Therese SÃ¸rlie

List of Publications by Year
in descending order

74	25,112	109321 35	85541 71
papers	citations	h-index	g-index

78	78	78	23177
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Molecular portraits of human breast tumours. Nature, 2000, 406, 747-752.	27.8	13,397
2	Repeated observation of breast tumor subtypes in independent gene expression data sets. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 8418-8423.	7.1	4,849
3	Microarray analysis reveals a major direct role of DNA copy number alteration in the transcriptional program of human breast tumors. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12963-12968.	7.1	1,098
4	Robustness, scalability, and integration of a wound-response gene expression signature in predicting breast cancer survival. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 3738-3743.	7.1	934
5	Distinct patterns of DNA copy number alteration are associated with different clinicopathological features and geneâ€expression subtypes of breast cancer. Genes Chromosomes and Cancer, 2006, 45, 1033-1040.	2.8	464
6	Molecular portraits of breast cancer: tumour subtypes as distinct disease entities. European Journal of Cancer, 2004, 40, 2667-2675.	2.8	336
7	Cell-Type-Specific Responses to Chemotherapeutics in Breast Cancer. Cancer Research, 2004, 64, 4218-4226.	0.9	321
8	Distinct molecular mechanisms underlying clinically relevant subtypes of breast cancer: gene expression analyses across three different platforms. BMC Genomics, 2006, 7, 127.	2.8	314
9	Gene Expression Patterns in Ovarian Carcinomas. Molecular Biology of the Cell, 2003, 14, 4376-4386.	2.1	302
10	Tripleâ€negative breast cancer: Present challenges and new perspectives. Molecular Oncology, 2010, 4, 209-229.	4.6	252
11	Integrated molecular profiles of invasive breast tumors and ductal carcinoma in situ (DCIS) reveal differential vascular and interleukin signaling. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 2802-2807.	7.1	149
12	Glycan gene expression signatures in normal and malignant breast tissue; possible role in diagnosis and progression. Molecular Oncology, 2010, 4, 98-118.	4.6	147
13	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. Science Translational Medicine, 2010, 2, 38ra47.	12.4	138
14	An independent poor-prognosis subtype of breast cancer defined by a distinct tumor immune microenvironment. Nature Communications, 2019, 10, 5499.	12.8	132
15	Presence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancer. Molecular Oncology, 2007, 1, 160-171.	4.6	128
16	Frequent aberrant DNA methylation of ABCB1, FOXC1, PPP2R2B and PTEN in ductal carcinoma in situ and early invasive breast cancer. Breast Cancer Research, 2010, 12, R3.	5.0	128
17	Gene expression profiles do not consistently predict the clinical treatment response in locally advanced breast cancer. Molecular Cancer Therapeutics, 2006, 5, 2914-2918.	4.1	114
18	Re-definition of claudin-low as a breast cancer phenotype. Nature Communications, 2020, 11, 1787.	12.8	108

