Angela Cox

List of Publications by Citations

209 papers	18,942 citations	66 h-index	135 g-index
217 ext. papers	22,148 ext. citations	10.7 avg, IF	4.66 L-index

#	Paper	IF	Citations
209	Genome-wide association study identifies novel breast cancer susceptibility loci. *Nature*, **2007**, 447, 1087-93	50.4	1957
208	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
207	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
206	Subtyping of breast cancer by immunohistochemistry to investigate a relationship between subtype and short and long term survival: a collaborative analysis of data for 10,159 cases from 12 studies. *PLoS Medicine*, **2010**, 7, e1000279	11.6	616
205	A common coding variant in CASP8 is associated with breast cancer risk. *Nature Genetics*, **2007**, 39, 352-8	36.3	557
204	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. *Journal of the National Cancer Institute*, **2011**, 103, 250-63	9.7	513
203	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, 304-11	2.2	435
202	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
201	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
200	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
199	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
198	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. *Nature Genetics*, **2009**, 41, 585-90	36.3	393
197	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
196	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. *Nature Genetics*, **2009**, 41, 1116-21	36.3	360
195	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
194	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
193	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. *PLoS Genetics*, **2008**, 4, e1000054	6	280

192	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. *Nature Genetics*, **2010**, 42, 885-92	36.3	276
191	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
190	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. *Nature Genetics*, **2011**, 43, 1210-4	36.3	253
189	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. *Breast Cancer Research*, **2013**, 15, R92	8.3	248
188	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. *Nature Genetics*, **2017**, 49, 1126-1132	36.3	246
187	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. *Nature Genetics*, **2011**, 43, 785-91	36.3	243
186	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
185	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
184	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
183	Association of a common variant of the CASP8 gene with reduced risk of breast cancer. *Journal of the National Cancer Institute*, **2004**, 96, 1866-9	9.7	173
182	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
181	An analysis of linkage disequilibrium in the interleukin-1 gene cluster, using a novel grouping method for multiallelic markers. *American Journal of Human Genetics*, **1998**, 62, 1180-8	11	165
180	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. *Nature Genetics*, **2013**, 45, 868-76	36.3	147
179	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. *Journal of the National Cancer Institute*, **2018**, 110, 855-862	9.7	145
178	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. *Human Molecular Genetics*, **2012**, 21, 5373-84	5.6	143
177	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2011**, 20, 3289-303	5.6	140
176	Contemporary Occupational Carcinogen Exposure and Bladder Cancer: A Systematic Review and Meta-analysis. *JAMA Oncology*, **2015**, 1, 1282-90	13.4	135
175	Interleukin-1 receptor antagonist allele (IL1RN*2) associated with nephropathy in diabetes mellitus. *Human Genetics*, **1996**, 97, 369-74	6.3	135

174	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *Journal of Clinical Oncology*, **2012**, 30, 4308-16	2.2	134
173	Multiple novel prostate cancer predisposition loci confirmed by an international study: the PRACTICAL Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 2052-61	4	134
172	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. *Carcinogenesis*, **2014**, 35, 1012-9	4.6	121
171	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
170	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. *PLoS Genetics*, **2013**, 9, e1003284	6	112
169	The interleukin 1 receptor antagonist gene allele 2 as a predictor of pouchitis following colectomy and IPAA in ulcerative colitis. *Gastroenterology*, **2001**, 121, 805-11	13.3	111
168	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. *Human Molecular Genetics*, **2013**, 22, 408-15	5.6	109
167	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
166	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
165	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
164	Common breast cancer susceptibility loci are associated with triple-negative breast cancer. *Cancer Research*, **2011**, 71, 6240-9	10.1	100
163	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
162	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Research*, **2012**, 72, 1795-803	10.1	93
161	A potential role for the XRCC2 R188H polymorphic site in DNA-damage repair and breast cancer. *Human Molecular Genetics*, **2002**, 11, 1433-8	5.6	93
160	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. *PLoS Genetics*, **2013**, 9, e1003173	6	90
159	Risk of estrogen receptor-positive and -negative breast cancer and single-nucleotide polymorphism 2q35-rs13387042. *Journal of the National Cancer Institute*, **2009**, 101, 1012-8	9.7	90
158	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
157	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

