 2014, 15, 647-661.	7.7	224
65	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. Nature Communications, 2014, 5, 4330.	5.8	102
66	Distinct Chemokine Signaling Regulates Integrin Ligand Specificity to Dictate Tissue-Specific Lymphocyte Homing. Developmental Cell, 2014, 30, 61-70.	3.1	75
67	Mouse SCNT ESCs Have Lower Somatic Mutation Load Than SyngeneicÂiPSCs. Stem Cell Reports, 2014, 2, 399-405.	2.3	20
68	Analysis of protein-coding mutations in hiPSCs and their possible role during somatic cell reprogramming. Nature Communications, 2013, 4, 1382.	5.8	58
69	The Presenilin-1 Î”E9 Mutation Results in Reduced Î³-Secretase Activity, but Not Total Loss of PS1 Function, in Isogenic Human Stem Cells. Cell Reports, 2013, 5, 974-985.	2.9	168
70	Massively parallel polymerase cloning and genome sequencing of single cells using nanoliter microwells. Nature Biotechnology, 2013, 31, 1126-1132.	9.4	231
71	On the design of clone-based haplotyping. Genome Biology, 2013, 14, R100.	13.9	18
72	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. Cell, 2013, 153, 692-706.	13.5	440

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73	Microfluidic devices with permeable polymer barriers for capture and transport of biomolecules and cells. Lab on A Chip, 2013, 13, 3389.	3.1	13
74	The Unique Disulfide Bond-stabilized W1 Î²4-Î²1 Loop in the Î±4 Î²-Propeller Domain Regulates Integrin Î±4Î²7 Affinity and Signaling. Journal of Biological Chemistry, 2013, 288, 14228-14237.	1.6	12
75	Disruption of disulfide-restriction at integrin knees induces activation and ligand-independent signaling of Î±4Î²7. Journal of Cell Science, 2013, 126, 5030-41.	1.2	8
76	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. Cell Research, 2013, 23, 329-339.	5.7	152
77	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2013, 5, 59.	4.8	3
78	Chromatin signature of widespread monoallelic expression. ELife, 2013, 2, e01256.	2.8	71
79	The regulation of integrin function by divalent cations. Cell Adhesion and Migration, 2012, 6, 20-29.	1.1	205
80	A public resource facilitating clinical use of genomes. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11920-11927.	3.3	194
81	Tet1 controls meiosis by regulating meiotic gene expression. Nature, 2012, 492, 443-447.	13.7	255
82	Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. Cell, 2012, 151, 1431-1442.	13.5	501
83	Library-free methylation sequencing with bisulfite padlock probes. Nature Methods, 2012, 9, 270-272.	9.0	92
84	Evolutionary History and Adaptation from High-Coverage Whole-Genome Sequences of Diverse African Hunter-Gatherers. Cell, 2012, 150, 457-469.	13.5	289
85	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, 16196-16201.	3.3	152
86	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. Cell Research, 2012, 22, 168-177.	5.7	452
87	Genome-wide mapping of the sixth base. Genome Biology, 2011, 12, 116.	13.9	0
88	Specific Sorting of Single Bacterial Cells with Microfabricated Fluorescence-Activated Cell Sorting and Tyramide Signal Amplification Fluorescence in Situ Hybridization. Analytical Chemistry, 2011, 83, 7269-7275.	3.2	50
89	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	9.4	968
90	Genome-wide Regulation of 5hmC, 5mC, and Gene Expression by Tet1 Hydroxylase in Mouse Embryonic Stem Cells. Molecular Cell, 2011, 42, 451-464.	4.5	551

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91	Targeted Gene Correction of Laminopathy-Associated LMNA Mutations in Patient-Specific iPSCs. Cell Stem Cell, 2011, 8, 688-694.	5.2	214
92	Human oocytes reprogram somatic cells to a pluripotent state. Nature, 2011, 478, 70-75.	13.7	221
93	Somatic coding mutations in human induced pluripotent stem cells. Nature, 2011, 471, 63-67.	13.7	1,147
94	Recapitulation of premature ageing with iPSCs from Hutchinsonâ€“Gilford progeria syndrome. Nature, 2011, 472, 221-225.	13.7	510
95	Mediators and dynamics of DNA methylation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 281-298.	6.6	7
96	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. Nucleic Acids Research, 2011, 39, e127-e127.	6.5	61
97	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, 6537-6542.	3.3	150
98	Rapid identification of heterozygous mutations in Drosophila melanogaster using genomic capture sequencing. Genome Research, 2010, 20, 981-988.	2.4	30
99	Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome. Genome Research, 2010, 20, 883-889.	2.4	343
100	Multiplex padlock targeted sequencing reveals human hypermutable CpG variations. Genome Research, 2009, 19, 1606-1615.	2.4	62
101	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. Nature Biotechnology, 2009, 27, 353-360.	9.4	458
102	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. Nature Methods, 2009, 6, 613-618.	9.0	149
103	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, 103-106.	5.2	171
104	Genome-Wide Identification of Human RNA Editing Sites by Parallel DNA Capturing and Sequencing. Science, 2009, 324, 1210-1213.	6.0	483
105	A Robust Approach to Identifying Tissue-Specific Gene Expression Regulatory Variants Using Personalized Human Induced Pluripotent Stem Cells. PLoS Genetics, 2009, 5, e1000718.	1.5	55
106	Multiplex amplification of large sets of human exons. Nature Methods, 2007, 4, 931-936.	9.0	392
107	Finding the Needles in the Metagenome Haystack. Microbial Ecology, 2007, 53, 475-485.	1.4	68
108	Sequencing genomes from single cells by polymerase cloning. Nature Biotechnology, 2006, 24, 680-686.	9.4	388

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109	Long-range polony haplotyping of individual human chromosome molecules. Nature Genetics, 2006, 38, 382-387.	9.4	97
110	Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. Science, 2005, 309, 1728-1732.	6.0	1,189
111	Randomly distributed crossovers may generate block-like patterns of linkage disequilibrium: an act of genetic drift. Human Genetics, 2003, 113, 51-59.	1.8	41
112	The Effect of Single Nucleotide Polymorphism Identification Strategies on Estimates of Linkage Disequilibrium. Molecular Biology and Evolution, 2003, 20, 232-242.	3.5	67
113	HaploBlockFinder: haplotype block analyses. Bioinformatics, 2003, 19, 1300-1301.	1.8	112
114	Interrogating a High-Density SNP Map for Signatures of Natural Selection. Genome Research, 2002, 12, 1805-1814.	2.4	852
115	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, 1227-1234.	2.6	399
116	The Effect That Genotyping Errors Have on the Robustness of Common Linkage-Disequilibrium Measures. American Journal of Human Genetics, 2001, 68, 1447-1456.	2.6	110