

# Christos Sotiriou

## List of Publications by Year in descending order

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156  
papers

31,221  
citations

13099

68  
h-index

8167

148  
g-index

159  
all docs

159  
docs citations

159  
times ranked

31817  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 262-272.	6.3	1,824
2	Breast cancer classification and prognosis based on gene expression profiles from a population-based study. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10393-10398.	7.1	1,796
3	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
4	70-Gene Signature as an Aid to Treatment Decisions in Early-Stage Breast Cancer. <i>New England Journal of Medicine</i> , 2016, 375, 717-729.	27.0	1,427
5	Prognostic and Predictive Value of Tumor-Infiltrating Lymphocytes in a Phase III Randomized Adjuvant Breast Cancer Trial in Node-Positive Breast Cancer Comparing the Addition of Docetaxel to Doxorubicin With Doxorubicin-Based Chemotherapy: BIG 02-98. <i>Journal of Clinical Oncology</i> , 2013, 31, 860-867.	1.6	1,342
6	Gene-Expression Signatures in Breast Cancer. <i>New England Journal of Medicine</i> , 2009, 360, 790-800.	27.0	1,286
7	Validation and Clinical Utility of a 70-Gene Prognostic Signature for Women With Node-Negative Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2006, 98, 1183-1192.	6.3	1,128
8	Tumor-Infiltrating Lymphocytes and Response to Neoadjuvant Chemotherapy With or Without Carboplatin in Human Epidermal Growth Factor Receptor 2-Positive and Triple-Negative Primary Breast Cancers. <i>Journal of Clinical Oncology</i> , 2015, 33, 983-991.	1.6	863
9	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, 3207-3214.	7.0	839
10	CD4+ follicular helper T cell infiltration predicts breast cancer survival. <i>Journal of Clinical Investigation</i> , 2013, 123, 2873-2892.	8.2	813
11	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. <i>Nature Biotechnology</i> , 2010, 28, 827-838.	17.5	795
12	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.	5.0	765
13	Biological Processes Associated with Breast Cancer Clinical Outcome Depend on the Molecular Subtypes. <i>Clinical Cancer Research</i> , 2008, 14, 5158-5165.	7.0	745
14	Definition of Clinically Distinct Molecular Subtypes in Estrogen Receptor-Positive Breast Carcinomas Through Genomic Grade. <i>Journal of Clinical Oncology</i> , 2007, 25, 1239-1246.	1.6	711
15	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015, 21, 751-759.	30.7	711
16	Clinical relevance of host immunity in breast cancer: from TILs to the clinic. <i>Nature Reviews Clinical Oncology</i> , 2016, 13, 228-241.	27.6	679
17	hsa-miR-210 Is Induced by Hypoxia and Is an Independent Prognostic Factor in Breast Cancer. <i>Clinical Cancer Research</i> , 2008, 14, 1340-1348.	7.0	617
18	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	16.8	534