156	Combination of polymorphisms from genes related to estrogen metabolism and risk of prostate cancers: the hidden face of estrogens. *Journal of Clinical Oncology*, **2007**, 25, 3596-602	2.2	83
155	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. *Breast Cancer Research* , **2014**, 16, 3419	8.3	82
154	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
153	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	11.6	80
152	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
151	Association of folate-pathway gene polymorphisms with the risk of prostate cancer: a population-based nested case-control study, systematic review, and meta-analysis. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 2528-39	4	75
150	The role of genetic breast cancer susceptibility variants as prognostic factors. *Human Molecular Genetics*, **2012**, 21, 3926-39	5.6	75
149	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
148	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. *Breast Cancer Research*, **2010**, 12, R110	8.3	74
147	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. *Nature Communications*, **2016**, 7, 10933	17.4	70
146	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
145	Meta association of colorectal cancer confirms risk alleles at 8q24 and 18q21. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 616-21	4	66
144	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2011**, 20, 4693-706	5.6	66
143	Evaluation of the current knowledge limitations in breast cancer research: a gap analysis. *Breast Cancer Research*, **2008**, 10, R26	8.3	66
142	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
141	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
140	Genetic variants in the vitamin d receptor are associated with advanced prostate cancer at diagnosis: findings from the prostate testing for cancer and treatment study and a systematic review. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 2874-81	4	60
139	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

138	Role of tumour necrosis factor gene polymorphisms (-308 and -238) in breast cancer susceptibility and severity. *Breast Cancer Research*, **2004**, 6, R395-400	8.3	59
137	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
136	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
135	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
134	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
133	Five polymorphisms and breast cancer risk: results from the Breast Cancer Association Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 1610-6	4	53
132	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
131	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.3	51
130	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
129	Structure and polymorphism of the human gene for the interferon-induced p78 protein (MX1): evidence of association with alopecia areata in the Down syndrome region. *Human Genetics*, **2000**, 106, 639-45	6.3	49
128	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). *PLoS ONE*, **2012**, 7, e42380	3.7	49
127	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
126	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. *Breast Cancer Research and Treatment*, **2008**, 111, 139-44	4.4	48
125	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
124	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1121-9	4	46
123	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
122	Associations between an obesity related genetic variant (FTO rs9939609) and prostate cancer risk. *PLoS ONE*, **2010**, 5, e13485	3.7	46
121	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45

120	Association between a germline OCA2 polymorphism at chromosome 15q13.1 and estrogen receptor-negative breast cancer survival. *Journal of the National Cancer Institute*, **2010**, 102, 650-62	9.7	45
119	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. *EBioMedicine*, **2015**, 2, 681-9	8.8	44
118	MLH1 -93G>A promoter polymorphism and risk of mismatch repair deficient colorectal cancer. *International Journal of Cancer*, **2008**, 123, 2456-9	7.5	43
117	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
116	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
115	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. *Journal of Medical Genetics*, **2011**, 48, 477-84	5.8	42
114	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
113	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
112	Molecular cloning of the interleukin-1 gene cluster: construction of an integrated YAC/PAC contig and a partial transcriptional map in the region of chromosome 2q13. *Genomics*, **1997**, 41, 370-8	4.3	39
111	Thymidine selectively enhances growth suppressive effects of camptothecin/irinotecan in MSI+ cells and tumors containing a mutation of MRE11. *Clinical Cancer Research*, **2008**, 14, 5476-83	12.9	39
110	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
109	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285	6	38
108	MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973	3.7	37
107	Genetic variants in XRCC2: new insights into colorectal cancer tumorigenesis. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 2476-84	4	37
106	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
105	Mitotic defects in XRCC3 variants T241M and D213N and their relation to cancer susceptibility. *Human Molecular Genetics*, **2006**, 15, 1217-24	5.6	36
104	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
103	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. *Human Molecular Genetics*, **2014**, 23, 2490-7	5.6	35

102	11q13 is a susceptibility locus for hormone receptor positive breast cancer. *Human Mutation*, **2012**, 33, 1123-32	4.7	33
101	Missense variants in ATM in 26,101 breast cancer cases and 29,842 controls. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2143-51	4	31
100	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
99	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
98	Lung cancer and chronic obstructive pulmonary disease: From a clinical perspective. *Oncotarget*, **2017**, 8, 18513-18524	3.3	29
97	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. *Nature Communications*, **2018**, 9, 3221	17.4	29
96	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
95	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
94	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
93	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
92	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
91	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2011**, 20, 2222-31	4	27
90	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
89	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119	8.3	26
88	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
87	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
86	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
85	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

