Carlos Caldas

List of Publications by Citations

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401	59,149	104	239
papers	citations	h-index	g-index
454	70,331	13.4	7.13
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
401	Signatures of mutational processes in human cancer. *Nature*, **2013**, 500, 415-21	50.4	5895
400	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. *Nature*, **2012**, 486, 346-52	50.4	3479
399	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
398	Analysis of circulating tumor DNA to monitor metastatic breast cancer. *New England Journal of Medicine*, **2013**, 368, 1199-209	59.2	1560
397	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	36.3	1492
396	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. *Nature*, **2012**, 486, 395-9	50.4	1417
395	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
394	Non-invasive analysis of acquired resistance to cancer therapy by sequencing of plasma DNA. *Nature*, **2013**, 497, 108-12	50.4	1220
393	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. *Nature*, **2016**, 534, 47-54	50.4	1193
392	Liquid biopsies come of age: towards implementation of circulating tumour DNA. *Nature Reviews Cancer*, **2017**, 17, 223-238	31.3	1192
391	Patient-derived xenograft models: an emerging platform for translational cancer research. *Cancer Discovery*, **2014**, 4, 998-1013	24.4	1018
390	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. *Nature*, **2012**, 481, 389-93	50.4	1011
389	Frequent somatic mutations and homozygous deletions of the p16 (MTS1) gene in pancreatic adenocarcinoma. *Nature Genetics*, **1994**, 8, 27-32	36.3	980
388	Noninvasive identification and monitoring of cancer mutations by targeted deep sequencing of plasma DNA. *Science Translational Medicine*, **2012**, 4, 136ra68	17.5	882
387	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. *Nature*, **2009**, 461, 809-13	50.4	879
386	Genetic unmasking of an epigenetically silenced microRNA in human cancer cells. *Cancer Research*, **2007**, 67, 1424-9	10.1	795
385	The somatic mutation profiles of 2,433 breast cancers refines their genomic and transcriptomic landscapes. *Nature Communications*, **2016**, 7, 11479	17.4	779

384	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. *Genome Biology*, **2007**, 8, R214	18.3	742
383	Molecular classification and molecular forecasting of breast cancer: ready for clinical application?. *Journal of Clinical Oncology*, **2005**, 23, 7350-60	2.2	696
382	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	11.6	616
381	Clinical validity of circulating tumour cells in patients with metastatic breast cancer: a pooled analysis of individual patient data. *Lancet Oncology, The*, **2014**, 15, 406-14	21.7	566
380	Systematic comparison of microarray profiling, real-time PCR, and next-generation sequencing technologies for measuring differential microRNA expression. *Rna*, **2010**, 16, 991-1006	5.8	515
379	Driver mutations in TP53 are ubiquitous in high grade serous carcinoma of the ovary. *Journal of Pathology*, **2010**, 221, 49-56	9.4	485
378	Incidence of gastric cancer and breast cancer in CDH1 (E-cadherin) mutation carriers from hereditary diffuse gastric cancer families. *Gastroenterology*, **2001**, 121, 1348-53	13.3	485
377	Mutations truncating the EP300 acetylase in human cancers. *Nature Genetics*, **2000**, 24, 300-3	36.3	482
376	Helicobacter pylori and interleukin 1 genotyping: an opportunity to identify high-risk individuals for gastric carcinoma. *Journal of the National Cancer Institute*, **2002**, 94, 1680-7	9.7	475
375	p300/CBP and cancer. *Oncogene*, **2004**, 23, 4225-31	9.2	464
374	Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution. *Nature*, **2015**, 518, 422-6	50.4	451
373	Toward understanding and exploiting tumor heterogeneity. *Nature Medicine*, **2015**, 21, 846-53	50.5	441
372	Association between CD8+ T-cell infiltration and breast cancer survival in 12,439 patients. *Annals of Oncology*, **2014**, 25, 1536-43	10.3	433
371	A proinflammatory genetic profile increases the risk for chronic atrophic gastritis and gastric carcinoma. *Gastroenterology*, **2003**, 125, 364-71	13.3	415
370	Hereditary diffuse gastric cancer: updated consensus guidelines for clinical management and directions for future research. *Journal of Medical Genetics*, **2010**, 47, 436-44	5.8	411
369	Hereditary Diffuse Gastric Cancer Syndrome: CDH1 Mutations and Beyond. *JAMA Oncology*, **2015**, 1, 23-32	13.4	401
368	Hereditary diffuse gastric cancer: updated clinical guidelines with an emphasis on germline CDH1 mutation carriers. *Journal of Medical Genetics*, **2015**, 52, 361-74	5.8	385
367	An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. *Genome Biology*, **2007**, 8, R157	18.3	383

