

Paul D P Pharoah

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1674493/publications.pdf>

Version: 2024-02-01

829
papers

78,883
citations

419

132
h-index

851

244
g-index

892
all docs

892
docs citations

892
times ranked

62856
citing authors

#	ARTICLE	IF	CITATIONS
1	Risk-Adjusted Cancer Screening and Prevention (RiskAP): Complementing Screening for Early Disease Detection by a Learning Screening Based on Risk Factors. <i>Breast Care</i> , 2022, 17, 208-223.	1.4	6
2	Comprehensive epithelial tubo-ovarian cancer risk prediction model incorporating genetic and epidemiological risk factors. <i>Journal of Medical Genetics</i> , 2022, 59, 632-643.	3.2	33
3	MCM3 is a novel proliferation marker associated with longer survival for patients with tubo-ovarian high-grade serous carcinoma. <i>Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin</i> , 2022, 480, 855-871.	2.8	8
4	High Prediagnosis Inflammation-Related Risk Score Associated with Decreased Ovarian Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 443-452.	2.5	2
5	Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. <i>American Journal of Human Genetics</i> , 2022, 109, 116-135.	6.2	3
6	Reproductive factors do not influence survival with ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, , cebp.1091.2021.	2.5	1
7	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	4.4	6
8	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
9	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
10	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	7.1	51
11	Concerns About Methods Used in Modeling Study of Risk-Stratified Screening for Breast Cancer. <i>JAMA Oncology</i> , 2022, , .	7.1	3
12	Validated biomarker assays confirm that <scp>ARID1A</scp> loss is confounded with <scp>MMR</scp> deficiency, <scp>CD8</sup>+</sup> TIL</scp> infiltration, and provides no independent prognostic value in endometriosis-associated ovarian carcinomas. <i>Journal of Pathology</i> , 2022, 256, 388-401.	4.5	15
13	Multi-omic machine learning predictor of breast cancer therapy response. <i>Nature</i> , 2022, 601, 623-629.	27.8	187
14	Large-scale Integrated Analysis of Genetics and Metabolomic Data Reveals Potential Links Between Lipids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1216-1226.	2.5	3
15	A multi-level investigation of the genetic relationship between endometriosis and ovarian cancer histotypes. <i>Cell Reports Medicine</i> , 2022, 3, 100542.	6.5	26
16	Germline BRCA variants, lifestyle and ovarian cancer survival. <i>Gynecologic Oncology</i> , 2022, , .	1.4	2
17	A Genome-Wide Gene-Based Gene-Environment Interaction Study of Breast Cancer in More than 90,000 Women. <i>Cancer Research Communications</i> , 2022, 2, 211-219.	1.7	6
18	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. <i>Breast Cancer Research</i> , 2022, 24, 27.	5.0	15

#	ARTICLE	IF	CITATIONS
19	Beyond GWAS of Colorectal Cancer: Evidence of Interaction with Alcohol Consumption and Putative Causal Variant for the 10q24.2 Region. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1077-1089.	2.5	6
20	Genetic Regulation of DNA Methylation Yields Novel Discoveries in GWAS of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2022, 31, 1068-1076.	2.5	1
21	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. <i>Human Molecular Genetics</i> , 2022, 31, 3133-3143.	2.9	11
22	Relevance of the MHC region for breast cancer susceptibility in Asians. <i>Breast Cancer</i> , 2022, 29, 869-879.	2.9	1
23	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	8.2	19
24	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. <i>Journal of the National Cancer Institute</i> , 2022, 114, 1706-1719.	6.3	14
25	Associations of a breast cancer polygenic risk score with tumor characteristics and survival.. <i>Journal of Clinical Oncology</i> , 2022, 40, 563-563.	1.6	1
26	Molecular Subclasses of Clear Cell Ovarian Carcinoma and Their Impact on Disease Behavior and Outcomes. <i>Clinical Cancer Research</i> , 2022, 28, 4947-4956.	7.0	22
27	chromMAGMA: regulatory element-centric interrogation of risk variants. <i>Life Science Alliance</i> , 2022, 5, e202201446.	2.8	1
28	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. <i>Cancers</i> , 2022, 14, 3363.	3.7	2
29	Germline allelic expression of genes at 17q22 locus associates with risk of breast cancer. <i>European Journal of Cancer</i> , 2022, 172, 146-157.	2.8	0
30	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	6.3	45
31	Population-based targeted sequencing of 54 candidate genes identifies <i>PALB2</i> as a susceptibility gene for high-grade serous ovarian cancer. <i>Journal of Medical Genetics</i> , 2021, 58, 305-313.	3.2	26
32	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 453-461.	6.3	12
33	Expanding Our Understanding of Ovarian Cancer Risk: The Role of Incomplete Pregnancies. <i>Journal of the National Cancer Institute</i> , 2021, 113, 301-308.	6.3	8
34	Refined cut-off for TP53 immunohistochemistry improves prediction of TP53 mutation status in ovarian mucinous tumors: implications for outcome analyses. <i>Modern Pathology</i> , 2021, 34, 194-206.	5.5	21
35	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021, 160, 1164-1178.e6.	1.3	36
36	Genetically predicted circulating protein biomarkers and ovarian cancer risk. <i>Gynecologic Oncology</i> , 2021, 160, 506-513.	1.4	12

