Douglas Easton

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8351267/publications.pdf

Version: 2024-02-01

415 papers	57,773 citations	1459 107 h-index	1421 221 g-index
454 all docs	454 docs citations	454 times ranked	44175 citing authors

#	Article	IF	Citations
1	Identification of the breast cancer susceptibility gene BRCA2. Nature, 1995, 378, 789-792.	13.7	3,230
2	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
3	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	3.8	1,898
4	Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. Science, 1994, 265, 2088-2090.	6.0	1,725
5	The evolutionary history of lethal metastatic prostate cancer. Nature, 2015, 520, 353-357.	13.7	1,185
6	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
7	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	9.4	960
8	Cancer Incidence in BRCA1 Mutation Carriers. Journal of the National Cancer Institute, 2002, 94, 1358-1365.	3.0	947
9	Polygenic susceptibility to breast cancer and implications for prevention. Nature Genetics, 2002, 31, 33-36.	9.4	874
10	PALB2, which encodes a BRCA2-interacting protein, is a breast cancer susceptibility gene. Nature Genetics, 2007, 39, 165-167.	9.4	858
11	The Pathology of Familial Breast Cancer: Predictive Value of Immunohistochemical Markers Estrogen Receptor, Progesterone Receptor, HER-2, and p53 in Patients With Mutations in BRCA1 and BRCA2. Journal of Clinical Oncology, 2002, 20, 2310-2318.	0.8	770
12	Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. PLoS Medicine, 2010, 7, e1000279.	3.9	764
13	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	13.9	764
14	Breast-Cancer Risk in Families with Mutations in PALB2. New England Journal of Medicine, 2014, 371, 497-506.	13.9	745
15	Genome-wide association study identifies five new breast cancer susceptibility loci. Nature Genetics, 2010, 42, 504-507.	9.4	653
16	Multifactorial Analysis of Differences Between Sporadic Breast Cancers and Cancers Involving BRCA1 and BRCA2 Mutations. Journal of the National Cancer Institute, 1998, 90, 1138-1145.	3.0	652
17	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
18	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.	3.0	596

#	Article	IF	Citations
19	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
20	Prediction of BRCA1 Status in Patients with Breast Cancer Using Estrogen Receptor and Basal Phenotype. Clinical Cancer Research, 2005, 11, 5175-5180.	3.2	577
21	Polygenes, Risk Prediction, and Targeted Prevention of Breast Cancer. New England Journal of Medicine, 2008, 358, 2796-2803.	13.9	558
22	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
23	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
24	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
25	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.	1.1	513
26	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
27	Family history and the risk of breast cancer: A systematic review and meta-analysis. , 1997, 71, 800-809.		494
28	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
29	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
30	Variation in Cancer Risks, by Mutation Position, in BRCA2 Mutation Carriers. American Journal of Human Genetics, 2001, 68, 410-419.	2.6	459
31	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
32	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.	9.4	426
33	A Systematic Genetic Assessment of 1,433 Sequence Variants of Unknown Clinical Significance in the BRCA1 and BRCA2 Breast Cancerâ€"Predisposition Genes. American Journal of Human Genetics, 2007, 81, 873-883.	2.6	416
34	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	1.1	415
35	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. Nature, 2011, 480, 99-103.	13.7	413
36	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408

#	Article	IF	Citations
37	Association of Type and Location ofBRCA1andBRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	3.8	390
38	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	9.4	389
39	Using human genetics to understand the disease impacts of testosterone in men and women. Nature Medicine, 2020, 26, 252-258.	15.2	384
40	Analysis of the genetic phylogeny of multifocal prostate cancer identifies multiple independent clonal expansions in neoplastic and morphologically normal prostate tissue. Nature Genetics, 2015, 47, 367-372.	9.4	380
41	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	9.4	377
42	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
43	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
44	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
45	Germline BRCA mutation and outcome in young-onset breast cancer (POSH): a prospective cohort study. Lancet Oncology, The, 2018, 19, 169-180.	5.1	316
46	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
47	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.	9.4	309
48	Positional cloning of the Fanconi anaemia group A gene. Nature Genetics, 1996, 14, 324-328.	9.4	294
49	Genetic susceptibility to breast cancer. Molecular Oncology, 2010, 4, 174-191.	2.1	291
50	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
51	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
52	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	9.4	279
53	Effect of BRCA Mutations on Metastatic Relapse and Cause-specific Survival After Radical Treatment for Localised Prostate Cancer. European Urology, 2015, 68, 186-193.	0.9	279
54	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278

