Zemin Zhang

List of Publications by Year
in descending order

69	29,329	47006	91884
papers	citations	47	69
		h-index	g-index

75	75	75	37571
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	GEPIA: a web server for cancer and normal gene expression profiling and interactive analyses. Nucleic Acids Research, 2017, 45, W98-W102.	14.5	7,114
2	The Genomic Landscapes of Human Breast and Colorectal Cancers. Science, 2007, 318, 1108-1113.	12.6	3,049
3	GEPIA2: an enhanced web server for large-scale expression profiling and interactive analysis. Nucleic Acids Research, 2019, 47, W556-W560.	14.5	2,458
4	Landscape of Infiltrating T Cells in Liver Cancer Revealed by Single-Cell Sequencing. Cell, 2017, 169, 1342-1356.e16.	28.9	1,540
5	Diverse somatic mutation patterns and pathway alterations in human cancers. Nature, 2010, 466, 869-873.	27.8	1,189
6	The history and advances in cancer immunotherapy: understanding the characteristics of tumor-infiltrating immune cells and their therapeutic implications. Cellular and Molecular Immunology, 2020, 17, 807-821.	10.5	1,136
7	Global characterization of T cells in non-small-cell lung cancer by single-cell sequencing. Nature Medicine, 2018, 24, 978-985.	30.7	1,044
8	Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. Nature Genetics, 2012, 44, 1111-1116.	21.4	906
9	Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. Cell, 2019, 179, 829-845.e20.	28.9	897
10	Recurrent R-spondin fusions in colon cancer. Nature, 2012, 488, 660-664.	27.8	862
11	Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. Nature, 2018, 564, 268-272.	27.8	742
12	Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. Cell, 2020, 181, 442-459.e29.	28.9	741
13	A pan-cancer single-cell transcriptional atlas of tumor infiltrating myeloid cells. Cell, 2021, 184, 792-809.e23.	28.9	563
14	A comprehensive transcriptional portrait of human cancer cell lines. Nature Biotechnology, 2015, 33, 306-312.	17.5	556
15	Identification of an angiogenic mitogen selective for endocrine gland endothelium. Nature, 2001, 412, 877-884.	27.8	519
16	COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. Cell, 2021, 184, 1895-1913.e19.	28.9	512
17	Interleukin (IL)-22, a Novel Human Cytokine That Signals through the Interferon Receptor-related Proteins CRF2â€"4 and IL-22R. Journal of Biological Chemistry, 2000, 275, 31335-31339.	3.4	469
18	Pan-cancer single-cell landscape of tumor-infiltrating T cells. Science, 2021, 374, abe6474.	12.6	460

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19	The mutation spectrum revealed by paired genome sequences from a lung cancer patient. Nature, 2010, 465, 473-477.	27.8	453
20	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment. Genome Research, 2003, 13, 2265-2270.	5.5	305
21	Single-cell analyses reveal key immune cell subsets associated with response to PD-L1 blockade in triple-negative breast cancer. Cancer Cell, 2021, 39, 1578-1593.e8.	16.8	275
22	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. Genome Research, 2012, 22, 593-601.	5.5	257
23	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. Genome Research, 2012, 22, 2315-2327.	5.5	177
24	Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. Genomics, Proteomics and Bioinformatics, 2021, 19, 253-266.	6.9	167
25	Maternal Embryonic Leucine Zipper Kinase/Murine Protein Serine-Threonine Kinase 38 Is a Promising Therapeutic Target for Multiple Cancers. Cancer Research, 2005, 65, 9751-9761.	0.9	159
26	Assessment of computational methods for predicting the effects of missense mutations in human cancers. BMC Genomics, 2013, 14, S7.	2.8	153
27	Insights Gained from Single-Cell Analysis of Immune Cells in the Tumor Microenvironment. Annual Review of Immunology, 2021, 39, 583-609.	21.8	153
28	Temporal single-cell tracing reveals clonal revival and expansion of precursor exhausted T cells during anti-PD-1 therapy in lung cancer. Nature Cancer, 2022, 3, 108-121.	13.2	150
29	Immune phenotypic linkage between colorectal cancer and liver metastasis. Cancer Cell, 2022, 40, 424-437.e5.	16.8	129
30	CanPredict: a computational tool for predicting cancer-associated missense mutations. Nucleic Acids Research, 2007, 35, W595-W598.	14.5	125
31	MBASED: allele-specific expression detection in cancer tissues and cell lines. Genome Biology, 2014, 15, 405.	8.8	112
32	Distinguishing Cancer-Associated Missense Mutations from Common Polymorphisms. Cancer Research, 2007, 67, 465-473.	0.9	108
33	Tumour heterogeneity and intercellular networks of nasopharyngeal carcinoma at single cell resolution. Nature Communications, 2021, 12, 741.	12.8	104
34	Signal peptide prediction based on analysis of experimentally verified cleavage sites. Protein Science, 2009, 13, 2819-2824.	7.6	100
35	Diverse modes of genomic alteration in hepatocellular carcinoma. Genome Biology, 2014, 15, 436.	8.8	100
36	An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. Genes and Development, 2014, 28, 1068-1084.	5.9	95

