Ingrid Hedenfalk

List of Publications by Year
in descending order

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67 papers	4,769 citations	185998 28 h-index	106150 65 g-index
70 all docs	70 docs citations	70 times ranked	6655 citing authors

#	Article	IF	Citations
1	Abstract P2-08-11: How reliable are biomarkers assessed on a core needle biopsy? A study of paired core needle biopsies and surgical specimens in early breast cancer. Cancer Research, 2022, 82, P2-08-11-P2-08-11.	0.4	0
2	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12
3	Protein Signature Predicts Response to Neoadjuvant Treatment With Chemotherapy and Bevacizumab in HER2-Negative Breast Cancers. JCO Precision Oncology, 2021, 5, 286-306.	1.5	5
4	Homologous Recombination Repair Mechanisms in Serous Endometrial Cancer. Cancers, 2021, 13, 254.	1.7	12
5	Distinct mechanisms of resistance to fulvestrant treatment dictate level of ER independence and selective response to CDK inhibitors in metastatic breast cancer. Breast Cancer Research, 2021, 23, 26.	2.2	19
6	Regulatory T lymphocyte infiltration in metastatic breast cancerâ€”an independent prognostic factor that changes with tumor progression. Breast Cancer Research, 2021, 23, 27.	2.2	33
7	Oncogenic translation directs spliceosome dynamics revealing an integral role for SF3A3 in breast cancer. Molecular Cell, 2021, 81, 1453-1468.e12.	4.5	31
8	MET Expression and Cancer Stem Cell Networks Impact Outcome in High-Grade Serous Ovarian Cancer. Genes, 2021, 12, 742.	1.0	6
9	Evaluation of multiple transcriptomic gene risk signatures in male breast cancer. Npj Breast Cancer, 2021, 7, 98.	2.3	4
10	High density of stroma-localized CD11c-positive macrophages is associated with longer overall survival in high-grade serous ovarian cancer. Gynecologic Oncology, 2020, 159, 860-868.	0.6	4
11	SOX2 is a promising predictor of relapse and death in advanced stage high-grade serous ovarian cancer patients with residual disease after debulking surgery. Molecular and Cellular Oncology, 2020, 7, 1805094.	0.3	7
12	PD-1/PD-L1 expression and tumor-infiltrating lymphocytes are prognostically favorable in advanced high-grade serous ovarian carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 477, 83-91.	1.4	41
13	A multiplex biomarker assay improves the diagnostic performance of HE4 and CA125 in ovarian tumor patients. PLoS ONE, 2020, 15, e0240418.	1.1	15
14	Simvastatin is a potential candidate drug in ovarian clear cell carcinomas. Oncotarget, 2020, 11, 3660-3674.	0.8	4
15	Detecting TP53 mutations in diagnostic and archival liquid-based Pap samples from ovarian cancer patients using an ultra-sensitive ddPCR method. Scientific Reports, 2019, 9, 15506.	1.6	10
16	Afadin cooperates with Claudin-2 to promote breast cancer metastasis. Genes and Development, 2019, 33, 180-193.	2.7	45
17	Extracellular lipid loading augments hypoxic paracrine signaling and promotes glioma angiogenesis and macrophage infiltration. Journal of Experimental and Clinical Cancer Research, 2019, 38, 241.	3.5	21
18	Crizotinib and PARP inhibitors act synergistically by triggering apoptosis in high-grade serous ovarian cancer. Oncotarget, 2019, 10, 6981-6996.	0.8	9

