

Christine Desmedt

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

169 papers	20,639 citations	49 h-index	143 g-index
232 ext. papers	24,715 ext. citations	7.7 avg, IF	5.7 L-index

#	Paper	IF	Citations
169	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
168	Gene expression profiling in breast cancer: understanding the molecular basis of histologic grade to improve prognosis. <i>Journal of the National Cancer Institute</i> , 2006 , 98, 262-72	9.7	1485
167	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012 , 486, 400-4	50.4	1264
166	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
165	Tumor infiltrating lymphocytes are prognostic in triple negative breast cancer and predictive for trastuzumab benefit in early breast cancer: results from the FinHER trial. <i>Annals of Oncology</i> , 2014 , 25, 1544-50	10.3	780
164	Strong time dependence of the 76-gene prognostic signature for node-negative breast cancer patients in the TRANSBIG multicenter independent validation series. <i>Clinical Cancer Research</i> , 2007 , 13, 3207-14	12.9	759
163	Meta-analysis of gene expression profiles in breast cancer: toward a unified understanding of breast cancer subtyping and prognosis signatures. <i>Breast Cancer Research</i> , 2008 , 10, R65	8.3	658
162	Definition of clinically distinct molecular subtypes in estrogen receptor-positive breast carcinomas through genomic grade. <i>Journal of Clinical Oncology</i> , 2007 , 25, 1239-46	2.2	650
161	Biological processes associated with breast cancer clinical outcome depend on the molecular subtypes. <i>Clinical Cancer Research</i> , 2008 , 14, 5158-65	12.9	641
160	CD4+ follicular helper T cell infiltration predicts breast cancer survival. <i>Journal of Clinical Investigation</i> , 2013 , 123, 2873-92	15.9	554
159	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015 , 21, 751-9	50.5	521
158	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017 , 32, 169-184.e7	24.3	346
157	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. <i>BMC Genomics</i> , 2008 , 9, 239	4.5	272
156	Amplification of LAPT4B and YWHAZ contributes to chemotherapy resistance and recurrence of breast cancer. <i>Nature Medicine</i> , 2010 , 16, 214-8	50.5	262
155	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014 , 345, 1251343	33.3	250
154	A three-gene model to robustly identify breast cancer molecular subtypes. <i>Journal of the National Cancer Institute</i> , 2012 , 104, 311-25	9.7	218
153	Genomic index of sensitivity to endocrine therapy for breast cancer. <i>Journal of Clinical Oncology</i> , 2010 , 28, 4111-9	2.2	203

152	Genomic Characterization of Primary Invasive Lobular Breast Cancer. <i>Journal of Clinical Oncology</i> , 2016 , 34, 1872-81	2.2	175
151	Global microRNA expression profiling identifies MiR-210 associated with tumor proliferation, invasion and poor clinical outcome in breast cancer. <i>PLoS ONE</i> , 2011 , 6, e20980	3.7	175
150	DNA methylation profiling reveals a predominant immune component in breast cancers. <i>EMBO Molecular Medicine</i> , 2011 , 3, 726-41	12	167
149	Gene modules and response to neoadjuvant chemotherapy in breast cancer subtypes: a pooled analysis. <i>Journal of Clinical Oncology</i> , 2012 , 30, 1996-2004	2.2	167
148	A comparative study of survival models for breast cancer prognostication based on microarray data: does a single gene beat them all?. <i>Bioinformatics</i> , 2008 , 24, 2200-8	7.2	157
147	Genomic grade index is associated with response to chemotherapy in patients with breast cancer. <i>Journal of Clinical Oncology</i> , 2009 , 27, 3185-91	2.2	153
146	Multifactorial approach to predicting resistance to anthracyclines. <i>Journal of Clinical Oncology</i> , 2011 , 29, 1578-86	2.2	143
145	HER2 and TOP2A as predictive markers for anthracycline-containing chemotherapy regimens as adjuvant treatment of breast cancer: a meta-analysis of individual patient data. <i>Lancet Oncology</i> , 2011 , 12, 1134-42	21.7	141
144	Principles Governing A-to-I RNA Editing in the Breast Cancer Transcriptome. <i>Cell Reports</i> , 2015 , 13, 277-89	10.6	137
143	Comparison of prognostic gene expression signatures for breast cancer. <i>BMC Genomics</i> , 2008 , 9, 394	4.5	110
142	Assessment of an RNA interference screen-derived mitotic and ceramide pathway metagene as a predictor of response to neoadjuvant paclitaxel for primary triple-negative breast cancer: a retrospective analysis of five clinical trials. <i>Lancet Oncology</i> , 2010 , 11, 358-65	21.7	97
141	Polysomy 17 in HER-2/neu status elaboration in breast cancer: effect on daily practice. <i>Clinical Cancer Research</i> , 2005 , 11, 4393-9	12.9	87
140	Topoisomerase-II alpha expression as a predictive marker in a population of advanced breast cancer patients randomly treated either with single-agent doxorubicin or single-agent docetaxel. <i>Molecular Cancer Therapeutics</i> , 2004 , 3, 1207-14	6.1	83
139	Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations. <i>Nature Communications</i> , 2017 , 8, 14944	17.4	79
138	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016 , 7, 12910	17.4	74
137	Improvement of the clinical applicability of the Genomic Grade Index through a qRT-PCR test performed on frozen and formalin-fixed paraffin-embedded tissues. <i>BMC Genomics</i> , 2009 , 10, 424	4.5	67
136	Proliferation: the most prominent predictor of clinical outcome in breast cancer. <i>Cell Cycle</i> , 2006 , 5, 2198-202	4.7	67
135	Correction for chromosome-17 is critical for the determination of true Her-2/neu gene amplification status in breast cancer. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2572-9	6.1	67