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19	Tumor-Infiltrating Lymphocytes and Prognosis: A Pooled Individual Patient Analysis of Early-Stage Triple-Negative Breast Cancers. <i>Journal of Clinical Oncology</i> , 2019, 37, 559-569.	1.6	505
20	Tumor-Infiltrating Lymphocytes and Associations With Pathological Complete Response and Event-Free Survival in HER2-Positive Early-Stage Breast Cancer Treated With Lapatinib and Trastuzumab. <i>JAMA Oncology</i> , 2015, 1, 448.	7.1	482
21	Assessing Tumor-Infiltrating Lymphocytes in Solid Tumors: A Practical Review for Pathologists and Proposal for a Standardized Method From the International Immunooncology Biomarkers Working Group: Part 1: Assessing the Host Immune Response, TILs in Invasive Breast Carcinoma and Ductal Carcinoma In Situ, Metastatic Tumor Deposits and Areas for Further Research. <i>Advances in Anatomic Pathology</i> , 2017, 24, 235-251.	4.3	469
22	Taking gene-expression profiling to the clinic: when will molecular signatures become relevant to patient care?. <i>Nature Reviews Cancer</i> , 2007, 7, 545-553.	28.4	423
23	The 2019 World Health Organization classification of tumours of the breast. <i>Histopathology</i> , 2020, 77, 181-185.	2.9	395
24	Dissecting the Heterogeneity of Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 1879-1887.	1.6	388
25	<i>PIK3CA</i> mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor-positive breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10208-10213.	7.1	324
26	Elucidating Prognosis and Biology of Breast Cancer Arising in Young Women Using Gene Expression Profiling. <i>Clinical Cancer Research</i> , 2012, 18, 1341-1351.	7.0	303
27	Amplification of <i>LAPTM4B</i> and <i>YWHAZ</i> contributes to chemotherapy resistance and recurrence of breast cancer. <i>Nature Medicine</i> , 2010, 16, 214-218.	30.7	301
28	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. <i>BMC Genomics</i> , 2008, 9, 239.	2.8	300
29	Luminal B Breast Cancer: Molecular Characterization, Clinical Management, and Future Perspectives. <i>Journal of Clinical Oncology</i> , 2014, 32, 2794-2803.	1.6	298
30	Relevance of Tumor-Infiltrating Immune Cell Composition and Functionality for Disease Outcome in Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2017, 109, djw192.	6.3	296
31	A Five-Gene Molecular Grade Index and <i>HOXB13:IL17BR</i> Are Complementary Prognostic Factors in Early Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2008, 14, 2601-2608.	7.0	283
32	A Three-Gene Model to Robustly Identify Breast Cancer Molecular Subtypes. <i>Journal of the National Cancer Institute</i> , 2012, 104, 311-325.	6.3	272
33	Genomic Characterization of Primary Invasive Lobular Breast Cancer. <i>Journal of Clinical Oncology</i> , 2016, 34, 1872-1881.	1.6	249
34	Different Prognostic Value of Cytokeratin-19 mRNA-Positive Circulating Tumor Cells According to Estrogen Receptor and HER2 Status in Early-Stage Breast Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 5194-5202.	1.6	238
35	Genomic Index of Sensitivity to Endocrine Therapy for Breast Cancer. <i>Journal of Clinical Oncology</i> , 2010, 28, 4111-4119.	1.6	235
36	<i>Fat1</i> deletion promotes hybrid EMT state, tumour stemness and metastasis. <i>Nature</i> , 2021, 589, 448-455.	27.8	232

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37	<i>PIK3CA</i> Mutations Are Associated With Lower Rates of Pathologic Complete Response to Anti-Human Epidermal Growth Factor Receptor 2 (HER2) Therapy in Primary HER2-Overexpressing Breast Cancer. <i>Journal of Clinical Oncology</i> , 2014, 32, 3212-3220.	1.6	231
38	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.	2.5	214
39	DNA methylation profiling reveals a predominant immune component in breast cancers. <i>EMBO Molecular Medicine</i> , 2011, 3, 726-741.	6.9	210
40	<i>PIK3CA</i> Mutations Are Associated With Decreased Benefit to Neoadjuvant Human Epidermal Growth Factor Receptor 2-Targeted Therapies in Breast Cancer. <i>Journal of Clinical Oncology</i> , 2015, 33, 1334-1339.	1.6	201
41	Gene Modules and Response to Neoadjuvant Chemotherapy in Breast Cancer Subtypes: A Pooled Analysis. <i>Journal of Clinical Oncology</i> , 2012, 30, 1996-2004.	1.6	194
42	Gene expression profiles derived from fine needle aspiration correlate with response to systemic chemotherapy in breast cancer. <i>Breast Cancer Research</i> , 2002, 4, R3.	5.0	186
43	Luminal breast cancer: from biology to treatment. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 494-506.	27.6	183
44	Principles Governing A-to-I RNA Editing in the Breast Cancer Transcriptome. <i>Cell Reports</i> , 2015, 13, 277-289.	6.4	179
45	Determination of oestrogen-receptor status and ERBB2 status of breast carcinoma: a gene-expression profiling study. <i>Lancet Oncology</i> , The, 2007, 8, 203-211.	10.7	175
46	Genomic Grade Index Is Associated With Response to Chemotherapy in Patients With Breast Cancer. <i>Journal of Clinical Oncology</i> , 2009, 27, 3185-3191.	1.6	173
47	Tumor-infiltrating lymphocyte composition, organization and PD-1/ PD-L1 expression are linked in breast cancer. <i>Oncotarget</i> , 2017, 6, e1257452.	4.6	169
48	Interactions between immunity, proliferation and molecular subtype in breast cancer prognosis. <i>Genome Biology</i> , 2013, 14, R34.	9.6	168
49	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> , The, 2011, 12, 1134-1142.	10.7	165
50	RANK-ligand (RANKL) expression in young breast cancer patients and during pregnancy. <i>Breast Cancer Research</i> , 2015, 17, 24.	5.0	149
51	The path to a better biomarker: application of a risk management framework for the implementation of PD-L1 and TILs as immunology biomarkers in breast cancer clinical trials and daily practice. <i>Journal of Pathology</i> , 2020, 250, 667-684.	4.5	142
52	Phylogenetic analysis of metastatic progression in breast cancer using somatic mutations and copy number aberrations. <i>Nature Communications</i> , 2017, 8, 14944.	12.8	126
53	Comparison of prognostic gene expression signatures for breast cancer. <i>BMC Genomics</i> , 2008, 9, 394.	2.8	123
54	RNA Sequencing to Predict Response to Neoadjuvant Anti-HER2 Therapy. <i>JAMA Oncology</i> , 2017, 3, 227.	7.1	118

