Jianjiong Gao

List of Publications by Year in descending order

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149 papers	132,794 citations	6613 79 h-index	12597 132 g-index
162 all docs	162 docs citations	162 times ranked	110861 citing authors

#	Article	IF	Citations
1	The cBio Cancer Genomics Portal: An Open Platform for Exploring Multidimensional Cancer Genomics Data. Cancer Discovery, 2012, 2, 401-404.	9.4	12,801
2	Integrative Analysis of Complex Cancer Genomics and Clinical Profiles Using the cBioPortal. Science Signaling, 2013, 6, pl1.	3.6	11,344
3	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
4	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
5	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
6	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
7	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
8	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
9	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
10	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
11	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
12	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
13	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
14	Integrative Clinical Genomics of Advanced Prostate Cancer. Cell, 2015, 161, 1215-1228.	28.9	2,660
15	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
16	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
17	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
18	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	30.7	2,473

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19	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
20	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
21	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
22	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
23	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	27.8	1,966
24	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
25	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
26	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
27	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
28	Integrated genomic characterization of oesophageal carcinoma. Nature, 2017, 541, 169-175.	27.8	1,448
29	OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.	3.0	1,266
30	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
31	AACR Project GENIE: Powering Precision Medicine through an International Consortium. Cancer Discovery, 2017, 7, 818-831.	9.4	1,235
32	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	27.8	1,158
33	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
34	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
35	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
36	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683

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37	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.	17.5	634
38	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
39	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	21.4	601
40	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	16.8	589
41	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.	9.4	490
42	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
43	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
44	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
45	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
46	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
47	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
48	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
49	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	329
50	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
51	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. Nature Genetics, 2014, 46, 424-426.	21.4	291
52	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	3.0	286
53	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
54	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	9.4	275

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55	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	9.4	275
56	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
57	The expanding landscape of â€˜oncohistoneâ€™ mutations in human cancers. Nature, 2019, 567, 473-478.	27.8	271
58	Musite, a Tool for Global Prediction of General and Kinase-specific Phosphorylation Sites. Molecular and Cellular Proteomics, 2010, 9, 2586-2600.	3.8	233
59	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
60	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients. Cell, 2022, 185, 563-575.e11.	28.9	223
61	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	16.8	213
62	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
63	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. Nature, 2016, 531, 471-475.	27.8	202
64	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. BMC Bioinformatics, 2010, 11, 5.	2.6	180
65	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
66	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. Genome Medicine, 2017, 9, 4.	8.2	170
67	Harnessing multimodal data integration to advance precision oncology. Nature Reviews Cancer, 2022, 22, 114-126.	28.4	168
68	BioJava: an open-source framework for bioinformatics in 2012. Bioinformatics, 2012, 28, 2693-2695.	4.1	160
69	Unifying cancer and normal RNA sequencing data from different sources. Scientific Data, 2018, 5, 180061.	5.3	152
70	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
71	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
72	P3DB: a plant protein phosphorylation database. Nucleic Acids Research, 2009, 37, D960-D962.	14.5	115

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73	Steganalysis Based on Multiple Features Formed by Statistical Moments of Wavelet Characteristic Functions. Lecture Notes in Computer Science, 2005, , 262-277.	1.3	113
74	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. Molecular and Cellular Proteomics, 2019, 18, 1893-1898.	3.8	106
75	A phase II study of frontline paclitaxel/carboplatin/bevacizumab, paclitaxel/carboplatin/temsirolimus, or ixabepilone/carboplatin/bevacizumab in advanced/recurrent endometrial cancer. Gynecologic Oncology, 2018, 150, 274-281.	1.4	105
76	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. Nature Genetics, 2020, 52, 448-457.	21.4	104
77	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. Cell Systems, 2015, 1, 197-209.	6.2	94
78	Image Steganalysis Based on Moments of Characteristic Functions Using Wavelet Decomposition, Prediction-Error Image, and Neural Network. , 0, , .		90
79	Phosphoproteomic Analysis of Seed Maturation in Arabidopsis, Rapeseed, and Soybean Â Â Â. Plant Physiology, 2012, 159, 517-528.	4.8	89
80	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
81	Multimodal data integration using machine learning improves risk stratification of high-grade serous ovarian cancer. Nature Cancer, 2022, 3, 723-733.	13.2	82
82	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. Annals of Oncology, 2017, 28, 3015-3021.	1.2	79
83	P3DB 3.0: From plant phosphorylation sites to protein networks. Nucleic Acids Research, 2014, 42, D1206-D1213.	14.5	75
84	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. Blood, 2021, 137, 2103-2113.	1.4	57
85	OncoTree: A Cancer Classification System for Precision Oncology. JCO Clinical Cancer Informatics, 2021, 5, 221-230.	2.1	51
86	P3DB: An Integrated Database for Plant Protein Phosphorylation. Frontiers in Plant Science, 2012, 3, 206.	3.6	50
87	Integrated Genomics for Pinpointing Survival Loci within Arm-Level Somatic Copy Number Alterations. Cancer Cell, 2016, 29, 737-750.	16.8	50
88	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. Bioinformatics, 2017, 33, 2238-2240.	4.1	50
89	Effective steganalysis based on statistical moments of wavelet characteristic function. , 2005, , .		49
90	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. Genome Medicine, 2017, 9, 113.	8.2	47