134	Change in the microenvironment of breast cancer studied by FTIR imaging. <i>Analyst, The</i> , 2013 , 138, 4058-4065	5.5	65
133	DNA methylation-based immune response signature improves patient diagnosis in multiple cancers. <i>Journal of Clinical Investigation</i> , 2017 , 127, 3090-3102	15.9	63
132	Next-generation sequencing in breast cancer: first take home messages. <i>Current Opinion in Oncology</i> , 2012 , 24, 597-604	4.2	62
131	Uncovering the genomic heterogeneity of multifocal breast cancer. <i>Journal of Pathology</i> , 2015 , 236, 457-466	5.6	61
130	The Gene expression Grade Index: a potential predictor of relapse for endocrine-treated breast cancer patients in the BIG 1-98 trial. <i>BMC Medical Genomics</i> , 2009 , 2, 40	3.7	58
129	A single-cell map of intratumoral changes during anti-PD1 treatment of patients with breast cancer. <i>Nature Medicine</i> , 2021 , 27, 820-832	50.5	57
128	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019 , 29, 356-366	9.7	55
127	Immune Infiltration in Invasive Lobular Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 768-776	9.7	55
126	Infrared imaging in breast cancer: automated tissue component recognition and spectral characterization of breast cancer cells as well as the tumor microenvironment. <i>Analyst, The</i> , 2014 , 139, 1044-56	5	55
125	International expert consensus on primary systemic therapy in the management of early breast cancer: highlights of the Fourth Symposium on Primary Systemic Therapy in the Management of Operable Breast Cancer, Cremona, Italy (2010). <i>Journal of the National Cancer Institute Monographs</i> , 2011 , 2011, 147-51	4.8	55
124	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015 , 25, 814-24	9.7	52
123	Bortezomib (PS-341, Velcade) increases the efficacy of trastuzumab (Herceptin) in HER-2-positive breast cancer cells in a synergistic manner. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 3042-51	6.1	51
122	Reliability of tumor-infiltrating lymphocyte and tertiary lymphoid structure assessment in human breast cancer. <i>Modern Pathology</i> , 2017 , 30, 1204-1212	9.8	50
121	TP53 mutation-correlated genes predict the risk of tumor relapse and identify MPS1 as a potential therapeutic kinase in TP53-mutated breast cancers. <i>Molecular Oncology</i> , 2014 , 8, 508-19	7.9	49
120	Biology of breast cancer during pregnancy using genomic profiling. <i>Endocrine-Related Cancer</i> , 2014 , 21, 545-54	5.7	48
119	Predicting Anthracycline Benefit: TOP2A and CEP17-Not Only but Also. <i>Journal of Clinical Oncology</i> , 2015 , 33, 1680-7	2.2	47
118	A significant proportion of elderly patients develop hormone-dependant "luminal-B" tumours associated with aggressive characteristics. <i>Critical Reviews in Oncology/Hematology</i> , 2008 , 67, 80-92	7	46
117	Characterization of human breast cancer tissues by infrared imaging. <i>Analyst, The</i> , 2016 , 141, 606-19	5	45

