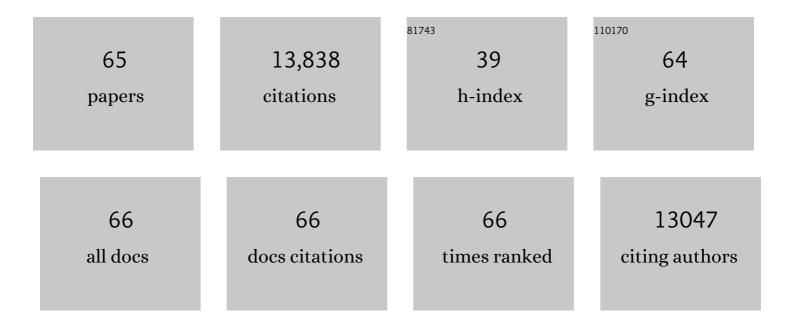
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	<scp>MammaPrint</scp> and <scp>BluePrint</scp> comprehensively capture the cancer hallmarks in earlyâ€stage breast cancer patients. Genes Chromosomes and Cancer, 2022, 61, 148-160.	1.5	11
2	Outcome of Patients With an Ultralow-Risk 70-Gene Signature in the MINDACT Trial. Journal of Clinical Oncology, 2022, 40, 1335-1345.	0.8	28
3	High concordance of 70â€gene recurrence risk signature and 80â€gene molecular subtyping signature between core needle biopsy and surgical resection specimens in earlyâ€stage breast cancer. Journal of Surgical Oncology, 2022, 125, 596-602.	0.8	6
4	70-gene signature as an aid for treatment decisions in early breast cancer: updated results of the phase 3 randomised MINDACT trial with an exploratory analysis by age. Lancet Oncology, The, 2021, 22, 476-488.	5.1	179
5	Controlling technical variation amongst 6693 patient microarrays of the randomized MINDACT trial. Communications Biology, 2020, 3, 397.	2.0	7
6	Investigating the concordance in molecular subtypes of primary colorectal tumors and their matched synchronous liver metastasis. International Journal of Cancer, 2020, 147, 2303-2315.	2.3	14
7	Decentralization of Next-Generation RNA Sequencing-Based MammaPrint® and BluePrint® Kit at University Hospitals Leuven and Curie Institute Paris. Translational Oncology, 2019, 12, 1557-1565.	1.7	6
8	MammaPrint and BluePrint Molecular Diagnostics Using Targeted RNA Next-Generation Sequencing Technology. Journal of Molecular Diagnostics, 2019, 21, 808-823.	1.2	15
9	Immunohistochemical versus molecular (BluePrint and MammaPrint) subtyping of breast carcinoma. Outcome results from the EORTC 10041/BIG 3-04 MINDACT trial. Breast Cancer Research and Treatment, 2018, 167, 123-131.	1.1	51
10	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, <i>BRCA1</i> -like status, tumor-infiltrating immune cells and survival. OncoImmunology, 2018, 7, e1509820.	2.1	80
11	A breast cancer gene signature for indolent disease. Breast Cancer Research and Treatment, 2017, 164, 461-466.	1.1	19
12	DNA repair deficiency biomarkers and the 70-gene ultra-high risk signature as predictors of veliparib/carboplatin response in the I-SPY 2 breast cancer trial. Npj Breast Cancer, 2017, 3, 31.	2.3	64
13	A Computational Workflow Translates a 58-Gene Signature to a Formalin-Fixed, Paraffin-Embedded Sample-Based Companion Diagnostic for Personalized Treatment of the BRAF-Mutation-Like Subtype of Colorectal Cancers. High-Throughput, 2017, 6, 16.	4.4	3
14	The BRCA1ness signature is associated significantly with response to PARP inhibitor treatment versus control in the I-SPY 2 randomized neoadjuvant setting. Breast Cancer Research, 2017, 19, 99.	2.2	58
15	70-Gene Signature as an Aid to Treatment Decisions in Early-Stage Breast Cancer. New England Journal of Medicine, 2016, 375, 717-729.	13.9	1,427
16	Prognostic Value of MammaPrint [®] in Invasive Lobular Breast Cancer. Biomarker Insights, 2016, 11, BMI.S38435.	1.0	31
17	Equivalence of MammaPrint array types in clinical trials and diagnostics. Breast Cancer Research and Treatment, 2016, 156, 279-287.	1.1	57
18	Discordant assessment of tumor biomarkers by histopathological and molecular assays in the EORTC randomized controlled 10041/BIG 03-04 MINDACT trial breast cancer. Breast Cancer Research and Treatment, 2016, 155, 463-469.	1.1	19

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19	Neoadjuvant tamoxifen synchronizes ERα binding and gene expression profiles related to outcome and proliferation. Oncotarget, 2016, 7, 33901-33918.	0.8	13
