

# Ute Hamann

## List of Publications by Year in descending order

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154  
papers

16,438  
citations

47409

49  
h-index

20625

120  
g-index

157  
all docs

157  
docs citations

157  
times ranked

20211  
citing authors

#	ARTICLE	IF	CITATIONS
1	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
2	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in <i>BRCA1</i> and <i>BRCA2</i> compared with those harboring protein truncating variants. <i>Genetics in Medicine</i> , 2022, 24, 119-129.	1.1	10
3	Prevalence of <i>BRCA1</i> and <i>BRCA2</i> Germline Mutations in Patients of African Descent with Early-Onset and Familial Colombian Breast Cancer. <i>Oncologist</i> , 2022, 27, e151-e157.	1.9	0
4	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	0.8	90
5	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
7	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
8	Chasing the origin of 23 recurrent <i>BRCA1</i> mutations in Pakistani breast and ovarian cancer patients. <i>International Journal of Cancer</i> , 2022, , .	2.3	4
9	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	1.6	2
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	3.6	19
11	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1706-1719.	3.0	14
12	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	3.0	45
13	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.	2.9	5
14	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
15	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. <i>Cancers</i> , 2021, 13, 2370.	1.7	4
16	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 <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	1.1	16
17	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.	2.6	6
18	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.	2.2	7

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19	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9
20	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642.	1.1	19
21	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, 19787.	1.6	2
22	Epigenetic quantification of circulating immune cells in peripheral blood of triple-negative breast cancer patients. <i>Clinical Epigenetics</i> , 2021, 13, 207.	1.8	2
23	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
24	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
25	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	1.1	82
26	DNA methylation of the long intergenic noncoding RNA 299 gene in triple-negative breast cancer: results from a prospective study. <i>Scientific Reports</i> , 2020, 10, 11762.	1.6	10
27	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	39
28	Genetic Variability in the microRNA Binding Sites of <i>BMP1B</i> , <i>TGFBR1</i> , <i>IQGAP1</i> , <i>KRAS</i> , <i>SETD8</i> and <i>RYR3</i> and Risk of Breast Cancer in Colombian Women. <i>OncoTargets and Therapy</i> , 2020, Volume 13, 12281-12287.	1.0	2
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	Germline <i>HOXB13</i> mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	1.6	2
31	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
32	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
33	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
34	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.	1.1	14
35	Prevalence of <i>RECQL</i> germline variants in Pakistani early-onset and familial breast cancer patients. <i>Hereditary Cancer in Clinical Practice</i> , 2020, 18, 25.	0.6	6
36	The <i>FANCM</i> :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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37	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5
38	Spectrum and prevalence of BRCA1/2 germline mutations in Pakistani breast cancer patients: results from a large comprehensive study. <i>Hereditary Cancer in Clinical Practice</i> , 2019, 17, 27.	0.6	24
39	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
40	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.	2.9	19
41	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
42	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
43	Prediction and clinical utility of a contralateral breast cancer risk model. <i>Breast Cancer Research</i> , 2019, 21, 144.	2.2	24
44	Low Prevalence of the Four Common Colombian Founder Mutations in <i>BRCA1</i> and <i>BRCA2</i> in Early-Onset and Familial Afro-Colombian Patients with Breast Cancer. <i>Oncologist</i> , 2019, 24, e475-e479.	1.9	4
45	Long intergenic noncoding RNA 299 methylation in peripheral blood is a biomarker for triple-negative breast cancer. <i>Epigenomics</i> , 2019, 11, 81-93.	1.0	32
46	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
47	Interaction between genetic ancestry and common breast cancer susceptibility variants in Colombian women. <i>International Journal of Cancer</i> , 2019, 144, 2181-2191.	2.3	9
48	Prevalence of PALB2 Germline Mutations in Early-onset and Familial Breast/Ovarian Cancer Patients from Pakistan. <i>Cancer Research and Treatment</i> , 2019, 51, 992-1000.	1.3	9
49	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	1.1	19
50	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
51	Tissue-Specific Down-Regulation of the Long Non-Coding RNAs PCAT18 and LINC01133 in Gastric Cancer Development. <i>International Journal of Molecular Sciences</i> , 2018, 19, 3881.	1.8	37
52	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
53	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
54	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75

