Kun Zhang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3312909/publications.pdf

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	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
2	Effective Cancer Subtype and Stage Prediction via Dropfeature-DNNs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 107-120.	3.0	1
3	Brain Functional Connectivity Analysis via Graphical Deep Learning. IEEE Transactions on Biomedical Engineering, 2022, 69, 1696-1706.	4.2	5
4	Deciphering the Increased Prevalence of TP53 Mutations in Metastatic Prostate Cancer. Cancer Informatics, 2022, 21, 117693512210870.	1.9	3
5	A Novel Allosteric Inhibitor Targets PLK1 in Triple Negative Breast Cancer Cells. Biomolecules, 2022, 12, 531.	4.0	3
6	A single-cell regulatory map of postnatal lung alveologenesis in humans and mice. Cell Genomics, 2022, 2, 100108.	6.5	13
7	Driver gene detection through Bayesian network integration of mutation and expression profiles. Bioinformatics, 2022, 38, 2781-2790.	4.1	2
8	A reference tissue atlas for the human kidney. Science Advances, 2022, 8, .	10.3	67
9	5-Azacytidine Transiently Restores Dysregulated Erythroid Differentiation Gene Expression in TET2-Deficient Erythroleukemia Cells. Molecular Cancer Research, 2021, 19, 451-464.	3.4	3
10	Acquisition of Letrozole Resistance Through Activation of the p38/MAPK Signaling Cascade. Anticancer Research, 2021, 41, 583-599.	1.1	6
11	Adaptive robust local online density estimation for streaming data. International Journal of Machine Learning and Cybernetics, 2021, 12, 1803-1824.	3.6	5
12	Quantitative Proteomic Profiling Identifies a Potential Novel Chaperone Marker in Resistant Breast Cancer. Frontiers in Oncology, 2021, 11, 540134.	2.8	4
13	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
14	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
15	Seeking the exclusive binding region of phenylalkylamine derivatives on human Tâ€type calcium channels via homology modeling and molecular dynamics simulation approach. Pharmacology Research and Perspectives, 2021, 9, e00783.	2.4	1
16	A deep imputation and inference framework for estimating personalized and race-specific causal effects of genomic alterations on PSA. Journal of Bioinformatics and Computational Biology, 2021, 19, 2150016.	0.8	2
17	A machine learning framework for predicting drugâ€“drug interactions. Scientific Reports, 2021, 11, 17619.	3.3	19
18	Charting oncogenicity of genes and variants across lineages via multiplexed screens in teratomas. IScience, 2021, 24, 103149.	4.1	2

#	Article	IF	Citations
19	Ensemble Manifold Regularized Multi-Modal Graph Convolutional Network for Cognitive Ability Prediction. IEEE Transactions on Biomedical Engineering, 2021, 68, 3564-3573.	4.2	20
20	Single-cell transcriptomics reveals opposing roles of Shp2 in Myc-driven liver tumor cells and microenvironment. Cell Reports, 2021, 37, 109974.	6.4	26
21	Deciphering the Polygenic Basis of Racial Disparities in Prostate Cancer By an Integrative Analysis of Genomic and Transcriptomic Data. Cancer Prevention Research, 2021, , .	1.5	2
22	Insufficient Lycopene Intake Is Associated With High Risk of Prostate Cancer: A Cross-Sectional Study From the National Health and Nutrition Examination Survey (2003â€“2010). Frontiers in Public Health, 2021, 9, 792572.	2.7	8
23	CSRDA: Cost-sensitive Regularized Dual Averaging for Handling Imbalanced and High-dimensional Streaming Data. , 2021, , .		3
24	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
25	Non-invasive early detection of cancer four years before conventional diagnosis using a blood test. Nature Communications, 2020, 11, 3475.	12.8	341
26	RETrace: simultaneous retrospective lineage tracing and methylation profiling of single cells. Genome Research, 2020, 30, 602-610.	5.5	14
27	Tools for the analysis of high-dimensional single-cell RNA sequencing data. Nature Reviews Nephrology, 2020, 16, 408-421.	9.6	80
28	In silico unravelling pathogen-host signaling cross-talks via pathogen mimicry and human protein-protein interaction networks. Computational and Structural Biotechnology Journal, 2020, 18, 100-113.	4.1	12
29	SEER and Gene Expression Data Analysis Deciphers Racial Disparity Patterns in Prostate Cancer Mortality and the Public Health Implication. Scientific Reports, 2020, 10, 6820.	3.3	8
30	Inferring Personalized and Race-Specific Causal Effects of Genomic Aberrations on Gleason Scores: A Deep Latent Variable Model. Frontiers in Oncology, 2020, 10, 272.	2.8	1
31	Fusion Lasso and Its Applications to Cancer Subtype and Stage Prediction. , 2020, , .		2
32	A Simple Ensemble Learning Knowledge Distillation. Frontiers in Artificial Intelligence and Applications, 2020, , .	0.3	1
33	Genome and transcriptome profiling of family in human prostate cancer. American Journal of Clinical and Experimental Urology, 2020, 8, 116-128.	0.4	0
34	Circular RNAs add diversity to androgen receptor isoform repertoire in castration-resistant prostate cancer. Oncogene, 2019, 38, 7060-7072.	5.9	31
35	Learning discriminative subregions and pattern orders for facial genderÂclassification. Image and Vision Computing, 2019, 89, 144-157.	4.5	2
36	Cellular Recruitment by Podocyte-Derived Pro-migratory Factors in Assembly of the Human Renal Filter. IScience, 2019, 20, 402-414.	4.1	11

