# Robert Winqvist

List of Publications by Year
in descending order

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| 165 | 16,277 | 30551 | 21239 |
|---|---|---|---|
| papers | citations | 56 h-index | 119 g-index |

| 173 | 173 | 173 | 21255 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65. | 2.0 | 6 |
| 2 | Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2. | 2.2 | 15 |
| 3 | Truncating TINF2 p.Tyr312Ter variant and inherited breast cancer susceptibility. Familial Cancer, 2022, , . | 0.9 | 1 |
| 4 | CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854. | 2.9 | 5 |
| 5 | Exome sequencing identifies a recurrent variant in SERPINA3 associating with hereditary susceptibility to breast cancer. European Journal of Cancer, 2021, 143, 46-51. | 1.3 | 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?. Cancers, 2021, 13, 2370. | 1.7 | 4 |
| 7 | Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203. | 2.6 | 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. Breast Cancer Research, 2021, 23, 86. | 2.2 | 7 |
| 9 | Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145. | 2.9 | 9 |
| 10 | Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642. | 1.1 | 19 |
| 11 | Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787. | 1.6 | 2 |
| 12 | Evaluating the role of MLH3 p.Ser1188Ter variant in inherited breast cancer predisposition. Genetics in Medicine, 2020, 22, 663-664. | 1.1 | 2 |
| 13 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73. | 9.4 | 120 |
| 14 | 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 |
| 15 | Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848. | 2.6 | 39 |
| 16 | Evaluating the role of NTHL1 p.Q90* allele in inherited breast cancer predisposition. Molecular Genetics & Genomic Medicine, 2020, 8, e1493. | 0.6 | 5 |
| 17 | Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581. | 9.4 | 265 |
| 18 | Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468. | 0.6 | 32 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312. | 5.8 | 30 |
| 20 | Homologous recombination DNA repair defects in PALB2-associated breast cancers. Npj Breast Cancer, 2019, 5, 23. | 2.3 | 39 |
| 21 | BRCA1 mislocalization leads to aberrant DNA damage response in heterozygous ABRAXAS1 mutation carrier cells. Human Molecular Genetics, 2019, 28, 4148-4160. | 1.4 | 4 |
| 22 | Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431. | 5.8 | 88 |
| 23 | Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741. | 5.8 | 90 |
| 24 | Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657. | 2.9 | 52 |
| 25 | Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34. | 2.6 | 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. | 0.9 | 81 |
| 27 | The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741. | 1.1 | 19 |
| 28 | 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 |
| 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. | 1.6 | 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. | 9.4 | 184 |
| 31 | BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799. | 0.4 | 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. | 9.4 | 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. | 1.6 | 20 |
| 34 | Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94. | 13.7 | 1,099 |
| 35 | Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778. | 9.4 | 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. | 1.1 | 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. | 0.9 | 45 |
| 38 | Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119. | 2.2 | 43 |
| 39 | PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782. | 0.8 | 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. | 0.8 | 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. | 3.9 | 118 |
| 42 | Targeted Next-Generation Sequencing Identifies a Recurrent Mutation in MCPH1 Associating with Hereditary Breast Cancer Susceptibility. PLoS Genetics, 2016, 12, e1005816. | 1.5 | 22 |
| 43 | Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316. | 1.1 | 12 |
| 44 | 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 |
| 45 | PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811. | 1.5 | 174 |
| 46 | 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 |
| 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. | 2.2 | 31 |
| 48 | Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22. | 2.2 | 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. | 0.8 | 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. | 2.6 | 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. | 1.4 | 33 |
| 52 | FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770. | 2.3 | 13 |
| 53 | rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874. | 1.6 | 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. | 7.7 | 157 |

