Charles M Perou

List of Publications by Year
in descending order

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	Molecular portraits of human breast tumours. Nature, 2000, 406, 747-752.	27.8	13,397
2	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
3	Gene expression patterns of breast carcinomas distinguish tumor subclasses with clinical implications. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 10869-10874.	7.1	9,721
4	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
5	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	27.8	6,879
6	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
7	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
8	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	16.8	6,138
9	Repeated observation of breast tumor subtypes in independent gene expression data sets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8418-8423.	7.1	4,849
10	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572
11	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
12	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
13	Supervised Risk Predictor of Breast Cancer Based on Intrinsic Subtypes. Journal of Clinical Oncology, 2009, 27, 1160-1167.	1.6	3,730
14	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
15	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
16	Pathological complete response and long-term clinical benefit in breast cancer: the CTNeoBC pooled analysis. Lancet, The, 2014, 384, 164-172.	13.7	3,224
17	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
18	Race, Breast Cancer Subtypes, and Survival in the Carolina Breast Cancer Study. JAMA - Journal of the American Medical Association, 2006, 295, 2492.	7.4	3,135

#	Article	IF	Citations
19	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
20	Personalizing the treatment of women with early breast cancer: highlights of the St Gallen International Expert Consensus on the Primary Therapy of Early Breast Cancer 2013. Annals of Oncology, 2013, 24, 2206-2223.	1.2	2,805
21	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
22	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
23	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
24	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
25	Immunohistochemical and Clinical Characterization of the Basal-Like Subtype of Invasive Breast Carcinoma. Clinical Cancer Research, 2004, 10, 5367-5374.	7.0	2,393
26	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
27	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
28	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
29	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	16.8	2,078
30	Systematic variation in gene expression patterns in human cancer cell lines. Nature Genetics, 2000, 24, 227-235.	21.4	1,946
31	Ki67 Index, HER2 Status, and Prognosis of Patients With Luminal B Breast Cancer. Journal of the National Cancer Institute, 2009, 101, 736-750.	6.3	1,844
32	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
33	The Triple Negative Paradox: Primary Tumor Chemosensitivity of Breast Cancer Subtypes. Clinical Cancer Research, 2007, 13, 2329-2334.	7.0	1,786
34	Phenotypic and molecular characterization of the claudin-low intrinsic subtype of breast cancer. Breast Cancer Research, 2010, 12, R68.	5.0	1,748
35	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
36	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695

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37	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
38	Breast Cancer Molecular Subtypes Respond Differently to Preoperative Chemotherapy. Clinical Cancer Research, 2005, 11, 5678-5685.	7.0	1,618
39	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
40	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
41	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
42	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	27.8	1,384
43	Identification of Genes Periodically Expressed in the Human Cell Cycle and Their Expression in Tumors. Molecular Biology of the Cell, 2002, 13, 1977-2000.	2.1	1,352
44	Residual breast cancers after conventional therapy display mesenchymal as well as tumor-initiating features. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 13820-13825.	7.1	1,257
45	Distinctive gene expression patterns in human mammary epithelial cells and breast cancers. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 9212-9217.	7.1	1,256
46	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
47	Concordance among Gene-Expression€"Based Predictors for Breast Cancer. New England Journal of Medicine, 2006, 355, 560-569.	27.0	1,201
48	The molecular portraits of breast tumors are conserved across microarray platforms. BMC Genomics, 2006, 7, 96.	2.8	1,169
49	Integrated genomic and molecular characterization of cervical cancer. Nature, 2017, 543, 378-384.	27.8	1,158
50	Diversity of gene expression in adenocarcinoma of the lung. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 13784-13789.	7.1	1,151
51	Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12963-12968.	7.1	1,098
52	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
53	Deconstructing the molecular portraits of breast cancer. Molecular Oncology, 2011, 5, 5-23.	4.6	1,059
54	Basal-Like Breast Cancer Defined by Five Biomarkers Has Superior Prognostic Value than Triple-Negative Phenotype. Clinical Cancer Research, 2008, 14, 1368-1376.	7.0	1,040

