Thilo DÃ¶rk

List of Publications by Year
in descending order

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Version: 2024-02-01

355 papers	27,003 citations	11235 73 h-index	9346 148 g-index
378 all docs	378 docs citations	378 times ranked	28828 citing authors

#	Article	IF	Citations
1	Cancer in Children With Fanconi Anemia and Ataxia-Telangiectasiaâ€"A Nationwide Register-Based Cohort Study in Germany. Journal of Clinical Oncology, 2022, 40, 32-39.	0.8	17
2	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
3	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
4	Causation and causal inference in obstetrics-gynecology. American Journal of Obstetrics and Gynecology, 2022, 226, 12-23.	0.7	2
5	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
6	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
7	Exome sequencing identifies RASSF1 and KLK3 germline variants in an Iranian multiple-case breast cancer family. European Journal of Medical Genetics, 2022, 65, 104425.	0.7	1
8	OUP accepted manuscript. Human Molecular Genetics, 2022, , .	1.4	1
9	Variants in genes encoding the SUR1-TRPM4 non-selective cation channel and sudden infant death syndrome (SIDS): potentially increased risk for cerebral edema. International Journal of Legal Medicine, 2022, , 1.	1.2	1
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
11	Associations of a breast cancer polygenic risk score with tumor characteristics and survival.. Journal of Clinical Oncology, 2022, 40, 563-563.	0.8	1
12	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 217-228.	1.1	12
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.	1.5	26
14	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	2.3	35
15	Genetic association study of fatal pulmonary embolism. International Journal of Legal Medicine, 2021, 135, 143-151.	1.2	3
16	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.	2.9	5
17	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	5.8	19
18	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532

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19	Gene variants associated with obstructive sleep apnea (OSA) in relation to sudden infant death syndrome (SIDS). International Journal of Legal Medicine, 2021, 135, 1499-1506.	1.2	7
20	Persistent DNA Double-Strand Breaks After Repeated Diagnostic CT Scans in Breast Epithelial Cells and Lymphocytes. Frontiers in Oncology, 2021, 11, 634389.	1.3	2
21	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	1.7	4
22	MicroRNA Profiles of Maternal and Neonatal Endothelial Progenitor Cells in Preeclampsia. International Journal of Molecular Sciences, 2021, 22, 5320.	1.8	12
23	Association of genomic variants at <scp>PAX8</scp> and <scp>PBX2</scp> with cervical cancer risk. International Journal of Cancer, 2021, 149, 893-900.	2.3	7
24	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.	1.0	6
25	Identification of a Locus Near ULK1 Associated With Progression-Free Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1669-1680.	1.1	5
26	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.	2.6	6
27	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
28	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.	2.2	7
29	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
30	NK Cell-Mediated Eradication of Ovarian Cancer Cells with a Novel Chimeric Antigen Receptor Directed against CD44. Biomedicines, 2021, 9, 1339.	1.4	18
31	Performance of a six-methylation-marker assay on self-collected cervical samples â€“ A feasibility study. Journal of Virological Methods, 2021, 295, 114219.	1.0	8
32	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.	1.1	19
33	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
34	Genomic Risk Factors for Cervical Cancer. Cancers, 2021, 13, 5137.	1.7	21
35	Multi-tissue transcriptome-wide association study identifies eight candidate genes and tissue-specific gene expression underlying endometrial cancer susceptibility. Communications Biology, 2021, 4, 1211.	2.0	11
36	First Prospective Cross-Sectional Study on the Impact of Immigration Background and Education in Early Detection of Breast Cancer. Breast Care, 2021, 16, 516-522.	0.8	1

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37	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.	3.0	35
38	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	2.3	13
39	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
40	RAD50 regulates mitotic progression independent of DNA repair functions. FASEB Journal, 2020, 34, 2812-2820.	0.2	9
41	Exome sequencing study of Russian breast cancer patients suggests a predisposing role for USP39. Breast Cancer Research and Treatment, 2020, 179, 731-742.	1.1	9
42	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. American Journal of Human Genetics, 2020, 107, 622-635.	2.6	14
43	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39
44	Evidence of pathogenicity for the leaky splice variant c. 1066â€6T >Gâ€‰in ATM. American Journal of Medical Genetics, Part A, 2020, 182, 2971-2975.	0.7	5
45	Genetic Susceptibility to Endometrial Cancer: Risk Factors and Clinical Management. Cancers, 2020, 12, 2407.	1.7	32
46	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
47	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
48	Human <scp>RAD50</scp> deficiency: Confirmation of a distinctive phenotype. American Journal of Medical Genetics, Part A, 2020, 182, 1378-1386.	0.7	21
49	Association of genomic variants at the human leukocyte antigen locus with cervical cancer risk, HPV status and gene expression levels. International Journal of Cancer, 2020, 147, 2458-2468.	2.3	12
50	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
51	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
52	Recommendations Related to Genetic Testing for Breast Cancer. JAMA - Journal of the American Medical Association, 2020, 323, 188.	3.8	0
53	Genomeâ€wide SNP typing of ancient DNA: Determination of hair and eye color of Bronze Age humans from their skeletal remains. American Journal of Physical Anthropology, 2020, 172, 99-109.	2.1	6
54	Germline variation of Ribonuclease H2 genes in ovarian cancer patients. Journal of Ovarian Research, 2020, 13, 146.	1.3	1

