Carlos Caldas

List of Publications by Year
in descending order

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410	77,660	993	567
papers	citations	114 h-index	263 g-index

454	454	454	84474
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	13.7	4,708
3	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
4	Analysis of Circulating Tumor DNA to Monitor Metastatic Breast Cancer. New England Journal of Medicine, 2013, 368, 1199-1209.	13.9	1,884
5	Liquid biopsies come of age: towards implementation of circulating tumour DNA. Nature Reviews Cancer, 2017, 17, 223-238.	12.8	1,786
6	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	13.7	1,778
7	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
8	Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. Nature Genetics, 2005, 37, 391-400.	9.4	1,710
9	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. Nature, 2012, 481, 389-393.	13.7	1,655
10	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	13.7	1,535
11	Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. Nature, 2013, 497, 108-112.	13.7	1,443
12	Patient-Derived Xenograft Models: An Emerging Platform for Translational Cancer Research. Cancer Discovery, 2014, 4, 998-1013.	7.7	1,341
13	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. Nature Communications, 2016, 7, 11479.	5.8	1,221
14	Noninvasive Identification and Monitoring of Cancer Mutations by Targeted Deep Sequencing of Plasma DNA. Science Translational Medicine, 2012, 4, 136ra68.	5.8	1,086
15	Frequent somatic mutations and homozygous deletions of the p16 (MTS1) gene in pancreatic adenocarcinoma. Nature Genetics, 1994, 8, 27-32.	9.4	1,063
16	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. Nature, 2009, 461, 809-813.	13.7	984
17	Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. Cancer Research, 2007, 67, 1424-1429.	0.4	883
18	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. Genome Biology, 2007, 8, R214.	13.9	828

#	Article	IF	Citations
19	Molecular Classification and Molecular Forecasting of Breast Cancer: Ready for Clinical Application?. Journal of Clinical Oncology, 2005, 23, 7350-7360.	0.8	798
20	Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. PLoS Medicine, 2010, 7, e1000279.	3.9	764
21	Clinical validity of circulating tumour cells in patients with metastatic breast cancer: a pooled analysis of individual patient data. Lancet Oncology, The, 2014, 15, 406-414.	5.1	703
22	Driver mutations in TP53 are ubiquitous in high grade serous carcinoma of the ovary. Journal of Pathology, 2010, 221, 49-56.	2.1	617
23	Association between CD8+ T-cell infiltration and breast cancer survival in 12 439 patients. Annals of Oncology, 2014, 25, 1536-1543.	0.6	610
24	Toward understanding and exploiting tumor heterogeneity. Nature Medicine, 2015, 21, 846-853.	15.2	604
25	Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. Rna, 2010, 16, 991-1006.	1.6	588
26	Incidence of gastric cancer and breast cancer in CDH1 (E-cadherin) mutation carriers from hereditary diffuse gastric cancer families. Gastroenterology, 2001, 121, 1348-1353.	0.6	579
27	Helicobacter pylori and Interleukin 1 Genotyping: An Opportunity to Identify High-Risk Individuals for Gastric Carcinoma. Journal of the National Cancer Institute, 2002, 94, 1680-1687.	3.0	563
28	p300/CBP and cancer. Oncogene, 2004, 23, 4225-4231.	2.6	547
29	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. Nature, 2015, 518, 422-426.	13.7	545
30	Mutations truncating the EP300 acetylase in human cancers. Nature Genetics, 2000, 24, 300-303.	9.4	543
31	Hereditary Diffuse Gastric Cancer Syndrome. JAMA Oncology, 2015, 1, 23.	3.4	540
32	Interrogating open issues in cancer precision medicine with patient-derived xenografts. Nature Reviews Cancer, 2017, 17, 254-268.	12.8	527
33	Progesterone receptor modulates ERÎ± action in breast cancer. Nature, 2015, 523, 313-317.	13.7	504
34	Hereditary diffuse gastric cancer: updated consensus guidelines for clinical management and directions for future research. Journal of Medical Genetics, 2010, 47, 436-444.	1.5	495
35	Hereditary diffuse gastric cancer: updated clinical guidelines with an emphasis on germlineCDH1mutation carriers. Journal of Medical Genetics, 2015, 52, 361-374.	1.5	479
36	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

