

Jianjiong Gao

List of Publications by Citations

Source: <https://exaly.com/author-pdf/5142925/jianjiong-gao-publications-by-citations.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. <i>Cancer Discovery</i> , 2012 , 2, 401-4	24.4	8578
135	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012 , 490, 61-70	50.4	8025
134	Integrative analysis of complex cancer genomics and clinical profiles using the cBioPortal. <i>Science Signaling</i> , 2013 , 6, p1	8.8	7715
133	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7	50.4	5640
132	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013 , 45, 1113-20	36.3	3933
131	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9	50.4	3659
130	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50	50.4	3310
129	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
128	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012 , 489, 519-25	50.4	2820
127	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
126	Comprehensive genomic characterization of head and neck squamous cell carcinomas. <i>Nature</i> , 2015 , 517, 576-82	50.4	2332
125	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013 , 499, 43-9	50.4	2184
124	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
123	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
122	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96	56.2	1807
121	Integrative clinical genomics of advanced prostate cancer. <i>Cell</i> , 2015 , 161, 1215-1228	56.2	1765
120	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754

119	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25	56.2	1713
118	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90	56.2	1660
117	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , 2017 , 23, 703-713	50.5	1638
116	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
115	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
114	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
113	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
112	Integrated genomic characterization of oesophageal carcinoma. <i>Nature</i> , 2017 , 541, 169-175	50.4	965
111	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
110	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6	56.2	888
109	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
108	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020 , 578, 82-93	50.4	840
107	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
106	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , 2017 , 2017,	3.6	699
105	AACR Project GENIE: Powering Precision Medicine through an International Consortium. <i>Cancer Discovery</i> , 2017 , 7, 818-831	24.4	629
104	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. <i>Nature Biotechnology</i> , 2016 , 34, 155-63	44.5	465
103	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
102	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405

101	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , 2018 , 50, 645-651	36.3	380
100	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
99	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
98	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2018 , 33, 125-136.e3	24.3	338
97	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736.e3	24.3	324
96	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
95	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , 2017 , 7, 596-609	24.4	317
94	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018 , 33, 706-720.e9	24.3	275
93	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565	24.4	258
92	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
91	Recurrent SMARCA4 mutations in small cell carcinoma of the ovary. <i>Nature Genetics</i> , 2014 , 46, 424-6	36.3	231
90	Characterization of HPV and host genome interactions in primary head and neck cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15544-9	11.5	229
89	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
88	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
87	Musite, a tool for global prediction of general and kinase-specific phosphorylation sites. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2586-600	7.6	187
86	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , 2018 , 8, 49-58	24.4	180
85	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
84	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , 2018 , 8, 174-183	24.4	162

83	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2	10.6	159
82	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
81	The expanding landscape of TncohistoneTmutations in human cancers. <i>Nature</i> , 2019 , 567, 473-478	50.4	151
80	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , 2017 , 2017,	3.6	151
79	Deletions linked to TP53 loss drive cancer through p53-independent mechanisms. <i>Nature</i> , 2016 , 531, 471-475	50.4	142
78	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020 , 181, 236-249	56.2	140
77	BioJava: an open-source framework for bioinformatics in 2012. <i>Bioinformatics</i> , 2012 , 28, 2693-5	7.2	136
76	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e3	10.2	133
75	The BridgeDb framework: standardized access to gene, protein and metabolite identifier mapping services. <i>BMC Bioinformatics</i> , 2010 , 11, 5	3.6	125
74	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
73	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , 2017 , 9, 4	14.4	117
72	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018 , 33, 450-462.e10	24.3	114
71	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
70	P3DB: a plant protein phosphorylation database. <i>Nucleic Acids Research</i> , 2009 , 37, D960-2	20.1	96
69	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
68	Phosphoproteomic analysis of seed maturation in Arabidopsis, rapeseed, and soybean. <i>Plant Physiology</i> , 2012 , 159, 517-28	6.6	79
67	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015 , 1, 197-209	10.6	72
66	Steganalysis Based on Multiple Features Formed by Statistical Moments of Wavelet Characteristic Functions. <i>Lecture Notes in Computer Science</i> , 2005 , 262-277	0.9	72