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55	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.	0.4	49
56	A Splice Site Variant of CDK12 and Breast Cancer in Three Eurasian Populations. Frontiers in Oncology, 2019, 9, 493.	1.3	4
57	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
58	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. EBioMedicine, 2019, 48, 203-211.	2.7	14
59	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
60	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
61	BARD1 is a Low/Moderate Breast Cancer Risk Gene: Evidence Based on an Association Study of the Central European p.Q564X Recurrent Mutation. Cancers, 2019, 11, 740.	1.7	25
62	Preeclampsia-Associated Alteration of DNA Methylation in Fetal Endothelial Progenitor Cells. Frontiers in Cell and Developmental Biology, 2019, 7, 32.	1.8	17
63	Towards controlled terminology for reporting germline cancer susceptibility variants: an ENIGMA report. Journal of Medical Genetics, 2019, 56, 347-357.	1.5	32
64	Functional classification of ATM variants in ataxiaâ€telangiectasia patients. Human Mutation, 2019, 40, 1713-1730.	1.1	27
65	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
66	Genotypeâ€“phenotype correlations in ataxia telangiectasia patients with ATM c.3576G>A and c.8147T>C mutations. Journal of Medical Genetics, 2019, 56, 308-316.	1.5	29
67	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
68	Characterization of a Novel Third-Generation Anti-CD24-CAR against Ovarian Cancer. International Journal of Molecular Sciences, 2019, 20, 660.	1.8	70
69	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. European Journal of Epidemiology, 2019, 34, 591-600.	2.5	16
70	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
71	Late-Onset Antibody Deficiency Due to Monoallelic Alterations in NFKB1. Frontiers in Immunology, 2019, 10, 2618.	2.2	29
72	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711

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73	Evidence for an association of interferon gene variants with sudden infant death syndrome. International Journal of Legal Medicine, 2019, 133, 863-869.	1.2	8
74	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.4	22
75	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
76	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
77	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129.	2.9	15
78	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
79	Exome sequencing and caseâ€“control analyses identify RCC1 as a candidate breast cancer susceptibility gene. International Journal of Cancer, 2018, 142, 2512-2517.	2.3	17
80	Assessment of a FBXW8 frameshift mutation, c.1312_1313delGT, in breast cancer patients and controls from Central Europe. Cancer Genetics, 2018, 220, 38-43.	0.2	1
81	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2018, 47, 450-459.	0.9	15
82	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.	0.4	54
83	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
84	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
85	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
86	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
87	Prospective cross-sectional-study on influence of immigration background and education on breast cancer survival in a real-world setting.. Journal of Clinical Oncology, 2018, 36, e18650-e18650.	0.8	0
88	Abstract 230: Joint genome-wide association study of endometrial cancer and ovarian cancer identifies a novel genetic risk region at 14q23.3. , 2018, , .		0
89	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. British Journal of Cancer, 2017, 116, 524-535.	2.9	23
90	Assessment of an APOBEC3B truncating mutation, c.783delG, in patients with breast cancer. Breast Cancer Research and Treatment, 2017, 162, 31-37.	1.1	5

