

John W M Martens

List of Publications by Year in descending order

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Version: 2024-02-01

254
papers

22,504
citations

13865

67
h-index

10445

139
g-index

268
all docs

268
docs citations

268
times ranked

32875
citing authors

#	ARTICLE	IF	CITATIONS
1	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
2	Mutational Processes Molding the Genomes of 21 Breast Cancers. <i>Cell</i> , 2012, 149, 979-993.	28.9	1,673
3	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012, 486, 400-404.	27.8	1,535
4	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , 2009, 462, 1005-1010.	27.8	776
5	HRDetect is a predictor of BRCA1 and BRCA2 deficiency based on mutational signatures. <i>Nature Medicine</i> , 2017, 23, 517-525.	30.7	769
6	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
7	Subtypes of Breast Cancer Show Preferential Site of Relapse. <i>Cancer Research</i> , 2008, 68, 3108-3114.	0.9	674
8	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	16.8	534
9	<i>CCAT2</i> , a novel noncoding RNA mapping to 8q24, underlies metastatic progression and chromosomal instability in colon cancer. <i>Genome Research</i> , 2013, 23, 1446-1461.	5.5	526
10	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
11	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
12	Anti-Epithelial Cell Adhesion Molecule Antibodies and the Detection of Circulating Normal-Like Breast Tumor Cells. <i>Journal of the National Cancer Institute</i> , 2009, 101, 61-66.	6.3	407
13	Four miRNAs associated with aggressiveness of lymph node-negative, estrogen receptor-positive human breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13021-13026.	7.1	374
14	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
15	Genes Associated With Breast Cancer Metastatic to Bone. <i>Journal of Clinical Oncology</i> , 2006, 24, 2261-2267.	1.6	278
16	Pan-cancer landscape of homologous recombination deficiency. <i>Nature Communications</i> , 2020, 11, 5584.	12.8	262
17	The genomic landscape of metastatic breast cancer highlights changes in mutation and signature frequencies. <i>Nature Genetics</i> , 2019, 51, 1450-1458.	21.4	250
18	Distinct gene mutation profiles among luminal-type and basal-type breast cancer cell lines. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 53-64.	2.5	247

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19	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016, 7, 11383.	12.8	235
20	Targeted sequencing by proximity ligation for comprehensive variant detection and local haplotyping. <i>Nature Biotechnology</i> , 2014, 32, 1019-1025.	17.5	231
21	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	27.8	229
22	Efficacy of Cabazitaxel in Castration-resistant Prostate Cancer Is Independent of the Presence of AR-V7 in Circulating Tumor Cells. <i>European Urology</i> , 2015, 68, 939-945.	1.9	223
23	mRNA and microRNA Expression Profiles in Circulating Tumor Cells and Primary Tumors of Metastatic Breast Cancer Patients. <i>Clinical Cancer Research</i> , 2011, 17, 3600-3618.	7.0	207
24	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201
25	The DNA cytosine deaminase APOBEC3B promotes tamoxifen resistance in ER-positive breast cancer. <i>Science Advances</i> , 2016, 2, e1601737.	10.3	175
26	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174
27	Molecular characterization of circulating tumor cells in large quantities of contaminating leukocytes by a multiplex real-time PCR. <i>Breast Cancer Research and Treatment</i> , 2009, 118, 455-468.	2.5	171
28	miRNA expression profiling of 51 human breast cancer cell lines reveals subtype and driver mutation-specific miRNAs. <i>Breast Cancer Research</i> , 2013, 15, R33.	5.0	170
29	<i>CCAT2</i> , a novel long non-coding RNA in breast cancer: expression study and clinical correlations. <i>Oncotarget</i> , 2013, 4, 1748-1762.	1.8	169
30	Functional <i>Ex Vivo</i> Assay to Select Homologous Recombination-Deficient Breast Tumors for PARP Inhibitor Treatment. <i>Clinical Cancer Research</i> , 2014, 20, 4816-4826.	7.0	144
31	5-Fluorouracil treatment induces characteristic T>G mutations in human cancer. <i>Nature Communications</i> , 2019, 10, 4571.	12.8	143
32	Elevated APOBEC3B Correlates with Poor Outcomes for Estrogen-Receptor-Positive Breast Cancers. <i>Hormones and Cancer</i> , 2014, 5, 405-413.	4.9	140
33	The genomic landscape of metastatic castration-resistant prostate cancers reveals multiple distinct genotypes with potential clinical impact. <i>Nature Communications</i> , 2019, 10, 5251.	12.8	130
34	<i>KRAS</i> and <i>BRAF</i> mutation status in circulating colorectal tumor cells and their correlation with primary and metastatic tumor tissue. <i>International Journal of Cancer</i> , 2013, 133, 130-141.	5.1	128
35	Application of circulating tumor DNA in prospective clinical oncology trials – standardization of preanalytical conditions. <i>Molecular Oncology</i> , 2017, 11, 295-304.	4.6	123
36	Breast cancer genome and transcriptome integration implicates specific mutational signatures with immune cell infiltration. <i>Nature Communications</i> , 2016, 7, 12910.	12.8	119