116	Transfer of clinically relevant gene expression signatures in breast cancer: from Affymetrix microarray to Illumina RNA-Sequencing technology. <i>BMC Genomics</i> , 2014 , 15, 1008	4.5	45
115	Gene expression predictors in breast cancer: current status, limitations and perspectives. <i>European Journal of Cancer</i> , 2008 , 44, 2714-20	7.5	45
114	p-53 gene mutations as a predictive marker in a population of advanced breast cancer patients randomly treated with doxorubicin or docetaxel in the context of a phase III clinical trial. <i>Annals of Oncology</i> , 2007 , 18, 997-1003	10.3	45
113	Unraveling Triple-Negative Breast Cancer Tumor Microenvironment Heterogeneity: Towards an Optimized Treatment Approach. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 708-719	9.7	45
112	Type I interferon/IRF7 axis instigates chemotherapy-induced immunological dormancy in breast cancer. <i>Oncogene</i> , 2019 , 38, 2814-2829	9.2	45
111	Epstein-Barr Virus Infection of Mammary Epithelial Cells Promotes Malignant Transformation. <i>EBioMedicine</i> , 2016 , 9, 148-160	8.8	44
110	Implication of tumor microenvironment in the resistance to chemotherapy in breast cancer patients. <i>Current Opinion in Oncology</i> , 2010 , 22, 547-51	4.2	42
109	Tumor-Infiltrating Lymphocytes in Patients Receiving Trastuzumab/Pertuzumab-Based Chemotherapy: A TRYPHAENA Substudy. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 69-77	9.7	40
108	Cyclophosphamide dose intensification may circumvent anthracycline resistance of p53 mutant breast cancers. <i>Oncologist</i> , 2010 , 15, 246-52	5.7	40
107	Breast cancer and melanoma cell line identification by FTIR imaging after formalin-fixation and paraffin-embedding. <i>Analyst, The</i> , 2013 , 138, 4083-91	5	39
106	Characterization and clinical evaluation of CD10+ stroma cells in the breast cancer microenvironment. <i>Clinical Cancer Research</i> , 2012 , 18, 1004-14	12.9	39
105	Impact of cyclins E, neutrophil elastase and proteinase 3 expression levels on clinical outcome in primary breast cancer patients. <i>International Journal of Cancer</i> , 2006 , 119, 2539-45	7.5	37
104	A fuzzy gene expression-based computational approach improves breast cancer prognostication. <i>Genome Biology</i> , 2010 , 11, R18	18.3	36
103	Quantitation of HER2 expression or HER2:HER2 dimers and differential survival in a cohort of metastatic breast cancer patients carefully selected for trastuzumab treatment primarily by FISH. <i>Diagnostic Molecular Pathology</i> , 2009 , 18, 22-9		36
102	Constitutive phosphorylated STAT3-associated gene signature is predictive for trastuzumab resistance in primary HER2-positive breast cancer. <i>BMC Medicine</i> , 2015 , 13, 177	11.4	35
101	Genomic grade adds prognostic value in invasive lobular carcinoma. <i>Annals of Oncology</i> , 2013 , 24, 377-384	16.3	35
100	An advanced discrete state-discrete event multiscale simulation model of the response of a solid tumor to chemotherapy: Mimicking a clinical study. <i>Journal of Theoretical Biology</i> , 2010 , 266, 124-39	2.3	35
99	HER-2 as a target for breast cancer therapy. <i>Clinical Cancer Research</i> , 2009 , 15, 1848-52	12.9	32

