Joe G Dennis

List of Publications by Citations

175 papers	11,877 citations	52 h-index	106 g-index
197 ext. papers	15,540 ext. citations	11.9 avg, IF	3.86 L-index

#	Paper	IF	Citations
175	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
174	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
173	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
172	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. *Nature Genetics*, **2013**, 45, 385-91, 391e1-2	36.3	413
171	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
170	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
169	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
168	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
167	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936	36.3	340
166	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
165	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
164	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
163	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	36.3	257
162	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
161	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
160	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk. *PLoS Genetics*, **2013**, 9, e1003212	6	209
159	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190

158	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
157	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
156	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
155	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. *Nature Genetics*, **2015**, 47, 164-71	36.3	177
154	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	11	167
153	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	153
152	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
151	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
150	A genome-wide association scan (GWAS) for mean telomere length within the COGS project: identified loci show little association with hormone-related cancer risk. *Human Molecular Genetics*, **2013**, 22, 5056-64	5.6	107
149	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, 1052-67	24.4	104
148	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. *Radiotherapy and Oncology*, **2014**, 111, 178-85	5.3	102
147	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. *Journal of Clinical Oncology*, **2017**, 35, 2240-2250	2.2	101
146	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
145	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
144	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. *PLoS Genetics*, **2013**, 9, e1003173	6	90
143	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. *Human Molecular Genetics*, **2013**, 22, 2520-8	5.6	88
142	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
141	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	5.8	83

140	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
139	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, 1046-60	11	80
138	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76
137	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. *Human Molecular Genetics*, **2013**, 22, 2539-50	5.6	75
136	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
135	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
134	Prevalence of the HOXB13 G84E germline mutation in British men and correlation with prostate cancer risk, tumour characteristics and clinical outcomes. *Annals of Oncology*, **2015**, 26, 756-761	10.3	67
133	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	65
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	11	59
131	Evaluating genome-wide association study-identified breast cancer risk variants in African-American women. *PLoS ONE*, **2013**, 8, e58350	3.7	58
130	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
129	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
128	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. *Human Molecular Genetics*, **2016**, 25, 2256-2268	5.6	55
127	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. *Human Molecular Genetics*, **2015**, 24, 5589-602	5.6	54
126	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. *International Journal of Epidemiology*, **2018**, 47, 526-536	7.8	53
125	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
124	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
123	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. *Journal of the National Cancer Institute*, **2020**, 112, 1242-1250	9.7	51

122	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.3	51
121	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
120	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111	5.6	48
119	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
118	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Human Molecular Genetics*, **2015**, 24, 1478-92	5.6	46
117	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	8.3	46
116	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
115	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Research*, **2015**, 75, 2457-67	10.1	45
114	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
113	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
112	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	11	43
111	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 1503-1510	4	42
110	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
109	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. *Nature Communications*, **2015**, 6, 8234	17.4	40
108	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
107	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
106	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285	6	38
105	MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973	3.7	37

104	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
103	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98	5.6	35
102	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Human Molecular Genetics*, **2014**, 23, 2490-7	5.6	35
101	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
100	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	8.1	34
99	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. *Breast Cancer Research*, **2016**, 18, 124	8.3	34
98	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. *Nature Communications*, **2020**, 11, 3353	17.4	32
97	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	10.1	32
96	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. *Human Molecular Genetics*, **2015**, 24, 3595-607	5.6	32
95	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. *Nature Communications*, **2020**, 11, 3833	17.4	31
94	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
93	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. *Human Genetics*, **2015**, 134, 231-45	6.3	30
92	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
91	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46,450 cases and 42,461 controls from the breast cancer association consortium. *Human Molecular Genetics*, **2014**, 23, 1934-46	5.6	28
90	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	10.1	28
89	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
88	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. *Scientific Reports*, **2015**, 5, 17369	4.9	27
87	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	11	26

86	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. *International Journal of Cancer*, **2015**, 136, E685-96	7.5	26
85	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317	7.5	26
84	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. *Breast Cancer Research*, **2016**, 18, 98	8.3	26
83	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	8.3	25
82	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, 1574-84	4	24
81	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	5.6	24
80	FastPop: a rapid principal component derived method to infer intercontinental ancestry using genetic data. *BMC Bioinformatics*, **2016**, 17, 122	3.6	24
79	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24
78	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
77	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). *Journal of Genetics and Genome Research*, **2015**, 2,		22
76	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. *Human Genetics*, **2014**, 133, 481-97	6.3	21
75	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	3.3	21
74	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. *Carcinogenesis*, **2017**, 38, 511-518	4.6	20
73	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. *Carcinogenesis*, **2015**, 36, 1341-53	4.6	20
72	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
71	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocrine-Related Cancer*, **2015**, 22, 851-61	5.7	19
70	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
69	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. *Breast Cancer Research*, **2019**, 21, 68	8.3	18