#	Article	IF	Citations
37	A Multi-Label Learning Framework for Drug Repurposing. Pharmaceutics, 2019, 11, 466.	4.5	14
38	Identification of a 1p21 independent functional variant for abdominal obesity. International Journal of Obesity, 2019, 43, 2480-2490.	3.4	5
39	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
40	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
41	A Computational Framework for Predicting Direct Contacts and Substructures within Protein Complexes. Biomolecules, 2019, 9, 656.	4.0	0
42	High-throughput sequencing of the transcriptome and chromatin accessibility in the same cell. Nature Biotechnology, 2019, 37, 1452-1457.	17.5	550
43	System network analysis of genomics and transcriptomics data identified type 1 diabetes-associated pathway and genes. Genes and Immunity, 2019, 20, 500-508.	4.1	11
44	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
45	LncEGFL7OS regulates human angiogenesis by interacting with MAX at the EGFL7/miR-126 locus. ELife, 2019, 8, .	6.0	17
46	PD-L1 instead of PD-1 status is associated with the clinical features in human primary prostate tumors. American Journal of Clinical and Experimental Urology, 2019, 7, 159-169.	0.4	13
47	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
48	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
49	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
50	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	17.5	762
51	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. Methods in Molecular Biology, 2018, 1708, 365-382.	0.9	1
52	Online Density Estimation over Streaming Data: A Local Adaptive Solution. , 2018, , .		4
53	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
54	Driver gene mutations based clustering of tumors: methods and applications. Bioinformatics, 2018, 34, i404-i411.	4.1	6

#	Article	IF	Citations
55	SPIN1 promotes tumorigenesis by blocking the uL18 (universal large ribosomal subunit protein) Tj ETQq1 1 0.784314 rgBT /Overlock 10	6.0	53
56	Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on M. tuberculosis. BMC Genomics, 2018, 19, 505.	2.8	11
57	Reply to â€˜DNA methylation haplotypes as cancer markersâ€™. Nature Genetics, 2018, 50, 1063-1066.	21.4	1
58	Bagging. , 2018, , 258-263.		0
59	Stratifying tissue heterogeneity with scalable single-cell assays. Nature Methods, 2017, 14, 238-239.	19.0	4
60	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
61	A computational framework for distinguishing directversusindirect interactions in human functional proteinâ€“protein interaction networks. Integrative Biology (United Kingdom), 2017, 9, 595-606.	1.3	7
62	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
63	Significant Prognostic Features and Patterns of Somatic TP53 Mutations in Human Cancers. Cancer Informatics, 2017, 16, 117693511769126.	1.9	16
64	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
65	CSTG: An Effective Framework for Cost-sensitive Sparse Online Learning. , 2017, 2017, 759-767.		6
66	Assessing characteristics of RNA amplification methods for single cell RNA sequencing. BMC Genomics, 2016, 17, 966.	2.8	34
67	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
68	Computational discovery of Epstein-Barr virus targeted human genes and signalling pathways. Scientific Reports, 2016, 6, 30612.	3.3	9
69	Targeted methylation sequencing reveals dysregulated Wnt signaling in Parkinson disease. Journal of Genetics and Genomics, 2016, 43, 587-592.	3.9	52
70	Characterization of chromatin accessibility with a transposome hypersensitive sites sequencing (THS-seq) assay. Genome Biology, 2016, 17, 20.	8.8	55
71	Mutant TP53 disrupts age-related accumulation patterns of somatic mutations in multiple cancer types. Cancer Genetics, 2016, 209, 376-380.	0.4	10
72	The Homeobox Transcription Factor RHOX10 Drives Mouse Spermatogonial Stem Cell Establishment. Cell Reports, 2016, 17, 149-164.	6.4	50

