

Robert Winqvist

List of Publications by Year in descending order

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Version: 2024-02-01

165
papers

16,277
citations

26630
56
h-index

18647
119
g-index

173
all docs

173
docs citations

173
times ranked

19492
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
3	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . <i>New England Journal of Medicine</i> , 2014, 371, 497-506.	27.0	745
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
5	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. <i>Journal of the National Cancer Institute</i> , 2011, 103, 250-263.	6.3	596
6	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
7	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
8	The clinical value of somatic TP53 gene mutations in 1,794 patients with breast cancer.. <i>Clinical Cancer Research</i> , 2006, 12, 1157-1167.	7.0	495
9	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
10	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	428
11	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
12	A recurrent mutation in PALB2 in Finnish cancer families. <i>Nature</i> , 2007, 446, 316-319.	27.8	402
13	Genome-wide association studies identify four ER negative“specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
14	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
15	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor“negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	21.4	309
16	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
17	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor“negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
18	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	1.6	270

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19	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
20	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	21.4	256
21	Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. <i>Clinical Cancer Research</i> , 2004, 10, 2473-2481.	7.0	224
22	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201
23	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	21.4	184
24	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. <i>Carcinogenesis</i> , 2005, 27, 1593-1599.	2.8	179
25	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174
26	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
27	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
28	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
29	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	8.4	118
30	Unstable DNA may be responsible for the incomplete penetrance of the myotonic dystrophy phenotype. <i>Human Molecular Genetics</i> , 1992, 1, 467-473.	2.9	115
31	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6240-6249.	0.9	109
32	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	3.5	105
33	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
34	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.9	100
35	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
36	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98

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37	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	5.0	97
38	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
39	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
40	Penetrance Analysis of the <i>PALB2</i> c.1592delT Founder Mutation. <i>Clinical Cancer Research</i> , 2008, 14, 4667-4671.	7.0	90
41	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
42	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
43	ACUTE MYELOGENOUS LEUKAEMIA WITH C-MYC AMPLIFICATION AND DOUBLE MINUTE CHROMOSOMES. <i>Lancet</i> , The, 1985, 326, 1035-1039.	13.7	84
44	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	1.9	81
45	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	2.9	80
46	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
47	Evidence of Founder Mutations in Finnish BRCA1 and BRCA2 Families. <i>American Journal of Human Genetics</i> , 1998, 62, 1544-1548.	6.2	77
48	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	6.3	77
49	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
50	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. <i>European Journal of Human Genetics</i> , 2000, 8, 757-763.	2.8	75
51	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.9	75
52	Analysis of 11q21-24 loss of heterozygosity candidate target genes in breast cancer: Indications of TSLC1 promoter hypermethylation. <i>Genes Chromosomes and Cancer</i> , 2002, 34, 384-389.	2.8	74
53	myc oncogenes: activation and amplification. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1987, 907, 1-32.	7.4	73
54	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	2.9	71

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55	A common region of loss of heterozygosity in Wilms' tumor and embryonal rhabdomyosarcoma distal to the D11S988 locus on chromosome 11p15.5. Human Genetics, 1996, 97, 163-170.	3.8	67
56	Heterozygous mutations in PALB2 cause DNA replication and damage response defects. Nature Communications, 2013, 4, 2578.	12.8	60
57	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.	6.2	59
58	Machine learning identifies interacting genetic variants contributing to breast cancer risk: A case study in Finnish cases and controls. Scientific Reports, 2018, 8, 13149.	3.3	58
59	Human familial and sporadic breast cancer: analysis of the coding regions of the 17 β -hydroxysteroid dehydrogenase 2 gene (EDH17B2) using a single-strand conformation polymorphism assay. Human Genetics, 1994, 93, 319-324.	3.8	56
60	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
61	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.	2.5	54
62	Breast Cancerâ€Associated <i>Abraxas</i> Mutation Disrupts Nuclear Localization and DNA Damage Response Functions. Science Translational Medicine, 2012, 4, 122ra23.	12.4	54
63	Loss of heterozygosity at chromosomes 3, 6, 8, 11, 16, and 17 in ovarian cancer.. Cancer Genetics and Cytogenetics, 2000, 122, 49-54.	1.0	53
64	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
65	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
66	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
67	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.	2.5	51
68	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
69	Cell lineage involvement of recurrent chromosomal abnormalities in hematologic neoplasms. Genes Chromosomes and Cancer, 1994, 10, 95-102.	2.8	48
70	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
71	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
72	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43