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91	Correlation between posttranslational modification and intrinsic disorder in protein. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 94-103.	0.7	45
92	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	21.4	44
93	Overcome tumor heterogeneity-imposed therapeutic barriers through convergent genomic biomarker discovery: A braided cancer river model of kidney cancer. Seminars in Cell and Developmental Biology, 2017, 64, 98-106.	5.0	43
94	Multiomic Integration of Public Oncology Databases in Bioconductor. JCO Clinical Cancer Informatics, 2020, 4, 958-971.	2.1	42
95	rcellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. Bioinformatics, 2016, 32, 1272-1274.	4.1	39
96	Integrated digital pathology at scale: A solution for clinical diagnostics and cancer research at a large academic medical center. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 1874-1884.	4.4	39
97	Modeling biological and genetic diversity in upper tract urothelial carcinoma with patient derived xenografts. Nature Communications, 2020, 11, 1975.	12.8	37
98	MITI minimum information guidelines for highly multiplexed tissue images. Nature Methods, 2022, 19, 262-267.	19.0	37
99	Characteristics and Outcome of AKT1E17K-Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. Cancer Discovery, 2020, 10, 526-535.	9.4	36
100	An integrative somatic mutation analysis to identify pathways linked with survival outcomes across 19 cancer types. Bioinformatics, 2016, 32, 1643-1651.	4.1	35
101	Multicenter phase II study of temozolomide and myeloablative chemotherapy with autologous stem cell transplant for newly diagnosed anaplastic oligodendroglioma. Neuro-Oncology, 2017, 19, 1380-1390.	1.2	35
102	The performance of BRCA1 immunohistochemistry for detecting germline, somatic, and epigenetic BRCA1 loss in high-grade serous ovarian cancer. Annals of Oncology, 2014, 25, 2372-2378.	1.2	31
103	Oncologist use and perception of large panel next-generation tumor sequencing. Annals of Oncology, 2017, 28, 2298-2304.	1.2	31
104	Predicting and Analyzing Protein Phosphorylation Sites in Plants Using Musite. Frontiers in Plant Science, 2012, 3, 186.	3.6	27
105	Effector prediction in host-pathogen interaction based on a Markov model of a ubiquitous EPIYA motif. BMC Genomics, 2010, 11, S1.	2.8	26
106	Collection, integration and analysis of cancer genomic profiles: from data to insight. Current Opinion in Genetics and Development, 2014, 24, 92-98.	3.3	22
107	Steganalysis Using High-Dimensional Features Derived from Co-occurrence Matrix and Class-Wise Non-Principal Components Analysis (CNPCA). Lecture Notes in Computer Science, 2006, , 49-60.	1.3	21
108	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. Nucleic Acids Research, 2016, 44, D986-D991.	14.5	21