65	A phase II study of frontline paclitaxel/carboplatin/bevacizumab, paclitaxel/carboplatin/temsirolimus, or ixabepilone/carboplatin/bevacizumab in advanced/recurrent endometrial cancer. <i>Gynecologic Oncology</i> , 2018 , 150, 274-281	4.9	67
64	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018 , 5, 180068.2	8.2	66
63	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
62	A harmonized meta-knowledgebase of clinical interpretations of somatic genomic variants in cancer. <i>Nature Genetics</i> , 2020 , 52, 448-457	36.3	58
61	PDB 3.0: From plant phosphorylation sites to protein networks. <i>Nucleic Acids Research</i> , 2014 , 42, D12062-131	13.1	57
60	Lossless Data Hiding Using Histogram Shifting Method Based on Integer Wavelets. <i>Lecture Notes in Computer Science</i> , 2006 , 323-332	0.9	57
59	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.3	56
58	Image steganalysis based on moments of characteristic functions using wavelet decomposition, prediction-error image, and neural network		56
57	Clinical and molecular characterization of patients with cancer of unknown primary in the modern era. <i>Annals of Oncology</i> , 2017 , 28, 3015-3021	10.3	52
56	Integration and Analysis of CPTAC Proteomics Data in the Context of Cancer Genomics in the cBioPortal. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1893-1898	7.6	50
55	Correlation between posttranslational modification and intrinsic disorder in protein. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012 , 94-103	1.3	44
54	P(3)DB: An Integrated Database for Plant Protein Phosphorylation. <i>Frontiers in Plant Science</i> , 2012 , 3, 206	6.2	40
53	Overcome tumor heterogeneity-imposed therapeutic barriers through convergent genomic biomarker discovery: A braided cancer river model of kidney cancer. <i>Seminars in Cell and Developmental Biology</i> , 2017 , 64, 98-106	7.5	37
52	PathwayMapper: a collaborative visual web editor for cancer pathways and genomic data. <i>Bioinformatics</i> , 2017 , 33, 2238-2240	7.2	31
51	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017 , 9, 113	14.4	31
50	Integrated Genomics for Pinpointing Survival Loci within Arm-Level Somatic Copy Number Alterations. <i>Cancer Cell</i> , 2016 , 29, 737-750	24.3	31
49	rCellMiner: exploring molecular profiles and drug response of the NCI-60 cell lines in R. <i>Bioinformatics</i> , 2016 , 32, 1272-4	7.2	30
48	Effective steganalysis based on statistical moments of wavelet characteristic function 2005 ,		27

47	The performance of BRCA1 immunohistochemistry for detecting germline, somatic, and epigenetic BRCA1 loss in high-grade serous ovarian cancer. <i>Annals of Oncology</i> , 2014 , 25, 2372-2378	10.3	26
46	Oncologist use and perception of large panel next-generation tumor sequencing. <i>Annals of Oncology</i> , 2017 , 28, 2298-2304	10.3	24
45	Predicting and analyzing protein phosphorylation sites in plants using musite. <i>Frontiers in Plant Science</i> , 2012 , 3, 186	6.2	24
44	Multicenter phase II study of temozolomide and myeloablative chemotherapy with autologous stem cell transplant for newly diagnosed anaplastic oligodendroglioma. <i>Neuro-Oncology</i> , 2017 , 19, 1380-1390	13.90	20
43	Effector prediction in host-pathogen interaction based on a Markov model of a ubiquitous EPIYA motif. <i>BMC Genomics</i> , 2010 , 11 Suppl 3, S1	4.5	20
42	Characteristics and Outcome of -Mutant Breast Cancer Defined through AACR Project GENIE, a Clinicogenomic Registry. <i>Cancer Discovery</i> , 2020 , 10, 526-535	24.4	19
41	Genomic profiling identifies somatic mutations predicting thromboembolic risk in patients with solid tumors. <i>Blood</i> , 2021 , 137, 2103-2113	2.2	19
40	Harnessing multimodal data integration to advance precision oncology. <i>Nature Reviews Cancer</i> , 2021 ,	31.3	18
39	Modeling biological and genetic diversity in upper tract urothelial carcinoma with patient derived xenografts. <i>Nature Communications</i> , 2020 , 11, 1975	17.4	17
38	Collection, integration and analysis of cancer genomic profiles: from data to insight. <i>Current Opinion in Genetics and Development</i> , 2014 , 24, 92-8	4.9	17
37	Disrupting KATP channels diminishes the estrogen-mediated protection in female mutant mice during ischemia-reperfusion. <i>Clinical Proteomics</i> , 2014 , 11, 19	5	16
36	Steganalysis Using High-Dimensional Features Derived from Co-occurrence Matrix and Class-Wise Non-Principal Components Analysis (CNPCA). <i>Lecture Notes in Computer Science</i> , 2006 , 49-60	0.9	15
35	An integrative somatic mutation analysis to identify pathways linked with survival outcomes across 19 cancer types. <i>Bioinformatics</i> , 2016 , 32, 1643-51	7.2	14
34	A New Machine Learning Approach for Protein Phosphorylation Site Prediction in Plants. <i>Lecture Notes in Computer Science</i> , 2009 , 18-29	0.9	13
33	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016 , 44, D986-91	20.1	11
32	Genomic characterization of metastatic patterns from prospective clinical sequencing of 25,000 patients.. <i>Cell</i> , 2022 , 185, 563-575.e11	56.2	11
31	OncoTree: A Cancer Classification System for Precision Oncology. <i>JCO Clinical Cancer Informatics</i> , 2021 , 5, 221-230	5.2	11
30	PiHelper: an open source framework for drug-target and antibody-target data. <i>Bioinformatics</i> , 2013 , 29, 2071-2	7.2	10