#	ARTICLE	IF	CITATIONS
37	A comprehensive re-assessment of the association between vitamin D and cancer susceptibility using Mendelian randomization. <i>Nature Communications</i> , 2021, 12, 246.	12.8	39
38	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
39	Genetically predicted circulating concentrations of micronutrients and risk of colorectal cancer among individuals of European descent: a Mendelian randomization study. <i>American Journal of Clinical Nutrition</i> , 2021, 113, 1490-1502.	4.7	27
40	NHS announces a pilot of a blood test for early detection of many cancers. <i>Journal of Medical Screening</i> , 2021, 28, 1-2.	2.3	2
41	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	12.8	19
42	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021, 70, 1325-1334.	12.1	44
43	Meta-analysis of the association between emphysematous change on thoracic computerized tomography scan and recurrent pneumothorax. <i>QJM - Monthly Journal of the Association of Physicians</i> , 2021, , .	0.5	0
44	Breast Cancer Risk Genes " Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	27.0	532
45	Germline and Somatic Genetic Variants in the p53 Pathway Interact to Affect Cancer Risk, Progression, and Drug Response. <i>Cancer Research</i> , 2021, 81, 1667-1680.	0.9	32
46	Benefit, Harm, and Cost-effectiveness Associated With Magnetic Resonance Imaging Before Biopsy in Age-based and Risk-stratified Screening for Prostate Cancer. <i>JAMA Network Open</i> , 2021, 4, e2037657.	5.9	34
47	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1168-1176.	6.3	41
48	Response to Li and Hopper. <i>American Journal of Human Genetics</i> , 2021, 108, 527-529.	6.2	5
49	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?. <i>Cancers</i> , 2021, 13, 2370.	3.7	4
50	Joint IARC/NCI International Cancer Seminar Series Report: expert consensus on future directions for ovarian carcinoma research. <i>Carcinogenesis</i> , 2021, 42, 785-793.	2.8	6
51	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.7	6
52	Identification of a Locus Near <i>ULK1</i> Associated With Progression-Free Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1669-1680.	2.5	5
53	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. <i>Nature Communications</i> , 2021, 12, 4198.	12.8	24
54	A systematic review assessing the existence of pneumothorax-only variants of FLCN. Implications for lifelong surveillance of renal tumours. <i>European Journal of Human Genetics</i> , 2021, 29, 1595-1600.	2.8	12

#	ARTICLE	IF	CITATIONS
55	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203.	6.2	6
56	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.	3.8	18
57	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. Human Genetics and Genomics Advances, 2021, 2, 100041.	1.7	6
58	Association of germline genetic variants with breast cancer-specific survival in patient subgroups defined by clinic-pathological variables related to tumor biology and type of systemic treatment. Breast Cancer Research, 2021, 23, 86.	5.0	7
59	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
60	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
61	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. Breast Cancer Research, 2021, 23, 94.	5.0	4
62	Clinical Impact of the Predict Prostate Risk Communication Tool in Men Newly Diagnosed with Nonmetastatic Prostate Cancer: A Multicentre Randomised Controlled Trial. European Urology, 2021, 80, 661-669.	1.9	7
63	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.	2.5	19
64	Long-term opiate use and risk of cardiovascular mortality: results from the Golestan Cohort Study. European Journal of Preventive Cardiology, 2021, 28, 98-106.	1.8	13
65	A Combined Proteomics and Mendelian Randomization Approach to Investigate the Effects of Aspirin-Targeted Proteins on Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 564-575.	2.5	10
66	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
67	Care of men with cancer-predisposing BRCA variants. BMJ, The, 2021, 375, n2376.	6.0	1
68	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. Nutrients, 2021, 13, 4164.	4.1	3
69	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	7.9	83
70	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. Journal of the National Cancer Institute, 2020, 112, 179-190.	6.3	71
71	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228â€™%951 Women of European Descent. Journal of the National Cancer Institute, 2020, 112, 295-304.	6.3	35
72	A prospective study of tea drinking temperature and risk of esophageal squamous cell carcinoma. International Journal of Cancer, 2020, 146, 18-25.	5.1	57