#	Article	IF	Citations
55	Multiple loci on 8q24 associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1058-1060.	9.4	273
56	Cancer Risks Associated With Germline PALB2 Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	0.8	270
57	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
58	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
59	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	9.4	264
60	Evidence for further breast cancer susceptibility genes in addition toBRCA1 andBRCA2 in a population-based study. Genetic Epidemiology, 2001, 21, 1-18.	0.6	263
61	Localization to Xq27 of a susceptibility gene for testicular germ-cell tumours. Nature Genetics, 2000, 24, 197-200.	9.4	260
62	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.	2.6	257
63	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
64	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
65	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, .	3.0	242
66	A germline mutation in the androgen receptor gene in two brothers with breast cancer and Reifenstein syndrome. Nature Genetics, 1992, 2, 132-134.	9.4	241
67	Genome-wide association study identifies three new melanoma susceptibility loci. Nature Genetics, 2011, 43, 1108-1113.	9.4	230
68	Mutational spectrum in a worldwide study of 29,700 families withBRCA1orBRCA2mutations. Human Mutation, 2018, 39, 593-620.	1.1	224
69	Genome-wide association studies in cancer. Human Molecular Genetics, 2008, 17, R109-R115.	1.4	222
70	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
71	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	9.4	220
72	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	9.4	218

#	Article	IF	Citations
73	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.	2.6	217
74	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	9.4	210
75	The genetic epidemiology of prostate cancer and its clinical implications. Nature Reviews Urology, 2014, 11, 18-31.	1.9	207
76	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
77	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
78	Risk of cutaneous melanoma associated with a family history of the disease. International Journal of Cancer, 1995, 62, 377-381.	2.3	191
79	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
80	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
81	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	9.4	182
82	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
83	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
84	The Contributions of Breast Density and Common Genetic Variation to Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	3.0	174
85	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. Nature Communications, 2019, 10, 2154.	5.8	172
86	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.	0.4	169
87	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
88	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. PLoS Genetics, 2014, 10, e1004102.	1.5	167
89	CHEK2*1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€"Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	0.8	162
90	Risk models for familial ovarian and breast cancer. , 2000, 18, 173-190.		157

#	Article	IF	Citations
91	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
92	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.4	153
93	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. Nature Genetics, 2000, 26, 362-364.	9.4	152
94	BRCA1 and BRCA2 mutations in a population-based study of male breast cancer. Breast Cancer Research, 2001, 4, R2.	2.2	152
95	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.	1.4	152
96	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
97	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.	0.8	152
98	Multiple Novel Prostate Cancer Predisposition Loci Confirmed by an International Study: The PRACTICAL Consortium. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2052-2061.	1.1	148
99	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	1.5	148
100	Familial male breast cancer is not linked to the BRCA1 locus on chromosome 17q. Nature Genetics, 1994, 7, 103-107.	9.4	146
101	The contribution of rare variation to prostate cancer heritability. Nature Genetics, 2016, 48, 30-35.	9.4	139
102	Germline Mutation in BRCA1 or BRCA2 and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. Clinical Cancer Research, 2015, 21, 652-657.	3.2	138
103	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
104	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.	2.2	136
105	CHEK2 variant I157T may be associated with increased breast cancer risk. International Journal of Cancer, 2004, 111, 543-547.	2.3	134
106	A Full-Likelihood Method for the Evaluation of Causality of Sequence Variants from Family Data. American Journal of Human Genetics, 2003, 73, 652-655.	2.6	130
107	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	3.0	129
108	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	3.0	129

#	Article	IF	Citations
109	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
110	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. International Journal of Epidemiology, 2016, 45, 896-908.	0.9	124
111	Prostate Cancer Risks for Male BRCA1 and BRCA2 Mutation Carriers: A Prospective Cohort Study. European Urology, 2020, 77, 24-35.	0.9	124
112	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	9.4	120
113	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
114	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
115	Cumulative Burden of Colorectal Cancerâ€"Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	0.6	110
116	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. Nature Genetics, 2011, 43, 185-187.	9.4	109
117	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
118	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	1.4	106
119	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
120	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. Journal of the National Cancer Institute, 2020, 112, 1242-1250.	3.0	106
121	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
122	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
123	Where are the prostate cancer genes??A summary of eight genome wide searches. Prostate, 2003, 57, 261-269.	1.2	104
124	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	1.4	100
125	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
126	A genomic approach to therapeutic target validation identifies a glucose-lowering GLP1R variant protective for coronary heart disease. Science Translational Medicine, 2016, 8, 341ra76.	5.8	100

