

# Christina Curtis

## List of Publications by Year in descending order

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Version: 2024-02-01

84  
papers

17,303  
citations

70961

41  
h-index

64668

79  
g-index

105  
all docs

105  
docs citations

105  
times ranked

29769  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	13.7	4,708
2	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	13.7	1,778
3	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4009-4014.	3.3	1,471
4	Clonal replacement of tumor-specific T cells following PD-1 blockade. Nature Medicine, 2019, 25, 1251-1259.	15.2	974
5	A Big Bang model of human colorectal tumor growth. Nature Genetics, 2015, 47, 209-216.	9.4	867
6	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	6.0	781
7	Sensitive and specific multi-cancer detection and localization using methylation signatures in cell-free DNA. Annals of Oncology, 2020, 31, 745-759.	0.6	770
8	The shaping and functional consequences of the microRNA landscape in breast cancer. Nature, 2013, 497, 378-382.	13.7	370
9	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. Cell, 2018, 173, 1398-1412.e22.	13.5	362
10	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	5.8	356
11	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	13.5	334
12	Quantitative evidence for early metastatic seeding in colorectal cancer. Nature Genetics, 2019, 51, 1113-1122.	9.4	315
13	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. Cell Stem Cell, 2017, 21, 78-90.e6.	5.2	280
14	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	13.7	239
15	Quantification of subclonal selection in cancer from bulk sequencing data. Nature Genetics, 2018, 50, 895-903.	9.4	222
16	Multi-cancer analysis of clonality and the timing of systemic spread in paired primary tumors and metastases. Nature Genetics, 2020, 52, 701-708.	9.4	203
17	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. Nature, 2020, 580, 136-141.	13.7	203
18	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. Genome Biology, 2014, 15, 431.	3.8	178

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19	Between-region genetic divergence reflects the mode and tempo of tumor evolution. <i>Nature Genetics</i> , 2017, 49, 1015-1024.	9.4	144
20	A p53 Super-tumor Suppressor Reveals a Tumor Suppressive p53-Ptpn14-Yap Axis in Pancreatic Cancer. <i>Cancer Cell</i> , 2017, 32, 460-473.e6.	7.7	142
21	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	13.5	135
22	Transcriptional profiling of MnSOD-mediated lifespan extension in <i>Drosophila</i> reveals a species-general network of aging and metabolic genes. <i>Genome Biology</i> , 2007, 8, R262.	13.9	123
23	<i>ZNF703</i> is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. <i>EMBO Molecular Medicine</i> , 2011, 3, 167-180.	3.3	119
24	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. <i>Science Translational Medicine</i> , 2013, 5, 181re1.	5.8	108
25	Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice. <i>Nature Genetics</i> , 2018, 50, 483-486.	9.4	101
26	Inter-cellular CRISPR screens reveal regulators of cancer cell phagocytosis. <i>Nature</i> , 2021, 597, 549-554.	13.7	95
27	Bayesian Network Inference Modeling Identifies <i>TRIB1</i> as a Novel Regulator of Cell-Cycle Progression and Survival in Cancer Cells. <i>Cancer Research</i> , 2017, 77, 1575-1585.	0.4	94
28	Swift: primary data analysis for the Illumina Solexa sequencing platform. <i>Bioinformatics</i> , 2009, 25, 2194-2199.	1.8	83
29	The pitfalls of platform comparison: DNA copy number array technologies assessed. <i>BMC Genomics</i> , 2009, 10, 588.	1.2	80
30	Characterizing the ecological and evolutionary dynamics of cancer. <i>Nature Genetics</i> , 2020, 52, 759-767.	9.4	77
31	Single-cell analyses define a continuum of cell state and composition changes in the malignant transformation of polyps to colorectal cancer. <i>Nature Genetics</i> , 2022, 54, 985-995.	9.4	77
32	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	1.5	76
33	The <i>AMBRA1</i> E3 ligase adaptor regulates the stability of cyclin D. <i>Nature</i> , 2021, 592, 794-798.	13.7	76
34	A CRISPR/Cas9-Engineered <i>ARID1A</i> -Deficient Human Gastric Cancer Organoid Model Reveals Essential and Nonessential Modes of Oncogenic Transformation. <i>Cancer Discovery</i> , 2021, 11, 1562-1581.	7.7	75
35	Single-Molecule Genomic Data Delineate Patient-Specific Tumor Profiles and Cancer Stem Cell Organization. <i>Cancer Research</i> , 2013, 73, 41-49.	0.4	68
36	Cell of Origin Influences Pancreatic Cancer Subtype. <i>Cancer Discovery</i> , 2021, 11, 660-677.	7.7	58

