Jianjiong Gao

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/5142925/jianjiong-gao-publications-by-year.pdf
Version: 2024-04-24

136 papers	89,009 citations	72 h-index	162 g-index
162 ext. papers	115,229 ext. citations	22.3 avg, IF	9.32 L-index

#	Paper	IF	Citations
136	Semisupervised Training of a Brain MRI Tumor Detection Model Using Mined Annotations.. *Radiology*, **2022**, 210817	20.5	0
135	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer.. *JCO Clinical Cancer Informatics*, **2022**, 6, e2100144	5.2	0
134	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients.. *Cell*, **2022**, 185, 563-575.e11	56.2	11
133	MITI minimum information guidelines for highly multiplexed tissue images.. *Nature Methods*, **2022**, 19, 262-267	21.6	2
132	The context-specific role of germline pathogenicity in tumorigenesis. *Nature Genetics*, **2021**, 53, 1577-1585	36.3	6
131	Harnessing multimodal data integration to advance precision oncology. *Nature Reviews Cancer*, **2021**,	31.3	18
130	OncoTree: A Cancer Classification System for Precision Oncology. *JCO Clinical Cancer Informatics*, **2021**, 5, 221-230	5.2	11
129	CD38 in Advanced Prostate Cancers. *European Urology*, **2021**, 79, 736-746	10.2	0
128	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	8.6	7
127	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. *Blood*, **2021**, 137, 2103-2113	2.2	19
126	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 349	5.8	1
125	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. *Nature Genetics*, **2020**, 52, 448-457	36.3	58
124	Leveraging Systematic Functional Analysis to Benchmark an Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. *Cancer Research*, **2020**, 80, 4233-4243	10.1	9
123	Characteristics and Outcome of -Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. *Cancer Discovery*, **2020**, 10, 526-535	24.4	19
122	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
121	Modeling biological and genetic diversity in upper tract urothelial carcinoma with patient derived xenografts. *Nature Communications*, **2020**, 11, 1975	17.4	17
120	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. *Cell*, **2020**, 181, 236-249	56.2	140

119	How oncogenic mutations activate human MAP kinase 1 (MEK1): a molecular dynamics simulation study. *Journal of Biomolecular Structure and Dynamics*, **2020**, 38, 3942-3958	3.6	3
118	Multiomic Integration of Public Oncology Databases in Bioconductor. *JCO Clinical Cancer Informatics*, **2020**, 4, 958-971	5.2	7
117	The expanding landscape of Toncohistone Tmutations in human cancers. *Nature*, **2019**, 567, 473-478	50.4	151
116	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. *Molecular and Cellular Proteomics*, **2019**, 18, 1893-1898	7.6	50
115	Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. *Blood*, **2019**, 134, 2148-2148	2.2	0
114	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. *Blood*, **2019**, 134, 633-633	2.2	
113	Comprehensive Genomic Analysis of Metastatic Non-Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. *JCO Precision Oncology*, **2019**, 3,	3.6	4
112	Unifying cancer and normal RNA sequencing data from different sources. *Scientific Data*, **2018**, 5, 180061	8.2	66
111	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
110	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
109	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
108	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
107	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
106	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
105	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
104	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
103	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
102	The Immune Landscape of Cancer. *Immunity*, **2018**, 48, 812-830.e14	32.3	1754

101	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
100	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
99	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
98	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
97	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
96	G2S: a web-service for annotating genomic variants on 3D protein structures. *Bioinformatics*, **2018**, 34, 1949-1950	7.2	7
95	Accelerating Discovery of Functional Mutant Alleles in Cancer. *Cancer Discovery*, **2018**, 8, 174-183	24.4	162
94	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. *Cancer Cell*, **2018**, 33, 125-136.e3	24.3	338
93	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
92	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
91	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	24.3	275
90	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
89	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
88	The long tail of oncogenic drivers in prostate cancer. *Nature Genetics*, **2018**, 50, 645-651	36.3	380
87	Systematic Functional Annotation of Somatic Mutations in Cancer. *Cancer Cell*, **2018**, 33, 450-462.e10	24.3	114
86	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas **2018**,		5
85	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. *Cancer Discovery*, **2018**, 8, 49-58	24.4	180
84	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85

