

Charles M Perou

List of Publications by Year in descending order

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Version: 2024-02-01

502
papers

233,447
citations

73

172
h-index

16

462
g-index

529
all docs

529
docs citations

529
times ranked

143102
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene-Level Germline Contributions to Clinical Risk of Recurrence Scores in Black and White Patients with Breast Cancer. <i>Cancer Research</i> , 2022, 82, 25-35.	0.9	10
2	TP53 Pathway Function, Estrogen Receptor Status, and Breast Cancer Risk Factors in the Carolina Breast Cancer Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 124-131.	2.5	2
3	Development and validation of the new HER2DX assay for predicting pathological response and survival outcome in early-stage HER2-positive breast cancer. <i>EBioMedicine</i> , 2022, 75, 103801.	6.1	47
4	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
5	CALGB 40603 (Alliance): Long-Term Outcomes and Genomic Correlates of Response and Survival After Neoadjuvant Chemotherapy With or Without Carboplatin and Bevacizumab in Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2022, 40, 1323-1334.	1.6	62
6	Evaluating the efficacy of a priming dose of cyclophosphamide prior to pembrolizumab to treat metastatic triple negative breast cancer. , 2022, 10, e003427.		11
7	Abstract P3-15-01: Patients and Researchers Together (PART); a patient-centered tumor tissue collection PARTnership between patients and researchers to increase tissue donations for breast cancer research. <i>Cancer Research</i> , 2022, 82, P3-15-01-P3-15-01.	0.9	0
8	Patient-Derived Triple-Negative Breast Cancer Organoids Provide Robust Model Systems That Recapitulate Tumor Intrinsic Characteristics. <i>Cancer Research</i> , 2022, 82, 1174-1192.	0.9	21
9	Integrated Metabolic Profiling and Transcriptional Analysis Reveals Therapeutic Modalities for Targeting Rapidly Proliferating Breast Cancers. <i>Cancer Research</i> , 2022, 82, 665-680.	0.9	5
10	Challenges and Gaps in Clinical Trial Genomic Data Management. <i>JCO Clinical Cancer Informatics</i> , 2022, 6, e2100193.	2.1	0
11	Chemotherapy Coupled to Macrophage Inhibition Induces T-cell and B-cell Infiltration and Durable Regression in Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2022, 82, 2281-2297.	0.9	22
12	The landscape of immune microenvironments in racially-diverse breast cancer patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, , .	2.5	7
13	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1706-1719.	6.3	14
14	Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases. <i>Npj Breast Cancer</i> , 2022, 8, .	5.2	1
15	Prognostic and predictive implications of the intrinsic subtypes and gene expression signatures in early-stage HER2+ breast cancer: A pooled analysis of CALGB 40601, NeoALTTO, and NSABP B-41 trials.. <i>Journal of Clinical Oncology</i> , 2022, 40, 509-509.	1.6	4
16	14-gene immunoglobulin (IGG) and proliferation signatures and association with overall survival across cancer-types.. <i>Journal of Clinical Oncology</i> , 2022, 40, 2636-2636.	1.6	6
17	Integrated DNA and RNA Sequencing Reveals Drivers of Endocrine Resistance in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 3618-3629.	7.0	12
18	Molecular signatures of in situ to invasive progression for basal-like breast cancers: An integrated mouse model and human DCIS study. <i>Npj Breast Cancer</i> , 2022, 8, .	5.2	4

