

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 | 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 |
| 2 | The Genomic Landscapes of Human Breast and Colorectal Cancers. <i>Science</i> , 2007, 318, 1108-1113. | 6.0 | 3,049 |
| 3 | 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 |
| 4 | 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 |
| 5 | Diverse somatic mutation patterns and pathway alterations in human cancers. <i>Nature</i> , 2010, 466, 869-873. | 13.7 | 1,189 |
| 6 | 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 |
| 7 | 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 |
| 8 | Comprehensive genomic analysis identifies SOX2 as a frequently amplified gene in small-cell lung cancer. <i>Nature Genetics</i> , 2012, 44, 1111-1116. | 9.4 | 906 |
| 9 | Landscape and Dynamics of Single Immune Cells in Hepatocellular Carcinoma. <i>Cell</i> , 2019, 179, 829-845.e20. | 13.5 | 897 |
| 10 | Recurrent R-spondin fusions in colon cancer. <i>Nature</i> , 2012, 488, 660-664. | 13.7 | 862 |
| 11 | Lineage tracking reveals dynamic relationships of T cells in colorectal cancer. <i>Nature</i> , 2018, 564, 268-272. | 13.7 | 742 |
| 12 | Single-Cell Analyses Inform Mechanisms of Myeloid-Targeted Therapies in Colon Cancer. <i>Cell</i> , 2020, 181, 442-459.e29. | 13.5 | 741 |
| 13 | A pan-cancer single-cell transcriptional atlas of tumor infiltrating myeloid cells. <i>Cell</i> , 2021, 184, 792-809.e23. | 13.5 | 563 |
| 14 | A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015, 33, 306-312. | 9.4 | 556 |
| 15 | Identification of an angiogenic mitogen selective for endocrine gland endothelium. <i>Nature</i> , 2001, 412, 877-884. | 13.7 | 519 |
| 16 | COVID-19 immune features revealed by a large-scale single-cell transcriptome atlas. <i>Cell</i> , 2021, 184, 1895-1913.e19. | 13.5 | 512 |
| 17 | Interleukin (IL)-22, a Novel Human Cytokine That Signals through the Interferon Receptor-related Proteins CRF2 β 4 and IL-22R. <i>Journal of Biological Chemistry</i> , 2000, 275, 31335-31339. | 1.6 | 469 |
| 18 | Pan-cancer single-cell landscape of tumor-infiltrating T cells. <i>Science</i> , 2021, 374, abe6474. | 6.0 | 460 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------|-----------|
| 19 | The mutation spectrum revealed by paired genome sequences from a lung cancer patient. <i>Nature</i> , 2010, 465, 473-477. | 13.7 | 453 |
| 20 | 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 |
| 21 | 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 |
| 22 | The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. <i>Genome Research</i> , 2012, 22, 593-601. | 2.4 | 257 |
| 23 | Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012, 22, 2315-2327. | 2.4 | 177 |
| 24 | Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 253-266. | 3.0 | 167 |
| 25 | 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 |
| 26 | Assessment of computational methods for predicting the effects of missense mutations in human cancers. <i>BMC Genomics</i> , 2013, 14, S7. | 1.2 | 153 |
| 27 | 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 |
| 28 | 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 |
| 29 | Immune phenotypic linkage between colorectal cancer and liver metastasis. <i>Cancer Cell</i> , 2022, 40, 424-437.e5. | 7.7 | 129 |
| 30 | CanPredict: a computational tool for predicting cancer-associated missense mutations. <i>Nucleic Acids Research</i> , 2007, 35, W595-W598. | 6.5 | 125 |
| 31 | MBASED: allele-specific expression detection in cancer tissues and cell lines. <i>Genome Biology</i> , 2014, 15, 405. | 3.8 | 112 |
| 32 | Distinguishing Cancer-Associated Missense Mutations from Common Polymorphisms. <i>Cancer Research</i> , 2007, 67, 465-473. | 0.4 | 108 |
| 33 | Tumour heterogeneity and intercellular networks of nasopharyngeal carcinoma at single cell resolution. <i>Nature Communications</i> , 2021, 12, 741. | 5.8 | 104 |
| 34 | Signal peptide prediction based on analysis of experimentally verified cleavage sites. <i>Protein Science</i> , 2009, 13, 2819-2824. | 3.1 | 100 |
| 35 | Diverse modes of genomic alteration in hepatocellular carcinoma. <i>Genome Biology</i> , 2014, 15, 436. | 3.8 | 100 |
| 36 | An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. <i>Genes and Development</i> , 2014, 28, 1068-1084. | 2.7 | 95 |

