

# Giovanni Ciriello

## List of Publications by Citations

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

58 papers	16,268 citations	32 h-index	63 g-index
63 ext. papers	20,897 ext. citations	22 avg, IF	5.41 L-index

#	Paper	IF	Citations
58	The somatic genomic landscape of glioblastoma. <i>Cell</i> , <b>2013</b> , 155, 462-77	56.2	2900
57	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 2481-98	59.2	1828
56	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , <b>2015</b> , 161, 1681-96	56.2	1807
55	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , <b>2015</b> , 163, 1011-25	56.2	1713
54	Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , <b>2014</b> , 159, 676-90	56.2	1660
53	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124
52	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , <b>2015</b> , 163, 506-19	56.2	1055
51	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , <b>2013</b> , 45, 1127-33	36.3	889
50	Mutual exclusivity analysis identifies oncogenic network modules. <i>Genome Research</i> , <b>2012</b> , 22, 398-406	9.7	452
49	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , <b>2016</b> , 29, 723-736	24.3	324
48	Generation of tumor-targeted human T lymphocytes from induced pluripotent stem cells for cancer therapy. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 928-33	44.5	261
47	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2016</b> , 14, 2476-89	10.6	228
46	An epidemiologic and genomic investigation into the obesity paradox in renal cell carcinoma. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 1862-70	9.7	161
45	Synaptic proximity enables NMDAR signalling to promote brain metastasis. <i>Nature</i> , <b>2019</b> , 573, 526-531	50.4	158
44	Loss of the HVEM Tumor Suppressor in Lymphoma and Restoration by Modified CAR-T Cells. <i>Cell</i> , <b>2016</b> , 167, 405-418.e13	56.2	154
43	SQSTM1 is a pathogenic target of 5q copy number gains in kidney cancer. <i>Cancer Cell</i> , <b>2013</b> , 24, 738-50	24.3	111
42	Pan-Cancer Landscape of Aberrant DNA Methylation across Human Tumors. <i>Cell Reports</i> , <b>2018</b> , 25, 1066-1080.e8	10.6	104

41	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. <i>Genome Biology</i> , <b>2015</b> , 16, 45	18.3	101
40	Comprehensive Genetic Landscape of Uveal Melanoma by Whole-Genome Sequencing. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 1190-1198	11	99
39	The molecular diversity of Luminal A breast tumors. <i>Breast Cancer Research and Treatment</i> , <b>2013</b> , 141, 409-20	4.4	90
38	Comparison of computational methods for the identification of topologically associating domains. <i>Genome Biology</i> , <b>2018</b> , 19, 217	18.3	86
37	AlignNemo: a local network alignment method to integrate homology and topology. <i>PLoS ONE</i> , <b>2012</b> , 7, e38107	3.7	73
36	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , <b>2015</b> , 1, 197-209	10.6	72
35	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
34	A review on models and algorithms for motif discovery in protein-protein interaction networks. <i>Briefings in Functional Genomics &amp; Proteomics</i> , <b>2008</b> , 7, 147-56		66
33	The molecular basis of breast cancer pathological phenotypes. <i>Journal of Pathology</i> , <b>2017</b> , 241, 375-391	9.4	62
32	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. <i>Cancer Cell</i> , <b>2017</b> , 32, 155-168.e6	24.3	61
31	EZH2 oncogenic mutations drive epigenetic, transcriptional, and structural changes within chromatin domains. <i>Nature Genetics</i> , <b>2019</b> , 51, 517-528	36.3	52
30	The Oncogenic Action of NRF2 Depends on De-glycation by Fructosamine-3-Kinase. <i>Cell</i> , <b>2019</b> , 178, 807-819.e21	36.2	51
29	Pan-cancer inference of intra-tumor heterogeneity reveals associations with different forms of genomic instability. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007669	6	43
28	Genetic and epigenetic inactivation of controls mTORC1 and response to EZH2 inhibition in follicular lymphoma. <i>Science Translational Medicine</i> , <b>2017</b> , 9,	17.5	32
27	Uncoupling protein 2 reprograms the tumor microenvironment to support the anti-tumor immune cycle. <i>Nature Immunology</i> , <b>2019</b> , 20, 206-217	19.1	31
26	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , <b>2014</b> , 157, 753	56.2	29
25	Finding 3D motifs in ribosomal RNA structures. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e29	20.1	28
24	Frequent disruption of the RB pathway in indolent follicular lymphoma suggests a new combination therapy. <i>Journal of Experimental Medicine</i> , <b>2014</b> , 211, 1379-91	16.6	26

