

Heli Nevanlinna

List of Publications by Year in Descending Order

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Version: 2024-04-23

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

235
papers

23,195
citations

75
h-index

149
g-index

245
ext. papers

27,331
ext. citations

10.5
avg, IF

4.88
L-index

#	Paper	IF	Citations
235	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , 2022 , 5, 65	6.7	0
234	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , 2022 , 24, 2	8.3	3
233	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. <i>JAMA Oncology</i> , 2022 ,	13.4	4
232	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. <i>Genome Medicine</i> , 2022 , 14, 51	14.4	0
231	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 217-228	4	7
230	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021 , 11, 19787	4.9	0
229	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. <i>Genetics in Medicine</i> , 2021 , 23, 1726-1737	8.1	2
228	Expression of markers of stem cell characteristics, epithelial-mesenchymal transition, basal-like phenotype, proliferation, and androgen receptor in metaplastic breast cancer and their prognostic impact. <i>Acta Oncologica</i> , 2021 , 60, 1233-1239	3.2	0
227	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	11	1
226	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. <i>Scientific Reports</i> , 2021 , 11, 14763	4.9	0
225	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 453-461	9.7	4
224	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	8.7	2
223	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021 , 12, 1078	17.4	4
222	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021 , 384, 428-439	59.2	143
221	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2021 ,	9.7	3
220	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	8.3	1
219	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021 , 125, 1135-1145	8.7	0

218	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	36.3	76
217	Constitutional mosaicism for a BRCA2 mutation as a cause of early-onset breast cancer. <i>Familial Cancer</i> , 2020 , 19, 307-310	3	4
216	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020 , 10, 9688	4.9	2
215	SNPs in lncRNA Regions and Breast Cancer Risk. <i>Frontiers in Genetics</i> , 2020 , 11, 550	4.5	6
214	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants: Results From the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). <i>JAMA Oncology</i> , 2020 , 6, 1218-1230	13.4	25
213	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. <i>Journal of the National Cancer Institute</i> , 2020 , 112, 1242-1250	9.7	51
212	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , 2020 , 44, 442-468	2.6	9
211	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
210	The Spectrum of Protein Truncating Variants in European Breast Cancer Cases. <i>Cancers</i> , 2020 , 12,	6.6	7
209	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. <i>Breast Cancer Research and Treatment</i> , 2020 , 181, 423-434	4.4	7
208	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020 , 80, 624-638	10.1	22
207	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56
206	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020 , 38, 674-685	2.2	133
205	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020 , 22, 1653-1666	8.1	34
204	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020 , 107, 837-848	11	12
203	Association of germline variation with the survival of women with pathogenic variants and breast cancer. <i>Npj Breast Cancer</i> , 2020 , 6, 44	7.8	3
202	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019 , 9, 12524	4.9	2
201	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45

200	Large scale multifactorial likelihood quantitative analysis of BRCA1 and BRCA2 variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019 , 40, 1557-1578	4.7	52
199	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. <i>British Journal of Cancer</i> , 2019 , 121, 180-192	8.7	13
198	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
197	Recurrent moderate-risk mutations in Finnish breast and ovarian cancer patients. <i>International Journal of Cancer</i> , 2019 , 145, 2692-2700	7.5	9
196	Metaplastic carcinoma of the breast: Prognosis and response to systemic treatment in metastatic disease. <i>Breast Journal</i> , 2019 , 25, 418-424	1.2	17
195	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019 , 120, 647-657	8.7	28
194	Reply-Letter to the editor. <i>Breast Journal</i> , 2019 , 25, 1332	1.2	
193	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019 , 5, 38	7.8	12
192	BRCA1 mislocalization leads to aberrant DNA damage response in heterozygous ABRAXAS1 mutation carrier cells. <i>Human Molecular Genetics</i> , 2019 , 28, 4148-4160	5.6	2
191	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019 , 21, 144	8.3	11
190	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
189	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 350-364	9.7	22
188	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2019 , 79, 505-517	10.1	28
187	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018 , 39, 729-741	4.7	16
186	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018 , 118, 1123-1129	8.7	10
185	Mutational spectrum in a worldwide study of 29,700 families with BRCA1 or BRCA2 mutations. <i>Human Mutation</i> , 2018 , 39, 593-620	4.7	138
184	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018 , 8, 6574	4.9	19
183	Family history influences the tumor characteristics and prognosis of breast cancers developing during postmenopausal hormone therapy. <i>Familial Cancer</i> , 2018 , 17, 321-331	3	2