20	High concordance of protein (by IHC), gene (by FISH; HER2 only), and microarray readout (by) Tj ETQq0 0 0 rg Oncology, 2014, 25, 816-823.	gBT /Overlocl 0.6	k 10 Tf 50 707 50
21	MammaPrint Molecular Diagnostics on Formalin-Fixed, Paraffin-Embedded Tissue. Journal of Molecular Diagnostics, 2014, 16, 190-197.	1.2	90
22	Additional prognostic value of the 70-gene signature (MammaPrint®) among breast cancer patients with 4–9 positive lymph nodes. Breast, 2013, 22, 682-690.	0.9	47
23	Performance characteristics of the MammaPrint [®] breast cancer diagnostic gene signature. Personalized Medicine, 2013, 10, 801-811.	0.8	23
24	Independent Validation of a Prognostic Genomic Signature (ColoPrint) for Patients With Stage II Colon Cancer. Annals of Surgery, 2013, 257, 1053-1058.	2.1	102
25	A diagnostic gene profile for molecular subtyping of breast cancer associated with treatment response. Breast Cancer Research and Treatment, 2012, 133, 37-47.	1.1	121
26	Gene Expression Signature to Improve Prognosis Prediction of Stage II and III Colorectal Cancer. Journal of Clinical Oncology, 2011, 29, 17-24.	0.8	487
27	Impact of mammographic screening on the detection of good and poor prognosis breast cancers. Breast Cancer Research and Treatment, 2011, 130, 725-734.	1.1	76
28	Comparison of MammaPrint and TargetPrint results with clinical parameters in German patients with early stage breast cancer. International Journal of Molecular Medicine, 2010, 26, 837-43.	1.8	21
29	The 70-gene signature as a response predictor for neoadjuvant chemotherapy in breast cancer. Breast Cancer Research and Treatment, 2010, 119, 551-558.	1.1	220
30	Clinical Utility of the 70-gene MammaPrint Profile in a Japanese Population. Japanese Journal of Clinical Oncology, 2010, 40, 508-512.	0.6	35
31	Biological Functions of the Genes in the Mammaprint Breast Cancer Profile Reflect the Hallmarks of Cancer. Biomarker Insights, 2010, 5, BMI.S6184.	1.0	103
32	The 70-gene prognosis signature predicts early metastasis in breast cancer patients between 55 and 70 years of age. Annals of Oncology, 2010, 21, 717-722.	0.6	129
33	MammaPrint® Translating Research into a Diagnostic Test. , 2010, , 165-184.		3
34	Microarray-Based Determination of Estrogen Receptor, Progesterone Receptor, and HER2 Receptor Status in Breast Cancer. Clinical Cancer Research, 2009, 15, 7003-7011.	3.2	87
35	Gene expression profiling: Decoding breast cancer. Surgical Oncology, 2009, 18, 366-378.	0.8	27
36	Implementation of a novel microarrayâ€based diagnostic test for cancer of unknown primary. International Journal of Cancer, 2009, 125, 1390-1397.	2.3	45

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37	The 70-gene prognosis-signature predicts disease outcome in breast cancer patients with 1–3 positive lymph nodes in an independent validation study. Breast Cancer Research and Treatment, 2009, 116, 295-302.	1.1	260
38	Validation of 70-gene prognosis signature in node-negative breast cancer. Breast Cancer Research and Treatment, 2009, 117, 483-495.	1.1	154
39	Comparison of gene expression profiles predicting progression in breast cancer patients treated with tamoxifen. Breast Cancer Research and Treatment, 2009, 113, 275-283.	1.1	56
40	A gene expression profile for detection of sufficient tumour cells in breast tumour tissue: microarray diagnosis eligibility. BMC Medical Genomics, 2009, 2, 52.	0.7	11
41	PRAME expression and clinical outcome of breast cancer. British Journal of Cancer, 2008, 99, 398-403.	2.9	90
42	Gene Expression Profiling to Identify the Histogenetic Origin of Metastatic Adenocarcinomas of Unknown Primary. Journal of Clinical Oncology, 2008, 26, 4435-4441.	0.8	176
43	Analysis of the MammaPrint Breast Cancer Assay in a Predominantly Postmenopausal Cohort. Clinical Cancer Research, 2008, 14, 2988-2993.	3.2	140