#	Article	IF	Citations
127	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	1.4	99
128	Radiogenomics: Radiobiology Enters the Era of Big Data and Team Science. International Journal of Radiation Oncology Biology Physics, 2014, 89, 709-713.	0.4	99
129	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99
130	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
131	CanRisk Toolâ€"A Web Interface for the Prediction of Breast and Ovarian Cancer Risk and the Likelihood of Carrying Genetic Pathogenic Variants. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 469-473.	1.1	98
132	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.	2.2	97
133	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
134	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
135	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
136	Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541.	0.8	90
137	Localisation of the Fanconi anaemia complementation group A gene to chromosome 16q24.3. Nature Genetics, 1995, 11, 338-340.	9.4	89
138	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
139	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.	2.2	88
140	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
141	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
142	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
143	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	5.8	88
144	Implications of polygenic risk-stratified screening for prostate cancer on overdiagnosis. Genetics in Medicine, 2015, 17, 789-795.	1.1	87

#	Article	IF	Citations
145	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. Human Molecular Genetics, 2013, 22, 2539-2550.	1.4	86
146	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
147	Most common â€˜sporadicâ€™ cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	1.4	85
148	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
149	Inherited Genetic Susceptibility to Breast Cancer. American Journal of Pathology, 2013, 183, 1038-1051.	1.9	82
150	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.	1.1	82
151	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. Human Molecular Genetics, 2012, 21, 456-462.	1.4	81
152	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
153	Incorporating truncating variants in PALB2, CHEK2, and ATM into the BOADICEA breast cancer risk model. Genetics in Medicine, 2016, 18, 1190-1198.	1.1	80
154	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.	2.2	78
155	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
156	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	9.4	77
157	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
158	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
159	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. Nature Genetics, 2017, 49, 341-348.	9.4	75
160	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
161	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
162	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 2008, 123, 380-388.	2.3	73

#	Article	IF	Citations
163	The rs10993994 Risk Allele for Prostate Cancer Results in Clinically Relevant Changes in Microseminoprotein-Beta Expression in Tissue and Urine. PLoS ONE, 2010, 5, e13363.	1.1	73
164	Cancer mortality in relatives of women with ovarian cancer: The OPCS study. , 1996, 65, 284-294.		72
165	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. PLoS Medicine, 2016, 13, e1002118.	3.9	69
166	Ovarian and breast cancer risks to women in families with two or more cases of ovarian cancer. International Journal of Cancer, 2000, 87, 110-117.	2.3	68
167	Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515.	1.4	68
168	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.	1.4	68
169	Rare, protein-truncating variants inATM,CHEK2andPALB2, but notXRCC2, are associated with increased breast cancer risks. Journal of Medical Genetics, 2017, 54, 732-741.	1.5	68
170	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	1.4	67
171	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
172	A Cross-Cancer Genetic Association Analysis of the DNA Repair and DNA Damage Signaling Pathways for Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 193-200.	1.1	66
173	Familial risks of breast cancer. Breast Cancer Research, 2002, 4, 179-81.	2.2	65
174	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
175	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	3.0	63
176	Generalizability of established prostate cancer risk variants in men of <scp>A</scp>frican ancestry. International Journal of Cancer, 2015, 136, 1210-1217.	2.3	62
177	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	1.6	62
178	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
179	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
180	The influence of obesity-related factors in the etiology of renal cell carcinomaâ€”A mendelian randomization study. PLoS Medicine, 2019, 16, e1002724.	3.9	59

#	Article	IF	Citations
181	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&I). Journal of Personalized Medicine, 2021, 11, 511.	1.1	59
182	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. Nature Communications, 2018, 9, 1340.	5.8	58
183	A Genome-Wide Association Study of Prognosis in Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1140-1143.	1.1	57
184	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.	2.2	57
185	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	3.0	57
186	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
187	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
188	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
189	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
190	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.4	55
191	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	1.2	54
192	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
193	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
194	A risk prediction algorithm for ovarian cancer incorporatingBRCA1, BRCA2, common alleles and other familial effects. Journal of Medical Genetics, 2015, 52, 465-475.	1.5	52
195	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. Breast Cancer Research, 2016, 18, 124.	2.2	52
196	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	2.9	52
197	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	2.3	51
198	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