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55	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
56	Identification of conserved gene expression features between murine mammary carcinoma models and human breast tumors. Genome Biology, 2007, 8, R76.	9.6	1,009
57	Allele-specific copy number analysis of tumors. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 16910-16915.	7.1	979
58	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. Nucleic Acids Research, 2010, 38, e178-e178.	14.5	946
59	Phenotypic evaluation of the basal-like subtype of invasive breast carcinoma. Modern Pathology, 2006, 19, 264-271.	5.5	932
60	Genome-wide analysis of DNA copy-number changes using cDNA microarrays. Nature Genetics, 1999, 23, 41-46.	21.4	928
61	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
62	Impact of the Addition of Carboplatin and/or Bevacizumab to Neoadjuvant Once-per-Week Paclitaxel Followed by Dose-Dense Doxorubicin and Cyclophosphamide on Pathologic Complete Response Rates in Stage II to III Triple-Negative Breast Cancer: CALGB 40603 (Alliance). Journal of Clinical Oncology, 2015, 33, 13-21.	1.6	782
63	Characterization of a Naturally Occurring Breast Cancer Subset Enriched in Epithelial-to-Mesenchymal Transition and Stem Cell Characteristics. Cancer Research, 2009, 69, 4116-4124.	0.9	768
64	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
65	Epidemiology of basal-like breast cancer. Breast Cancer Research and Treatment, 2008, 109, 123-139.	2.5	747
66	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
67	A custom microarray platform for analysis of microRNA gene expression. Nature Methods, 2004, 1, 47-53.	19.0	704
68	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
69	A Comparison of PAM50 Intrinsic Subtyping with Immunohistochemistry and Clinical Prognostic Factors in Tamoxifen-Treated Estrogen Receptor€"Positive Breast Cancer. Clinical Cancer Research, 2010, 16, 5222-5232.	7.0	676
70	Estrogen and Progesterone Receptor Testing in Breast Cancer: ASCO/CAP Guideline Update. Journal of Clinical Oncology, 2020, 38, 1346-1366.	1.6	673
71	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
72	Carboplatin in BRCA1/2-mutated and triple-negative breast cancer BRCAness subgroups: the TNT Trial. Nature Medicine, 2018, 24, 628-637.	30.7	649

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73	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
74	Dynamic Reprogramming of the Kinome in Response to Targeted MEK Inhibition in Triple-Negative Breast Cancer. Cell, 2012, 149, 307-321.	28.9	637
75	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
76	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
77	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
78	Molecular classification of head and neck squamous cell carcinomas using patterns of gene expression. Cancer Cell, 2004, 5, 489-500.	16.8	589
79	Endocrine-Therapy-Resistant ESR1 Variants Revealed by Genomic Characterization of Breast-Cancer-Derived Xenografts. Cell Reports, 2013, 4, 1116-1130.	6.4	539
80	A single-cell and spatially resolved atlas of human breast cancers. Nature Genetics, 2021, 53, 1334-1347.	21.4	535
81	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
82	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
83	Common markers of proliferation. Nature Reviews Cancer, 2006, 6, 99-106.	28.4	522
84	Evaluating the comparability of gene expression in blood and brain. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 261-268.	1.7	512
85	Progesterone receptor modulates ERα action in breast cancer. Nature, 2015, 523, 313-317.	27.8	504
86	Expression of Cytokeratins 17 and 5 Identifies a Group of Breast Carcinomas with Poor Clinical Outcome. American Journal of Pathology, 2002, 161, 1991-1996.	3.8	494
87	Identification and mutation analysis of the complete gene for Chediak–Higashi syndrome. Nature Genetics, 1996, 14, 307-311.	21.4	485
88	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
89	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
90	Prognostic Significance of Progesterone Receptor–Positive Tumor Cells Within Immunohistochemically Defined Luminal A Breast Cancer. Journal of Clinical Oncology, 2013, 31, 203-209.	1.6	464