84	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. *Genetic Epidemiology*, **2014**, 38, 84-93	2.6	24
83	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24
82	Identification of candidate driver genes in common focal chromosomal aberrations of microsatellite stable colorectal cancer. *PLoS ONE*, **2013**, 8, e83859	3.7	23
81	A breast cancer risk haplotype in the caspase-8 gene. *Cancer Research*, **2009**, 69, 2724-8	10.1	23
80	FANCD2 re-expression is associated with glioma grade and chemical inhibition of the Fanconi Anaemia pathway sensitises gliomas to chemotherapeutic agents. *Oncotarget*, **2014**, 5, 6414-24	3.3	22
79	Human PIF1 helicase supports DNA replication and cell growth under oncogenic-stress. *Oncotarget*, **2014**, 5, 11381-98	3.3	22
78	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
77	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
76	Associations of folate, vitamin B12, homocysteine, and folate-pathway polymorphisms with prostate-specific antigen velocity in men with localized prostate cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 2833-8	4	20
75	Identification of new genetic risk factors for prostate cancer. *Asian Journal of Andrology*, **2009**, 11, 49-55	2.8	20
74	Endostatin gene variation and protein levels in breast cancer susceptibility and severity. *BMC Cancer*, **2007**, 7, 107	4.8	20
73	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocrine-Related Cancer*, **2015**, 22, 851-61	5.7	19
72	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
71	Fine-mapping CASP8 risk variants in breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2012**, 21, 176-81	4	19
70	Interleukin-1 receptor antagonist allele (ILIRN*2) associated with nephropathy in diabetes mellitus **1996**, 97, 369		19
69	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2015**, 1, 18-32	5.3	18
68	Association analysis of IL1A and IL1B variants in alopecia areata. *Heredity*, **2001**, 87, 215-9	3.6	18
67	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18

66	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. *International Journal of Cancer*, **2021**, 148, 1077-1086	7.5	18
65	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91	4	17
64	9q31.2-rs865686 as a susceptibility locus for estrogen receptor-positive breast cancer: evidence from the Breast Cancer Association Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2012**, 21, 1783-91	4	17
63	Structure and polymorphism of the human gene for the interferon-induced p78 protein (MX1): evidence of association with alopecia areata in the Down syndrome region. *Human Genetics*, **2000**, 106, 639-645	6.3	17
62	Consensus Analysis of Whole Transcriptome Profiles from Two Breast Cancer Patient Cohorts Reveals Long Non-Coding RNAs Associated with Intrinsic Subtype and the Tumour Microenvironment. *PLoS ONE*, **2016**, 11, e0163238	3.7	17
61	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. *Breast Cancer Research and Treatment*, **2016**, 157, 117-31	4.4	17
60	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. *Blood*, **2019**, 133, 1130-1139	2.2	17
59	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
58	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
57	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
56	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93	2.8	15
55	hapConstructor: automatic construction and testing of haplotypes in a Monte Carlo framework. *Bioinformatics*, **2008**, 24, 2105-7	7.2	14
54	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
53	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
52	Ultrabithorax mutations map to distant sites within the bithorax complex of Drosophila. *Nature*, **1984**, 309, 635-637	50.4	13
51	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 935-942	4	12
50	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. *Oncotarget*, **2019**, 10, 1760-1774	3.3	12
49	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

48	Comparing the efficacy of SNP filtering methods for identifying a single causal SNP in a known association region. *Annals of Human Genetics*, **2014**, 78, 50-61	2.2	12
47	A naturally occurring mutation in an ATP-binding domain of the recombination repair gene XRCC3 ablates its function without causing cancer susceptibility. *Human Molecular Genetics*, **2003**, 12, 915-23	5.6	12
46	Levels of DNA Methylation Vary at CpG Sites across the BRCA1 Promoter, and Differ According to Triple Negative and "BRCA-Like" Status, in Both Blood and Tumour DNA. *PLoS ONE*, **2016**, 11, e0160174	3.7	12
45	Altered RECQL5 expression in urothelial bladder carcinoma increases cellular proliferation and makes RECQL5 helicase activity a novel target for chemotherapy. *Oncotarget*, **2016**, 7, 76140-76150	3.3	12
44	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
43	Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. *Genetic Epidemiology*, **2016**, 40, 176-87	2.6	12
42	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. *Carcinogenesis*, **2018**, 39, 336-346	4.6	11
41	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. *Human Molecular Genetics*, **2014**, 23, 6034-46	5.6	11
40	The human gene encoding the interleukin-1 receptor accessory protein (IL1RAP) maps to chromosome 3q28 by fluorescence in situ hybridization and radiation hybrid mapping. *Genomics*, **1998**, 47, 325-6	4.3	11
39	Novel interleukin-1 receptor antagonist exon polymorphisms and their use in allele-specific mRNA assessment **1996**, 97, 723		11
38	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11
37	Very low PSA concentrations and deletions of the KLK3 gene. *Clinical Chemistry*, **2013**, 59, 234-44	5.5	10
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