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37	A novel independence test for somatic alterations in cancer shows that biology drives mutual exclusivity but chance explains most co-occurrence. <i>Genome Biology</i> , 2016, 17, 261.	8.8	114
38	Breast cancer genomics and immuno-oncological markers to guide immune therapies. <i>Seminars in Cancer Biology</i> , 2018, 52, 178-188.	9.6	111
39	Detection of circulating tumor cells in breast cancer may improve through enrichment with anti-CD146. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 33-41.	2.5	110
40	Loss of E-cadherin is not a necessity for epithelial to mesenchymal transition in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2013, 138, 47-57.	2.5	110
41	Tumor cell migration screen identifies SRPK1 as breast cancer metastasis determinant. <i>Journal of Clinical Investigation</i> , 2015, 125, 1648-1664.	8.2	110
42	Pathway analysis of gene signatures predicting metastasis of node-negative primary breast cancer. <i>BMC Cancer</i> , 2007, 7, 182.	2.6	109
43	Multicenter Study Using Paraffin-Embedded Tumor Tissue Testing PITX2 DNA Methylation As a Marker for Outcome Prediction in Tamoxifen-Treated, Node-Negative Breast Cancer Patients. <i>Journal of Clinical Oncology</i> , 2008, 26, 5036-5042.	1.6	105
44	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
45	Gene length corrected trimmed mean of M-values (GeTMM) processing of RNA-seq data performs similarly in intersample analyses while improving intrasample comparisons. <i>BMC Bioinformatics</i> , 2018, 19, 236.	2.6	105
46	Association of DNA Methylation of Phosphoserine Aminotransferase with Response to Endocrine Therapy in Patients with Recurrent Breast Cancer. <i>Cancer Research</i> , 2005, 65, 4101-4117.	0.9	104
47	DNA-methylation of the homeodomain transcription factor PITX2 reliably predicts risk of distant disease recurrence in tamoxifen-treated, node-negative breast cancer patients – Technical and clinical validation in a multi-centre setting in collaboration with the European Organisation for Research and Treatment of Cancer (EORTC) PathoBiology group. <i>European Journal of Cancer</i> , 2007, 43, 1679-1686.	2.8	103
48	DNA hypermethylation of PITX2 is a marker of poor prognosis in untreated lymph node-negative hormone receptor-positive breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2008, 111, 429-437.	2.5	103
49	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
50	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
51	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	5.0	97
52	Identification of a Putative Protein Profile Associated with Tamoxifen Therapy Resistance in Breast Cancer. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1278-1294.	3.8	94
53	Cancer-associated fibroblast-derived Gremlin 1 promotes breast cancer progression. <i>Breast Cancer Research</i> , 2019, 21, 109.	5.0	94
54	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93

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55	Methylated genes as new cancer biomarkers. <i>European Journal of Cancer</i> , 2009, 45, 335-346.	2.8	92
56	Deubiquitinase Activity Profiling Identifies UCHL1 as a Candidate Oncoprotein That Promotes TGF β -Induced Breast Cancer Metastasis. <i>Clinical Cancer Research</i> , 2020, 26, 1460-1473.	7.0	92
57	Spatial immunophenotypes predict response to anti-PD1 treatment and capture distinct paths of T cell evasion in triple negative breast cancer. <i>Nature Communications</i> , 2021, 12, 5668.	12.8	91
58	DNA Methylation Markers Predict Outcome in Node-Positive, Estrogen Receptor-Positive Breast Cancer with Adjuvant Anthracycline-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2009, 15, 315-323.	7.0	89
59	The circular RNome of primary breast cancer. <i>Genome Research</i> , 2019, 29, 356-366.	5.5	85
60	Patterns and incidence of chromosomal instability and their prognostic relevance in breast cancer subtypes. <i>Breast Cancer Research and Treatment</i> , 2011, 128, 23-30.	2.5	83
61	Selection of Personalized Patient Therapy through the Use of Knowledge-Based Computational Models That Identify Tumor-Driving Signal Transduction Pathways. <i>Cancer Research</i> , 2014, 74, 2936-2945.	0.9	82
62	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	2.9	80
63	Comparative Proteome Analysis Revealing an 11-Protein Signature for Aggressive Triple-Negative Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, djt376.	6.3	77
64	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
65	A Systematic Analysis of Oncogenic Gene Fusions in Primary Colon Cancer. <i>Cancer Research</i> , 2017, 77, 3814-3822.	0.9	76
66	Copy Number Alterations that Predict Metastatic Capability of Human Breast Cancer. <i>Cancer Research</i> , 2009, 69, 3795-3801.	0.9	75
67	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. <i>Nature Genetics</i> , 2017, 49, 341-348.	21.4	75
68	ESR1 mutations: Moving towards guiding treatment decision-making in metastatic breast cancer patients. <i>Cancer Treatment Reviews</i> , 2017, 52, 33-40.	7.7	75
69	Proteomics Pipeline for Biomarker Discovery of Laser Capture Microdissected Breast Cancer Tissue. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2012, 17, 155-164.	2.7	72
70	Aging of stromal-derived human breast fibroblasts might contribute to breast cancer progression. <i>Thrombosis and Haemostasis</i> , 2003, 89, 393-404.	3.4	69
71	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015, 25, 814-824.	5.5	69
72	Interferon-Stimulated Genes Are Involved in Cross-resistance to Radiotherapy in Tamoxifen-Resistant Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 3397-3408.	7.0	68

