

# Zemin Zhang

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

29,329  
citations

46984

47  
h-index

91828

69  
g-index

75  
all docs

75  
docs citations

75  
times ranked

37571  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell RNA sequencing reveals intrahepatic and peripheral immune characteristics related to disease phases in HBV-infected patients. <i>Gut</i> , 2023, 72, 153-167.	6.1	42
2	An Asia-specific variant of human IgG1 represses colorectal tumorigenesis by shaping the tumor microenvironment. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	14
3	Temporal single-cell tracing reveals clonal revival and expansion of precursor exhausted T cells during anti-PD-1 therapy in lung cancer. <i>Nature Cancer</i> , 2022, 3, 108-121.	5.7	150
4	Immune phenotypic linkage between colorectal cancer and liver metastasis. <i>Cancer Cell</i> , 2022, 40, 424-437.e5.	7.7	129
5	Tumour heterogeneity and intercellular networks of nasopharyngeal carcinoma at single cell resolution. <i>Nature Communications</i> , 2021, 12, 741.	5.8	104
6	A pan-cancer single-cell transcriptional atlas of tumor infiltrating myeloid cells. <i>Cell</i> , 2021, 184, 792-809.e23.	13.5	563
7	iMAP: integration of multiple single-cell datasets by adversarial paired transfer networks. <i>Genome Biology</i> , 2021, 22, 63.	3.8	26
8	Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 253-266.	3.0	167
9	Insights Gained from Single-Cell Analysis of Immune Cells in the Tumor Microenvironment. <i>Annual Review of Immunology</i> , 2021, 39, 583-609.	9.5	153
10	STARTRAC analyses of scRNAseq data from tumor models reveal T cell dynamics and therapeutic targets. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	15
11	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19.	13.5	512
12	Single-cell analyses reveal key immune cell subsets associated with response to PD-L1 blockade in triple-negative breast cancer. <i>Cancer Cell</i> , 2021, 39, 1578-1593.e8.	7.7	275
13	Resolving the intertwining of inflammation and fibrosis in human heart failure at single-cell level. <i>Basic Research in Cardiology</i> , 2021, 116, 55.	2.5	87
14	Pan-cancer single-cell landscape of tumor-infiltrating T cells. <i>Science</i> , 2021, 374, abe6474.	6.0	460
15	Distinct epigenetic features of tumor-reactive CD8+ T cells in colorectal cancer patients revealed by genome-wide DNA methylation analysis. <i>Genome Biology</i> , 2020, 21, 2.	3.8	77
16	Landscape of transcript isoforms in single T cells infiltrating in non-small-cell lung cancer. <i>Journal of Genetics and Genomics</i> , 2020, 47, 373-388.	1.7	10
17	Reconstruction of cell spatial organization from single-cell RNA sequencing data based on ligand-receptor mediated self-assembly. <i>Cell Research</i> , 2020, 30, 763-778.	5.7	92
18	An entropy-based metric for assessing the purity of single cell populations. <i>Nature Communications</i> , 2020, 11, 3155.	5.8	83

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19	Stepwise immune alterations in multiple myeloma progression. <i>Nature Cancer</i> , 2020, 1, 477-479.	5.7	1
20	Dynamics of peripheral T cell clones during PD-1 blockade in non-small cell lung cancer. <i>Cancer Immunology, Immunotherapy</i> , 2020, 69, 2599-2611.	2.0	21
21	The history and advances in cancer immunotherapy: understanding the characteristics of tumor-infiltrating immune cells and their therapeutic implications. <i>Cellular and Molecular Immunology</i> , 2020, 17, 807-821.	4.8	1,136
22	Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. <i>Cell</i> , 2020, 181, 442-459.e29.	13.5	741
23	SciBet as a portable and fast single cell type identifier. <i>Nature Communications</i> , 2020, 11, 1818.	5.8	90
24	Deep single-cell RNA sequencing data of individual T cells from treatment-naïve colorectal cancer patients. <i>Scientific Data</i> , 2019, 6, 131.	2.4	49
25	LILRB1 Blockade Enhances Bispecific T Cell Engager Antibody-Induced Tumor Cell Killing by Effector CD8+ T Cells. <i>Journal of Immunology</i> , 2019, 203, 1076-1087.	0.4	35
26	Recharacterizing Tumor-Infiltrating Lymphocytes by Single-Cell RNA Sequencing. <i>Cancer Immunology Research</i> , 2019, 7, 1040-1046.	1.6	57
27	Identification of transcriptional isoforms associated with survival in cancer patient. <i>Journal of Genetics and Genomics</i> , 2019, 46, 413-421.	1.7	3
28	Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 829-845.e20.	13.5	897
29	Understanding tumor-infiltrating lymphocytes by single cell RNA sequencing. <i>Advances in Immunology</i> , 2019, 144, 217-245.	1.1	21
30	GEPIA2: an enhanced web server for large-scale expression profiling and interactive analysis. <i>Nucleic Acids Research</i> , 2019, 47, W556-W560.	6.5	2,458
31	Systematic comparative analysis of single-nucleotide variant detection methods from single-cell RNA sequencing data. <i>Genome Biology</i> , 2019, 20, 242.	3.8	80
32	Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. <i>Nature Medicine</i> , 2018, 24, 978-985.	15.2	1,044
33	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. <i>Nature</i> , 2018, 564, 268-272.	13.7	742
34	GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. <i>Nucleic Acids Research</i> , 2017, 45, W98-W102.	6.5	7,114
35	Landscape of Infiltrating T Cells in Liver Cancer Revealed by Single-Cell Sequencing. <i>Cell</i> , 2017, 169, 1342-1356.e16.	13.5	1,540
36	Adenylate kinase hCINAP determines self-renewal of colorectal cancer stem cells by facilitating LDHA phosphorylation. <i>Nature Communications</i> , 2017, 8, 15308.	5.8	52

