Giovanni Ciriello

List of Publications by Year in Descending Order

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	Methods for the Analysis of Topologically Associating Domains (TADs). *Methods in Molecular Biology*, **2022**, 2301, 39-59	1.4	1
57	Frequent 4EBP1 Amplification Induces Synthetic Dependence on FGFR Signaling in Cancer. *Cancers*, **2022**, 14, 2397	6.6	1
56	Sustained androgen receptor signaling is a determinant of melanoma cell growth potential and tumorigenesis. *Journal of Experimental Medicine*, **2021**, 218,	16.6	6
55	Cancer Cells Retrace a Stepwise Differentiation Program during Malignant Progression. *Cancer Discovery*, **2021**, 11, 2638-2657	24.4	4
54	The many faces of cancer evolution. *IScience*, **2021**, 24, 102403	6.1	4
53	Histone acetylation dynamics modulates chromatin conformation and allele-specific interactions at oncogenic loci. *Nature Genetics*, **2021**, 53, 650-662	36.3	8
52	Systematic inference and comparison of multi-scale chromatin sub-compartments connects spatial organization to cell phenotypes. *Nature Communications*, **2021**, 12, 2439	17.4	5
51	Nongenetic Evolution Drives Lung Adenocarcinoma Spatial Heterogeneity and Progression. *Cancer Discovery*, **2021**, 11, 1490-1507	24.4	11
50	Cell-autonomous inflammation of BRCA1-deficient ovarian cancers drives both tumor-intrinsic immunoreactivity and immune resistance via STING. *Cell Reports*, **2021**, 36, 109412	10.6	12
49	Systematic assessment of gene co-regulation within chromatin domains determines differentially active domains across human cancers. *Genome Biology*, **2021**, 22, 218	18.3	1
48	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. *Nature Cancer*, **2020**, 1, 653-664	15.4	11
47	One size does not fit all for mutational signatures.. *Nature Cancer*, **2020**, 1, 158-159	15.4	
46	Cathepsin S Regulates Antigen Processing and T Cell Activity in Non-Hodgkin Lymphoma. *Cancer Cell*, **2020**, 37, 674-689.e12	24.3	23
45	Exploring chromatin conformation and gene co-expression through graph embedding. *Bioinformatics*, **2020**, 36, i700-i708	7.2	2
44	Discovering functional evolutionary dependencies in human cancers. *Nature Genetics*, **2020**, 52, 1198-1207	36.3	3
43	Uncoupling protein 2 reprograms the tumor microenvironment to support the anti-tumor immune cycle. *Nature Immunology*, **2019**, 20, 206-217	19.1	31
42	EZH2 oncogenic mutations drive epigenetic, transcriptional, and structural changes within chromatin domains. *Nature Genetics*, **2019**, 51, 517-528	36.3	52