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91	Breast Cancer Subtypes and Response to Docetaxel in Node-Positive Breast Cancer: Use of an Immunohistochemical Definition in the BCIRG 001 Trial. Journal of Clinical Oncology, 2009, 27, 1168-1176.	1.6	461
92	Molecular Characterization of Basal-Like and Non-Basal-Like Triple-Negative Breast Cancer. Oncologist, 2013, 18, 123-133.	3.7	454
93	Molecular Stratification of Triple-Negative Breast Cancers. Oncologist, 2011, 16, 61-70.	3.7	452
94	The Genome Architecture of the Collaborative Cross Mouse Genetic Reference Population. Genetics, 2012, 190, 389-401.	2.9	435
95	Standardizing global gene expression analysis between laboratories and across platforms. Nature Methods, 2005, 2, 351-356.	19.0	416
96	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
97	TBCRC 001: Randomized Phase II Study of Cetuximab in Combination With Carboplatin in Stage IV Triple-Negative Breast Cancer. Journal of Clinical Oncology, 2012, 30, 2615-2623.	1.6	413
98	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
99	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
100	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
101	A Renewable Tissue Resource of Phenotypically Stable, Biologically and Ethnically Diverse, Patient-Derived Human Breast Cancer Xenograft Models. Cancer Research, 2013, 73, 4885-4897.	0.9	394
102	MR Imaging Radiomics Signatures for Predicting the Risk of Breast Cancer Recurrence as Given by Research Versions of MammaPrint, Oncotype DX, and PAM50 Gene Assays. Radiology, 2016, 281, 382-391.	7.3	387
103	Triple-Negative Breast Cancer: Risk Factors to Potential Targets. Clinical Cancer Research, 2008, 14, 8010-8018.	7.0	380
104	Pathologic Complete Response Predicts Recurrence-Free Survival More Effectively by Cancer Subset: Results From the I-SPY 1 TRIALâ€"CALGB 150007/150012, ACRIN 6657. Journal of Clinical Oncology, 2012, 30, 3242-3249.	1.6	379
105	Asparagine bioavailability governs metastasis in a model of breast cancer. Nature, 2018, 554, 378-381.	27.8	362
106	Adjustment of systematic microarray data biases. Bioinformatics, 2004, 20, 105-114.	4.1	360
107	A Novel Lung Metastasis Signature Links Wnt Signaling with Cancer Cell Self-Renewal and Epithelial-Mesenchymal Transition in Basal-like Breast Cancer. Cancer Research, 2009, 69, 5364-5373.	0.9	360
108	Development and verification of the PAM50-based Prosigna breast cancer gene signature assay. BMC Medical Genomics, 2015, 8, 54.	1.5	352

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109	Intrinsic Breast Tumor Subtypes, Race, and Long-Term Survival in the Carolina Breast Cancer Study. Clinical Cancer Research, 2010, 16, 6100-6110.	7.0	351
110	Population Differences in Breast Cancer: Survey in Indigenous African Women Reveals Over-Representation of Triple-Negative Breast Cancer. Journal of Clinical Oncology, 2009, 27, 4515-4521.	1.6	341
111	A model of breast cancer heterogeneity reveals vascular mimicry as a driver of metastasis. Nature, 2015, 520, 358-362.	27.8	336
112	Molecular Heterogeneity and Response to Neoadjuvant Human Epidermal Growth Factor Receptor 2 Targeting in CALGB 40601, a Randomized Phase III Trial of Paclitaxel Plus Trastuzumab With or Without Lapatinib. Journal of Clinical Oncology, 2016, 34, 542-549.	1.6	336
113	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
114	Expression of Autotaxin and Lysophosphatidic Acid Receptors Increases Mammary Tumorigenesis, Invasion, and Metastases. Cancer Cell, 2009, 15, 539-550.	16.8	332
115	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
116	Cell-Type-Specific Responses to Chemotherapeutics in Breast Cancer. Cancer Research, 2004, 64, 4218-4226.	0.9	321
117	Characterization of HPV and host genome interactions in primary head and neck cancers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15544-15549.	7.1	317
118	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
119	Molecular Portraits and 70-Gene Prognosis Signature Are Preserved throughout the Metastatic Process of Breast Cancer. Cancer Research, 2005, 65, 9155-9158.	0.9	302
120	Estrogen-Regulated Genes Predict Survival in Hormone Receptor–Positive Breast Cancers. Journal of Clinical Oncology, 2006, 24, 1656-1664.	1.6	300
121	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
122	Chemotherapy response and recurrence-free survival in neoadjuvant breast cancer depends on biomarker profiles: results from the I-SPY 1 TRIAL (CALGB 150007/150012; ACRIN 6657). Breast Cancer Research and Treatment, 2012, 132, 1049-1062.	2.5	286
123	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
124	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor–negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
125	Molecular portraits and the family tree of cancer. Nature Genetics, 2002, 32, 533-540.	21.4	275
126	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272

