Carlos Caldas

List of Publications by Year
in descending order

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410 papers	77,660 citations	993 114 h-index	567 263 g-index
454 all docs	454 docs citations	454 times ranked	84474 citing authors

#	Article	IF	Citations
1	Clinical utility of whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 32-39.	4.3	35
2	Analytical demands to use whole-genome sequencing in precision oncology. Seminars in Cancer Biology, 2022, 84, 16-22.	4.3	22
3	Clinical interpretation of whole-genome and whole-transcriptome sequencing for precision oncology. Seminars in Cancer Biology, 2022, 84, 23-31.	4.3	10
4	Clonal populations of a human TNBC model display significant functional heterogeneity and divergent growth dynamics in distinct contexts. Oncogene, 2022, 41, 112-124.	2.6	6
5	Residual cancer burden after neoadjuvant chemotherapy and long-term survival outcomes in breast cancer: a multicentre pooled analysis of 5161 patients. Lancet Oncology, The, 2022, 23, 149-160.	5.1	148
6	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	13.7	187
7	The Molecular Tumor Board Portal supports clinical decisions and automated reporting for precision oncology. Nature Cancer, 2022, 3, 251-261.	5.7	44
8	Nucleoporin-93 reveals a common feature of aggressive breast cancers: robust nucleocytoplasmic transport of transcription factors. Cell Reports, 2022, 38, 110418.	2.9	12
9	Modeling the Prognostic Impact of Circulating Tumor Cells Enumeration in Metastatic Breast Cancer for Clinical Trial Design Simulation. Oncologist, 2022, 27, e561-e570.	1.9	5
10	Preclinical In Vivo Validation of the RAD51 Test for Identification of Homologous Recombination-Deficient Tumors and Patient Stratification. Cancer Research, 2022, 82, 1646-1657.	0.4	40
11	Breast tumor microenvironment structures are associated with genomic features and clinical outcome. Nature Genetics, 2022, 54, 660-669.	9.4	88
12	Allelic expression imbalance of PIK3CA mutations is frequent in breast cancer and prognostically significant. Npj Breast Cancer, 2022, 8, .	2.3	1
13	Germline allelic expression of genes at 17q22 locus associates with risk of breast cancer. European Journal of Cancer, 2022, 172, 146-157.	1.3	0
14	Serial Analysis of Circulating Tumor Cells in Metastatic Breast Cancer Receiving First-Line Chemotherapy. Journal of the National Cancer Institute, 2021, 113, 443-452.	3.0	22
15	NRG1 fusions in breast cancer. Breast Cancer Research, 2021, 23, 3.	2.2	18
16	Abstract GS4-08: Clinical utility of repeated circulating tumor cell (CTC) enumeration as early treatment monitoring tool in metastatic breast cancer (MBC) - a global pooled analysis with individual patient data. , 2021, , .		2
17	FGFR1 amplification or overexpression and hormonal resistance in luminal breast cancer: rationale for a triple blockade of ER, CDK4/6, and FGFR1. Breast Cancer Research, 2021, 23, 21.	2.2	22
18	Time-resolved single-cell analysis of Brca1 associated mammary tumourigenesis reveals aberrant differentiation of luminal progenitors. Nature Communications, 2021, 12, 1502.	5.8	34

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19	Landscapes of cellular phenotypic diversity in breast cancer xenografts and their impact on drug response. Nature Communications, 2021, 12, 1998.	5.8	37
20	PI3K activation promotes resistance to eribulin in HER2-negative breast cancer. British Journal of Cancer, 2021, 124, 1581-1591.	2.9	12
21	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. Npj Breast Cancer, 2021, 7, 46.	2.3	6
22	Intestinal microbiota influences clinical outcome and side effects of early breast cancer treatment. Cell Death and Differentiation, 2021, 28, 2778-2796.	5.0	72
23	Deciphering the signaling network of breast cancer improves drug sensitivity prediction. Cell Systems, 2021, 12, 401-418.e12.	2.9	22