#	ARTICLE	IF	CITATIONS
73	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.	1.9	21
74	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	5.1	13
75	Identification of novel epithelial ovarian cancer loci in women of African ancestry. International Journal of Cancer, 2020, 146, 2987-2998.	5.1	18
76	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
77	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
78	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. International Journal of Epidemiology, 2020, 49, 1117-1131.	1.9	41
79	Identification of Novel Loci and New Risk Variant in Known Loci for Colorectal Cancer Risk in East Asians. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 477-486.	2.5	25
80	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. Journal of Clinical Oncology, 2020, 38, 674-685.	1.6	270
81	Association Between Levels of Sex Hormones and Risk of Esophageal Adenocarcinoma and Barrett's Esophagus. Clinical Gastroenterology and Hepatology, 2020, 18, 2701-2709.e3.	4.4	12
82	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. American Journal of Human Genetics, 2020, 107, 622-635.	6.2	14
83	Cancer Screening, Surrogates of Survival, and the Soma. Cancer Cell, 2020, 38, 433-437.	16.8	14
84	Breast cancer risk factors and their effects on survival: a Mendelian randomisation study. BMC Medicine, 2020, 18, 327.	5.5	40
85	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444.	6.2	124
86	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	12.8	88
87	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	21.4	367
88	Rare Germline Genetic Variants and the Risks of Epithelial Ovarian Cancer. Cancers, 2020, 12, 3046.	3.7	22
89	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
90	Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. BMC Medicine, 2020, 18, 229.	5.5	28

#	ARTICLE	IF	CITATIONS
91	Sex-Specific Genetic Associations for Barrett's Esophagus and Esophageal Adenocarcinoma. <i>Gastroenterology</i> , 2020, 159, 2065-2076.e1.	1.3	16
92	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
93	The challenge of early detection in cancer. <i>Science</i> , 2020, 368, 589-590.	12.6	70
94	Usual physical activity and subsequent hospital usage over 20 years in a general population: the EPIC-Norfolk cohort. <i>BMC Geriatrics</i> , 2020, 20, 165.	2.7	10
95	The effect of sample size on polygenic hazard models for prostate cancer. <i>European Journal of Human Genetics</i> , 2020, 28, 1467-1475.	2.8	14
96	Comparative performance and external validation of the multivariable PREDICT Prostate tool for non-metastatic prostate cancer: a study in 69,206 men from Prostate Cancer data Base Sweden (PCBaSe). <i>BMC Medicine</i> , 2020, 18, 139.	5.5	10
97	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	27.6	178
98	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	3.3	2
99	Development and Validation of the Gene Expression Predictor of High-grade Serous Ovarian Carcinoma Molecular SubTYPE (ProTYPE). <i>Clinical Cancer Research</i> , 2020, 26, 5411-5423.	7.0	43
100	Household Fuel Use and the Risk of Gastrointestinal Cancers: The Golestan Cohort Study. <i>Environmental Health Perspectives</i> , 2020, 128, 67002.	6.0	19
101	Clinical and pathological associations of PTEN expression in ovarian cancer: a multicentre study from the Ovarian Tumour Tissue Analysis Consortium. <i>British Journal of Cancer</i> , 2020, 123, 793-802.	6.4	35
102	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 860-870.	2.5	26
103	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. <i>Nature Communications</i> , 2020, 11, 1217.	12.8	46
104	Functional informed genome-wide interaction analysis of body mass index, diabetes and colorectal cancer risk. <i>Cancer Medicine</i> , 2020, 9, 3563-3573.	2.8	7
105	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1731-1738.	2.5	27
106	Menopausal hormone therapy prior to the diagnosis of ovarian cancer is associated with improved survival. <i>Gynecologic Oncology</i> , 2020, 158, 702-709.	1.4	15
107	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
108	Urinary TERT promoter mutations are detectable up to 10 years prior to clinical diagnosis of bladder cancer: Evidence from the Golestan Cohort Study. <i>EBioMedicine</i> , 2020, 53, 102643.	6.1	51

#	ARTICLE	IF	CITATIONS
109	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in <i>RAD51C</i> and <i>RAD51D</i> . Journal of the National Cancer Institute, 2020, 112, 1242-1250.	6.3	106
110	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
111	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
112	Opium use and subsequent incidence of cancer: results from the Golestan Cohort Study. The Lancet Global Health, 2020, 8, e649-e660.	6.3	59
113	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14
114	Combining measures of immune infiltration shows additive effect on survival prediction in high-grade serous ovarian carcinoma. British Journal of Cancer, 2020, 122, 1803-1810.	6.4	23
115	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.	21.4	138
116	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597.	12.8	193
117	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. Cancer Research, 2019, 79, 505-517.	0.9	49
118	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
119	Sex specific associations in genome wide association analysis of renal cell carcinoma. European Journal of Human Genetics, 2019, 27, 1589-1598.	2.8	27
120	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
121	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
122	Evidence of a Causal Association Between Cancer and Alzheimer's Disease: a Mendelian Randomization Analysis. Scientific Reports, 2019, 9, 13548.	3.3	26
123	Understanding of prognosis in non-metastatic prostate cancer: a randomised comparative study of clinician estimates measured against the PREDICT prostate prognostic model. British Journal of Cancer, 2019, 121, 715-718.	6.4	12
124	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
125	Overestimation of the Benefit-to-Harm Ratio of Risk-Based Mammography Screening in the United Kingdom—Reply. JAMA Oncology, 2019, 5, 428.	7.1	1
126	Models predicting survival to guide treatment decision-making in newly diagnosed primary non-metastatic prostate cancer: a systematic review. BMJ Open, 2019, 9, e029149.	1.9	15