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19	Receiver operating characteristic curves and confidence bands for support vector machines. <i>Biometrics</i> , 2021, 77, 1422-1430.	1.4	8
20	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	6.3	45
21	Outcomes of Hormone-Receptor Positive, HER2-Negative Breast Cancers by Race and Tumor Biological Features. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkaa072.	2.9	14
22	Serial single-cell profiling analysis of metastatic TNBC during Nab-paclitaxel and pembrolizumab treatment. <i>Breast Cancer Research and Treatment</i> , 2021, 185, 85-94.	2.5	15
23	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. <i>Briefings in Bioinformatics</i> , 2021, 22, 416-427.	6.5	156
24	Inherited predisposition to breast cancer in the Carolina Breast Cancer Study. <i>Npj Breast Cancer</i> , 2021, 7, 6.	5.2	8
25	Abstract OT-09-08: Solti-1502 aRIANNA: Targeting PAM50 HER2-enriched intrinsic subtype with enzalutamide in hormone receptor-positive/HER2-negative metastatic breast cancer. , 2021, , .		1
26	Independent Validation of the PAM50-Based Chemo-Endocrine Score (CES) in Hormone Receptor-Positive HER2-Positive Breast Cancer Treated with Neoadjuvant Anti-HER2-Based Therapy. <i>Clinical Cancer Research</i> , 2021, 27, 3116-3125.	7.0	9
27	Abstract PS18-12: Comparative analysis of differential gene expression by ancestry using primary breast cancers from Nigeria and the cancer genome atlas (TCGA). , 2021, , .		0
28	Clinical and genomic assessment of PD-L1 SP142 expression in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021, 188, 165-178.	2.5	13
29	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021, 372, .	12.6	85
30	ULK1 inhibition overcomes compromised antigen presentation and restores antitumor immunity in LKB1-mutant lung cancer. <i>Nature Cancer</i> , 2021, 2, 503-514.	13.2	72
31	FOXA1 and adaptive response determinants to HER2 targeted therapy in TBCRC 036. <i>Npj Breast Cancer</i> , 2021, 7, 51.	5.2	11
32	Highly metastatic claudin-low mammary cancers can originate from luminal epithelial cells. <i>Nature Communications</i> , 2021, 12, 3742.	12.8	24
33	FOXA1 overexpression suppresses interferon signaling and immune response in cancer. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	48
34	Oestrogen receptor activity in hormone-dependent breast cancer during chemotherapy. <i>EBioMedicine</i> , 2021, 69, 103451.	6.1	7
35	Multik: an automated tool to determine optimal cluster numbers in single-cell RNA sequencing data. <i>Genome Biology</i> , 2021, 22, 232.	8.8	16
36	Entinostat induces antitumor immune responses through immune editing of tumor neoantigens. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	43

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37	Single allele loss-of-function mutations select and sculpt conditional cooperative networks in breast cancer. <i>Nature Communications</i> , 2021, 12, 5238.	12.8	8
38	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	21.4	535
39	PDGFR β is an essential therapeutic target for BRCA1-deficient mammary tumors. <i>Breast Cancer Research</i> , 2021, 23, 10.	5.0	9
40	Inhibition of estrogen signaling in myeloid cells increases tumor immunity in melanoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	40
41	Anti-PD-1 Checkpoint Therapy Can Promote the Function and Survival of Regulatory T Cells. <i>Journal of Immunology</i> , 2021, 207, 2598-2607.	0.8	10
42	A multi-omic single-cell landscape of human gynecologic malignancies. <i>Molecular Cell</i> , 2021, 81, 4924-4941.e10.	9.7	36
43	Tumor Suppressor PLK2 May Serve as a Biomarker in Triple-Negative Breast Cancer for Improved Response to PLK1 Therapeutics. <i>Cancer Research Communications</i> , 2021, 1, 178-193.	1.7	8
44	Joint and individual analysis of breast cancer histologic images and genomic covariates. <i>Annals of Applied Statistics</i> , 2021, 15, 1697-1722.	1.1	4
45	Molecular analysis of TCGA breast cancer histologic types. <i>Cell Genomics</i> , 2021, 1, 100067.	6.5	37
46	Bimodal age distribution at diagnosis in breast cancer persists across molecular and genomic classifications. <i>Breast Cancer Research and Treatment</i> , 2020, 179, 185-195.	2.5	11
47	Borderline Estrogen Receptor-Positive Breast Cancers in Black and White Women. <i>Journal of the National Cancer Institute</i> , 2020, 112, 728-736.	6.3	19
48	Survival, Pathologic Response, and Genomics in CALGB 40601 (Alliance), a Neoadjuvant Phase III Trial of Paclitaxel-Trastuzumab With or Without Lapatinib in HER2-Positive Breast Cancer. <i>Journal of Clinical Oncology</i> , 2020, 38, 4184-4193.	1.6	74
49	Identification of BBOX1 as a Therapeutic Target in Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2020, 10, 1706-1721.	9.4	35
50	Stimulation of Oncogene-Specific Tumor-Infiltrating T Cells through Combined Vaccine and \pm PD-1 Enable Sustained Antitumor Responses against Established HER2 Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 4670-4681.	7.0	31
51	A multivariable prognostic score to guide systemic therapy in early-stage HER2-positive breast cancer: a retrospective study with an external evaluation. <i>Lancet Oncology</i> , The, 2020, 21, 1455-1464.	10.7	52
52	A pan-cancer analysis of the frequency of DNA alterations across cell cycle activity levels. <i>Oncogene</i> , 2020, 39, 5430-5440.	5.9	23
53	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. <i>Genome Biology</i> , 2020, 21, 42.	8.8	60
54	HER2-enriched subtype and pathological complete response in HER2-positive breast cancer: A systematic review and meta-analysis. <i>Cancer Treatment Reviews</i> , 2020, 84, 101965.	7.7	92

