Kun Zhang

List of Publications by Year
in descending order

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116 papers	21,691 citations	19657 61 h-index	21540 114 g-index
132 all docs	132 docs citations	132 times ranked	33624 citing authors

#	Article	IF	Citations
1	Accurate Multiplex Polony Sequencing of an Evolved Bacterial Genome. Science, 2005, 309, 1728-1732.	12.6	1,189
2	Somatic coding mutations in human induced pluripotent stem cells. Nature, 2011, 471, 63-67.	27.8	1,147
3	Increased methylation variation in epigenetic domains across cancer types. Nature Genetics, 2011, 43, 768-775.	21.4	968
4	In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. Nature, 2016, 540, 144-149.	27.8	906
5	Interrogating a High-Density SNP Map for Signatures of Natural Selection. Genome Research, 2002, 12, 1805-1814.	5.5	852
6	Neuronal subtypes and diversity revealed by single-nucleus RNA sequencing of the human brain. Science, 2016, 352, 1586-1590.	12.6	822
7	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	17.5	762
8	Genome-wide Regulation of 5hmC, 5mC, and Gene Expression by Tet1 Hydroxylase in Mouse Embryonic Stem Cells. Molecular Cell, 2011, 42, 451-464.	9.7	551
9	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 2019, 37, 1452-1457.	17.5	550
10	Recapitulation of premature ageing with iPSCs from Hutchinsonâ€“Gilford progeria syndrome. Nature, 2011, 472, 221-225.	27.8	510
11	Whole-Genome Sequencing in Autism Identifies Hot Spots for De Novo Germline Mutation. Cell, 2012, 151, 1431-1442.	28.9	501
12	Genome-Wide Identification of Human RNA Editing Sites by Parallel DNA Capturing and Sequencing. Science, 2009, 324, 1210-1213.	12.6	483
13	Targeted bisulfite sequencing reveals changes in DNA methylation associated with nuclear reprogramming. Nature Biotechnology, 2009, 27, 353-360.	17.5	458
14	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. Cell Research, 2012, 22, 168-177.	12.0	452
15	Genome-wide Analysis Reveals TET- and TDG-Dependent 5-Methylcytosine Oxidation Dynamics. Cell, 2013, 153, 692-706.	28.9	440
16	Fluorescent in situ sequencing (FISSEQ) of RNA for gene expression profiling in intact cells and tissues. Nature Protocols, 2015, 10, 442-458.	12.0	422
17	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.	6.2	399
18	Multiplex amplification of large sets of human exons. Nature Methods, 2007, 4, 931-936.	19.0	392

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19	Sequencing genomes from single cells by polymerase cloning. Nature Biotechnology, 2006, 24, 680-686.	17.5	388
20	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.	21.4	384
21	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
22	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. Nature Methods, 2016, 13, 241-244.	19.0	356
23	Allele-specific methylation is prevalent and is contributed by CpG-SNPs in the human genome. Genome Research, 2010, 20, 883-889.	5.5	343
24	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. Nature Communications, 2020, 11, 3475.	12.8	341
25	A multimodal cell census and atlas of the mammalian primary motor cortex. Nature, 2021, 598, 86-102.	27.8	316
26	Single-nucleus analysis of accessible chromatin in developing mouse forebrain reveals cell-type-specific transcriptional regulation. Nature Neuroscience, 2018, 21, 432-439.	14.8	290
27	Evolutionary History and Adaptation from High-Coverage Whole-Genome Sequences of Diverse African Hunter-Gatherers. Cell, 2012, 150, 457-469.	28.9	289
28	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
29	Tet1 controls meiosis by regulating meiotic gene expression. Nature, 2012, 492, 443-447.	27.8	255
30	Massively parallel polymerase cloning and genome sequencing of single cells using nanoliter microwells. Nature Biotechnology, 2013, 31, 1126-1132.	17.5	231
31	Advances in the profiling of DNA modifications: cytosine methylation and beyond. Nature Reviews Genetics, 2014, 15, 647-661.	16.3	224
32	Human oocytes reprogram somatic cells to a pluripotent state. Nature, 2011, 478, 70-75.	27.8	221
33	Targeted Gene Correction of Laminopathy-Associated LMNA Mutations in Patient-Specific iPSCs. Cell Stem Cell, 2011, 8, 688-694.	11.1	214
34	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.	3.3	209
35	A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. Nature Communications, 2019, 10, 2832.	12.8	206
36	The regulation of integrin function by divalent cations. Cell Adhesion and Migration, 2012, 6, 20-29.	2.7	205