68	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. *Genetic Epidemiology*, **2015**, 39, 689-97	2.6	18
67	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
66	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. *Breast Cancer Research*, **2015**, 17, 18	8.3	17
65	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. *International Journal of Epidemiology*, **2020**, 49, 1117-1131	7.8	17
64	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. *Blood*, **2019**, 133, 1130-1139	2.2	17
63	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. *Nature Communications*, **2020**, 11, 1217	17.4	16
62	The BRCA2 c.68-7T□□A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
61	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	4.9	16
60	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	8.3	16
59	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. *European Journal of Human Genetics*, **2017**, 25, 432-438	5.3	15
58	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. *PLoS ONE*, **2015**, 10, e0128106	3.7	15
57	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. *Journal of the National Cancer Institute*, **2021**, 113, 329-337	9.7	14
56	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
55	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. *Nature Communications*, **2014**, 5, 4051	17.4	13
54	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. *International Journal of Epidemiology*, **2020**, 49, 216-232	7.8	13
53	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. *International Journal of Cancer*, **2021**, 148, 307-319	7.5	13
52	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, 256-71	4.6	12
51	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12

50	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51	8.3	12
49	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. *Human Molecular Genetics*, **2014**, 23, 6034-46	5.6	11
48	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11
47	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. *EBioMedicine*, **2019**, 48, 203-211	8.8	9
46	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
45	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9
44	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. *Journal of the National Cancer Institute*, **2021**, 113, 1168-1176	9.7	9
43	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. *Human Molecular Genetics*, **2016**, 25, 3600-3612	5.6	9
42	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. *International Journal of Cancer*, **2020**, 146, 2130-2138	7.5	9
41	Population Study of Ovarian Cancer Risk Prediction for Targeted Screening and Prevention. *Cancers* , **2020**, 12,	6.6	8
40	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	3.3	7
39	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, 137-54	6.3	6
38	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers		5
37	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. *Human Genetics*, **2021**, 140, 1353-1365	6.3	5
36	External Validation of Risk Prediction Models Incorporating Common Genetic Variants for Incident Colorectal Cancer Using UK Biobank. *Cancer Prevention Research*, **2020**, 13, 509-520	3.2	4
35	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
34	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. *Oncotarget*, **2016**, 7, 69097-69110	3.3	4
33	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4

32	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e707	2.3	3
31	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
30	- a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget*, **2017**, 8, 102769-102782	3.3	3
29	Association of germline variation with the survival of women with pathogenic variants and breast cancer. *Npj Breast Cancer*, **2020**, 6, 44	7.8	3
28	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. *Journal of the National Cancer Institute*, **2021**,	9.7	3
27	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
26	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
25	rs2735383, located at a microRNA binding site in the 3QUTR of NBS1, is not associated with breast cancer risk. *Scientific Reports*, **2016**, 6, 36874	4.9	2
24	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. *Human Molecular Genetics*, **2013**, 22, 4239-4239	5.6	2
23	Fine-mapping of 150 breast cancer risk regions identifies 178 high confidence target genes		2
22	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2
21	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. *Genetics in Medicine*, **2021**, 23, 1726-1737	8.1	2
20	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	8.7	2
19	Polygenic risk scores for prediction of breast cancer risk in Asian populations.. *Genetics in Medicine*, **2021**,	8.1	2
18	Clustering of known low and moderate risk alleles rather than a novel recessive high-risk gene in non-BRCA1/2 sib trios affected with breast cancer. *International Journal of Cancer*, **2020**, 147, 2708-2716	7.5	1
17	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
16	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1
15	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. *Nature Communications*, **2021**, 12, 4198	17.4	1

List of Publications

14	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	11	1
13	Detecting rare copy number variants from Illumina genotyping arrays with the CamCNV pipeline: Segmentation of z-scores improves detection and reliability. *Genetic Epidemiology*, **2021**, 45, 237-248	2.6	1
12	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	8.3	1
11	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. *Breast Cancer Research*, **2021**, 23, 94	8.3	1
10	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. *Breast Cancer Research*, **2022**, 24, 27	8.3	1
9	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
8	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0
7	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
6	A Genome-Wide Gene-Based Gene–Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, **2022**, 2, 211-219		0
5	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
4	Authors' response: Associations of obesity and circulating insulin and glucose with breast cancer risk. *International Journal of Epidemiology*, **2019**, 48, 1016-1017	7.8	
3	Body mass index and type 2 diabetes and breast cancer survival: a Mendelian randomization study. *American Journal of Cancer Research*, **2021**, 11, 3921-3934	4.4	
2	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9	
1	Relevance of the MHC region for breast cancer susceptibility in Asians.. *Breast Cancer*, **2022**, 1	3.4	