

Angela Cox

List of Publications by Year in Descending Order

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Version: 2024-04-10

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , 2022 , 5, 65	6.7	0
208	Gene-gene interaction of AhRwith and within the Wntcascade affects susceptibility to lung cancer.. <i>European Journal of Medical Research</i> , 2022 , 27, 14	4.8	
207	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , 2022 , 24, 2	8.3	3
206	Iam hiQ-a novel pair of accuracy indices for imputed genotypes.. <i>BMC Bioinformatics</i> , 2022 , 23, 50	3.6	0
205	A biobank perspective on use of tissue samples donated by trial participants.. <i>Lancet Oncology</i> , 2022 , 23, e205	21.7	2
204	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	11	1
203	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	9.7	14
202	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. <i>International Journal of Cancer</i> , 2021 , 148, 1077-1086	7.5	18
201	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	8.7	2
200	The utility of the Laplace effect size prior distribution in Bayesian fine-mapping studies. <i>Genetic Epidemiology</i> , 2021 , 45, 386-401	2.6	2
199	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	8.3	1
198	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021 , 125, 1135-1145	8.7	0
197	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021 , 596, 393-397	50.4	28
196	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	4	4
195	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	36.3	76
194	Protein-altering germline mutations implicate novel genes related to lung cancer development. <i>Nature Communications</i> , 2020 , 11, 2220	17.4	6
193	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , 2020 , 44, 442-468	2.6	9

192	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020 , 11, 312	17.4	20
191	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020 , 52, 56-73	36.3	56
190	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020 , 107, 837-848	11	12
189	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45
188	Elevated Platelet Count Appears to Be Causally Associated with Increased Risk of Lung Cancer: A Mendelian Randomization Analysis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 935-942	4	12
187	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. <i>Oncotarget</i> , 2019 , 10, 1760-1774	3.3	12
186	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019 , 10, 1741	17.4	47
185	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019 , 120, 647-657	8.7	28
184	Using GWAS top hits to inform priors in Bayesian fine-mapping association studies. <i>Genetic Epidemiology</i> , 2019 , 43, 675-689	2.6	6
183	Bayesian variable selection using partially observed categorical prior information in fine-mapping association studies. <i>Genetic Epidemiology</i> , 2019 , 43, 690-703	2.6	3
182	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
181	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. <i>Blood</i> , 2019 , 133, 1130-1139	2.2	17
180	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019 , 48, 795-806	7.8	52
179	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018 , 39, 729-741	4.7	16
178	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018 , 7, 1978-1987	4.8	40
177	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. <i>Carcinogenesis</i> , 2018 , 39, 336-346	4.6	11
176	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 526-536	7.8	53
175	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 855-862	9.7	145

174	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
173	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. <i>Nature Communications</i> , 2018 , 9, 3221	17.4	29
172	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	36.3	101
171	Genome-Wide Analysis of Circulating Cell-Free DNA Copy Number Detects Active Melanoma and Predicts Survival. <i>Clinical Chemistry</i> , 2018 , 64, 1338-1346	5.5	7
170	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 2789-2799	10.1	49
169	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	36.3	257
168	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017 , 49, 1126-1132	36.3	246
167	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
166	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
165	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017 , 19, 119	8.3	26
164	Lung cancer and chronic obstructive pulmonary disease: From a clinical perspective. <i>Oncotarget</i> , 2017 , 8, 18513-18524	3.3	29
163	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017 , 141, 1830-1840	7.5	13
162	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017 , 19, 599-603	6.3	51
161	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
160	- a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017 , 8, 102769-102782	3.3	3
159	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016 , 141, 386-401	4.9	15
158	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	5.6	24
157	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 1503-1510	4	42