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|----|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 37 | 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 |
| 38 | SciBet as a portable and fast single cell type identifier. <i>Nature Communications</i> , 2020, 11, 1818. | 5.8 | 90 |
| 39 | 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 |
| 40 | A profile hidden Markov model for signal peptides generated by HMMER. <i>Bioinformatics</i> , 2003, 19, 307-308. | 1.8 | 85 |
| 41 | An entropy-based metric for assessing the purity of single cell populations. <i>Nature Communications</i> , 2020, 11, 3155. | 5.8 | 83 |
| 42 | 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 |
| 43 | Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014, 5, 3830. | 5.8 | 77 |
| 44 | 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 |
| 45 | Understanding the Genetic Mechanisms of Cancer Drug Resistance Using Genomic Approaches. <i>Trends in Genetics</i> , 2016, 32, 127-137. | 2.9 | 69 |
| 46 | Recharacterizing Tumor-Infiltrating Lymphocytes by Single-Cell RNA Sequencing. <i>Cancer Immunology Research</i> , 2019, 7, 1040-1046. | 1.6 | 57 |
| 47 | 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 |
| 48 | 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 |
| 49 | Inferring the functional effects of mutation through clusters of mutations in homologous proteins. <i>Human Mutation</i> , 2010, 31, 264-271. | 1.1 | 48 |
| 50 | Genome-wide identification of chromosomal regions of increased tumor expression by transcriptome analysis. <i>Cancer Research</i> , 2003, 63, 5781-4. | 0.4 | 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. <i>Endocrinology</i> , 2003, 144, 2606-2616. | 1.4 | 45 |
| 52 | Bioinformatics and cancer target discovery. <i>Drug Discovery Today</i> , 2004, 9, 795-802. | 3.2 | 42 |
| 53 | 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 |
| 54 | Genomic landscape of liver cancer. <i>Nature Genetics</i> , 2012, 44, 1075-1077. | 9.4 | 41 |

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|----|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----------|
| 55 | 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 |
| 56 | Bi-Directional SIFT Predicts a Subset of Activating Mutations. <i>PLoS ONE</i> , 2009, 4, e8311. | 1.1 | 33 |
| 57 | iMAP: integration of multiple single-cell datasets by adversarial paired transfer networks. <i>Genome Biology</i> , 2021, 22, 63. | 3.8 | 26 |
| 58 | Large-scale integrative network-based analysis identifies common pathways disrupted by copy number alterations across cancers. <i>BMC Genomics</i> , 2013, 14, 440. | 1.2 | 21 |
| 59 | Understanding tumor-infiltrating lymphocytes by single cell RNA sequencing. <i>Advances in Immunology</i> , 2019, 144, 217-245. | 1.1 | 21 |
| 60 | 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 |
| 61 | Computational prediction of the functional effects of amino acid substitutions in signal peptides using a model-based approach. <i>Human Mutation</i> , 2009, 30, 99-106. | 1.1 | 20 |
| 62 | 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 |
| 63 | 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 |
| 64 | 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 |
| 65 | Cleavage and Identification of Proteins: A Modified Aspartyl-Prolyl Cleavage. <i>Analytical Chemistry</i> , 2000, 72, 5431-5436. | 3.2 | 10 |
| 66 | 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 |
| 67 | Integrative analysis of two cell lines derived from a non-small-lung cancer patient—a panomics approach. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014, , 75-86. | 0.7 | 4 |
| 68 | Identification of transcriptional isoforms associated with survival in cancer patient. <i>Journal of Genetics and Genomics</i> , 2019, 46, 413-421. | 1.7 | 3 |
| 69 | Stepwise immune alterations in multiple myeloma progression. <i>Nature Cancer</i> , 2020, 1, 477-479. | 5.7 | 1 |