

Heli Nevanlinna

List of Publications by Year in descending order

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Version: 2024-02-01

238
papers

30,268
citations

5876

81
h-index

5364

164
g-index

245
all docs

245
docs citations

245
times ranked

26856
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 1117-1130.	2.6	3,105
2	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007, 447, 1087-1093.	13.7	2,165
3	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
4	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
5	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . <i>New England Journal of Medicine</i> , 2014, 371, 497-506.	13.9	745
6	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
7	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. <i>Journal of the National Cancer Institute</i> , 2011, 103, 250-263.	3.0	596
8	A common coding variant in <i>CASP8</i> is associated with breast cancer risk. <i>Nature Genetics</i> , 2007, 39, 352-358.	9.4	591
9	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
10	Breast Cancer Risk Genes Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	13.9	532
11	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, 304-311.	0.8	521
12	Pathology of Breast and Ovarian Cancers among <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from the Consortium of Investigators of Modifiers of <i>BRCA1/2</i> (CIMBA). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 134-147.	1.1	513
13	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	9.4	513
14	Multiple independent variants at the <i>TERT</i> locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	9.4	493
15	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
16	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
17	A <i>CHEK2</i> Genetic Variant Contributing to a Substantial Fraction of Familial Breast Cancer. <i>American Journal of Human Genetics</i> , 2002, 71, 432-438.	2.6	402
18	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2015, 313, 1347.	3.8	390

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19	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
20	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
21	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
22	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
23	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010, 42, 874-879.	9.4	321
24	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	1.5	315
25	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. <i>Nature Genetics</i> , 2010, 42, 885-892.	9.4	309
26	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
27	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	9.4	279
28	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	0.8	270
29	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	9.4	265
30	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, 937-948.	2.6	257
31	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
32	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.	1.5	244
33	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010, 42, 880-884.	9.4	235
34	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.	3.0	225
35	Mutational spectrum in a worldwide study of 29,700 families with <i>BRCA1</i> or <i>BRCA2</i> mutations. <i>Human Mutation</i> , 2018, 39, 593-620.	1.1	224
36	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221

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37	RAD51 135Gâ†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, 1186-1200.	2.6	217
38	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	2.6	201
39	The CHEK2 gene and inherited breast cancer susceptibility. <i>Oncogene</i> , 2006, 25, 5912-5919.	2.6	184
40	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	9.4	184
41	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, 844-853.	9.4	181
42	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
43	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Implications for Risk Prediction. <i>Cancer Research</i> , 2010, 70, 9742-9754.	0.4	169
44	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, 5373-5384.	1.4	168
45	<i>CHEK2</i>*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€Specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316.	0.8	162
46	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, 15172-15177.	3.3	162
47	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, 1529-1531.	3.0	159
48	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
49	Amplification of <i>gfr4</i> gene in human breast and gynecological cancers. <i>International Journal of Cancer</i> , 1993, 54, 378-382.	2.3	154
50	Age- and Tumor Subtypeâ€Specific Breast Cancer Risk Estimates for <i>CH</i><i>EK</i><i>2</i>*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	152
51	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	0.8	152
52	Aberrations of the MRE11â€RAD50â€NBS1 DNA damage sensor complex in human breast cancer: <i>MRE11</i> as a candidate familial cancerâ€predisposing gene. <i>Molecular Oncology</i> , 2008, 2, 296-316.	2.1	147
53	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	5.8	144
54	Breast Cancer Patients with p53 Pro72 Homozygous Genotype Have a Poorer Survival. <i>Clinical Cancer Research</i> , 2005, 11, 5098-5103.	3.2	138

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55	CHEK2 variant I157T may be associated with increased breast cancer risk. <i>International Journal of Cancer</i> , 2004, 111, 543-547.	2.3	134
56	Low proportion of BRCA1 and BRCA2 mutations in Finnish breast cancer families: evidence for additional susceptibility genes. <i>Human Molecular Genetics</i> , 1997, 6, 2309-2315.	1.4	128
57	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	9.4	125
58	RAD51C is a susceptibility gene for ovarian cancer. <i>Human Molecular Genetics</i> , 2011, 20, 3278-3288.	1.4	124
59	The Breast Cancer Susceptibility Mutation <i>PALB2</i> 1592delT Is Associated with an Aggressive Tumor Phenotype. <i>Clinical Cancer Research</i> , 2009, 15, 3214-3222.	3.2	122
60	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
61	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	3.9	118
62	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
63	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in <i>RAD51C</i> and <i>RAD51D</i> . <i>Journal of the National Cancer Institute</i> , 2020, 112, 1242-1250.	3.0	106
64	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	1.5	105
65	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
66	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. <i>Human Mutation</i> , 2019, 40, 1557-1578.	1.1	102
67	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	100
68	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.4	100
69	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2009, 18, 4442-4456.	1.4	99
70	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	3.0	99
71	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	98
72	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98