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55	Microtubule-Associated Protein-tau is a Bifunctional Predictor of Endocrine Sensitivity and Chemotherapy Resistance in Estrogen Receptor-Positive Breast Cancer. <i>Clinical Cancer Research</i> , 2007, 13, 2061-2067.	7.0	115
56	The tale of TILs in breast cancer: A report from The International Immuno-Oncology Biomarker Working Group. <i>Npj Breast Cancer</i> , 2021, 7, 150.	5.2	112
57	Pitfalls in assessing stromal tumor infiltrating lymphocytes (sTILs) in breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 17.	5.2	106
58	Portraying breast cancers with long noncoding RNAs. <i>Science Advances</i> , 2016, 2, e1600220.	10.3	102
59	Tumor <i>PIK3CA</i> Genotype and Prognosis in Early-Stage Breast Cancer: A Pooled Analysis of Individual Patient Data. <i>Journal of Clinical Oncology</i> , 2018, 36, 981-990.	1.6	95
60	CD73 Promotes Resistance to HER2/ErbB2 Antibody Therapy. <i>Cancer Research</i> , 2017, 77, 5652-5663.	0.9	90
61	Report on computational assessment of Tumor Infiltrating Lymphocytes from the International Immuno-Oncology Biomarker Working Group. <i>Npj Breast Cancer</i> , 2020, 6, 16.	5.2	90
62	The Prognostic Role of Androgen Receptor in Patients with Early-Stage Breast Cancer: A Meta-analysis of Clinical and Gene Expression Data. <i>Clinical Cancer Research</i> , 2017, 23, 2702-2712.	7.0	82
63	Reliability of tumor-infiltrating lymphocyte and tertiary lymphoid structure assessment in human breast cancer. <i>Modern Pathology</i> , 2017, 30, 1204-1212.	5.5	81
64	Genomic aberrations in young and elderly breast cancer patients. <i>BMC Medicine</i> , 2015, 13, 266.	5.5	80
65	Genomic and Transcriptomic Analyses of Breast Cancer Primaries and Matched Metastases in AURORA, the Breast International Group (BIG) Molecular Screening Initiative. <i>Cancer Discovery</i> , 2021, 11, 2796-2811.	9.4	79
66	Proliferation: the Most Prominent Predictor of Clinical Outcome in Breast Cancer. <i>Cell Cycle</i> , 2006, 5, 2198-2202.	2.6	76
67	Next-generation sequencing in breast cancer. <i>Current Opinion in Oncology</i> , 2012, 24, 597-604.	2.4	76
68	Immune Infiltration in Invasive Lobular Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2018, 110, 768-776.	6.3	76
69	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.	2.8	74
70	Circulating Tumor DNA in HER2-Amplified Breast Cancer: A Translational Research Substudy of the NeoALTO Phase III Trial. <i>Clinical Cancer Research</i> , 2019, 25, 3581-3588.	7.0	73
71	Molecular Profiling: Moving Away from Tumor Philately. <i>Science Translational Medicine</i> , 2010, 2, 47ps43.	12.4	71
72	Prognostic Implications of PD-L1 Expression in Breast Cancer: Systematic Review and Meta-analysis of Immunohistochemistry and Pooled Analysis of Transcriptomic Data. <i>Clinical Cancer Research</i> , 2019, 25, 5717-5726.	7.0	71