156	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	4.9	2
155	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016 , 6, 1052-67	24.4	104
154	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
153	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016 , 7, 12675	17.4	53
152	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	4.9	16
151	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016 , 7, 10933	17.4	70
150	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016 , 34, 2750-60	2.2	107
149	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016 , 23, 77-91	5.7	41
148	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016 , 53, 298-309	5.8	83
147	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016 , 48, 374-86	36.3	93
146	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , 2016 , 114, 298-304	8.7	5
145	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, 137-54	6.3	6
144	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	65
143	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
142	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. <i>PLoS ONE</i> , 2016 , 11, e0160174	3.7	12
141	Altered RECQL5 expression in urothelial bladder carcinoma increases cellular proliferation and makes RECQL5 helicase activity a novel target for chemotherapy. <i>Oncotarget</i> , 2016 , 7, 76140-76150	3.3	12
140	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016 , 7, 80140-80163	3.3	21
139	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	11.6	80

138	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016 , 11, e0160316	3.7	11
137	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. <i>PLoS ONE</i> , 2016 , 11, e0163238	3.7	17
136	Discordant Haplotype Sequencing Identifies Functional Variants at the 2q33 Breast Cancer Risk Locus. <i>Cancer Research</i> , 2016 , 76, 1916-25	10.1	5
135	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016 , 139, 1303-1317	7.5	26
134	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
133	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	8.3	25
132	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. <i>Breast Cancer Research and Treatment</i> , 2016 , 157, 117-31	4.4	17
131	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016 , 18, 22	8.3	31
130	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, 679-93	2.8	15
129	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016 , 48, 667-674	36.3	56
128	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	11	43
127	Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. <i>Genetic Epidemiology</i> , 2016 , 40, 176-87	2.6	12
126	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015 , 36, 256-71	4.6	12
125	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
124	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015 , 97, 22-34	11	26
123	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
122	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1121-9	4	46
121	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. <i>Human Genetics</i> , 2015 , 134, 231-45	6.3	30

120	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
119	Contemporary Occupational Carcinogen Exposure and Bladder Cancer: A Systematic Review and Meta-analysis. <i>JAMA Oncology</i> , 2015 , 1, 1282-90	13.4	135
118	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
117	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2015 , 22, 851-61	5.7	19
116	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, 1680-91	4	17
115	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 285-98	5.6	35
114	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 1478-92	5.6	46
113	Novel bayes factors that capture expert uncertainty in prior density specification in genetic association studies. <i>Genetic Epidemiology</i> , 2015 , 39, 239-48	2.6	9
112	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. <i>International Journal of Cancer</i> , 2015 , 136, E685-96	7.5	26
111	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015 , 5, 17369	4.9	27
110	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015 , 17, 58	8.3	24
109	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015 , 6, 37979-94	3.3	19
108	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
107	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2015 , 1, 18-32	5.3	18
106	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015 , 2, 681-9	8.8	44
105	Inherited mutations in 17 breast cancer susceptibility genes among a large triple-negative breast cancer cohort unselected for family history of breast cancer. <i>Journal of Clinical Oncology</i> , 2015 , 33, 304-11 ²	435	
104	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
103	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015 , 96, 5-20	11	59

102	Patient-Reported Outcomes (PRO) in the Setting of Relapsed Myeloma: The Influence of Treatment Strategies and Genetic Variants Predict Quality of Life and Pain Experience. <i>Blood</i> , 2015 , 126, 3180-3180 ^{2,2}		
101	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. <i>Human Molecular Genetics</i> , 2014 , 23, 1934-46	5.6	28
100	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. <i>Genetic Epidemiology</i> , 2014 , 38, 84-93	2.6	24
99	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. <i>Carcinogenesis</i> , 2014 , 35, 1012-9	4.6	121
98	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
97	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
96	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
95	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
94	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
93	Comparing the efficacy of SNP filtering methods for identifying a single causal SNP in a known association region. <i>Annals of Human Genetics</i> , 2014 , 78, 50-61	2.2	12
92	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
91	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014 , 16, 3419	8.3	82
90	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. <i>Human Molecular Genetics</i> , 2014 , 23, 2490-7	5.6	35
89	FANCD2 re-expression is associated with glioma grade and chemical inhibition of the Fanconi Anaemia pathway sensitises gliomas to chemotherapeutic agents. <i>Oncotarget</i> , 2014 , 5, 6414-24	3.3	22
88	Human PIF1 helicase supports DNA replication and cell growth under oncogenic-stress. <i>Oncotarget</i> , 2014 , 5, 11381-98	3.3	22
87	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium 2014 , n/a-n/a		1
86	Fine-scale mapping of the FGFR2 breast cancer risk locus: putative functional variants differentially bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013 , 93, 1046-60	11	80
85	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, 371-84, 384e1-2	36.3	422