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73	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	2.4	67
74	Decreased expression of ABAT and STC2 hallmarks ER α -positive inflammatory breast cancer and endocrine therapy resistance in advanced disease. <i>Molecular Oncology</i> , 2015, 9, 1218-1233.	4.6	64
75	T lymphocytes facilitate brain metastasis of breast cancer by inducing Guanylate-Binding Protein 1 expression. <i>Acta Neuropathologica</i> , 2018, 135, 581-599.	7.7	63
76	Somatic mutation detection using various targeted detection assays in paired samples of circulating tumor DNA, primary tumor and metastases from patients undergoing resection of colorectal liver metastases. <i>Molecular Oncology</i> , 2016, 10, 1575-1584.	4.6	61
77	APOBEC3G Expression Correlates with T-Cell Infiltration and Improved Clinical Outcomes in High-grade Serous Ovarian Carcinoma. <i>Clinical Cancer Research</i> , 2016, 22, 4746-4755.	7.0	59
78	Survival and contralateral breast cancer in CHEK2 1100delC breast cancer patients: impact of adjuvant chemotherapy. <i>British Journal of Cancer</i> , 2014, 111, 1004-1013.	6.4	58
79	Uncovering the signaling landscape controlling breast cancer cell migration identifies novel metastasis driver genes. <i>Nature Communications</i> , 2019, 10, 2983.	12.8	58
80	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	56
81	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, 104.	5.0	56
82	MicroRNAs as possible indicators of drug sensitivity in breast cancer cell lines. <i>PLoS ONE</i> , 2019, 14, e0216400.	2.5	54
83	Endocrine therapy resistance in estrogen receptor (ER)-positive breast cancer. <i>Drug Discovery Today</i> , 2016, 21, 1181-1188.	6.4	53
84	Functional <i>in vivo</i> Assay Reveals Homologous Recombination Deficiency in Breast Cancer Beyond BRCA Gene Defects. <i>Clinical Cancer Research</i> , 2018, 24, 6277-6287.	7.0	53
85	DNA methylation as a biomarker in breast cancer. <i>Future Oncology</i> , 2009, 5, 1245-1256.	2.4	52
86	Estrogen receptor mutations and splice variants determined in liquid biopsies from metastatic breast cancer patients. <i>Molecular Oncology</i> , 2018, 12, 48-57.	4.6	52
87	High protein expression of EZH2 is related to unfavorable outcome to tamoxifen in metastatic breast cancer. <i>Annals of Oncology</i> , 2014, 25, 2185-2190.	1.2	51
88	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015, 13, 156.	5.5	51
89	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
90	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018, 8, 6574.	3.3	51

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91	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 104-119.	6.9	51
92	Characterizing steroid hormone receptor chromatin binding landscapes in male and female breast cancer. <i>Nature Communications</i> , 2018, 9, 482.	12.8	50
93	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	2.5	49
94	CD49f-based selection of circulating tumor cells (CTCs) improves detection across breast cancer subtypes. <i>Cancer Letters</i> , 2012, 319, 49-55.	7.2	48
95	A kinase inhibitor screen identifies a dual cdc7/CDK9 inhibitor to sensitise triple-negative breast cancer to EGFR-targeted therapy. <i>Breast Cancer Research</i> , 2019, 21, 77.	5.0	48
96	Generating human prostate cancer organoids from leukapheresis enriched circulating tumour cells. <i>European Journal of Cancer</i> , 2021, 150, 179-189.	2.8	47
97	Correlation of breast cancer susceptibility loci with patient characteristics, metastasis-free survival, and mRNA expression of the nearest genes. <i>Breast Cancer Research and Treatment</i> , 2012, 133, 843-851.	2.5	46
98	DNA damage responsive microRNAs misexpressed in human cancer modulate therapy sensitivity. <i>Molecular Oncology</i> , 2014, 8, 458-468.	4.6	46
99	Gene expression profiles in circulating tumor cells to predict prognosis in metastatic breast cancer patients. <i>Annals of Oncology</i> , 2015, 26, 510-516.	1.2	46
100	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019, 10, 1749.	12.8	46
101	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	45
102	Genomic profiling of CHEK2*1100delC-mutated breast carcinomas. <i>BMC Cancer</i> , 2015, 15, 877.	2.6	44
103	Estrogen Receptor Pathway Activity Score to Predict Clinical Response or Resistance to Neoadjuvant Endocrine Therapy in Primary Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2020, 19, 680-689.	4.1	44
104	Optimized nLC-MS workflow for laser capture microdissected breast cancer tissue. <i>Journal of Proteomics</i> , 2012, 75, 2844-2854.	2.4	42
105	Whole genome sequencing of metastatic colorectal cancer reveals prior treatment effects and specific metastasis features. <i>Nature Communications</i> , 2021, 12, 574.	12.8	39
106	High TWIST1 mRNA expression is associated with poor prognosis in lymph node-negative and estrogen receptor-positive human breast cancer and is co-expressed with stromal as well as ECM related genes. <i>Breast Cancer Research</i> , 2012, 14, R123.	5.0	38
107	The advantage of laser capture microdissection over whole tissue analysis in proteomic profiling studies. <i>Proteomics</i> , 2016, 16, 1474-1485.	2.2	38
108	Gene expression profiling assigns CHEK2 1100delC breast cancers to the luminal intrinsic subtypes. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 439-448.	2.5	37