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127	Genomic Analysis of Immune Cell Infiltrates Across 11 Tumor Types. Journal of the National Cancer Institute, 2016, 108, djw144.	6.3	271
128	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
129	Quantitative MRI radiomics in the prediction of molecular classifications of breast cancer subtypes in the TCGA/TCIA data set. Npj Breast Cancer, 2016, 2, .	5.2	266
130	Towards a novel classification of human malignancies based on gene expression patterns. Journal of Pathology, 2001, 195, 41-52.	4.5	265
131	Gene Expression Profiling Reveals Reproducible Human Lung Adenocarcinoma Subtypes in Multiple Independent Patient Cohorts. Journal of Clinical Oncology, 2006, 24, 5079-5090.	1.6	263
132	Ductal Carcinoma <i>In situ</i> and the Emergence of Diversity during Breast Cancer Evolution. Clinical Cancer Research, 2008, 14, 370-378.	7.0	262
133	Comparison of RNA-Seq by poly (A) capture, ribosomal RNA depletion, and DNA microarray for expression profiling. BMC Genomics, 2014, 15, 419.	2.8	262
134	Lung Squamous Cell Carcinoma mRNA Expression Subtypes Are Reproducible, Clinically Important, and Correspond to Normal Cell Types. Clinical Cancer Research, 2010, 16, 4864-4875.	7.0	259
135	A 50-Gene Intrinsic Subtype Classifier for Prognosis and Prediction of Benefit from Adjuvant Tamoxifen. Clinical Cancer Research, 2012, 18, 4465-4472.	7.0	258
136	ÂB-Crystallin is a novel oncoprotein that predicts poor clinical outcome in breast cancer. Journal of Clinical Investigation, 2005, 116, 261-270.	8.2	256
137	Mutation of GATA3 in human breast tumors. Oncogene, 2004, 23, 7669-7678.	5.9	250
138	PAM50 Breast Cancer Subtyping by RT-qPCR and Concordance with Standard Clinical Molecular Markers. BMC Medical Genomics, 2012, 5, 44.	1.5	250
139	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
140	Practical implications of gene-expression-based assays for breast oncologists. Nature Reviews Clinical Oncology, 2012, 9, 48-57.	27.6	242
141	EGFR associated expression profiles vary with breast tumor subtype. BMC Genomics, 2007, 8, 258.	2.8	234
142	Prognostic B-cell Signatures Using mRNA-Seq in Patients with Subtype-Specific Breast and Ovarian Cancer. Clinical Cancer Research, 2014, 20, 3818-3829.	7.0	230
143	A Genome-Wide Screen for Promoter Methylation in Lung Cancer Identifies Novel Methylation Markers for Multiple Malignancies. PLoS Medicine, 2006, 3, e486.	8.4	228
144	Multiple Roles of Cyclin-Dependent Kinase 4/6 Inhibitors in Cancer Therapy. Journal of the National Cancer Institute, 2012, 104, 476-487.	6.3	228