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37	<i>Drosophila melanogaster</i> p53 has developmental stage-specific and sex-specific effects on adult life span indicative of sexual antagonistic pleiotropy. <i>Aging</i> , 2009, 1, 903-936.	1.4	58
38	The m <sup>6</sup> A RNA demethylase FTO is a HIF-independent synthetic lethal partner with the VHL tumor suppressor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21441-21449.	3.3	56
39	Metabolic Profiling Reveals a Dependency of Human Metastatic Breast Cancer on Mitochondrial Serine and One-Carbon Unit Metabolism. <i>Molecular Cancer Research</i> , 2022, 18, 599-611.	1.5	56
40	The Breast Cancer Oncogene EMSY Represses Transcription of Antimetastatic microRNA miR-31. <i>Molecular Cell</i> , 2014, 53, 806-818.	4.5	55
41	A screen of apoptosis and senescence regulatory genes for life span effects when over-expressed in <i>Drosophila</i> . <i>Aging</i> , 2009, 1, 191-211.	1.4	52
42	Harnessing Tumor Evolution to Circumvent Resistance. <i>Trends in Genetics</i> , 2018, 34, 639-651.	2.9	49
43	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. <i>Cancer Research</i> , 2015, 75, 194-202.	0.4	48
44	Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing. <i>ELife</i> , 2020, 9, .	2.8	47
45	Zmat3 Is a Key Splicing Regulator in the p53 Tumor Suppression Program. <i>Molecular Cell</i> , 2020, 80, 452-469.e9.	4.5	44
46	Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. <i>Nature Communications</i> , 2019, 10, 657.	5.8	43
47	Pathologic and molecular responses to neoadjuvant trastuzumab and/or lapatinib from a phase II randomized trial in HER2-positive breast cancer (TRIO-US B07). <i>Nature Communications</i> , 2020, 11, 5824.	5.8	42
48	Spatial proteomic characterization of HER2-positive breast tumors through neoadjuvant therapy predicts response. <i>Nature Cancer</i> , 2021, 2, 400-413.	5.7	41
49	Looking backward in time to define the chronology of metastasis. <i>Nature Communications</i> , 2020, 11, 3213.	5.8	39
50	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	2.1	38
51	Big Bang Tumor Growth and Clonal Evolution. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a028381.	2.9	38
52	Explaining differences in saturation levels for Affymetrix GeneChip® arrays. <i>Nucleic Acids Research</i> , 2007, 35, 4154-4163.	6.5	37
53	A population genetics perspective on the determinants of intra-tumor heterogeneity. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2017, 1867, 109-126.	3.3	37
54	Many private mutations originate from the first few divisions of a human colorectal adenoma. <i>Journal of Pathology</i> , 2015, 237, 355-362.	2.1	30

