

Jianhua Zhang

List of Publications by Year in descending order

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111
papers

11,095
citations

66315

42
h-index

33869

99
g-index

122
all docs

122
docs citations

122
times ranked

19813
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. <i>Clinical Cancer Research</i> , 2023, 27, 852-864.	3.2	61
2	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. <i>Hepatology</i> , 2022, 75, 955-967.	3.6	25
3	Mouse IntraDuctal (MIND): an <i>in vivo</i> model for studying the underlying mechanisms of DCIS malignancy. <i>Journal of Pathology</i> , 2022, 256, 186-201.	2.1	12
4	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. <i>Nature Communications</i> , 2022, 13, 42.	5.8	27
5	Expansion of Candidate HPV-Specific T Cells in the Tumor Microenvironment during Chemoradiotherapy Is Prognostic in HPV16+ Cancers. <i>Cancer Immunology Research</i> , 2022, 10, 259-271.	1.6	10
6	²²³ Ra Induces Transient Functional Bone Marrow Toxicity. <i>Journal of Nuclear Medicine</i> , 2022, 63, 1544-1550.	2.8	2
7	Spatially resolved transcriptomics of high-grade serous ovarian carcinoma. <i>IScience</i> , 2022, 25, 103923.	1.9	23
8	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. <i>Npj Precision Oncology</i> , 2022, 6, 21.	2.3	7
9	Genomic and Single-Cell Landscape Reveals Novel Drivers and Therapeutic Vulnerabilities of Transformed Cutaneous T-cell Lymphoma. <i>Cancer Discovery</i> , 2022, 12, 1294-1313.	7.7	18
10	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	4.7	9
11	Immunogenomic intertumor heterogeneity across primary and metastatic sites in a patient with lung adenocarcinoma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 172.	3.5	2
12	Multi-modal molecular programs regulate melanoma cell state. <i>Nature Communications</i> , 2022, 13, .	5.8	9
13	Fusobacterium is enriched in oral cancer and promotes induction of programmed death-ligand 1 (PD-L1). <i>Neoplasia</i> , 2022, 31, 100813.	2.3	14
14	Neoadjuvant Chemotherapy Increases Cytotoxic T Cell, Tissue Resident Memory T Cell, and B Cell Infiltration in Resectable NSCLC. <i>Journal of Thoracic Oncology</i> , 2021, 16, 127-139.	0.5	48
15	Multi-omic molecular profiling reveals potentially targetable abnormalities shared across multiple histologies of brain metastasis. <i>Acta Neuropathologica</i> , 2021, 141, 303-321.	3.9	30
16	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. <i>Nature Communications</i> , 2021, 12, 687.	5.8	30
17	Distinct T cell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. <i>IScience</i> , 2021, 24, 102053.	1.9	6
18	Precision medicine: preliminary results from the Initiative for Molecular Profiling and Advanced Cancer Therapy 2 (IMPACT2) study. <i>Npj Precision Oncology</i> , 2021, 5, 21.	2.3	12

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19	Characterization of the Immune Landscape of EGFR-Mutant NSCLC Identifies CD73/Adenosine Pathway as a Potential Therapeutic Target. <i>Journal of Thoracic Oncology</i> , 2021, 16, 583-600.	0.5	62
20	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2607.	5.8	61
21	Whole-Genome Sequencing of Common Salivary Gland Carcinomas: Subtype-Restricted and Shared Genetic Alterations. <i>Clinical Cancer Research</i> , 2021, 27, 3960-3969.	3.2	14
22	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. <i>Nature Communications</i> , 2021, 12, 2722.	5.8	74
23	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. <i>Nature Communications</i> , 2021, 12, 2877.	5.8	35
24	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. <i>Nature Medicine</i> , 2021, 27, 1432-1441.	15.2	216
25	Telomere dysfunction instigates inflammation in inflammatory bowel disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	28
26	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. <i>Acta Neuropathologica</i> , 2021, 142, 565-590.	3.9	12
27	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7411.	1.8	3
28	Oncogene-specific differences in tumor mutational burden, PD-L1 expression, and outcomes from immunotherapy in non-small cell lung cancer. , 2021, 9, e002891.		107
29	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. <i>Frontiers in Oncology</i> , 2021, 11, 705627.	1.3	7
30	USP21 deubiquitinase elevates macropinocytosis to enable oncogenic KRAS bypass in pancreatic cancer. <i>Genes and Development</i> , 2021, 35, 1327-1332.	2.7	18
31	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. <i>Nature Medicine</i> , 2021, 27, 141-151.	15.2	134
32	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. <i>Nature Communications</i> , 2021, 12, 6071.	5.8	44
33	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	3.2	0
34	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. <i>Nature Communications</i> , 2021, 12, 6655.	5.8	24
35	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. <i>Nature Communications</i> , 2021, 12, 7081.	5.8	16
36	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	3.2	6