98	Loss of ARID1A Activates ANXA1, which Serves as a Predictive Biomarker for Trastuzumab Resistance. <i>Clinical Cancer Research</i> , 2016 , 22, 5238-5248	12.9	30
97	Evolving paradigms in multifocal breast cancer. <i>Seminars in Cancer Biology</i> , 2015 , 31, 111-8	12.7	29
96	The technologically integrated oncosimulator: combining multiscale cancer modeling with information technology in the in silico oncology context. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2014 , 18, 840-54	7.2	29
95	Modeling invasive breast cancer: growth factors propel progression of HER2-positive premalignant lesions. <i>Oncogene</i> , 2012 , 31, 3569-83	9.2	28
94	Recurrence dynamics of breast cancer according to baseline body mass index. <i>European Journal of Cancer</i> , 2017 , 87, 10-20	7.5	27
93	A gene signature to predict high tumor-infiltrating lymphocytes after neoadjuvant chemotherapy and outcome in patients with triple-negative breast cancer. <i>Annals of Oncology</i> , 2018 , 29, 162-169	10.3	26
92	Gene expression profiling in breast cancer. <i>Annals of Oncology</i> , 2006 , 17 Suppl 10, x259-62	10.3	24
91	Association between SPARC mRNA expression, prognosis and response to neoadjuvant chemotherapy in early breast cancer: a pooled in-silico analysis. <i>PLoS ONE</i> , 2013 , 8, e62451	3.7	23
90	Circulating tumor DNA in early response assessment and monitoring of advanced colorectal cancer treated with a multi-kinase inhibitor. <i>Oncotarget</i> , 2018 , 9, 17756-17769	3.3	21
89	Transcriptomic and genomic features of invasive lobular breast cancer. <i>Seminars in Cancer Biology</i> , 2017 , 44, 98-105	12.7	20
88	Discrimination between healthy and tumor tissues on formalin-fixed paraffin-embedded breast cancer samples using IR imaging. <i>Spectroscopy</i> , 2010 , 24, 67-72		20
87	Imprint of parity and age at first pregnancy on the genomic landscape of subsequent breast cancer. <i>Breast Cancer Research</i> , 2019 , 21, 25	8.3	20
86	The Genomic Grade Assay Compared With Ki67 to Determine Risk of Distant Breast Cancer Recurrence. <i>JAMA Oncology</i> , 2016 , 2, 217-24	13.4	19
85	Development and validation of gene expression profile signatures in early-stage breast cancer. <i>Cancer Investigation</i> , 2009 , 27, 1-10	2.1	19
84	A semantic grid infrastructure enabling integrated access and analysis of multilevel biomedical data in support of postgenomic clinical trials on cancer. <i>IEEE Transactions on Information Technology in Biomedicine</i> , 2008 , 12, 205-17		19
83	The "Oncosimulator": a multilevel, clinically oriented simulation system of tumor growth and organism response to therapeutic schemes. Towards the clinical evaluation of in silico oncology. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , 2007 , 2007, 6629-32		19
82	CCR 20th Anniversary Commentary: Gene-Expression Signature in Breast Cancer--Where Did It Start and Where Are We Now?. <i>Clinical Cancer Research</i> , 2015 , 21, 4743-6	12.9	18
81	Impact of tumor sequencing on the use of anticancer drugs. <i>Current Opinion in Oncology</i> , 2014 , 26, 347-56	5.2	18

