Jianhua Zhang

List of Publications by Year
in descending order

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	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	13.5	2,318
2	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. Science, 2014, 346, 256-259.	6.0	834
3	Identification of Double-stranded Genomic DNA Spanning All Chromosomes with Mutated KRAS and p53 DNA in the Serum Exosomes of Patients with Pancreatic Cancer. Journal of Biological Chemistry, 2014, 289, 3869-3875.	1.6	826
4	Integrated molecular analysis of tumor biopsies on sequential CTLA-4 and PD-1 blockade reveals markers of response and resistance. Science Translational Medicine, 2017, 9, .	5.8	689
5	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	7.7	433
6	KRAS-IRF2 Axis Drives Immune Suppression and Immune Therapy Resistance in Colorectal Cancer. Cancer Cell, 2019, 35, 559-572.e7.	7.7	353
7	Preleukaemic clonal haemopoiesis and risk of therapy-related myeloid neoplasms: a case-control study. Lancet Oncology, The, 2017, 18, 100-111.	5.1	296
8	PPM1D Mutations Drive Clonal Hematopoiesis in Response to Cytotoxic Chemotherapy. Cell Stem Cell, 2018, 23, 700-713.e6.	5.2	272
9	MuSE: accounting for tumor heterogeneity using a sample-specific error model improves sensitivity and specificity in mutation calling from sequencing data. Genome Biology, 2016, 17, 178.	3.8	231
10	Gut microbiota signatures are associated with toxicity to combined CTLA-4 and PD-1 blockade. Nature Medicine, 2021, 27, 1432-1441.	15.2	216
11	Clonal evolution of acute myeloid leukemia revealed by high-throughput single-cell genomics. Nature Communications, 2020, 11, 5327.	5.8	208
12	Epigenetic Activation of WNT5A Drives Glioblastoma Stem Cell Differentiation and Invasive Growth. Cell, 2016, 167, 1281-1295.e18.	13.5	207
13	Neoadjuvant PD-L1 plus CTLA-4 blockade in patients with cisplatin-ineligible operable high-risk urothelial carcinoma. Nature Medicine, 2020, 26, 1845-1851.	15.2	193
14	Mechanisms of nuclear content loading to exosomes. Science Advances, 2019, 5, eaax8849.	4.7	176
15	Synthetic essentiality of chromatin remodelling factor CHD1 in PTEN-deficient cancer. Nature, 2017, 542, 484-488.	13.7	173
16	Metabolic reprogramming toward oxidative phosphorylation identifies a therapeutic target for mantle cell lymphoma. Science Translational Medicine, 2019, 11, .	5.8	161
17	TCR Repertoire Intratumor Heterogeneity in Localized Lung Adenocarcinomas: An Association with Predicted Neoantigen Heterogeneity and Postsurgical Recurrence. Cancer Discovery, 2017, 7, 1088-1097.	7.7	160
18	Comprehensive T cell repertoire characterization of non-small cell lung cancer. Nature Communications, 2020, 11, 603.	5.8	140

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19	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	15.2	134
20	Genomic heterogeneity of multiple synchronous lung cancer. Nature Communications, 2016, 7, 13200.	5.8	132
21	Genomic and immune heterogeneity are associated with differential responses to therapy in melanoma. Npj Genomic Medicine, 2017, 2, .	1.7	120
22	Oncogenic KRAS-Driven Metabolic Reprogramming in Pancreatic Cancer Cells Utilizes Cytokines from the Tumor Microenvironment. Cancer Discovery, 2020, 10, 608-625.	7.7	119
23	Neoantigen responses, immune correlates, and favorable outcomes after ipilimumab treatment of patients with prostate cancer. Science Translational Medicine, 2020, 12, .	5.8	108
24	Oncogene-specific differences in tumor mutational burden, PD-L1 expression, and outcomes from immunotherapy in non-small cell lung cancer. , 2021, 9, e002891.		107