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73	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.	1.5	67
74	CDK4 phosphorylation status and a linked gene expression profile predict sensitivity to palbociclib. <i>EMBO Molecular Medicine</i> , 2017, 9, 1052-1066.	6.9	65
75	A common language in neoadjuvant breast cancer clinical trials: proposals for standard definitions and endpoints. <i>Lancet Oncology</i> , The, 2012, 13, e240-e248.	10.7	64
76	Infrared imaging in breast cancer: automated tissue component recognition and spectral characterization of breast cancer cells as well as the tumor microenvironment. <i>Analyst</i> , The, 2014, 139, 1044.	3.5	62
77	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.	6.3	60
78	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, 508-519.	4.6	59
79	Biology of breast cancer during pregnancy using genomic profiling. <i>Endocrine-Related Cancer</i> , 2014, 21, 545-554.	3.1	58
80	Evaluation of biological pathways involved in chemotherapy response in breast cancer. <i>Breast Cancer Research</i> , 2008, 10, R37.	5.0	53
81	Genomic Grade Index: An important tool for assessing breast cancer tumor grade and prognosis. <i>Critical Reviews in Oncology/Hematology</i> , 2011, 77, 20-29.	4.4	53
82	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.	2.8	52
83	Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. <i>BMC Medical Genomics</i> , 2009, 2, 37.	1.5	51
84	A fuzzy gene expression-based computational approach improves breast cancer prognostication. <i>Genome Biology</i> , 2010, 11, R18.	9.6	47
85	Characterization and Clinical Evaluation of CD10+ Stroma Cells in the Breast Cancer Microenvironment. <i>Clinical Cancer Research</i> , 2012, 18, 1004-1014.	7.0	46
86	Inhibition of RANK signaling in breast cancer induces an anti-tumor immune response orchestrated by CD8+ T cells. <i>Nature Communications</i> , 2020, 11, 6335.	12.8	46
87	Constitutive phosphorylated STAT3-associated gene signature is predictive for trastuzumab resistance in primary HER2-positive breast cancer. <i>BMC Medicine</i> , 2015, 13, 177.	5.5	45
88	Proliferation and estrogen signaling can distinguish patients at risk for early versus late relapse among estrogen receptor positive breast cancers. <i>Breast Cancer Research</i> , 2013, 15, R86.	5.0	44
89	Liquid biopsy-based clinical research in early breast cancer: The EORTC 90091-10093 Treat CTC trial. <i>European Journal of Cancer</i> , 2016, 63, 97-104.	2.8	44
90	Loss of ARID1A Activates ANXA1, which Serves as a Predictive Biomarker for Trastuzumab Resistance. <i>Clinical Cancer Research</i> , 2016, 22, 5238-5248.	7.0	43