29	CORRELATION BETWEEN POSTTRANSLATIONAL MODIFICATION AND INTRINSIC DISORDER IN PROTEIN 2011 ,		10
28	The Musite open-source framework for phosphorylation-site prediction. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 12, S9	3.6	10
27	Leveraging Systematic Functional Analysis to Benchmark an Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. <i>Cancer Research</i> , 2020 , 80, 4233-4243	10.1	9
26	BioJava-ModFinder: identification of protein modifications in 3D structures from the Protein Data Bank. <i>Bioinformatics</i> , 2017 , 33, 2047-2049	7.2	8
25	BridgeDb app: unifying identifier mapping services for Cytoscape. <i>F1000Research</i> , 2014 , 3, 148	3.6	8
24	G2S: a web-service for annotating genomic variants on 3D protein structures. <i>Bioinformatics</i> , 2018 , 34, 1949-1950	7.2	7
23	Multomic Integration of Public Oncology Databases in Bioconductor. <i>JCO Clinical Cancer Informatics</i> , 2020 , 4, 958-971	5.2	7
22	Integrated digital pathology at scale: A solution for clinical diagnostics and cancer research at a large academic medical center. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021 , 28, 1874-1884	8.6	7
21	Abstract 5277: The cBioPortal for cancer genomics and its application in precision oncology 2016 ,		6
20	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021 , 53, 1577-1583	5.3	6
19	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. <i>Surgical Pathology Clinics</i> , 2015 , 8, 269-88	3.9	5
18	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas 2018 ,		5
17	OncoKB: Annotation of the oncogenic effect and treatment implications of somatic mutations in cancer.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 11583-11583	2.2	5
16	A harmonized meta-knowledgebase of clinical interpretations of cancer genomic variants		5
15	Translational Bioinformatics and Clinical Research (Biomedical) Informatics. <i>Clinics in Laboratory Medicine</i> , 2016 , 36, 153-81	2.1	4
14	Image Steganalysis Based on Statistical Moments of Wavelet Subband Histograms in DFT Domain 2005 ,		4
13	Enabling cross-study analysis of RNA-Sequencing data		4
12	Comprehensive Genomic Analysis of Metastatic Non-Clear-Cell Renal Cell Carcinoma to Identify Therapeutic Targets. <i>JCO Precision Oncology</i> , 2019 , 3,	3.6	4

11	How oncogenic mutations activate human MAP kinase 1 (MEK1): a molecular dynamics simulation study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020 , 38, 3942-3958	3.6	3
10	MITI minimum information guidelines for highly multiplexed tissue images.. <i>Nature Methods</i> , 2022 , 19, 262-267	21.6	2
9	Detecting Cancer Survival Related Gene Markers Based on Rectified Factor Network. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 349	5.8	1
8	Immune and malignant cell phenotypes of ovarian cancer are determined by distinct mutational processes		1
7	Analysis and Prediction of Protein Posttranslational Modification Sites 2013 , 91-106		0
6	Semisupervised Training of a Brain MRI Tumor Detection Model Using Mined Annotations.. <i>Radiology</i> , 2022 , 210817	20.5	0
5	Genome Nexus: A Comprehensive Resource for the Annotation and Interpretation of Genomic Variants in Cancer.. <i>JCO Clinical Cancer Informatics</i> , 2022 , 6, e2100144	5.2	0
4	Annotation of Somatic Genomic Variants in Hematologic Diseases Using OncoKB, a Precision Oncology Knowledgebase. <i>Blood</i> , 2019 , 134, 2148-2148	2.2	0
3	CD38 in Advanced Prostate Cancers. <i>European Urology</i> , 2021 , 79, 736-746	10.2	0
2	Extended Mutational Profiling By MSK-IMPACTTM Identifies Mutations Predicting Thromboembolic Risk in Patients with Solid Tumor Malignancy. <i>Blood</i> , 2019 , 134, 633-633	2.2	
1	The long tail of significantly mutated genes in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2017 , 35, 131-131	2.2	