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109	mRNA expression profiles in circulating tumor cells of metastatic colorectal cancer patients. <i>Molecular Oncology</i> , 2015, 9, 920-932.	4.6	37
110	Steps forward for cancer precision medicine. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 1-2.	46.4	37
111	High-throughput isolation of circulating tumor DNA: a comparison of automated platforms. <i>Molecular Oncology</i> , 2019, 13, 392-402.	4.6	37
112	Molecular characteristics of circulating tumor cells resemble the liver metastasis more closely than the primary tumor in metastatic colorectal cancer. <i>Oncotarget</i> , 2016, 7, 59058-59069.	1.8	37
113	Ageing of stromal-derived human breast fibroblasts might contribute to breast cancer progression. <i>Thrombosis and Haemostasis</i> , 2003, 89, 393-404.	3.4	37
114	Molecular characterization of irinotecan (SN-38) resistant human breast cancer cell lines. <i>BMC Cancer</i> , 2016, 16, 34.	2.6	35
115	Polyomavirus T Antigen Induces APOBEC3B Expression Using an LXCXE-Dependent and TP53-Independent Mechanism. <i>MBio</i> , 2019, 10, .	4.1	35
116	Stem cell-like transcriptional reprogramming mediates metastatic resistance to mTOR inhibition. <i>Oncogene</i> , 2017, 36, 2737-2749.	5.9	34
117	IGF1R signaling drives antiestrogen resistance through PAK2/PIX activation in luminal breast cancer. <i>Oncogene</i> , 2018, 37, 1869-1884.	5.9	34
118	Phosphoserine aminotransferase 1 is associated to poor outcome on tamoxifen therapy in recurrent breast cancer. <i>Scientific Reports</i> , 2017, 7, 2099.	3.3	33
119	Confirmation of a metastasis-specific microRNA signature in primary colon cancer. <i>Scientific Reports</i> , 2018, 8, 5242.	3.3	33
120	Mitochondrial DNA content in breast cancer: Impact on <i>in vitro</i> and <i>in vivo</i> phenotype and patient prognosis. <i>Oncotarget</i> , 2016, 7, 29166-29176.	1.8	33
121	Male breast cancer precursor lesions: analysis of the EORTC 10085/TBCRC/BIG/NABCG International Male Breast Cancer Program. <i>Modern Pathology</i> , 2017, 30, 509-518.	5.5	32
122	Association of microRNA-7 and its binding partner CDR1-AS with the prognosis and prediction of 1st-line tamoxifen therapy in breast cancer. <i>Scientific Reports</i> , 2018, 8, 9657.	3.3	32
123	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
124	Concentrations of TIMP1 mRNA Splice Variants and TIMP-1 Protein Are Differentially Associated with Prognosis in Primary Breast Cancer. <i>Clinical Chemistry</i> , 2007, 53, 1280-1288.	3.2	31
125	4 protein signature predicting tamoxifen treatment outcome in recurrent breast cancer. <i>Molecular Oncology</i> , 2016, 10, 24-39.	4.6	31
126	Progressive APOBEC3B mRNA expression in distant breast cancer metastases. <i>PLoS ONE</i> , 2017, 12, e0171343.	2.5	31

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127	Stromal cells promote anti-estrogen resistance of breast cancer cells through an insulin-like growth factor binding protein 5 (IGFBP5)/B-cell leukemia/lymphoma 3 (Bcl-3) axis. <i>Oncotarget</i> , 2015, 6, 39307-39328.	1.8	31
128	Cell-free DNA mutations as biomarkers in breast cancer patients receiving tamoxifen. <i>Oncotarget</i> , 2016, 7, 43412-43418.	1.8	30
129	Comprehensive evaluation of methods to assess overall and cell-specific immune infiltrates in breast cancer. <i>Breast Cancer Research</i> , 2019, 21, 151.	5.0	30
130	CHEK2*1100delC homozygosity in the Netherlands prevalence and risk of breast and lung cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 46-51.	2.8	29
131	Tumor-Specific Mitochondrial DNA Variants Are Rarely Detected in Cell-Free DNA. <i>Neoplasia</i> , 2018, 20, 687-696.	5.3	28
132	Comparison of variant allele frequency and number of mutant molecules as units of measurement for circulating tumor DNA. <i>Molecular Oncology</i> , 2021, 15, 57-66.	4.6	28
133	Androgen receptor expression in circulating tumor cells of patients with metastatic breast cancer. <i>International Journal of Cancer</i> , 2019, 145, 1083-1089.	5.1	27
134	The molecular genetic make-up of male breast cancer. <i>Endocrine-Related Cancer</i> , 2019, 26, 779-794.	3.1	27
135	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	5.0	26
136	Multi-targeted kinase inhibition alleviates mTOR inhibitor resistance in triple-negative breast cancer. <i>Breast Cancer Research and Treatment</i> , 2019, 178, 263-274.	2.5	26
137	Clonality, Antigen Recognition, and Suppression of CD8+ T Cells Differentially Affect Prognosis of Breast Cancer Subtypes. <i>Clinical Cancer Research</i> , 2020, 26, 505-517.	7.0	26
138	Annexin-A1 and caldesmon are associated with resistance to tamoxifen in estrogen receptor positive recurrent breast cancer. <i>Oncotarget</i> , 2016, 7, 3098-3110.	1.8	26
139	An 8-gene mRNA expression profile in circulating tumor cells predicts response to aromatase inhibitors in metastatic breast cancer patients. <i>BMC Cancer</i> , 2016, 16, 123.	2.6	25
140	Characterization of the mechanism by which the RB/E2F pathway controls expression of the cancer genomic DNA deaminase APOBEC3B. <i>ELife</i> , 2020, 9, .	6.0	25
141	BRCA1-deficient breast cancer cell lines are resistant to MEK inhibitors and show distinct sensitivities to 6-thioguanine. <i>Scientific Reports</i> , 2016, 6, 28217.	3.3	23
142	AR splice variants in circulating tumor cells of patients with castration-resistant prostate cancer: relation with outcome to cabazitaxel. <i>Molecular Oncology</i> , 2019, 13, 1795-1807.	4.6	23
143	GATA3 mRNA expression, but not mutation, associates with longer progression-free survival in ER-positive breast cancer patients treated with first-line tamoxifen for recurrent disease. <i>Cancer Letters</i> , 2016, 376, 104-109.	7.2	22
144	Co-regulated gene expression of splicing factors as drivers of cancer progression. <i>Scientific Reports</i> , 2019, 9, 5484.	3.3	22

