Arto Mannermaa

List of Publications by Year in descending order

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108	12,112	76031	32181
papers	citations	42 h-index	105 g-index

108	108	108	17526
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
3	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
5	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
6	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
7	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
8	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
9	Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
10	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
11	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
12	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	0.8	270
13	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
14	NAD(P)H:quinone oxidoreductase 1 NQO1*2 genotype (P187S) is a strong prognostic and predictive factor in breast cancer. Nature Genetics, 2008, 40, 844-853.	9.4	181
15	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
16	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. Nature Genetics, 2000, 26, 362-364.	9.4	152
17	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
18	Age- and Tumor Subtypeâ€"Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152

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19	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	1.3	145
20	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
21	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
22	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
23	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
24	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
25	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
26	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80
27	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
28	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
29	Genetic Polymorphisms and Protein Expression of NRF2 and Sulfiredoxin Predict Survival Outcomes in Breast Cancer. Cancer Research, 2012, 72, 5537-5546.	0.4	73
30	Feasibility and acceptance of screening for fragile X mutations in low-risk pregnancies. European Journal of Human Genetics, 1999, 7, 212-216.	1.4	70
31	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
32	Nrf2 and SQSTM1/p62 jointly contribute to mesenchymal transition and invasion in glioblastoma. Oncogene, 2019, 38, 7473-7490.	2.6	61
33	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	2.6	59
34	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
35	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
36	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56

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37	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	2.2	56
38	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
39	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
40	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	2.3	51
41	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
42	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
43	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptorâ€“Negative Breast Cancer Survival. Journal of the National Cancer Institute, 2010, 102, 650-662.	3.0	48
44	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
45	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
46	Severity of Cardiovascular Disease, Apolipoprotein E Genotype, and Brain Pathology in Aging and Dementia. Annals of the New York Academy of Sciences, 2000, 903, 244-251.	1.8	39
47	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
48	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	2.2	39
49	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
50	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
51	KEAP1 Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. Clinical Cancer Research, 2015, 21, 1591-1601.	3.2	37
52	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	2.6	37
53	Overexpression of MicroRNA-200c Predicts Poor Outcome in Patients with PR-Negative Breast Cancer. PLoS ONE, 2014, 9, e109508.	1.1	37
54	Predicting breast cancer risk using interacting genetic and demographic factors and machine learning. Scientific Reports, 2020, 10, 11044.	1.6	36

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55	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
56	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	1.4	33
57	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
58	ST14Gene Variant and Decreased Matriptase Protein Expression Predict Poor Breast Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2133-2142.	1.1	29
59	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
60	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
61	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
62	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
63	Low expression levels of hepsin and TMPRSS3 are associated with poor breast cancer survival. BMC Cancer, 2015, 15, 431.	1.1	26
64	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. Breast Cancer Research and Treatment, 2017, 166, 217-226.	1.1	26
65	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
66	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
67	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2015, 1, 18-32.	1.3	24
68	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	1.1	24
69	Deletion in the FMR1 gene in a fragile-X male. , 1996, 64, 293-295.		23
70	Type II Transmembrane Serine Protease Gene Variants Associate with Breast Cancer. PLoS ONE, 2014, 9, e102519.	1.1	23
71	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	0.8	21
72	Multi-level dilated residual network for biomedical image segmentation. Scientific Reports, 2021, 11, 14105.	1.6	21

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73	SNP-SNP interaction analysis of NF-Î³B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
74	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
75	Highâ€throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	1.3	19
76	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	2.3	19
77	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. Breast Cancer Research and Treatment, 2013, 138, 529-542.	1.1	18
78	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	1.1	18
79	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
80	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
81	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
82	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
83	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
84	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
85	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	3.0	14
86	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	2.3	13
87	Antenatal genetic screening for congenital nephrosis. Prenatal Diagnosis, 2001, 21, 81-84.	1.1	12
88	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
89	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
90	MicroRNAs Associated With Biological Pathways of Left- and Right-sided Colorectal Cancer. Anticancer Research, 2020, 40, 3713-3722.	0.5	11

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91	Peritumor to tumor apparent diffusion coefficient ratio is associated with biologically more aggressive breast cancer features and correlates with the prognostication tools. PLoS ONE, 2020, 15, e0235278.	1.1	11
92	GASC1 expression in lung carcinoma is associated with smoking and prognosis of squamous cell carcinoma. Histology and Histopathology, 2014, 29, 797-804.	0.5	11
93	XRCC1 rs25487 polymorphism predicts the survival of patients after postoperative radiotherapy and adjuvant chemotherapy for breast cancer. Anticancer Research, 2014, 34, 3031-7.	0.5	11
94	The debatable presence of PIWIâ€interacting RNAs in invasive breast cancer. Cancer Medicine, 2021, 10, 3593-3603.	1.3	10
95	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
96	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
97	Cellular hyaluronan is associated with a poor prognosis in renal cell carcinoma. Urologic Oncology: Seminars and Original Investigations, 2020, 38, 686.e11-686.e22.	0.8	8
98	High Cell-Free DNA Integrity Is Associated with Poor Breast Cancer Survival. Cancers, 2021, 13, 4679.	1.7	8
99	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	2.9	7
100	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
101	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
102	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	2.6	6
103	Circulating Cell-Free DNA Reflects the Clonal Evolution of Breast Cancer Tumors. Cancers, 2022, 14, 1332.	1.7	6
104	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	0.7	6
105	SIP1 predicts progression and poor prognosis in pharyngeal squamous cell carcinoma. Histology and Histopathology, 2015, 30, 569-79.	0.5	5
106	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
107	High regional mortality due to malignant melanoma in Eastern Finland may be explained by the increase in aggressive melanoma types. BMC Cancer, 2021, 21, 1155.	1.1	3
108	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2