Anthony J Swerdlow

List of Publications by Year
in descending order

195 papers	17,333 citations	18465 62 h-index	18115 120 g-index
206 all docs	206 docs citations	206 times ranked	21448 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
2	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
3	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
4	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
5	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.	9.4	493
6	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
7	Myocardial Infarction Mortality Risk After Treatment for Hodgkin Disease: A Collaborative British Cohort Study. Journal of the National Cancer Institute, 2007, 99, 206-214.	3.0	411
8	Genome-wide association studies identify four ER negative–specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
9	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
10	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
11	Ovarian Cancer Risk Factors by Histologic Subtype: An Analysis From the Ovarian Cancer Cohort Consortium. Journal of Clinical Oncology, 2016, 34, 2888-2898.	0.8	349
12	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
13	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
14	Epidemiology of Health Effects of Radiofrequency Exposure. Environmental Health Perspectives, 2004, 112, 1741-1754.	2.8	262
15	Genome-wide association study of glioma subtypes identifies specific differences in genetic susceptibility to glioblastoma and non-glioblastoma tumors. Nature Genetics, 2017, 49, 789-794.	9.4	259
16	Mortality in Women with Turner Syndrome in Great Britain: A National Cohort Study. Journal of Clinical Endocrinology and Metabolism, 2008, 93, 4735-4742.	1.8	258
17	Cancer Incidence and Mortality in Men with Klinefelter Syndrome: A Cohort Study. Journal of the National Cancer Institute, 2005, 97, 1204-1210.	3.0	246
18	Mortality in Patients with Klinefelter Syndrome in Britain: A Cohort Study. Journal of Clinical Endocrinology and Metabolism, 2005, 90, 6516-6522.	1.8	234

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19	The INTERPHONE study: design, epidemiological methods, and description of the study population. European Journal of Epidemiology, 2007, 22, 647-664.	2.5	225
20	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218
21	Association of Body Mass Index and Age With Subsequent Breast Cancer Risk in Premenopausal Women. JAMA Oncology, 2018, 4, e181771.	3.4	210
22	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.	2.6	201
23	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
24	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
25	Tamoxifen Treatment for Breast Cancer and Risk of Endometrial Cancer: A Case-Control Study. Journal of the National Cancer Institute, 2005, 97, 375-384.	3.0	181
26	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
27	A genome-wide association study of Hodgkin's lymphoma identifies new susceptibility loci at 2p16.1 (REL), 8q24.21 and 10p14 (GATA3). Nature Genetics, 2010, 42, 1126-1130.	9.4	177
28	Second Cancer Risk After Chemotherapy for Hodgkin's Lymphoma: A Collaborative British Cohort Study. Journal of Clinical Oncology, 2011, 29, 4096-4104.	0.8	175
29	Cancer incidence in women with Turner syndrome in Great Britain: a national cohort study. Lancet Oncology, The, 2008, 9, 239-246.	5.1	174
30	*PALB2*, *CHEK2* and *ATM* rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
31	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
32	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
33	Family history and risk of breast cancer: an analysis accounting for family structure. Breast Cancer Research and Treatment, 2017, 165, 193-200.	1.1	155
34	Age- and Tumor Subtype–Specific Breast Cancer Risk Estimates for *CHEK2**1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
35	Breast Cancer Risk After Supradiaphragmatic Radiotherapy for Hodgkin's Lymphoma in England and Wales: A National Cohort Study. Journal of Clinical Oncology, 2012, 30, 2745-2752.	0.8	142
36	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. Nature Genetics, 2020, 52, 494-504.	9.4	138