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37	A proinflammatory genetic profile increases the risk for chronic atrophic gastritis and gastric carcinoma. Gastroenterology, 2003, 125, 364-371.	0.6	450
38	An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. Genome Biology, 2007, 8, R157.	13.9	433
39	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. Nature Genetics, 2017, 49, 1476-1486.	9.4	427
40	Prognostic and predictive value of PDL1 expression in breast cancer. Oncotarget, 2015, 6, 5449-5464.	0.8	424
41	Early Gastric Cancer in Young, Asymptomatic Carriers of Germ-Line E-Cadherin Mutations. New England Journal of Medicine, 2001, 344, 1904-1909.	13.9	420
42	Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. Nature Communications, 2015, 6, 8760.	5.8	409
43	Interleukin 1B and interleukin 1RN polymorphisms are associated with increased risk of gastric carcinoma. Gastroenterology, 2001, 121, 823-829.	0.6	402
44	Molecular heterogeneity of breast carcinomas and the cancer stem cell hypothesis. Nature Reviews Cancer, 2007, 7, 791-799.	12.8	397
45	EMSY Links the BRCA2 Pathway to Sporadic Breast and Ovarian Cancer. Cell, 2003, 115, 523-535.	13.5	389
46	MicroRNAâ€"implications for cancer. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2008, 452, 1-10.	1.4	386
47	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. Nature Communications, 2017, 8, 14432.	5.8	379
48	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. Cell Stem Cell, 2015, 16, 712-724.	5.2	376
49	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 2016, 167, 260-274.e22.	13.5	376
50	The shaping and functional consequences of the microRNA landscape in breast cancer. Nature, 2013, 497, 378-382.	13.7	370
51	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. Cell, 2018, 173, 1398-1412.e22.	13.5	362
52	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	5.8	356
53	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
54	Endogenous Purification Reveals GREB1 as a Key Estrogen Receptor Regulatory Factor. Cell Reports, 2013, 3, 342-349.	2.9	319

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55	The Implications of Clonal Genome Evolution for Cancer Medicine. New England Journal of Medicine, 2013, 368, 842-851.	13.9	316
56	Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. Nature Genetics, 2014, 46, 837-843.	9.4	302
57	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. Nature Cell Biology, 2018, 20, 954-965.	4.6	291
58	Chromatin modifier enzymes, the histone code and cancer. European Journal of Cancer, 2005, 41, 2381-2402.	1.3	290
59	PREDICT: a new UK prognostic model that predicts survival following surgery for invasive breast cancer. Breast Cancer Research, 2010, 12, R1.	2.2	285
60	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. Genome Biology, 2007, 8, R215.	13.9	275
61	Caring for patients with cancer in the COVID-19 era. Nature Medicine, 2020, 26, 665-671.	15.2	269
62	A new genome-driven integrated classification of breast cancer and its implications. EMBO Journal, 2013, 32, 617-628.	3.5	267
63	Maintaining Tumor Heterogeneity in Patient-Derived Tumor Xenografts. Cancer Research, 2015, 75, 2963-2968.	0.4	267
64	Phenotypic and functional characterisation of the luminal cell hierarchy of the mammary gland. Breast Cancer Research, 2012, 14, R134.	2.2	260
65	Allele-Specific Up-Regulation of FGFR2 Increases Susceptibility to Breast Cancer. PLoS Biology, 2008, 6, e108.	2.6	254
66	Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. BMC Genomics, 2012, 13, 591.	1.2	251
67	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. Genome Biology, 2012, 13, R124.	13.9	247
68	Model of the early development of diffuse gastric cancer in E-cadherin mutation carriers and its implications for patient screening. Journal of Pathology, 2004, 203, 681-687.	2.1	242
69	TP53 Mutation Spectrum in Breast Cancer Is Subtype Specific and Has Distinct Prognostic Relevance. Clinical Cancer Research, 2014, 20, 3569-3580.	3.2	240
70	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. Nature, 2019, 567, 399-404.	13.7	239
71	Integrative analysis of genome-wide loss of heterozygosity and monoallelic expression at nucleotide resolution reveals disrupted pathways in triple-negative breast cancer. Genome Research, 2012, 22, 1995-2007.	2.4	237
72	Human and mouse oligonucleotide-based array CGH. Nucleic Acids Research, 2005, 33, e192-e192.	6.5	231