182	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 855-862	9.7	145
181	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018 , 78, 5419-5430	10.1	32
180	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018 , 13, e0197561	3.7	9
179	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	3
178	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	36.3	101
177	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2018 , 9, 4249-4257	3.3	8
176	Gene-panel testing of breast and ovarian cancer patients identifies a recurrent RAD51C duplication. <i>Clinical Genetics</i> , 2018 , 93, 595-602	4	8
175	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017 , 116, 524-535	8.7	18
174	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 2789-2799	10.1	49
173	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	36.3	257
172	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017 , 49, 680-691	36.3	190
171	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	4.9	10
170	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
169	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
168	CHEK2 c.1100delC mutation is associated with an increased risk for male breast cancer in Finnish patient population. <i>BMC Cancer</i> , 2017 , 17, 620	4.8	21
167	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017 , 19, 119	8.3	26
166	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017 , 35, 2240-2250	2.2	101
165	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	4.4	17

164	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. <i>Nature Communications</i> , 2017 , 8, 1632	17.4	13
163	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. <i>Breast Cancer Research and Treatment</i> , 2017 , 161, 117-134	4.4	15
162	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599-603	6.3	51
161	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
160	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2017 , 8, 18381-18398	3.3	7
159	- a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017 , 8, 102769-102782	3.3	3
158	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
157	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	5.6	24
156	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. <i>International Journal of Cancer</i> , 2016 , 139, 2760-2770	7.5	10
155	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	4.9	2
154	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, 1052-67	24.4	104
153	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. <i>Breast Cancer Research</i> , 2016 , 18, 112	8.3	25
152	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
151	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53
150	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	4.9	16
149	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 2750-60	2.2	107
148	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
147	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93

146	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , 2016 , 114, 298-304	8.7	5
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, 137-54	6.3	6
144	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
143	Screening of HELQ in breast and ovarian cancer families. <i>Familial Cancer</i> , 2016 , 15, 19-23	3	4
142	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
141	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016 , 7, 69097-69110	3.3	4
140	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. <i>Oncotarget</i> , 2016 , 7, 72381-72394	3.3	11
139	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	3.3	21
138	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	11.6	80
137	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS ONE</i> , 2016 , 11, e0158801	3.7	7
136	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016 , 11, e0160316	3.7	11
135	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 884-95	7.8	45
134	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
133	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
132	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016 , 18, 98	8.3	26
131	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	8.3	25
130	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016 , 135, 741-56	6.3	18
129	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. <i>Breast Cancer Research and Treatment</i> , 2016 , 157, 117-31	4.4	17

128	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016 , 18, 22	8.3	31
127	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, 679-93	2.8	15
126	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
125	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. <i>Breast Cancer Research</i> , 2016 , 18, 15	8.3	58
124	Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. <i>Breast Cancer Research and Treatment</i> , 2016 , 158, 463-9	4.4	16
123	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016 , 45, 1619-1630	7.8	77
122	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	11	43
121	Somatic MED12 mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. <i>Prostate</i> , 2016 , 76, 22-31	4.2	25
120	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015 , 47, 164-71	36.3	177
119	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
118	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1574-84	4	24
117	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	11	26
116	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
115	RAD51, XRCC3, and XRCC2 mutation screening in Finnish breast cancer families. <i>SpringerPlus</i> , 2015 , 4, 92		17
114	Evaluating the ovarian cancer gonadotropin hypothesis: a candidate gene study. <i>Gynecologic Oncology</i> , 2015 , 136, 542-8	4.9	12
113	INPP4B and RAD50 have an interactive effect on survival after breast cancer. <i>Breast Cancer Research and Treatment</i> , 2015 , 149, 363-71	4.4	8
112	Association of type and location of BRCA1 and BRCA2 mutations with risk of breast and ovarian cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 1347-61	27.4	286
111	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015 , 6, 8234	17.4	40