83	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. *Cancer Discovery*, **2018**, 8, 1548-1565	24.4	258
82	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
81	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	4.9	67
80	Integrated genomic and molecular characterization of cervical cancer. *Nature*, **2017**, 543, 378-384	50.4	755
79	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. *Genome Medicine*, **2017**, 9, 4	14.4	117
78	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. *Nature Medicine*, **2017**, 23, 703-713	50.5	1638
77	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	20
76	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
75	AACR Project GENIE: Powering Precision Medicine through an International Consortium. *Cancer Discovery*, **2017**, 7, 818-831	24.4	629
74	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. *Bioinformatics*, **2017**, 33, 2238-2240	7.2	31
73	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. *Cancer Discovery*, **2017**, 7, 596-609	24.4	317
72	Integrated genomic characterization of oesophageal carcinoma. *Nature*, **2017**, 541, 169-175	50.4	965
71	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. *Annals of Oncology*, **2017**, 28, 3015-3021	10.3	52
70	BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. *Bioinformatics*, **2017**, 33, 2047-2049	7.2	8
69	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. *Genome Medicine*, **2017**, 9, 113	14.4	31
68	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,	3.6	151
67	OncoKB: A Precision Oncology Knowledge Base. *JCO Precision Oncology*, **2017**, 2017,	3.6	699
66	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451

65	Oncologist use and perception of large panel next-generation tumor sequencing. *Annals of Oncology*, **2017**, 28, 2298-2304	10.3	24
64	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	7.5	37
63	The long tail of significantly mutated genes in prostate cancer.. *Journal of Clinical Oncology*, **2017**, 35, 131-131	2.2	
62	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. *Nucleic Acids Research*, **2016**, 44, D986-91	20.1	11
61	rcellminer: exploring molecular profiles and drug response of the NCI-60 cell lines in R. *Bioinformatics*, **2016**, 32, 1272-4	7.2	30
60	An integrative somatic mutation analysis to identify pathways linked with survival outcomes across 19 cancer types. *Bioinformatics*, **2016**, 32, 1643-51	7.2	14
59	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. *Nature*, **2016**, 531, 471-475	50.4	142
58	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. *Clinics in Laboratory Medicine*, **2016**, 36, 153-81	2.1	4
57	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. *Nature Biotechnology*, **2016**, 34, 155-63	44.5	465
56	Abstract 5277: The cBioPortal for cancer genomics and its application in precision oncology **2016**,		6
55	OncoKB: Annotation of the oncogenic effect and treatment implications of somatic mutations in cancer.. *Journal of Clinical Oncology*, **2016**, 34, 11583-11583	2.2	5
54	Integrated Genomics for Pinpointing Survival Loci within Arm-Level Somatic Copy Number Alterations. *Cancer Cell*, **2016**, 29, 737-750	24.3	31
53	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
52	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
51	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
50	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. *Surgical Pathology Clinics*, **2015**, 8, 269-88	3.9	5
49	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
48	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. *Cell Systems*, **2015**, 1, 197-209	10.6	72

(2013-2015)