#	Article	IF	Citations
199	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
200	Combined quantitative measures of ER, PR, HER2, and KI67 provide more prognostic information than categorical combinations in luminal breast cancer. Modern Pathology, 2019, 32, 1244-1256.	2.9	51
201	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	3.4	51
202	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	1.4	50
203	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
204	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	5.8	50
205	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	1.1	49
206	Evaluating the power to discriminate between highly correlated SNPs in genetic association studies. Genetic Epidemiology, 2010, 34, 463-468.	0.6	48
207	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	1.1	48
208	Characterization of the Cancer Spectrum in Men With GermlineBRCA1andBRCA2Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	3.4	48
209	Evaluation of Fanconi Anemia genes in familial breast cancer predisposition. Cancer Research, 2003, 63, 8596-9.	0.4	48
210	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
211	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	5.8	46
212	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	0.9	45
213	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
214	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	1.1	44
215	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326.	1.8	44
216	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	6.1	44

#	Article	IF	Citations
217	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	2.2	43
218	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	2.3	43
219	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	5.8	43
220	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
221	A comprehensive examination of breast cancer risk loci in African American women. Human Molecular Genetics, 2014, 23, 5518-5526.	1.4	42
222	Genome-wide association study of endometrial cancer in E2C2. Human Genetics, 2014, 133, 211-224.	1.8	42
223	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	2.2	42
224	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	0.9	41
225	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2020, 22, 8.	2.2	41
226	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. Journal of the National Cancer Institute, 2021, 113, 1168-1176.	3.0	41
227	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	1.4	40
228	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. Nature Communications, 2017, 8, 1892.	5.8	40
229	Identification of Women at High Risk of Breast Cancer Who Need Supplemental Screening. Radiology, 2020, 297, 327-333.	3.6	40
230	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study. PLoS ONE, 2020, 15, e0229999.	1.1	40
231	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
232	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. European Urology, 2017, 72, 747-754.	0.9	39
233	Association of Genomic Domains in BRCA1 and BRCA2 with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.4	39
234	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	2.6	39

#	Article	IF	Citations
235	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	1.4	38
236	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. Carcinogenesis, 2017, 38, 511-518.	1.3	38
237	Evaluation of Association Methods for Analysing Modifiers of Disease Risk in Carriers of Highâ€Risk Mutations. Genetic Epidemiology, 2012, 36, 274-291.	0.6	37
238	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 934-945.	1.1	37
239	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
240	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
241	Identification of four new susceptibility loci for testicular germ cell tumour. Nature Communications, 2015, 6, 8690.	5.8	36
242	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. Nature Communications, 2020, 11, 1536.	5.8	36
243	Absence of evidence for a familial breast cancer susceptibility gene at chromosome 8p12-p22. Oncogene, 2000, 19, 4170-4173.	2.6	35
244	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
245	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780.	0.9	35
246	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
247	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
248	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	1.5	34
249	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
250	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
251	Inherited mutations in BRCA1 and BRCA2 in an unselected multiethnic cohort of Asian patients with breast cancer and healthy controls from Malaysia. Journal of Medical Genetics, 2018, 55, 97-103.	1.5	34
252	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. Journal of the National Cancer Institute, 2021, 113, 434-442.	3.0	34

#	Article	IF	Citations
253	Oral contraceptive use and ovarian cancer risk for BRCA1/2 mutation carriers: an international cohort study. American Journal of Obstetrics and Gynecology, 2021, 225, 51.e1-51.e17.	0.7	34
254	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	1.1	33
255	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
256	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. JNCI Cancer Spectrum, 2018, 2, pky023.	1.4	33
257	Comprehensive epithelial tubo-ovarian cancer risk prediction model incorporating genetic and epidemiological risk factors. Journal of Medical Genetics, 2022, 59, 632-643.	1.5	33
258	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
259	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. American Journal of Human Genetics, 2016, 98, 1159-1169.	2.6	32
260	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	0.6	32
261	Reply to â€œVariation in KLK genes, prostate-specific antigen and risk of prostate cancerâ€. Nature Genetics, 2008, 40, 1035-1036.	9.4	31
262	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	1.4	31
263	Multi-stage genome-wide association study identifies new susceptibility locus for testicular germ cell tumour on chromosome 3q25. Human Molecular Genetics, 2015, 24, 1169-1176.	1.4	31
264	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
265	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
266	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	2.2	31
267	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. International Journal of Cancer, 2019, 144, 1195-1204.	2.3	31
268	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.	3.0	30
269	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	5.8	30
270	Apparent humanBRCA1 knockout caused by mispriming during polymerase chain reaction: Implications for genetic testing. Genes Chromosomes and Cancer, 2001, 31, 96-98.	1.5	29

