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	Methotrexate-related central neurotoxicity: clinical characteristics, risk factors and genome-wide association study in children treated for acute lymphoblastic leukemia. Haematologica, 2022, 107, 635-643.	3.5	16
2	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
3	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants. Genetics in Medicine, 2022, 24, 119-129.	2.4	10
4	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	1.6	90
5	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
6	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
7	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
8	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
9	TRACEBACK: Testing of Historical Tubo-Ovarian Cancer Patients for Hereditary Risk Genes as a Cancer Prevention Strategy in Family Members. Journal of Clinical Oncology, 2022, , JCO2102108.	1.6	3
10	Epigenome erosion and SOX10 drive neural crest phenotypic mimicry in triple-negative breast cancer. Npj Breast Cancer, 2022, 8, 57.	5.2	11
11	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
12	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
13	Population-based targeted sequencing of 54 candidate genes identifiesPALB2as a susceptibility gene for high-grade serous ovarian cancer. Journal of Medical Genetics, 2021, 58, 305-313.	3.2	26
14	Evaluating the role of alcohol consumption in breast and ovarian cancer susceptibility using populationâ€based cohort studies and twoâ€sample Mendelian randomization analyses. International Journal of Cancer, 2021, 148, 1338-1350.	5.1	9
15	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
16	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
17	RNF168 regulates R-loop resolution and genomic stability in BRCA1/2-deficient tumors. Journal of Clinical Investigation, 2021, 131, .	8.2	38
18	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

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19	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. Human Genetics and Genomics Advances, 2021, 2, 100042.	1.7	6
20	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	2.5	5
21	The predictive ability of the 313 variantâ€“based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	2.4	16
22	Abstract 758: The clinical utility of BRCA1/2 pathogenic variants in breast cancer patient prognosis. , 2021, , .		0
23	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
24	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
25	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
26	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
27	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
28	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
29	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€‰951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	6.3	35
30	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
31	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	8.8	27
32	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	1.9	41
33	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
34	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
35	Immune Cell Associations with Cancer Risk. IScience, 2020, 23, 101296.	4.1	6
36	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39

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37	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	5.2	5
38	eQTL Colocalization Analyses Identify NTN4 as a Candidate Breast Cancer Risk Gene. American Journal of Human Genetics, 2020, 107, 778-787.	6.2	29
39	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
40	Copy Number Variation and Ovarian Cancer Riskâ€"Letter. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1278-1278.	2.5	1
41	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (PrOTYPE). Clinical Cancer Research, 2020, 26, 5411-5423.	7.0	43
42	Nicholas Gordon Martin. Twin Research and Human Genetics, 2020, 23, 72-73.	0.6	0
43	SNPs in lncRNA Regions and Breast Cancer Risk. Frontiers in Genetics, 2020, 11, 550.	2.3	14
44	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
45	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. Gynecologic Oncology, 2020, 158, 702-709.	1.4	15
46	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
47	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
48	Candidate Causal Variants at the 8p12 Breast Cancer Risk Locus Regulate DUSP4. Cancers, 2020, 12, 170.	3.7	6
49	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
50	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	8.8	21
51	Genome-Wide Association Meta-Analysis of Single-Nucleotide Polymorphisms and Symptomatic Venous Thromboembolism during Therapy for Acute Lymphoblastic Leukemia and Lymphoma in Caucasian Children. Cancers, 2020, 12, 1285.	3.7	5
52	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
53	LobSig is a multigene predictor of outcome in invasive lobular carcinoma. Npj Breast Cancer, 2019, 5, 18.	5.2	28
54	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28

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55	â€œI am not a statisticâ€•ovarian cancer survivorsâ€™ views of factors that influenced their long-term survival. Gynecologic Oncology, 2019, 155, 461-467.	1.4	19
56	The molecular origin and taxonomy of mucinous ovarian carcinoma. Nature Communications, 2019, 10, 3935.	12.8	110
57	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
58	The spectrum of BRCA1 and BRCA2 pathogenic sequence variants in Middle Eastern, North African, and South European countries. Human Mutation, 2019, 40, e1-e23.	2.5	34
59	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	6.4	19
60	BRCA1andBRCA2pathogenic sequence variants in women of African origin or ancestry. Human Mutation, 2019, 40, 1781-1796.	2.5	26
61	Whole-genome sequencing reveals clinically relevant insights into the aetiology of familial breast cancers. Annals of Oncology, 2019, 30, 1071-1079.	1.2	64
62	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
63	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. Gynecologic Oncology, 2019, 153, 343-355.	1.4	28
64	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
65	Germline deletion of ETV6 in familial acute lymphoblastic leukemia. Blood Advances, 2019, 3, 1039-1046.	5.2	21
66	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
67	Is Schizophrenia a Risk Factor for Breast Cancer?â€”Evidence From Genetic Data. Schizophrenia Bulletin, 2019, 45, 1251-1256.	4.3	24
68	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	6.3	30
69	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
70	A comprehensive geneâ€“environment interaction analysis in Ovarian Cancer using genomeâ€wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	5.1	12
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 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