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37	Humanized Mice Reveal Differential Immunogenicity of Cells Derived from Autologous Induced Pluripotent Stem Cells. Cell Stem Cell, 2015, 17, 353-359.	11.1	198
38	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.	7.1	194
39	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.	11.1	171
40	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.	6.4	168
41	Performance evaluation of pathogenicity-computation methods for missense variants. Nucleic Acids Research, 2018, 46, 7793-7804.	14.5	168
42	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.	7.1	152
43	Dynamics of 5-methylcytosine and 5-hydroxymethylcytosine during germ cell reprogramming. Cell Research, 2013, 23, 329-339.	12.0	152
44	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.	7.1	150
45	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. Nature Methods, 2009, 6, 613-618.	19.0	149
46	VarCards: an integrated genetic and clinical database for coding variants in the human genome. Nucleic Acids Research, 2018, 46, D1039-D1048.	14.5	148
47	The lncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression. Cell Reports, 2015, 11, 137-148.	6.4	127
48	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.	11.1	113
49	HaploBlockFinder: haplotype block analyses. Bioinformatics, 2003, 19, 1300-1301.	4.1	112
50	The Effect That Genotyping Errors Have on the Robustness of Common Linkage-Disequilibrium Measures. American Journal of Human Genetics, 2001, 68, 1447-1456.	6.2	110
51	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. Nature Communications, 2014, 5, 4330.	12.8	102
52	Long-range polony haplotyping of individual human chromosome molecules. Nature Genetics, 2006, 38, 382-387.	21.4	97
53	Targeted sequencing and functional analysis reveal brain-size-related genes and their networks in autism spectrum disorders. Molecular Psychiatry, 2017, 22, 1282-1290.	7.9	95
54	Rationale and design of the Kidney Precision Medicine Project. Kidney International, 2021, 99, 498-510.	5.2	94

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55	Library-free methylation sequencing with bisulfite padlock probes. Nature Methods, 2012, 9, 270-272.	19.0	92
56	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.	6.4	85
57	Genetic evidence of gender difference in autism spectrum disorder supports the female-protective effect. Translational Psychiatry, 2020, 10, 4.	4.8	84
58	Tools for the analysis of high-dimensional single-cell RNA sequencing data. Nature Reviews Nephrology, 2020, 16, 408-421.	9.6	80
59	Distinct Chemokine Signaling Regulates Integrin Ligand Specificity to Dictate Tissue-Specific Lymphocyte Homing. Developmental Cell, 2014, 30, 61-70.	7.0	75
60	Chromatin signature of widespread monoallelic expression. ELife, 2013, 2, e01256.	6.0	71
61	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.	14.3	69
62	Finding the Needles in the Metagenome Haystack. Microbial Ecology, 2007, 53, 475-485.	2.8	68
63	The Effect of Single Nucleotide Polymorphism Identification Strategies on Estimates of Linkage Disequilibrium. Molecular Biology and Evolution, 2003, 20, 232-242.	8.9	67
64	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	10.3	67
65	PAK2 Haploinsufficiency Results in Synaptic Cytoskeleton Impairment and Autism-Related Behavior. Cell Reports, 2018, 24, 2029-2041.	6.4	64
66	Visualizing and Interpreting Single-Cell Gene Expression Datasets with Similarity Weighted Nonnegative Embedding. Cell Systems, 2018, 7, 656-666.e4.	6.2	63
67	Transcriptomic signature associated with carcinogenesis and aggressiveness of papillary thyroid carcinoma. Theranostics, 2018, 8, 4345-4358.	10.0	63
68	Multiplex padlock targeted sequencing reveals human hypermutable CpG variations. Genome Research, 2009, 19, 1606-1615.	5.5	62
69	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. Nucleic Acids Research, 2011, 39, e127-e127.	14.5	61
70	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.	2.3	59
71	Analysis of protein-coding mutations in hiPSCs and their possible role during somatic cell reprogramming. Nature Communications, 2013, 4, 1382.	12.8	58
72	Mechanical signals regulate and activate SNAIL1 protein to control the fibrogenic response of CAFs. Journal of Cell Science, 2016, 129, 1989-2002.	2.0	57