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91	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. <i>Cancer Discovery</i> , 2022, 12, 1022-1045.	9.4	43
92	Core Biopsies Can Be Used to Distinguish Differences in Expression Profiling by cDNA Microarrays. <i>Journal of Molecular Diagnostics</i> , 2002, 4, 30-36.	2.8	41
93	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, 2539-2545.	5.1	39
94	The use of gene-expression profiling to better understand the clinical heterogeneity of estrogen receptor positive breast cancers and tamoxifen response. <i>Critical Reviews in Oncology/Hematology</i> , 2007, 61, 187-194.	4.4	39
95	Bringing Molecular Prognosis and Prediction to the Clinic. <i>Clinical Breast Cancer</i> , 2005, 6, 61-76.	2.4	36
96	Recurrence dynamics of breast cancer according to baseline body mass index. <i>European Journal of Cancer</i> , 2017, 87, 10-20.	2.8	35
97	Evolving paradigms in multifocal breast cancer. <i>Seminars in Cancer Biology</i> , 2015, 31, 111-118.	9.6	34
98	Transcriptomic and genomic features of invasive lobular breast cancer. <i>Seminars in Cancer Biology</i> , 2017, 44, 98-105.	9.6	34
99	Tumor infiltrating lymphocyte stratification of prognostic staging of early-stage triple negative breast cancer. <i>Npj Breast Cancer</i> , 2022, 8, 3.	5.2	33
100	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
101	Downregulation of the FTO m6A RNA demethylase promotes EMT-mediated progression of epithelial tumors and sensitivity to Wnt inhibitors. <i>Nature Cancer</i> , 2021, 2, 611-628.	13.2	30
102	The evolution of treatment strategies: Aiming at the target. <i>Breast</i> , 2007, 16, 10-16.	2.2	29
103	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.	2.5	27
104	Feasibility Study of EndoTAG-1, a Tumor Endothelial Targeting Agent, in Combination with Paclitaxel followed by FEC as Induction Therapy in HER2-Negative Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0154009.	2.5	27
105	Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. <i>Cancer Investigation</i> , 2009, 27, 1-10.	1.3	23
106	<i>CCR</i> 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, 4743-4746.	7.0	23
107	Phylogenetic reconstruction of breast cancer reveals two routes of metastatic dissemination associated with distinct clinical outcome. <i>EBioMedicine</i> , 2020, 56, 102793.	6.1	22
108	Characterization of Stromal Tumor-infiltrating Lymphocytes and Genomic Alterations in Metastatic Lobular Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 6254-6265.	7.0	22

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109	Genomic Grade Index (GGI): Feasibility in Routine Practice and Impact on Treatment Decisions in Early Breast Cancer. <i>PLoS ONE</i> , 2013, 8, e66848.	2.5	21
110	The Genomic Grade Assay Compared With Ki67 to Determine Risk of Distant Breast Cancer Recurrence. <i>JAMA Oncology</i> , 2016, 2, 217.	7.1	21
111	Fine Tuning of the Van Nuys Prognostic Index (VNPI) 2003 by Integrating the Genomic Grade Index (GGI): New Tools for Ductal Carcinoma In Situ (DCIS). <i>Breast Journal</i> , 2011, 17, 343-351.	1.0	20
112	Genomic hotspots but few recurrent fusion genes in breast cancer. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 331-338.	2.8	18
113	pAKT pathway activation is associated with PIK3CA mutations and good prognosis in luminal breast cancer in contrast to p-mTOR pathway activation. <i>Npj Breast Cancer</i> , 2019, 5, 7.	5.2	18
114	NR2F2 controls malignant squamous cell carcinoma state by promoting stemness and invasion and repressing differentiation. <i>Nature Cancer</i> , 2021, 2, 1152-1169.	13.2	17
115	Low CD10 mRNA Expression Identifies High-Risk Ductal Carcinoma In Situ (DCIS). <i>PLoS ONE</i> , 2010, 5, e12100.	2.5	16
116	Application of a risk-management framework for integration of stromal tumor-infiltrating lymphocytes in clinical trials. <i>Npj Breast Cancer</i> , 2020, 6, 15.	5.2	16
117	No significant viral transcription detected in whole breast cancer transcriptomes. <i>BMC Cancer</i> , 2015, 15, 147.	2.6	15
118	18FDG-PET/CT and molecular markers to predict response to neoadjuvant chemotherapy and outcome in HER2-negative advanced luminal breast cancers patients. <i>Oncotarget</i> , 2018, 9, 16343-16353.	1.8	15
119	Breast cancer gene expression profiling: clinical trial and practice implications. <i>Pharmacogenomics</i> , 2005, 6, 49-58.	1.3	14
120	Prognostic and Predictive Impact of Beta-2 Adrenergic Receptor Expression in HER2-Positive Breast Cancer. <i>Clinical Breast Cancer</i> , 2020, 20, 262-273.e7.	2.4	14
121	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, 30306-30316.	1.8	14
122	Association of T-Cell Receptor Repertoire Use With Response to Combined Trastuzumab-Lapatinib Treatment of HER2-Positive Breast Cancer. <i>JAMA Oncology</i> , 2018, 4, e181564.	7.1	13
123	Reactive stroma and trastuzumab resistance in HER2-positive early breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 266-276.	5.1	13
124	Alpha-smooth Muscle Actin Expression in the Stroma Predicts Resistance to Trastuzumab in Patients with Early-stage HER2-positive Breast Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 6156-6163.	7.0	12
125	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, e58-e69.	4.4	10
126	Gene Profiling Assay and Application: The Predictive Role in Primary Therapy. <i>Journal of the National Cancer Institute Monographs</i> , 2011, 2011, 124-127.	2.1	9



