Georgia Chenevix-Trench

List of Publications by Year
in descending order

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508	54,339	2975	1676
papers	citations	93 h-index	214 g-index

532	532	532	50941
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Mutations of the BRAF gene in human cancer. Nature, 2002, 417, 949-954.	27.8	9,374
2	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	27.8	2,802
3	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
4	Mutations of the Human Homolog of Drosophila patched in the Nevoid Basal Cell Carcinoma Syndrome. Cell, 1996, 85, 841-851.	28.9	2,150
5	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
6	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
7	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	27.0	764
8	Intragenic ERBB2 kinase mutations in tumours. Nature, 2004, 431, 525-526.	27.8	757
9	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
10	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
11	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
12	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
13	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	7.4	546
14	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
15	Pathology of Breast and Ovarian Cancers among BRCA1 and BRCA2 Mutation Carriers: Results from the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	2.5	513
16	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
17	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
18	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

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19	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
20	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
21	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
22	CHEK2*1100delC and Susceptibility to Breast Cancer: A Collaborative Analysis Involving 10,860 Breast Cancer Cases and 9,065 Controls from 10 Studies. American Journal of Human Genetics, 2004, 74, 1175-1182.	6.2	422
23	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	7.4	390
24	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
25	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
26	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
27	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
28	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
29	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
30	Nevoid basal cell carcinoma syndrome: Review of 118 affected individuals. American Journal of Medical Genetics Part A, 1994, 50, 282-290.	2.4	318
31	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
32	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
33	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
34	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
35	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
36	A recurrent germline PAX5 mutation confers susceptibility to pre-B cell acute lymphoblastic leukemia. Nature Genetics, 2013, 45, 1226-1231.	21.4	270

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37	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
38	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
39	Dose-Response Association of CD8⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. JAMA Oncology, 2017, 3, e173290.	7.1	260
40	Common Breast Cancer-Predisposition Alleles Are Associated with Breast Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. American Journal of Human Genetics, 2008, 82, 937-948.	6.2	257
41	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
42	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
43	Gastric adenocarcinoma and proximal polyposis of the stomach (GAPPS): a new autosomal dominant syndrome. Gut, 2012, 61, 774-779.	12.1	242
44	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, .	6.3	242
45	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
46	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	2.5	224
47	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
48	Dominant Negative ATM Mutations in Breast Cancer Families. Journal of the National Cancer Institute, 2002, 94, 205-215.	6.3	217
49	RAD51 135Gâ†'C Modifies Breast Cancer Risk among BRCA2 Mutation Carriers: Results from a Combined Analysis of 19 Studies. American Journal of Human Genetics, 2007, 81, 1186-1200.	6.2	217
50	The BRCA1-Î"11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.9	208
51	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
52	Point Mutations in Exon 1B of APC Reveal Gastric Adenocarcinoma and Proximal Polyposis of the Stomach as a Familial Adenomatous Polyposis Variant. American Journal of Human Genetics, 2016, 98, 830-842.	6.2	201
53	Glutathione S-transferase M1 and T1 polymorphisms: susceptibility to colon cancer and age of onset. Carcinogenesis, 1995, 16, 1655-1657.	2.8	193
54	Rare variants in the ATMgene and risk of breast cancer. Breast Cancer Research, 2011, 13, R73.	5.0	188

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55	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
56	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
57	Isolation and characterization of human patched 2 (PTCH2), a putative tumour suppressor gene inbasal cell carcinoma and medulloblastoma on chromosome 1p32. Human Molecular Genetics, 1999, 8, 291-297.	2.9	175
58	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
59	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.9	169
60	Rare, Evolutionarily Unlikely Missense Substitutions in ATM Confer Increased Risk of Breast Cancer. American Journal of Human Genetics, 2009, 85, 427-446.	6.2	165
61	Incessant ovulation, inflammation and epithelial ovarian carcinogenesis: Revisiting old hypotheses. Molecular and Cellular Endocrinology, 2006, 247, 4-21.	3.2	162
62	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
63	Genetic and Histopathologic Evaluation ofBRCA1andBRCA2DNA Sequence Variants of Unknown Clinical Significance. Cancer Research, 2006, 66, 2019-2027.	0.9	153
64	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
65	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
66	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.	1.6	152
67	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
68	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	7.0	138
69	An international initiative to identify genetic modifiers of cancer risk in BRCA1 and BRCA2 mutation carriers: the Consortium of Investigators of Modifiers of BRCA1 and BRCA2 (CIMBA). Breast Cancer Research, 2007, 9, 104.	5.0	136
70	Analysis of cancer risk and BRCA1 and BRCA2mutation prevalence in the kConFab familial breast cancer resource. Breast Cancer Research, 2006, 8, R12.	5.0	135
71	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, 5056-5064.	2.9	130
72	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128