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55	Microscaled proteogenomic methods for precision oncology. Nature Communications, 2020, 11, 532.	12.8	78
56	Virus expression detection reveals RNA-sequencing contamination in TCGA. BMC Genomics, 2020, 21, 79.	2.8	21
57	Estrogen and Progesterone Receptor Testing in Breast Cancer: ASCO/CAP Guideline Update. Journal of Clinical Oncology, 2020, 38, 1346-1366.	1.6	673
58	Estrogen and Progesterone Receptor Testing in Breast Cancer: American Society of Clinical Oncology/College of American Pathologists Guideline Update. Archives of Pathology and Laboratory Medicine, 2020, 144, 545-563.	2.5	205
59	FGFR4 regulates tumor subtype differentiation in luminal breast cancer and metastatic disease. Journal of Clinical Investigation, 2020, 130, 4871-4887.	8.2	49
60	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. BMC Bioinformatics, 2020, 21, 30.	2.6	32
61	Alterations in Wnt- and/or STAT3 signaling pathways and the immune microenvironment during metastatic progression. Oncogene, 2019, 38, 5942-5958.	5.9	10
62	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. Cell, 2019, 179, 1191-1206.e21.	28.9	291
63	The MMTV-Wnt1 murine model produces two phenotypically distinct subtypes of mammary tumors with unique therapeutic responses to an EGFR inhibitor. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	8
64	Breast cancer PAM50 signature: correlation and concordance between RNA-Seq and digital multiplexed gene expression technologies in a triple negative breast cancer series. BMC Genomics, 2019, 20, 452.	2.8	36
65	The Immune Microenvironment in Hormone Receptor-Positive Breast Cancer Before and After Preoperative Chemotherapy. Clinical Cancer Research, 2019, 25, 4644-4655.	7.0	76
66	I-Boost: an integrative boosting approach for predicting survival time with multiple genomics platforms. Genome Biology, 2019, 20, 52.	8.8	7
67	The long-term prognostic and predictive capacity of cyclin D1 gene amplification in 2305 breast tumours. Breast Cancer Research, 2019, 21, 34.	5.0	48
68	Separation of breast cancer and organ microenvironment transcriptomes in metastases. Breast Cancer Research, 2019, 21, 36.	5.0	36
69	MERTK mediated novel site Akt phosphorylation alleviates SAV1 suppression. Nature Communications, 2019, 10, 1515.	12.8	25
70	Prolyl hydroxylase substrate adenylosuccinate lyase is an oncogenic driver in triple negative breast cancer. Nature Communications, 2019, 10, 5177.	12.8	27
71	Genetic determinants of the molecular portraits of epithelial cancers. Nature Communications, 2019, 10, 5666.	12.8	21
72	Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas. Cancer Causes and Control, 2019, 30, 31-39.	1.8	14

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73	Improved indel detection in DNA and RNA via realignment with ABRA2. <i>Bioinformatics</i> , 2019, 35, 2966-2973.	4.1	55
74	A mouse model featuring tissue-specific deletion of p53 and Brca1 gives rise to mammary tumors with genomic and transcriptomic similarities to human basal-like breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 174, 143-155.	2.5	18
75	Genomic-based predictive biomarkers to anti-HER2 therapies: A combined analysis of CALGB 40601 (Alliance) and PAMELA clinical trials.. <i>Journal of Clinical Oncology</i> , 2019, 37, 571-571.	1.6	6
76	The association between copy number aberration, DNA methylation and gene expression in tumor samples. <i>Nucleic Acids Research</i> , 2018, 46, 3009-3018.	14.5	51
77	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	28.9	2,277
78	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	28.9	1,670
79	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.	28.9	1,718
80	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	28.9	228
81	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
82	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
83	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
84	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
85	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	333
86	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
87	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	6.4	245
88	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	6.4	205
89	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	523
90	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.4	683