80	'In silico' oncology for clinical decision making in the context of nephroblastoma. <i>Klinische Padiatrie</i> , 2009 , 221, 141-9	0.9	17
79	Frequent incidence of BARD1-truncating mutations in germline DNA from triple-negative breast cancer patients. <i>Clinical Genetics</i> , 2016 , 89, 336-40	4	17
78	Abstract S1-05: Tumor infiltrating lymphocytes (TILs) indicate trastuzumab benefit in early-stage HER2-positive breast cancer (HER2+ BC) 2013 ,		15
77	mutations in metastatic lobular breast cancer patients. <i>Npj Breast Cancer</i> , 2019 , 5, 9	7.8	15
76	Catalog of genetic progression of human cancers: breast cancer. <i>Cancer and Metastasis Reviews</i> , 2016 , 35, 49-62	9.6	14
75	A meta-analysis of phase III trials evaluating the predictive value of HER2 and topoisomerase II alpha in early breast cancer patients treated with CMF or anthracycline-based adjuvant therapy. 2009 ,		14
74	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019 , 21, 151	8.3	14
73	Tumor characteristics and outcome by androgen receptor expression in triple-negative breast cancer patients treated with neo-adjuvant chemotherapy. <i>Breast Cancer Research and Treatment</i> , 2019 , 176, 699-708	4.4	13
72	A key genomic subtype associated with lymphovascular invasion in invasive breast cancer. <i>British Journal of Cancer</i> , 2019 , 120, 1129-1136	8.7	12
71	Breast cancer diagnosed during pregnancy is associated with enrichment of non-silent mutations, mismatch repair deficiency signature and mucin mutations. <i>Npj Breast Cancer</i> , 2018 , 4, 23	7.8	12
70	MAGI1, a New Potential Tumor Suppressor Gene in Estrogen Receptor Positive Breast Cancer. <i>Cancers</i> , 2020 , 12,	6.6	11
69	Informed consent, biobank research, and locality: perceptions of breast cancer patients in three European countries. <i>Journal of Empirical Research on Human Research Ethics</i> , 2014 , 9, 48-55	1.6	11
68	Estrogens decrease gamma-ray-induced senescence and maintain cell cycle progression in breast cancer cells independently of p53. <i>International Journal of Radiation Oncology Biology Physics</i> , 2007 , 67, 1187-200	4	11
67	Integrative proteomic and gene expression analysis identify potential biomarkers for adjuvant trastuzumab resistance: analysis from the Fin-her phase III randomized trial. <i>Oncotarget</i> , 2015 , 6, 30306-33	7.3	11
66	Body Mass Index and Tumor-Infiltrating Lymphocytes in Triple-Negative Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 146-153	9.7	11
65	Genomic, Transcriptomic, Epigenetic, and Immune Profiling of Mucinous Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 742-746	9.7	10
64	Molecular biology in breast cancer: should molecular classifiers be assessed by conventional tools or by gene expression arrays?. <i>Critical Reviews in Oncology/Hematology</i> , 2012 , 84 Suppl 1, e58-69	7	10
63	Predicting risk of breast cancer recurrence using gene-expression profiling. <i>Pharmacogenomics</i> , 2007 , 8, 101-11	2.6	10

62	Breast cancer gene expression profiling: clinical trial and practice implications. <i>Pharmacogenomics</i> , 2005 , 6, 49-58	2.6	10
61	Predicting the efficacy of anthracyclines in breast cancer (BC) patients: Results of the neoadjuvant TOP trial. <i>Journal of Clinical Oncology</i> , 2009 , 27, 523-523	2.2	10
60	Phylogenetic reconstruction of breast cancer reveals two routes of metastatic dissemination associated with distinct clinical outcome. <i>EBioMedicine</i> , 2020 , 56, 102793	8.8	10
59	Characterization of Stromal Tumor-infiltrating Lymphocytes and Genomic Alterations in Metastatic Lobular Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 6254-6265	12.9	10
58	TOP2A protein by quantitative immunofluorescence as a predictor of response to epirubicin in the neoadjuvant treatment of breast cancer. <i>Future Oncology</i> , 2013 , 9, 1477-87	3.6	9
57	Gene profiling assay and application: the predictive role in primary therapy. <i>Journal of the National Cancer Institute Monographs</i> , 2011 , 2011, 124-7	4.8	8
56	Prediction of early distant relapses on tamoxifen in early-stage breast cancer (BC): A potential tool for adjuvant aromatase inhibitor (AI) tailoring. <i>Journal of Clinical Oncology</i> , 2005 , 23, 509-509	2.2	7
55	Association between the histopathological growth patterns of liver metastases and survival after hepatic surgery in breast cancer patients. <i>Npj Breast Cancer</i> , 2020 , 6, 64	7.8	7
54	Tumor dormancy at bedside: A late awakening. <i>Breast</i> , 2019 , 45, 61-63	3.6	6
53	Low residual proliferation after short-term letrozole therapy is an early predictive marker of response in high proliferative ER-positive breast cancer. <i>Endocrine-Related Cancer</i> , 2011 , 18, 721-30	5.7	6
52	Comprehensive analysis integrating both clinicopathological and gene expression data in more than 1,500 samples: Proliferation captured by gene expression grade index appears to be the strongest prognostic factor in breast cancer (BC). <i>Journal of Clinical Oncology</i> , 2006 , 24, 507-507	2.2	6
51	Clinical Implications of Body Mass Index in Metastatic Breast Cancer Patients Treated With Abemaciclib and Endocrine Therapy. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 462-470	9.7	6
50	The AURORA pilot study for molecular screening of patients with advanced breast cancer-a study of the breast international group. <i>Npj Breast Cancer</i> , 2017 , 3, 23	7.8	5
49	Assessment of stromal tumor infiltrating lymphocytes and immunohistochemical features in invasive micropapillary breast carcinoma with long-term outcomes. <i>Breast Cancer Research and Treatment</i> , 2020 , 184, 985-998	4.4	5
48	Does Physical Activity Have an Impact on Recurrence Dynamics in Early Breast Cancer Patients?. <i>Journal of Clinical Medicine</i> , 2021 , 10,	5.1	5
47	Is cancer biology different in older patients?. <i>The Lancet Healthy Longevity</i> , 2021 , 2, e663-e677	9.5	5
46	Late effects of adjuvant chemotherapy adumbrate dormancy complexity in breast cancer. <i>Breast</i> , 2020 , 52, 64-70	3.6	4
45	90_PR Gene Modules and Pathological Complete Response to Neoadjuvant Chemotherapy in Breast Cancer. A Pooled Analysis. <i>Annals of Oncology</i> , 2012 , 23, ii17	10.3	4