#	ARTICLE	IF	CITATIONS
127	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. <i>Modern Pathology</i> , 2019, 32, 1834-1846.	5.5	54
128	Authors'™ response: Associations of obesity and circulating insulin and glucose with breast cancer risk. <i>International Journal of Epidemiology</i> , 2019, 48, 1016-1017.	1.9	1
129	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. <i>Molecular Genetics & Genomic Medicine</i> , 2019, 7, e707.	1.2	9
130	Going to extremes: determinants of extraordinary response and survival in patients with cancer. <i>Nature Reviews Cancer</i> , 2019, 19, 339-348.	28.4	35
131	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. <i>Nature Communications</i> , 2019, 10, 2154.	12.8	172
132	Evaluation of vitamin D biosynthesis and pathway target genes reveals UGT2A1/2 and EGFR polymorphisms associated with epithelial ovarian cancer in African American Women. <i>Cancer Medicine</i> , 2019, 8, 2503-2513.	2.8	6
133	A transcriptome-wide association study of high-grade serous epithelial ovarian cancer identifies new susceptibility genes and splice variants. <i>Nature Genetics</i> , 2019, 51, 815-823.	21.4	89
134	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
135	Individual and Combined Effects of Environmental Risk Factors for Esophageal Cancer Based on Results From the Golestan Cohort Study. <i>Gastroenterology</i> , 2019, 156, 1416-1427.	1.3	123
136	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	1.4	28
137	Individual prognosis at diagnosis in nonmetastatic prostate cancer: Development and external validation of the PREDICT Prostate multivariable model. <i>PLoS Medicine</i> , 2019, 16, e1002758.	8.4	56
138	Dynamics of breast-cancer relapse reveal late-recurring ER-positive genomic subgroups. <i>Nature</i> , 2019, 567, 399-404.	27.8	239
139	Combined quantitative measures of ER, PR, HER2, and Ki67 provide more prognostic information than categorical combinations in luminal breast cancer. <i>Modern Pathology</i> , 2019, 32, 1244-1256.	5.5	51
140	Body mass index and the association between low-density lipoprotein cholesterol as predicted by HMGCR genetic variants and breast cancer risk. <i>International Journal of Epidemiology</i> , 2019, 48, 1727-1730.	1.9	3
141	No Association Between Vitamin D Status and Risk of Barrett's Esophagus or Esophageal Adenocarcinoma: A Mendelian Randomization Study. <i>Clinical Gastroenterology and Hepatology</i> , 2019, 17, 2227-2235.e1.	4.4	16
142	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
143	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. <i>European Journal of Epidemiology</i> , 2019, 34, 591-600.	5.7	16
144	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. <i>Human Genetics</i> , 2019, 138, 307-326.	3.8	44

#	ARTICLE	IF	CITATIONS
145	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
146	Polygenic risk-tailored screening for prostate cancer: A benefit-harm and cost-effectiveness modelling study. PLoS Medicine, 2019, 16, e1002998.	8.4	56
147	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
148	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29
149	European Breast Cancer Council manifesto 2018: Genetic risk prediction testing in breast cancer. European Journal of Cancer, 2019, 106, 45-53.	2.8	15
150	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780.	1.9	35
151	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	2.4	415
152	Targeted Resequencing of the Coding Sequence of 38 Genes Near Breast Cancer GWAS Loci in a Large Case-Control Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 822-825.	2.5	7
153	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. Biological Psychiatry, 2019, 85, 946-955.	1.3	69
154	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
155	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. Cancer Research, 2019, 79, 467-481.	0.9	22
156	A comprehensive gene-environment interaction analysis in Ovarian Cancer using genome-wide significant common variants. International Journal of Cancer, 2019, 144, 2192-2205.	5.1	12
157	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
158	Title is missing!. , 2019, 16, e1002998.		0
159	Title is missing!. , 2019, 16, e1002998.		0
160	Title is missing!. , 2019, 16, e1002998.		0
161	Title is missing!. , 2019, 16, e1002998.		0
162	MyD88 and TLR4 Expression in Epithelial Ovarian Cancer. Mayo Clinic Proceedings, 2018, 93, 307-320.	3.0	22