23	Using MEMo to discover mutual exclusivity modules in cancer. <i>Current Protocols in Bioinformatics</i> , <b>2013</b> , Chapter 8, Unit 8.17	24.2	26
22	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. <i>Cancer Cell</i> , <b>2020</b> , 37, 674-689.e12	24.3	23
21	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. <i>PLoS Computational Biology</i> , <b>2016</b> , 12, e1004765	5	23
20	Collection, integration and analysis of cancer genomic profiles: from data to insight. <i>Current Opinion in Genetics and Development</i> , <b>2014</b> , 24, 92-8	4.9	17
19	Pan-SRC kinase inhibition blocks B-cell receptor oncogenic signaling in non-Hodgkin lymphoma. <i>Blood</i> , <b>2018</b> , 131, 2345-2356	2.2	15
18	Cell-autonomous inflammation of BRCA1-deficient ovarian cancers drives both tumor-intrinsic immunoreactivity and immune resistance via STING. <i>Cell Reports</i> , <b>2021</b> , 36, 109412	10.6	12
17	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , <b>2020</b> , 1, 653-664	15.4	11
16	Impact of recurrent copy number alterations and cancer gene mutations on the predictive accuracy of prognostic models in clear cell renal cell carcinoma. <i>Journal of Urology</i> , <b>2014</b> , 192, 24-9	2.5	11
15	Nongenetic Evolution Drives Lung Adenocarcinoma Spatial Heterogeneity and Progression. <i>Cancer Discovery</i> , <b>2021</b> , 11, 1490-1507	24.4	11
14	Analysis of interactions between ribosomal proteins and RNA structural motifs. <i>BMC Bioinformatics</i> , <b>2010</b> , 11 Suppl 1, S41	3.6	10
13	Histone acetylation dynamics modulates chromatin conformation and allele-specific interactions at oncogenic loci. <i>Nature Genetics</i> , <b>2021</b> , 53, 650-662	36.3	8
12	Sustained androgen receptor signaling is a determinant of melanoma cell growth potential and tumorigenesis. <i>Journal of Experimental Medicine</i> , <b>2021</b> , 218,	16.6	6
11	Systematic inference and comparison of multi-scale chromatin sub-compartments connects spatial organization to cell phenotypes. <i>Nature Communications</i> , <b>2021</b> , 12, 2439	17.4	5
10	Cancer Cells Retrace a Stepwise Differentiation Program during Malignant Progression. <i>Cancer Discovery</i> , <b>2021</b> , 11, 2638-2657	24.4	4
9	The many faces of cancer evolution. <i>IScience</i> , <b>2021</b> , 24, 102403	6.1	4
8	Discovering functional evolutionary dependencies in human cancers. <i>Nature Genetics</i> , <b>2020</b> , 52, 1198-1207.	26.3	3
7	Exploring chromatin conformation and gene co-expression through graph embedding. <i>Bioinformatics</i> , <b>2020</b> , 36, i700-i708	7.2	2
6	Dynamic Emergence of Observed and Hidden Intra-tumor Heterogeneity. <i>IScience</i> , <b>2019</b> , 21, 157-167	6.1	1

5	Methods for the Analysis of Topologically Associating Domains (TADs). <i>Methods in Molecular Biology</i> , <b>2022</b> , 2301, 39-59	1.4	1
4	Systematic assessment of gene co-regulation within chromatin domains determines differentially active domains across human cancers. <i>Genome Biology</i> , <b>2021</b> , 22, 218	18.3	1
3	Frequent 4EBP1 Amplification Induces Synthetic Dependence on FGFR Signaling in Cancer. <i>Cancers</i> , <b>2022</b> , 14, 2397	6.6	1
2	One size does not fit all for mutational signatures.. <i>Nature Cancer</i> , <b>2020</b> , 1, 158-159	15.4	
1	Actionable secondary driver mutations in BRAFWT and NRASWT metastatic cutaneous melanoma using the Caris Molecular Intelligence profiling.. <i>Journal of Clinical Oncology</i> , <b>2016</b> , 34, e21021-e21021	2.2	