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37	Understanding the Genetic Mechanisms of Cancer Drug Resistance Using Genomic Approaches. Trends in Genetics, 2016, 32, 127-137.	2.9	69
38	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	9.4	556
39	Diverse modes of genomic alteration in hepatocellular carcinoma. Genome Biology, 2014, 15, 436.	3.8	100
40	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. Nature Communications, 2014, 5, 3830.	5.8	77
41	MBASED: allele-specific expression detection in cancer tissues and cell lines. Genome Biology, 2014, 15, 405.	3.8	112
42	An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. Genes and Development, 2014, 28, 1068-1084.	2.7	95
43	Integrative analysis of two cell lines derived from a non-small-lung cancer patient—a panomics approach. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2014, , 75-86.	0.7	4
44	Assessment of computational methods for predicting the effects of missense mutations in human cancers. BMC Genomics, 2013, 14, S7.	1.2	153
45	Large-scale integrative network-based analysis identifies common pathways disrupted by copy number alterations across cancers. BMC Genomics, 2013, 14, 440.	1.2	21
46	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. Genome Research, 2012, 22, 2315-2327.	2.4	177
47	Recurrent R-spondin fusions in colon cancer. Nature, 2012, 488, 660-664.	13.7	862
48	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. Genome Research, 2012, 22, 593-601.	2.4	257
49	Genomic landscape of liver cancer. Nature Genetics, 2012, 44, 1075-1077.	9.4	41
50	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. Nature Genetics, 2012, 44, 1111-1116.	9.4	906
51	Inferring the functional effects of mutation through clusters of mutations in homologous proteins. Human Mutation, 2010, 31, 264-271.	1.1	48
52	The mutation spectrum revealed by paired genome sequences from a lung cancer patient. Nature, 2010, 465, 473-477.	13.7	453
53	Diverse somatic mutation patterns and pathway alterations in human cancers. Nature, 2010, 466, 869-873.	13.7	1,189
54	Computational prediction of the functional effects of amino acid substitutions in signal peptides using a model-based approach. Human Mutation, 2009, 30, 99-106.	1.1	20

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55	Analytical methods for inferring functional effects of single base pair substitutions in human cancers. <i>Human Genetics</i> , 2009, 126, 481-498.	1.8	19
56	Signal peptide prediction based on analysis of experimentally verified cleavage sites. <i>Protein Science</i> , 2009, 13, 2819-2824.	3.1	100
57	Bi-Directional SIFT Predicts a Subset of Activating Mutations. <i>PLoS ONE</i> , 2009, 4, e8311.	1.1	33
58	CanPredict: a computational tool for predicting cancer-associated missense mutations. <i>Nucleic Acids Research</i> , 2007, 35, W595-W598.	6.5	125
59	Distinguishing Cancer-Associated Missense Mutations from Common Polymorphisms. <i>Cancer Research</i> , 2007, 67, 465-473.	0.4	108
60	The Genomic Landscapes of Human Breast and Colorectal Cancers. <i>Science</i> , 2007, 318, 1108-1113.	6.0	3,049
61	Maternal Embryonic Leucine Zipper Kinase/Murine Protein Serine-Threonine Kinase 38 Is a Promising Therapeutic Target for Multiple Cancers. <i>Cancer Research</i> , 2005, 65, 9751-9761.	0.4	159
62	Bioinformatics and cancer target discovery. <i>Drug Discovery Today</i> , 2004, 9, 795-802.	3.2	42
63	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment. <i>Genome Research</i> , 2003, 13, 2265-2270.	2.4	305
64	A profile hidden Markov model for signal peptides generated by HMMER. <i>Bioinformatics</i> , 2003, 19, 307-308.	1.8	85
65	Mouse Endocrine Gland-Derived Vascular Endothelial Growth Factor: A Distinct Expression Pattern from Its Human Ortholog Suggests Different Roles as a Regulator of Organ-Specific Angiogenesis. <i>Endocrinology</i> , 2003, 144, 2606-2616.	1.4	45
66	Genome-wide identification of chromosomal regions of increased tumor expression by transcriptome analysis. <i>Cancer Research</i> , 2003, 63, 5781-4.	0.4	48
67	Identification of an angiogenic mitogen selective for endocrine gland endothelium. <i>Nature</i> , 2001, 412, 877-884.	13.7	519
68	Interleukin (IL)-22, a Novel Human Cytokine That Signals through the Interferon Receptor-related Proteins CRF2 $\alpha$ 4 and IL-22R. <i>Journal of Biological Chemistry</i> , 2000, 275, 31335-31339.	1.6	469
69	Cleavage and Identification of Proteins: A Modified Aspartyl-Prolyl Cleavage. <i>Analytical Chemistry</i> , 2000, 72, 5431-5436.	3.2	10