

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	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
3	Truncating TINF2 p.Tyr312Ter variant and inherited breast cancer susceptibility. <i>Familial Cancer</i> , 2022, , .	1.9	1
4	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
5	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.	2.8	11
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?. <i>Cancers</i> , 2021, 13, 2370.	3.7	4
7	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
8	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
9	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	6.4	9
10	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
11	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
12	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
13	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
14	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
15	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	6.2	39
16	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
17	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
18	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32

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19	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
20	Homologous recombination DNA repair defects in PALB2-associated breast cancers. Npj Breast Cancer, 2019, 5, 23.	5.2	39
21	BRCA1 mislocalization leads to aberrant DNA damage response in heterozygous ABRAXAS1 mutation carrier cells. Human Molecular Genetics, 2019, 28, 4148-4160.	2.9	4
22	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
23	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
24	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
25	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
26	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
27	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
28	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
29	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
30	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
31	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
32	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
33	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.	3.3	20
34	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
35	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
36	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

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37	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
38	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
39	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
40	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
41	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.	8.4	118
42	Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. PLoS Genetics, 2016, 12, e1005816.	3.5	22
43	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
44	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
45	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
46	Patient survival and tumor characteristics associated with CHEK2:p.I157T – findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
47	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
48	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
49	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.	1.8	21
50	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
51	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.	2.9	33
52	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	5.1	13
53	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
54	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157

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55	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
56	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
57	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
58	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
59	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
60	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.	3.8	8
61	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
62	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
63	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
64	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
65	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
66	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
67	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
68	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.	6.2	76
69	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
70	<i>KEAP1</i> Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. Clinical Cancer Research, 2015, 21, 1591-1601.	7.0	37
71	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
72	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.	6.2	37

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73	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
74	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
75	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
76	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
77	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.	2.9	38
78	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
79	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
80	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
81	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
82	Recurrent CYP2C19 deletion allele is associated with triple-negative breast cancer. BMC Cancer, 2014, 14, 902.	2.6	18
83	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
84	Breast-Cancer Risk in Families With Mutations in PALB2. Obstetrical and Gynecological Survey, 2014, 69, 659-660.	0.4	1
85	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
86	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
87	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	27.0	745
88	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
89	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
90	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

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91	Assessment of Targeted and Non-Targeted Responses in Cells Deficient in ATM Function following Exposure to Low and High Dose X-Rays. PLoS ONE, 2014, 9, e93211.	2.5	7
92	Heterozygous mutations in PALB2 cause DNA replication and damage response defects. Nature Communications, 2013, 4, 2578.	12.8	60
93	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.	6.2	98
94	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.	21.4	493
95	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
96	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.	6.2	201
97	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
98	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
99	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
100	The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104.	2.3	8
101	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
102	Breast Cancer-associated ATRX Mutation Disrupts Nuclear Localization and DNA Damage Response Functions. Science Translational Medicine, 2012, 4, 122ra23.	12.4	54
103	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
104	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
105	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
106	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.	2.5	17
107	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
108	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

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109	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€“Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	2.5	27
110	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
111	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
112	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.	7.2	22
113	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.	2.5	54
114	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
115	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.	4.5	10
116	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 Consortiumâ€“. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	2.9	71
117	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6240-6249.	0.9	109
118	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.	2.5	12
119	Screening for large genomic rearrangements of the BRIP1 and CHK1 genes in Finnish breast cancer families. <i>Familial Cancer</i> , 2010, 9, 537-540.	1.9	13
120	Long-term observational follow-up study of breast cancer diagnosed in women â‰¥40 years old. <i>Breast</i> , 2010, 19, 456-461.	2.2	19
121	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	21.4	309
122	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
123	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
124	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
125	Mutation analysis of the AATF gene in breast cancer families. <i>BMC Cancer</i> , 2009, 9, 457.	2.6	8
126	Haplotypes of the I157T CHEK2 germline mutation in ethnically diverse populations. <i>Familial Cancer</i> , 2009, 8, 473-478.	1.9	6