#	Reference		
41	The Oncogenic Action of NRF2 Depends on De-glycation by Fructosamine-3-Kinase. *Cell*, **2019**, 178, 807-819.e21	56.2	11
40	Dynamic Emergence of Observed and Hidden Intra-tumor Heterogeneity. *IScience*, **2019**, 21, 157-167	6.1	1
39	Synaptic proximity enables NMDAR signalling to promote brain metastasis. *Nature*, **2019**, 573, 526-531	50.4	158
38	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
37	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
36	Pan-SRC kinase inhibition blocks B-cell receptor oncogenic signaling in non-Hodgkin lymphoma. *Blood*, **2018**, 131, 2345-2356	2.2	15
35	Comparison of computational methods for the identification of topologically associating domains. *Genome Biology*, **2018**, 19, 217	18.3	86
34	Pan-Cancer Landscape of Aberrant DNA Methylation across Human Tumors. *Cell Reports*, **2018**, 25, 1066-1080.e8	10.6	304
33	Pan-cancer inference of intra-tumor heterogeneity reveals associations with different forms of genomic instability. *PLoS Genetics*, **2018**, 14, e1007669	6	43
32	Conditional Selection of Genomic Alterations Dictates Cancer Evolution and Oncogenic Dependencies. *Cancer Cell*, **2017**, 32, 155-168.e6	24.3	61
31	Genetic and epigenetic inactivation of controls mTORC1 and response to EZH2 inhibition in follicular lymphoma. *Science Translational Medicine*, **2017**, 9,	17.5	32
30	The molecular basis of breast cancer pathological phenotypes. *Journal of Pathology*, **2017**, 241, 375-391	9.4	62
29	Comprehensive Genetic Landscape of Uveal Melanoma by Whole-Genome Sequencing. *American Journal of Human Genetics*, **2016**, 99, 1190-1198	11	99
28	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. *Cell Reports*, **2016**, 14, 2476-89	10.6	228
27	Actionable secondary driver mutations in BRAFWT and NRASWT metastatic cutaneous melanoma using the Caris Molecular Intelligence profiling.. *Journal of Clinical Oncology*, **2016**, 34, e21021-e21021	2.2	
26	A Multi-Method Approach for Proteomic Network Inference in 11 Human Cancers. *PLoS Computational Biology*, **2016**, 12, e1004765	5	23
25	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*, **2016**, 29, 723-736	24.3	324
24	Loss of the HVEM Tumor Suppressor in Lymphoma and Restoration by Modified CAR-T Cells. *Cell*, **2016**, 167, 405-418.e13	56.2	154

23	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
22	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
21	Systematic identification of cancer driving signaling pathways based on mutual exclusivity of genomic alterations. *Genome Biology*, **2015**, 16, 45	18.3	101
20	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
19	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. *Cell Systems*, **2015**, 1, 197-209	10.6	72
18	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
17	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
16	Frequent disruption of the RB pathway in indolent follicular lymphoma suggests a new combination therapy. *Journal of Experimental Medicine*, **2014**, 211, 1379-91	16.6	26
15	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
14	The Somatic Genomic Landscape of Glioblastoma. *Cell*, **2014**, 157, 753	56.2	29
13	Impact of recurrent copy number alterations and cancer gene mutations on the predictive accuracy of prognostic models in clear cell renal cell carcinoma. *Journal of Urology*, **2014**, 192, 24-9	2.5	11
12	Generation of tumor-targeted human T lymphocytes from induced pluripotent stem cells for cancer therapy. *Nature Biotechnology*, **2013**, 31, 928-33	44.5	261
11	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
10	The molecular diversity of Luminal A breast tumors. *Breast Cancer Research and Treatment*, **2013**, 141, 409-20	4.4	90
9	Emerging landscape of oncogenic signatures across human cancers. *Nature Genetics*, **2013**, 45, 1127-33	36.3	889
8	SQSTM1 is a pathogenic target of 5q copy number gains in kidney cancer. *Cancer Cell*, **2013**, 24, 738-50	24.3	111
7	Using MEMo to discover mutual exclusivity modules in cancer. *Current Protocols in Bioinformatics*, **2013**, Chapter 8, Unit 8.17	24.2	26
6	An epidemiologic and genomic investigation into the obesity paradox in renal cell carcinoma. *Journal of the National Cancer Institute*, **2013**, 105, 1862-70	9.7	161

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5	Mutual exclusivity analysis identifies oncogenic network modules. *Genome Research*, **2012**, 22, 398-406	9.7	452
4	AlignNemo: a local network alignment method to integrate homology and topology. *PLoS ONE*, **2012**, 7, e38107	3.7	73
3	Analysis of interactions between ribosomal proteins and RNA structural motifs. *BMC Bioinformatics*, **2010**, 11 Suppl 1, S41	3.6	10
2	Finding 3D motifs in ribosomal RNA structures. *Nucleic Acids Research*, **2009**, 37, e29	20.1	28
1	A review on models and algorithms for motif discovery in protein-protein interaction networks. *Briefings in Functional Genomics & Proteomics*, **2008**, 7, 147-56		66