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37	Smoking and risk of breast cancer in the Generations Study cohort. Breast Cancer Research, 2017, 19, 118.	2.2	133
38	Anthropometric and Hormonal Risk Factors for Male Breast Cancer: Male Breast Cancer Pooling Project Results. Journal of the National Cancer Institute, 2014, 106, djt465-djt465.	3.0	131
39	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
40	Epidemiologic Evidence on Mobile Phones and Tumor Risk. Epidemiology, 2009, 20, 639-652.	1.2	121
41	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
42	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
43	Cancer Risks in Patients Treated With Growth Hormone in Childhood: The SAGhE European Cohort Study. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 1661-1672.	1.8	113
44	Genome-wide association study identifies multiple susceptibility loci for glioma. Nature Communications, 2015, 6, 8559.	5.8	112
45	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
46	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	9.4	99
47	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
48	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.	2.6	98
49	Mobile Phones, Brain Tumors, and the Interphone Study: Where Are We Now?. Environmental Health Perspectives, 2011, 119, 1534-1538.	2.8	94
50	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	1.5	94
51	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
52	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
53	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
54	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.	0.9	88

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55	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
56	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
57	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
58	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
59	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
60	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
61	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	1.3	70
62	Endometrial cancer survival after breast cancer in relation to tamoxifen treatment: Pooled results from three countries. Breast Cancer Research, 2012, 14, R91.	2.2	69
63	Effects of Single-Agent and Combination Chemotherapy for Gestational Trophoblastic Tumors on Risks of Second Malignancy and Early Menopause. Journal of Clinical Oncology, 2015, 33, 472-478.	0.8	67
64	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
65	Functional antibody and T cell immunity following SARS-CoV-2 infection, including by variants of concern, in patients with cancer: the CAPTURE study. Nature Cancer, 2021, 2, 1321-1337.	5.7	66
66	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
67	Variation at 3p24.1 and 6q23.3 influences the risk of Hodgkin's lymphoma. Nature Communications, 2013, 4, 2549.	5.8	62
68	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
69	Genetic overlap between endometriosis and endometrial cancer: evidence from cross–disease genetic correlation and GWAS meta–analyses. Cancer Medicine, 2018, 7, 1978-1987.	1.3	62
70	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. Journal of the National Cancer Institute, 2020, 112, 278-285.	3.0	61
71	Temporal Stability and Determinants of White Blood Cell DNA Methylation in the Breakthrough Generations Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 221-229.	1.1	60
72	Current knowledge and future research directions in treatment-related second primary malignancies. European Journal of Cancer, Supplement, 2014, 12, 5-17.	2.2	59

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73	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
74	Psychological stress, adverse life events and breast cancer incidence: a cohort investigation in 106,000 women in the United Kingdom. Breast Cancer Research, 2016, 18, 72.	2.2	58
75	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	5.8	58
76	Menopausal hormone therapy and breast cancer: what is the true size of the increased risk?. British Journal of Cancer, 2016, 115, 607-615.	2.9	57
77	Long-term mortality after childhood growth hormone treatment: the SAGhE cohort study. Lancet Diabetes and Endocrinology,the, 2020, 8, 683-692.	5.5	57
78	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	2.2	56
79	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
80	A combination of the immunohistochemical markers CK7 and SATB2 is highly sensitive and specific for distinguishing primary ovarian mucinous tumors from colorectal and appendiceal metastases. Modern Pathology, 2019, 32, 1834-1846.	2.9	54
81	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
82	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
83	Description of the SAGhE Cohort: A Large European Study of Mortality and Cancer Incidence Risks after Childhood Treatment with Recombinant Growth Hormone. Hormone Research in Paediatrics, 2015, 84, 172-183.	0.8	51
84	Fine‑scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	2.3	51
85	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	1.6	51
86	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	1.4	50
87	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
88	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
89	Comparative validation of the BOADICEA and Tyrer-Cuzick breast cancer risk models incorporating classical risk factors and polygenic risk in a population-based prospective cohort of women of European ancestry. Breast Cancer Research, 2021, 23, 22.	2.2	49
90	Risk of Premature Menopause After Treatment for Hodgkin's Lymphoma. Journal of the National Cancer Institute, 2014, 106, .	3.0	48

