

Christina Curtis

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

17,303
citations

71102

41
h-index

64796

79
g-index

105
all docs

105
docs citations

105
times ranked

29769
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.4	56
2	Patient perspectives on window of opportunity clinical trials in early-stage breast cancer. <i>Breast Cancer Research and Treatment</i> , 2022, , 1.	2.5	0
3	The Mettl3 epitranscriptomic writer amplifies p53 stress responses. <i>Molecular Cell</i> , 2022, 82, 2370-2384.e10.	9.7	22
4	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.	21.4	77
5	Combinatorial immunotherapies overcome MYC-driven immune evasion in triple negative breast cancer. <i>Nature Communications</i> , 2022, 13, .	12.8	21
6	Molecular Heterogeneity and Evolution in Breast Cancer. <i>Annual Review of Cancer Biology</i> , 2021, 5, 79-94.	4.5	14
7	A High-Dimensional Window into the Micro-Environment of Triple Negative Breast Cancer. <i>Cancers</i> , 2021, 13, 316.	3.7	16
8	Androgen receptor agonists as breast cancer therapeutics. <i>Nature Medicine</i> , 2021, 27, 198-199.	30.7	7
9	The oncogene AAMDC links PI3K-AKT-mTOR signaling with metabolic reprogramming in estrogen receptor-positive breast cancer. <i>Nature Communications</i> , 2021, 12, 1920.	12.8	19
10	An expanded universe of cancer targets. <i>Cell</i> , 2021, 184, 1142-1155.	28.9	135
11	Cell of Origin Influences Pancreatic Cancer Subtype. <i>Cancer Discovery</i> , 2021, 11, 660-677.	9.4	58
12	The AMBRA1 E3 ligase adaptor regulates the stability of cyclin D. <i>Nature</i> , 2021, 592, 794-798.	27.8	76
13	Spatial proteomic characterization of HER2-positive breast tumors through neoadjuvant therapy predicts response. <i>Nature Cancer</i> , 2021, 2, 400-413.	13.2	41
14	A tumor "personality" test to guide therapeutic decision making. <i>Cancer Cell</i> , 2021, 39, 747-749.	16.8	2
15	Transcriptome and genome evolution during HER2-amplified breast neoplasia. <i>Breast Cancer Research</i> , 2021, 23, 73.	5.0	2
16	Abstract 123: A CRISPR/Cas9-engineered ARID1A-deficient human gastric cancer organoid model reveals essential and non-essential modes of oncogenic transformation. , 2021, , .		1
17	Inter-cellular CRISPR screens reveal regulators of cancer cell phagocytosis. <i>Nature</i> , 2021, 597, 549-554.	27.8	95
18	Preface. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1876, 188617.	7.4	0

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19	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.	9.4	75
20	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.	12.8	42
21	Characterizing the ecological and evolutionary dynamics of cancer. <i>Nature Genetics</i> , 2020, 52, 759-767.	21.4	77
22	The m ⁶ 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.	7.1	56
23	Zmat3 Is a Key Splicing Regulator in the p53 Tumor Suppression Program. <i>Molecular Cell</i> , 2020, 80, 452-469.e9.	9.7	44
24	Multi-cancer analysis of clonality and the timing of systemic spread in paired primary tumors and metastases. <i>Nature Genetics</i> , 2020, 52, 701-708.	21.4	203
25	CRISPR screens in cancer spheroids identify 3D growth-specific vulnerabilities. <i>Nature</i> , 2020, 580, 136-141.	27.8	203
26	Quantifying mutations in healthy blood. <i>Science</i> , 2020, 367, 1426-1427.	12.6	4
27	Looking backward in time to define the chronology of metastasis. <i>Nature Communications</i> , 2020, 11, 3213.	12.8	39
28	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
29	Sensitive and specific multi-cancer detection and localization using methylation signatures in cell-free DNA. <i>Annals of Oncology</i> , 2020, 31, 745-759.	1.2	770
30	Novel insights into breast cancer copy number genetic heterogeneity revealed by single-cell genome sequencing. <i>ELife</i> , 2020, 9, .	6.0	47
31	Clonal replacement of tumor-specific T cells following PD-1 blockade. <i>Nature Medicine</i> , 2019, 25, 1251-1259.	30.7	974
32	Quantitative evidence for early metastatic seeding in colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 1113-1122.	21.4	315
33	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. <i>Nature</i> , 2019, 567, 399-404.	27.8	239
34	Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. <i>Nature Communications</i> , 2019, 10, 657.	12.8	43
35	Chromatin regulators mediate anthracycline sensitivity in breast cancer. <i>Nature Medicine</i> , 2019, 25, 1721-1727.	30.7	27
36	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.	7.1	26

