

# Kun Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

101  
papers

4,885  
citations

218677

26  
h-index

118850

62  
g-index

105  
all docs

105  
docs citations

105  
times ranked

9583  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	17.5	762
2	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 2019, 37, 1452-1457.	17.5	550
3	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
4	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
5	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. Nature Communications, 2020, 11, 3475.	12.8	341
6	Whole-Genome Sequencing Analysis Reveals High Specificity of CRISPR/Cas9 and TALEN-Based Genome Editing in Human iPSCs. Cell Stem Cell, 2014, 15, 12-13.	11.1	315
7	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
8	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. Nature Methods, 2009, 6, 613-618.	19.0	149
9	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
10	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. Nature Communications, 2014, 5, 4330.	12.8	102
11	Direct mining of discriminative and essential frequent patterns via model-based search tree. , 2008, , .		83
12	A positive role of c-Myc in regulating androgen receptor and its splice variants in prostate cancer. Oncogene, 2019, 38, 4977-4989.	5.9	80
13	Tools for the analysis of high-dimensional single-cell RNA sequencing data. Nature Reviews Nephrology, 2020, 16, 408-421.	9.6	80
14	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	10.3	67
15	RS-Forest: A Rapid Density Estimator for Streaming Anomaly Detection. , 2014, 2014, 600-609.		61
16	The Sequence Structures of Human MicroRNA Molecules and Their Implications. PLoS ONE, 2013, 8, e54215.	2.5	56
17	Forecasting skewed biased stochastic ozone days: analyses, solutions and beyond. Knowledge and Information Systems, 2008, 14, 299-326.	3.2	55
18	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. Genome Biology, 2016, 17, 20.	8.8	55

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19	SPIN1 promotes tumorigenesis by blocking the uL18 (universal large ribosomal subunit protein) Tj ETQq1 1 0.784314 rgBT /Overlock 10	6.0	53
20	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. Journal of Genetics and Genomics, 2016, 43, 587-592.	3.9	52
21	The Homeobox Transcription Factor RHOX10 Drives Mouse Spermatogonial Stem Cell Establishment. Cell Reports, 2016, 17, 149-164.	6.4	50
22	New Noncoding Lytic Transcripts Derived from the Epstein-Barr Virus Latency Origin of Replication, <i>oriP</i> , Are Hyperedited, Bind the Paraspeckle Protein, NONO/p54nrb, and Support Viral Lytic Transcription. Journal of Virology, 2015, 89, 7120-7132.	3.4	46
23	Alu distribution and mutation types of cancer genes. BMC Genomics, 2011, 12, 157.	2.8	39
24	miRNA-mRNA Correlation-Network Modules in Human Prostate Cancer and the Differences between Primary and Metastatic Tumor Subtypes. PLoS ONE, 2012, 7, e40130.	2.5	38
25	Racial disparities in patient survival and tumor mutation burden, and the association between tumor mutation burden and cancer incidence rate. Scientific Reports, 2017, 7, 13639.	3.3	37
26	Assessing characteristics of RNA amplification methods for single cell RNA sequencing. BMC Genomics, 2016, 17, 966.	2.8	34
27	Hyperinsulinemia enhances interleukin-17-induced inflammation to promote prostate cancer development in obese mice through inhibiting glycogen synthase kinase 3-mediated phosphorylation and degradation of interleukin-17 receptor. Oncotarget, 2016, 7, 13651-13666.	1.8	32
28	Circular RNAs add diversity to androgen receptor isoform repertoire in castration-resistant prostate cancer. Oncogene, 2019, 38, 7060-7072.	5.9	31
29	Single-cell transcriptomics reveals opposing roles of Shp2 in Myc-driven liver tumor cells and microenvironment. Cell Reports, 2021, 37, 109974.	6.4	26
30	Integrative Genomics and Transcriptomics Analysis Reveals Potential Mechanisms for Favorable Prognosis of Patients with HPV-Positive Head and Neck Carcinomas. Scientific Reports, 2016, 6, 24927.	3.3	25
31	Ensemble Manifold Regularized Multi-Modal Graph Convolutional Network for Cognitive Ability Prediction. IEEE Transactions on Biomedical Engineering, 2021, 68, 3564-3573.	4.2	20
32	Iterative sampling based frequent itemset mining for big data. International Journal of Machine Learning and Cybernetics, 2015, 6, 875-882.	3.6	19
33	A machine learning framework for predicting drug-drug interactions. Scientific Reports, 2021, 11, 17619.	3.3	19
34	Increased transcription and high translation efficiency lead to accumulation of androgen receptor splice variant after androgen deprivation therapy. Cancer Letters, 2021, 504, 37-48.	7.2	17
35	LncEGFL7OS regulates human angiogenesis by interacting with MAX at the EGFL7/miR-126 locus. ELife, 2019, 8, .	6.0	17
36	Classifying Imbalanced Data Streams via Dynamic Feature Group Weighting with Importance Sampling. , 2014, 2014, 722-730.		16