#	ARTICLE	IF	CITATIONS
163	The Landscape of Somatic Genetic Alterations in Breast Cancers From ATM Germline Mutation Carriers. <i>Journal of the National Cancer Institute</i> , 2018, 110, 1030-1034.	6.3	90
164	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. <i>International Journal of Cancer</i> , 2018, 143, 746-757.	5.1	19
165	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	6.4	15
166	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018, 7, 1978-1987.	2.8	62
167	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. <i>Nature Communications</i> , 2018, 9, 1340.	12.8	58
168	Development and External Validation of Prediction Models for 10-Year Survival of Invasive Breast Cancer. Comparison with PREDICT and CancerMath. <i>Clinical Cancer Research</i> , 2018, 24, 2110-2115.	7.0	15
169	Cost-effectiveness of Population-Based BRCA1, BRCA2, RAD51C, RAD51D, BRIP1, PALB2 Mutation Testing in Unselected General Population Women. <i>Journal of the National Cancer Institute</i> , 2018, 110, 714-725.	6.3	138
170	Determining Risk of Barrett's Esophagus and Esophageal Adenocarcinoma Based on Epidemiologic Factors and Genetic Variants. <i>Gastroenterology</i> , 2018, 154, 1273-1281.e3.	1.3	67
171	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 526-536.	1.9	88
172	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. <i>Human Molecular Genetics</i> , 2018, 27, 853-859.	2.9	20
173	Germline BRCA mutation and outcome in young-onset breast cancer (POSH): a prospective cohort study. <i>Lancet Oncology</i> , The, 2018, 19, 169-180.	10.7	316
174	Opium Use and Risk of Pancreatic Cancer: A Prospective Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 268-273.	2.5	22
175	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. <i>BMJ: British Medical Journal</i> , 2018, 360, j5757.	2.3	153
176	Assessment of moderate coffee consumption and risk of epithelial ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2018, 47, 450-459.	1.9	15
177	Germline pathogenic variants in PALB2 and other cancer-predisposing genes in families with hereditary diffuse gastric cancer without CDH1 mutation: a whole-exome sequencing study. <i>The Lancet Gastroenterology and Hepatology</i> , 2018, 3, 489-498.	8.1	87
178	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018, 8, 6574.	3.3	51
179	Interactions Between Genetic Variants and Environmental Factors Affect Risk of Esophageal Adenocarcinoma and Barrett's Esophagus. <i>Clinical Gastroenterology and Hepatology</i> , 2018, 16, 1598-1606.e4.	4.4	16
180	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. <i>American Journal of Epidemiology</i> , 2018, 187, 366-377.	3.4	8

#	ARTICLE	IF	CITATIONS
181	Common Genetic Variation and Susceptibility to Ovarian Cancer: Current Insights and Future Directions. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 395-404.	2.5	33
182	Meta-Analysis of Genome-Wide Association Studies (GWAS) of Late Toxicity in 3,874 Men Treated with Radiation for Prostate Cancer. <i>International Journal of Radiation Oncology Biology Physics</i> , 2018, 102, e738-e739.	0.8	1
183	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3707.	12.8	86
184	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. <i>Blood</i> , 2018, 132, 2040-2052.	1.4	17
185	Alcohol consumption and future hospital usage: The EPIC-Norfolk prospective population study. <i>PLoS ONE</i> , 2018, 13, e0200747.	2.5	2
186	Pre-operative stromal stiffness measured by shear wave elastography is independently associated with breast cancer-specific survival. <i>Breast Cancer Research and Treatment</i> , 2018, 171, 383-389.	2.5	27
187	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. <i>Journal of Medical Genetics</i> , 2018, 55, 546-554.	3.2	38
188	Mendelian randomisation study of age at menarche and age at menopause and the risk of colorectal cancer. <i>British Journal of Cancer</i> , 2018, 118, 1639-1647.	6.4	16
189	Cost-effectiveness and Benefit-to-Harm Ratio of Risk-Stratified Screening for Breast Cancer. <i>JAMA Oncology</i> , 2018, 4, 1504.	7.1	199
190	Age, HIV status, and research context determined attrition in a longitudinal cohort in Nigeria. <i>Journal of Clinical Epidemiology</i> , 2018, 100, 32-43.	5.0	7
191	The importance of using public data to validate reported associations. <i>PLoS Genetics</i> , 2018, 14, e1007416.	3.5	0
192	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. <i>Journal of Pathology: Clinical Research</i> , 2018, 4, 250-261.	3.0	70
193	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
194	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	2.5	9
195	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178
196	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. <i>International Journal of Molecular Sciences</i> , 2018, 19, 2473.	4.1	3
197	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	21.4	652
198	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018, 9, 2256.	12.8	88

