

Charles M Perou

List of Publications by Year in descending order

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Version: 2024-02-01

501
papers

233,447
citations

90

172
h-index

17

462
g-index

529
all docs

529
docs citations

529
times ranked

154676
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.	0.4	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.	1.1	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.	2.7	47
4	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	2.0	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.	0.8	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.	0.4	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.	0.4	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.	0.4	5
10	Challenges and Gaps in Clinical Trial Genomic Data Management. <i>JCO Clinical Cancer Informatics</i> , 2022, 6, e2100193.	1.0	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.	0.4	22
12	The landscape of immune microenvironments in racially-diverse breast cancer patients. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, , .	1.1	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.	3.0	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, .	2.3	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.	0.8	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.	0.8	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.	3.2	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, .	2.3	4

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19	Receiver operating characteristic curves and confidence bands for support vector machines. <i>Biometrics</i> , 2021, 77, 1422-1430.	0.8	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.	3.0	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.	1.4	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.	1.1	15
23	SCDC: bulk gene expression deconvolution by multiple single-cell RNA sequencing references. <i>Briefings in Bioinformatics</i> , 2021, 22, 416-427.	3.2	156
24	Inherited predisposition to breast cancer in the Carolina Breast Cancer Study. <i>Npj Breast Cancer</i> , 2021, 7, 6.	2.3	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.	3.2	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.	1.1	13
29	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021, 372, .	6.0	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.	5.7	72
31	FOXA1 and adaptive response determinants to HER2 targeted therapy in TBCRC 036. <i>Npj Breast Cancer</i> , 2021, 7, 51.	2.3	11
32	Highly metastatic claudin-low mammary cancers can originate from luminal epithelial cells. <i>Nature Communications</i> , 2021, 12, 3742.	5.8	24
33	FOXA1 overexpression suppresses interferon signaling and immune response in cancer. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	48
34	Oestrogen receptor activity in hormone-dependent breast cancer during chemotherapy. <i>EBioMedicine</i> , 2021, 69, 103451.	2.7	7
35	Multik: an automated tool to determine optimal cluster numbers in single-cell RNA sequencing data. <i>Genome Biology</i> , 2021, 22, 232.	3.8	16
36	Entinostat induces antitumor immune responses through immune editing of tumor neoantigens. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	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.	5.8	8
38	A single-cell and spatially resolved atlas of human breast cancers. <i>Nature Genetics</i> , 2021, 53, 1334-1347.	9.4	535
39	PDGFR β is an essential therapeutic target for BRCA1-deficient mammary tumors. <i>Breast Cancer Research</i> , 2021, 23, 10.	2.2	9
40	Inhibition of estrogen signaling in myeloid cells increases tumor immunity in melanoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	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.	0.4	10
42	A multi-omic single-cell landscape of human gynecologic malignancies. <i>Molecular Cell</i> , 2021, 81, 4924-4941.e10.	4.5	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.	0.7	8
44	Joint and individual analysis of breast cancer histologic images and genomic covariates. <i>Annals of Applied Statistics</i> , 2021, 15, 1697-1722.	0.5	4
45	Molecular analysis of TCGA breast cancer histologic types. <i>Cell Genomics</i> , 2021, 1, 100067.	3.0	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.	1.1	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.	3.0	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.	0.8	74
49	Identification of BBOX1 as a Therapeutic Target in Triple-Negative Breast Cancer. <i>Cancer Discovery</i> , 2020, 10, 1706-1721.	7.7	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.	3.2	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.	5.1	52
52	A pan-cancer analysis of the frequency of DNA alterations across cell cycle activity levels. <i>Oncogene</i> , 2020, 39, 5430-5440.	2.6	23
53	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. <i>Genome Biology</i> , 2020, 21, 42.	3.8	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.	3.4	92