366	Progesterone receptor modulates ERα action in breast cancer. *Nature*, **2015**, 523, 313-7	50.4	376
365	Interrogating open issues in cancer precision medicine with patient-derived xenografts. *Nature Reviews Cancer*, **2017**, 17, 254-268	31.3	369
364	Molecular heterogeneity of breast carcinomas and the cancer stem cell hypothesis. *Nature Reviews Cancer*, **2007**, 7, 791-9	31.3	365
363	Interleukin 1B and interleukin 1RN polymorphisms are associated with increased risk of gastric carcinoma. *Gastroenterology*, **2001**, 121, 823-9	13.3	365
362	Early gastric cancer in young, asymptomatic carriers of germ-line E-cadherin mutations. *New England Journal of Medicine*, **2001**, 344, 1904-9	59.2	361
361	EMSY links the BRCA2 pathway to sporadic breast and ovarian cancer. *Cell*, **2003**, 115, 523-35	56.2	345
360	Multifocal clonal evolution characterized using circulating tumour DNA in a case of metastatic breast cancer. *Nature Communications*, **2015**, 6, 8760	17.4	334
359	MicroRNA: implications for cancer. *Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin*, **2008**, 452, 1-10	5.1	331
358	The shaping and functional consequences of the microRNA landscape in breast cancer. *Nature*, **2013**, 497, 378-82	50.4	321
357	Prognostic and predictive value of PDL1 expression in breast cancer. *Oncotarget*, **2015**, 6, 5449-64	3.3	313
356	Combined Single-Cell Functional and Gene Expression Analysis Resolves Heterogeneity within Stem Cell Populations. *Cell Stem Cell*, **2015**, 16, 712-24	18	286
355	Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. *PLoS Medicine*, **2016**, 13, e1002194	11.6	282
354	Quantitative image analysis of cellular heterogeneity in breast tumors complements genomic profiling. *Science Translational Medicine*, **2012**, 4, 157ra143	17.5	277
353	The implications of clonal genome evolution for cancer medicine. *New England Journal of Medicine*, **2013**, 368, 842-51	59.2	275
352	A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. *Cell*, **2016**, 167, 260-274.e22	56.2	274
351	Chromatin modifier enzymes, the histone code and cancer. *European Journal of Cancer*, **2005**, 41, 2381-402	7.5	260
350	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. *Nature Genetics*, **2017**, 49, 1476-1486	36.3	255
349	CX-5461 is a DNA G-quadruplex stabilizer with selective lethality in BRCA1/2 deficient tumours. *Nature Communications*, **2017**, 8, 14432	17.4	251