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73	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, 575-580.	2.3	97
74	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419.	2.2	97
75	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	1.5	94
76	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
77	A combined analysis of genome-wide association studies in breast cancer. <i>Breast Cancer Research and Treatment</i> , 2011, 126, 717-727.	1.1	90
78	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
79	Familial breast cancer in southern Finland. <i>European Journal of Cancer</i> , 2000, 36, 1143-1148.	1.3	89
80	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.	2.2	88
81	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
82	Histopathological features of breast tumours in BRCA1, BRCA2 and mutation-negative breast cancer families. <i>Breast Cancer Research</i> , 2004, 7, R93-100.	2.2	86
83	A probability model for predicting BRCA1 and BRCA2 mutations in breast and breast-ovarian cancer families. <i>British Journal of Cancer</i> , 2001, 84, 704-708.	2.9	85
84	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139.	1.4	84
85	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.	1.1	82
86	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.	2.2	78
87	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
88	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
89	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	2.6	76
90	Multiple founder effects and geographical clustering of BRCA1 and BRCA2 families in Finland. <i>European Journal of Human Genetics</i> , 2000, 8, 757-763.	1.4	75

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91	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
92	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 884-895.	0.9	71
93	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.	1.1	70
94	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, 3304-3321.	1.4	68
95	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. <i>Human Molecular Genetics</i> , 2015, 24, 5955-5964.	1.4	68
96	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
97	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
98	Ki67 and cyclin A as prognostic factors in early breast cancer. What are the optimal cut-off values?. <i>Histopathology</i> , 2007, 51, 491-498.	1.6	61
99	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	2.6	59
100	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.	2.2	57
101	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.	2.2	57
102	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
103	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.	1.1	55
104	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, 368-372.	2.3	54
105	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.	0.4	54
106	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	1.4	53
107	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
108	Evaluation of RAD50 in familial breast cancer predisposition. <i>International Journal of Cancer</i> , 2006, 118, 2911-2916.	2.3	51

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109	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. <i>BMC Medicine</i> , 2015, 13, 156.	2.3	51
110	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	2.3	51
111	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.	1.6	51
112	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
113	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
114	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.	0.4	49
115	BRCA1 and BRCA2 mutations among 233 unselected Finnish ovarian carcinoma patients. <i>European Journal of Human Genetics</i> , 2001, 9, 424-430.	1.4	48
116	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
117	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.	1.5	47
118	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
119	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44
120	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
121	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	43
122	Identification of Inherited Genetic Variations Influencing Prognosis in Early-Onset Breast Cancer. <i>Cancer Research</i> , 2013, 73, 1883-1891.	0.4	42
123	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. <i>PLoS ONE</i> , 2014, 9, e101488.	1.1	42
124	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.	2.2	42
125	A Finnish founder mutation in RAD51D: analysis in breast, ovarian, prostate, and colorectal cancer: Table 1. <i>Journal of Medical Genetics</i> , 2012, 49, 429-432.	1.5	41
126	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40

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127	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285.	1.5	39
128	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.	2.2	39
129	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.4	39
130	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	39
131	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, 116-119.	2.9	38
132	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	1.4	38
133	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, 934-945.	1.1	37
134	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	2.6	37
135	Metaplastic carcinoma of the breast: Prognosis and response to systemic treatment in metastatic disease. <i>Breast Journal</i> , 2019, 25, 418-424.	0.4	36
136	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.	1.1	34
137	Somatic <i>MED12</i> mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. <i>Prostate</i> , 2016, 76, 22-31.	1.2	33
138	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	1.4	33
139	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
140	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	0.8	31
141	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
142	Height and Body Mass Index as Modifiers of Breast Cancer Risk in <i>BRCA1</i> / <i>BRCA2</i> Mutation Carriers: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2019, 111, 350-364.	3.0	30
143	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
144	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.	1.1	29

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145	Overabundant FANCD2, alone and combined with NQO1, is a sensitive marker of adverse prognosis in breast cancer. <i>Annals of Oncology</i> , 2013, 24, 2780-2785.	0.6	28
146	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, 1574-1584.	1.1	28
147	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
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