

Robert Winqvist

List of Publications by Year in descending order

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Version: 2024-02-01

165
papers

16,277
citations

30551

56
h-index

21239

119
g-index

173
all docs

173
docs citations

173
times ranked

21255
citing authors

#	ARTICLE	IF	CITATIONS
1	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
3	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . <i>New England Journal of Medicine</i> , 2014, 371, 497-506.	13.9	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.	2.6	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.	3.0	596
6	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	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.	9.4	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.	3.2	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.	9.4	493
10	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	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.	9.4	426
12	A recurrent mutation in PALB2 in Finnish cancer families. <i>Nature</i> , 2007, 446, 316-319.	13.7	402
13	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	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.	9.4	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.	9.4	309
16	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	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.	9.4	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.	0.8	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.	9.4	265
20	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
21	Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. <i>Clinical Cancer Research</i> , 2004, 10, 2473-2481.	3.2	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.	2.6	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.	9.4	184
24	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. <i>Carcinogenesis</i> , 2005, 27, 1593-1599.	1.3	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.	1.5	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.	7.7	157
27	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
28	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	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.	3.9	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.	1.4	115
31	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6240-6249.	0.4	109
32	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	1.5	105
33	Evidence that breast cancer risk at the 2q35 locus is mediated through <i>IGFBP5</i> regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
34	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	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.	3.0	99
36	Fine-Scale Mapping of the <i>FGFR2</i> Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind <i>FOXA1</i> and <i>E2F1</i> . <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	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.	2.2	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.	1.5	94
39	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
40	Penetrance Analysis of the <i>PALB2</i> c.1592delT Founder Mutation. <i>Clinical Cancer Research</i> , 2008, 14, 4667-4671.	3.2	90
41	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
42	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
43	ACUTE MYELOGENOUS LEUKAEMIA WITH C-MYC AMPLIFICATION AND DOUBLE MINUTE CHROMOSOMES. <i>Lancet</i> , The, 1985, 326, 1035-1039.	6.3	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.	0.9	81
45	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	1.4	80
46	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
47	Evidence of Founder Mutations in Finnish BRCA1 and BRCA2 Families. <i>American Journal of Human Genetics</i> , 1998, 62, 1544-1548.	2.6	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.	3.0	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.	2.6	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.	1.4	75
51	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	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.	1.5	74
53	<i>myc</i> oncogenes: activation and amplification. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 1987, 907, 1-32.	3.3	73
54	Associations of common variants at 1p11.2 and 14q24.1 (<i>RAD51L1</i>) 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.	1.4	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. <i>Human Genetics</i> , 1996, 97, 163-170.	1.8	67
56	Heterozygous mutations in PALB2 cause DNA replication and damage response defects. <i>Nature Communications</i> , 2013, 4, 2578.	5.8	60
57	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	2.6	59
58	Machine learning identifies interacting genetic variants contributing to breast cancer risk: A case study in Finnish cases and controls. <i>Scientific Reports</i> , 2018, 8, 13149.	1.6	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. <i>Human Genetics</i> , 1994, 93, 319-324.	1.8	56
60	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
61	Further evidence for the contribution of the RAD51C gene in hereditary breast and ovarian cancer susceptibility. <i>Breast Cancer Research and Treatment</i> , 2011, 130, 1003-1010.	1.1	54
62	Breast Cancer-associated <i>Abraxas</i> Mutation Disrupts Nuclear Localization and DNA Damage Response Functions. <i>Science Translational Medicine</i> , 2012, 4, 122ra23.	5.8	54
63	Loss of heterozygosity at chromosomes 3, 6, 8, 11, 16, and 17 in ovarian cancer. <i>Cancer Genetics and Cytogenetics</i> , 2000, 122, 49-54.	1.0	53
64	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	1.4	53
65	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
66	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	2.3	51
67	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012, 7, e42380.	1.1	51
68	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
69	Cell lineage involvement of recurrent chromosomal abnormalities in hematologic neoplasms. <i>Genes Chromosomes and Cancer</i> , 1994, 10, 95-102.	1.5	48
70	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
71	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
72	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	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.	2.3	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.	1.1	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.	1.4	41
77	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
78	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
79	Patient survival and tumor characteristics associated with CHEK2:p.1157T findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
80	Homologous recombination DNA repair defects in PALB2-associated breast cancers. <i>Npj Breast Cancer</i> , 2019, 5, 23.	2.3	39
81	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	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.	1.4	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.	0.6	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.	1.3	37
85	KEAP1 Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. <i>Clinical Cancer Research</i> , 2015, 21, 1591-1601.	3.2	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.	2.6	37
87	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132.	1.1	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 17 β -Hydroxysteroid Dehydrogenase Type 1 Gene 2 (EDH17B2) in Vitro. <i>Genomics</i> , 1994, 23, 250-252.	1.3	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.	1.5	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.	1.4	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. <i>Human Molecular Genetics</i> , 2014, 23, 1934-1946.	1.4	32
92	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
93	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	0.8	31
94	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
95	Mutation analysis of the ATR gene in breast and ovarian cancer families. <i>Breast Cancer Research</i> , 2005, 7, R495-501.	2.2	30
96	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
97	Rare Copy Number Variants Observed in Hereditary Breast Cancer Cases Disrupt Genes in Estrogen Signaling and TP53 Tumor Suppression Network. <i>PLoS Genetics</i> , 2012, 8, e1002734.	1.5	28
98	Genome-wide scanning for linkage in Finnish breast cancer families. <i>European Journal of Human Genetics</i> , 2004, 12, 98-104.	1.4	27
99	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor-Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	1.1	27
100	Increasing oxidative damage and loss of mismatch repair enzymes during breast carcinogenesis. <i>European Journal of Cancer</i> , 2006, 42, 2653-2659.	1.3	26
101	Somatic mutation analysis of MYH11 in breast and prostate cancer. <i>BMC Cancer</i> , 2008, 8, 263.	1.1	26
102	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	2.2	26
103	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. <i>Breast Cancer Research and Treatment</i> , 2017, 166, 217-226.	1.1	26
104	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
105	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	1.1	24
106	The gene for 17beta-hydroxysteroid dehydrogenase maps to human chromosome 17, bands q12-q21, and shows an RFLP with Scal. <i>Human Genetics</i> , 1990, 85, 473-6.	1.8	22
107	Screening for large genomic rearrangements in the FANCA gene reveals extensive deletion in a Finnish breast cancer family. <i>Cancer Letters</i> , 2011, 302, 113-118.	3.2	22
108	Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. <i>PLoS Genetics</i> , 2016, 12, e1005816.	1.5	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.	1.3	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.	0.8	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.	3.2	20
112	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	0.8	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.	1.6	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.	0.9	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.	1.6	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.	1.1	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.	1.1	19
119	Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. <i>Breast Cancer Research</i> , 2010, 12, R50.	2.2	18
120	Recurrent CYP2C19 deletion allele is associated with triple-negative breast cancer. <i>BMC Cancer</i> , 2014, 14, 902.	1.1	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.	1.1	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.	1.0	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.	5.8	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.	1.8	15
126	Screening for RAD51 and BRCA2 BRC repeat mutations in breast and ovarian cancer families. <i>Cancer Letters</i> , 2006, 236, 142-147.	3.2	15