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| 55 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375. | 5.8 | 93 |
| 56 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675. | 5.8 | 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. | 1.6 | 19 |
| 58 | 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 |
| 59 | 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 |
| 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. | 1.8 | 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. | 3.0 | 77 |
| 62 | RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788. | 1.1 | 26 |
| 63 | Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58. | 2.2 | 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. | 0.2 | 0 |
| 65 | SNP-SNP interaction analysis of NF-Î¹B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994. | 0.8 | 20 |
| 66 | Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, . | 3.0 | 428 |
| 67 | Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984. | 1.4 | 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. | 2.6 | 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. | 1.3 | 14 |
| 70 | KEAP1 Genetic Polymorphisms Associate with Breast Cancer Risk and Survival Outcomes. Clinical Cancer Research, 2015, 21, 1591-1601. | 3.2 | 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. | 9.4 | 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. | 2.6 | 37 |

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| 73 | Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, . | 3.0 | 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. | 9.4 | 357 |
| 75 | Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219. | 3.0 | 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. | 1.1 | 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. | 1.4 | 38 |
| 78 | MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973. | 1.1 | 49 |
| 79 | Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285. | 1.5 | 39 |
| 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 | 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 |
| 82 | Recurrent CYP2C19 deletion allele is associated with triple-negative breast cancer. BMC Cancer, 2014, 14, 902. | 1.1 | 18 |
| 83 | Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419. | 2.2 | 97 |
| 84 | Breast-Cancer Risk in Families With Mutations in PALB2. Obstetrical and Gynecological Survey, 2014, 69, 659-660. | 0.2 | 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. | 1.4 | 32 |
| 86 | Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97. | 13.7 | 548 |
| 87 | Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506. | 13.9 | 745 |
| 88 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999. | 5.8 | 105 |
| 89 | Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046. | 1.4 | 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. | 2.2 | 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. | 1.1 | 7 |
| 92 | Heterozygous mutations in PALB2 cause DNA replication and damage response defects. Nature Communications, 2013, 4, 2578. | 5.8 | 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. | 2.6 | 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. | 9.4 | 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. | 2.6 | 201 |
| 97 | Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398. | 9.4 | 374 |
| 98 | Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361. | 9.4 | 960 |
| 99 | Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173. | 1.5 | 105 |
| 100 | The UGT1A6_19_GG genotype is a breast cancer risk factor. Frontiers in Genetics, 2013, 4, 104. | 1.1 | 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. | 1.5 | 28 |
| 102 | Breast Cancerâ€“Associated Abraxas Mutation Disrupts Nuclear Localization and DNA Damage Response Functions. Science Translational Medicine, 2012, 4, 122ra23. | 5.8 | 54 |
| 103 | 19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803. | 0.4 | 100 |
| 104 | The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939. | 1.4 | 80 |
| 105 | Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318. | 9.4 | 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. | 1.1 | 17 |
| 107 | 11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132. | 1.1 | 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. | 1.1 | 51 |