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145	Targeted MS Assay Predicting Tamoxifen Resistance in Estrogen-Receptor-Positive Breast Cancer Tissues and Sera. <i>Journal of Proteome Research</i> , 2016, 15, 1230-1242.	3.7	21
146	Circulating Tumor Cell Enumeration and Characterization in Metastatic Castration-Resistant Prostate Cancer Patients Treated with Cabazitaxel. <i>Cancers</i> , 2019, 11, 1212.	3.7	21
147	Clinical significance of the nuclear receptor co-regulator DC-SCRIPT in breast cancer: an independent retrospective validation study. <i>Breast Cancer Research</i> , 2010, 12, R103.	5.0	20
148	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	1.8	20
149	Associations between AR-V7 status in circulating tumour cells, circulating tumour cell count and survival in men with metastatic castration-resistant prostate cancer. <i>European Journal of Cancer</i> , 2019, 121, 48-54.	2.8	20
150	ER and PI3K Pathway Activity in Primary ER Positive Breast Cancer Is Associated with Progression-Free Survival of Metastatic Patients under First-Line Tamoxifen. <i>Cancers</i> , 2020, 12, 802.	3.7	20
151	Liquid Biopsies to Select Patients for Perioperative Chemotherapy in Muscle-invasive Bladder Cancer: A Systematic Review. <i>European Urology Oncology</i> , 2021, 4, 204-214.	5.4	20
152	Differential reprogramming of breast cancer subtypes in 3D cultures and implications for sensitivity to targeted therapy. <i>Scientific Reports</i> , 2021, 11, 7259.	3.3	20
153	Splicing factors control triple-negative breast cancer cell mitosis through SUN2 interaction and sororin intron retention. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 82.	8.6	20
154	Prognostic significance of nuclear expression of UMP-CMP kinase in triple negative breast cancer patients. <i>Scientific Reports</i> , 2016, 6, 32027.	3.3	19
155	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016, 2, 138-153.	3.0	19
156	Integrative analysis of genomic amplification-dependent expression and loss-of-function screen identifies ASAP1 as a driver gene in triple-negative breast cancer progression. <i>Oncogene</i> , 2020, 39, 4118-4131.	5.9	19
157	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	12.8	19
158	Evaluation of the ability of adjuvant tamoxifen benefit gene signatures to predict outcome of hormone-naïve estrogen receptor-positive breast cancer patients treated with tamoxifen in the advanced setting. <i>Molecular Oncology</i> , 2014, 8, 1679-1689.	4.6	18
159	The Predictive Value of PITX2 DNA Methylation for High-Risk Breast Cancer Therapy: Current Guidelines, Medical Needs, and Challenges. <i>Disease Markers</i> , 2017, 2017, 1-14.	1.3	18
160	The Prevalence of CD146 Expression in Breast Cancer Subtypes and Its Relation to Outcome. <i>Cancers</i> , 2018, 10, 134.	3.7	18
161	Detection of tumor-derived extracellular vesicles in plasma from patients with solid cancer. <i>BMC Cancer</i> , 2021, 21, 315.	2.6	18
162	Mesenchymal stem cells and carcinoma-associated fibroblasts sensitize breast cancer cells in 3D cultures to kinase inhibitors. <i>International Journal of Oncology</i> , 2011, 39, 689-96.	3.3	17

