Jaana M Hartikainen

List of Publications by Year
in descending order

90 papers	11,597 citations	100601 38 h-index	49824 91 g-index
93 all docs	93 docs citations	93 times ranked	15812 citing authors

#	Article	IF	Citations
1	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
2	Circulating Cell-Free DNA Reflects the Clonal Evolution of Breast Cancer Tumors. Cancers, 2022, 14, 1332.	1.7	6
3	MCF10CA Breast Cancer Cells Utilize Hyaluronan-Coated EV-Rich Trails for Coordinated Migration. Frontiers in Oncology, 2022, 12, 869417.	1.3	6
4	M1 Macrophages Induce Protumor Inflammation in Melanoma Cells through TNFRâ€“NF-ÎºB Signaling. Journal of Investigative Dermatology, 2022, 142, 3041-3051.e10.	0.3	7
5	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
6	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	1.7	4
7	The debatable presence of PIWIâ€interacting RNAs in invasive breast cancer. Cancer Medicine, 2021, 10, 3593-3603.	1.3	10
8	Chromatin-directed proteomics-identified network of endogenous androgen receptor in prostate cancer cells. Oncogene, 2021, 40, 4567-4579.	2.6	20
9	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	2.2	7
10	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
11	Clinical and epidemiological observations on individual radiation sensitivity and susceptibility. International Journal of Radiation Biology, 2020, 96, 324-339.	1.0	35
12	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
13	MicroRNAs Associated With Biological Pathways of Left- and Right-sided Colorectal Cancer. Anticancer Research, 2020, 40, 3713-3722.	0.5	11
14	High mutation burden of circulating cellâ€free DNA in earlyâ€stage breast cancer patients is associated with a poor relapseâ€free survival. Cancer Medicine, 2020, 9, 5922-5931.	1.3	9
15	Predicting breast cancer risk using interacting genetic and demographic factors and machine learning. Scientific Reports, 2020, 10, 11044.	1.6	36
16	Nrf2 and SQSTM1/p62 jointly contribute to mesenchymal transition and invasion in glioblastoma. Oncogene, 2019, 38, 7473-7490.	2.6	61
17	CD44s Assembles Hyaluronan Coat on Filopodia and Extracellular Vesicles and Induces Tumorigenicity of MKN74 Gastric Carcinoma Cells. Cells, 2019, 8, 276.	1.8	26
18	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52

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19	Rare missense mutations in RECQL and POLG associate with inherited predisposition to breast cancer. International Journal of Cancer, 2018, 142, 2286-2292.	2.3	15
20	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	1.6	51
21	Machine learning identifies interacting genetic variants contributing to breast cancer risk: A case study in Finnish cases and controls. Scientific Reports, 2018, 8, 13149.	1.6	58
22	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. Scientific Reports, 2017, 7, 681.	1.6	20
23	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
24	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
25	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
26	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
27	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	2.2	31
28	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154.	1.8	8
29	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
30	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
31	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	2.3	34
32	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	1.1	6
33	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
34	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
35	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
36	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76

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37	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14
38	KEAP1 Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. Clinical Cancer Research, 2015, 21, 1591-1601.	3.2	37
39	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
40	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
41	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. Breast Cancer Research, 2015, 17, 18.	2.2	20
42	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	2.3	51
43	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
44	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
45	Finnish Fanconi anemia mutations and hereditary predisposition to breast and prostate cancer. Clinical Genetics, 2015, 88, 68-73.	1.0	17
46	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
47	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
48	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
49	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
50	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	2.2	97
51	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	1.4	32
52	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	0.6	28
53	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. British Journal of Cancer, 2014, 110, 1088-1100.	2.9	21
54	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105

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55	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
56	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
57	Type II Transmembrane Serine Protease Gene Variants Associate with Breast Cancer. PLoS ONE, 2014, 9, e102519.	1.1	23
58	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
59	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
60	Matriptaseâ€2 gene (TMPRSS6) variants associate with breast cancer survival, and reduced expression is related to tripleâ€negative breast cancer. International Journal of Cancer, 2013, 133, 2334-2340.	2.3	28
61	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
62	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
63	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
64	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	1.5	136
65	The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104.	1.1	8
66	Breast Cancerâ€“Associated Abraxas Mutation Disrupts Nuclear Localization and DNA Damage Response Functions. Science Translational Medicine, 2012, 4, 122ra23.	5.8	54
67	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.4	100
68	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80
69	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
70	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	1.1	17
71	Genetic Polymorphisms and Protein Expression of NRF2 and Sulfiredoxin Predict Survival Outcomes in Breast Cancer. Cancer Research, 2012, 72, 5537-5546.	0.4	73
72	Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. PLoS ONE, 2012, 7, e35706.	1.1	11

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73	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
74	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	1.1	51
75	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€“Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	1.1	27
76	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
77	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	1.4	152
78	Further evidence for the contribution of the RAD51C gene in hereditary breast and ovarian cancer susceptibility. Breast Cancer Research and Treatment, 2011, 130, 1003-1010.	1.1	54
79	Evaluation of variation in the phosphoinositide-3-kinase catalytic subunit alpha oncogene and breast cancer risk. British Journal of Cancer, 2011, 105, 1934-1939.	2.9	4
80	ST14Gene Variant and Decreased Matriptase Protein Expression Predict Poor Breast Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2133-2142.	1.1	29
81	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
82	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
83	Screening for BRCA1 and BRCA2 mutations in Eastern Finnish breast/ovarian cancer families. Clinical Genetics, 2007, 72, 311-320.	1.0	13
84	A BRCA2 mutation, 4088insA, in a Finnish breast and ovarian cancer family associated with favourable clinical course. Anticancer Research, 2007, 27, 4295-300.	0.5	1
85	Refinement of the 22q12-q13 Breast Cancerâ€“Associated Region: Evidence of TMPRSS6 as a Candidate Gene in an Eastern Finnish Population. Clinical Cancer Research, 2006, 12, 1454-1462.	3.2	43
86	An autosome-wide scan for linkage disequilibrium-based association in sporadic breast cancer cases in eastern Finland: three candidate regions found. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 75-80.	1.1	25
87	A Finnish BRCA1 exon 12 4216-2nt A to G splice acceptor site mutation causes aberrant splicing and frameshift, leading to protein truncation. , 2000, 15, 120-120.		7
88	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. European Journal of Human Genetics, 2000, 8, 757-763.	1.4	75
89	Late Infantile Neuronal Ceroid Lipofuscinosis Is Due to Splicing Mutations in the CLN2 Gene. Molecular Genetics and Metabolism, 1999, 67, 162-168.	0.5	27
90	Two common mutations in the CLN2 gene underlie late infantile neuronal ceroid lipoluscinosis. Clinical Genetics, 1998, 54, 234-238.	1.0	32