110	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	36.3	226
109	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015 , 36, 1341-53	4.6	20
108	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015 , 13, 156	11.4	37
107	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015 , 24, 5955-64	5.6	48
106	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
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, 1680-91	4	17
104	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, 285-98	5.6	35
103	Candidate genetic modifiers for breast and ovarian cancer risk in BRCA1 and BRCA2 mutation carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 308-16	4	20
102	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015 , 39, 689-97	2.6	18
101	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. <i>BMC Cancer</i> , 2015 , 15, 978	4.8	6
100	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015 , 17, 61	8.3	16
99	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24
98	Assessing associations between the AURKA-HMMR-TPX2-TUBG1 functional module and breast cancer risk in BRCA1/2 mutation carriers. <i>PLoS ONE</i> , 2015 , 10, e0120020	3.7	26
97	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015 , 10, e0128106	3.7	15
96	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015 , 6, 37979-94	3.3	19
95	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
94	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. <i>Clinical Cancer Research</i> , 2015 , 21, 4086-4096	12.9	10
93	Inherited mutations in 17 breast cancer susceptibility genes among a large triple-negative breast cancer cohort unselected for family history of breast cancer. <i>Journal of Clinical Oncology</i> , 2015 , 33, 304- \uparrow ²		435

92	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
91	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	11	59
90	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. <i>Oncotarget</i> , 2015 , 6, 7390-407	3.3	14
89	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015 , 2,		22
88	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 15172-7	11.5	128
87	Alcohol consumption and survival after a breast cancer diagnosis: a literature-based meta-analysis and collaborative analysis of data for 29,239 cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 934-45	4	29
86	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
85	Breast-cancer risk in families with mutations in PALB2. <i>New England Journal of Medicine</i> , 2014 , 371, 497-506	50.6	576
84	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
83	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	8.3	12
82	A genome wide meta-analysis study for identification of common variation associated with breast cancer prognosis. <i>PLoS ONE</i> , 2014 , 9, e101488	3.7	24
81	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
80	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
79	DNA glycosylases involved in base excision repair may be associated with cancer risk in BRCA1 and BRCA2 mutation carriers. <i>PLoS Genetics</i> , 2014 , 10, e1004256	6	33
78	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014 , 5, 4051	17.4	13
77	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
76	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	8.3	82
75	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2014 , 16, 3416	8.3	46

74	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium 2014 , n/a-n/a		1
73	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013 , 45, 362-70, 370e1-2	36.3	267
72	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, 1046-60	11	80
71	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, 371-84, 384e1-2	36.3	422
70	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	11	167
69	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. <i>International Journal of Cancer</i> , 2013 , 132, 2044-55	7.5	9
68	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
67	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
66	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome-wide interaction study. <i>Endocrine-Related Cancer</i> , 2013 , 20, 875-87	5.7	19
65	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. <i>PLoS Genetics</i> , 2013 , 9, e1003173	6	90
64	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk. <i>PLoS Genetics</i> , 2013 , 9, e1003212	6	209
63	Overabundant FANCD2, alone and combined with NQO1, is a sensitive marker of adverse prognosis in breast cancer. <i>Annals of Oncology</i> , 2013 , 24, 2780-5	10.3	16
62	Identification of inherited genetic variations influencing prognosis in early-onset breast cancer. <i>Cancer Research</i> , 2013 , 73, 1883-91	10.1	36
61	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013 , 4, 1628	17.4	124
60	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013 , 4, 1627	17.4	85
59	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2012 , 14, R33	8.3	70
58	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237
57	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012 , 21, 5373-84	5.6	143