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55	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
56	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
57	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
58	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
59	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.	1.1	18
60	Contribution of BRCA1 large genomic rearrangements to early-onset and familial breast/ovarian cancer in Pakistan. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 191-201.	1.1	13
61	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
62	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
63	Imputation of missing genotypes within LD-blocks relying on the basic coalescent and beyond: consideration of population growth and structure. <i>BMC Genomics</i> , 2017, 18, 798.	1.2	5
64	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
65	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.	0.8	14
66	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	9
67	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
68	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
69	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.	1.1	10
70	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
71	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
72	<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

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73	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
74	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. <i>Breast Cancer Research and Treatment</i> , 2016, 157, 117-131.	1.1	18
75	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
76	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, 679-693.	0.8	21
77	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
78	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
79	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
80	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.	1.6	2
81	A novel deleterious c.2656G>T MSH2 germline mutation in a Pakistani family with a phenotypic overlap of hereditary breast and ovarian cancer and Lynch syndrome. <i>Hereditary Cancer in Clinical Practice</i> , 2016, 14, 14.	0.6	6
82	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
83	High prevalence and predominance of BRCA1 germline mutations in Pakistani triple-negative breast cancer patients. <i>BMC Cancer</i> , 2016, 16, 673.	1.1	26
84	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
85	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
86	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.	1.6	19
87	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
88	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
89	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, 137-154.	1.8	8
90	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18

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91	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
92	Inbreeding and homozygosity in breast cancer survival. Scientific Reports, 2015, 5, 16467.	1.6	4
93	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
94	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
95	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
96	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
97	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
98	Absence of the FANCM c.5101C>T mutation in BRCA1/2-negative triple-negative breast cancer patients from Pakistan. Breast Cancer Research and Treatment, 2015, 152, 229-230.	1.1	7
99	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
100	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
101	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	1.3	14
102	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
103	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
104	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
105	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
106	Association of Type and Location of <i>BRCA1</i> and <i>BRCA2</i> Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
107	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
108	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99



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109	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, 1680-1691.	1.1	24
110	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 308-316.	1.1	22
111	Association between the BsmI Polymorphism in the Vitamin D Receptor Gene and Breast Cancer Risk: Results from a Pakistani Case-Control Study. <i>PLoS ONE</i> , 2015, 10, e0141562.	1.1	37
112	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. <i>Oncotarget</i> , 2015, 6, 7390-7407.	0.8	15
113	Systematic Pathway Enrichment Analysis of a Genome-Wide Association Study on Breast Cancer Survival Reveals an Influence of Genes Involved in Cell Adhesion and Calcium Signaling on the Patients' Clinical Outcome. <i>PLoS ONE</i> , 2014, 9, e98229.	1.1	16
114	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	1.1	49
115	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	5.8	16
116	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
117	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>Breast Cancer Research</i> , 2014, 16, 3416.	2.2	57
118	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
119	Practical investigation of the performance of robust logistic regression to predict the genetic risk of hypertension. <i>BMC Proceedings</i> , 2014, 8, S65.	1.8	4
120	Evidence that breast cancer risk at the 2q35 locus is mediated through <i>IGFBP5</i> regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
121	Deleterious <i>RAD51C</i> germline mutations rarely predispose to breast and ovarian cancer in Pakistan. <i>Breast Cancer Research and Treatment</i> , 2014, 145, 775-784.	1.1	28
122	Genetic variation at <i>CYP3A</i> is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	2.2	14
123	Associations between pre-defined occupational job tasks and breast cancer risk. <i>Occupational and Environmental Medicine</i> , 2014, 71, A84.1-A84.	1.3	0
124	Constitutional <i>CHEK2</i> mutations are infrequent in early-onset and familial breast/ovarian cancer patients from Pakistan. <i>BMC Cancer</i> , 2013, 13, 312.	1.1	21
125	Fine-Scale Mapping of the <i>FGFR2</i> Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind <i>FOXA1</i> and <i>E2F1</i> . <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	98
126	Exploring the association between genetic variation in the <i>SUMO</i> isopeptidase gene <i>USPL1</i> and breast cancer through integration of data from the population-based <i>GENICA</i> study and external genetic databases. <i>International Journal of Cancer</i> , 2013, 133, 362-372.	2.3	13