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73	The CYP3A4*1B polymorphism has no functional significance and is not associated with risk of breast or ovarian cancer. Pharmacogenetics and Genomics, 2002, 12, 355-366.	5.7	126
74	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
75	Genomic instability occurs in colorectal carcinomas but not in adenomas. Human Mutation, 1993, 2, 351-354.	2.5	124
76	HER3 and downstream pathways are involved in colonization of brain metastases from breast cancer. Breast Cancer Research, 2010, 12, R46.	5.0	122
77	Breast cancer stem cells: treatment resistance and therapeutic opportunities. Carcinogenesis, 2011, 32, 650-658.	2.8	120
78	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
79	?-Catenin mutation and expression analysis in ovarian cancer: Exon 3 mutations and nuclear translocation in 16% of endometrioid tumours. International Journal of Cancer, 1999, 82, 625-629.	5.1	119
80	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
81	Analysis of gene amplification in head-and-neck squamous-cell carcinomas. International Journal of Cancer, 1991, 48, 511-515.	5.1	115
82	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. Molecular Psychiatry, 2012, 17, 1116-1129.	7.9	112
83	A genome wide linkage search for breast cancer susceptibility genes. Genes Chromosomes and Cancer, 2006, 45, 646-655.	2.8	111
84	Gene expression profiling of tumour epithelial and stromal compartments during breast cancer progression. Breast Cancer Research and Treatment, 2012, 135, 153-165.	2.5	111
85	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	1.9	111
86	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
87	Tumour-specific distribution of BRCA1 promoter region methylation supports a pathogenetic role in breast and ovarian cancer. Carcinogenesis, 2000, 21, 147-151.	2.8	108
88	Mutation of ERBB2 Provides a Novel Alternative Mechanism for the Ubiquitous Activation of RAS-MAPK in Ovarian Serous Low Malignant Potential Tumors. Molecular Cancer Research, 2008, 6, 1678-1690.	3.4	108
89	ABCA Transporter Gene Expression and Poor Outcome in Epithelial Ovarian Cancer. Journal of the National Cancer Institute, 2014, 106, .	6.3	107
90	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	6.3	106

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91	CDX2, a human homologue of Drosophila caudal, is mutated in both alleles in a replication error positive colorectal cancer. Oncogene, 1998, 17, 657-659.	5.9	105
92	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
93	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
94	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
95	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
96	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	2.9	99
97	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
98	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
99	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
100	Integrated genomic and transcriptomic analysis of human brain metastases identifies alterations of potential clinical significance. Journal of Pathology, 2015, 237, 363-378.	4.5	98
101	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
102	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
103	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
104	Germ-line mutations inBRCA1 orBRCA2 in the normal breast are associated with altered expression of estrogen-responsive proteins and the predominance of progesterone receptor A. Genes Chromosomes and Cancer, 2004, 39, 236-248.	2.8	91
105	Interplay between BRCA1 and RHAMM Regulates Epithelial Apicobasal Polarization and May Influence Risk of Breast Cancer. PLoS Biology, 2011, 9, e1001199.	5.6	91
106	ABCB1 (MDR 1) Polymorphisms and Progression-Free Survival among Women with Ovarian Cancer following Paclitaxel/Carboplatin Chemotherapy. Clinical Cancer Research, 2008, 14, 5594-5601.	7.0	90
107	The Landscape of Somatic Genetic Alterations in Breast Cancers From ATM Germline Mutation Carriers. Journal of the National Cancer Institute, 2018, 110, 1030-1034.	6.3	90
108	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90

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109	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	1.6	90
110	Population-based estimates of breast cancer risks associated withATMgene variants c.7271T>G and c.1066-6T>G (IVS10-6T>G) from the Breast Cancer Family Registry. Human Mutation, 2006, 27, 1122-1128.	2.5	88
111	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	5.0	88
112	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
113	Subtypes of familial breast tumours revealed by expression and copy number profiling. Breast Cancer Research and Treatment, 2010, 123, 661-677.	2.5	86
114	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
115	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	2.9	85
116	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 2009, 18, 1131-1139.	2.9	84
117	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
118	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.	2.4	82
119	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
120	DNA Methylome of Familial Breast Cancer Identifies Distinct Profiles Defined by Mutation Status. American Journal of Human Genetics, 2010, 86, 420-433.	6.2	80
121	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
122	Rad51 supports triple negative breast cancer metastasis. Oncotarget, 2014, 5, 3261-3272.	1.8	80
123	Classification of BRCA1 missense variants of unknown clinical significance. Journal of Medical Genetics, 2005, 42, 138-146.	3.2	79
124	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2007, 67, 3027-3035.	0.9	78
125	Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	5.0	78
126	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	21.4	78