24	TSHZ2 is an EGF-regulated tumor suppressor that binds to the cytokinesis regulator PRC1 and inhibits metastasis. Science Signaling, 2021, 14, .	1.6	7
25	High-throughput surface marker screen on primary human breast tissues reveals further cellular heterogeneity. Breast Cancer Research, 2021, 23, 66.	2.2	5
26	The temporal mutational and immune tumour microenvironment remodelling of HER2-negative primary breast cancers. Npj Breast Cancer, 2021, 7, 73.	2.3	2
27	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	13.7	71
28	Functional genomics approaches to improve preâ€clinical drug screening and biomarker discovery. EMBO Molecular Medicine, 2021, 13, e13189.	3.3	5
29	Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. Npj Precision Oncology, 2021, 5, 83.	2.3	4
30	Metabolic imaging with hyperpolarized [1-13C] pyruvate in patient-derived preclinical mouse models of breast cancer. STAR Protocols, 2021, 2, 100608.	0.5	2
31	3D deformable registration of longitudinal abdominopelvic CT images using unsupervised deep learning. Computer Methods and Programs in Biomedicine, 2021, 208, 106261.	2.6	9
32	DNA methylation landscapes of 1538 breast cancers reveal a replication-linked clock, epigenomic instability and cis-regulation. Nature Communications, 2021, 12, 5406.	5.8	29
33	Germline <scp>APOBEC3B</scp> deletion increases somatic hypermutation in Asian breast cancer that is associated with Her2 subtype, <scp>PIK3CA</scp> mutations and immune activation. International Journal of Cancer, 2021, 148, 2489-2501.	2.3	15
34	Hyperpolarized Carbon-13 MRI for Early Response Assessment of Neoadjuvant Chemotherapy in Breast Cancer Patients. Cancer Research, 2021, 81, 6004-6017.	0.4	25
35	Determinants of anti-PD-1 response and resistance in clear cell renal cell carcinoma. Cancer Cell, 2021, 39, 1497-1518.e11.	7.7	126
36	Positive correlation between transcriptomic stemness and PI3K/AKT/mTOR signaling scores in breast cancer, and a counterintuitive relationship with PIK3CA genotype. PLoS Genetics, 2021, 17, e1009876.	1.5	14

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37	Fbxl17 is rearranged in breast cancer and loss of its activity leads to increased global O-GlcNAcylation. Cellular and Molecular Life Sciences, 2020, 77, 2605-2620.	2.4	10
38	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. Nature Genetics, 2020, 52, 187-197.	9.4	108
39	Association Between Levels of Sex Hormones and Risk of Esophageal Adenocarcinoma and Barrettâ€™s Esophagus. Clinical Gastroenterology and Hepatology, 2020, 18, 2701-2709.e3.	2.4	12
40	Metabolic Imaging Detects Resistance to PI3KÎ± Inhibition Mediated by Persistent FOXM1 Expression in ER+ Breast Cancer. Cancer Cell, 2020, 38, 516-533.e9.	7.7	38
41	Hyperpolarized ¹³C MRI of Tumor Metabolism Demonstrates Early Metabolic Response to Neoadjuvant Chemotherapy in Breast Cancer. Radiology Imaging Cancer, 2020, 2, e200017.	0.7	40
42	Towards a cancer mission in Horizon Europe: recommendations. Molecular Oncology, 2020, 14, 1589-1615.	2.1	33
43	Landscape of G-quadruplex DNA structural regions in breast cancer. Nature Genetics, 2020, 52, 878-883.	9.4	122
44	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	5.8	60
45	Sex-Specific Genetic Associations for Barrettâ€™s Esophagus and Esophageal Adenocarcinoma. Gastroenterology, 2020, 159, 2065-2076.e1.	0.6	16
46	Association of Sperm-Associated Antigen 5 and Treatment Response in Patients With Estrogen Receptorâ€"Positive Breast Cancer. JAMA Network Open, 2020, 3, e209486.	2.8	2
47	Age-correlated protein and transcript expression in breast cancer and normal breast tissues is dominated by host endocrine effects. Nature Cancer, 2020, 1, 518-532.	5.7	11