44	Gene-Expression and Immunohistochemical Study of Specific T-Cell Subsets and Accessory Cell Types in the Transformation and Prognosis of Follicular Lymphoma. Journal of Clinical Oncology, 2007, 25, 390-398.	0.8	221
45	Use of 70-gene signature to predict prognosis of patients with node-negative breast cancer: a prospective community-based feasibility study (RASTER). Lancet Oncology, The, 2007, 8, 1079-1087.	5.1	268
46	Robust interlaboratory reproducibility of a gene expression signature measurement consistent with the needs of a new generation of diagnostic tools. BMC Genomics, 2007, 8, 148.	1.2	46
47	Converting a breast cancer microarray signature into a high-throughput diagnostic test. BMC Genomics, 2006, 7, 278.	1.2	429
48	Validation and Clinical Utility of a 70-Gene Prognostic Signature for Women With Node-Negative Breast Cancer. Journal of the National Cancer Institute, 2006, 98, 1183-1192.	3.0	1,128
49	Mechanisms and Effects of Loss of Human Leukocyte Antigen Class II Expression in Immune-Privileged Site-Associated B-Cell Lymphoma. Clinical Cancer Research, 2006, 12, 2698-2705.	3.2	71
50	Gene Expression Profiles of Primary Breast Carcinomas from Patients at High Risk for Local Recurrence after Breast-Conserving Therapy. Clinical Cancer Research, 2006, 12, 5705-5712.	3.2	56
51	Gene expression profiling in follicular lymphoma to assess clinical aggressiveness and to guide the choice of treatment. Blood, 2005, 105, 301-307.	0.6	208
52	No common denominator for breast cancer lymph node metastasis. British Journal of Cancer, 2005, 93, 924-932.	2.9	82
53	Molecular Portraits and 70-Gene Prognosis Signature Are Preserved throughout the Metastatic Process of Breast Cancer. Cancer Research, 2005, 65, 9155-9158.	0.4	302
54	Gene expression profiles of primary breast tumors maintained in distant metastases. Proceedings of the United States of America, 2003, 100, 15901-15905.	3.3	404

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55	Very late relapse in diffuse large B-cell lymphoma represents clonally related disease and is marked by germinal center cell features. Blood, 2003, 102, 324-327.	0.6	40
56	A Gene-Expression Signature as a Predictor of Survival in Breast Cancer. New England Journal of Medicine, 2002, 347, 1999-2009.	13.9	5,759
57	B-cell–autonomous somatic mutation deficit following bone marrow transplant. Blood, 2000, 96, 1064-1069.	0.6	28
58	B-cell–autonomous somatic mutation deficit following bone marrow transplant. Blood, 2000, 96, 1064-1069.	0.6	6
59	Human B cells accumulate immunoglobulin V gene somatic mutations in a cell contact-dependent manner in cultures supported by activated T cells but not in cultures supported by CD40 ligand. Clinical and Experimental Immunology, 1999, 116, 441-448.	1.1	7
60	Motif-specific probes identify individual genes and detect somatic mutations. Molecular Immunology, 1999, 36, 599-610.	1.0	4
61	Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient. Clinical and Experimental Immunology, 1997, 107, 372-380.	1.1	10
62	Non-stochastic utilization of Ig V region genes in unselected human peripheral B cells. Molecular Immunology, 1996, 33, 553-560.	1.0	65
63	VH repertoire in human B lymphocytes stimulated by CD40 ligand and IL-4: Evidence for positive and negative selection mechanisms coupled to CD40 activation. Molecular Immunology, 1996, 33, 1369-1376.	1.0	7
64	Polymorphism and Utilization of Human V _H Genes ^a . Annals of the New York Academy of Sciences, 1995, 764, 50-61.	1.8	51
65	Anomalous Diversification of the Antibody Repertoire following Bone Marrow Transplantation (Sup) a / Sup) Annals of the New York Academy of Sciences 1995, 764, 312-314	1.8	5