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73	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
74	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
75	Cancer genetics of epigenetic genes. Human Molecular Genetics, 2007, 16, R28-R49.	1.4	223
76	Differential expression of selected histone modifier genes in human solid cancers. BMC Genomics, 2006, 7, 90.	1.2	209
77	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer. Nature Cancer, 2020, 1, 163-175.	5.7	209
78	The Extracellular Matrix Protein TGFBI Induces Microtubule Stabilization and Sensitizes Ovarian Cancers to Paclitaxel. Cancer Cell, 2007, 12, 514-527.	7.7	202
79	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
80	Breast Cancer Molecular Stratification. American Journal of Pathology, 2017, 187, 2152-2162.	1.9	198
81	Personalized circulating tumor DNA analysis to detect residual disease after neoadjuvant therapy in breast cancer. Science Translational Medicine, 2019, 11, .	5.8	197
82	Sizing up miRNAs as cancer genes. Nature Medicine, 2005, 11, 712-714.	15.2	189
83	Bcl-2 Is a Prognostic Marker in Breast Cancer Independently of the Nottingham Prognostic Index. Clinical Cancer Research, 2006, 12, 2468-2475.	3.2	188
84	Alphaâ€6 integrin is necessary for the tumourigenicity of a stem cellâ€like subpopulation within the MCF7 breast cancer cell line. International Journal of Cancer, 2008, 122, 298-304.	2.3	187
85	Multi-omic machine learning predictor of breast cancer therapy response. Nature, 2022, 601, 623-629.	13.7	187
86	A Recurrent Chromosome Breakpoint in Breast Cancer at the NRG1/Neuregulin 1/Heregulin Gene. Cancer Research, 2004, 64, 6840-6844.	0.4	185
87	Germline CDH1 deletions in hereditary diffuse gastric cancer families. Human Molecular Genetics, 2009, 18, 1545-1555.	1.4	185
88	Master regulators of FGFR2 signalling and breast cancer risk. Nature Communications, 2013, 4, 2464.	5.8	180
89	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. Genome Biology, 2014, 15, 431.	3.8	178
90	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. Nature Genetics, 2013, 45, 1487-1493.	9.4	174

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91	JARID1B Is a Luminal Lineage-Driving Oncogene in Breast Cancer. Cancer Cell, 2014, 25, 762-777.	7.7	170
92	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
93	Identification of CDH1 germline missense mutations associated with functional inactivation of the E-cadherin protein in young gastric cancer probands. Human Molecular Genetics, 2003, 12, 575-582.	1.4	167
94	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. Cell, 2019, 179, 1207-1221.e22.	13.5	162
95	Meta-analysis confirms BCL2 is an independent prognostic marker in breast cancer. BMC Cancer, 2008, 8, 153.	1.1	159
96	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
97	Screening E-cadherin in gastric cancer families reveals germline mutations only in hereditary diffuse gastric cancer kindred. Human Mutation, 2002, 19, 510-517.	1.1	153
98	Molecular Classification of Breast Carcinomas Using Tissue Microarrays. Diagnostic Molecular Pathology, 2003, 12, 27-34.	2.1	153
99	Molecular genetic profiles of colitis-associated neoplasms. Gastroenterology, 1994, 107, 420-428.	0.6	152
100	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	1.4	152
101	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
102	A 1â€‰Mb minimal amplicon at 8p11â€“12 in breast cancer identifies new candidate oncogenes. Oncogene, 2005, 24, 5235-5245.	2.6	146
103	Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. BMC Cancer, 2010, 10, 604.	1.1	144
104	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
105	Common occurrence of APC and K-ras gene mutations in the spectrum of colitis-associated neoplasias. Gastroenterology, 1995, 108, 383-392.	0.6	139
106	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. Science Translational Medicine, 2010, 2, 38ra47.	5.8	138
107	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
108	Identification and validation of prognostic markers in breast cancer with the complementary use of array-CGH and tissue microarrays. Journal of Pathology, 2005, 205, 388-396.	2.1	137