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109	CD38 in Advanced Prostate Cancers. European Urology, 2021, 79, 736-746.	1.9	21
110	Disrupting KATP channels diminishes the estrogen-mediated protection in female mutant mice during ischemia-reperfusion. Clinical Proteomics, 2014, 11, 19.	2.1	19
111	Leveraging Systematic Functional Analysis to Benchmark an In Silico Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. Cancer Research, 2020, 80, 4233-4243.	0.9	18
112	CORRELATION BETWEEN POSTTRANSLATIONAL MODIFICATION AND INTRINSIC DISORDER IN PROTEIN. , 2011, , .		16
113	A New Machine Learning Approach for Protein Phosphorylation Site Prediction in Plants. Lecture Notes in Computer Science, 2009, , 18-29.	1.3	15
114	Abstract 5277: The cBioPortal for cancer genomics and its application in precision oncology. Cancer Research, 2016, 76, 5277-5277.	0.9	14
115	PiHelper: an open source framework for drug-target and antibody-target data. Bioinformatics, 2013, 29, 2071-2072.	4.1	13
116	The Musite open-source framework for phosphorylation-site prediction. BMC Bioinformatics, 2010, 11, S9.	2.6	12
117	Abstract 923: The cBioPortal for Cancer Genomics: An intuitive open-source platform for exploration, analysis and visualization of cancer genomics data. Cancer Research, 2018, 78, 923-923.	0.9	11
118	BridgeDb app: unifying identifier mapping services for Cytoscape. F1000Research, 2014, 3, 148.	1.6	11
119	G2S: a web-service for annotating genomic variants on 3D protein structures. Bioinformatics, 2018, 34, 1949-1950.	4.1	10
120	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
121	BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. Bioinformatics, 2017, 33, 2047-2049.	4.1	8
122	OncoKB: Annotation of the oncogenic effect and treatment implications of somatic mutations in cancer.. Journal of Clinical Oncology, 2016, 34, 11583-11583.	1.6	8
123	Image Steganalysis Based on Statistical Moments of Wavelet Subband Histograms in DFT Domain. , 2005, , .		7
124	Comprehensive Genomic Analysis of Metastatic Nonâ€“Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. JCO Precision Oncology, 2019, 3, 1-18.	3.0	7
125	How oncogenic mutations activate human MAP kinase 1 (MEK1): a molecular dynamics simulation study. Journal of Biomolecular Structure and Dynamics, 2020, 38, 3942-3958.	3.5	7
126	Semisupervised Training of a Brain MRI Tumor Detection Model Using Mined Annotations. Radiology, 2022, 303, 80-89.	7.3	7

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127	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Clinics in Laboratory Medicine, 2016, 36, 153-181.	1.4	6
128	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. Surgical Pathology Clinics, 2015, 8, 269-288.	1.7	5
129	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer. JCO Clinical Cancer Informatics, 2022, 6, e2100144.	2.1	4
130	Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. Blood, 2019, 134, 2148-2148.	1.4	3
131	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. Frontiers in Bioengineering and Biotechnology, 2020, 8, 349.	4.1	2
132	Abstract 5140: Individual patient cancer profiles in the cBio Cancer Genomic Portal.. , 2013, , .		2
133	Abstract 4271: The cBioPortal for Cancer Genomics as a clinical decision support tool. , 2014, , .		2
134	Abstract 2607: The cBioPortal for Cancer Genomics: an open source platform for accessing and interpreting complex cancer genomics data in the era of precision medicine. , 2017, , .		1
135	Abstract 375: Oncologist use and perception of large panel next generation tumor sequencing. , 2017, , .		1
136	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. Blood, 2019, 134, 633-633.	1.4	1
137	BridgeDb: standardized access to gene, protein and metabolite identifier mapping services. Nature Precedings, 2010, , .	0.1	0
138	Abstract LB-91: SMARCA4 mutations in small cell carcinoma of the ovary. , 2014, , .		0
139	Musite: Tool for Predicting Protein Phosphorylation Sites. , 2016, , 1393-1397.		0
140	Abstract 3606: Identification of oncogenic mutation hotspots via three-dimensional proximity. , 2016, , .		0
141	Abstract 4366: Identifying novel recurrent mutations reveals candidate actionable mutations. , 2016, , .		0
142	The long tail of significantly mutated genes in prostate cancer.. Journal of Clinical Oncology, 2017, 35, 131-131.	1.6	0
143	Abstract 3566: The long tail of significantly mutated genes in prostate cancer. , 2017, , .		0
144	Abstract 3024: Genomic characterization of organ-specific metastasis from prospective clinical sequencing of 20,000 cancer patients. , 2018, , .		0

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145	Abstract 2736: A molecular and histopathologic map of cancer metastasis. , 2019, , .		0
146	Abstract 910: The cBioPortal for cancer genomics. , 2019, , .		0
147	Abstract 3208: OncoKB, a precision oncology knowledgebase. , 2020, , .		0
148	Abstract 3209: The cBioPortal for Cancer Genomics. , 2020, , .		0
149	Abstract 1109: Integrative analysis of clinical and genomic information identifies predictive markers of metastatic risk. , 2020, , .		0