84	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. <i>Breast Cancer Research</i> , 2013 , 15, R92	8.3	248
83	Very low PSA concentrations and deletions of the KLK3 gene. <i>Clinical Chemistry</i> , 2013 , 59, 234-44	5.5	10
82	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	11	167
81	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
80	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. <i>Nature Genetics</i> , 2013 , 45, 385-91, 391e1-2	36.3	413
79	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
78	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013 , 45, 868-76	36.3	147
77	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. <i>Human Molecular Genetics</i> , 2013 , 22, 408-15	5.6	109
76	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. <i>PLoS Genetics</i> , 2013 , 9, e1003173	6	90
75	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. <i>PLoS Genetics</i> , 2013 , 9, e1003284	6	112
74	Circulating cell-free DNA: a potential biomarker in lung cancer. <i>Lung Cancer Management</i> , 2013 , 2, 407-426		
73	Identification of candidate driver genes in common focal chromosomal aberrations of microsatellite stable colorectal cancer. <i>PLoS ONE</i> , 2013 , 8, e83859	3.7	23
72	Associations of ATR and CHEK1 single nucleotide polymorphisms with breast cancer. <i>PLoS ONE</i> , 2013 , 8, e68578	3.7	8
71	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012 , 44, 312-8	36.3	237
70	Lack of association between polymorphisms in the interleukin-1 gene cluster and familial thrombophilia. <i>Thrombosis Research</i> , 2012 , 129, 629-34	8.2	
69	9q31.2-rs865686 as a susceptibility locus for estrogen receptor-positive breast cancer: evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 1783-91	4	17
68	A BCL2 promoter polymorphism rs2279115 is not associated with BCL2 protein expression or patient survival in breast cancer patients. <i>SpringerPlus</i> , 2012 , 1, 38		8
67	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012 , 21, 5373-84	5.6	143

66	Breast cancer risk and 6q22.33: combined results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. <i>PLoS ONE</i> , 2012 , 7, e35706	3.7	10
65	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012 , 33, 1123-32	4.7	33
64	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. <i>Cancer Research</i> , 2012 , 72, 1795-803	3.1	93
63	Fine-mapping CASP8 risk variants in breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 176-81	4	19
62	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. <i>Journal of Clinical Oncology</i> , 2012 , 30, 4308-16	2.2	134
61	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012 , 21, 3926-39	5.6	75
60	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012 , 7, e42380	3.7	49
59	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. <i>Journal of Medical Genetics</i> , 2011 , 48, 477-84	5.8	42
58	Confirmation of 5p12 as a susceptibility locus for progesterone-receptor-positive, lower grade breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011 , 20, 2222-31	4	27
57	Associations of breast cancer risk factors with tumor subtypes: a pooled analysis from the Breast Cancer Association Consortium studies. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 250-63	9.7	513
56	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011 , 20, 3289-303	5.6	140
55	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011 , 43, 1210-4	36.3	253
54	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011 , 43, 785-91	36.3	243
53	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. <i>Human Molecular Genetics</i> , 2011 , 20, 4693-706	5.6	66
52	7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. <i>Journal of Medical Genetics</i> , 2011 , 48, 698-702	5.8	5
51	Common breast cancer susceptibility loci are associated with triple-negative breast cancer. <i>Cancer Research</i> , 2011 , 71, 6240-9	10.1	100
50	The causal roles of vitamin B(12) and transcobalamin in prostate cancer: can Mendelian randomization analysis provide definitive answers?. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2011 , 2, 316-27	0.9	9
49	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, 885-92	36.3	276

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2	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2
1	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1