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145	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228
146	Combined immune checkpoint blockade as a therapeutic strategy for <i>BRCA1</i> -mutated breast cancer. Science Translational Medicine, 2017, 9, .	12.4	227
147	Differential Pathogenesis of Lung Adenocarcinoma Subtypes Involving Sequence Mutations, Copy Number, Chromosomal Instability, and Methylation. PLoS ONE, 2012, 7, e36530.	2.5	225
148	FOXA1 Expression in Breast Cancerâ€"Correlation with Luminal Subtype A and Survival. Clinical Cancer Research, 2007, 13, 4415-4421.	7.0	220
149	The functional loss of the retinoblastoma tumour suppressor is a common event in basal-like and luminal B breast carcinomas. Breast Cancer Research, 2008, 10, R75.	5.0	216
150	An integrated genomics approach identifies drivers of proliferation in luminal-subtype human breast cancer. Nature Genetics, 2014, 46, 1051-1059.	21.4	215
151	MicroRNA-30c inhibits human breast tumour chemotherapy resistance by regulating TWF1 and IL-11. Nature Communications, 2013, 4, 1393.	12.8	209
152	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. JAMA Oncology, 2017, 3, 1654.	7.1	208
153	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	6.4	205
154	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
155	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	204
156	A Six-Gene Signature Predicts Survival of Patients with Localized Pancreatic Ductal Adenocarcinoma. PLoS Medicine, 2010, 7, e1000307.	8.4	202
157	Breast Carcinomas Arising at a Young Age: Unique Biology or a Surrogate for Aggressive Intrinsic Subtypes?. Journal of Clinical Oncology, 2011, 29, e18-e20.	1.6	200
158	The Genomic Landscape of Breast Cancer as a Therapeutic Roadmap. Cancer Discovery, 2013, 3, 27-34.	9.4	200
159	Tumor mutational burden is a determinant of immune-mediated survival in breast cancer. OncoImmunology, 2018, 7, e1490854.	4.6	200
160	Merging two gene-expression studies via cross-platform normalization. Bioinformatics, 2008, 24, 1154-1160.	4.1	198
161	<i>PIK3CA</i> and <i>PIK3CB</i> Inhibition Produce Synthetic Lethality when Combined with Estrogen Deprivation in Estrogen Receptorâ€"Positive Breast Cancer. Cancer Research, 2009, 69, 3955-3962.	0.9	198
162	Molecular Stratification of Triple-Negative Breast Cancers. Oncologist, 2010, 15, 39-48.	3.7	197

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163	TP53 genomics predict higher clinical and pathologic tumor response in operable early-stage breast cancer treated with docetaxel-capecitabineÂÂ±Âtrastuzumab. Breast Cancer Research and Treatment, 2012, 132, 781-791.	2.5	194
164	Image analysis with deep learning to predict breast cancer grade, ER status, histologic subtype, and intrinsic subtype. Npj Breast Cancer, 2018, 4, 30.	5.2	193
165	Identification of the murine beige gene by YAC complementation and positional cloning. Nature Genetics, 1996, 13, 303-308.	21.4	192
166	How Many Etiological Subtypes of Breast Cancer: Two, Three, Four, Or More?. Journal of the National Cancer Institute, 2014, 106, dju165-dju165.	6.3	191
167	Genomic analysis identifies unique signatures predictive of brain, lung, and liver relapse. Breast Cancer Research and Treatment, 2012, 132, 523-535.	2.5	189
168	Transcriptomic classification of genetically engineered mouse models of breast cancer identifies human subtype counterparts. Genome Biology, 2013, 14, R125.	9.6	188
169	Comparative oncogenomics identifies breast tumors enriched in functional tumor-initiating cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2778-2783.	7.1	187
170	Identification of a basal-like subtype of breast ductal carcinoma in situ. Human Pathology, 2007, 38, 197-204.	2.0	185
171	Defining the cellular precursors to human breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2772-2777.	7.1	185
172	Molecular Features and Survival Outcomes of the Intrinsic Subtypes Within HER2-Positive Breast Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	178
173	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
174	Classification and risk stratification of invasive breast carcinomas using a real-time quantitative RT-PCR assay. Breast Cancer Research, 2006, 8, R23.	5.0	176
175	Mammary development meets cancer genomics. Nature Medicine, 2009, 15, 842-844.	30.7	171
176	Molecular Subtypes in Breast Cancer Evaluation and Management: Divide and Conquer. Cancer Investigation, 2008, 26, 1-10.	1.3	170
177	Characterization of cell lines derived from breast cancers and normal mammary tissues for the study of the intrinsic molecular subtypes. Breast Cancer Research and Treatment, 2013, 142, 237-255.	2.5	169
178	Mutant <i>PIK3CA</i> accelerates HER2-driven transgenic mammary tumors and induces resistance to combinations of anti-HER2 therapies. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14372-14377.	7.1	168
179	Intrinsic Subtypes and Gene Expression Profiles in Primary and Metastatic Breast Cancer. Cancer Research, 2017, 77, 2213-2221.	0.9	168
180	A compact VEGF signature associated with distant metastases and poor outcomes. BMC Medicine, 2009, 7, 9.	5.5	162

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181	Systems Biology and Genomics of Breast Cancer. Cold Spring Harbor Perspectives in Biology, 2011, 3, a003293-a003293.	5.5	156
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