#	ARTICLE	IF	CITATIONS
199	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	21.4	184
200	Abstract 1225: Rare variants in DNA damage repair genes are associated with male breast cancer predisposition. , 2018, , .		1
201	A gene expression prognostic signature for overall survival in patients with high-grade serous ovarian cancer.. <i>Journal of Clinical Oncology</i> , 2018, 36, 5583-5583.	1.6	1
202	Abstract 2971: Digital image analysis based IHC4+C assay and prognosis in hormone receptor-positive breast cancer. , 2018, , .		0
203	Abstract 1498: The role of tissues specific super-enhancers in mediating the genetic risk of ovarian cancer. , 2018, , .		0
204	Abstract 225: Tumor-infiltrating CD8-positive T-lymphocytes in tubo-ovarian high-grade serous cancer are associated with multiple germline variants in 22q12.1 in a genome-wide association analysis. , 2018, , .		0
205	Abstract 2211: Patient level polygenic risk scores and continuous estrogen receptor expression in breast cancer. , 2018, , .		0
206	Abstract 2271: Pathway analysis suggests biological processes driven by germline genetic associations with breast cancer prognosis. , 2018, , .		0
207	Weibull regression with Bayesian variable selection to identify prognostic tumour markers of breast cancer survival. <i>Statistical Methods in Medical Research</i> , 2017, 26, 414-436.	1.5	20
208	Dietary Protein Sources and All-Cause and Cause-Specific Mortality: The Golestan Cohort Study in Iran. <i>American Journal of Preventive Medicine</i> , 2017, 52, 237-248.	3.0	54
209	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	6.4	23
210	Cigarette smoking is associated with adverse survival among women with ovarian cancer: Results from a pooled analysis of 19 studies. <i>International Journal of Cancer</i> , 2017, 140, 2422-2435.	5.1	25
211	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.9	75
212	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
213	Accuracy of the online prognostication tools PREDICT and Adjuvant! for early-stage breast cancer patients younger than 50 years. <i>European Journal of Cancer</i> , 2017, 78, 37-44.	2.8	38
214	Lymphocyte density determined by computational pathology validated as a predictor of response to neoadjuvant chemotherapy in breast cancer: secondary analysis of the ARTemis trial. <i>Annals of Oncology</i> , 2017, 28, 1832-1835.	1.2	36
215	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	12.8	106
216	Dairy Food Intake and All-Cause, Cardiovascular Disease, and Cancer Mortality. <i>American Journal of Epidemiology</i> , 2017, 185, 697-711.	3.4	53

#	ARTICLE	IF	CITATIONS
217	Mortality from respiratory diseases associated with opium use: a population-based cohort study. <i>Thorax</i> , 2017, 72, 1028-1034.	5.6	24
218	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
219	Germline variation in inflammation-related pathways and risk of Barrett's oesophagus and oesophageal adenocarcinoma. <i>Cut</i> , 2017, 66, 1739-1747.	12.1	38
220	Integration of Population-Level Genotype Data with Functional Annotation Reveals Over-Representation of Long Noncoding RNAs at Ovarian Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 116-125.	2.5	6
221	Genetic epidemiology of ovarian cancer and prospects for polygenic risk prediction. <i>Gynecologic Oncology</i> , 2017, 147, 705-713.	1.4	69
222	Dose-Response Association of CD8 ⁺ Tumor-Infiltrating Lymphocytes and Survival Time in High-Grade Serous Ovarian Cancer. <i>JAMA Oncology</i> , 2017, 3, e173290.	7.1	260
223	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
224	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
225	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. <i>International Journal of Cancer</i> , 2017, 141, 1830-1840.	5.1	20
226	RE: Personalized Prognostic Prediction Models for Breast Cancer Recurrence and Survival Incorporating Multidimensional Data. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	1
227	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. <i>British Journal of Cancer</i> , 2017, 117, 734-743.	6.4	7
228	Rare, protein-truncating variants in <i>ATM</i> , <i>CHEK2</i> and <i>PALB2</i> , but not <i>XRCC2</i> , are associated with increased breast cancer risks. <i>Journal of Medical Genetics</i> , 2017, 54, 732-741.	3.2	68
229	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. <i>European Urology</i> , 2017, 72, 747-754.	1.9	39
230	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. <i>Nature Communications</i> , 2017, 8, 1892.	12.8	40
231	Validation of the online prediction tool PREDICT v. 2.0 in the Dutch breast cancer population. <i>European Journal of Cancer</i> , 2017, 86, 364-372.	2.8	32
232	An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation. <i>Breast Cancer Research</i> , 2017, 19, 58.	5.0	161
233	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	2.4	67
234	No Evidence That Genetic Variation in the Myeloid-Derived Suppressor Cell Pathway Influences Ovarian Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 420-424.	2.5	3