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55	Microscaled proteogenomic methods for precision oncology. <i>Nature Communications</i> , 2020, 11, 532.	5.8	78
56	Virus expression detection reveals RNA-sequencing contamination in TCGA. <i>BMC Genomics</i> , 2020, 21, 79.	1.2	21
57	Estrogen and Progesterone Receptor Testing in Breast Cancer: ASCO/CAP Guideline Update. <i>Journal of Clinical Oncology</i> , 2020, 38, 1346-1366.	0.8	673
58	Estrogen and Progesterone Receptor Testing in Breast Cancer: American Society of Clinical Oncology/College of American Pathologists Guideline Update. <i>Archives of Pathology and Laboratory Medicine</i> , 2020, 144, 545-563.	1.2	205
59	FGFR4 regulates tumor subtype differentiation in luminal breast cancer and metastatic disease. <i>Journal of Clinical Investigation</i> , 2020, 130, 4871-4887.	3.9	49
60	Unlocking the transcriptomic potential of formalin-fixed paraffin embedded clinical tissues: comparison of gene expression profiling approaches. <i>BMC Bioinformatics</i> , 2020, 21, 30.	1.2	32
61	Alterations in Wnt- and/or STAT3 signaling pathways and the immune microenvironment during metastatic progression. <i>Oncogene</i> , 2019, 38, 5942-5958.	2.6	10
62	B Cells and T Follicular Helper Cells Mediate Response to Checkpoint Inhibitors in High Mutation Burden Mouse Models of Breast Cancer. <i>Cell</i> , 2019, 179, 1191-1206.e21.	13.5	291
63	The MMTV-Wnt1 murine model produces two phenotypically distinct subtypes of mammary tumors with unique therapeutic responses to an EGFR inhibitor. <i>DMM Disease Models and Mechanisms</i> , 2019, 12, .	1.2	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. <i>BMC Genomics</i> , 2019, 20, 452.	1.2	36
65	The Immune Microenvironment in Hormone Receptor-Positive Breast Cancer Before and After Preoperative Chemotherapy. <i>Clinical Cancer Research</i> , 2019, 25, 4644-4655.	3.2	76
66	I-Boost: an integrative boosting approach for predicting survival time with multiple genomics platforms. <i>Genome Biology</i> , 2019, 20, 52.	3.8	7
67	The long-term prognostic and predictive capacity of cyclin D1 gene amplification in 2305 breast tumours. <i>Breast Cancer Research</i> , 2019, 21, 34.	2.2	48
68	Separation of breast cancer and organ microenvironment transcriptomes in metastases. <i>Breast Cancer Research</i> , 2019, 21, 36.	2.2	36
69	MERTK mediated novel site Akt phosphorylation alleviates SAV1 suppression. <i>Nature Communications</i> , 2019, 10, 1515.	5.8	25
70	Prolyl hydroxylase substrate adenylosuccinate lyase is an oncogenic driver in triple negative breast cancer. <i>Nature Communications</i> , 2019, 10, 5177.	5.8	27
71	Genetic determinants of the molecular portraits of epithelial cancers. <i>Nature Communications</i> , 2019, 10, 5666.	5.8	21
72	Differences in race, molecular and tumor characteristics among women diagnosed with invasive ductal and lobular breast carcinomas. <i>Cancer Causes and Control</i> , 2019, 30, 31-39.	0.8	14

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73	Improved indel detection in DNA and RNA via realignment with ABRA2. <i>Bioinformatics</i> , 2019, 35, 2966-2973.	1.8	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.	1.1	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.	0.8	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.	6.5	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.	13.5	2,277
78	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	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.	13.5	1,718
80	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
81	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
82	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
83	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
84	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	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.	2.9	333
86	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
87	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	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.	2.9	205
89	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	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.	2.9	683