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109	A 4-Gene Signature Predicts Survival of Patients With Resected Adenocarcinoma of the Esophagus, Junction, and Gastric Cardia. Gastroenterology, 2010, 139, 1995-2004.e15.	0.6	135
110	BCL11A is a triple-negative breast cancer gene with critical functions in stem and progenitor cells. Nature Communications, 2015, 6, 5987.	5.8	135
111	p300 regulates p53-dependent apoptosis after DNA damage in colorectal cancer cells by modulation of PUMA/p21 levels. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7386-7391.	3.3	133
112	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
113	Dysregulated expression of Fau and MELK is associated with poor prognosis in breast cancer. Breast Cancer Research, 2009, 11, R60.	2.2	129
114	K-ras mutation and pancreatic adenocarcinoma. International Journal of Gastrointestinal Cancer, 1995, 18, 1-6.	0.4	127
115	Determinants of anti-PD-1 response and resistance in clear cell renal cell carcinoma. Cancer Cell, 2021, 39, 1497-1518.e11.	7.7	126
116	Predictive markers of anthracycline benefit: a prospectively planned analysis of the UK National Epirubicin Adjuvant Trial (NEAT/BR9601). Lancet Oncology, The, 2010, 11, 266-274.	5.1	122
117	Landscape of G-quadruplex DNA structural regions in breast cancer. Nature Genetics, 2020, 52, 878-883.	9.4	122
118	G-Quadruplex DNA as a Molecular Target for Induced Synthetic Lethality in Cancer Cells. Journal of the American Chemical Society, 2013, 135, 9640-9643.	6.6	121
119	Saliva samples are a viable alternative to blood samples as a source of DNA for high throughput genotyping. BMC Medical Genomics, 2012, 5, 19.	0.7	120
120	Circulating Tumor DNA to Monitor Metastatic Breast Cancer. New England Journal of Medicine, 2013, 369, 93-94.	13.9	120
121	ZNF703 is a common Luminal B breast cancer oncogene that differentially regulates luminal and basal progenitors in human mammary epithelium. EMBO Molecular Medicine, 2011, 3, 167-180.	3.3	119
122	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. Nature Communications, 2016, 7, 12910.	5.8	119
123	Characterisation of microRNA expression in post-natal mouse mammary gland development. BMC Genomics, 2009, 10, 548.	1.2	117
124	ctDNA monitoring using patient-specific sequencing and integration of variant reads. Science Translational Medicine, 2020, 12, .	5.8	116
125	Efficacy of neoadjuvant bevacizumab added to docetaxel followed by fluorouracil, epirubicin, and cyclophosphamide, for women with HER2-negative early breast cancer (ARTemis): an open-label, randomised, phase 3 trial. Lancet Oncology, The, 2015, 16, 656-666.	5.1	114
126	A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the Proliferation, Immune response and RNA splicing modules in breast cancer. Breast Cancer Research, 2008, 10, R93.	2.2	113

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127	Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. Molecular Oncology, 2014, 8, 1326-1338.	2.1	109
128	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. PLoS Computational Biology, 2007, 3, e161.	1.5	108
129	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. Science Translational Medicine, 2013, 5, 181re1.	5.8	108
130	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. Nature Genetics, 2020, 52, 187-197.	9.4	108
131	Effects of the addition of gemcitabine, and paclitaxel-first sequencing, in neoadjuvant sequential epirubicin, cyclophosphamide, and paclitaxel for women with high-risk early breast cancer (Neo-tAnGo): an open-label, 2Ã—2 factorial randomised phase 3 trial. Lancet Oncology, The, 2014, 15, 201-212.	5.1	106
132	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
133	APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. Cell Reports, 2015, 13, 108-121.	2.9	105
134	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
135	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. Cell Research, 2018, 28, 719-729.	5.7	105
136	Common Germline Genetic Variation in Antioxidant Defense Genes and Survival After Diagnosis of Breast Cancer. Journal of Clinical Oncology, 2007, 25, 3015-3023.	0.8	102
137	Cellâ€free circulating tumour DNA as a liquid biopsy in breast cancer. Molecular Oncology, 2016, 10, 464-474.	2.1	101
138	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
139	MLL2, the second human homolog of the Drosophila trithorax gene, maps to 19q13.1 and is amplified in solid tumor cell lines. Oncogene, 1999, 18, 7975-7984.	2.6	100
140	Regulation of p53 tetramerization and nuclear export by ARC. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 20826-20831.	3.3	100
141	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
142	Pharmacogenomic Identification of Novel Determinants of Response to Chemotherapy in Colon Cancer. Cancer Research, 2006, 66, 2765-2777.	0.4	99
143	Degenerate Oligonucleotide Primed-Polymerase Chain Reaction-Based Array Comparative Genomic Hybridization for Extensive Amplicon Profiling of Breast Cancers. American Journal of Pathology, 2001, 158, 1623-1631.	1.9	98
144	Microâ€RNAs and breast cancer. Molecular Oncology, 2010, 4, 230-241.	2.1	96

