

# Christos Sotiriou

## List of Publications by Year in descending order

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Version: 2024-02-01

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	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
2	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
3	Ontogeny and Vulnerabilities of Drug-Tolerant Persisters in HER2+ Breast Cancer. <i>Cancer Discovery</i> , 2022, 12, 1022-1045.	9.4	43
4	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
5	Interrogating breast cancer heterogeneity using single and pooled circulating tumor cell analysis. <i>Npj Breast Cancer</i> , 2022, 8, .	5.2	8
6	STAT3 activation in HER2-â€positive breast cancers: Analysis of data from a large prospective trial. <i>International Journal of Cancer</i> , 2021, 148, 1529-1535.	5.1	6
7	Fat1 deletion promotes hybrid EMT state, tumour stemness and metastasis. <i>Nature</i> , 2021, 589, 448-455.	27.8	232
8	Heparanase: a potential marker of worse prognosis in estrogen receptor-positive breast cancer. <i>Npj Breast Cancer</i> , 2021, 7, 67.	5.2	8
9	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
10	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
11	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
12	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
13	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
14	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
15	Heterogeneity of Circulating Tumor Cellâ€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
16	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
17	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
18	Reactive stroma and trastuzumab resistance in HER2â€positive early breast cancer. <i>International Journal of Cancer</i> , 2020, 147, 266-276.	5.1	13

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19	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
20	Molecular biology of breast cancer. , 2020, , 449-461.		0
21	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
22	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
23	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
24	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
25	Pitfalls in assessing stromal tumor infiltrating lymphocytes (sTILs) in breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 17.	5.2	106
26	Late effects of adjuvant chemotherapy adumbrate dormancy complexity in breast cancer. <i>Breast</i> , 2020, 52, 64-70.	2.2	8
27	The path to a better biomarker: application of a risk management framework for the implementation of PD-L1 and TILs as immuno-oncology biomarkers in breast cancer clinical trials and daily practice. <i>Journal of Pathology</i> , 2020, 250, 667-684.	4.5	142
28	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
29	The 2019 World Health Organization classification of tumours of the breast. <i>Histopathology</i> , 2020, 77, 181-185.	2.9	395
30	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
31	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
32	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
33	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
34	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
35	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
36	Immune Infiltration in Invasive Lobular Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2018, 110, 768-776.	6.3	76

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37	<scp>G</scp>enomic hotspots but few recurrent fusion genes in breast cancer. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 331-338.	2.8	18
38	Network science in clinical trials: A patient-centered approach. <i>Seminars in Cancer Biology</i> , 2018, 52, 135-150.	9.6	9
39	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
40	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
41	<i>Molecular Biology of Breast Cancer.</i> , 2018, , 569-588.		6
42	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
43	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
44	Transcriptomic and genomic features of invasive lobular breast cancer. <i>Seminars in Cancer Biology</i> , 2017, 44, 98-105.	9.6	34
45	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
46	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
47	<scp>CDK</scp>4 phosphorylation status and a linked gene expression profile predict sensitivity to palbociclib. <i>EMBO Molecular Medicine</i> , 2017, 9, 1052-1066.	6.9	65
48	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
49	Tumor-infiltrating lymphocyte composition, organization and PD-1/ PD-L1 expression are linked in breast cancer. <i>Oncolmmunology</i> , 2017, 6, e1257452.	4.6	169
50	Recurrence dynamics of breast cancer according to baseline body mass index. <i>European Journal of Cancer</i> , 2017, 87, 10-20.	2.8	35
51	CD73 Promotes Resistance to HER2/ErbB2 Antibody Therapy. <i>Cancer Research</i> , 2017, 77, 5652-5663.	0.9	90
52	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017, 32, 169-184.e7.	16.8	534
53	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
54	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