348	Endogenous purification reveals GREB1 as a key estrogen receptor regulatory factor. *Cell Reports*, **2013**, 3, 342-9	10.6	251
347	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. *Science*, **2014**, 345, 1251343	33.3	250
346	Ordering of mutations in preinvasive disease stages of esophageal carcinogenesis. *Nature Genetics*, **2014**, 46, 837-843	36.3	240
345	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. *Genome Biology*, **2007**, 8, R215	18.3	230
344	Promoter of lncRNA Gene PVT1 Is a Tumor-Suppressor DNA Boundary Element. *Cell*, **2018**, 173, 1398-1412.e22	56.2	226
343	Allele-specific up-regulation of FGFR2 increases susceptibility to breast cancer. *PLoS Biology*, **2008**, 6, e108	9.7	220
342	Human and mouse oligonucleotide-based array CGH. *Nucleic Acids Research*, **2005**, 33, e192	20.1	219
341	Maintaining Tumor Heterogeneity in Patient-Derived Tumor Xenografts. *Cancer Research*, **2015**, 75, 2963-8	16.1	218
340	A new genome-driven integrated classification of breast cancer and its implications. *EMBO Journal*, **2013**, 32, 617-28	13	212
339	Phenotypic and functional characterisation of the luminal cell hierarchy of the mammary gland. *Breast Cancer Research*, **2012**, 14, R134	8.3	211
338	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, 681-7	9.4	205
337	PREDICT: a new UK prognostic model that predicts survival following surgery for invasive breast cancer. *Breast Cancer Research*, **2010**, 12, R1	8.3	204
336	Caring for patients with cancer in the COVID-19 era. *Nature Medicine*, **2020**, 26, 665-671	50.5	201
335	Cancer genetics of epigenetic genes. *Human Molecular Genetics*, **2007**, 16 Spec No 1, R28-49	5.6	200
334	Differential expression of selected histone modifier genes in human solid cancers. *BMC Genomics*, **2006**, 7, 90	4.5	186
333	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	9.7	181
332	Shieldin complex promotes DNA end-joining and counters homologous recombination in BRCA1-null cells. *Nature Cell Biology*, **2018**, 20, 954-965	23.4	178
331	Copynumber: Efficient algorithms for single- and multi-track copy number segmentation. *BMC Genomics*, **2012**, 13, 591	4.5	175

330	The extracellular matrix protein TGFBI induces microtubule stabilization and sensitizes ovarian cancers to paclitaxel. *Cancer Cell*, **2007**, 12, 514-27	24.3	171
329	A recurrent chromosome breakpoint in breast cancer at the NRG1/neuregulin 1/heregulin gene. *Cancer Research*, **2004**, 64, 6840-4	10.1	170
328	Alpha-6 integrin is necessary for the tumourigenicity of a stem cell-like subpopulation within the MCF7 breast cancer cell line. *International Journal of Cancer*, **2008**, 122, 298-304	7.5	168
327	TP53 mutation spectrum in breast cancer is subtype specific and has distinct prognostic relevance. *Clinical Cancer Research*, **2014**, 20, 3569-80	12.9	167
326	Bcl-2 is a prognostic marker in breast cancer independently of the Nottingham Prognostic Index. *Clinical Cancer Research*, **2006**, 12, 2468-75	12.9	163
325	Germline CDH1 deletions in hereditary diffuse gastric cancer families. *Human Molecular Genetics*, **2009**, 18, 1545-55	5.6	159
324	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. *Nature*, **2017**, 543, 714-718	50.4	157
323	DriverNet: uncovering the impact of somatic driver mutations on transcriptional networks in cancer. *Genome Biology*, **2012**, 13, R124	18.3	156
322	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. *Nature Genetics*, **2013**, 45, 1487-93	36.3	151
321	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, 575-82	5.6	145
320	Molecular classification of breast carcinomas using tissue microarrays. *Diagnostic Molecular Pathology*, **2003**, 12, 27-34		142
319	Screening E-cadherin in gastric cancer families reveals germline mutations only in hereditary diffuse gastric cancer kindred. *Human Mutation*, **2002**, 19, 510-7	4.7	142
318	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, 3289-303	5.6	140
317	Molecular genetic profiles of colitis-associated neoplasms. *Gastroenterology*, **1994**, 107, 420-8	13.3	136
316	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	40	131
315	JARID1B is a luminal lineage-driving oncogene in breast cancer. *Cancer Cell*, **2014**, 25, 762-77	24.3	131
314	Genome-driven integrated classification of breast cancer validated in over 7,500 samples. *Genome Biology*, **2014**, 15, 431	18.3	130
313	Meta-analysis confirms BCL2 is an independent prognostic marker in breast cancer. *BMC Cancer*, **2008**, 8, 153	4.8	130