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37	Significant Prognostic Features and Patterns of Somatic <i>TP53</i> Mutations in Human Cancers. <i>Cancer Informatics</i> , 2017, 16, 117693511769126.	1.9	16
38	Characterization of Genome-Methylome Interactions in 22 Nuclear Pedigrees. <i>PLoS ONE</i> , 2014, 9, e99313.	2.5	15
39	miRNA-Mediated Relationships between Cis-SNP Genotypes and Transcript Intensities in Lymphocyte Cell Lines. <i>PLoS ONE</i> , 2012, 7, e31429.	2.5	15
40	A Multi-Label Learning Framework for Drug Repurposing. <i>Pharmaceutics</i> , 2019, 11, 466.	4.5	14
41	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. <i>Genome Research</i> , 2020, 30, 602-610.	5.5	14
42	PD-L1 instead of PD-1 status is associated with the clinical features in human primary prostate tumors. <i>American Journal of Clinical and Experimental Urology</i> , 2019, 7, 159-169.	0.4	13
43	A single-cell regulatory map of postnatal lung alveologenesis in humans and mice. <i>Cell Genomics</i> , 2022, 2, 100108.	6.5	13
44	svdPPCS: an effective singular value decomposition-based method for conserved and divergent co-expression gene module identification. <i>BMC Bioinformatics</i> , 2010, 11, 338.	2.6	12
45	In silico unravelling pathogen-host signaling cross-talks via pathogen mimicry and human protein-protein interaction networks. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 100-113.	4.1	12
46	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on <i>M. tuberculosis</i> . <i>BMC Genomics</i> , 2018, 19, 505.	2.8	11
47	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. <i>IScience</i> , 2019, 20, 402-414.	4.1	11
48	System network analysis of genomics and transcriptomics data identified type 1 diabetes-associated pathway and genes. <i>Genes and Immunity</i> , 2019, 20, 500-508.	4.1	11
49	Mutant TP53 disrupts age-related accumulation patterns of somatic mutations in multiple cancer types. <i>Cancer Genetics</i> , 2016, 209, 376-380.	0.4	10
50	An Integrated Approach for RNA-seq Data Normalization. <i>Cancer Informatics</i> , 2016, 15, CIN.S39781.	1.9	10
51	High-resolution RNA allelotyping along the inactive X chromosome: evidence of RNA polymerase III in regulating chromatin configuration. <i>Scientific Reports</i> , 2017, 7, 45460.	3.3	10
52	Computational discovery of Epstein-Barr virus targeted human genes and signalling pathways. <i>Scientific Reports</i> , 2016, 6, 30612.	3.3	9
53	SEER and Gene Expression Data Analysis Deciphers Racial Disparity Patterns in Prostate Cancer Mortality and the Public Health Implication. <i>Scientific Reports</i> , 2020, 10, 6820.	3.3	8
54	Insufficient Lycopene Intake Is Associated With High Risk of Prostate Cancer: A Cross-Sectional Study From the National Health and Nutrition Examination Survey (2003-2010). <i>Frontiers in Public Health</i> , 2021, 9, 792572.	2.7	8

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55	A computational framework for distinguishing direct<i></i>versus</i>indirect interactions in human functional proteinâ€“protein interaction networks. Integrative Biology (United Kingdom), 2017, 9, 595-606.	1.3	7
56	Breaking the computational barrier: a divide-conquer and aggregate based approach for Alu insertion site characterisation. International Journal of Computational Biology and Drug Design, 2009, 2, 302.	0.3	6
57	Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data. BMC Genomics, 2013, 14, 584.	2.8	6
58	CSTG: An Effective Framework for Cost-sensitive Sparse Online Learning. , 2017, 2017, 759-767.		6
59	Driver gene mutations based clustering of tumors: methods and applications. Bioinformatics, 2018, 34, i404-i411.	4.1	6
60	Neglog: Homology-Based Negative Data Sampling Method for Genome-Scale Reconstruction of Human Proteinâ€“Protein Interaction Networks. International Journal of Molecular Sciences, 2019, 20, 5075.	4.1	6
61	Acquisition of Letrozole Resistance Through Activation of the p38/MAPK Signaling Cascade. Anticancer Research, 2021, 41, 583-599.	1.1	6
62	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	3.4	5
63	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
64	Adaptive robust local online density estimation for streaming data. International Journal of Machine Learning and Cybernetics, 2021, 12, 1803-1824.	3.6	5
65	Th17 cells promote tumor growth in an immunocompetent orthotopic mouse model of prostate cancer. American Journal of Clinical and Experimental Urology, 2019, 7, 249-261.	0.4	5
66	Brain Functional Connectivity Analysis via Graphical Deep Learning. IEEE Transactions on Biomedical Engineering, 2022, 69, 1696-1706.	4.2	5
67	Inferring Polymorphism-Induced Regulatory Gene Networks Active in Human Lymphocyte Cell Lines by Weighted Linear Mixed Model Analysis of Multiple RNA-Seq Datasets. PLoS ONE, 2013, 8, e78868.	2.5	4
68	Stratifying tissue heterogeneity with scalable single-cell assays. Nature Methods, 2017, 14, 238-239.	19.0	4
69	Online Density Estimation over Streaming Data: A Local Adaptive Solution. , 2018, , .		4
70	Robust RNA-seq data analysis using an integrated method of ROC curve and Kolmogorovâ€“Smirnov test. Communications in Statistics Part B: Simulation and Computation, 2022, 51, 7444-7457.	1.2	4
71	Quantitative Proteomic Profiling Identifies a Potential Novel Chaperone Marker in Resistant Breast Cancer. Frontiers in Oncology, 2021, 11, 540134.	2.8	4
72	Comprehensive Analysis of Multiple Cohort Datasets Deciphers the Utility of Germline Single-Nucleotide Polymorphisms in Prostate Cancer Diagnosis. Cancer Prevention Research, 2021, 14, 741-752.	1.5	4