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55	RNA Sequencing to Predict Response to Neoadjuvant Anti-HER2 Therapy. <i>JAMA Oncology</i> , 2017, 3, 227.	7.1	118
56	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	27.8	1,760
57	Loss of <i>ARID1A</i> Activates <i>ANXA1</i> , which Serves as a Predictive Biomarker for Trastuzumab Resistance. <i>Clinical Cancer Research</i> , 2016, 22, 5238-5248.	7.0	43
58	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
59	Portraying breast cancers with long noncoding RNAs. <i>Science Advances</i> , 2016, 2, e1600220.	10.3	102
60	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
61	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
62	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
63	Genomic Characterization of Primary Invasive Lobular Breast Cancer. <i>Journal of Clinical Oncology</i> , 2016, 34, 1872-1881.	1.6	249
64	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
65	Genomic aberrations in young and elderly breast cancer patients. <i>BMC Medicine</i> , 2015, 13, 266.	5.5	80
66	<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
67	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
68	<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
69	Evolving paradigms in multifocal breast cancer. <i>Seminars in Cancer Biology</i> , 2015, 31, 111-118.	9.6	34
70	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015, 21, 751-759.	30.7	711
71	No significant viral transcription detected in whole breast cancer transcriptomes. <i>BMC Cancer</i> , 2015, 15, 147.	2.6	15
72	RANK-ligand (RANKL) expression in young breast cancer patients and during pregnancy. <i>Breast Cancer Research</i> , 2015, 17, 24.	5.0	149

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73	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
74	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
75	Principles Governing A-to-I RNA Editing in the Breast Cancer Transcriptome. <i>Cell Reports</i> , 2015, 13, 277-289.	6.4	179
76	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
77	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
78	<i>TP53</i> mutation-associated genes predict the risk of tumor relapse and identify <i>MPS1</i> as a potential therapeutic kinase in <i>TP53</i> -mutated breast cancers. <i>Molecular Oncology</i> , 2014, 8, 508-519.	4.6	59
79	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.	3.5	62
80	Luminal B Breast Cancer: Molecular Characterization, Clinical Management, and Future Perspectives. <i>Journal of Clinical Oncology</i> , 2014, 32, 2794-2803.	1.6	298
81	<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
82	Biology of breast cancer during pregnancy using genomic profiling. <i>Endocrine-Related Cancer</i> , 2014, 21, 545-554.	3.1	58
83	Molecular Testing in Breast Cancer. , 2014, , 169-188.		0
84	Interactions between immunity, proliferation and molecular subtype in breast cancer prognosis. <i>Genome Biology</i> , 2013, 14, R34.	9.6	168
85	Luminal breast cancer: from biology to treatment. <i>Nature Reviews Clinical Oncology</i> , 2013, 10, 494-506.	27.6	183
86	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
87	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
88	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
89	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
90	CD4+ follicular helper T cell infiltration predicts breast cancer survival. <i>Journal of Clinical Investigation</i> , 2013, 123, 2873-2892.	8.2	813

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91	Next-generation sequencing in breast cancer. <i>Current Opinion in Oncology</i> , 2012, 24, 597-604.	2.4	76
92	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
93	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
94	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
95	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
96	Should we assess HER2 status by Oncotype DX®?. <i>Nature Reviews Clinical Oncology</i> , 2012, 9, 12-14.	27.6	8
97	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
98	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
99	Dissecting the Heterogeneity of Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 1879-1887.	1.6	388
100	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
101	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
102	Multiple-input multiple-output causal strategies for gene selection. <i>BMC Bioinformatics</i> , 2011, 12, 458.	2.6	4
103	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
104	Time to move forward from "first-generation" prognostic gene signatures in early breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 128, 643-645.	2.5	1
105	Consistent metagenes from cancer expression profiles yield agent specific predictors of chemotherapy response. <i>BMC Bioinformatics</i> , 2011, 12, 310.	2.6	4
106	DNA methylation profiling reveals a predominant immune component in breast cancers. <i>EMBO Molecular Medicine</i> , 2011, 3, 726-741.	6.9	210
107	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
108	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