#	ARTICLE	IF	CITATIONS
235	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	2.5	278
236	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	242
237	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	45
238	Testâ€Retest Reliability of Self-Reported Sexual Behavior History in Urbanized Nigerian Women. <i>Frontiers in Public Health</i> , 2017, 5, 172.	2.7	10
239	Association between tumour infiltrating lymphocytes, histotype and clinical outcome in epithelial ovarian cancer. <i>BMC Cancer</i> , 2017, 17, 657.	2.6	48
240	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	5.0	43
241	Abstract 1289: Evaluation of vitamin D receptor regulated genes reveals EGFR polymorphism is associated with high-grade serous ovarian cancer in African American women. , 2017, , .		1
242	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. <i>Oncotarget</i> , 2017, 8, 18381-18398.	1.8	14
243	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. <i>Oncotarget</i> , 2017, 8, 50930-50940.	1.8	43
244	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. <i>Oncotarget</i> , 2017, 8, 64670-64684.	1.8	7
245	<i>PHIP</i>- a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	1.8	9
246	Abstract 5502: Functional evaluation of superenhancers as mediators of epithelial ovarian cancer risk. , 2017, , .		0
247	Abstract 1299: Common germline risk loci and the tumor anticancer immune response in breast cancer. , 2017, , .		0
248	Abstract 1307: Identification of novel epithelial ovarian cancer loci in women of African ancestry from the Ovarian Cancer Association Consortium. , 2017, , .		0
249	Abstract 2258: Genome-wide association studies of breast cancer prognosis. , 2017, , .		0
250	Abstract 1308: Transcriptome-wide association study among 66,450 women to identify candidate susceptible genes for ovarian cancer risk. , 2017, , .		0
251	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. <i>Oncotarget</i> , 2016, 7, 80140-80163.	1.8	31
252	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , 2016, 13, e1002105.	8.4	118

#	ARTICLE	IF	CITATIONS
253	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	2.5	10
254	Patterns of Immune Infiltration in Breast Cancer and Their Clinical Implications: A Gene-Expression-Based Retrospective Study. PLoS Medicine, 2016, 13, e1002194.	8.4	473
255	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
256	P-B25â€fInfluence of spirituality and modesty on acceptance of self sampling for cervical cancer screening. Journal of Acquired Immune Deficiency Syndromes (1999), 2016, 71, 84.	2.1	1
257	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895.	1.9	71
258	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
259	Exome genotyping arrays to identify rare and low frequency variants associated with epithelial ovarian cancer risk. Human Molecular Genetics, 2016, 25, 3600-3612.	2.9	17
260	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
261	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
262	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. Breast Cancer Research, 2016, 18, 64.	5.0	31
263	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. Breast Cancer Research, 2016, 18, 124.	5.0	52
264	Decline in Antigenicity of Tumor Markers by Storage Time Using Pathology Sections Cut From Tissue Microarrays. Applied Immunohistochemistry and Molecular Morphology, 2016, 24, 221-226.	1.2	10
265	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. Human Genetics, 2016, 135, 741-756.	3.8	19
266	Incorporating truncating variants in PALB2, CHEK2, and ATM into the BOADICEA breast cancer risk model. Genetics in Medicine, 2016, 18, 1190-1198.	2.4	80
267	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
268	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. Cancer Causes and Control, 2016, 27, 679-693.	1.8	21
269	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
270	The BRCA1-Î”11q Alternative Splice Isoform Bypasses Germline Mutations and Promotes Therapeutic Resistance to PARP Inhibition and Cisplatin. Cancer Research, 2016, 76, 2778-2790.	0.9	208

#	ARTICLE	IF	CITATIONS
271	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.9	100
272	Common genetic variation associated with increased susceptibility to prostate cancer does not increase risk of radiotherapy toxicity. <i>British Journal of Cancer</i> , 2016, 114, 1165-1174.	6.4	17
273	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	1.9	111
274	Risk Prediction for Epithelial Ovarian Cancer in 11 United Statesâ€‘Based Case-Control Studies: Incorporation of Epidemiologic Risk Factors and 17 Confirmed Genetic Loci. <i>American Journal of Epidemiology</i> , 2016, 184, 555-569.	3.4	32
275	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. <i>American Journal of Human Genetics</i> , 2016, 99, 903-911.	6.2	59
276	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. <i>EBioMedicine</i> , 2016, 10, 150-163.	6.1	69
277	Population-Based Precision Cancer Screening: A Symposium on Evidence, Epidemiology, and Next Steps. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1449-1455.	2.5	43
278	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	5.1	43
279	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33
280	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1503-1510.	2.5	64
281	Genome-wide association studies in oesophageal adenocarcinoma and Barrett's oesophagus: a large-scale meta-analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1363-1373.	10.7	133
282	A splicing variant of <i>TERT</i> identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. <i>International Journal of Cancer</i> , 2016, 139, 2646-2654.	5.1	7
283	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
284	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
285	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€‘ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
286	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	3.3	19
287	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , 2016, 7, 10979.	12.8	50
288	Prognostic value of automated Ki67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, 104.	5.0	56