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37	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. <i>Gut</i> , 2020, 69, 18-31.	6.1	94
38	Distinct co-acquired alterations and genomic evolution during TKI treatment in non-small-cell lung cancer patients with or without acquired T790M mutation. <i>Oncogene</i> , 2020, 39, 1846-1859.	2.6	29
39	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. <i>Nature Communications</i> , 2020, 11, 5327.	5.8	208
40	Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma. <i>Nature Medicine</i> , 2020, 26, 1845-1851.	15.2	193
41	Microbial Diversity and Composition Is Associated with Patient-Reported Toxicity during Chemoradiation Therapy for Cervical Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2020, 107, 163-171.	0.4	46
42	Telomere dysfunction activates YAP1 to drive tissue inflammation. <i>Nature Communications</i> , 2020, 11, 4766.	5.8	42
43	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. <i>Clinical Cancer Research</i> , 2020, 26, 5477-5486.	3.2	15
44	Multimomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. <i>Genome Biology</i> , 2020, 21, 271.	3.8	36
45	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. <i>Science Translational Medicine</i> , 2020, 12, .	5.8	108
46	Combination of PD-1 Inhibitor and OX40 Agonist Induces Tumor Rejection and Immune Memory in Mouse Models of Pancreatic Cancer. <i>Gastroenterology</i> , 2020, 159, 306-319.e12.	0.6	82
47	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. <i>Journal of Thoracic Disease</i> , 2020, 12, 1952-1959.	0.6	6
48	Oncogenic KRAS-Driven Metabolic Reprogramming in Pancreatic Cancer Cells Utilizes Cytokines from the Tumor Microenvironment. <i>Cancer Discovery</i> , 2020, 10, 608-625.	7.7	119
49	Tumor Microenvironment Remodeling Enables Bypass of Oncogenic KRAS Dependency in Pancreatic Cancer. <i>Cancer Discovery</i> , 2020, 10, 1058-1077.	7.7	87
50	Thirty-three years later: Two distinct cases of acute lymphoblastic leukemia in one patient. <i>American Journal of Hematology</i> , 2020, 95, 1117-1120.	2.0	0
51	Efficacy of venetoclax in high risk relapsed mantle cell lymphoma (<sc>MCL</sc>) – outcomes and mutation profile from venetoclax resistant <sc>MCL</sc> patients. <i>American Journal of Hematology</i> , 2020, 95, 623-629.	2.0	54
52	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. <i>Cell Reports</i> , 2020, 31, 107502.	2.9	69
53	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. <i>Nature Communications</i> , 2020, 11, 1839.	5.8	15
54	Genomic profiles and clinical outcomes of de novo blastoid/pleomorphic MCL are distinct from those of transformed MCL. <i>Blood Advances</i> , 2020, 4, 1038-1050.	2.5	43