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91	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
92	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
93	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
94	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
95	PAM50 and Risk of Recurrence Scores for Interval Breast Cancers. <i>Cancer Prevention Research</i> , 2018, 11, 327-336.	0.7	7
96	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
97	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
98	Pathological Response in a Triple-Negative Breast Cancer Cohort Treated with Neoadjuvant Carboplatin and Docetaxel According to Lehmann's Refined Classification. <i>Clinical Cancer Research</i> , 2018, 24, 1845-1852.	3.2	84
99	Asparagine bioavailability governs metastasis in a model of breast cancer. <i>Nature</i> , 2018, 554, 378-381.	13.7	362
100	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
101	Intrinsic subtypes and benefit from postmastectomy radiotherapy in node-positive premenopausal breast cancer patients who received adjuvant chemotherapy – results from two independent randomized trials. <i>Acta Oncologica</i> , 2018, 57, 38-43.	0.8	22
102	Frequency of breast cancer subtypes among African American women in the AMBER consortium. <i>Breast Cancer Research</i> , 2018, 20, 12.	2.2	27
103	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. <i>Nature Medicine</i> , 2018, 24, 628-637.	15.2	649
104	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
105	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284
106	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400
107	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
108	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	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.	7.7	478
110	GATA3 zinc finger 2 mutations reprogram the breast cancer transcriptional network. <i>Nature Communications</i> , 2018, 9, 1059.	5.8	72
111	Reported Biologic Differences in Breast Cancer by Race Due to Disparities in Screening—Reply. <i>JAMA Oncology</i> , 2018, 4, 883.	3.4	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.	1.1	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.	0.8	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.	3.0	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.	3.3	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.	3.6	14
117	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	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.	2.9	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.	2.3	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.	0.4	22
121	TP53 protein levels, RNA-based pathway assessment, and race among invasive breast cancer cases. <i>Npj Breast Cancer</i> , 2018, 4, 13.	2.3	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.	3.2	82
123	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
124	Functional Annotation of ESR1 Gene Fusions in Estrogen Receptor-Positive Breast Cancer. <i>Cell Reports</i> , 2018, 24, 1434-1444.e7.	2.9	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.	2.9	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.	3.2	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.	2.2	6
128	VHL substrate transcription factor ZHX2 as an oncogenic driver in clear cell renal cell carcinoma. <i>Science</i> , 2018, 361, 290-295.	6.0	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.	3.4	79
130	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. <i>Oncolmmunology</i> , 2018, 7, e1490854.	2.1	200
131	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
132	Multiple Instance Learning for Heterogeneous Images: Training a CNN for Histopathology. <i>Lecture Notes in Computer Science</i> , 2018, , 254-262.	1.0	36
133	Integrated RNA and DNA sequencing reveals early drivers of metastatic breast cancer. <i>Journal of Clinical Investigation</i> , 2018, 128, 1371-1383.	3.9	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.	3.2	108
135	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
136	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	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.	7.7	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, .	1.6	43
139	Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2213-2221.	0.4	168
140	Amplification of SOX4 promotes PI3K/Akt signaling in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2017, 162, 439-450.	1.1	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.	2.3	47
142	A murine preclinical syngeneic transplantation model for breast cancer precision medicine. <i>Science Advances</i> , 2017, 3, e1600957.	4.7	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.	3.4	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.	3.2	28

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145	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	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, .	5.8	227
147	Progesterone Receptor Isoform Ratio: A Breast Cancer Prognostic and Predictive Factor for Antiprogestin Responsiveness. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	3.0	49
148	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. <i>Nature Communications</i> , 2017, 8, 14864.	5.8	112
149	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
150	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	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.	0.5	136
152	Nuclear Localized LSR: A Novel Regulator of Breast Cancer Behavior and Tumorigenesis. <i>Molecular Cancer Research</i> , 2017, 15, 165-178.	1.5	23
153	Docetaxel-Loaded PLGA Nanoparticles Improve Efficacy in Taxane-Resistant Triple-Negative Breast Cancer. <i>Nano Letters</i> , 2017, 17, 242-248.	4.5	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.	3.2	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.	3.2	43
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