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| 109 | 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 |
| 110 | Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263. | 3.0 | 596 |
| 111 | A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214. | 9.4 | 279 |
| 112 | Screening for large genomic rearrangements in the FANCA gene reveals extensive deletion in a Finnish breast cancer family. Cancer Letters, 2011, 302, 113-118. | 3.2 | 22 |
| 113 | Further evidence for the contribution of the RAD51C gene in hereditary breast and ovarian cancer susceptibility. Breast Cancer Research and Treatment, 2011, 130, 1003-1010. | 1.1 | 54 |
| 114 | Mutation screening of the RNF8, UBC13 and MMS2 genes in Northern Finnish breast cancer families. BMC Medical Genetics, 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. Journal of Pathology, 2011, 224, 301-305. | 2.1 | 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€. Human Molecular Genetics, 2011, 20, 4693-4706. | 1.4 | 71 |
| 117 | Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249. | 0.4 | 109 |
| 118 | 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. | 1.1 | 12 |
| 119 | Screening for large genomic rearrangements of the BRIP1 and CHK1 genes in Finnish breast cancer families. Familial Cancer, 2010, 9, 537-540. | 0.9 | 13 |
| 120 | Long-term observational follow-up study of breast cancer diagnosed in women â‰¤40 years old. Breast, 2010, 19, 456-461. | 0.9 | 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. Nature Genetics, 2010, 42, 885-892. | 9.4 | 309 |
| 122 | Inactivation of Palb2 gene leads to mesoderm differentiation defect and early embryonic lethality in mice. Human Molecular Genetics, 2010, 19, 3021-3029. | 1.4 | 41 |
| 123 | Mutation analysis of the gene encoding the PALB2-binding protein MRG15 in BRCA1/2-negative breast cancer families. Journal of Human Genetics, 2010, 55, 842-843. | 1.1 | 6 |
| 124 | Genome-wide search for breast cancer linkage in large Icelandic non-BRCA1/2 families. Breast Cancer Research, 2010, 12, R50. | 2.2 | 18 |
| 125 | Mutation analysis of the AATF gene in breast cancer families. BMC Cancer, 2009, 9, 457. | 1.1 | 8 |
| 126 | Haplotypes of the I157T CHEK2 germline mutation in ethnically diverse populations. Familial Cancer, 2009, 8, 473-478. | 0.9 | 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. | 1.1 | 42 |
| 128 | Somatic mutation analysis of MYH11in breast and prostate cancer. BMC Cancer, 2008, 8, 263. | 1.1 | 26 |
| 129 | Germline alterations in the CLSPN gene in breast cancer families. Cancer Letters, 2008, 261, 93-97. | 3.2 | 15 |
| 130 | Penetrance Analysis of the PALB2 c.1592delT Founder Mutation. Clinical Cancer Research, 2008, 14, 4667-4671. | 3.2 | 90 |
| 131 | Germline alterations in the 53BP1 gene in breast and ovarian cancer families. Cancer Letters, 2007, 245, 337-340. | 3.2 | 12 |
| 132 | A recurrent mutation in PALB2 in Finnish cancer families. Nature, 2007, 446, 316-319. | 13.7 | 402 |
| 133 | Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. Carcinogenesis, 2006, 28, 1040-1045. | 1.3 | 21 |
| 134 | Screening for RAD51 and BRCA2 BRC repeat mutations in breast and ovarian cancer families. Cancer Letters, 2006, 236, 142-147. | 3.2 | 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. | 1.3 | 37 |
| 136 | Increasing oxidative damage and loss of mismatch repair enzymes during breast carcinogenesis. European Journal of Cancer, 2006, 42, 2653-2659. | 1.3 | 26 |
| 137 | The clinical value of somatic TP53 gene mutations in 1,794 patients with breast cancer.. Clinical Cancer Research, 2006, 12, 1157-1167. | 3.2 | 495 |
| 138 | Association of commonATM polymorphism with bilateral breast cancer. International Journal of Cancer, 2005, 116, 69-72. | 2.3 | 42 |
| 139 | RAD50 and NBS1 are breast cancer susceptibility genes associated with genomic instability. Carcinogenesis, 2005, 27, 1593-1599. | 1.3 | 179 |
| 140 | Mutation analysis of the ATRgene in breast and ovarian cancer families. Breast Cancer Research, 2005, 7, R495-501. | 2.2 | 30 |
| 141 | Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. Clinical Cancer Research, 2004, 10, 2473-2481. | 3.2 | 224 |
| 142 | Genome-wide scanning for linkage in Finnish breast cancer families. European Journal of Human Genetics, 2004, 12, 98-104. | 1.4 | 27 |
| 143 | Characterization and expression of the human WNT4; lack of associated germline mutations in highâ€"to moderateâ€"risk breast and ovarian cancer. Cancer Letters, 2004, 213, 83-90. | 3.2 | 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. | 1.5 | 74 |