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127	Network science in clinical trials: A patient-centered approach. <i>Seminars in Cancer Biology</i> , 2018, 52, 135-150.	9.6	9
128	FDG positron emission tomography imaging and ctDNA detection as an early dynamic biomarker of everolimus efficacy in advanced luminal breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 125.	5.2	9
129	Incorporation of TILs in daily breast cancer care: how much evidence can we bear?. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2022, 480, 147-162.	2.8	9
130	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, 721-730.	3.1	8
131	Should we assess HER2 status by Oncotype DX®?. <i>Nature Reviews Clinical Oncology</i> , 2012, 9, 12-14.	27.6	8
132	Late effects of adjuvant chemotherapy adumbrate dormancy complexity in breast cancer. <i>Breast</i> , 2020, 52, 64-70.	2.2	8
133	Heparanase: a potential marker of worse prognosis in estrogen receptor-positive breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 67.	5.2	8
134	Integrated Molecular and Immune Phenotype of HER2-Positive Breast Cancer and Response to Neoadjuvant Therapy: A NeoALTTO Exploratory Analysis. <i>Clinical Cancer Research</i> , 2021, 27, 6307-6313.	7.0	8
135	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. <i>Npj Breast Cancer</i> , 2022, 8, .	5.2	8
136	Better translation from bench to bedside: Breakthroughs in the individualized treatment of cancer. <i>Critical Care Medicine</i> , 2009, 37, S22-S29.	0.9	7
137	Molecular Biology of Breast Cancer. , 2018, , 569-588.		6
138	STAT3 activation in HER2 positive breast cancers: Analysis of data from a large prospective trial. <i>International Journal of Cancer</i> , 2021, 148, 1529-1535.	5.1	6
139	Copy Number Aberration Analysis to Predict Response to Neoadjuvant Anti-HER2 Therapy: Results from the NeoALTTO Phase III Clinical Trial. <i>Clinical Cancer Research</i> , 2021, 27, 5607-5618.	7.0	5
140	Heterogeneity of Circulating Tumor Cell-Associated Genomic Gains in Breast Cancer and Its Association with the Host Immune Response. <i>Cancer Research</i> , 2021, 81, 6196-6206.	0.9	5
141	Multiple-input multiple-output causal strategies for gene selection. <i>BMC Bioinformatics</i> , 2011, 12, 458.	2.6	4
142	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. <i>BMC Bioinformatics</i> , 2011, 12, 310.	2.6	4
143	Feasibility of developing reliable gene expression modules from FFPE derived RNA profiled on Affymetrix arrays. <i>PLoS ONE</i> , 2018, 13, e0203346.	2.5	4
144	Adaptive immune signature in HER2-positive breast cancer in NCCTG (Alliance) N9831 and NeoALTTO trials. <i>Npj Breast Cancer</i> , 2022, 8, .	5.2	4

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145	Aiming at the target: improved adjuvant medical therapy. Breast, 2009, 18, S25-S30.	2.2	3
146	Molecular Biology of Breast Cancer. , 2010, , 341-349.		3
147	New Tools for Assessing Breast Cancer Recurrence. Cancer Treatment and Research, 2008, 141, 99-118.	0.5	3
148	Genomic and Molecular Classification of Breast Cancer. , 2006, , 595-621.		2
149	Molecular Biology of Breast Cancer. , 2009, , 501-517.		1
150	Time to move forward from "first-generation" prognostic gene signatures in early breast cancer. Breast Cancer Research and Treatment, 2011, 128, 643-645.	2.5	1
151	Strategies to Incorporate Translational Research Science into Clinical Trials in Breast Cancer. Current Breast Cancer Reports, 2010, 2, 208-213.	1.0	0
152	Molecular biology of breast cancer. , 2020, , 449-461.		0
153	Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. Translational Medicine Series, 2007, , 121-136.	0.0	0
154	Introduction to Gene Expression Profiling in Breast Cancer. , 2010, , 295-314.		0
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