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109	Global MicroRNA Expression Profiling Identifies MiR-210 Associated with Tumor Proliferation, Invasion and Poor Clinical Outcome in Breast Cancer. PLoS ONE, 2011, 6, e20980.	2.5	214
110	The prognostic and predictive value of gene expression signatures in breast cancer. , 2011, , 4-12.		0
111	Strategies to Incorporate Translational Research Science into Clinical Trials in Breast Cancer. Current Breast Cancer Reports, 2010, 2, 208-213.	1.0	0
112	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	17.5	795
113	Amplification of LAPT4B and YWHAZ contributes to chemotherapy resistance and recurrence of breast cancer. Nature Medicine, 2010, 16, 214-218.	30.7	301
114	Molecular Biology of Breast Cancer. , 2010, , 341-349.		3
115	Low CD10 mRNA Expression Identifies High-Risk Ductal Carcinoma In Situ (DCIS). PLoS ONE, 2010, 5, e12100.	2.5	16
116	Molecular Profiling: Moving Away from Tumor Philately. Science Translational Medicine, 2010, 2, 47ps43.	12.4	71
117	<i>PIK3CA</i> mutations associated with gene signature of low mTORC1 signaling and better outcomes in estrogen receptor-positive breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10208-10213.	7.1	324
118	Genomic Index of Sensitivity to Endocrine Therapy for Breast Cancer. Journal of Clinical Oncology, 2010, 28, 4111-4119.	1.6	235
119	A fuzzy gene expression-based computational approach improves breast cancer prognostication. Genome Biology, 2010, 11, R18.	9.6	47
120	Introduction to Gene Expression Profiling in Breast Cancer. , 2010, , 295-314.		0
121	Molecular Biology of Breast Cancer. , 2009, , 501-517.		1
122	Genomic Grade Index Is Associated With Response to Chemotherapy in Patients With Breast Cancer. Journal of Clinical Oncology, 2009, 27, 3185-3191.	1.6	173
123	Improvement of the clinical applicability of the Genomic Grade Index through a qRT-PCR test performed on frozen and formalin-fixed paraffin-embedded tissues. BMC Genomics, 2009, 10, 424.	2.8	74
124	Aiming at the target: improved adjuvant medical therapy. Breast, 2009, 18, S25-S30.	2.2	3
125	Gene expression profiling identifies activated growth factor signaling in poor prognosis (Luminal-B) estrogen receptor positive breast cancer. BMC Medical Genomics, 2009, 2, 37.	1.5	51
126	The Gene expression Grade Index: a potential predictor of relapse for endocrine-treated breast cancer patients in the BIG 1-98 trial. BMC Medical Genomics, 2009, 2, 40.	1.5	67



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127	Gene-Expression Signatures in Breast Cancer. <i>New England Journal of Medicine</i> , 2009, 360, 790-800.	27.0	1,286
128	Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. <i>Cancer Investigation</i> , 2009, 27, 1-10.	1.3	23
129	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
130	Predicting prognosis using molecular profiling in estrogen receptor-positive breast cancer treated with tamoxifen. <i>BMC Genomics</i> , 2008, 9, 239.	2.8	300
131	Comparison of prognostic gene expression signatures for breast cancer. <i>BMC Genomics</i> , 2008, 9, 394.	2.8	123
132	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
133	Evaluation of biological pathways involved in chemotherapy response in breast cancer. <i>Breast Cancer Research</i> , 2008, 10, R37.	5.0	53
134	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
135	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
136	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
137	New Tools for Assessing Breast Cancer Recurrence. <i>Cancer Treatment and Research</i> , 2008, 141, 99-118.	0.5	3
138	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
139	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
140	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
141	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
142	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
143	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
144	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

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145	The evolution of treatment strategies: Aiming at the target. <i>Breast</i> , 2007, 16, 10-16.	2.2	29
146	Development and Validation of Gene Expression Profile Signatures in Early-Stage Breast Cancer. <i>Translational Medicine Series</i> , 2007, , 121-136.	0.0	0
147	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
148	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
149	Proliferation: the Most Prominent Predictor of Clinical Outcome in Breast Cancer. <i>Cell Cycle</i> , 2006, 5, 2198-2202.	2.6	76
150	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
151	Genomic and Molecular Classification of Breast Cancer. , 2006, , 595-621.		2
152	Bringing Molecular Prognosis and Prediction to the Clinic. <i>Clinical Breast Cancer</i> , 2005, 6, 61-76.	2.4	36
153	Breast cancer gene expression profiling: clinical trial and practice implications. <i>Pharmacogenomics</i> , 2005, 6, 49-58.	1.3	14
154	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
155	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
156	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