44	Abstract 986: Unraveling breast cancer progression through geographical and temporal sequencing 2014 ,		4
43	Genome-wide gene expression profiling to predict resistance to anthracyclines in breast cancer patients. <i>Genomics Data</i> , 2013 , 1, 7-10		3
42	Body Mass Index and Weight Change in Patients With HER2-Positive Early Breast Cancer: Exploratory Analysis of the ALTTO BIG 2-06 Trial. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2021 , 19, 181-189	7.3	3
41	Microscopic tumor foci in axillary lymph nodes may reveal the recurrence dynamics of breast cancer. <i>Cancer Communications</i> , 2019 , 39, 35	9.4	2
40	Multiple-input multiple-output causal strategies for gene selection. <i>BMC Bioinformatics</i> , 2011 , 12, 458	3.6	2
39	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. <i>BMC Bioinformatics</i> , 2011 , 12, 310	3.6	2
38	Erratum to [When should I start using a new biomarker: Focus on Expression arrays][EJC Supplement, 5 (2007) 97104]. <i>European Journal of Cancer</i> , 2008 , 44, 326-328	7.5	2
37	Abstract P2-11-02: Understanding the biology and prognosis of PIK3CA gene mutations in primary breast cancer using gene expression profiling: A pooled analysis 2013 ,		2
36	Tumor infiltrating lymphocytes before and after dual HER2 blockade in HER2-amplified early breast cancer: A TRYPHAENA substudy.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 11507-11507	2.2	2
35	Impact of body mass index (BMI) and weight change after treatment in patients (pts) with HER2-positive (HER2+) early breast cancer (EBC): Secondary analysis of the ALTTO BIG 2-06 trial.. <i>Journal of Clinical Oncology</i> , 2018 , 36, 10067-10067	2.2	2
34	Abstract P3-01-13: Association between the histopathological growth patterns (HGP) of liver metastases (LM) and survival after hepatic surgery in patients with oligometastatic breast cancer (BC) 2020 ,		2
33	Breast adipocyte size associates with ipsilateral invasive breast cancer risk after ductal carcinoma in situ. <i>Npj Breast Cancer</i> , 2021 , 7, 31	7.8	2
32	How Researchers, Clinicians and Patient Advocates Can Accelerate Lobular Breast Cancer Research. <i>Cancers</i> , 2021 , 13,	6.6	2
31	Downregulation of the FTO mA RNA demethylase promotes EMT-mediated progression of epithelial tumors and sensitivity to Wnt inhibitors.. <i>Nature Cancer</i> , 2021 , 2, 611-628	15.4	2
30	Inter-observer agreement for the histological diagnosis of invasive lobular breast carcinoma. <i>Journal of Pathology: Clinical Research</i> , 2021 ,	5.3	2
29	Loss of E-cadherin leads to Id2-dependent inhibition of cell cycle progression in metastatic lobular breast cancer.. <i>Oncogene</i> , 2022 ,	9.2	2
28	Clinico-pathological and transcriptomic determinants of SLFN11 expression in invasive breast carcinoma 2015 , 3,		1
27	Time to move forward from "first-generation" prognostic gene signatures in early breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011 , 128, 643-5	4.4	1