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55	Comprehensive T cell repertoire characterization of non-small cell lung cancer. <i>Nature Communications</i> , 2020, 11, 603.	5.8	140
56	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. <i>Oncotarget</i> , 2020, 11, 1-14.	0.8	1
57	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2020, 18, 1300-1304.	2.3	4
58	KRT-232 and navitoclax enhance trametinib's anti-Cancer activity in non-small cell lung cancer patient-derived xenografts with KRAS mutations. <i>American Journal of Cancer Research</i> , 2020, 10, 4464-4475.	1.4	5
59	Single-Cell Characterization of Acute Myeloid Leukemia (AML) and Its Microenvironment Identifies Signatures of Resistance to PD-1 Blockade Based Therapy. <i>Blood</i> , 2020, 136, 29-31.	0.6	0
60	Hypomethylating Agents Do Not Alter Novel Splicing Events in Myeloid Neoplasms. <i>Blood</i> , 2020, 136, 37-38.	0.6	0
61	MYC protein expression is an important prognostic factor in acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2019, 60, 37-48.	0.6	54
62	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. <i>Nature Communications</i> , 2019, 10, 2978.	5.8	91
63	Global impact of somatic structural variation on the DNA methylome of human cancers. <i>Genome Biology</i> , 2019, 20, 209.	3.8	40
64	USP21 deubiquitinase promotes pancreas cancer cell stemness via Wnt pathway activation. <i>Genes and Development</i> , 2019, 33, 1361-1366.	2.7	65
65	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. <i>Cell Reports</i> , 2019, 26, 1518-1532.e9.	2.9	70
66	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. <i>Science Translational Medicine</i> , 2019, 11, .	5.8	161
67	KRAS-IRF2 Axis Drives Immune Suppression and Immune Therapy Resistance in Colorectal Cancer. <i>Cancer Cell</i> , 2019, 35, 559-572.e7.	7.7	353
68	Mechanisms of nuclear content loading to exosomes. <i>Science Advances</i> , 2019, 5, eaax8849.	4.7	176
69	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). <i>Blood</i> , 2019, 134, 458-458.	0.6	4
70	A Preexisting Rare <i>PIK3CA</i> E545K Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in <i>NRAS</i> Melanoma and Is Dependent on S6K1 Signaling. <i>Cancer Discovery</i> , 2018, 8, 556-567.	7.7	55
71	Genomic profiling of dedifferentiated liposarcoma compared to matched well-differentiated liposarcoma reveals higher genomic complexity and a common origin. <i>Journal of Physical Education and Sports Management</i> , 2018, 4, a002386.	0.5	45
72	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. <i>Modern Pathology</i> , 2018, 31, 947-955.	2.9	56

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73	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. <i>Blood</i> , 2018, 131, 1820-1832.	0.6	40
74	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cell-free DNA by next-generation sequencing. <i>Cancer</i> , 2018, 124, 1061-1069.	2.0	11
75	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. <i>Cell Stem Cell</i> , 2018, 23, 700-713.e6.	5.2	272
76	Combined Analysis of Antigen Presentation and T-cell Recognition Reveals Restricted Immune Responses in Melanoma. <i>Cancer Discovery</i> , 2018, 8, 1366-1375.	7.7	80
77	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. <i>Nature Communications</i> , 2018, 9, 2496.	5.8	39
78	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. <i>Oncotarget</i> , 2018, 9, 29495-29507.	0.8	18
79	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. <i>Frontiers in Microbiology</i> , 2018, 9, 297.	1.5	19
80	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. <i>Nature Communications</i> , 2018, 9, 2670.	5.8	79
81	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. <i>Cell Reports</i> , 2018, 24, 515-527.	2.9	70
82	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. <i>PLoS Computational Biology</i> , 2018, 14, e1006266.	1.5	8
83	Abstract 4686: T cell repertoire evolution from the normal lung to invasive lung adenocarcinoma. , 2018, , .		2
84	Comprehensive Genomic Analysis of IDH Inhibitor-Treated AML Samples Delineates Molecular Mechanisms of Differentiation and Heterogeneous Patterns of Acquired Resistance. <i>Blood</i> , 2018, 132, 441-441.	0.6	3
85	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. <i>Blood</i> , 2018, 132, 1801-1801.	0.6	4
86	Abstract 213: Exome sequencing of paired primary and relapsed small cell lung cancers reveals increased copy number aberration complexity to be associated with disease relapse. , 2018, , .		3
87	High Prevalence of PPM1D Mutations in Therapy-Related AML/MDS Is Due to Context-Specific Clonal Hematopoiesis. <i>Blood</i> , 2018, 132, 746-746.	0.6	0
88	Clinical Heterogeneity of AML Is Associated with Mutational Heterogeneity. <i>Blood</i> , 2018, 132, 5240-5240.	0.6	2
89	Distinct Gene Expression Patterns of Minimal Residual Disease (MRD) Cells in High-Risk AML Patients Identified By RNA-Sequencing. <i>Blood</i> , 2018, 132, 2757-2757.	0.6	0
90	Integrated molecular analysis of tumor biopsies on sequential CTLA-4 and PD-1 blockade reveals markers of response and resistance. <i>Science Translational Medicine</i> , 2017, 9, .	5.8	689