#	Article	IF	Citations
271	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	0.6	29
272	Identification of 31 loci for mammographic density phenotypes and their associations with breast cancer risk. Nature Communications, 2020, 11, 5116.	5.8	29
273	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
274	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	2.3	28
275	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	5.8	28
276	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	1.1	27
277	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	1.4	27
278	Chromatin interactome mapping at 139 independent breast cancer risk signals. Genome Biology, 2020, 21, 8.	3.8	27
279	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	1.1	27
280	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27
281	Genetic Variation in Prostate-Specific Antigenâ€“Detected Prostate Cancer and the Effect of Control Selection on Genetic Association Studies. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1356-1365.	1.1	26
282	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.	2.2	26
283	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	2.2	26
284	BRCA1andBRCA2pathogenic sequence variants in women of African origin or ancestry. Human Mutation, 2019, 40, 1781-1796.	1.1	26
285	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	1.1	26
286	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	1.6	25
287	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). Journal of Genetics and Genome Research, 2015, 2, .	0.3	25
288	Familial cancer risks to offspring from mothers with 2 primary breast cancers: Leads to cancer syndromes. International Journal of Cancer, 2000, 88, 87-91.	2.3	24

#	Article	IF	Citations
289	Polymorphisms of an Innate Immune Gene, Toll-Like Receptor 4, and Aggressive Prostate Cancer Risk: A Systematic Review and Meta-Analysis. PLoS ONE, 2014, 9, e110569.	1.1	24
290	Area and Volumetric Density Estimation in Processed Full-Field Digital Mammograms for Risk Assessment of Breast Cancer. PLoS ONE, 2014, 9, e110690.	1.1	24
291	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
292	Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. Breast Cancer Research and Treatment, 2016, 158, 463-469.	1.1	24
293	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	2.2	24
294	Is Schizophrenia a Risk Factor for Breast Cancer?â€"Evidence From Genetic Data. Schizophrenia Bulletin, 2019, 45, 1251-1256.	2.3	24
295	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for BRCA1 and BRCA2 Mutation Carriers: Results from The BRCA1 and BRCA2 Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 368-378.	1.1	24
296	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	5.8	24
297	Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. British Journal of Cancer, 2016, 115, 624-631.	2.9	23
298	Exome array analysis identifies ETFB as a novel susceptibility gene for anthracycline-induced cardiotoxicity in cancer patients. Breast Cancer Research and Treatment, 2018, 167, 249-256.	1.1	23
299	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	1.4	23
300	Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	0.6	22
301	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22
302	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
303	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2020, 49, 216-232.	0.9	21
304	Non-coding RNAs underlie genetic predisposition to breast cancer. Genome Biology, 2020, 21, 7.	3.8	21
305	SNP-SNP interaction analysis of NF-Î¹B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	0.8	20
306	Geneâ€"environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	2.3	20

#	Article	IF	Citations
307	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. Human Molecular Genetics, 2018, 27, 853-859.	1.4	20
308	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. European Urology, 2018, 74, 248-252.	0.9	20
309	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	2.2	19
310	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
311	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	1.4	19
312	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
313	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
314	Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. Cancer Research, 2018, 78, 6329-6338.	0.4	19
315	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.	2.9	19
316	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
317	Breast and Prostate Cancer Risks for MaleBRCA1andBRCA2Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	3.0	19
318	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
319	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	3.6	19
320	Localisation of the breast-ovarian cancer susceptibility gene (BRCAI) on 17q12â€“21 to an interval of î‹ºIcM. Genes Chromosomes and Cancer, 1994, 10, 71-76.	1.5	18
321	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. Breast Cancer Research and Treatment, 2013, 138, 529-542.	1.1	18
322	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
323	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.	1.1	18
324	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