312	A 1 Mb minimal amplicon at 8p11-12 in breast cancer identifies new candidate oncogenes. *Oncogene*, **2005**, 24, 5235-45	9.2	130
311	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	7	129
310	Master regulators of FGFR2 signalling and breast cancer risk. *Nature Communications*, **2013**, 4, 2464	17.4	128
309	Identification and validation of prognostic markers in breast cancer with the complementary use of array-CGH and tissue microarrays. *Journal of Pathology*, **2005**, 205, 388-96	9.4	128
308	Common occurrence of APC and K-ras gene mutations in the spectrum of colitis-associated neoplasias. *Gastroenterology*, **1995**, 108, 383-92	13.3	127
307	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, 7386-91	11.5	125
306	Genomic architecture characterizes tumor progression paths and fate in breast cancer patients. *Science Translational Medicine*, **2010**, 2, 38ra47	17.5	122
305	A 4-gene signature predicts survival of patients with resected adenocarcinoma of the esophagus, junction, and gastric cardia. *Gastroenterology*, **2010**, 139, 1995-2004.e15	13.3	116
304	Breast Cancer Molecular Stratification: From Intrinsic Subtypes to Integrative Clusters. *American Journal of Pathology*, **2017**, 187, 2152-2162	5.8	114
303	Circulating tumor DNA to monitor metastatic breast cancer. *New England Journal of Medicine*, **2013**, 369, 93-4	59.2	109
302	Predictive markers of anthracycline benefit: a prospectively planned analysis of the UK National Epirubicin Adjuvant Trial (NEAT/BR9601). *Lancet Oncology, The*, **2010**, 11, 266-74	21.7	109
301	Dysregulated expression of Fau and MELK is associated with poor prognosis in breast cancer. *Breast Cancer Research*, **2009**, 11, R60	8.3	109
300	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. *Nature*, **2019**, 567, 399-404	50.4	108
299	Personalized circulating tumor DNA analysis to detect residual disease after neoadjuvant therapy in breast cancer. *Science Translational Medicine*, **2019**, 11,	17.5	106
298	Characterisation of microRNA expression in post-natal mouse mammary gland development. *BMC Genomics*, **2009**, 10, 548	4.5	104
297	Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. *BMC Cancer*, **2010**, 10, 604	4.8	104
296	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	8.3	104
295	G-quadruplex DNA as a molecular target for induced synthetic lethality in cancer cells. *Journal of the American Chemical Society*, **2013**, 135, 9640-3	16.4	101

294	K-ras mutation and pancreatic adenocarcinoma. *International Journal of Gastrointestinal Cancer*, **1995**, 18, 1-6		98
293	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, 167-80	12	97
292	Integration of genomic, transcriptomic and proteomic data identifies two biologically distinct subtypes of invasive lobular breast cancer. *Scientific Reports*, **2016**, 6, 18517	4.9	96
291	Genome-wide association studies in oesophageal adenocarcinoma and Barrett�s oesophagus: a large-scale meta-analysis. *Lancet Oncology, The*, **2016**, 17, 1363-1373	21.7	94
290	BCL11A is a triple-negative breast cancer gene with critical functions in stem and progenitor cells. *Nature Communications*, **2015**, 6, 5987	17.4	94
289	Systematic analysis of challenge-driven improvements in molecular prognostic models for breast cancer. *Science Translational Medicine*, **2013**, 5, 181re1	17.5	94
288	Pharmacogenomic identification of novel determinants of response to chemotherapy in colon cancer. *Cancer Research*, **2006**, 66, 2765-77	10.1	94
287	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, 656-66	21.7	93
286	Common germline genetic variation in antioxidant defense genes and survival after diagnosis of breast cancer. *Journal of Clinical Oncology*, **2007**, 25, 3015-23	2.2	93
285	Elucidating the altered transcriptional programs in breast cancer using independent component analysis. *PLoS Computational Biology*, **2007**, 3, e161	5	92
284	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, 7975-84	9.2	92
283	Imaging mass cytometry and multiplatform genomics define the phenogenomic landscape of breast cancer.. *Nature Cancer*, **2020**, 1, 163-175	15.4	90
282	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, 2�2 factorial randomised phase 3 trial. *Lancet Oncology, The*, **2014**, 15, 201-12	21.7	89
281	Regulation of p53 tetramerization and nuclear export by ARC. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 20826-31	11.5	89
280	Saliva samples are a viable alternative to blood samples as a source of DNA for high throughput genotyping. *BMC Medical Genomics*, **2012**, 5, 19	3.7	88
279	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
278	Degenerate oligonucleotide primed-polymerase chain reaction-based array comparative genomic hybridization for extensive amplicon profiling of breast cancers : a new approach for the molecular analysis of paraffin-embedded cancer tissue. *American Journal of Pathology*, **2001**, 158, 1623-31	5.8	87
277	Micro-RNAs and breast cancer. *Molecular Oncology*, **2010**, 4, 230-41	7.9	86