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127	Analysis of large deletions in BRCA1, BRCA2 and PALB2 genes in Finnish breast and ovarian cancer families. BMC Cancer, 2008, 8, 146.	2.6	42
128	Somatic mutation analysis of MYH11 in breast and prostate cancer. BMC Cancer, 2008, 8, 263.	2.6	26
129	Germline alterations in the CLSPN gene in breast cancer families. Cancer Letters, 2008, 261, 93-97.	7.2	15
130	Penetrance Analysis of the PALB2 c.1592delT Founder Mutation. Clinical Cancer Research, 2008, 14, 4667-4671.	7.0	90
131	Germline alterations in the 53BP1 gene in breast and ovarian cancer families. Cancer Letters, 2007, 245, 337-340.	7.2	12
132	A recurrent mutation in PALB2 in Finnish cancer families. Nature, 2007, 446, 316-319.	27.8	402
133	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. Carcinogenesis, 2006, 28, 1040-1045.	2.8	21
134	Screening for RAD51 and BRCA2 BRC repeat mutations in breast and ovarian cancer families. Cancer Letters, 2006, 236, 142-147.	7.2	15
135	Identification of a common polymorphism in the TopBP1 gene associated with hereditary susceptibility to breast and ovarian cancer. European Journal of Cancer, 2006, 42, 2647-2652.	2.8	37
136	Increasing oxidative damage and loss of mismatch repair enzymes during breast carcinogenesis. European Journal of Cancer, 2006, 42, 2653-2659.	2.8	26
137	The clinical value of somatic TP53 gene mutations in 1,794 patients with breast cancer.. Clinical Cancer Research, 2006, 12, 1157-1167.	7.0	495
138	Association of common ATM polymorphism with bilateral breast cancer. International Journal of Cancer, 2005, 116, 69-72.	5.1	42
139	RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis, 2005, 27, 1593-1599.	2.8	179
140	Mutation analysis of the ATR gene in breast and ovarian cancer families. Breast Cancer Research, 2005, 7, R495-501.	5.0	30
141	Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. Clinical Cancer Research, 2004, 10, 2473-2481.	7.0	224
142	Genome-wide scanning for linkage in Finnish breast cancer families. European Journal of Human Genetics, 2004, 12, 98-104.	2.8	27
143	Characterization and expression of the human WNT4; lack of associated germline mutations in high to moderate risk breast and ovarian cancer. Cancer Letters, 2004, 213, 83-90.	7.2	20
144	Analysis of 11q21-24 loss of heterozygosity candidate target genes in breast cancer: Indications of TSLC1 promoter hypermethylation. Genes Chromosomes and Cancer, 2002, 34, 384-389.	2.8	74

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145	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
146	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
147	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
148	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
149	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
150	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
151	Evidence of Founder Mutations in Finnish BRCA1 and BRCA2 Families. <i>American Journal of Human Genetics</i> , 1998, 62, 1544-1548.	6.2	77
152	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
153	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.	3.8	67
154	Population variation at the polymorphic ApaLI restriction enzyme site in intron 5 of the WT1 gene. <i>Clinical Genetics</i> , 1996, 50, 555-557.	2.0	0
155	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
156	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.	3.8	56
157	Cell lineage involvement of recurrent chromosomal abnormalities in hematologic neoplasms. <i>Genes Chromosomes and Cancer</i> , 1994, 10, 95-102.	2.8	48
158	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.	2.9	34
159	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
160	The gene for 17 β -hydroxysteroid dehydrogenase maps to human chromosome 17, bands q12-q21, and shows an RFLP with Scal. <i>Human Genetics</i> , 1990, 85, 473-6.	3.8	22
161	Linkage disequilibrium detected between dystrophin myotonica and APOC2 locus in the Finnish population. <i>Human Genetics</i> , 1990, 85, 541-5.	3.8	6
162	A new RFLP withStul 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

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163	myc oncogenes: activation and amplification. Biochimica Et Biophysica Acta: Reviews on Cancer, 1987, 907, 1-32.	7.4	73
164	ACUTE MYELOGENOUS LEUKAEMIA WITH C-MYC AMPLIFICATION AND DOUBLE MINUTE CHROMOSOMES. Lancet, The, 1985, 326, 1035-1039.	13.7	84
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