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73	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. Genome Biology, 2016, 17, 20.	8.8	55
74	A Robust Approach to Identifying Tissue-Specific Gene Expression Regulatory Variants Using Personalized Human Induced Pluripotent Stem Cells. PLoS Genetics, 2009, 5, e1000718.	3.5	55
75	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. Journal of Genetics and Genomics, 2016, 43, 587-592.	3.9	52
76	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.	12.0	51
77	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.	6.5	50
78	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.	2.3	50
79	Randomly distributed crossovers may generate block-like patterns of linkage disequilibrium: an act of genetic drift. Human Genetics, 2003, 113, 51-59.	3.8	41
80	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.	7.1	41
81	Mapping Cellular Reprogramming via Pooled Overexpression Screens with Paired Fitness and Single-Cell RNA-Sequencing Readout. Cell Systems, 2018, 7, 548-555.e8.	6.2	35
82	DNA methylation identifies genetically and prognostically distinct subtypes of myelodysplastic syndromes. Blood Advances, 2019, 3, 2845-2858.	5.2	32
83	Defining the Teratoma as a Model for Multi-lineage Human Development. Cell, 2020, 183, 1402-1419.e18.	28.9	32
84	Discovery of genomic loci of the human cerebral cortex using genetically informed brain atlases. Science, 2022, 375, 522-528.	12.6	31
85	Rapid identification of heterozygous mutations in Drosophila melanogaster using genomic capture sequencing. Genome Research, 2010, 20, 981-988.	5.5	30
86	Temporal analyses of postnatal liver development and maturation by single-cell transcriptomics. Developmental Cell, 2022, 57, 398-414.e5.	7.0	30
87	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2014, 5, 59-68.	11.0	26
88	A comparative study of the genetic components of three subcategories of autism spectrum disorder. Molecular Psychiatry, 2019, 24, 1720-1731.	7.9	22
89	Mouse SCNT ESCs Have Lower Somatic Mutation Load Than SyngeneicÂiPSCs. Stem Cell Reports, 2014, 2, 399-405.	4.8	20
90	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.	1.7	20

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91	On the design of clone-based haplotyping. Genome Biology, 2013, 14, R100.	9.6	18
92	The role of the NMD factor UPF3B in olfactory sensory neurons. ELife, 2020, 9, .	6.0	18
93	Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). Nature Protocols, 2021, 16, 4992-5029.	12.0	18
94	Characterization of Genome-Methylome Interactions in 22 Nuclear Pedigrees. PLoS ONE, 2014, 9, e99313.	2.5	15
95	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. Genome Research, 2020, 30, 602-610.	5.5	14
96	Microfluidic devices with permeable polymer barriers for capture and transport of biomolecules and cells. Lab on A Chip, 2013, 13, 3389.	6.0	13
97	TET1s deficiency exacerbates oscillatory shear flow-induced atherosclerosis. International Journal of Biological Sciences, 2022, 18, 2163-2180.	6.4	13
98	A single-cell regulatory map of postnatal lung alveologenesis in humans and mice. Cell Genomics, 2022, 2, 100108.	6.5	13
99	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.	3.4	12
100	Development and Bias Assessment of a Method for Targeted Metagenomic Sequencing of Marine Cyanobacteria. Applied and Environmental Microbiology, 2014, 80, 1116-1125.	3.1	12
101	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. IScience, 2019, 20, 402-414.	4.1	11
102	Dedifferentiationâ€associated inflammatory factors of longâ€term expanded human hepatocytes exacerbate their elimination by macrophages during liver engraftment. Hepatology, 2022, 76, 1690-1705.	7.3	11
103	High-resolution RNA allelotyping along the inactive X chromosome: evidence of RNA polymerase III in regulating chromatin configuration. Scientific Reports, 2017, 7, 45460.	3.3	10
104	Disruption of disulfide-restriction at integrin knees induces activation and ligand-independent signaling of Î±4Î²7. Journal of Cell Science, 2013, 126, 5030-41.	2.0	8
105	Mediators and dynamics of DNA methylation. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 281-298.	6.6	7
106	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.	2.5	5
107	A new approach to decode DNA methylome and genomic variants simultaneously from double strand bisulfite sequencing. Briefings in Bioinformatics, 2021, 22, .	6.5	5
108	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.	6.0	3

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109	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. Molecular Cancer Research, 2021, 19, 451-464.	3.4	3
110	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2013, 5, 59.	11.0	3
111	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. IScience, 2021, 24, 103149.	4.1	2
112	Gel-seq: A Method for Simultaneous Sequencing Library Preparation of DNA and RNA Using Hydrogel Matrices. Journal of Visualized Experiments, 2018, , .	0.3	1
113	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. Methods in Molecular Biology, 2018, 1708, 365-382.	0.9	1
114	Reply to â€˜DNA methylation haplotypes as cancer markersâ€™. Nature Genetics, 2018, 50, 1063-1066.	21.4	1
115	Genome-wide mapping of the sixth base. Genome Biology, 2011, 12, 116.	9.6	0
116	DNA Methylation Identifies Genetically and Prognostically Distinct Subtypes of MDS. Blood, 2018, 132, 106-106.	1.4	0