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91	Evaluation of RAG1 mutations in an adult with combined immunodeficiency and progressive multifocal leukoencephalopathy. Clinical Immunology, 2017, 179, 1-7.	1.4	24
92	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
93	Limited role of interferon-kappa (IFNK) truncating mutations in common variable immunodeficiency. Cytokine, 2017, 96, 71-74.	1.4	2
94	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
95	History of hypertension, heart disease, and diabetes and ovarian cancer patient survival: evidence from the ovarian cancer association consortium. Cancer Causes and Control, 2017, 28, 469-486.	0.8	28
96	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
97	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
98	Improved Killing of Ovarian Cancer Stem Cells by Combining a Novel Chimeric Antigen Receptorâ€“Based Immunotherapy and Chemotherapy. Human Gene Therapy, 2017, 28, 886-896.	1.4	65
99	History of thyroid disease and survival of ovarian cancer patients: results from the Ovarian Cancer Association Consortium, a brief report. British Journal of Cancer, 2017, 117, 1063-1069.	2.9	16
100	History of Comorbidities and Survival of Ovarian Cancer Patients, Results from the Ovarian Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1470-1473.	1.1	10
101	Analysis of a RECQL splicing mutation, c.1667_1667+3delAGTA, in breast cancer patients and controls from Central Europe. Familial Cancer, 2017, 16, 181-186.	0.9	20
102	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
103	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.	1.1	3
104	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
105	Clinical and Biological Manifestation of RNF168 Deficiency in Two Polish Siblings. Frontiers in Immunology, 2017, 8, 1683.	2.2	14
106	Functional dissection of breast cancer risk-associated TERT promoter variants. Oncotarget, 2017, 8, 67203-67217.	0.8	21
107	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. Oncotarget, 2017, 8, 50930-50940.	0.8	43
108	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. Oncotarget, 2017, 8, 64670-64684.	0.8	7

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109	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
110	Guideline adherence and clinical outcome in vulnerable and healthy breast cancer patients: Results of a prospective cross-sectional study in Germany.. Journal of Clinical Oncology, 2017, 35, e18132-e18132.	0.8	0
111	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.	0.8	31
112	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.	3.9	118
113	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
114	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	0.9	71
115	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
116	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
117	The search for new candidate genes involved in ovarian cancer pathogenesis by exome sequencing. Russian Journal of Genetics, 2016, 52, 1105-1109.	0.2	2
118	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	2.2	39
119	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.	2.2	31
120	Rare ATAD5 missense variants in breast and ovarian cancer patients. Cancer Letters, 2016, 376, 173-177.	3.2	21
121	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	1.8	19
122	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
123	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.	0.8	21
124	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
125	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 1619-1630.	0.9	111
126	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.	2.6	59

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127	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.	1.4	33
128	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.	1.1	64
129	Frameshift variant <scp>FANCL</scp>*c.1096_1099dupATTA is not associated with high breast cancer risk. Clinical Genetics, 2016, 90, 385-386.	1.0	3
130	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.	1.6	2
131	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.	7.7	157
132	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
133	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.	1.6	19
134	MCM3APandPOMPMutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. Human Mutation, 2016, 37, 257-268.	1.1	18
135	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
136	Recreational physical inactivity and mortality in women with invasive epithelial ovarian cancer: evidence from the Ovarian Cancer Association Consortium. British Journal of Cancer, 2016, 115, 95-101.	2.9	39
137	Allogeneic-matched sibling stem cell transplantation in a 13-year-old boy with ataxia telangiectasia and EBV-positive non-Hodgkin lymphoma. Bone Marrow Transplantation, 2016, 51, 1271-1274.	1.3	24
138	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
139	Candidate gene variants of the immune system and sudden infant death syndrome. International Journal of Legal Medicine, 2016, 130, 1025-1033.	1.2	19
140	PPM1DMosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. Journal of the National Cancer Institute, 2016, 108, djv347.	3.0	43
141	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.	1.5	94
142	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	9.4	125
143	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. Human Genetics, 2016, 135, 137-154.	1.8	8
144	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	3.0	77

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145	Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10.	0.5	37
146	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
147	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
148	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	0.8	5
149	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	0.8	13
150	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.	1.6	35
151	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
152	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.	0.2	0
153	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
154	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
155	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
156	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
157	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.	2.6	76
158	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.	1.3	14
159	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
160	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
161	Genome-wide significant risk associations for mucinous ovarian carcinoma. Nature Genetics, 2015, 47, 888-897.	9.4	78
162	Polymorphisms in genes of respiratory control and sudden infant death syndrome. International Journal of Legal Medicine, 2015, 129, 977-984.	1.2	14

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163	Network-Based Integration of GWAS and Gene Expression Identifies a HOX-Centric Network Associated with Serous Ovarian Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1574-1584.	1.1	28
164	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.	2.6	37
165	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.	1.1	56
166	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	0.6	15
167	Novel ATM mutation in a German patient presenting as generalized dystonia without classical signs of ataxia-telangiectasia. Journal of Neurology, 2015, 262, 768-770.	1.8	17
168	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.	1.8	34
169	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	5.8	63
170	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
171	Common variants at theCHEK2gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	1.3	24
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