25	Multiplex profiling of peritoneal metastases from gastric adenocarcinoma identified novel targets and molecular subtypes that predict treatment response. Gut, 2020, 69, 18-31.	6.1	94
26	Multi-region exome sequencing reveals genomic evolution from preneoplasia to lung adenocarcinoma. Nature Communications, 2019, 10, 2978.	5.8	91
27	Tumor Microenvironment Remodeling Enables Bypass of Oncogenic KRAS Dependency in Pancreatic Cancer. Cancer Discovery, 2020, 10, 1058-1077.	7.7	87
28	Clinical implications of *TP53* mutations in myelodysplastic syndromes treated with hypomethylating agents. Oncotarget, 2016, 7, 14172-14187.	0.8	86
29	Combination of PD-1 Inhibitor and OX40 Agonist Induces Tumor Rejection and Immune Memory in Mouse Models of Pancreatic Cancer. Gastroenterology, 2020, 159, 306-319.e12.	0.6	82
30	Combined Analysis of Antigen Presentation and T-cell Recognition Reveals Restricted Immune Responses in Melanoma. Cancer Discovery, 2018, 8, 1366-1375.	7.7	80
31	Integrative genomic analysis of adult mixed phenotype acute leukemia delineates lineage associated molecular subtypes. Nature Communications, 2018, 9, 2670.	5.8	79
32	Immune evolution from preneoplasia to invasive lung adenocarcinomas and underlying molecular features. Nature Communications, 2021, 12, 2722.	5.8	74
33	A Pan-Cancer Compendium of Genes Deregulated by Somatic Genomic Rearrangement across More Than 1,400 Cases. Cell Reports, 2018, 24, 515-527.	2.9	70
34	Pre-existing Functional Heterogeneity of Tumorigenic Compartment as the Origin of Chemoresistance in Pancreatic Tumors. Cell Reports, 2019, 26, 1518-1532.e9.	2.9	70
35	Molecular Analysis of Clinically Defined Subsets of High-Grade Serous Ovarian Cancer. Cell Reports, 2020, 31, 107502.	2.9	69
36	USP21 deubiquitinase promotes pancreas cancer cell stemness via Wnt pathway activation. Genes and Development, 2019, 33, 1361-1366.	2.7	65

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37	Characterization of the Immune Landscape of EGFR-Mutant NSCLC Identifies CD73/Adenosine Pathway as a Potential Therapeutic Target. Journal of Thoracic Oncology, 2021, 16, 583-600.	0.5	62
38	Proteogenomic Analysis of Salivary Adenoid Cystic Carcinomas Defines Molecular Subtypes and Identifies Therapeutic Targets. Clinical Cancer Research, 2023, 27, 852-864.	3.2	61
39	Leukemia stemness and co-occurring mutations drive resistance to IDH inhibitors in acute myeloid leukemia. Nature Communications, 2021, 12, 2607.	5.8	61
40	Multiregion gene expression profiling reveals heterogeneity in molecular subtypes and immunotherapy response signatures in lung cancer. Modern Pathology, 2018, 31, 947-955.	2.9	56
41	A Preexisting Rare *PIK3CA* E545K Subpopulation Confers Clinical Resistance to MEK plus CDK4/6 Inhibition in *NRAS* Melanoma and Is Dependent on S6K1 Signaling. Cancer Discovery, 2018, 8, 556-567.	7.7	55
42	MYC protein expression is an important prognostic factor in acute myeloid leukemia. Leukemia and Lymphoma, 2019, 60, 37-48.	0.6	54
43	Efficacy of venetoclax in high risk relapsed mantle cell lymphoma (MCL) â€•outcomes and mutation profile from venetoclax resistant MCL patients. American Journal of Hematology, 2020, 95, 623-629.	2.0	54
44	Neoadjuvant Chemotherapy Increases Cytotoxic T Cell, Tissue Resident Memory T Cell, and B Cell Infiltration in Resectable NSCLC. Journal of Thoracic Oncology, 2021, 16, 127-139.	0.5	48