48	Transcriptional profiling reveals a subset of human breast tumors that retain wt TP53 but display mutant p53â€associated features. Molecular Oncology, 2020, 14, 1640-1652.	2.1	8
49	Trial watch : the gut microbiota as a tool to boost the clinical efficacy of anticancer immunotherapy. OncoImmunology, 2020, 9, 1774298.	2.1	22
50	ctDNA monitoring using patient-specific sequencing and integration of variant reads. Science Translational Medicine, 2020, 12, .	5.8	116
51	Representative Sequencing: Unbiased Sampling of Solid Tumor Tissue. Cell Reports, 2020, 31, 107550.	2.9	51
52	The GATA3 X308_Splice breast cancer mutation is a hormone context-dependent oncogenic driver. Oncogene, 2020, 39, 5455-5467.	2.6	12
53	Cancer-associated fibroblast compositions change with breast cancer progression linking the ratio of S100A4+ and PDPN+ CAFs to clinical outcome. Nature Cancer, 2020, 1, 692-708.	5.7	159
54	Support systems to guide clinical decision-making in precision oncology: The Cancer Core Europe Molecular Tumor Board Portal. Nature Medicine, 2020, 26, 992-994.	15.2	56

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55	Imaging breast cancer using hyperpolarized carbon-13 MRI. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2092-2098.	3.3	138
56	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. Nature Cancer, 2020, 1, 163-175.	5.7	209
57	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
58	Caring for patients with cancer in the COVID-19 era. Nature Medicine, 2020, 26, 665-671.	15.2	269
59	Genetic Alterations in the PI3K/AKT Pathway and Baseline AKT Activity Define AKT Inhibitor Sensitivity in Breast Cancer Patient-derived Xenografts. Clinical Cancer Research, 2020, 26, 3720-3731.	3.2	21
60	The molecular landscape of Asian breast cancers reveals clinically relevant population-specific differences. Nature Communications, 2020, 11, 6433.	5.8	37
61	DNA copy number motifs are strong and independent predictors of survival in breast cancer. Communications Biology, 2020, 3, 153.	2.0	9
62	Six versus 12 monthsâ€™ adjuvant trastuzumab in patients with HER2-positive early breast cancer: the PERSEPHONE non-inferiority RCT. Health Technology Assessment, 2020, 24, 1-190.	1.3	11
63	Deep Sequencing of B Cell Receptor Repertoires From COVID-19 Patients Reveals Strong Convergent Immune Signatures. Frontiers in Immunology, 2020, 11, 605170.	2.2	101
64	Personalized circulating tumor DNA analysis to detect residual disease after neoadjuvant therapy in breast cancer. Science Translational Medicine, 2019, 11, .	5.8	197
65	BET Inhibition as a Rational Therapeutic Strategy for Invasive Lobular Breast Cancer. Clinical Cancer Research, 2019, 25, 7139-7150.	3.2	18
66	POSEIDON Trial Phase 1b Results: Safety, Efficacy and Circulating Tumor DNA Response of the Beta Isoform-Sparing PI3K Inhibitor Taselisib (GDC-0032) Combined with Tamoxifen in Hormone Receptor Positive Metastatic Breast Cancer Patients. Clinical Cancer Research, 2019, 25, 6598-6605.	3.2	17
67	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	13.5	162
68	Cancer Core Europe: A translational research infrastructure for a European mission on cancer. Molecular Oncology, 2019, 13, 521-527.	2.1	38
69	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	2.4	85
70	Chlorambucil targets <scp>BRCA</scp> 1/2â€deficient tumours and counteracts <scp>PARP</scp> inhibitor resistance. EMBO Molecular Medicine, 2019, 11, e9982.	3.3	26
71	Chromosome 12p Amplification in Triple-Negative/BRCA1-Mutated Breast Cancer Associates with Emergence of Docetaxel Resistance and Carboplatin Sensitivity. Cancer Research, 2019, 79, 4258-4270.	0.4	17
72	EN1 Is a Transcriptional Dependency in Triple-Negative Breast Cancer Associated with Brain Metastasis. Cancer Research, 2019, 79, 4173-4183.	0.4	47