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19	Characterizing steroid hormone receptor chromatin binding landscapes in male and female breast cancer. Nature Communications, 2018, 9, 482.	5.8	50
20	Characterization of male breast cancer: results of the EORTC 10085/TBCRC/BIG/NABCG International Male Breast Cancer Program. Annals of Oncology, 2018, 29, 405-417.	0.6	246
21	Assessment of early response biomarkers in relation to longâ€term survival in patients with HER2â€negative breast cancer receiving neoadjuvant chemotherapy plus bevacizumab: Results from the Phase II PROMIX trial. International Journal of Cancer, 2018, 142, 618-628.	2.3	27
22	Claudin-4 Expression is Associated With Survival in Ovarian Cancer But Not With Chemotherapy Response. International Journal of Gynecological Pathology, 2018, 37, 101-109.	0.9	31
23	Ghrelin expression is associated with a favorable outcome in male breast cancer. Scientific Reports, 2018, 8, 13586.	1.6	8
24	Dynamic evaluation of the immune infiltrate and immune function genes as predictive markers for neoadjuvant chemotherapy in hormone receptor positive, HER2 negative breast cancer. OncoImmunology, 2018, 7, e1466017.	2.1	18
25	A Case-Matched Gender Comparison Transcriptomic Screen Identifies eIF4E and eIF5 as Potential Prognostic Markers in Male Breast Cancer. Clinical Cancer Research, 2017, 23, 2575-2583.	3.2	16
26	An HIF-1Î±/VEGF-A Axis in Cytotoxic T Cells Regulates Tumor Progression. Cancer Cell, 2017, 32, 669-683.e5.	7.7	352
27	Involvement of Chromatin Remodeling Genes and the Rho GTPases RhoB and CDC42 in Ovarian Clear Cell Carcinoma. Frontiers in Oncology, 2017, 7, 109.	1.3	20
28	Gene expression modules in primary breast cancers as risk factors for organotropic patterns of first metastatic spread: a case control study. Breast Cancer Research, 2017, 19, 113.	2.2	5
29	Transcriptional Profiling of Breast Cancer Metastases Identifies Liver Metastasisâ€“Selective Genes Associated with Adverse Outcome in Luminal A Primary Breast Cancer. Clinical Cancer Research, 2016, 22, 146-157.	3.2	38
30	Genome methylation patterns in male breast cancer â€“ Identification of an epitype with hypermethylation of polycomb target genes. Molecular Oncology, 2015, 9, 1565-1579.	2.1	14
31	Statin-induced anti-proliferative effects via cyclin D1 and p27 in a window-of-opportunity breast cancer trial. Journal of Translational Medicine, 2015, 13, 133.	1.8	53
32	Sex Steroid Hormone Receptor Expression Affects Ovarian Cancer Survival. Translational Oncology, 2015, 8, 424-433.	1.7	27
33	Molecular subtype and tumor characteristics of breast cancer metastases as assessed by gene expression significantly influence patient post-relapse survival. Annals of Oncology, 2015, 26, 81-88.	0.6	75
34	Global Transcriptional Changes Following Statin Treatment in Breast Cancer. Clinical Cancer Research, 2015, 21, 3402-3411.	3.2	44
35	Clinical and molecular complexity of breast cancer metastases. Seminars in Cancer Biology, 2015, 35, 85-95.	4.3	118
36	Abstract S6-05: Characterization of male breast cancer: First results of the EORTC10085/TBCRC/BIG/NABCG International Male BC Program. , 2015, , .		20