45	Microbial Diversity and Composition Is Associated with Patient-Reported Toxicity during Chemoradiation Therapy for Cervical Cancer. International Journal of Radiation Oncology Biology Physics, 2020, 107, 163-171.	0.4	46
46	Genomic profiling of dedifferentiated liposarcoma compared to matched well-differentiated liposarcoma reveals higher genomic complexity and a common origin. Journal of Physical Education and Sports Management, 2018, 4, a002386.	0.5	45
47	Single cell T cell landscape and T cell receptor repertoire profiling of AML in context of PD-1 blockade therapy. Nature Communications, 2021, 12, 6071.	5.8	44
48	Genomic profiles and clinical outcomes of de novo blastoid/pleomorphic MCL are distinct from those of transformed MCL. Blood Advances, 2020, 4, 1038-1050.	2.5	43
49	Telomere dysfunction activates YAP1 to drive tissue inflammation. Nature Communications, 2020, 11, 4766.	5.8	42
50	4-1BB Agonist Focuses CD8+ Tumor-Infiltrating T-Cell Growth into a Distinct Repertoire Capable of Tumor Recognition in Pancreatic Cancer. Clinical Cancer Research, 2017, 23, 7263-7275.	3.2	41
51	Clinical implications of cancer gene mutations in patients with chronic lymphocytic leukemia treated with lenalidomide. Blood, 2018, 131, 1820-1832.	0.6	40
52	Global impact of somatic structural variation on the DNA methylome of human cancers. Genome Biology, 2019, 20, 209.	3.8	40
53	KMT2D/MLL2 inactivation is associated with recurrence in adult-type granulosa cell tumors of the ovary. Nature Communications, 2018, 9, 2496.	5.8	39
54	DNA methylation intratumor heterogeneity in localized lung adenocarcinomas. Oncotarget, 2017, 8, 21994-22002.	0.8	39

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55	Multiomics profiling of primary lung cancers and distant metastases reveals immunosuppression as a common characteristic of tumor cells with metastatic plasticity. Genome Biology, 2020, 21, 271.	3.8	36
56	Longitudinal single-cell profiling reveals molecular heterogeneity and tumor-immune evolution in refractory mantle cell lymphoma. Nature Communications, 2021, 12, 2877.	5.8	35
57	Copy number alterations detected as clonal hematopoiesis of indeterminate potential. Blood Advances, 2017, 1, 1031-1036.	2.5	30
58	Multi-omic molecular profiling reveals potentially targetable abnormalities shared across multiple histologies of brain metastasis. Acta Neuropathologica, 2021, 141, 303-321.	3.9	30
59	Evolution of DNA methylome from precancerous lesions to invasive lung adenocarcinomas. Nature Communications, 2021, 12, 687.	5.8	30
60	Distinct co-acquired alterations and genomic evolution during TKI treatment in non-small-cell lung cancer patients with or without acquired T790M mutation. Oncogene, 2020, 39, 1846-1859.	2.6	29
61	Telomere dysfunction instigates inflammation in inflammatory bowel disease. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	28
62	Prediction of biomarkers and therapeutic combinations for anti-PD-1 immunotherapy using the global gene network association. Nature Communications, 2022, 13, 42.	5.8	27
63	Gut microbiome features associated with liver fibrosis in Hispanics, a population at high risk for fatty liver disease. Hepatology, 2022, 75, 955-967.	3.6	25
64	Cold and heterogeneous T cell repertoire is associated with copy number aberrations and loss of immune genes in small-cell lung cancer. Nature Communications, 2021, 12, 6655.	5.8	24
65	Spatially resolved transcriptomics of high-grade serous ovarian carcinoma. IScience, 2022, 25, 103923.	1.9	23
66	Spatio-Temporal Genomic Heterogeneity, Phylogeny, and Metastatic Evolution in Salivary Adenoid Cystic Carcinoma. Journal of the National Cancer Institute, 2017, 109, .	3.0	19