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73	6 versus 12 months of adjuvant trastuzumab for HER2-positive early breast cancer (PERSEPHONE): 4-year disease-free survival results of a randomised phase 3 non-inferiority trial. Lancet, The, 2019, 393, 2599-2612.	6.3	225
74	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	2.9	95
75	A key genomic subtype associated with lymphovascular invasion in invasive breast cancer. British Journal of Cancer, 2019, 120, 1129-1136.	2.9	25
76	EZH2 Is Overexpressed in BRCA1-like Breast Tumors and Predictive for Sensitivity to High-Dose Platinum-Based Chemotherapy. Clinical Cancer Research, 2019, 25, 4351-4362.	3.2	33
77	PDLIM2 Is a Marker of Adhesion and Î²-Catenin Activity in Triple-Negative Breast Cancer. Cancer Research, 2019, 79, 2619-2633.	0.4	14
78	Cancer Treatment in the Genomic Era. Annual Review of Biochemistry, 2019, 88, 247-280.	5.0	24
79	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	13.7	239
80	miR-342-5p as a Potential Regulator of HER2 Breast Cancer Cell Growth. MicroRNA (Shariqah, United) Tj ETQq0 0 0 rgBT /Overlock 10 Tf	0.6	27
81	Combined quantitative measures of ER, PR, HER2, and KI67 provide more prognostic information than categorical combinations in luminal breast cancer. Modern Pathology, 2019, 32, 1244-1256.	2.9	51
82	No Association Between Vitamin D Status and Risk of Barrett's Esophagus or Esophageal Adenocarcinoma: A Mendelian Randomization Study. Clinical Gastroenterology and Hepatology, 2019, 17, 2227-2235.e1.	2.4	16
83	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
84	Clonal replacement and heterogeneity in breast tumors treated with neoadjuvant HER2-targeted therapy. Nature Communications, 2019, 10, 657.	5.8	43
85	Tumor diversity and the trade-off between universal cancer tasks. Nature Communications, 2019, 10, 5423.	5.8	53
86	PathTracer: High-sensitivity detection of differential pathway activity in tumours. Scientific Reports, 2019, 9, 16332.	1.6	2
87	The clinical use of circulating tumor cells (CTCs) enumeration for staging of metastatic breast cancer (MBC): International expert consensus paper. Critical Reviews in Oncology/Hematology, 2019, 134, 39-45.	2.0	200
88	Next Generation-Targeted Amplicon Sequencing (NG-TAS): an optimised protocol and computational pipeline for cost-effective profiling of circulating tumour DNA. Genome Medicine, 2019, 11, 1.	3.6	84
89	Therapeutic relevance of the PP2A-B55 inhibitory kinase MASTL/Greatwall in breast cancer. Cell Death and Differentiation, 2018, 25, 828-840.	5.0	67
90	High USP6NL Levels in Breast Cancer Sustain Chronic AKT Phosphorylation and GLUT1 Stability Fueling Aerobic Glycolysis. Cancer Research, 2018, 78, 3432-3444.	0.4	54

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91	SILAC identifies LAD1 as a filamin-binding regulator of actin dynamics in response to EGF and a marker of aggressive breast tumors. Science Signaling, 2018, 11, .	1.6	41
92	Determining Risk of Barrettâ€™s Esophagus and Esophageal Adenocarcinoma Based on Epidemiologic Factors and GeneticÂVariants. Gastroenterology, 2018, 154, 1273-1281.e3.	0.6	67
93	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. Cell, 2018, 173, 1398-1412.e22.	13.5	362
94	Germline pathogenic variants in PALB2 and other cancer-predisposing genes in families with hereditary diffuse gastric cancer without CDH1 mutation: a whole-exome sequencing study. The Lancet Gastroenterology and Hepatology, 2018, 3, 489-498.	3.7	87
95	Shallow whole genome sequencing for robust copy number profiling of formalin-fixed paraffin-embedded breast cancers. Experimental and Molecular Pathology, 2018, 104, 161-169.	0.9	25
96	Interactions Between Genetic Variants and Environmental Factors Affect Risk of Esophageal Adenocarcinoma and Barrettâ€™s Esophagus. Clinical Gastroenterology and Hepatology, 2018, 16, 1598-1606.e4.	2.4	16