26	210 Anthracyclines and topoisomerase II alpha ¿what is beyond?. <i>European Journal of Cancer, Supplement</i> , 2010 , 8, 120	1.6	1
25	Translating multiscale cancer models into clinical trials: Simulating breast cancer tumor dynamics within the framework of the ¿trial of Principle¿clinical trial and the ACGT project. 2008 ,		1
24	When should I start using a new biomarker: Focus on expression arrays?. <i>European Journal of Cancer, Supplement</i> , 2007 , 5, 97-104	1.6	1
23	Genomic heterogeneity in primary breast cancer: Clinical implications.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 11004-11004	2.2	1
22	Obesity and menopausal status impact the features and molecular phenotype of invasive lobular breast cancer. <i>Breast Cancer Research and Treatment</i> , 2021 , 191, 451	4.4	1
21	Computational Intelligence in Clinical Oncology: Lessons Learned from an Analysis of a Clinical Study. <i>Studies in Computational Intelligence</i> , 2008 , 237-268	0.8	1
20	A gene signature of chemo-immunization to predict outcome in patients with triple negative breast cancer treated with neoadjuvant chemotherapy.. <i>Journal of Clinical Oncology</i> , 2017 , 35, 575-575	2.2	1
19	Digital analysis of distant and cancer-associated mammary adipocytes. <i>Breast</i> , 2020 , 54, 179-186	3.6	1
18	Correlation of Trop-2 expression with clinicopathological characteristics, sTILs, AR expression and outcome in primary TNBC.. <i>Journal of Clinical Oncology</i> , 2021 , 39, e12558-e12558	2.2	1
17	The genomic landscape of carcinomas with mucinous differentiation. <i>Scientific Reports</i> , 2021 , 11, 9478	4.9	1
16	Spatial interplay of lymphocytes and fibroblasts in estrogen receptor-positive HER2-negative breast cancer.. <i>Npj Breast Cancer</i> , 2022 , 8, 56	7.8	1
15	Histopathological growth patterns of liver metastasis: updated consensus guidelines for pattern scoring, perspectives and recent mechanistic insights. <i>British Journal of Cancer</i> ,	8.7	1
14	Tumor Infiltrating Lymphocytes in Breast Cancer: Implementation of a New Histopathological Biomarker 2022 , 207-243		1
13	Comparison of the tumor immune microenvironment of primary hormone receptor-negative HER2-positive and triple negative breast cancer. <i>Npj Breast Cancer</i> , 2021 , 7, 128	7.8	0
12	Doubling back on centromere 17 in early breast cancer. <i>Lancet Oncology, The</i> , 2010 , 11, 216-7	21.7	
11	Strategies to Incorporate Translational Research Science into Clinical Trials in Breast Cancer. <i>Current Breast Cancer Reports</i> , 2010 , 2, 208-213	0.8	
10	ACGT: A platform to facilitate future clinico-genomic research on breast cancer. <i>European Journal of Cancer, Supplement</i> , 2008 , 6, 17-18	1.6	
9	Genomic and Molecular Classification of Breast Cancer 2006 , 595-621		

- 8 Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. *Translational Medicine Series*, **2007**, 121-136
- 7 Metastasis by semi-quantitative oestrogen receptor expression in stage I-III early diagnosed triple positive breast cancer patients.. *Journal of Clinical Oncology*, **2020**, 38, e13031-e13031 2.2
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