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37	Reconstruction of cell spatial organization from single-cell RNA sequencing data based on ligand-receptor mediated self-assembly. Cell Research, 2020, 30, 763-778.	12.0	92
38	SciBet as a portable and fast single cell type identifier. Nature Communications, 2020, 11, 1818.	12.8	90
39	Resolving the intertwining of inflammation and fibrosis in human heart failure at single-cell level. Basic Research in Cardiology, 2021, 116, 55.	5.9	87
40	A profile hidden Markov model for signal peptides generated by HMMER. Bioinformatics, 2003, 19, 307-308.	4.1	85
41	An entropy-based metric for assessing the purity of single cell populations. Nature Communications, 2020, 11, 3155.	12.8	83
42	Systematic comparative analysis of single-nucleotide variant detection methods from single-cell RNA sequencing data. Genome Biology, 2019, 20, 242.	8.8	80
43	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. Nature Communications, 2014, 5, 3830.	12.8	77
44	Distinct epigenetic features of tumor-reactive CD8+ T cells in colorectal cancer patients revealed by genome-wide DNA methylation analysis. Genome Biology, 2020, 21, 2.	8.8	77
45	Understanding the Genetic Mechanisms of Cancer Drug Resistance Using Genomic Approaches. Trends in Genetics, 2016, 32, 127-137.	6.7	69
46	Recharacterizing Tumor-Infiltrating Lymphocytes by Single-Cell RNA Sequencing. Cancer Immunology Research, 2019, 7, 1040-1046.	3.4	57
47	Adenylate kinase hCINAP determines self-renewal of colorectal cancer stem cells by facilitating LDHA phosphorylation. Nature Communications, 2017, 8, 15308.	12.8	52
48	Deep single-cell RNA sequencing data of individual T cells from treatment-naïve colorectal cancer patients. Scientific Data, 2019, 6, 131.	5.3	49
49	Inferring the functional effects of mutation through clusters of mutations in homologous proteins. Human Mutation, 2010, 31, 264-271.	2.5	48
50	Genome-wide identification of chromosomal regions of increased tumor expression by transcriptome analysis. Cancer Research, 2003, 63, 5781-4.	0.9	48
51	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. Endocrinology, 2003, 144, 2606-2616.	2.8	45
52	Bioinformatics and cancer target discovery. Drug Discovery Today, 2004, 9, 795-802.	6.4	42
53	Single-cell RNA sequencing reveals intrahepatic and peripheral immune characteristics related to disease phases in HBV-infected patients. Gut, 2023, 72, 153-167.	12.1	42
54	Genomic landscape of liver cancer. Nature Genetics, 2012, 44, 1075-1077.	21.4	41

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55	LILRB1 Blockade Enhances Bispecific T Cell Engager Antibody–Induced Tumor Cell Killing by Effector CD8+ T Cells. Journal of Immunology, 2019, 203, 1076-1087.	0.8	35
56	Bi-Directional SIFT Predicts a Subset of Activating Mutations. PLoS ONE, 2009, 4, e8311.	2.5	33
57	iMAP: integration of multiple single-cell datasets by adversarial paired transfer networks. Genome Biology, 2021, 22, 63.	8.8	26
58	Large-scale integrative network-based analysis identifies common pathways disrupted by copy number alterations across cancers. BMC Genomics, 2013, 14, 440.	2.8	21
59	Understanding tumor-infiltrating lymphocytes by single cell RNA sequencing. Advances in Immunology, 2019, 144, 217-245.	2.2	21
60	Dynamics of peripheral T cell clones during PD-1 blockade in non-small cell lung cancer. Cancer Immunology, Immunotherapy, 2020, 69, 2599-2611.	4.2	21
61	Computational prediction of the functional effects of amino acid substitutions in signal peptides using a model-based approach. Human Mutation, 2009, 30, 99-106.	2.5	20
62	Analytical methods for inferring functional effects of single base pair substitutions in human cancers. Human Genetics, 2009, 126, 481-498.	3.8	19
63	STARTRAC analyses of scRNAseq data from tumor models reveal T cell dynamics and therapeutic targets. Journal of Experimental Medicine, 2021, 218, .	8.5	15
64	An Asia-specific variant of human IgG1 represses colorectal tumorigenesis by shaping the tumor microenvironment. Journal of Clinical Investigation, 2022, 132, .	8.2	14
65	Cleavage and Identification of Proteins: A Modified Aspartyl–Prolyl Cleavage. Analytical Chemistry, 2000, 72, 5431-5436.	6.5	10
66	Landscape of transcript isoforms in single T cells infiltrating in non-small-cell lung cancer. Journal of Genetics and Genomics, 2020, 47, 373-388.	3.9	10
67	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
68	Identification of transcriptional isoforms associated with survival in cancer patient. Journal of Genetics and Genomics, 2019, 46, 413-421.	3.9	3
69	Stepwise immune alterations in multiple myeloma progression. Nature Cancer, 2020, 1, 477-479.	13.2	1