56	NQO1 expression correlates inversely with NFB activation in human breast cancer. <i>Breast Cancer Research and Treatment</i> , 2012 , 132, 955-68	4.4	20
55	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. <i>Cancer Research</i> , 2012 , 72, 1795-803	3.1	93
54	A Finnish founder mutation in RAD51D: analysis in breast, ovarian, prostate, and colorectal cancer. <i>Journal of Medical Genetics</i> , 2012 , 49, 429-32	5.8	35
53	Pathology of breast and ovarian cancers among BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 134-47	4	411
52	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4308-16	2.2	134
51	Genome-wide association study for ovarian cancer susceptibility using pooled DNA. <i>Twin Research and Human Genetics</i> , 2012 , 15, 615-623	2.2	8
50	Glycodelin expression associates with differential tumour phenotype and outcome in sporadic and familial non-BRCA1/2 breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2011 , 128, 85-95	4.4	14
49	A combined analysis of genome-wide association studies in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011 , 126, 717-27	4.4	85
48	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, 250-63	9.7	513
47	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011 , 43, 1210-4	36.3	253
46	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2011 , 20, 3304-21	5.6	62
45	RAD51C is a susceptibility gene for ovarian cancer. <i>Human Molecular Genetics</i> , 2011 , 20, 3278-88	5.6	111
44	MiR-34a expression has an effect for lower risk of metastasis and associates with expression patterns predicting clinical outcome in breast cancer. <i>PLoS ONE</i> , 2011 , 6, e26122	3.7	65
43	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010 , 42, 880-4	36.3	210
42	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010 , 42, 874-9	36.3	277
41	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, 885-92	36.3	276
40	Common breast cancer susceptibility alleles and the risk of breast cancer for BRCA1 and BRCA2 mutation carriers: implications for risk prediction. <i>Cancer Research</i> , 2010 , 70, 9742-54	10.1	147
39	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009 , 18, 1131-9	3.9	75

38	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2009 , 18, 4442-56	5.6	91
37	The breast cancer susceptibility mutation PALB2 1592delT is associated with an aggressive tumor phenotype. <i>Clinical Cancer Research</i> , 2009 , 15, 3214-22	12.9	106
36	Cyclin D1 expression is associated with poor prognostic features in estrogen receptor positive breast cancer. <i>Breast Cancer Research and Treatment</i> , 2009 , 113, 75-82	4.4	49
35	NAD(P)H:quinone oxidoreductase 1 NQO1*2 genotype (P187S) is a strong prognostic and predictive factor in breast cancer. <i>Nature Genetics</i> , 2008 , 40, 844-53	36.3	163
34	Aberrations of the MRE11-RAD50-NBS1 DNA damage sensor complex in human breast cancer: MRE11 as a candidate familial cancer-predisposing gene. <i>Molecular Oncology</i> , 2008 , 2, 296-316	7.9	120
33	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. <i>PLoS Genetics</i> , 2008 , 4, e1000054	6	280
32	Common breast cancer-predisposition alleles are associated with breast cancer risk in BRCA1 and BRCA2 mutation carriers. <i>American Journal of Human Genetics</i> , 2008 , 82, 937-48	11	218
31	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007 , 39, 352-8	36.3	557
30	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007 , 447, 1087-93	19.4	1957
29	Ki67 and cyclin A as prognostic factors in early breast cancer. What are the optimal cut-off values?. <i>Histopathology</i> , 2007 , 51, 491-8	7.3	57
28	RAD51 135G-->C modifies breast cancer risk among BRCA2 mutation carriers: results from a combined analysis of 19 studies. <i>American Journal of Human Genetics</i> , 2007 , 81, 1186-200	11	204
27	Evaluation of the role of Finnish ataxia-telangiectasia mutations in hereditary predisposition to breast cancer. <i>Carcinogenesis</i> , 2007 , 28, 1040-5	4.6	16
26	Evaluation of RAD50 in familial breast cancer predisposition. <i>International Journal of Cancer</i> , 2006 , 118, 2911-6	7.5	47
25	The CHEK2 gene and inherited breast cancer susceptibility. <i>Oncogene</i> , 2006 , 25, 5912-9	9.2	158
24	Relationship of patients age to histopathological features of breast tumours in BRCA1 and BRCA2 and mutation-negative breast cancer families. <i>Breast Cancer Research</i> , 2005 , 7, R465-9	8.3	51
23	Histopathological features of breast tumours in BRCA1, BRCA2 and mutation-negative breast cancer families. <i>Breast Cancer Research</i> , 2005 , 7, R93-100	8.3	75
22	Correlation of CHEK2 protein expression and c.1100delC mutation status with tumor characteristics among unselected breast cancer patients. <i>International Journal of Cancer</i> , 2005 , 113, 575-80	7.5	85
21	Breast cancer patients with p53 Pro72 homozygous genotype have a poorer survival. <i>Clinical Cancer Research</i> , 2005 , 11, 5098-103	12.9	126