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127	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
128	Double-Strand Break Repair Gene Polymorphisms and Risk of Breast or Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 319-323.	2.5	77
129	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
130	Evidence for a time-dependent association between FOLR1 expression and survival from ovarian carcinoma: implications for clinical testing. An Ovarian Tumour Tissue Analysis consortium study. British Journal of Cancer, 2014, 111, 2297-2307.	6.4	76
131	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
132	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 245-250.	2.5	75
133	A Genome-Wide Association Study of Caffeine-Related Sleep Disturbance: Confirmation of a Role for a Common Variant in the Adenosine Receptor. Sleep, 2012, 35, 967-975.	1.1	75
134	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
135	A Role for Common Genomic Variants in the Assessment of Familial Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4330-4336.	1.6	74
136	Polymorphisms at the glutathione S-transferase GSTM1, GSTT1 and GSTP1 loci: risk of ovarian cancer by histological subtype. Carcinogenesis, 2001, 22, 67-72.	2.8	73
137	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	5.1	73
138	A Novel Corepressor, BCoR-L1, Represses Transcription through an Interaction with CtBP. Journal of Biological Chemistry, 2007, 282, 15248-15257.	3.4	72
139	Clinical Classification ofBRCA1andBRCA2DNA Sequence Variants: The Value of Cytokeratin Profiles and Evolutionary Analysisâ€"A Report From the kConFab Investigators. Journal of Clinical Oncology, 2008, 26, 1657-1663.	1.6	72
140	A fine-scale dissection of the DNA double-strand break repair machinery and its implications for breast cancer therapy. Nucleic Acids Research, 2014, 42, 6106-6127.	14.5	72
141	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	5.0	71
142	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
143	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
144	Distinct phenotype in maternal uniparental disomy of chromosome 14. American Journal of Medical Genetics Part A, 1994, 51, 147-149.	2.4	70

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145	Meta-analysis of the global gene expression profile of triple-negative breast cancer identifies genes for the prognostication and treatment of aggressive breast cancer. Oncogenesis, 2014, 3, e100-e100.	4.9	70
146	Androgen Receptor Exon 1 CAG Repeat Length and Breast Cancer in Women Before Age Forty Years. Journal of the National Cancer Institute, 1999, 91, 961-966.	6.3	69
147	Role of genetic polymorphisms and ovarian cancer susceptibility. Molecular Oncology, 2009, 3, 171-181.	4.6	69
148	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	2.9	68
149	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
150	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
151	Common chromosomal fragile site FRA16D mutation in cancer cells. Human Molecular Genetics, 2005, 14, 1341-1349.	2.9	66
152	Treatment of Triple-Negative Breast Cancer Using Anti-EGFRâ€"Directed Radioimmunotherapy Combined with Radiosensitizing Chemotherapy and PARP Inhibitor. Journal of Nuclear Medicine, 2013, 54, 913-921.	5.0	66
153	Association Between Single-Nucleotide Polymorphisms in Hormone Metabolism and DNA Repair Genes and Epithelial Ovarian Cancer: Results from Two Australian Studies and an Additional Validation Set. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2557-2565.	2.5	65
154	Analysis of RAD51C germline mutations in high-risk breast and ovarian cancer families and ovarian cancer patients. Human Mutation, 2012, 33, 95-99.	2.5	64
155	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	1.2	64
156	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.9	63
157	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
158	Targeted massively parallel sequencing of a panel of putative breast cancer susceptibility genes in a large cohort of multiple-case breast and ovarian cancer families. Journal of Medical Genetics, 2016, 53, 34-42.	3.2	63
159	Gene expression profiling of formalinâ€fixed, paraffinâ€embedded familial breast tumours using the whole genomeâ€DASL assay. Journal of Pathology, 2010, 221, 452-461.	4.5	62
160	Reduced expression of intercellular adhesion molecule-1 in ovarian adenocarcinomas. British Journal of Cancer, 2001, 85, 1351-1358.	6.4	60
161	Common variants associated with breast cancer in genome-wide association studies are modifiers of breast cancer risk in BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2010, 19, 2886-2897.	2.9	60
162	Heregulin-HER3-HER2 signaling promotes matrix metalloproteinase-dependent blood-brain-barrier transendothelial migration of human breast cancer cell lines. Oncotarget, 2015, 6, 3932-3946.	1.8	60

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163	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
164	Identification of BRCA1 missense substitutions that confer partial functional activity: potential moderate risk variants?. Breast Cancer Research, 2007, 9, R82.	5.0	58
165	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
166	Platinum Sensitivityâ€"Related Germline Polymorphism Discovered via a Cell-Based Approach and Analysis of Its Association with Outcome in Ovarian Cancer Patients. Clinical Cancer Research, 2011, 17, 5490-5500.	7.0	57
167	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.	5.0	57
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