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91	Risk Factors for Breast Cancer at Young Ages in Twins: An International Population-Based Study. Journal of the National Cancer Institute, 2002, 94, 1238-1246.	3.0	47
92	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.	3.0	45
93	Genetic Variants at Chromosomes 2q35, 5p12, 6q25.1, 10q26.13, and 16q12.1 Influence the Risk of Breast Cancer in Men. PLoS Genetics, 2011, 7, e1002290.	1.5	43
94	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
95	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	2.2	43
96	Analgesic Use and Ovarian Cancer Risk: An Analysis in the Ovarian Cancer Cohort Consortium. Journal of the National Cancer Institute, 2019, 111, 137-145.	3.0	43
97	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	0.9	43
98	Night shift work and risk of breast cancer in women: the Generations Study cohort. British Journal of Cancer, 2019, 121, 172-179.	2.9	41
99	Mitochondrial DNA Copy Number in Peripheral Blood Cells and Risk of Developing Breast Cancer. Cancer Research, 2015, 75, 2844-2850.	0.4	40
100	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
101	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	40
102	Cancer, COVID-19, and Antiviral Immunity: The CAPTURE Study. Cell, 2020, 183, 4-10.	13.5	40
103	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	1.5	39
104	Location of Gliomas in Relation to Mobile Telephone Use: A Case-Case and Case-Specular Analysis. American Journal of Epidemiology, 2011, 174, 2-11.	1.6	38
105	Effect of population breast screening on breast cancer mortality up to 2005 in England and Wales: an individual-level cohort study. British Journal of Cancer, 2017, 116, 246-252.	2.9	38
106	Domestic light at night and breast cancer risk: a prospective analysis of 105 000 UK women in the Generations Study. British Journal of Cancer, 2018, 118, 600-606.	2.9	38
107	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
108	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 781-794.	0.9	37

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109	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	1.1	35
110	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
111	The Risk of Ovarian Cancer Increases with an Increase in the Lifetime Number of Ovulatory Cycles: An Analysis from the Ovarian Cancer Cohort Consortium (OC3). Cancer Research, 2020, 80, 1210-1218.	0.4	35
112	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
113	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
114	Circulating antiâ€Mᬼllerian hormone and breast cancer risk: A study in ten prospective cohorts. International Journal of Cancer, 2018, 142, 2215-2226.	2.3	32
115	Influence of obesity-related risk factors in the aetiology of glioma. British Journal of Cancer, 2018, 118, 1020-1027.	2.9	32
116	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
117	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
118	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
119	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	1.6	31
120	Risk of Meningioma in European Patients Treated With Growth Hormone in Childhood: Results From the SAGhE Cohort. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 658-664.	1.8	31
121	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. Journal of the National Cancer Institute, 2012, 104, 657-669.	3.0	30
122	Breast cancer risk prediction in women aged 35â€"50â€‰years: impact of including sex hormone concentrations in the Gail model. Breast Cancer Research, 2019, 21, 42.	2.2	30
123	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
124	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	0.6	29
125	Mortality and cancer incidence in males with Y polysomy in Britain: a cohort study. Human Genetics, 2007, 121, 691-696.	1.8	28
126	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28