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91	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
92	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	6.4	119
93	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
94	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
95	PAM50 and Risk of Recurrence Scores for Interval Breast Cancers. Cancer Prevention Research, 2018, 11, 327-336.	1.5	7
96	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
97	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
98	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. Clinical Cancer Research, 2018, 24, 1845-1852.	7.0	84
99	Asparagine bioavailability governs metastasis in a model of breast cancer. Nature, 2018, 554, 378-381.	27.8	362
100	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
101	Intrinsic subtypes and benefit from postmastectomy radiotherapy in node-positive premenopausal breast cancer patients who received adjuvant chemotherapy â€” results from two independent randomized trials. Acta Oncol ³ gica, 2018, 57, 38-43.	1.8	22
102	Frequency of breast cancer subtypes among African American women in the AMBER consortium. Breast Cancer Research, 2018, 20, 12.	5.0	27
103	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. Nature Medicine, 2018, 24, 628-637.	30.7	649
104	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
105	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
106	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
107	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
108	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396

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109	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
110	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. <i>Nature Communications</i> , 2018, 9, 1059.	12.8	72
111	Reported Biologic Differences in Breast Cancer by Race Due to Disparities in Screening—Reply. <i>JAMA Oncology</i> , 2018, 4, 883.	7.1	0
112	A Phase I Trial of the PI3K Inhibitor Buparlisib Combined With Capecitabine in Patients With Metastatic Breast Cancer. <i>Clinical Breast Cancer</i> , 2018, 18, 289-297.	2.4	21
113	Reproductive risk factor associations with lobular and ductal carcinoma in the Carolina Breast Cancer Study. <i>Cancer Causes and Control</i> , 2018, 29, 25-32.	1.8	9
114	Racial Differences in PAM50 Subtypes in the Carolina Breast Cancer Study. <i>Journal of the National Cancer Institute</i> , 2018, 110, 176-182.	6.3	104
115	DPYSL3 modulates mitosis, migration, and epithelial-to-mesenchymal transition in claudin-low breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11978-E11987.	7.1	40
116	Identification of Jun loss promotes resistance to histone deacetylase inhibitor entinostat through Myc signaling in luminal breast cancer. <i>Genome Medicine</i> , 2018, 10, 86.	8.2	14
117	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β 2 Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.2	134
118	Cdh1 and Pik3ca Mutations Cooperate to Induce Immune-Related Invasive Lobular Carcinoma of the Breast. <i>Cell Reports</i> , 2018, 25, 702-714.e6.	6.4	47
119	Image analysis with deep learning to predict breast cancer grade, ER status, histologic subtype, and intrinsic subtype. <i>Npj Breast Cancer</i> , 2018, 4, 30.	5.2	193
120	FGFR1-Activated Translation of WNT Pathway Components with Structured 5' UTRs Is Vulnerable to Inhibition of EIF4A-Dependent Translation Initiation. <i>Cancer Research</i> , 2018, 78, 4229-4240.	0.9	22
121	TP53 protein levels, RNA-based pathway assessment, and race among invasive breast cancer cases. <i>Npj Breast Cancer</i> , 2018, 4, 13.	5.2	18
122	Pathological Response and Survival in Triple-Negative Breast Cancer Following Neoadjuvant Carboplatin plus Docetaxel. <i>Clinical Cancer Research</i> , 2018, 24, 5820-5829.	7.0	82
123	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
124	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. <i>Cell Reports</i> , 2018, 24, 1434-1444.e7.	6.4	73
125	Single-Cell Transcriptomes Distinguish Stem Cell State Changes and Lineage Specification Programs in Early Mammary Gland Development. <i>Cell Reports</i> , 2018, 24, 1653-1666.e7.	6.4	125
126	Integrated Analysis of RNA and DNA from the Phase III Trial CALGB 40601 Identifies Predictors of Response to Trastuzumab-Based Neoadjuvant Chemotherapy in HER2-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 5292-5304.	7.0	73