20	CHEK2 variant I157T may be associated with increased breast cancer risk. <i>International Journal of Cancer</i> , 2004 , 111, 543-7	7.5	114
19	Average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations detected in case Series unselected for family history: a combined analysis of 22 studies. <i>American Journal of Human Genetics</i> , 2003 , 72, 1117-30	11	2643
18	A CHEK2 genetic variant contributing to a substantial fraction of familial breast cancer. <i>American Journal of Human Genetics</i> , 2002 , 71, 432-8	11	354
17	Survival of breast cancer patients in BRCA1, BRCA2, and non-BRCA1/2 breast cancer families: a relative survival analysis from Finland. <i>International Journal of Cancer</i> , 2001 , 93, 368-72	7.5	48
16	Involvement of BRCA1 and BRCA2 in breast cancer in a western Finnish sub-population. <i>Genetic Epidemiology</i> , 2001 , 20, 239-46	2.6	7
15	Risk of cancer in BRCA1 and BRCA2 mutation-positive and -negative breast cancer families (Finland). <i>Cancer Causes and Control</i> , 2001 , 12, 739-46	2.8	22
14	Germline TP53 alterations in Finnish breast cancer families are rare and occur at conserved mutation-prone sites. <i>British Journal of Cancer</i> , 2001 , 84, 116-9	8.7	29
13	BRCA1 and BRCA2 mutations among 233 unselected Finnish ovarian carcinoma patients. <i>European Journal of Human Genetics</i> , 2001 , 9, 424-30	5.3	43
12	Haplotype analysis in Icelandic and Finnish BRCA2 999del5 breast cancer families. <i>European Journal of Human Genetics</i> , 2001 , 9, 773-9	5.3	21
11	BRCA1 and BRCA2 mutations among Finnish ovarian carcinoma families. <i>International Journal of Oncology</i> , 2001 , 18, 831-5	1	8
10	A probability model for predicting BRCA1 and BRCA2 mutations in breast and breast-ovarian cancer families. <i>British Journal of Cancer</i> , 2001 , 84, 704-8	8.7	74
9	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. <i>European Journal of Human Genetics</i> , 2000 , 8, 757-63	5.3	64
8	Population-based study of BRCA1 and BRCA2 mutations in 1035 unselected Finnish breast cancer patients. <i>Journal of the National Cancer Institute</i> , 2000 , 92, 1529-31	9.7	140
7	Familial breast cancer in southern Finland: how prevalent are breast cancer families and can we trust the family history reported by patients?. <i>European Journal of Cancer</i> , 2000 , 36, 1143-8	7.5	84
6	Familial Breast Cancer in Southern Finland. <i>Disease Markers</i> , 1999 , 15, 105-105	3.2	78
5	Low proportion of BRCA1 and BRCA2 mutations in Finnish breast cancer families: evidence for additional susceptibility genes. <i>Human Molecular Genetics</i> , 1997 , 6, 2309-15	5.6	106
4	Amplification of fgfr4 gene in human breast and gynecological cancers. <i>International Journal of Cancer</i> , 1993 , 54, 378-82	7.5	127
3	The genes for CD37, CD53, and R2, all members of a novel gene family, are located on different chromosomes. <i>Immunogenetics</i> , 1993 , 37, 461-5	3.2	12

2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes	1
1	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses	2