67	Linking Associations of Rare Low-Abundance Species to Their Environments by Association Networks. Frontiers in Microbiology, 2018, 9, 297.	1.5	19
68	Toll-like receptor 4: a target for chemoprevention of hepatocellular carcinoma in obesity and steatohepatitis. Oncotarget, 2018, 9, 29495-29507.	0.8	18
69	USP21 deubiquitinase elevates macropinocytosis to enable oncogenic KRAS bypass in pancreatic cancer. Genes and Development, 2021, 35, 1327-1332.	2.7	18
70	Genomic and Single-Cell Landscape Reveals Novel Drivers and Therapeutic Vulnerabilities of Transformed Cutaneous T-cell Lymphoma. Cancer Discovery, 2022, 12, 1294-1313.	7.7	18
71	The histologic phenotype of lung cancers is associated with transcriptomic features rather than genomic characteristics. Nature Communications, 2021, 12, 7081.	5.8	16
72	Evolution of Genomic and T-cell Repertoire Heterogeneity of Malignant Pleural Mesothelioma Under Dasatinib Treatment. Clinical Cancer Research, 2020, 26, 5477-5486.	3.2	15

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73	Spatially resolved analyses link genomic and immune diversity and reveal unfavorable neutrophil activation in melanoma. Nature Communications, 2020, 11, 1839.	5.8	15
74	Whole-Genome Sequencing of Common Salivary Gland Carcinomas: Subtype-Restricted and Shared Genetic Alterations. Clinical Cancer Research, 2021, 27, 3960-3969.	3.2	14
75	Fusobacterium is enriched in oral cancer and promotes induction of programmed death-ligand 1 (PD-L1). Neoplasia, 2022, 31, 100813.	2.3	14
76	Precision medicine: preliminary results from the Initiative for Molecular Profiling and Advanced Cancer Therapy 2 (IMPACT2) study. Npj Precision Oncology, 2021, 5, 21.	2.3	12
77	Enhancer reprogramming in PRC2-deficient malignant peripheral nerve sheath tumors induces a targetable de-differentiated state. Acta Neuropathologica, 2021, 142, 565-590.	3.9	12
78	Mouse-IntraDuctal (MIND): an in vivo model for studying the underlying mechanisms of DCIS malignancy. Journal of Pathology, 2022, 256, 186-201.	2.1	12
79	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cell-free DNA by next-generation sequencing. Cancer, 2018, 124, 1061-1069.	2.0	11
80	Expansion of Candidate HPV-Specific T Cells in the Tumor Microenvironment during Chemoradiotherapy Is Prognostic in HPV16+ Cancers. Cancer Immunology Research, 2022, 10, 259-271.	1.6	10
81	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	4.7	9
82	Multi-modal molecular programs regulate melanoma cell state. Nature Communications, 2022, 13, .	5.8	9
83	FusionPathway: Prediction of pathways and therapeutic targets associated with gene fusions in cancer. PLoS Computational Biology, 2018, 14, e1006266.	1.5	8
84	Decoupling Lineage-Associated Genes in Acute Myeloid Leukemia Reveals Inflammatory and Metabolic Signatures Associated With Outcomes. Frontiers in Oncology, 2021, 11, 705627.	1.3	7
85	Multi-site desmoplastic small round cell tumors are genetically related and immune-cold. Npj Precision Oncology, 2022, 6, 21.	2.3	7
86	Genomic assessment distinguishes intrapulmonary metastases from synchronous primary lung cancers. Journal of Thoracic Disease, 2020, 12, 1952-1959.	0.6	6
87	Distinct T-cell receptor repertoire diversity of clinically defined high-grade serous ovarian cancer treatment subgroups. IScience, 2021, 24, 102053.	1.9	6
88	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. Clinical Cancer Research, 2021, 27, 5049-5061.	3.2	6