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73	Exclusion of large deletions and other rearrangements in BRCA1 and BRCA2 in Finnish breast and ovarian cancer families. <i>Cancer Genetics and Cytogenetics</i> , 2001, 129, 120-123.	1.0	42
74	Association of common ATM polymorphism with bilateral breast cancer. <i>International Journal of Cancer</i> , 2005, 116, 69-72.	5.1	42
75	Analysis of large deletions in BRCA1, BRCA2 and PALB2 genes in Finnish breast and ovarian cancer families. <i>BMC Cancer</i> , 2008, 8, 146.	2.6	42
76	Inactivation of Palb2 gene leads to mesoderm differentiation defect and early embryonic lethality in mice. <i>Human Molecular Genetics</i> , 2010, 19, 3021-3029.	2.9	41
77	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
78	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	3.5	39
79	Patient survival and tumor characteristics associated with CHEK2:p.1157T → C findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	5.0	39
80	Homologous recombination DNA repair defects in PALB2-associated breast cancers. <i>Npj Breast Cancer</i> , 2019, 5, 23.	5.2	39
81	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
82	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	38
83	Chromosome 11q22.3-q25 LOH in Ovarian Cancer: Association with a More Aggressive Disease Course and Involved Subregions. <i>Gynecologic Oncology</i> , 1998, 71, 299-304.	1.4	37
84	Identification of a common polymorphism in the TopBP1 gene associated with hereditary susceptibility to breast and ovarian cancer. <i>European Journal of Cancer</i> , 2006, 42, 2647-2652.	2.8	37
85	KEAP1 Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. <i>Clinical Cancer Research</i> , 2015, 21, 1591-1601.	7.0	37
86	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	6.2	37
87	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132.	2.5	35
88	A Point Mutation in the Putative TATA Box, Detected in Nondiseased Individuals and Patients with Hereditary Breast Cancer, Decreases Promoter Activity of the 17β-Hydroxysteroid Dehydrogenase Type 1 Gene 2 (EDH17B2) in Vitro. <i>Genomics</i> , 1994, 23, 250-252.	2.9	34
89	Loss of heterozygosity at 11q23.1 and survival in breast cancer: Results of a large European study. <i>Genes Chromosomes and Cancer</i> , 1999, 25, 212-221.	2.8	34
90	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33

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91	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.	2.9	32
92	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
93	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
94	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.	5.0	31
95	Mutation analysis of the ATR gene in breast and ovarian cancer families. Breast Cancer Research, 2005, 7, R495-501.	5.0	30
96	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
97	Rare Copy Number Variants Observed in Hereditary Breast Cancer Cases Disrupt Genes in Estrogen Signaling and TP53 Tumor Suppression Network. PLoS Genetics, 2012, 8, e1002734.	3.5	28
98	Genome-wide scanning for linkage in Finnish breast cancer families. European Journal of Human Genetics, 2004, 12, 98-104.	2.8	27
99	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor-Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
100	Increasing oxidative damage and loss of mismatch repair enzymes during breast carcinogenesis. European Journal of Cancer, 2006, 42, 2653-2659.	2.8	26
101	Somatic mutation analysis of MYH11 in breast and prostate cancer. BMC Cancer, 2008, 8, 263.	2.6	26
102	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
103	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.	2.5	26
104	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
105	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.	2.5	24
106	The gene for 17beta-hydroxysteroid dehydrogenase maps to human chromosome 17, bands q12-q21, and shows an RFLP with Scal. Human Genetics, 1990, 85, 473-6.	3.8	22
107	Screening for large genomic rearrangements in the FANCA gene reveals extensive deletion in a Finnish breast cancer family. Cancer Letters, 2011, 302, 113-118.	7.2	22
108	Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. PLoS Genetics, 2016, 12, e1005816.	3.5	22

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109	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. <i>Carcinogenesis</i> , 2006, 28, 1040-1045.	2.8	21
110	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016, 27, 679-693.	1.8	21
111	Characterization and expression of the human WNT4; lack of associated germline mutations in high- to moderate-risk breast and ovarian cancer. <i>Cancer Letters</i> , 2004, 213, 83-90.	7.2	20
112	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	1.8	20
113	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. <i>Scientific Reports</i> , 2017, 7, 681.	3.3	20
114	Germ-Line TP53 Mutations in Finnish Cancer Families Exhibiting Features of the Li-Fraumeni Syndrome and Negative for BRCA1 and BRCA2. <i>Cancer Genetics and Cytogenetics</i> , 1999, 112, 9-14.	1.0	19
115	Long-term observational follow-up study of breast cancer diagnosed in women \geq 40 years old. <i>Breast</i> , 2010, 19, 456-461.	2.2	19
116	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	3.3	19
117	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	2.5	19
118	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642.	2.5	19
119	Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. <i>Breast Cancer Research</i> , 2010, 12, R50.	5.0	18
120	Recurrent CYP2C19 deletion allele is associated with triple-negative breast cancer. <i>BMC Cancer</i> , 2014, 14, 902.	2.6	18
121	Mapping of amplified c-myc oncogene, sister chromatid exchanges, and karyotypic analysis of the COLO 205 colon carcinoma cell line. <i>Cancer Genetics and Cytogenetics</i> , 1985, 18, 251-264.	1.0	17
122	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1783-1791.	2.5	17
123	Molecular cloning, expression and chromosomal localization of a human gene encoding a 33 kDa putative metallopeptidase (PRSM1). <i>Gene</i> , 1996, 174, 135-143.	2.2	16
124	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	12.8	16
125	Improved carrier testing for multiple endocrine neoplasia, type 1, using new microsatellite-type DNA markers. <i>Human Genetics</i> , 1995, 96, 449-53.	3.8	15
126	Screening for RAD51 and BRCA2 BRC repeat mutations in breast and ovarian cancer families. <i>Cancer Letters</i> , 2006, 236, 142-147.	7.2	15