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145	TGFÎ² induces the formation of tumour-initiating cells in claudinlow breast cancer. Nature Communications, 2012, 3, 1055.	5.8	95
146	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. Cell Reports, 2019, 27, 2690-2708.e10.	2.9	95
147	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. Cancer Research, 2017, 77, e62-e66.	0.4	92
148	Evidence for a role of FGF-2 and FGF receptors in the proliferation of non-small cell lung cancer cells. , 1999, 83, 415-423.		91
149	The molecular outlook. Nature, 2002, 415, 484-485.	13.7	91
150	Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel. Clinical Cancer Research, 2014, 20, 2466-2475.	3.2	91
151	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
152	Breast tumor microenvironment structures are associated with genomic features and clinical outcome. Nature Genetics, 2022, 54, 660-669.	9.4	88
153	A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. Breast Cancer Research, 2008, 10, R73.	2.2	87
154	Cancer stem cell markers in breast cancer: pathological, clinical and prognostic significance. Breast Cancer Research, 2011, 13, R118.	2.2	87
155	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
156	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
157	Comparative study of endoscopic surveillance in hereditary diffuse gastric cancer according to CDH1 mutation status. Gastrointestinal Endoscopy, 2018, 87, 408-418.	0.5	85
158	The circular RNome of primary breast cancer. Genome Research, 2019, 29, 356-366.	2.4	85
159	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
160	Facilitating a culture of responsible and effective sharing of cancer genome data. Nature Medicine, 2016, 22, 464-471.	15.2	83
161	A consensus prognostic gene expression classifier for ER positive breast cancer. Genome Biology, 2006, 7, R101.	13.9	82
162	BEX2 Is Overexpressed in a Subset of Primary Breast Cancers and Mediates Nerve Growth Factor/Nuclear Factor-ÎºB Inhibition of Apoptosis in Breast Cancer Cell Lines. Cancer Research, 2007, 67, 6725-6736.	0.4	81

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163	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
164	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
165	The pitfalls of platform comparison: DNA copy number array technologies assessed. BMC Genomics, 2009, 10, 588.	1.2	80
166	Genomic gain of 5p15 leads to over-expression of Misu (NSUN2) in breast cancer. Cancer Letters, 2010, 289, 71-80.	3.2	80
167	Therapeutic Rationale to Target Highly Expressed CDK7 Conferring Poor Outcomes in Triple-Negative Breast Cancer. Cancer Research, 2017, 77, 3834-3845.	0.4	79
168	Aberrant splicing of the TSG101 and FHIT genes occurs frequently in multiple malignancies and in normal tissues and mimics alterations previously described in tumours. Oncogene, 1997, 15, 2119-2126.	2.6	78
169	Expression of androgen receptor splice variants in clinical breast cancers. Oncotarget, 2015, 6, 44728-44744.	0.8	77
170	CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. Breast Cancer Research, 2010, 12, R64.	2.2	76
171	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. PLoS Computational Biology, 2013, 9, e1003047.	1.5	76
172	Prospective cohort study assessing outcomes of patients from families fulfilling criteria for hereditary diffuse gastric cancer undergoing endoscopic surveillance. Gastrointestinal Endoscopy, 2014, 80, 78-87.	0.5	75
173	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. Bioinformatics, 2005, 21, 3025-3033.	1.8	73
174	Targeting BRCA1â€BER deficient breast cancer by ATM or DNAâ€PKcs blockade either alone or in combination with cisplatin for personalized therapy. Molecular Oncology, 2015, 9, 204-217.	2.1	72
175	Intestinal microbiota influences clinical outcome and side effects of early breast cancer treatment. Cell Death and Differentiation, 2021, 28, 2778-2796.	5.0	72
176	Exon scrambling of MLL transcripts occur commonly and mimic partial genomic duplication of the gene. Gene, 1998, 208, 167-176.	1.0	71
177	Clonal fitness inferred from time-series modelling of single-cell cancer genomes. Nature, 2021, 595, 585-590.	13.7	71
178	A Ki67/BCL2 index based on immunohistochemistry is highly prognostic in ERâ€positive breast cancer. Journal of Pathology, 2012, 226, 97-107.	2.1	70
179	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	2.4	69
180	DNA repair polymorphisms and the risk of stomach adenocarcinoma and severe chronic gastritis in the EPIC-EURGAST study. International Journal of Epidemiology, 2008, 37, 1316-1325.	0.9	68

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181	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	1.4	68
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