Angela Cox

List of Publications by Year
in descending order

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208	24,532	10389 72	8396 147
papers	citations	h-index	g-index

217	217	217	25435
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
4	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.	8.4	764
5	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
6	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, 250-263.	6.3	596
7	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
8	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
9	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	1.6	521
10	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
11	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
12	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
13	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. Nature Genetics, 2017, 49, 1126-1132.	21.4	472
14	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
15	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
16	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.	21.4	426
17	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	21.4	389
18	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374

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19	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
20	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. Breast Cancer Research, 2013, 15, R92.	5.0	320
21	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
22	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptorâ€“negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309
23	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
24	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
25	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
26	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
27	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
28	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. Journal of the National Cancer Institute, 2018, 110, 855-862.	6.3	225
29	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.	6.2	201
30	Association of a Common Variant of the CASP8 Gene With Reduced Risk of Breast Cancer. Journal of the National Cancer Institute, 2004, 96, 1866-1869.	6.3	188
31	Contemporary Occupational Carcinogen Exposure and Bladder Cancer. JAMA Oncology, 2015, 1, 1282.	7.1	184
32	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
33	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
34	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	21.4	179
35	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
36	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, 1180-1188.	6.2	176

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37	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
38	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, 5373-5384.	2.9	168
39	CHEK2*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€“Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	1.6	162
40	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
41	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, 3289-3303.	2.9	152
42	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
43	Multiple Novel Prostate Cancer Predisposition Loci Confirmed by an International Study: The PRACTICAL Consortium. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2052-2061.	2.5	148
44	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	2.8	145
45	Interleukin-1 receptor antagonist allele (ILIRN*2) associated with nephropathy in diabetes mellitus. Human Genetics, 1996, 97, 369-374.	3.8	141
46	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
47	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
48	The interleukin 1 receptor antagonist gene allele 2 as a predictor of pouchitis following colectomy and IPAA in ulcerative colitis. Gastroenterology, 2001, 121, 805-811.	1.3	121
49	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
50	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, 408-415.	2.9	118
51	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.	8.4	118
52	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
53	A potential role for the XRCC2 R188H polymorphic site in DNA-damage repair and breast cancer. Human Molecular Genetics, 2002, 11, 1433-1438.	2.9	106
54	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105

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55	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
56	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
57	Risk of Estrogen Receptorâ€“Positive and â€“Negative Breast Cancer and Singleâ€“Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	6.3	99
58	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
59	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
60	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
61	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	12.8	94
62	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
63	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
64	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
65	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, 3596-3602.	1.6	89
66	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, 2528-2539.	2.5	89
67	Evaluation of the current knowledge limitations in breast cancer research: a gap analysis. Breast Cancer Research, 2008, 10, R26.	5.0	88
68	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.	1.9	88
69	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
70	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.	5.0	82
71	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
72	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80

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73	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
74	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
75	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
76	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.	6.2	76
77	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
78	Causal relationships between body mass index, smoking and lung cancer: Univariable and multivariable Mendelian randomization. International Journal of Cancer, 2021, 148, 1077-1086.	5.1	73
79	Meta Association of Colorectal Cancer Confirms Risk Alleles at 8q24 and 18q21. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 616-621.	2.5	71
80	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
81	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
82	Role of tumour necrosis factor gene polymorphisms (-308 and -238) in breast cancer susceptibility and severity. Breast Cancer Research, 2004, 6, R395-400.	5.0	65
83	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, 2874-2881.	2.5	64
84	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.	2.5	64
85	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
86	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
87	Associations between an Obesity Related Genetic Variant (FTO rs9939609) and Prostate Cancer Risk. PLoS ONE, 2010, 5, e13485.	2.5	61
88	Identification of susceptibility pathways for the role of chromosome 15q25.1 in modifying lung cancer risk. Nature Communications, 2018, 9, 3221.	12.8	60
89	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.	6.2	59
90	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	2.5	57

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91	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	2.9	56
92	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
93	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
94	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1121-1129.	2.5	56
95	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.	3.8	54
96	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
97	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
98	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
99	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.	2.5	51
100	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. Breast Cancer Research and Treatment, 2008, 111, 139-144.	2.5	50
101	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
102	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
103	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptorâ€"Negative Breast Cancer Survival. Journal of the National Cancer Institute, 2010, 102, 650-662.	6.3	48
104	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	3.2	47
105	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, 370-378.	2.9	45
106	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
107	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.	6.3	45
108	MLH1 â^'93G>A promoter polymorphism and risk of mismatch repair deficient colorectal cancer. International Journal of Cancer, 2008, 123, 2456-2459.	5.1	44