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37	Contrasting breast cancer molecular subtypes across serial tumor progression stages: biological and prognostic implications. Oncotarget, 2015, 6, 33306-33318.	0.8	31
38	Nuclear HIF1A expression is strongly prognostic in sporadic but not familial male breast cancer. Modern Pathology, 2014, 27, 1223-1230.	2.9	23
39	Claudinâ€2 is an independent negative prognostic factor in breast cancer and specifically predicts early liver recurrences. Molecular Oncology, 2014, 8, 119-128.	2.1	61
40	Molecular profiling of male breast cancer â€" Lost in translation?. International Journal of Biochemistry and Cell Biology, 2014, 53, 526-535.	1.2	34
41	Molecular Subtyping of Serous Ovarian Tumors Reveals Multiple Connections to Intrinsic Breast Cancer Subtypes. PLoS ONE, 2014, 9, e107643.	1.1	17
42	The combination of Ki67, histological grade and estrogen receptor status identifies a low-risk group among 1,854 chemo-naÃ¯ve women with N0/N1 primary breast cancer. SpringerPlus, 2013, 2, 111.	1.2	12
43	High proliferation is associated with inferior outcome in male breast cancer patients. Modern Pathology, 2013, 26, 87-94.	2.9	27
44	Requirement of Apoptotic Protease-Activating Factor-1 for Bortezomib-Induced Apoptosis but Not for Fas-Mediated Apoptosis in Human Leukemic Cells. Molecular Pharmacology, 2013, 83, 245-255.	1.0	7
45	Molecular subtyping of male breast cancer using alternative definitions and its prognostic impact. Acta OncolÃ³gica, 2013, 52, 102-109.	0.8	45
46	The Landscape of Candidate Driver Genes Differs between Male and Female Breast Cancer. PLoS ONE, 2013, 8, e78299.	1.1	46
47	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	9.4	99
48	Co-targeting of the PI3K pathway improves the response of BRCA1 deficient breast cancer cells to PARP1 inhibition. Cancer Letters, 2012, 319, 232-241.	3.2	45
49	Gene expression profiling of primary male breast cancers reveals two unique subgroups and identifies N-acetyltransferase-1 (NAT1) as a novel prognostic biomarker. Breast Cancer Research, 2012, 14, R31.	2.2	100
50	Increased gene copy number of <i>KIT</i> and <i>VEGFR2</i> at 4q12 in primary breast cancer is related to an aggressive phenotype and impaired prognosis. Genes Chromosomes and Cancer, 2012, 51, 375-383.	1.5	31
51	Combination of the proliferation marker cyclin A, histological grade, and estrogen receptor status in a new variable with high prognostic impact in breast cancer. Breast Cancer Research and Treatment, 2012, 131, 33-40.	1.1	13
52	Similarities and differences in the characteristics and primary treatment of breast cancer in men and women â€" a population based study (Sweden). Acta OncolÃ³gica, 2011, 50, 1083-1088.	0.8	34
53	Laser capture microdissection (LCM) and whole genome amplification (WGA) of DNA from normal breast tissue --- optimization for genome wide array analyses. BMC Research Notes, 2011, 4, 69.	0.6	28
54	High-resolution genomic profiling of male breast cancer reveals differences hidden behind the similarities with female breast cancer. Breast Cancer Research and Treatment, 2011, 129, 747-760.	1.1	70

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55	Numb protein expression correlates with a basal-like phenotype and cancer stem cell markers in primary breast cancer. Breast Cancer Research and Treatment, 2010, 122, 315-324.	1.1	70
56	Genomic alterations in histopathologically normal breast tissue from <i>BRCA1</i> mutation carriers may be caused by BRCA1 haploinsufficiency. Genes Chromosomes and Cancer, 2010, 49, 78-90.	1.5	26
57	Tiling array-CGH for the assessment of genomic similarities among synchronous unilateral and bilateral invasive breast cancer tumor pairs. BMC Clinical Pathology, 2008, 8, 6.	1.8	28
58	RNA quality in frozen breast cancer samples and the influence on gene expression analysis - a comparison of three evaluation methods using microcapillary electrophoresis traces. BMC Molecular Biology, 2007, 8, 38.	3.0	89
59	High-throughput genomic technology in research and clinical management of breast cancer. Molecular signatures of progression from benign epithelium to metastatic breast cancer. Breast Cancer Research, 2006, 8, 213.	2.2	13
60	Microarrays in breast cancer research and clinical practice â€“ the future lies ahead. Endocrine-Related Cancer, 2006, 13, 1017-1031.	1.6	22
61	ERK1/2 inhibition increases antiestrogen treatment efficacy by interfering with hypoxia-induced downregulation of ERÎ±: a combination therapy potentially targeting hypoxic and dormant tumor cells. Oncogene, 2005, 24, 6835-6841.	2.6	45
62	Cyclin E Overexpression Obstructs Infiltrative Behavior in Breast Cancer: A Novel Role Reflected in the Growth Pattern of Medullary Breast Cancers. Cancer Research, 2005, 65, 9727-9734.	0.4	25
63	Characterization of a Novel Breast Carcinoma Xenograft and Cell Line Derived from a BRCA1 Germ-Line Mutation Carrier. Laboratory Investigation, 2003, 83, 387-396.	1.7	43
64	Molecular classification of familial non-BRCA1/BRCA2 breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2532-2537.	3.3	182
65	Gene Expression Profiling of Hereditary and Sporadic Ovarian Cancers Reveals Unique BRCA1 and BRCA2 Signatures. Journal of the National Cancer Institute, 2002, 94, 960-961.	3.0	19
66	Gene-Expression Profiles in Hereditary Breast Cancer. New England Journal of Medicine, 2001, 344, 539-548.	13.9	1,669
67	DNA methylation patterns in hereditary human cancers mimic sporadic tumorigenesis. Human Molecular Genetics, 2001, 10, 3001-3007.	1.4	374