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127	Transcriptome-Wide Association Study Identifies New Candidate Susceptibility Genes for Glioma. Cancer Research, 2019, 79, 2065-2071.	0.4	26
128	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
129	Development and Validation of a Melanoma Risk Score Based on Pooled Data from 16 Case–Control Studies. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 817-824.	1.1	25
130	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	1.6	25
131	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.	1.1	24
132	The Premenopausal Breast Cancer Collaboration: A Pooling Project of Studies Participating in the National Cancer Institute Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1360-1369.	1.1	23
133	Genome-wide association analysis identifies a meningioma risk locus at 11p15.5. Neuro-Oncology, 2018, 20, 1485-1493.	0.6	23
134	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
135	Genome-wide association study of anti-Müllerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. Human Molecular Genetics, 2019, 28, 1392-1401.	1.4	22
136	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
137	The Intracranial Distribution of Gliomas in Relation to Exposure From Mobile Phones: Analyses From the INTERPHONE Study. American Journal of Epidemiology, 2016, 184, 818-828.	1.6	21
138	Gene–environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	2.3	20
139	Tobacco and Alcohol in Relation to Male Breast Cancer: An Analysis of the Male Breast Cancer Pooling Project Consortium. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 520-531.	1.1	19
140	The *BRCA2* c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	1.1	19
141	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	2.3	19
142	Childhood body size and pubertal timing in relation to adult mammographic density phenotype. Breast Cancer Research, 2017, 19, 13.	2.2	18
143	The National Cancer Institute Cohort Consortium: An International Pooling Collaboration of 58 Cohorts from 20 Countries. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1307-1319.	1.1	18
144	Does growth hormone therapy increase the risk of cancer?. Nature Clinical Practice Endocrinology and Metabolism, 2006, 2, 530-531.	2.9	17

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145	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. Blood, 2018, 132, 2040-2052.	0.6	17
146	Adult weight change and premenopausal breast cancer risk: A prospective pooled analysis of data from 628,463 women. International Journal of Cancer, 2020, 147, 1306-1314.	2.3	17
147	Mortality and cancer incidence in women with extra X chromosomes: a cohort study in Britain. Human Genetics, 2005, 118, 255-260.	1.8	16
148	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
149	Validated biomarker assays confirm that <scp>ARID1A</scp> loss is confounded with <scp>MMR</scp> deficiency, <scp>CD8⁺ TIL</scp> infiltration, and provides no independent prognostic value in endometriosisâ€associated ovarian carcinomas. Journal of Pathology, 2022, 256, 388-401.	2.1	15
150	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	2.2	15
151	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	2.2	14
152	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
153	Radiologic Features of Breast Cancer after Mantle Radiation Therapy for Hodgkin Disease: A Study of 230 Cases. Radiology, 2014, 272, 73-78.	3.6	13
154	Genome-wide homozygosity signature and risk of Hodgkin lymphoma. Scientific Reports, 2015, 5, 14315.	1.6	13
155	Genome-wide association study meta-analysis identifies three novel loci for circulating anti-Mã¼llerian hormone levels in women. Human Reproduction, 2022, 37, 1069-1082.	0.4	13
156	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
157	Breast cancer risk in relation to history of preeclampsia and hyperemesis gravidarum: Prospective analysis in the Generations Study. International Journal of Cancer, 2018, 143, 782-792.	2.3	12
158	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
159	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12
160	Sharing data safely while preserving privacy. Lancet, The, 2019, 394, 1902.	6.3	11
161	Mortality and Cancer Incidence in Carriers of Balanced Robertsonian Translocations: A National Cohort Study. American Journal of Epidemiology, 2019, 188, 500-508.	1.6	9
162	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9

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163	*PHIP*- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
164	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
165	Maternal breast cancer risk in relation to birthweight and gestation of her offspring. Breast Cancer Research, 2018, 20, 110.	2.2	8
166	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2022, 480, 855-871.	1.4	8
167	Length of *FMR1* repeat alleles within the normal range does not substantially affect the risk of early menopause. Human Reproduction, 2016, 31, 2396-2403.	0.4	7
168	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
169	Mortality risks in patients with constitutional autosomal chromosome deletions in Britain: a cohort study. Human Genetics, 2008, 123, 215-224.	1.8	6
170	A Novel Approach to Exploring Potential Interactions among Single-Nucleotide Polymorphisms of Inflammation Genes in Gliomagenesis: An Exploratory Case-Only Study. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1683-1689.	1.1	6
171	Retrospective methods to estimate radiation dose at the site of breast cancer development after Hodgkin lymphoma radiotherapy. Clinical and Translational Radiation Oncology, 2017, 7, 20-27.	0.9	6
172	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
173	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
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