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127	Intrinsic molecular subtypes of breast cancers categorized as HER2-positive using an alternative chromosome 17 probe assay. <i>Breast Cancer Research</i> , 2018, 20, 75.	5.0	6
128	VHL substrate transcription factor ZHX2 as an oncogenic driver in clear cell renal cell carcinoma. <i>Science</i> , 2018, 361, 290-295.	12.6	134
129	Clinical implications of the non-luminal intrinsic subtypes in hormone receptor-positive breast cancer. <i>Cancer Treatment Reviews</i> , 2018, 67, 63-70.	7.7	79
130	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. <i>Oncotmunology</i> , 2018, 7, e1490854.	4.6	200
131	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	324
132	Multiple Instance Learning for Heterogeneous Images: Training a CNN for Histopathology. <i>Lecture Notes in Computer Science</i> , 2018, , 254-262.	1.3	36
133	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 1371-1383.	8.2	126
134	Efficacy of Neoadjuvant Carboplatin plus Docetaxel in Triple-Negative Breast Cancer: Combined Analysis of Two Cohorts. <i>Clinical Cancer Research</i> , 2017, 23, 649-657.	7.0	108
135	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	27.8	1,158
136	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	16.8	532
137	Enhancer Remodeling during Adaptive Bypass to MEK Inhibition Is Attenuated by Pharmacologic Targeting of the P-TEFb Complex. <i>Cancer Discovery</i> , 2017, 7, 302-321.	9.4	128
138	Pentraxin-3 is a PI3K signaling target that promotes stem cell-like traits in basal-like breast cancers. <i>Science Signaling</i> , 2017, 10, .	3.6	43
139	Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2213-2221.	0.9	168
140	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 439-450.	2.5	47
141	Patterns of cell cycle checkpoint deregulation associated with intrinsic molecular subtypes of human breast cancer cells. <i>Npj Breast Cancer</i> , 2017, 3, 9.	5.2	47
142	A murine preclinical syngeneic transplantation model for breast cancer precision medicine. <i>Science Advances</i> , 2017, 3, e1600957.	10.3	10
143	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017, 3, 1654.	7.1	208
144	A PAM50-Based Chemoendocrine Score for Hormone Receptor-Positive Breast Cancer with an Intermediate Risk of Relapse. <i>Clinical Cancer Research</i> , 2017, 23, 3035-3044.	7.0	28

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145	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
146	Combined immune checkpoint blockade as a therapeutic strategy for <i>BRCA1</i> -mutated breast cancer. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	227
147	Progesterone Receptor Isoform Ratio: A Breast Cancer Prognostic and Predictive Factor for Antiprogesterin Responsiveness. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	49
148	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	12.8	112
149	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
150	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
151	Lung Adenocarcinoma and Squamous Cell Carcinoma Gene Expression Subtypes Demonstrate Significant Differences in Tumor Immune Landscape. <i>Journal of Thoracic Oncology</i> , 2017, 12, 943-953.	1.1	136
152	Nuclear Localized LSR: A Novel Regulator of Breast Cancer Behavior and Tumorigenesis. <i>Molecular Cancer Research</i> , 2017, 15, 165-178.	3.4	23
153	Docetaxel-Loaded PLGA Nanoparticles Improve Efficacy in Taxane-Resistant Triple-Negative Breast Cancer. <i>Nano Letters</i> , 2017, 17, 242-248.	9.1	94
154	PAM50 Provides Prognostic Information When Applied to the Lymph Node Metastases of Advanced Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2017, 23, 7225-7231.	7.0	17
155	Gene Expression Signatures and Immunohistochemical Subtypes Add Prognostic Value to Each Other in Breast Cancer Cohorts. <i>Clinical Cancer Research</i> , 2017, 23, 7512-7520.	7.0	43
156	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	16.8	642
157	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
158	Metabolic reprogramming underlies metastatic potential in an obesity-responsive murine model of metastatic triple negative breast cancer. <i>Npj Breast Cancer</i> , 2017, 3, 26.	5.2	32
159	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
160	SynthEx: a synthetic-normal-based DNA sequencing tool for copy number alteration detection and tumor heterogeneity profiling. <i>Genome Biology</i> , 2017, 18, 66.	8.8	26
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