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19	Molecular diversity in ductal carcinoma in situ (DCIS) and early invasive breast cancer. Molecular Oncology, 2010, 4, 357-368.	4.6	107
20	Merging transcriptomics and metabolomics - advances in breast cancer profiling. BMC Cancer, 2010, 10, 628.	2.6	101
21	Molecular profiling and characterization of luminalâ€like and basalâ€like in vivo breast cancer xenograft models. Molecular Oncology, 2009, 3, 469-482.	4.6	96
22	Tumor initiating but differentiated luminal-like breast cancer cells are highly invasive in the absence of basal-like activity. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6124-6129.	7.1	96
23	Prognostic value of PAM50 and risk of recurrence score in patients with early-stage breast cancer with long-term follow-up. Breast Cancer Research, 2017, 19, 120.	5.0	93
24	Molecular Features of Subtype-Specific Progression from Ductal Carcinoma In Situ to Invasive Breast Cancer. Cell Reports, 2016, 16, 1166-1179.	6.4	85
25	Development and Validation of a Gene Profile Predicting Benefit of Postmastectomy Radiotherapy in Patients with High-Risk Breast Cancer: A Study of Gene Expression in the DBCG82bc Cohort. Clinical Cancer Research, 2014, 20, 5272-5280.	7.0	80
26	Influence of DNA copy number and mRNA levels on the expression of breast cancer related proteins. Molecular Oncology, 2013, 7, 704-718.	4.6	77
27	Molecular Classification of Breast Tumors: Toward Improved Diagnostics and Treatments. , 2007, 360, 91-114.		63
28	Molecular subtypes in ductal carcinoma in situ of the breast and their relation to prognosis: a population-based cohort study. BMC Cancer, 2013, 13, 512.	2.6	61
29	Genomics in breast cancerâ€"therapeutic implications. Nature Clinical Practice Oncology, 2005, 2, 26-33.	4.3	53
30	Best Practices for Spatial Profiling for Breast Cancer Research with the GeoMxÂ® Digital Spatial Profiler. Cancers, 2021, 13, 4456.	3.7	50
31	Glycanâ€related gene expression signatures in breast cancer subtypes; relation to survival. Molecular Oncology, 2015, 9, 861-876.	4.6	47
32	Interplay of choline metabolites and genes in patient-derived breast cancer xenografts. Breast Cancer Research, 2014, 16, R5.	5.0	45
33	The prognostic role of HER2 expression in ductal breast carcinoma in situ (DCIS); a population-based cohort study. BMC Cancer, 2015, 15, 468.	2.6	44
34	Introducing Molecular Subtyping of Breast Cancer Into the Clinic?. Journal of Clinical Oncology, 2009, 27, 1153-1154.	1.6	43
35	The importance of gene-centring microarray data. Lancet Oncology, The, 2010, 11, 719-720.	10.7	42
36	Combining Gene Signatures Improves Prediction of Breast Cancer Survival. PLoS ONE, 2011, 6, e17845.	2.5	38

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37	Relationship between the prognostic and predictive value of the intrinsic subtypes and a validated gene profile predictive of loco-regional control and benefit from post-mastectomy radiotherapy in patients with high-risk breast cancer. Acta OncolÃ³gica, 2014, 53, 1337-1346.	1.8	34
38	Lessons learned from the intrinsic subtypes of breast cancer in the quest for precision therapy. British Journal of Surgery, 2014, 101, 925-938.	0.3	34
39	Systematic assessment of prognostic gene signatures for breast cancer shows distinct influence of time and ER status. BMC Cancer, 2014, 14, 211.	2.6	34
40	Genetic variation in putative regulatory loci controlling gene expression in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 7735-7740.	7.1	32
41	Ischemia caused by time to freezing induces systematic microRNA and mRNA responses in cancer tissue. Molecular Oncology, 2011, 5, 564-576.	4.6	29
42	The tankyrase inhibitor G007-LK inhibits small intestine LGR5+ stem cell proliferation without altering tissue morphology. Biological Research, 2018, 51, 3.	3.4	27
43	Full sequencing of TP53 identifies identical mutations within in situ and invasive components in breast cancer suggesting clonal evolution. Molecular Oncology, 2009, 3, 214-219.	4.6	26
44	Subtypeâ€specific response to bevacizumab is reflected in the metabolome and transcriptome of breast cancer xenografts. Molecular Oncology, 2013, 7, 130-142.	4.6	26
45	Contrasting DCIS and invasive breast cancer by subtype suggests basal-like DCIS as distinct lesions. Npj Breast Cancer, 2020, 6, 26.	5.2	24
46	Screening for p53 Gene Mutations in Archived Tumors of Workers Occupationally Exposed to Carcinogens: Examples from Analysis of Bladder Tumors. Journal of Occupational and Environmental Medicine, 1995, 37, 59-68.	1.7	23
47	In Silico Ascription of Gene Expression Differences to Tumor and Stromal Cells in a Model to Study Impact on Breast Cancer Outcome. PLoS ONE, 2010, 5, e14002.	2.5	23
48	Intrinsic subtypes and benefit from postmastectomy radiotherapy in node-positive premenopausal breast cancer patients who received adjuvant chemotherapy â€“ results from two independent randomized trials. Acta OncolÃ³gica, 2018, 57, 38-43.	1.8	22
49	The expression of the long NEAT1_2 isoform is associated with human epidermal growth factor receptor 2-positive breast cancers. Scientific Reports, 2020, 10, 1277.	3.3	22
50	Mutation screening of BRCA1 using PTT and LOH analysis at 17q21 in breast carcinomas from familial and non-familial cases. Breast Cancer Research and Treatment, 1998, 48, 259-264.	2.5	20
51	Pathway based analysis of SNPs with relevance to 5â€FU therapy: Relation to intratumoral mRNA expression and survival. International Journal of Cancer, 2008, 123, 577-585.	5.1	20
52	AXL Is a Driver of Stemness in Normal Mammary Gland and Breast Cancer. IScience, 2020, 23, 101649.	4.1	20
53	Claudin-low-like mouse mammary tumors show distinct transcriptomic patterns uncoupled from genomic drivers. Breast Cancer Research, 2019, 21, 85.	5.0	18
54	Effects of anastrozole on the intratumoral gene expression in locally advanced breast cancer. Journal of Steroid Biochemistry and Molecular Biology, 2005, 95, 105-111.	2.5	16