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73	Characterization of a novel breast cancer cell line derived from a metastatic bone lesion of a breast cancer patient. Breast Cancer Research and Treatment, 2018, 170, 179-188.	2.5	5
74	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. Mayo Clinic Proceedings, 2018, 93, 307-320.	3.0	22
75	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
76	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	6.4	15
77	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	2.5	224
78	Genome-wide association study of paclitaxel and carboplatin disposition in women with epithelial ovarian cancer. Scientific Reports, 2018, 8, 1508.	3.3	3
79	Ovarian cancer risk, <scp>ALDH</scp>2 polymorphism and alcohol drinking: Asian data from the Ovarian Cancer Association Consortium. Cancer Science, 2018, 109, 435-445.	3.9	10
80	Mixed ductalâ€lobular carcinomas: evidence for progression from ductal to lobular morphology. Journal of Pathology, 2018, 244, 460-468.	4.5	31
81	Morphology and genomic hallmarks of breast tumours developed by ATM deleterious variant carriers. Breast Cancer Research, 2018, 20, 28.	5.0	35
82	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	1.9	15
83	Multidimensional phenotyping of breast cancer cell lines to guide preclinical research. Breast Cancer Research and Treatment, 2018, 167, 289-301.	2.5	27
84	The importance of using public data to validate reported associations. PLoS Genetics, 2018, 14, e1007416.	3.5	0
85	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	54
86	Guidelines for whole genome bisulphite sequencing of intact and FFPET DNA on the Illumina HiSeq X Ten. Epigenetics and Chromatin, 2018, 11, 24.	3.9	38
87	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	2.5	9
88	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	4.1	3
89	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
90	A gene expression prognostic signature for overall survival in patients with high-grade serous ovarian cancer.. Journal of Clinical Oncology, 2018, 36, 5583-5583.	1.6	1

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91	Abstract 2211: Patient level polygenic risk scores and continuous estrogen receptor expression in breast cancer. , 2018, , .		0
92	Abstract 2271: Pathway analysis suggests biological processes driven by germline genetic associations with breast cancer prognosis. , 2018, , .		0
93	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. Genetics in Medicine, 2017, 19, 30-35.	2.4	53
94	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. European Journal of Human Genetics, 2017, 25, 432-438.	2.8	26
95	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
96	Translating Germline Cancer Risk into Precision Prevention. Cell, 2017, 168, 566-570.	28.9	22
97	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
98	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
99	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
100	Integration of Population-Level Genotype Data with Functional Annotation Reveals Over-Representation of Long Noncoding RNAs at Ovarian Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 116-125.	2.5	6
101	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
102	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
103	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
104	Panel sequencing of 264 candidate susceptibility genes and segregation analysis in a cohort of non-BRCA1, non-BRCA2 breast cancer families. Breast Cancer Research and Treatment, 2017, 166, 937-949.	2.5	16
105	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	2.5	18
106	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 420-424.	2.5	3
107	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
108	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

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109	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
110	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
111	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
112	Functional dissection of breast cancer risk-associated TERT promoter variants. Oncotarget, 2017, 8, 67203-67217.	1.8	21
113	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	1.8	14
114	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. Oncotarget, 2017, 8, 64670-64684.	1.8	7
115	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
116	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
117	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	2.5	10
118	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
119	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
120	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
121	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	2.9	17
122	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
123	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
124	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
125	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
126	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43

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127	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
128	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
129	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
130	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
131	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
132	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
133	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
134	Systematic review with metaâ€analysis: fundic gland polyps and proton pump inhibitors. Alimentary Pharmacology and Therapeutics, 2016, 44, 915-925.	3.7	55
135	A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. International Journal of Cancer, 2016, 139, 2646-2654.	5.1	7
136	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
137	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
138	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
139	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
140	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
141	High content screening application for cell-type specific behaviour in heterogeneous primary breast epithelial subpopulations. Breast Cancer Research, 2016, 18, 18.	5.0	9
142	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
143	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
144	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

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145	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
146	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
147	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
148	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	1.0	37
149	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
150	Abstract 2598: Predicting breast and ovarian cancer risks for BRCA1 and BRCA2 mutation carriers using polygenic risk scores. , 2016, , .		1
151	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
152	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	1.8	5
153	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
154	Germline polymorphisms in an enhancer of PSIP1 are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	1.8	29
155	Abstract 797: A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. , 2016, , .		0
156	Abstract 134: Mutational landscape of breast cancers from PALB2 germline mutation carriers. , 2016, , .		0
157	Abstract 3451: Breast cancer risk factor associations by loss of E-cadherin tumor tissue expression: A pooled analysis of 5,896 cases in 12 studies from the Breast Cancer Association Consortium (BCAC). , 2016, , .		0
158	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
159	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
160	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	5.0	26
161	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
162	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0

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163	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	2.5	34
164	A Common Cancer Risk-Associated Allele in the hTERT Locus Encodes a Dominant Negative Inhibitor of Telomerase. PLoS Genetics, 2015, 11, e1005286.	3.5	35
165	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
166	Cep55 regulates embryonic growth and development by promoting Akt stability in zebrafish. FASEB Journal, 2015, 29, 1999-2009.	0.5	24
167	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
168	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	27.0	764
169	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
170	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
171	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
172	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
173	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
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