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109	Lung cancer and chronic obstructive pulmonary disease: From a clinical perspective. Oncotarget, 2017, 8, 18513-18524.	1.8	44
110	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
111	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
112	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
113	Thymidine Selectively Enhances Growth Suppressive Effects of Camptothecin/Irinotecan in MSI+ Cells and Tumors Containing a Mutation of MRE11. Clinical Cancer Research, 2008, 14, 5476-5483.	7.0	39
114	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
115	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
116	Genetic Variants inXRCC2: New Insights Into Colorectal Cancer Tumorigenesis. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2476-2484.	2.5	38
117	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
118	Mitotic defects in XRCC3 variants T241M and D213N and their relation to cancer susceptibility. Human Molecular Genetics, 2006, 15, 1217-1224.	2.9	37
119	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.	6.2	37
120	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
121	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.	3.3	35
122	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
123	Candidate locus analysis of the TERTâ€“CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
124	Human PIF1 helicase supports DNA replication and cell growth under oncogenic-stress. Oncotarget, 2014, 5, 11381-11398.	1.8	34
125	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	2.5	33
126	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.	2.9	33

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127	FANCD2 re-expression is associated with glioma grade and chemical inhibition of the Fanconi Anaemia pathway sensitises gliomas to chemotherapeutic agents. Oncotarget, 2014, 5, 6414-6424.	1.8	33
128	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, 1934-1946.	2.9	32
129	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
130	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.	1.8	31
131	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.	5.0	31
132	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	12.8	31
133	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
134	Identification of Candidate Driver Genes in Common Focal Chromosomal Aberrations of Microsatellite Stable Colorectal Cancer. PLoS ONE, 2013, 8, e83859.	2.5	29
135	Genome-wide interaction study of smoking behavior and non-small cell lung cancer risk in Caucasian population. Carcinogenesis, 2018, 39, 336-346.	2.8	29
136	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29
137	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
138	A Breast Cancer Risk Haplotype in the Caspase-8 Gene. Cancer Research, 2009, 69, 2724-2728.	0.9	27
139	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€"Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
140	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
141	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
142	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
143	Genetic interaction analysis among oncogenesis-related genes revealed novel genes and networks in lung cancer development. Oncotarget, 2019, 10, 1760-1774.	1.8	25
144	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.	3.0	24

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145	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
146	Identification of new genetic risk factors for prostate cancer. Asian Journal of Andrology, 2009, 11, 49-55.	1.6	23
147	Interleukin-1 receptor antagonist allele (IL1RN*2) associated with nephropathy in diabetes mellitus. Human Genetics, 1996, 97, 369-374.	3.8	23
148	Fine-Mapping CASP8 Risk Variants in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 176-181.	2.5	21
149	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.	2.5	21
150	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
151	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.	2.5	21
152	Endostatin gene variation and protein levels in breast cancer susceptibility and severity. BMC Cancer, 2007, 7, 107.	2.6	20
153	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, 2833-2838.	2.5	20
154	SNP-SNP interaction analysis of NF-ÎºB signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
155	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
156	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.	3.8	19
157	Association analysis of IL1A and IL1B variants in alopecia areata. Heredity, 2001, 87, 215-219.	2.6	19
158	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.	3.3	19
159	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
160	Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 623-642.	2.5	19
161	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.	1.8	19
162	Ultrabithorax mutations map to distant sites within the bithorax complex of Drosophila. Nature, 1984, 309, 635-637.	27.8	18

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163	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
164	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
165	hapConstructor: automatic construction and testing of haplotypes in a Monte Carlo framework. Bioinformatics, 2008, 24, 2105-2107.	4.1	17
166	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, 1783-1791.	2.5	17
167	Novel interleukin-1 receptor antagonist exon polymorphisms and their use in allele-specific mRNA assessment. Human Genetics, 1996, 97, 723-726.	3.8	17
168	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
169	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.	2.8	14
170	Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. Genetic Epidemiology, 2016, 40, 176-187.	1.3	14
171	Levels of DNA Methylation Vary at CpG Sites across the BRCA1 Promoter, and Differ According to Triple Negative and â€œBRCA-Likeâ€•Status, in Both Blood and Tumour DNA. PLoS ONE, 2016, 11, e0160174.	2.5	14
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