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127	Germline alterations in the CLSPN gene in breast cancer families. Cancer Letters, 2008, 261, 93-97.	7.2	15
128	Rare missense mutations in <i>RECQL</i> and <i>POLG</i> associate with inherited predisposition to breast cancer. International Journal of Cancer, 2018, 142, 2286-2292.	5.1	15
129	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
130	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
131	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.	2.8	14
132	Screening for large genomic rearrangements of the BRIP1 and CHK1 genes in Finnish breast cancer families. Familial Cancer, 2010, 9, 537-540.	1.9	13
133	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	5.1	13
134	Germline alterations in the 53BP1 gene in breast and ovarian cancer families. Cancer Letters, 2007, 245, 337-340.	7.2	12
135	Mutation screening of the MERIT40 gene encoding a novel BRCA1 and RAP80 interacting protein in breast cancer families. Breast Cancer Research and Treatment, 2010, 120, 165-168.	2.5	12
136	Evaluation of the need for routine clinical testing of PALB2 c.1592delT mutation in BRCA negative Northern Finnish breast cancer families. BMC Medical Genetics, 2013, 14, 82.	2.1	12
137	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
138	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
139	Exome sequencing identifies a recurrent variant in SERPINA3 associating with hereditary susceptibility to breast cancer. European Journal of Cancer, 2021, 143, 46-51.	2.8	11
140	Using mouse models to investigate the biological and physiological consequences of defects in the Fanconi anaemia/breast cancer DNA repair signalling pathway. Journal of Pathology, 2011, 224, 301-305.	4.5	10
141	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
142	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
143	Mutation analysis of the AATF gene in breast cancer families. BMC Cancer, 2009, 9, 457.	2.6	8
144	The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104.	2.3	8

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145	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. <i>Human Genetics</i> , 2016, 135, 137-154.	3.8	8
146	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. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7
147	Assessment of Targeted and Non-Targeted Responses in Cells Deficient in ATM Function following Exposure to Low and High Dose X-Rays. <i>PLoS ONE</i> , 2014, 9, e93211.	2.5	7
148	Linkage disequilibrium detected between dystrophin myotonia and APOC2 locus in the Finnish population. <i>Human Genetics</i> , 1990, 85, 541-5.	3.8	6
149	Haplotypes of the I157T CHEK2 germline mutation in ethnically diverse populations. <i>Familial Cancer</i> , 2009, 8, 473-478.	1.9	6
150	Mutation analysis of the gene encoding the PALB2-binding protein MRG15 in BRCA1/2-negative breast cancer families. <i>Journal of Human Genetics</i> , 2010, 55, 842-843.	2.3	6
151	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	6.2	6
152	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
153	A new RFLP with <i>StuI</i> and probe cX55.7 (DXS105) and its usefulness in carrier analysis of fragile X syndrome. <i>Human Genetics</i> , 1988, 80, 193-193.	3.8	5
154	Evaluating the role of <i>NTHL1</i> p.Q90* allele in inherited breast cancer predisposition. <i>Molecular Genetics & Genomic Medicine</i> , 2020, 8, e1493.	1.2	5
155	CYP3A7*1C allele: linking premenopausal oestrogen and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
156	Mutation screening of the RNF8, UBC13 and MMS2 genes in Northern Finnish breast cancer families. <i>BMC Medical Genetics</i> , 2011, 12, 98.	2.1	4
157	BRCA1 mislocalization leads to aberrant DNA damage response in heterozygous ABRAXAS1 mutation carrier cells. <i>Human Molecular Genetics</i> , 2019, 28, 4148-4160.	2.9	4
158	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?. <i>Cancers</i> , 2021, 13, 2370.	3.7	4
159	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	3.3	2
160	Evaluating the role of MLH3 p.Ser1188Ter variant in inherited breast cancer predisposition. <i>Genetics in Medicine</i> , 2020, 22, 663-664.	2.4	2
161	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, 19787.	3.3	2
162	Breast-Cancer Risk in Families With Mutations in PALB2. <i>Obstetrical and Gynecological Survey</i> , 2014, 69, 659-660.	0.4	1

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163	Truncating TINF2 p.Tyr312Ter variant and inherited breast cancer susceptibility. Familial Cancer, 2022, , .	1.9	1
164	Population variation at the polymorphic ApaLI restriction enzyme site in intron 5 of the WT1 gene. Clinical Genetics, 1996, 50, 555-557.	2.0	0
165	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0