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37	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. <i>Cell</i> , 2018, 173, 1398-1412.e22.	28.9	362
38	Mapping the in vivo fitness landscape of lung adenocarcinoma tumor suppression in mice. <i>Nature Genetics</i> , 2018, 50, 483-486.	21.4	101
39	Big Bang Tumor Growth and Clonal Evolution. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2018, 8, a028381.	6.2	38
40	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
41	A role for chromatin regulatory dynamics in breast cancer evolution. <i>Nature Medicine</i> , 2018, 24, 1309-1311.	30.7	2
42	Quantification of subclonal selection in cancer from bulk sequencing data. <i>Nature Genetics</i> , 2018, 50, 895-903.	21.4	222
43	Organoids reveal cancer dynamics. <i>Nature</i> , 2018, 556, 441-442.	27.8	16
44	Harnessing Tumor Evolution to Circumvent Resistance. <i>Trends in Genetics</i> , 2018, 34, 639-651.	6.7	49
45	Bayesian Network Inference Modeling Identifies TRIB1 as a Novel Regulator of Cell-Cycle Progression and Survival in Cancer Cells. <i>Cancer Research</i> , 2017, 77, 1575-1585.	0.9	94
46	A population genetics perspective on the determinants of intra-tumor heterogeneity. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2017, 1867, 109-126.	7.4	37
47	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.	16.8	142
48	Intestinal Enteroendocrine Lineage Cells Possess Homeostatic and Injury-Inducible Stem Cell Activity. <i>Cell Stem Cell</i> , 2017, 21, 78-90.e6.	11.1	280
49	Between-region genetic divergence reflects the mode and tempo of tumor evolution. <i>Nature Genetics</i> , 2017, 49, 1015-1024.	21.4	144
50	Early mutation bursts in colorectal tumors. <i>PLoS ONE</i> , 2017, 12, e0172516.	2.5	1
51	Population Genetics Approaches to Quantify Clonal Evolution. <i>Blood</i> , 2017, 130, SCI-37-SCI-37.	1.4	0
52	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.	5.0	11
53	Inferring Tumor Phylogenies from Multi-region Sequencing. <i>Cell Systems</i> , 2016, 3, 12-14.	6.2	12
54	Higher peripheral lymphocyte count to predict survival in triple-negative breast cancer (TNBC).. <i>Journal of Clinical Oncology</i> , 2016, 34, 1010-1010.	1.6	0

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55	Many private mutations originate from the first few divisions of a human colorectal adenoma. <i>Journal of Pathology</i> , 2015, 237, 355-362.	4.5	30
56	Genomic profiling of breast cancers. <i>Current Opinion in Obstetrics and Gynecology</i> , 2015, 27, 34-39.	2.0	19
57	A Big Bang model of human colorectal tumor growth. <i>Nature Genetics</i> , 2015, 47, 209-216.	21.4	867
58	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.	4.6	38
59	Contributions to Drug Resistance in Glioblastoma Derived from Malignant Cells in the Sub-Ependymal Zone. <i>Cancer Research</i> , 2015, 75, 194-202.	0.9	48
60	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. <i>Genome Biology</i> , 2014, 15, 431.	8.8	178
61	The Breast Cancer Oncogene EMSY Represses Transcription of Antimetastatic microRNA miR-31. <i>Molecular Cell</i> , 2014, 53, 806-818.	9.7	55
62	Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 4009-4014.	7.1	1,471
63	Single-Molecule Genomic Data Delineate Patient-Specific Tumor Profiles and Cancer Stem Cell Organization. <i>Cancer Research</i> , 2013, 73, 41-49.	0.9	68
64	The shaping and functional consequences of the microRNA landscape in breast cancer. <i>Nature</i> , 2013, 497, 378-382.	27.8	370
65	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	3.2	76
66	Precise inference of copy number alterations in tumor samples from SNP arrays. <i>Bioinformatics</i> , 2013, 29, 2964-2970.	4.1	12
67	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. <i>Science Translational Medicine</i> , 2013, 5, 181re1.	12.4	108
68	Abstract 5016: The human sub-ependymal zone harbors glioblastoma precursors and represents a distinct therapeutic target.. <i>Cancer Research</i> , 2013, 73, 5016-5016.	0.9	21
69	Abstract SY36-01: Exploiting intra-tumor heterogeneity through agent-based models of tumor growth to infer properties of human malignancies.. , 2013, , .		0
70	Abstract B020: A copy number and expression based classifier for breast cancer tumors. , 2013, , .		0
71	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. <i>Science Translational Medicine</i> , 2012, 4, 157ra143.	12.4	356
72	Calling Sample Mix-Ups in Cancer Population Studies. <i>PLoS ONE</i> , 2012, 7, e41815.	2.5	6

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73	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
74	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
75	<i>ZNF703</i> is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. EMBO Molecular Medicine, 2011, 3, 167-180.	6.9	119
76	The importance of platform annotation in interpreting microarray data. Lancet Oncology, The, 2010, 11, 717.	10.7	14
77	A sparse regulatory network of copy-number driven expression reveals putative breast cancer oncogenes. , 2010, , .		2
78	Swift: primary data analysis for the Illumina Solexa sequencing platform. Bioinformatics, 2009, 25, 2194-2199.	4.1	83
79	The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics, 2009, 10, 588.	2.8	80
80	Product Length, Dye Choice, and Detection Chemistry in the Bead-Emulsion Amplification of Millions of Single DNA Molecules in Parallel. Analytical Chemistry, 2009, 81, 5770-5776.	6.5	15
81	A screen of apoptosis and senescence regulatory genes for life span effects when over-expressed in Drosophila. Aging, 2009, 1, 191-211.	3.1	52
82	Drosophila melanogaster p53 has developmental stage-specific and sex-specific effects on adult life span indicative of sexual antagonistic pleiotropy. Aging, 2009, 1, 903-936.	3.1	58
83	Explaining differences in saturation levels for Affymetrix GeneChip® arrays. Nucleic Acids Research, 2007, 35, 4154-4163.	14.5	37
84	Transcriptional profiling of MnSOD-mediated lifespan extension in Drosophila reveals a species-general network of aging and metabolic genes. Genome Biology, 2007, 8, R262.	9.6	123