#	ARTICLE	IF	CITATIONS
163	Integrative Analysis of Genomics and Proteomics Data on Clinical Breast Cancer Tissue Specimens Extracted with Acid Guanidinium Thiocyanate–Phenol–Chloroform. <i>Journal of Proteome Research</i> , 2015, 14, 1627-1636.	3.7	17
164	Role of genetic variation in docetaxel-induced neutropenia and pharmacokinetics. <i>Pharmacogenomics Journal</i> , 2016, 16, 519-524.	2.0	17
165	Characterizing the invasion of different breast cancer cell lines with distinct E-cadherin status in 3D using a microfluidic system. <i>Biomedical Microdevices</i> , 2019, 21, 101.	2.8	17
166	Estrogens and Progestogens in Triple Negative Breast Cancer: Do They Harm?. <i>Cancers</i> , 2021, 13, 2506.	3.7	17
167	PIK3CA mutations in ductal carcinoma in situ and adjacent invasive breast cancer. <i>Endocrine-Related Cancer</i> , 2019, 26, 471-482.	3.1	17
168	DC-SCRIPT is a novel regulator of the tumor suppressor gene CDKN2B and induces cell cycle arrest in ER \pm -positive breast cancer cells. <i>Breast Cancer Research and Treatment</i> , 2015, 149, 693-703.	2.5	16
169	Proper genomic profiling of (<i>BRCA1</i>-mutated) basal-like breast carcinomas requires prior removal of tumor infiltrating lymphocytes. <i>Molecular Oncology</i> , 2015, 9, 877-888.	4.6	16
170	Dendritic Cells Actively Limit Interleukin-10 Production Under Inflammatory Conditions via DC-SCRIPT and Dual-Specificity Phosphatase 4. <i>Frontiers in Immunology</i> , 2018, 9, 1420.	4.8	16
171	SPEN is required for Xist upregulation during initiation of X chromosome inactivation. <i>Nature Communications</i> , 2021, 12, 7000.	12.8	16
172	Prognostic value of acquired uniparental disomy (aUPD) in primary breast cancer. <i>Breast Cancer Research and Treatment</i> , 2012, 132, 189-196.	2.5	15
173	Predicting paclitaxel-induced neutropenia using the DMET platform. <i>Pharmacogenomics</i> , 2015, 16, 1231-1241.	1.3	15
174	The 29.5 kb APOBEC3B Deletion Polymorphism Is Not Associated with Clinical Outcome of Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0161731.	2.5	15
175	An In-Depth Evaluation of the Validity and Logistics Surrounding the Testing of AR-V7 mRNA Expression in Circulating Tumor Cells. <i>Journal of Molecular Diagnostics</i> , 2018, 20, 316-325.	2.8	15
176	An increased cell cycle gene network determines MEK and Akt inhibitor double resistance in triple-negative breast cancer. <i>Scientific Reports</i> , 2019, 9, 13308.	3.3	15
177	The role of mitochondrial DNA in breast tumors. <i>Drug Discovery Today</i> , 2019, 24, 1202-1208.	6.4	15
178	An Optimized Workflow to Evaluate Estrogen Receptor Gene Mutations in Small Amounts of Cell-Free DNA. <i>Journal of Molecular Diagnostics</i> , 2019, 21, 123-137.	2.8	15
179	Low Tumor Mitochondrial DNA Content Is Associated with Better Outcome in Breast Cancer Patients Receiving Anthracycline-Based Chemotherapy. <i>Clinical Cancer Research</i> , 2017, 23, 4735-4743.	7.0	14
180	High mRNA expression of splice variant SYK short correlates with hepatic disease progression in chemonaive lymph node negative colon cancer patients. <i>PLoS ONE</i> , 2017, 12, e0185607.	2.5	14

#	ARTICLE	IF	CITATIONS
181	High ctDNA molecule numbers relate with poor outcome in advanced ER+, HER2 ⁺ postmenopausal breast cancer patients treated with everolimus and exemestane. <i>Molecular Oncology</i> , 2020, 14, 490-503.	4.6	14
182	Interconnectivity between molecular subtypes and tumor stage in colorectal cancer. <i>BMC Cancer</i> , 2020, 20, 850.	2.6	14
183	Optimizing Nanopore sequencing-based detection of structural variants enables individualized circulating tumor DNA-based disease monitoring in cancer patients. <i>Genome Medicine</i> , 2021, 13, 86.	8.2	14
184	Detection of Aneuploidy in Cerebrospinal Fluid from Patients with Breast Cancer Can Improve Diagnosis of Leptomeningeal Metastases. <i>Clinical Cancer Research</i> , 2021, 27, 2798-2806.	7.0	14
185	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	2.9	12
186	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
187	Sensitive detection of mitochondrial DNA variants for analysis of mitochondrial DNA-enriched extracts from frozen tumor tissue. <i>Scientific Reports</i> , 2018, 8, 2261.	3.3	12
188	Liquid biopsy in esophageal cancer: a case report of false-positive circulating tumor DNA detection due to clonal hematopoiesis. <i>Annals of Translational Medicine</i> , 2021, 9, 1264-1264.	1.7	12
189	Understanding drugs in breast cancer through drug sensitivity screening. <i>SpringerPlus</i> , 2015, 4, 611.	1.2	11
190	Elucidating the Underlying Functional Mechanisms of Breast Cancer Susceptibility Through Post-GWAS Analyses. <i>Frontiers in Genetics</i> , 2018, 9, 280.	2.3	11
191	JNK-Dependent cjun Phosphorylation Mitigates TGF β ² - and EGF-Induced Pre-Malignant Breast Cancer Cell Invasion by Suppressing AP-1-Mediated Transcriptional Responses. <i>Cells</i> , 2019, 8, 1481.	4.1	11
192	Metabotropic glutamate receptor 1 is associated with unfavorable prognosis in ER-negative and triple-negative breast cancer. <i>Scientific Reports</i> , 2020, 10, 22292.	3.3	11
193	MicroRNA expression in pre-treatment plasma of patients with benign breast diseases and breast cancer. <i>Oncotarget</i> , 2018, 9, 24335-24346.	1.8	11
194	Sensitivity to systemic therapy for metastatic breast cancer in CHEK2 1100delC mutation carriers. <i>Journal of Cancer Research and Clinical Oncology</i> , 2015, 141, 1879-1887.	2.5	10
195	Clinical performance of an analytically validated assay in comparison to microarray technology to assess PITX2 DNA-methylation in breast cancer. <i>Scientific Reports</i> , 2018, 8, 16861.	3.3	10
196	Incorporating liquid biopsies into treatment decision-making: obstacles and possibilities. <i>Drug Discovery Today</i> , 2019, 24, 1715-1719.	6.4	10
197	Novel methods to diagnose leptomeningeal metastases in breast cancer. <i>Neuro-Oncology</i> , 2019, 21, 428-439.	1.2	10
198	Intratumoral heterogeneity of second-harmonic generation scattering from tumor collagen and its effects on metastatic risk prediction. <i>BMC Cancer</i> , 2020, 20, 1217.	2.6	10