276	A RAD51 assay feasible in routine tumor samples calls PARP inhibitor response beyond BRCA mutation. *EMBO Molecular Medicine*, **2018**, 10,	12	85
275	Cell-free circulating tumour DNA as a liquid biopsy in breast cancer. *Molecular Oncology*, **2016**, 10, 464-74	7.9	82
274	The pitfalls of platform comparison: DNA copy number array technologies assessed. *BMC Genomics*, **2009**, 10, 588	4.5	79
273	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, 2466-75	12.9	78
272	A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. *Breast Cancer Research*, **2008**, 10, R73	8.3	78
271	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. *Science Translational Medicine*, **2016**, 8, 341ra76	17.5	77
270	Genomic and protein expression analysis reveals flap endonuclease 1 (FEN1) as a key biomarker in breast and ovarian cancer. *Molecular Oncology*, **2014**, 8, 1326-38	7.9	77
269	TGF□induces the formation of tumour-initiating cells in claudinlow breast cancer. *Nature Communications*, **2012**, 3, 1055	17.4	76
268	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, 2119-26	9.2	75
267	A consensus prognostic gene expression classifier for ER positive breast cancer. *Genome Biology*, **2006**, 7, R101	18.3	75
266	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. *Nature Communications*, **2016**, 7, 12910	17.4	74
265	Clonal Decomposition and DNA Replication States Defined by Scaled Single-Cell Genome Sequencing. *Cell*, **2019**, 179, 1207-1221.e22	56.2	73
264	Cancer stem cell markers in breast cancer: pathological, clinical and prognostic significance. *Breast Cancer Research*, **2011**, 13, R118	8.3	73
263	Evidence for a role of FGF-2 and FGF receptors in the proliferation of non-small cell lung cancer cells. *International Journal of Cancer*, **1999**, 83, 415-23	7.5	73
262	BEX2 is overexpressed in a subset of primary breast cancers and mediates nerve growth factor/nuclear factor-kappaB inhibition of apoptosis in breast cancer cell lines. *Cancer Research*, **2007**, 67, 6725-36	10.1	72
261	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	11.5	71
260	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	8.3	71
259	Comparative study of endoscopic surveillance in hereditary diffuse gastric cancer according to CDH1 mutation status. *Gastrointestinal Endoscopy*, **2018**, 87, 408-418	5.2	66

258	PDX-MI: Minimal Information for Patient-Derived Tumor Xenograft Models. *Cancer Research*, **2017**, 77, e62-e66	10.1	65
257	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	21.7	65
256	APOBEC3B-Mediated Cytidine Deamination Is Required for Estrogen Receptor Action in Breast Cancer. *Cell Reports*, **2015**, 13, 108-121	10.6	64
255	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, 917-28	8.7	64
254	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	5.2	63
253	Facilitating a culture of responsible and effective sharing of cancer genome data. *Nature Medicine*, **2016**, 22, 464-71	50.5	63
252	Exon scrambling of MLL transcripts occur commonly and mimic partial genomic duplication of the gene. *Gene*, **1998**, 208, 167-76	3.8	62
251	DNA repair polymorphisms and the risk of stomach adenocarcinoma and severe chronic gastritis in the EPIC-EURGAST study. *International Journal of Epidemiology*, **2008**, 37, 1316-25	7.8	62
250	A Ki67/BCL2 index based on immunohistochemistry is highly prognostic in ER-positive breast cancer. *Journal of Pathology*, **2012**, 226, 97-107	9.4	61
249	Biological and prognostic associations of miR-205 and let-7b in breast cancer revealed by in situ hybridization analysis of micro-RNA expression in arrays of archival tumour tissue. *Journal of Pathology*, **2012**, 227, 306-14	9.4	60
248	Prognostic significance of androgen receptor expression in invasive breast cancer: transcriptomic and protein expression analysis. *Breast Cancer Research and Treatment*, **2016**, 159, 215-27	4.4	59
247	Genomic gain of 5p15 leads to over-expression of Misu (NSUN2) in breast cancer. *Cancer Letters*, **2010**, 289, 71-80	9.9	59
246	Landscape of G-quadruplex DNA structural regions in breast cancer. *Nature Genetics*, **2020**, 52, 878-883	36.3	59
245	Therapeutic Rationale to Target Highly Expressed CDK7 Conferring Poor Outcomes in Triple-Negative Breast Cancer. *Cancer Research*, **2017**, 77, 3834-3845	10.1	58
244	The Genomic and Immune Landscapes of Lethal Metastatic Breast Cancer. *Cell Reports*, **2019**, 27, 2690-2708.e10	10.6	58
243	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	18.8	58
242	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. *Bioinformatics*, **2005**, 21, 3025-33	7.2	58
241	Integrative clustering reveals a novel split in the luminal A subtype of breast cancer with impact on outcome. *Breast Cancer Research*, **2017**, 19, 44	8.3	57