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55	Chromatin regulators mediate anthracycline sensitivity in breast cancer. <i>Nature Medicine</i> , 2019, 25, 1721-1727.	15.2	27
56	Assessment of <i>ERBB2</i> / <i>HER2</i> Status in <i>HER2</i> -Equivocal Breast Cancers by FISH and 2013/2014 ASCO-CAP Guidelines. <i>JAMA Oncology</i> , 2019, 5, 366.	3.4	26
57	The <i>Mettl3</i> epitranscriptomic writer amplifies p53 stress responses. <i>Molecular Cell</i> , 2022, 82, 2370-2384.e10.	4.5	22
58	Abstract 5016: The human sub-ependymal zone harbors glioblastoma precursors and represents a distinct therapeutic target.. <i>Cancer Research</i> , 2013, 73, 5016-5016.	0.4	21
59	Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer. <i>Nature Communications</i> , 2022, 13, .	5.8	21
60	Genomic profiling of breast cancers. <i>Current Opinion in Obstetrics and Gynecology</i> , 2015, 27, 34-39.	0.9	19
61	The oncogene <i>AAMDC</i> links PI3K-AKT-mTOR signaling with metabolic reprogramming in estrogen receptor-positive breast cancer. <i>Nature Communications</i> , 2021, 12, 1920.	5.8	19
62	Organoids reveal cancer dynamics. <i>Nature</i> , 2018, 556, 441-442.	13.7	16
63	A High-Dimensional Window into the Micro-Environment of Triple Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 316.	1.7	16
64	Product Length, Dye Choice, and Detection Chemistry in the Bead-Emulsion Amplification of Millions of Single DNA Molecules in Parallel. <i>Analytical Chemistry</i> , 2009, 81, 5770-5776.	3.2	15
65	The importance of platform annotation in interpreting microarray data. <i>Lancet Oncology</i> , The, 2010, 11, 717.	5.1	14
66	Molecular Heterogeneity and Evolution in Breast Cancer. <i>Annual Review of Cancer Biology</i> , 2021, 5, 79-94.	2.3	14
67	Precise inference of copy number alterations in tumor samples from SNP arrays. <i>Bioinformatics</i> , 2013, 29, 2964-2970.	1.8	12
68	Inferring Tumor Phylogenies from Multi-region Sequencing. <i>Cell Systems</i> , 2016, 3, 12-14.	2.9	12
69	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 70.	2.2	11
70	Androgen receptor agonists as breast cancer therapeutics. <i>Nature Medicine</i> , 2021, 27, 198-199.	15.2	7
71	Calling Sample Mix-Ups in Cancer Population Studies. <i>PLoS ONE</i> , 2012, 7, e41815.	1.1	6
72	Quantifying mutations in healthy blood. <i>Science</i> , 2020, 367, 1426-1427.	6.0	4

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73	A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , .		2
74	A role for chromatin regulatory dynamics in breast cancer evolution. Nature Medicine, 2018, 24, 1309-1311.	15.2	2
75	A tumor "personality" test to guide therapeutic decision making. Cancer Cell, 2021, 39, 747-749.	7.7	2
76	Transcriptome and genome evolution during HER2-amplified breast neoplasia. Breast Cancer Research, 2021, 23, 73.	2.2	2
77	Abstract 123: A CRISPR/Cas9-engineered ARID1A-deficient human gastric cancer organoid model reveals essential and non-essential modes of oncogenic transformation. , 2021, , .		1
78	Early mutation bursts in colorectal tumors. PLoS ONE, 2017, 12, e0172516.	1.1	1
79	Preface. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1876, 188617.	3.3	0
80	Abstract SY36-01: Exploiting intra-tumor heterogeneity through agent-based models of tumor growth to infer properties of human malignancies.. , 2013, , .		0
81	Abstract B020: A copy number and expression based classifier for breast cancer tumors. , 2013, , .		0
82	Higher peripheral lymphocyte count to predict survival in triple-negative breast cancer (TNBC).. Journal of Clinical Oncology, 2016, 34, 1010-1010.	0.8	0
83	Population Genetics Approaches to Quantify Clonal Evolution. Blood, 2017, 130, SCI-37-SCI-37.	0.6	0
84	Patient perspectives on window of opportunity clinical trials in early-stage breast cancer. Breast Cancer Research and Treatment, 2022, , 1.	1.1	0