89	Presence of 4 or More Driver Mutations Predicts Poor Response to Hypomethylating Agent (HMA) Therapy and Poor Overall Survival in MDS. Blood, 2015, 126, 1663-1663.	0.6	5
90	KRT-232 and navitoclax enhance trametinib's anti-Cancer activity in non-small cell lung cancer patient-derived xenografts with KRAS mutations. American Journal of Cancer Research, 2020, 10, 4464-4475.	1.4	5

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91	Pan-Myeloid Leukemia Analysis: Machine Learning-Based Approach to Predict Phenotype and Clinical Outcomes Using Mutation Data. Blood, 2018, 132, 1801-1801.	0.6	4
92	Comprehensive Analysis of Genotype and Prior Exposures in Therapy-Related Myeloid Neoplasms (t-MNs). Blood, 2019, 134, 458-458.	0.6	4
93	A Cryptic BCR-PDGFRB Fusion Resulting in a Chronic Myeloid Neoplasm With Monocytosis and Eosinophilia: A Novel Finding With Treatment Implications. Journal of the National Comprehensive Cancer Network: JNCCN, 2020, 18, 1300-1304.	2.3	4
94	Somatic Mutations in Circulating Cell-Free DNA and Risk for Hepatocellular Carcinoma in Hispanics. International Journal of Molecular Sciences, 2021, 22, 7411.	1.8	3
95	Comprehensive Genomic Analysis of IDH Inhibitor-Treated AML Samples Delineates Molecular Mechanisms of Differentiation and Heterogeneous Patterns of Acquired Resistance. Blood, 2018, 132, 441-441.	0.6	3
96	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
97	Abstract 4686: T cell repertoire evolution from the normal lung to invasive lung adenocarcinoma. , 2018, , .		2
98	Clinical Heterogeneity of AML Is Associated with Mutational Heterogeneity. Blood, 2018, 132, 5240-5240.	0.6	2
99	^{223}Ra Induces Transient Functional Bone Marrow Toxicity. Journal of Nuclear Medicine, 2022, 63, 1544-1550.	2.8	2
100	Immunogenomic intertumor heterogeneity across primary and metastatic sites in a patient with lung adenocarcinoma. Journal of Experimental and Clinical Cancer Research, 2022, 41, 172.	3.5	2
101	Clinical Relevance of Driver Mutations and Number of Driver Mutations in Patients with Myelodysplastic Syndromes and Chronic Myelomonocytic Leukemia. Blood, 2016, 128, 54-54.	0.6	1
102	Pathogenic mutations and overall survival in 3,084 patients with cancer: the Hellenic Cooperative Oncology Group Precision Medicine Initiative. Oncotarget, 2020, 11, 1-14.	0.8	1
103	Thirty‑three years later: Two distinct cases of acute lymphoblastic leukemia in one patient. American Journal of Hematology, 2020, 95, 1117-1120.	2.0	0
104	IKZF3 p.L162R Is a Recurrent Hotspot Mutation in Chronic Lymphocytic Leukemia (CLL). Blood, 2015, 126, 4136-4136.	0.6	0
105	Clonal Hematopoiesis Increases Risk of Therapy-Related Myeloid Neoplasms. Blood, 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. Blood, 2016, 128, 597-597.	0.6	0
107	High Prevalence of PPM1D Mutations in Therapy-Related AML/MDS Is Due to Context-Specific Clonal Hematopoiesis. Blood, 2018, 132, 746-746.	0.6	0
108	Distinct Gene Expression Patterns of Minimal Residual Disease (MRD) Cells in High-Risk AML Patients Identified By RNA-Sequencing. Blood, 2018, 132, 2757-2757.	0.6	0

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109	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. Clinical Cancer Research, 2021, 27, 5049-5061.	3.2	0
110	Single-Cell Characterization of Acute Myeloid Leukemia (AML) and Its Microenvironment Identifies Signatures of Resistance to PD-1 Blockade Based Therapy. Blood, 2020, 136, 29-31.	0.6	0
111	Hypomethylating Agents Do Not Alter Novel Splicing Events in Myeloid Neoplasms. Blood, 2020, 136, 37-38.	0.6	0