97	Comparative study of endoscopic surveillance in hereditary diffuse gastric cancer according to CDH1 mutation status. Gastrointestinal Endoscopy, 2018, 87, 408-418.	0.5	85
98	A <scp>RAD</scp> 51 assay feasible in routine tumor samples calls <scp>PARP</scp> inhibitor response beyond <scp>BRCA</scp> mutation. EMBO Molecular Medicine, 2018, 10, .	3.3	169
99	Cancer Core Europe: A European cancer research alliance realizing a research infrastructure with critical mass and programmatic approach to cure cancer in the 21st century. European Journal of Cancer, 2018, 103, 155-159.	1.3	15
100	Computational approach to discriminate human and mouse sequences in patient-derived tumour xenografts. BMC Genomics, 2018, 19, 19.	1.2	55
101	Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients. Journal of Molecular Diagnostics, 2018, 20, 883-892.	1.2	81
102	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. Cell Research, 2018, 28, 719-729.	5.7	105
103	Î±Eâ€catenin is a candidate tumor suppressor for the development of Eâ€cadherinâ€expressing lobularâ€type breast cancer. Journal of Pathology, 2018, 245, 456-467.	2.1	34
104	Dynamics of multiple resistance mechanisms in plasma DNA during EGFRâ€targeted therapies in nonâ€small cell lung cancer. EMBO Molecular Medicine, 2018, 10, .	3.3	61
105	Saccharomyces cerevisiae-like 1 (SEC14L1) is a prognostic factor in breast cancer associated with lymphovascular invasion. Modern Pathology, 2018, 31, 1675-1682.	2.9	13
106	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. Nature Cell Biology, 2018, 20, 954-965.	4.6	291
107	SOX4 can redirect TGF-Î²-mediated SMAD3-transcriptional output in a context-dependent manner to promote tumorigenesis. Nucleic Acids Research, 2018, 46, 9578-9590.	6.5	37
108	Abstract 3596: Biomarkers of response to CDK4/6 inhibitor (CDK4/6i) in hormone receptor (HR) positive and HER2-positive breast cancer (BC) patient-derived xenografts (PDX). , 2018, , .		1

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109	PERSEPHONE: 6 versus 12 months (m) of adjuvant trastuzumab in patients (pts) with HER2 positive (+) early breast cancer (EBC): Randomised phase 3 non-inferiority trial with definitive 4-year (yr) disease-free survival (DFS) results.. Journal of Clinical Oncology, 2018, 36, 506-506.	0.8	59
110	Global transcriptional analysis identifies a novel role for SOX4 in tumor-induced angiogenesis. ELife, 2018, 7, .	2.8	32
111	Interrogating open issues in cancer precision medicine with patient-derived xenografts. Nature Reviews Cancer, 2017, 17, 254-268.	12.8	527
112	Liquid biopsies come of age: towards implementation of circulating tumour DNA. Nature Reviews Cancer, 2017, 17, 223-238.	12.8	1,786
113	High-risk individualsâ€™ perceptions of reproductive genetic testing for CDH1 mutations. Familial Cancer, 2017, 16, 531-535.	0.9	7
114	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. Nature Communications, 2017, 8, 14432.	5.8	379
115	Ki67 expression in invasive breast cancer: the use of tissue microarrays compared with whole tissue sections. Breast Cancer Research and Treatment, 2017, 164, 341-348.	1.1	44
116	Addition of gemcitabine to paclitaxel, epirubicin, and cyclophosphamide adjuvant chemotherapy for women with early-stage breast cancer (tAnGo): final 10-year follow-up of an open-label, randomised, phase 3 trial. Lancet Oncology, The, 2017, 18, 755-769.	5.1	18
117	Therapeutic Rationale to Target Highly Expressed CDK7 Conferring Poor Outcomes in Triple-Negative Breast Cancer. Cancer Research, 2017, 77, 3834-3845.	0.4	79
118	Central pathology review with two-stage quality assurance for pathological response after neoadjuvant chemotherapy in the ARTemis Trial. Modern Pathology, 2017, 30, 1069-1077.	2.9	15