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127	Germline alterations in the CLSPN gene in breast cancer families. <i>Cancer Letters</i> , 2008, 261, 93-97.	3.2	15
128	Rare missense mutations in <i>RECQL</i> and <i>POLG</i> associate with inherited predisposition to breast cancer. <i>International Journal of Cancer</i> , 2018, 142, 2286-2292.	2.3	15
129	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
130	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	2.2	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. <i>Carcinogenesis</i> , 2015, 36, 256-271.	1.3	14
132	Screening for large genomic rearrangements of the BRIP1 and CHK1 genes in Finnish breast cancer families. <i>Familial Cancer</i> , 2010, 9, 537-540.	0.9	13
133	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. <i>International Journal of Cancer</i> , 2016, 139, 2760-2770.	2.3	13
134	Germline alterations in the 53BP1 gene in breast and ovarian cancer families. <i>Cancer Letters</i> , 2007, 245, 337-340.	3.2	12
135	Mutation screening of the MERIT40 gene encoding a novel BRCA1 and RAP80 interacting protein in breast cancer families. <i>Breast Cancer Research and Treatment</i> , 2010, 120, 165-168.	1.1	12
136	Evaluation of the need for routine clinical testing of PALB2 c.1592delT mutation in BRCA negative Northern Finnish breast cancer families. <i>BMC Medical Genetics</i> , 2013, 14, 82.	2.1	12
137	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	1.4	12
138	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
139	Exome sequencing identifies a recurrent variant in SERPINA3 associating with hereditary susceptibility to breast cancer. <i>European Journal of Cancer</i> , 2021, 143, 46-51.	1.3	11
140	Using mouse models to investigate the biological and physiological consequences of defects in the Fanconi anaemia/breast cancer DNA repair signalling pathway. <i>Journal of Pathology</i> , 2011, 224, 301-305.	2.1	10
141	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9
142	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	9
143	Mutation analysis of the AATF gene in breast cancer families. <i>BMC Cancer</i> , 2009, 9, 457.	1.1	8
144	The UGT1A6_19_GG genotype is a breast cancer risk factor. <i>Frontiers in Genetics</i> , 2013, 4, 104.	1.1	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.	1.8	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.	2.2	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.	1.1	7
148	Linkage disequilibrium detected between dystrophin myotonia and APOC2 locus in the Finnish population. <i>Human Genetics</i> , 1990, 85, 541-5.	1.8	6
149	Haplotypes of the 1157T CHEK2 germline mutation in ethnically diverse populations. <i>Familial Cancer</i> , 2009, 8, 473-478.	0.9	6
150	Mutation analysis of the gene encoding the PALB2-binding protein MRC15 in BRCA1/2-negative breast cancer families. <i>Journal of Human Genetics</i> , 2010, 55, 842-843.	1.1	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.	2.6	6
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