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| 145 | Exclusion of large deletions and other rearrangements in BRCA1 and BRCA2 in Finnish breast and ovarian cancer families. Cancer Genetics and Cytogenetics, 2001, 129, 120-123. | 1.0 | 42 |
| 146 | Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. European Journal of Human Genetics, 2000, 8, 757-763. | 1.4 | 75 |
| 147 | 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 |
| 148 | Germ-Line TP53 Mutations in Finnish Cancer Families Exhibiting Features of the Li-Fraumeni Syndrome and Negative for BRCA1 and BRCA2. Cancer Genetics and Cytogenetics, 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. Genes Chromosomes and Cancer, 1999, 25, 212-221. | 1.5 | 34 |
| 150 | Chromosome 11q22.3-q25 LOH in Ovarian Cancer: Association with a More Aggressive Disease Course and Involved Subregions. Gynecologic Oncology, 1998, 71, 299-304. | 0.6 | 37 |
| 151 | Evidence of Founder Mutations in Finnish BRCA1 and BRCA2 Families. American Journal of Human Genetics, 1998, 62, 1544-1548. | 2.6 | 77 |
| 152 | Molecular cloning, expression and chromosomal localization of a human gene encoding a 33 kDa putative metallopeptidase (PRSM1). Gene, 1996, 174, 135-143. | 1.0 | 16 |
| 153 | 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. | 1.8 | 67 |
| 154 | Population variation at the polymorphic ApaLI restriction enzyme site in intron 5 of the WT1 gene. Clinical Genetics, 1996, 50, 555-557. | 1.0 | 0 |
| 155 | Improved carrier testing for multiple endocrine neoplasia, type 1, using new microsatellite-type DNA markers. Human Genetics, 1995, 96, 449-53. | 1.8 | 15 |
| 156 | Human familial and sporadic breast cancer: analysis of the coding regions of the 17?-hydroxysteroid dehydrogenase 2 gene (EDH17B2) using a single-strand conformation polymorphism assay. Human Genetics, 1994, 93, 319-324. | 1.8 | 56 |
| 157 | Cell lineage involvement of recurrent chromosomal abnormalities in hematologic neoplasms. Genes Chromosomes and Cancer, 1994, 10, 95-102. | 1.5 | 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 17Î²-Hydroxysteroid Dehydrogenase Type 1 Gene 2 (EDH17B2) in Vitro. Genomics, 1994, 23, 250-252. | 1.3 | 34 |
| 159 | Unstable DNA may be responsible for the incomplete penetrance of the myotonic dystrophy phenotype. Human Molecular Genetics, 1992, 1, 467-473. | 1.4 | 115 |
| 160 | The gene for 17beta-hydroxysteroid dehydrogenase maps to human chromosome 17, bands q12?q21, and shows an RFLP with ScaI. Human Genetics, 1990, 85, 473-6. | 1.8 | 22 |
| 161 | Linkage disequilibrium detected between dystrophia myotonica and APOC2 locus in the Finnish population. Human Genetics, 1990, 85, 541-5. | 1.8 | 6 |
| 162 | A new RFLP withStuI and probe cX55.7 (DXS105) and its usefulness in carrier analysis of fragile X syndrome. Human Genetics, 1988, 80, 193-193. | 1.8 | 5 |

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| 163 | myc oncogenes: activation and amplification. Biochimica Et Biophysica Acta: Reviews on Cancer, 1987, 907, 1-32. | 3.3 | 73 |
| 164 | ACUTE MYELOGENOUS LEUKAEMIA WITH C-MYC AMPLIFICATION AND DOUBLE MINUTE CHROMOSOMES. Lancet, The, 1985, 326, 1035-1039. | 6.3 | 84 |
| 165 | Mapping of amplified c-myb oncogene, sister chromatid exchanges, and karyotypic analysis of the COLO 205 colon carcinoma cell line. Cancer Genetics and Cytogenetics, 1985, 18, 251-264. | 1.0 | 17 |