240	ctDNA monitoring using patient-specific sequencing and integration of variant reads. *Science Translational Medicine*, **2020**, 12,	17.5	57
239	Improving breast cancer survival analysis through competition-based multidimensional modeling. *PLoS Computational Biology*, **2013**, 9, e1003047	5	57
238	Fine scale mapping of the breast cancer 16q12 locus. *Human Molecular Genetics*, **2010**, 19, 2507-15	5.6	57
237	PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. *Bioinformatics*, **2006**, 22, 2269-75	7.2	57
236	Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients. *Journal of Molecular Diagnostics*, **2018**, 20, 883-892	5.1	57
235	MAP3K1 and MAP2K4 mutations are associated with sensitivity to MEK inhibitors in multiple cancer models. *Cell Research*, **2018**, 28, 719-729	24.7	57
234	Expression of androgen receptor splice variants in clinical breast cancers. *Oncotarget*, **2015**, 6, 44728-44	3.3	56
233	The circular RNome of primary breast cancer. *Genome Research*, **2019**, 29, 356-366	9.7	55
232	Targeting BRCA1-BER deficient breast cancer by ATM or DNA-PKcs blockade either alone or in combination with cisplatin for personalized therapy. *Molecular Oncology*, **2015**, 9, 204-17	7.9	55
231	ESR1 gene amplification in breast cancer: a common phenomenon?. *Nature Genetics*, **2008**, 40, 806-7; author reply 810-2	36.3	55
230	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	15.4	53
229	Therapeutic relevance of the PP2A-B55 inhibitory kinase MASTL/Greatwall in breast cancer. *Cell Death and Differentiation*, **2018**, 25, 828-840	12.7	53
228	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. *Genome Research*, **2015**, 25, 814-24	9.7	52
227	Lymphocyte Invasion in IC10/Basal-Like Breast Tumors Is Associated with Wild-Type TP53. *Molecular Cancer Research*, **2015**, 13, 493-501	6.6	48
226	Predicting Anthracycline Benefit: TOP2A and CEP17-Not Only but Also. *Journal of Clinical Oncology*, **2015**, 33, 1680-7	2.2	47
225	High-resolution magic angle spinning 1H NMR spectroscopy and reverse transcription-PCR analysis of apoptosis in a rat glioma. *Analytical Chemistry*, **2006**, 78, 1546-52	7.8	47
224	CDH1 c-160a promotor polymorphism is not associated with risk of stomach cancer. *International Journal of Cancer*, **2002**, 101, 196-7	7.5	47
223	ARID1A influences HDAC1/BRD4 activity, intrinsic proliferative capacity and breast cancer treatment response. *Nature Genetics*, **2020**, 52, 187-197	36.3	47

222	Genetic predisposition to gastro-oesophageal cancer. *Current Opinion in Genetics and Development*, **2010**, 20, 210-7	4.9	46
221	BRCA1-like signature in triple negative breast cancer: Molecular and clinical characterization reveals subgroups with therapeutic potential. *Molecular Oncology*, **2015**, 9, 1528-38	7.9	45
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