119	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. Breast Cancer Research, 2017, 19, 44.	2.2	85
120	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. Gut, 2017, 66, 1739-1747.	6.1	38
121	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
122	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
123	Rho-GTPase activating-protein 18: a biomarker associated with good prognosis in invasive breast cancer. British Journal of Cancer, 2017, 117, 1176-1184.	2.9	16
124	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics, 2017, 49, 1476-1486.	9.4	427
125	Breast Cancer Molecular Stratification. American Journal of Pathology, 2017, 187, 2152-2162.	1.9	198
126	Predicting treatment resistance and relapse through circulating DNA. Breast, 2017, 34, S31-S35.	0.9	17

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127	Intersect-then-combine approach: improving the performance of somatic variant calling in whole exome sequencing data using multiple aligners and callers. Genome Medicine, 2017, 9, 35.	3.6	48
128	The Psychosocial Impact of Undergoing Prophylactic Total Gastrectomy (PTG) to Manage the Risk of Hereditary Diffuse Gastric Cancer (HDGC). Journal of Genetic Counseling, 2017, 26, 752-762.	0.9	29
129	Further evidence to support bimodality of oestrogen receptor expression in breast cancer. Histopathology, 2017, 70, 456-465.	1.6	12
130	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
131	Integrative analysis of copy number and gene expression in breast cancer using formalin-fixed paraffin-embedded core biopsy tissue: a feasibility study. BMC Genomics, 2017, 18, 526.	1.2	11
132	The BRCA1ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. Breast Cancer Research, 2017, 19, 99.	2.2	58
133	Data-driven analysis of immune infiltrate in a large cohort of breast cancer and its association with disease progression, ER activity, and genomic complexity. Oncotarget, 2017, 8, 57121-57133.	0.8	31
134	Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. PLoS Medicine, 2016, 13, e1002194.	3.9	473
135	Genome co-amplification upregulates a mitotic gene network activity that predicts outcome and response to mitotic protein inhibitors in breast cancer. Breast Cancer Research, 2016, 18, 70.	2.2	11
136	Subtypeâ€specific microâ€RNA expression signatures in breast cancer progression. International Journal of Cancer, 2016, 139, 1117-1128.	2.3	53
137	Stratification and therapeutic potential of PML in metastatic breast cancer. Nature Communications, 2016, 7, 12595.	5.8	45
138	Modeling Breast Cancer Intertumor and Intratumor Heterogeneity Using Xenografts. Cold Spring Harbor Symposia on Quantitative Biology, 2016, 81, 227-230.	2.0	7
139	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. Scientific Reports, 2016, 6, 18517.	1.6	143
140	p120-catenin prevents multinucleation through control of MKLP1-dependent RhoA activity during cytokinesis. Nature Communications, 2016, 7, 13874.	5.8	17
141	Decline in Antigenicity of Tumor Markers by Storage Time Using Pathology Sections Cut From Tissue Microarrays. Applied Immunohistochemistry and Molecular Morphology, 2016, 24, 221-226.	0.6	10
142	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
143	Facilitating a culture of responsible and effective sharing of cancer genome data. Nature Medicine, 2016, 22, 464-471.	15.2	83
144	Nucleosome mapping in plasma DNA predicts cancer gene expression. Nature Genetics, 2016, 48, 1105-1106.	9.4	19

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145	Androgen and Estrogen Receptors in Breast Cancer Coregulate Human UDP-Glucuronosyltransferases 2B15 and 2B17. Cancer Research, 2016, 76, 5881-5893.	0.4	50
146	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. Lancet Oncology, The, 2016, 17, 1363-1373.	5.1	133