#	ARTICLE	IF	CITATIONS
199	Loss of Y-Chromosome during Male Breast Carcinogenesis. <i>Cancers</i> , 2020, 12, 631.	3.7	10
200	High-throughput and affordable genome-wide methylation profiling of circulating cell-free DNA by methylated DNA sequencing (MeD-seq) of LpnPI digested fragments. <i>Clinical Epigenetics</i> , 2021, 13, 196.	4.1	10
201	Circulating tumour cells to drive the use of neoadjuvant chemotherapy in patients with muscle-invasive bladder cancer. <i>ESMO Open</i> , 2022, 7, 100416.	4.5	10
202	Fusion transcripts and their genomic breakpoints in polyadenylated and ribosomal RNAâ€“minus RNA sequencing data. <i>GigaScience</i> , 2021, 10, .	6.4	10
203	mRNA expression profiles of colorectal liver metastases as a novel biomarker for early recurrence after partial hepatectomy. <i>Molecular Oncology</i> , 2016, 10, 1542-1550.	4.6	9
204	Interrogation of transcriptomic changes associated with drug-induced hepatic sinusoidal dilatation in colorectal cancer. <i>PLoS ONE</i> , 2018, 13, e0198099.	2.5	9
205	APOBEC3B Gene Expression in Ductal Carcinoma In Situ and Synchronous Invasive Breast Cancer. <i>Cancers</i> , 2019, 11, 1062.	3.7	9
206	Liquid Biopsy Based Circulating Biomarkers in Metastatic Prostate Cancer. <i>Frontiers in Oncology</i> , 0, 12, .	2.8	9
207	Functional RECAP (REpair CAPacity) assay identifies homologous recombination deficiency undetected by DNA-based BRCAness tests. <i>Oncogene</i> , 2022, 41, 3498-3506.	5.9	9
208	Clinical Validation of PITX2 DNA Methylation to Predict Outcome in High-Risk Breast Cancer Patients Treated with Anthracycline-Based Chemotherapy. <i>Breast Care</i> , 2018, 13, 425-433.	1.4	8
209	Prospects of Targeting the Gastrin Releasing Peptide Receptor and Somatostatin Receptor 2 for Nuclear Imaging and Therapy in Metastatic Breast Cancer. <i>PLoS ONE</i> , 2017, 12, e0170536.	2.5	8
210	<i>TP53</i> mutated glioblastoma stem-like cell cultures are sensitive to dual mTORC1/2 inhibition while resistance in <i>TP53</i> wild type cultures can be overcome by combined inhibition of mTORC1/2 and Bcl-2. <i>Oncotarget</i> , 2016, 7, 58435-58444.	1.8	8
211	The prognostic and predictive value of ESR1 fusion gene transcripts in primary breast cancer. <i>BMC Cancer</i> , 2022, 22, 165.	2.6	8
212	Genome-wide aneuploidy detected by mFastâ€“SeqS in circulating cell-free DNA is associated with poor response to pembrolizumab in patients with advanced urothelial cancer. <i>Molecular Oncology</i> , 2022, 16, 2086-2097.	4.6	8
213	Proteomic characterization of microdissected breast tissue environment provides a protein-level overview of malignant transformation. <i>Proteomics</i> , 2017, 17, 1600213.	2.2	7
214	Somatic Tumor Mutations Detected by Targeted Next Generation Sequencing in Minute Amounts of Serum-Derived Cell-Free DNA. <i>Scientific Reports</i> , 2017, 7, 2136.	3.3	7
215	Mitochondrial RNA Expression and Single Nucleotide Variants in Association with Clinical Parameters in Primary Breast Cancers. <i>Cancers</i> , 2018, 10, 500.	3.7	7
216	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7