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73	Somatic Mutations Favorable to Patient Survival Are Predominant in Ovarian Carcinomas. <i>PLoS ONE</i> , 2014, 9, e112561.	2.5	3
74	The modularity and dynamicity of miRNA-mRNA interactions in high-grade serous ovarian carcinomas and the prognostic implication. <i>Computational Biology and Chemistry</i> , 2016, 63, 3-14.	2.3	3
75	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. <i>Molecular Cancer Research</i> , 2021, 19, 451-464.	3.4	3
76	Deciphering the Increased Prevalence of TP53 Mutations in Metastatic Prostate Cancer. <i>Cancer Informatics</i> , 2022, 21, 117693512210870.	1.9	3
77	A Novel Allosteric Inhibitor Targets PLK1 in Triple Negative Breast Cancer Cells. <i>Biomolecules</i> , 2022, 12, 531.	4.0	3
78	CSRDA: Cost-sensitive Regularized Dual Averaging for Handling Imbalanced and High-dimensional Streaming Data. , 2021, , .		3
79	Multi-label $\ell_1, \ell_2$ -regularized logistic regression for predicting activation/inhibition relationships in human protein-protein interaction networks. <i>Scientific Reports</i> , 2016, 6, 36453.	3.3	2
80	Learning discriminative subregions and pattern orders for facial gender classification. <i>Image and Vision Computing</i> , 2019, 89, 144-157.	4.5	2
81	A deep imputation and inference framework for estimating personalized and race-specific causal effects of genomic alterations on PSA. <i>Journal of Bioinformatics and Computational Biology</i> , 2021, 19, 2150016.	0.8	2
82	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. <i>IScience</i> , 2021, 24, 103149.	4.1	2
83	Fusion Lasso and Its Applications to Cancer Subtype and Stage Prediction. , 2020, , .		2
84	Driver gene detection through Bayesian network integration of mutation and expression profiles. <i>Bioinformatics</i> , 2022, 38, 2781-2790.	4.1	2
85	Deciphering the Polygenic Basis of Racial Disparities in Prostate Cancer By an Integrative Analysis of Genomic and Transcriptomic Data. <i>Cancer Prevention Research</i> , 2021, , .	1.5	2
86	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. <i>Methods in Molecular Biology</i> , 2018, 1708, 365-382.	0.9	1
87	Reply to "DNA methylation haplotypes as cancer markers". <i>Nature Genetics</i> , 2018, 50, 1063-1066.	21.4	1
88	Inferring Personalized and Race-Specific Causal Effects of Genomic Aberrations on Gleason Scores: A Deep Latent Variable Model. <i>Frontiers in Oncology</i> , 2020, 10, 272.	2.8	1
89	Effective Cancer Subtype and Stage Prediction via Dropfeature-DNNs. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 107-120.	3.0	1
90	Seeking the exclusive binding region of phenylalkylamine derivatives on human T-type calcium channels via homology modeling and molecular dynamics simulation approach. <i>Pharmacology Research and Perspectives</i> , 2021, 9, e00783.	2.4	1

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91	Bagging. , 2009, , 206-210.		1
92	A Simple Ensemble Learning Knowledge Distillation. Frontiers in Artificial Intelligence and Applications, 2020, , .	0.3	1
93	Genetic alterations of interleukin-17 and related genes in human prostate cancer. American Journal of Clinical and Experimental Urology, 2019, 7, 352-377.	0.4	1
94	Efficient and fast identification of differentially methylated regions using whole-genome bisulfite sequencing data. Journal of Genetics and Genomics, 2018, 45, 455-457.	3.9	0
95	A Computational Framework for Predicting Direct Contacts and Substructures within Protein Complexes. Biomolecules, 2019, 9, 656.	4.0	0
96	Gene expression analysis reveals a pitfall in the molecular research of prostate tumors relevant to Gleason score. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050032.	0.8	0
97	Cytosine Methylation Patterns As Biomarkers in MDS. Blood, 2015, 126, 5226-5226.	1.4	0
98	Bagging. , 2016, , 1-5.		0
99	Methylation Profiling Among Patients with TET2 Mutations in Myelodysplastic Syndromes Is Associated with Overall Survival. Blood, 2016, 128, 3158-3158.	1.4	0
100	Bagging. , 2018, , 258-263.		0
101	Genome and transcriptome profiling of family in human prostate cancer. American Journal of Clinical and Experimental Urology, 2020, 8, 116-128.	0.4	0