#	Article	IF	Citations
325	A genetic study and meta-analysis of the genetic predisposition of prostate cancer in a Chinese population. Oncotarget, 2016, 7, 21393-21403.	0.8	18
326	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. Human Molecular Genetics, 2015, 24, 7406-7420.	1.4	17
327	Alzheimer disease is not associated with polymorphisms in the angiotensinogen and renin genes. American Journal of Medical Genetics Part A, 2001, 105, 761-764.	2.4	16
328	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
329	Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. Breast Cancer Research and Treatment, 2014, 143, 181-187.	1.1	16
330	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.	1.1	16
331	Splicing predictions, minigene analyses, and <scp>ACMG</scp>â€<scp>AMP</scp> clinical classification of 42 germline <scp>PALB2</scp> spliceâ€site variants. Journal of Pathology, 2022, 256, 321-334.	2.1	16
332	Risks of breast or ovarian cancer in BRCA1 or BRCA2 predictive test negatives: findings from the EMBRACE study. Genetics in Medicine, 2018, 20, 1575-1582.	1.1	15
333	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. Genome Medicine, 2021, 13, 15.	3.6	15
334	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	0.8	15
335	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	2.2	15
336	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	2.2	15
337	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
338	Incorporating Functional Genomic Information in Genetic Association Studies Using an Empirical Bayes Approach. Genetic Epidemiology, 2016, 40, 176-187.	0.6	14
339	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
340	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	1.4	14
341	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	1.1	14
342	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.	0.8	14

#	Article	IF	Citations
343	Predicting the Likelihood of Carrying a BRCA1 or BRCA2 Mutation in Asian Patients With Breast Cancer. Journal of Clinical Oncology, 2022, 40, 1542-1551.	0.8	14
344	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	3.0	14
345	Lymphocyte Telomere Length Is Long in BRCA1 and BRCA2 Mutation Carriers Regardless of Cancer-Affected Status. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1018-1024.	1.1	13
346	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	2.3	13
347	Serum Estradiol and 20 Site-Specific Cancers in Women: Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e467-e474.	1.8	13
348	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	1.4	12
349	Genome-wide association study of susceptibility loci for breast cancer in Sardinian population. BMC Cancer, 2015, 15, 383.	1.1	12
350	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	1.1	12
351	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	3.0	12
352	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. Human Molecular Genetics, 2022, 31, 3133-3143.	1.4	11
353	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.	1.1	10
354	Comprehensive Functional Characterization and Clinical Interpretation of 20 Splice-Site Variants of the RAD51C Gene. Cancers, 2020, 12, 3771.	1.7	10
355	Detecting rare copy number variants from Illumina genotyping arrays with the CamCNV pipeline: Segmentation ofÂzâ€scores improves detection and reliability. Genetic Epidemiology, 2021, 45, 237-248.	0.6	10
356	First international workshop of the ATM and cancer risk group (4-5 December 2019). Familial Cancer, 2022, 21, 211-227.	0.9	10
357	RAD51D Aberrant Splicing in Breast Cancer: Identification of Splicing Regulatory Elements and Minigene-Based Evaluation of 53 DNA Variants. Cancers, 2021, 13, 2845.	1.7	10
358	Telomere Length Shows No Association with BRCA1 and BRCA2 Mutation Status. PLoS ONE, 2014, 9, e86659.	1.1	10
359	pedigreejs: a web-based graphical pedigree editor. Bioinformatics, 2018, 34, 1069-1071.	1.8	9
360	Use of the BOADICEA Web Application in clinical practice: appraisals by clinicians from various countries. Familial Cancer, 2018, 17, 31-41.	0.9	9