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127	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, 371-384.	9.4	493
128	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
129	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
130	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
131	Estrogen Receptor Alpha and Nuclear Factor Y Coordinately Regulate the Transcription of the SUMO-Conjugating UBC9 Gene in MCF-7 Breast Cancer Cells. <i>PLoS ONE</i> , 2013, 8, e75695.	1.1	15
132	Prevalence of TP53 germ line mutations in young Pakistani breast cancer patients. <i>Familial Cancer</i> , 2012, 11, 307-311.	0.9	19
133	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
134	Identification of the deleterious 2080insA BRCA1 mutation in a male renal cell carcinoma patient from a family with multiple cancer diagnoses from Pakistan. <i>Familial Cancer</i> , 2011, 10, 709-712.	0.9	7
135	No association of polymorphisms in the cell polarity gene SCRIB with breast cancer risk. <i>Breast Cancer Research and Treatment</i> , 2011, 127, 259-264.	1.1	2
136	BRCA1-associated breast and ovarian cancer risks in Poland: no association with commonly studied polymorphisms. <i>Breast Cancer Research and Treatment</i> , 2010, 119, 201-211.	1.1	70
137	Polymorphisms in the UBC9 and PIAS3 genes of the SUMO-conjugating system and breast cancer risk. <i>Breast Cancer Research and Treatment</i> , 2010, 121, 185-194.	1.1	23
138	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
139	Family History, Genetic Testing, and Clinical Risk Prediction: Pooled Analysis of CHEK2*1100delC in 1,828 Bilateral Breast Cancers and 7,030 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 230-234.	1.1	47
140	Common variants in the UBC9 gene encoding the SUMO-conjugating enzyme are associated with breast tumor grade. <i>International Journal of Cancer</i> , 2009, 125, 596-602.	2.3	36
141	No association of miscarriage and BRCA carrier status in Pakistani breast/ovarian cancer patients with a history of parental consanguinity. <i>Breast Cancer Research and Treatment</i> , 2009, 116, 211-213.	1.1	3
142	Absence of the BRCA1 del (exons 9-12) mutation in breast/ovarian cancer families outside of Mexican Hispanics. <i>Breast Cancer Research and Treatment</i> , 2009, 117, 679-681.	1.1	19
143	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. <i>Breast Cancer Research and Treatment</i> , 2008, 111, 139-144.	1.1	50
144	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007, 39, 352-358.	9.4	591

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145	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007, 447, 1087-1093.	13.7	2,165
146	High proportion of BRCA1/2 founder mutations in Hispanic breast/ovarian cancer families from Colombia. <i>Breast Cancer Research and Treatment</i> , 2007, 103, 225-232.	1.1	86
147	The 3' untranslated region C>T polymorphism of prohibitin is a breast cancer risk modifier in Polish women carrying a BRCA1 mutation. <i>Breast Cancer Research and Treatment</i> , 2007, 104, 67-74.	1.1	15
148	Methylenetetrahydrofolate reductase polymorphisms modify BRCA1-associated breast and ovarian cancer risks. <i>Breast Cancer Research and Treatment</i> , 2007, 104, 299-308.	1.1	47
149	No association between BRCA mutations and sex ratio in offspring of Pakistani BRCA mutation carriers. <i>Breast Cancer Research and Treatment</i> , 2007, 107, 155-156.	1.1	1
150	Prevalence of BRCA1 and BRCA2 mutations in Pakistani breast and ovarian cancer patients. <i>International Journal of Cancer</i> , 2006, 119, 2832-2839.	2.3	98
151	Intronic TP53 Germline Sequence Variants Modify the Risk in German Breast/Ovarian Cancer Families. <i>Hereditary Cancer in Clinical Practice</i> , 2004, 2, 139.	0.6	2
152	Similar contributions of BRCA1 and BRCA2 germline mutations to early-onset breast cancer in Germany. <i>European Journal of Human Genetics</i> , 2003, 11, 464-467.	1.4	21
153	Survival and tumor characteristics of German hereditary breast cancer patients. <i>Breast Cancer Research and Treatment</i> , 2000, 59, 185-192.	1.1	48
154	Prevalence of FANCM germline variants in BRCA1/2 negative breast and/or ovarian cancer patients from Pakistan. <i>Familial Cancer</i> , 0, , .	0.9	0