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55	The Impact of Gene Expression Patterns in Breast Cancer. Clinical Chemistry, 2016, 62, 1150-1151.	3.2	13
56	Reliable PCR quantitation of estrogen, progesterone and ERBB2 receptor mRNA from formalin-fixed, paraffin-embedded tissue is independent of prior macro-dissection. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2013, 463, 775-786.	2.8	11
57	Sample Preparation Approach Influences PAM50 Risk of Recurrence Score in Early Breast Cancer. Cancers, 2021, 13, 6118.	3.7	10
58	A conditional transgenic mouse line for targeted expression of the stem cell marker LGR5. Developmental Biology, 2015, 404, 35-48.	2.0	9
59	A Bayesian two-way latent structure model for genomic data integration reveals few pan-genomic cluster subtypes in a breast cancer cohort. Bioinformatics, 2019, 35, 4886-4897.	4.1	9
60	Multi-Omics Marker Analysis Enables Early Prediction of Breast Tumor Progression. Frontiers in Genetics, 2021, 12, 670749.	2.3	9
61	Data integration from two microarray platforms identifies bi-allelic genetic inactivation of RIC8Ain a breast cancer cell line. BMC Medical Genomics, 2009, 2, 26.	1.5	8
62	On the molecular biology of breast cancer. Molecular Oncology, 2010, 4, 171-173.	4.6	8
63	Evaluation of MetriGenix custom 4Dâ„¢ arrays applied for detection of breast cancer subtypes. BMC Cancer, 2006, 6, 59.	2.6	7
64	NMD Microarray Analysis for Rapid Genome-Wide Screen of Mutated Genes in Cancer. Analytical Cellular Pathology, 2005, 27, 169-173.	1.4	7
65	Differential In Vivo Tumorigenicity of Distinct Subpopulations from a Luminal-Like Breast Cancer Xenograft. PLoS ONE, 2014, 9, e113278.	2.5	6
66	Epigenetic alterations at distal enhancers are linked to proliferation in human breast cancer. NAR Cancer, 2022, 4, zcac008.	3.1	6
67	GLI1â€induced mammary gland tumours are transplantable and maintain major molecular features. International Journal of Cancer, 2020, 146, 1125-1138.	5.1	5
68	Comparable cancerâ€relevant mutation profiles in synchronous ductal carcinoma in situ and invasive breast cancer. Cancer Reports, 2020, 3, e1248.	1.4	5
69	Can breast cancer be stopped? Modifiable risk factors of breast cancer among women with a prior benign or premalignant lesion. International Journal of Cancer, 2021, 149, 1247-1256.	5.1	5
70	How to personalise treatment in early breast cancer. European Journal of Cancer, 2011, 47, S310-S311.	2.8	4
71	A Longitudinal Study of the Association between Mammographic Density and Gene Expression in Normal Breast Tissue. Journal of Mammary Gland Biology and Neoplasia, 2019, 24, 163-175.	2.7	3
72	From autonomy to community; new perspectives on tumorigenicity and therapy resistance. Cancer Treatment Reviews, 2015, 41, 809-813.	7.7	2

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73	Mutation Screening of the TP53 Gene by Temporal Temperature Gel Electrophoresis (TTGE). Methods in Molecular Biology, 2014, 1105, 315-324.	0.9	1
74	Corrigendum to â€œPresence of bone marrow micrometastasis is associated with different recurrence risk within molecular subtypes of breast cancerâ€•[Mol. Oncol. 1 (2007) 160â€“171]. Molecular Oncology, 2010, 4, 169-169.	4.6	0