#	Article	IF	Citations
361	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561.	1.1	9
362	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. Molecular Genetics & Genomic Medicine, 2019, 7, e707.	0.6	9
363	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.	2.3	9
364	Potential of polygenic risk scores for improving population estimates of womenâ€™s breast cancer genetic risks. Genetics in Medicine, 2021, 23, 2114-2121.	1.1	9
365	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	2.9	9
366	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	0.8	9
367	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. Twin Research and Human Genetics, 2012, 15, 615-623.	0.3	8
368	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	1.4	8
369	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
370	Should Age-Dependent Absolute Risk Thresholds Be Used for Risk Stratification in Risk-Stratified Breast Cancer Screening?. Journal of Personalized Medicine, 2021, 11, 916.	1.1	8
371	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. Oncotarget, 2018, 9, 12630-12638.	0.8	8
372	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	2.9	7
373	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. British Journal of Cancer, 2017, 117, 734-743.	2.9	7
374	Targeted Resequencing of the Coding Sequence of 38 Genes Near Breast Cancer GWAS Loci in a Large Caseâ€“Control Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 822-825.	1.1	7
375	Cliniciansâ€™ use of breast cancer risk assessment tools according to their perceived importance of breast cancer risk factors: an international survey. Journal of Community Genetics, 2019, 10, 61-71.	0.5	7
376	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. Npj Breast Cancer, 2021, 7, 52.	2.3	7
377	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
378	Oral Contraceptive Use in BRCA1 and BRCA2 Mutation Carriers: Absolute Cancer Risks and Benefits. Journal of the National Cancer Institute, 2022, 114, 540-552.	3.0	7

#	Article	IF	Citations
379	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. BMC Cancer, 2015, 15, 978.	1.1	6
380	Prostate Cancer Risk by BRCA2 Genomic Regions. European Urology, 2020, 78, 494-497.	0.9	6
381	Candidate Causal Variants at the 8p12 Breast Cancer Risk Locus Regulate DUSP4. Cancers, 2020, 12, 170.	1.7	6
382	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. Npj Breast Cancer, 2021, 7, 46.	2.3	6
383	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
384	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.0	6
385	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	2.0	6
386	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	0.7	6
387	Risk Analysis of Prostate Cancer in PRACTICAL Consortiumâ€”Response. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 223-223.	1.1	5
388	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	1.6	5
389	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44.	2.3	5
390	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
391	Prostate cancer meta-analysis from more than 145,000 men to identify 65 novel prostate cancer susceptibility loci.. Journal of Clinical Oncology, 2017, 2017, 1-1.	0.8	5
392	Letter to the editor: a response to Mingâ€™s study on machine learning techniques for personalized breast cancer risk prediction. Breast Cancer Research, 2020, 22, 17.	2.2	4
393	Epidemiological and ES cellâ€based functional evaluation of BRCA2 variants identified in families with breast cancer. Human Mutation, 2021, 42, 200-212.	1.1	4
394	Characterisation of protein-truncating and missense variants in PALB2 in 15 768 women from Malaysia and Singapore. Journal of Medical Genetics, 2021, , jmedgenet-2020-107471.	1.5	4
395	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
396	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. Breast Cancer Research, 2021, 23, 94.	2.2	4

#	Article	IF	Citations
397	Germline breast cancer susceptibility genes, tumor characteristics, and survival. Genome Medicine, 2021, 13, 185.	3.6	3
398	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	1.1	3
399	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
400	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. Bioinformatics, 2017, 33, 1389-1391.	1.8	2
401	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	1.6	2
402	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2
403	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	1.6	2
404	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	1.6	2
405	Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of European Ancestry. Cancers, 2022, 14, 3363.	1.7	2
406	Authorsâ€™ response: Associations of obesity and circulating insulin and glucose with breast cancer risk. International Journal of Epidemiology, 2019, 48, 1016-1017.	0.9	1
407	Risk models for familial ovarian and breast cancer. Genetic Epidemiology, 2000, 18, 173.	0.6	1
408	OUP accepted manuscript. Human Molecular Genetics, 2022, , .	1.4	1
409	Relevance of the MHC region for breast cancer susceptibility in Asians. Breast Cancer, 2022, 29, 869-879.	1.3	1
410	Risk of breast or ovarian cancer in family members who do not carry the BRCA1 or BRCA2 family mutation: Findings from the EMBRACE study.. Journal of Clinical Oncology, 2017, 35, 1558-1558.	0.8	0
411	Body mass index and type 2 diabetes and breast cancer survival: a Mendelian randomization study. American Journal of Cancer Research, 2021, 11, 3921-3934.	1.4	0
412	Title is missing!. , 2020, 15, e0229999.		0
413	Title is missing!. , 2020, 15, e0229999.		0
414	Title is missing!. , 2020, 15, e0229999.		0

#	Article	IF	Citations
415	Title is missing!. , 2020, 15, e0229999.		0