#	Article	IF	Citations
73	Multi-label â„“2-regularized logistic regression for predicting activation/inhibition relationships in human protein-protein interaction networks. Scientific Reports, 2016, 6, 36453.	3.3	2
74	An Integrated Approach for RNA-seq Data Normalization. Cancer Informatics, 2016, 15, CIN.S39781.	1.9	10
75	The modularity and dynamicity of miRNAâ€“mRNA interactions in high-grade serous ovarian carcinomas and the prognostic implication. Computational Biology and Chemistry, 2016, 63, 3-14.	2.3	3
76	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
77	Bagging. , 2016, , 1-5.		0
78	Methylation Profiling Among Patients with TET2 Mutations in Myelodysplastic Syndromes Is Associated with Overall Survival. Blood, 2016, 128, 3158-3158.	1.4	0
79	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
80	New Noncoding Lytic Transcripts Derived from the Epstein-Barr Virus Latency Origin of Replication, oriP , Are Hyperedited, Bind the Paraspeckle Protein, NONO/p54nrb, and Support Viral Lytic Transcription. Journal of Virology, 2015, 89, 7120-7132.	3.4	46
81	Iterative sampling based frequent itemset mining for big data. International Journal of Machine Learning and Cybernetics, 2015, 6, 875-882.	3.6	19
82	Cytosine Methylation Patterns As Biomarkers in MDS. Blood, 2015, 126, 5226-5226.	1.4	0
83	Characterization of Genome-Methylome Interactions in 22 Nuclear Pedigrees. PLoS ONE, 2014, 9, e99313.	2.5	15
84	Somatic Mutations Favorable to Patient Survival Are Predominant in Ovarian Carcinomas. PLoS ONE, 2014, 9, e112561.	2.5	3
85	RS-Forest: A Rapid Density Estimator for Streaming Anomaly Detection. , 2014, 2014, 600-609.		61
86	Classifying Imbalanced Data Streams via Dynamic Feature Group Weighting with Importance Sampling. , 2014, 2014, 722-730.		16
87	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
88	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. Nature Communications, 2014, 5, 4330.	12.8	102
89	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
90	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

#	Article	IF	Citations
91	The Sequence Structures of Human MicroRNA Molecules and Their Implications. PLoS ONE, 2013, 8, e54215.	2.5	56
92	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
93	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
94	miRNA-Mediated Relationships between Cis-SNP Genotypes and Transcript Intensities in Lymphocyte Cell Lines. PLoS ONE, 2012, 7, e31429.	2.5	15
95	Alu distribution and mutation types of cancer genes. BMC Genomics, 2011, 12, 157.	2.8	39
96	svdPPCS: an effective singular value decomposition-based method for conserved and divergent co-expression gene module identification. BMC Bioinformatics, 2010, 11, 338.	2.6	12
97	Digital RNA allelotyping reveals tissue-specific and allele-specific gene expression in human. Nature Methods, 2009, 6, 613-618.	19.0	149
98	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
99	Bagging. , 2009, , 206-210.		1
100	Forecasting skewed biased stochastic ozone days: analyses, solutions and beyond. Knowledge and Information Systems, 2008, 14, 299-326.	3.2	55
101	Direct mining of discriminative and essential frequent patterns via model-based search tree. , 2008, , .		83