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91	Synthetic essentiality of chromatin remodelling factor CHD1 in PTEN-deficient cancer. <i>Nature</i> , 2017, 542, 484-488.	13.7	173
92	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. <i>Lancet Oncology</i> , The, 2017, 18, 100-111.	5.1	296
93	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	19
94	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.	7.7	433
95	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. <i>Npj Genomic Medicine</i> , 2017, 2, .	1.7	120
96	4-1BB Agonist Focuses CD8+ Tumor-Infiltrating T-Cell Growth into a Distinct Repertoire Capable of Tumor Recognition in Pancreatic Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7263-7275.	3.2	41
97	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. <i>Cancer Discovery</i> , 2017, 7, 1088-1097.	7.7	160
98	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. <i>Blood Advances</i> , 2017, 1, 1031-1036.	2.5	30
99	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. <i>Oncotarget</i> , 2017, 8, 21994-22002.	0.8	39
100	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. <i>Genome Biology</i> , 2016, 17, 178.	3.8	231
101	Epigenetic Activation of WNT5A Drives Glioblastoma Stem Cell Differentiation and Invasive Growth. <i>Cell</i> , 2016, 167, 1281-1295.e18.	13.5	207
102	Genomic heterogeneity of multiple synchronous lung cancer. <i>Nature Communications</i> , 2016, 7, 13200.	5.8	132
103	Clinical Relevance of Driver Mutations and Number of Driver Mutations in Patients with Myelodysplastic Syndromes and Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2016, 128, 54-54.	0.6	1
104	Clinical implications of TP53 mutations in myelodysplastic syndromes treated with hypomethylating agents. <i>Oncotarget</i> , 2016, 7, 14172-14187.	0.8	86
105	Clonal Hematopoiesis Increases Risk of Therapy-Related Myeloid Neoplasms. <i>Blood</i> , 2016, 128, 38-38.	0.6	0
106	Archetypes of AML Defined Using Whole Exome Sequencing and Clinical Characteristics in a Diverse Group of Patients. <i>Blood</i> , 2016, 128, 597-597.	0.6	0
107	Presence of 4 or More Driver Mutations Predicts Poor Response to Hypomethylating Agent (HMA) Therapy and Poor Overall Survival in MDS. <i>Blood</i> , 2015, 126, 1663-1663.	0.6	5
108	IKZF3 p.L162R Is a Recurrent Hotspot Mutation in Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2015, 126, 4136-4136.	0.6	0

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109	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
110	Identification of Double-stranded Genomic DNA Spanning All Chromosomes with Mutated KRAS and p53 DNA in the Serum Exosomes of Patients with Pancreatic Cancer. <i>Journal of Biological Chemistry</i> , 2014, 289, 3869-3875.	1.6	826
111	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. <i>Science</i> , 2014, 346, 256-259.	6.0	834