#	ARTICLE	IF	CITATIONS
217	A Method to Correlate mRNA Expression Datasets Obtained from Fresh Frozen and Formalin-Fixed, Paraffin-Embedded Tissue Samples: A Matter of Thresholds. <i>PLoS ONE</i> , 2015, 10, e0144097.	2.5	6
218	A Systematic Review of the Use of Circulating Cell-Free DNA Dynamics to Monitor Response to Treatment in Metastatic Breast Cancer Patients. <i>Cancers</i> , 2021, 13, 1811.	3.7	6
219	A pipeline for copy number profiling of single circulating tumour cells to assess inpatient tumour heterogeneity. <i>Molecular Oncology</i> , 2022, 16, 2981-3000.	4.6	6
220	Are Immune Signatures a Worthwhile Tool for Decision Making in Early-Stage Human Epidermal Growth Factor Receptor 2â€“Positive Breast Cancer?. <i>Journal of Clinical Oncology</i> , 2015, 33, 673-675.	1.6	5
221	Improved diagnosis and prognostication of patients with pleural malignant mesothelioma using biomarkers in pleural effusions and peripheral blood samples â€“ a short report. <i>Cellular Oncology (Dordrecht)</i> , 2017, 40, 511-519.	4.4	5
222	Increased MAPK1/3 Phosphorylation in Luminal Breast Cancer Related with PIK3CA Hotspot Mutations and Prognosis. <i>Translational Oncology</i> , 2017, 10, 854-866.	3.7	5
223	Performance of <i>BRCA1</i> 2 mutation prediction models in male breast cancer patients. <i>Clinical Genetics</i> , 2018, 93, 52-59.	2.0	5
224	Fundamentals of liquid biopsies in metastatic prostate cancer: from characterization to stratification. <i>Current Opinion in Oncology</i> , 2020, 32, 527-534.	2.4	5
225	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
226	SIAH2 protein expression in breast cancer is inversely related with ER status and outcome to tamoxifen therapy. <i>American Journal of Cancer Research</i> , 2016, 6, 270-84.	1.4	5
227	Apolipoprotein B mRNA-Editing Catalytic Polypeptide-Likeâ€“Induced Protein Changes in Estrogen Receptorâ€“Positive, Human Epidermal Growth Factor Receptor 2â€“Negative Breast Cancer Throughout Disease Progression. <i>JCO Precision Oncology</i> , 2022, 6, e2100190.	3.0	5
228	Evaluation of multiple transcriptomic gene risk signatures in male breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 98.	5.2	4
229	ESR1 Methylation Measured in Cell-Free DNA to Evaluate Endocrine Resistance in Metastatic Breast Cancer Patients. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5631.	4.1	4
230	Recurrent HOXB13 mutations in the Dutch population do not associate with increased breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 30026.	3.3	3
231	Proteome-wide onco-proteogenomic somatic variant identification in ER-positive breast cancer. <i>Clinical Biochemistry</i> , 2019, 66, 63-75.	1.9	3
232	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer. <i>Molecular Oncology</i> , 2021, 15, 3348-3362.	4.6	3
233	Harmonisation of multi-centre real-time reverse-transcribed PCR results of a candidate prognostic marker in breast cancer: An EU-FP6 supported study of members of the EORTC â€“ PathoBiology Group. <i>European Journal of Cancer</i> , 2009, 45, 74-81.	2.8	2
234	Growth and metastatic behavior of molecularly well-characterized human breast cancer cell lines in mice. <i>Breast Cancer Research and Treatment</i> , 2014, 148, 19-31.	2.5	2

#	ARTICLE	IF	CITATIONS
235	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	3.3	2
236	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	3.3	2
237	Circulating tumor cell-driven use of neoadjuvant chemotherapy in patients with muscle-invasive bladder cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 4523-4523.	1.6	2
238	Prognostic Value of Circulating Tumor Cell Characteristics May Be Biased by Their Quantity. <i>Journal of Clinical Oncology</i> , 2022, 40, 519-520.	1.6	2
239	Lost by Transcription: Fork Failures, Elevated Expression, and Clinical Consequences Related to Deletions in Metastatic Colorectal Cancer. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5080.	4.1	2
240	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. <i>Cancers</i> , 2022, 14, 3363.	3.7	2
241	Global proteomic characterization of microdissected estrogen receptor positive breast tumors. <i>Data in Brief</i> , 2015, 5, 399-402.	1.0	1
242	Circular RNA in Chemonaive Lymph Node Negative Colon Cancer Patients. <i>Cancers</i> , 2021, 13, 1903.	3.7	1
243	Transcriptomic Properties of HER2+ Ductal Carcinoma In Situ of the Breast Associate with Absence of Immune Cells. <i>Biology</i> , 2021, 10, 768.	2.8	1
244	A combined EpCAM and MCAM circulating tumor cell (CTC) CellSearch enrichment to improve CTC capture rate in stage II/III breast cancer: A Dutch Breast Cancer Trialists' Group (BOOG) side study.. <i>Journal of Clinical Oncology</i> , 2013, 31, e22106-e22106.	1.6	1
245	Identifying Transcripts with Tandem Duplications from RNA-Sequencing Data to Predict BRCA1-Type Primary Breast Cancer. <i>Cancers</i> , 2022, 14, 753.	3.7	1
246	Abstract P2-01-17: Circulating tumor cell count and levels of circulating tumor DNA are complementary prognostic biomarkers in metastatic breast cancer - A pilot study. <i>Cancer Research</i> , 2022, 82, P2-01-17-P2-01-17.	0.9	1
247	Review of: Demethylation of urokinase promoter as a prognostic marker in patients with breast carcinoma. <i>Breast Cancer Online: BCO</i> , 2004, 7, .	0.1	0
248	A panel of DNA methylation markers for the classification of consensus molecular subtypes 2 and 3 in patients with colorectal cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 3545-3545.	1.6	0
249	Prospective Evaluation of a Circulating Tumor Cell Sensitivity Profile to Predict Response to Cisplatin Chemotherapy in Metastatic Breast Cancer Patients. <i>Frontiers in Oncology</i> , 2021, 11, 697572.	2.8	0
250	mRNA expression profiles in circulating tumor cells (CTCs) of patients with metastatic breast cancer (MBC) treated with aromatase inhibitors (AI).. <i>Journal of Clinical Oncology</i> , 2013, 31, 11045-11045.	1.6	0
251	A pharmacogenetic model predicting low paclitaxel clearance based on the DMET platform.. <i>Journal of Clinical Oncology</i> , 2013, 31, 2597-2597.	1.6	0
252	Gene expression profiles of primary tumors versus circulating tumor cells in metastatic breast cancer.. <i>Journal of Clinical Oncology</i> , 2014, 32, 11017-11017.	1.6	0

#	ARTICLE	IF	CITATIONS
253	The complete genomic landscape of metastatic prostate cancer pinpoints clinically targetable subgroups.. Journal of Clinical Oncology, 2018, 36, 5014-5014.	1.6	0
254	Abstract P3-09-18: The association between genomic alterations and body mass index in patients with early breast cancer. Cancer Research, 2022, 82, P3-09-18-P3-09-18.	0.9	0