47	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
46	Integrative clinical genomics of advanced prostate cancer. *Cell*, **2015**, 161, 1215-1228	56.2	1765
45	Comprehensive genomic characterization of head and neck squamous cell carcinomas. *Nature*, **2015** , 517, 576-82	50.4	2332
44	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
43	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, 15544-9	11.5	229
42	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
41	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
40	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
39	Collection, integration and analysis of cancer genomic profiles: from data to insight. *Current Opinion in Genetics and Development*, **2014**, 24, 92-8	4.9	17
38	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	10.3	26
37	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
36	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. *Nature Genetics*, **2014**, 46, 424-6	36.3	231
35	P□DB 3.0: From plant phosphorylation sites to protein networks. *Nucleic Acids Research*, **2014**, 42, D1206-13	11.1	57
34	Disrupting KATP channels diminishes the estrogen-mediated protection in female mutant mice during ischemia-reperfusion. *Clinical Proteomics*, **2014**, 11, 19	5	16
33	BridgeDb app: unifying identifier mapping services for Cytoscape. *F1000Research*, **2014**, 3, 148	3.6	8
32	Analysis and Prediction of Protein Posttranslational Modification Sites **2013**, 91-106		0
31	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
30	The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, **2013**, 45, 1113-20	36.3	3933

29	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
28	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. *Science Signaling*, **2013**, 6, pl1	8.8	7715
27	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184
26	PiHelper: an open source framework for drug-target and antibody-target data. *Bioinformatics*, **2013**, 29, 2071-2	7.2	10
25	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. *Cancer Discovery*, **2012**, 2, 401-4	24.4	8578
24	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
23	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
22	Comprehensive genomic characterization of squamous cell lung cancers. *Nature*, **2012**, 489, 519-25	50.4	2820
21	Predicting and analyzing protein phosphorylation sites in plants using musite. *Frontiers in Plant Science*, **2012**, 3, 186	6.2	24
20	P(3)DB: An Integrated Database for Plant Protein Phosphorylation. *Frontiers in Plant Science*, **2012**, 3, 206	6.2	40
19	Phosphoproteomic analysis of seed maturation in Arabidopsis, rapeseed, and soybean. *Plant Physiology*, **2012**, 159, 517-28	6.6	79
18	BioJava: an open-source framework for bioinformatics in 2012. *Bioinformatics*, **2012**, 28, 2693-5	7.2	136
17	Correlation between posttranslational modification and intrinsic disorder in protein. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2012**, 94-103	1.3	44
16	CORRELATION BETWEEN POSTTRANSLATIONAL MODIFICATION AND INTRINSIC DISORDER IN PROTEIN **2011**,		10
15	Musite, a tool for global prediction of general and kinase-specific phosphorylation sites. *Molecular and Cellular Proteomics*, **2010**, 9, 2586-600	7.6	187
14	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. *BMC Bioinformatics*, **2010**, 11, 5	3.6	125
13	The Musite open-source framework for phosphorylation-site prediction. *BMC Bioinformatics*, **2010**, 11 Suppl 12, S9	3.6	10
12	Effector prediction in host-pathogen interaction based on a Markov model of a ubiquitous EPIYA motif. *BMC Genomics*, **2010**, 11 Suppl 3, S1	4.5	20

11	P3DB: a plant protein phosphorylation database. *Nucleic Acids Research*, **2009**, 37, D960-2	20.1	96
10	A New Machine Learning Approach for Protein Phosphorylation Site Prediction in Plants. *Lecture Notes in Computer Science*, **2009**, 18-29	0.9	13
9	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	0.9	15
8	Lossless Data Hiding Using Histogram Shifting Method Based on Integer Wavelets. *Lecture Notes in Computer Science*, **2006**, 323-332	0.9	57
7	Image Steganalysis Based on Statistical Moments of Wavelet Subband Histograms in DFT Domain **2005**,		4
6	Steganalysis Based on Multiple Features Formed by Statistical Moments of Wavelet Characteristic Functions. *Lecture Notes in Computer Science*, **2005**, 262-277	0.9	72
5	Effective steganalysis based on statistical moments of wavelet characteristic function **2005**,		27
4	Image steganalysis based on moments of characteristic functions using wavelet decomposition, prediction-error image, and neural network		56
3	Enabling cross-study analysis of RNA-Sequencing data		4
2	A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants		5
1	Immune and malignant cell phenotypes of ovarian cancer are determined by distinct mutational processes		1