Heli Nevanlinna

List of Publications by Year
in descending order

238 papers	30,268 citations	6840 81 h-index	6177 164 g-index
245 all docs	245 docs citations	245 times ranked	29158 citing authors

#	Article	IF	Citations
1	Breast and Prostate Cancer Risks for Male *BRCA1* and *BRCA2* Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
2	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
3	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
4	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
5	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
6	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
7	Associations of a breast cancer polygenic risk score with tumor characteristics and survival.. Journal of Clinical Oncology, 2022, 40, 563-563.	0.8	1
8	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
9	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12
10	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
11	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
12	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
13	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
14	High miR-30 Expression Associates with Improved Breast Cancer Patient Survival and Treatment Outcome. Cancers, 2021, 13, 2907.	1.7	3
15	The predictive ability of the 313 variantâ€"based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	1.1	16
16	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. Acta OncolÃ³gica, 2021, 60, 1233-1239.	0.8	6
17	Abstract 758: The clinical utility of BRCA1/2 pathogenic variants in breast cancer patient prognosis. , 2021, , .		0
18	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

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19	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. Scientific Reports, 2021, 11, 14763.	1.6	3
20	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
21	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
22	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
23	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
24	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
25	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	0.8	270
26	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	1.1	82
27	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
28	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	2.3	5
29	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
30	Constitutional mosaicism for a BRCA2 mutation as a cause of early-onset breast cancer. Familial Cancer, 2020, 19, 307-310.	0.9	10
31	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
32	SNPs in lncRNA Regions and Breast Cancer Risk. Frontiers in Genetics, 2020, 11, 550.	1.1	14
33	Characterization of the Cancer Spectrum in Men With Germline<i>BRCA1</i>and<i>BRCA2</i>Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
34	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in <i>RAD51C</i> and <i>RAD51D</i>. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	3.0	106
35	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
36	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30

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37	The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292.	1.7	11
38	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	1.1	14
39	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.4	49
40	Reply—Letter to the editor. Breast Journal, 2019, 25, 1332-1332.	0.4	0
41	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
42	BRCA1 mislocalization leads to aberrant DNA damage response in heterozygous ABRAXAS1 mutation carrier cells. Human Molecular Genetics, 2019, 28, 4148-4160.	1.4	4
43	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
44	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
45	Large scale multifactorial likelihood quantitative analysis of *BRCA1* and *BRCA2* variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	1.1	102
46	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	2.9	19
47	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
48	Recurrent moderate-risk mutations in Finnish breast and ovarian cancer patients. International Journal of Cancer, 2019, 145, 2692-2700.	2.3	19
49	Metaplastic carcinoma of the breast: Prognosis and response to systemic treatment in metastatic disease. Breast Journal, 2019, 25, 418-424.	0.4	36
50	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
51	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24
52	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
53	Height and Body Mass Index as Modifiers of Breast Cancer Risk in *BRCA1*/*2* Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	3.0	30
54	The *BRCA2* c.68-7T>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19

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55	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	2.9	15
56	Mutational spectrum in a worldwide study of 29,700 families with *BRCA1* or *BRCA2* mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
57	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	1.6	51
58	Family history influences the tumor characteristics and prognosis of breast cancers developing during postmenopausal hormone therapy. Familial Cancer, 2018, 17, 321-331.	0.9	4
59	Geneâ€panel testing of breast and ovarian cancer patients identifies a recurrent *RAD51C* duplication. Clinical Genetics, 2018, 93, 595-602.	1.0	11
60	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. Journal of the National Cancer Institute, 2018, 110, 855-862.	3.0	225
61	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.4	54
62	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
63	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
64	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
65	Meta-analysis of three genome-wide association studies identifies two loci that predict survival and treatment outcome in breast cancer. Oncotarget, 2018, 9, 4249-4257.	0.8	8
66	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
67	*BRCA2* Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
68	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
69	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
70	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
71	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
72	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289

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73	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
74	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	5.8	18
75	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. Breast Cancer Research and Treatment, 2017, 161, 117-134.	1.1	18
76	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
77	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
78	CHEK2 c.1100delC mutation is associated with an increased risk for male breast cancer in Finnish patient population. BMC Cancer, 2017, 17, 620.	1.1	29
79	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	2.2	43
80	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
81	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	0.8	14
82	<i>PHIP</i>- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
83	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
84	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
85	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
86	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
87	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
88	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
89	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
90	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

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91	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
92	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19
93	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	1.1	18
94	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
95	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
96	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
97	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	2.2	88
98	Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. Breast Cancer Research and Treatment, 2016, 158, 463-469.	1.1	24
99	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
100	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
101	Somatic *MED12* mutations in prostate cancer and uterine leiomyomas promote tumorigenesis through distinct mechanisms. Prostate, 2016, 76, 22-31.	1.2	33
102	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
103	FANCM c.5101C>T mutation associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2016, 139, 2760-2770.	2.3	13
104	rs2735383, located at a microRNA binding site in the 3′UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	1.6	2
105	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
106	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	2.2	42
107	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
108	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78

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109	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
110	Age- and Tumor Subtype–Specific Breast Cancer Risk Estimates for *CHEK2**1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
111	No evidence that protein truncating variants in *BRIP1* are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
112	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
113	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	2.9	7
114	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
115	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
116	Screening of HELQ in breast and ovarian cancer families. Familial Cancer, 2016, 15, 19-23.	0.9	7
117	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
118	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
119	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
120	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
121	Epithelial–Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
122	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	1.1	6
123	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	2.2	26
124	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
125	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
126	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44

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127	SNP-SNP interaction analysis of NF-Î²B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
128	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
129	Polymorphism at 19q13.41 Predicts Breast Cancer Survival Specifically after Endocrine Therapy. Clinical Cancer Research, 2015, 21, 4086-4096.	3.2	12
130	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	0.8	521
131	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
132	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
133	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
134	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
135	Network-Based Integration of GWAS and Gene Expression Identifies a *HOX*-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	1.1	28
136	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
137	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
138	RAD51, XRCC3, and XRCC2 mutation screening in Finnish breast cancer families. SpringerPlus, 2015, 4, 92.	1.2	21
139	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
140	INPP4B and RAD50 have an interactive effect on survival after breast cancer. Breast Cancer Research and Treatment, 2015, 149, 363-371.	1.1	8
141	Association of Type and Location of *BRCA1* and *BRCA2* Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
142	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
143	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
144	Common variants at the *CHEK2* gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24

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145	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	2.3	51
146	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	1.4	68
147	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
148	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
149	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
150	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
151	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
152	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
153	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	1.1	42
154	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
155	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
156	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
157	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
158	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
159	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
160	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	2.2	57
161	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	3.3	162
162	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	1.1	37

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163	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
164	Breast-Cancer Risk in Families with Mutations in *PALB2*. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
165	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
166	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
167	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2
168	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
169	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
170	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
171	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
172	Germline variation in TP53 regulatory network genes associates with breast cancer survival and treatment outcome. International Journal of Cancer, 2013, 132, 2044-2055.	2.3	11
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174	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
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