147	Prognostic significance of androgen receptor expression in invasive breast cancer: transcriptomic and protein expression analysis. Breast Cancer Research and Treatment, 2016, 159, 215-227.	1.1	81
148	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	13.5	376
149	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100
150	Reliable gene expression profiling of formalin-fixed paraffin-embedded breast cancer tissue (FFPE) using cDNA-mediated annealing, extension, selection, and ligation whole-genome (DASL WG) assay. BMC Medical Genomics, 2016, 9, 54.	0.7	11
151	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
152	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	5.8	1,221
153	Prognostic Value of MammaPrint^{Â®} in Invasive Lobular Breast Cancer. Biomarker Insights, 2016, 11, BMI.S38435.	1.0	31
154	An investigation of the factors effecting high-risk individualsâ€™ decision-making about prophylactic total gastrectomy and surveillance for hereditary diffuse gastric cancer (HDGC). Familial Cancer, 2016, 15, 665-676.	0.9	28
155	SPAG5 as a prognostic biomarker and chemotherapy sensitivity predictor in breast cancer: a retrospective, integrated genomic, transcriptomic, and protein analysis. Lancet Oncology, The, 2016, 17, 1004-1018.	5.1	105
156	Computational pathology of pre-treatment biopsies identifies lymphocyte density as a predictor of response to neoadjuvant chemotherapy in breast cancer. Breast Cancer Research, 2016, 18, 21.	2.2	66
157	Cellâ€free circulating tumour DNA as a liquid biopsy in breast cancer. Molecular Oncology, 2016, 10, 464-474.	2.1	101
158	Double-stranded microRNA mimics can induce length- and passenger strandâ€“dependent effects in a cell typeâ€“specific manner. Rna, 2016, 22, 193-203.	1.6	31
159	MYC functions are specific in biological subtypes of breast cancer and confers resistance to endocrine therapy in luminal tumours. British Journal of Cancer, 2016, 114, 917-928.	2.9	91
160	Disease-free (DFS) and overall survival (OS) at 3.4 years (yrs) for neoadjuvant bevacizumab (Bev) added to docetaxel followed by fluorouracil, epirubicin and cyclophosphamide (D-FEC), for women with HER2 negative early breast cancer: The ARTemis trial.. Journal of Clinical Oncology, 2016, 34, 1014-1014.	0.8	3
161	The Relationship between Common Genetic Markers of Breast Cancer Risk and Chemotherapy-Induced Toxicity: A Case-Control Study. PLoS ONE, 2016, 11, e0158984.	1.1	15
162	A retrospective study of SPAG5 expression and its clinical implications in >8,000 patients of ER positive (ER+) breast cancer (BC): Genomic, transcriptomic and protein analysis.. Journal of Clinical Oncology, 2016, 34, 575-575.	0.8	0

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163	Navigatorâ€3, a modulator of cell migration, may act as a suppressor of breast cancer progression. EMBO Molecular Medicine, 2015, 7, 299-314.	3.3	34
164	Context-Specific Effects of TGF-Î²/SMAD3 in Cancer Are Modulated by the Epigenome. Cell Reports, 2015, 13, 2480-2490.	2.9	43
165	A nested cohort study of 6,248 early breast cancer patients treated in neoadjuvant and adjuvant chemotherapy trials investigating the prognostic value of chemotherapy-related toxicities. BMC Medicine, 2015, 13, 306.	2.3	26
166	A co-culture genome-wide RNAi screen with mammary epithelial cells reveals transmembrane signals required for growth and differentiation. Breast Cancer Research, 2015, 17, 4.	2.2	24
167	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
168	Prognostic and predictive value of PDL1 expression in breast cancer. Oncotarget, 2015, 6, 5449-5464.	0.8	424
169	Polymorphisms in Genes of Relevance for Oestrogen and Oxytocin Pathways and Risk of Barrettâ€™s Oesophagus and Oesophageal Adenocarcinoma: A Pooled Analysis from the BEACON Consortium. PLoS ONE, 2015, 10, e0138738.	1.1	9
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