#	ARTICLE	IF	CITATIONS
289	The somatic mutation profiles of 2,433 breast cancers refine their genomic and transcriptomic landscapes. <i>Nature Communications</i> , 2016, 7, 11479.	12.8	1,221
290	Implications of using whole genome sequencing to test unselected populations for high risk breast cancer genes: a modelling study. <i>Hereditary Cancer in Clinical Practice</i> , 2016, 14, 12.	1.5	2
291	New paradigms for <i>BRCA1</i> / <i>BRCA2</i> testing in women with ovarian cancer: results of the Genetic Testing in Epithelial Ovarian Cancer (GTEOC) study. <i>Journal of Medical Genetics</i> , 2016, 53, 655-661.	3.2	57
292	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> / <i>EK</i> <i>2</i> *1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	1.6	152
293	Household Fuel Use and Cardiovascular Disease Mortality. <i>Circulation</i> , 2016, 133, 2360-2369.	1.6	66
294	Computational pathology of pre-treatment biopsies identifies lymphocyte density as a predictor of response to neoadjuvant chemotherapy in breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 21.	5.0	66
295	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016, 23, 77-91.	3.1	62
296	A Cross-Cancer Genetic Association Analysis of the DNA Repair and DNA Damage Signaling Pathways for Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 193-200.	2.5	66
297	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 780-790.	2.5	10
298	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016, 2, 138-153.	3.0	19
299	CWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. <i>Human Molecular Genetics</i> , 2016, 25, ddw092.	2.9	19
300	Personalized testing based on polygenic risk score is promising for more efficient population-based screening programs for common oncological diseases. <i>Annals of Oncology</i> , 2016, 27, 369-370.	1.2	5
301	<i>PPM1D</i> Mosaic Truncating Variants in Ovarian Cancer Cases May Be Treatment-Related Somatic Mutations. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv347.	6.3	43
302	The association between socioeconomic status and tumour stage at diagnosis of ovarian cancer: A pooled analysis of 18 case-control studies. <i>Cancer Epidemiology</i> , 2016, 41, 71-79.	1.9	20
303	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
304	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
305	Patients with a High Polygenic Risk of Breast Cancer do not have An Increased Risk of Radiotherapy Toxicity. <i>Clinical Cancer Research</i> , 2016, 22, 1413-1420.	7.0	16
306	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , 2016, 114, 298-304.	6.4	7

#	ARTICLE	IF	CITATIONS
307	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 446-454.	2.5	9
308	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.	3.8	8
309	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315.	6.3	77
310	Hypertension and mortality in the Golestan Cohort Study: A prospective study of 50,000 adults in Iran. Journal of Human Hypertension, 2016, 30, 260-267.	2.2	21
311	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
312	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
313	The Relationship between Common Genetic Markers of Breast Cancer Risk and Chemotherapy-Induced Toxicity: A Case-Control Study. PLoS ONE, 2016, 11, e0158984.	2.5	15
314	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110.	1.8	5
315	Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility: results from a large-scale collaboration. Oncotarget, 2016, 7, 72381-72394.	1.8	13
316	Germline polymorphisms in an enhancer of <i>PSIP1</i> are associated with progression-free survival in epithelial ovarian cancer. Oncotarget, 2016, 7, 6353-6368.	1.8	29
317	Abstract PR15: MYC distal enhancers underlie ovarian cancer susceptibility in the 8q24.21 locus.. , 2016, , .		0
318	Abstract B27: Investigation of small GTPase genes in epithelial ovarian cancer.. , 2016, , .		0
319	Abstract 797: A splicing variant of TERT identified by GWAS interacts with menopausal estrogen therapy in risk of ovarian cancer. , 2016, , .		0
320	Abstract 3451: Breast cancer risk factor associations by loss of E-cadherin tumor tissue expression: A pooled analysis of 5,896 cases in 12 studies from the Breast Cancer Association Consortium (BCAC). , 2016, , .		0
321	The Combined Effects of Healthy Lifestyle Behaviors on All-Cause Mortality: The Golestan Cohort Study. Archives of Iranian Medicine, 2016, 19, 752-761.	0.6	5
322	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
323	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.	3.3	35
324	A nested cohort study of 6,248 early breast cancer patients treated in neoadjuvant and adjuvant chemotherapy trials investigating the prognostic value of chemotherapy-related toxicities. BMC Medicine, 2015, 13, 306.	5.5	26

#	ARTICLE	IF	CITATIONS
325	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697.	1.3	22
326	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.	2.6	6
327	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
328	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	5.0	19
329	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. Journal of the National Cancer Institute, 2015, 107, .	6.3	129
330	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
331	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0
332	Do Health Professionals Need Additional Competencies for Stratified Cancer Prevention Based on Genetic Risk Profiling?. Journal of Personalized Medicine, 2015, 5, 191-212.	2.5	18
333	A review of the online prognostic model predict using the POSH cohort (women aged >=40 years at Tj ETQq1 1 0.784314 rgBT /Ove	1.6	6
334	The Clinical Performance of an Office-Based Risk Scoring System for Fatal Cardiovascular Diseases in North-East of Iran. PLoS ONE, 2015, 10, e0126779.	2.5	14
335	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106.	2.5	44
336	Polymorphisms in Genes of Relevance for Oestrogen and Oxytocin Pathways and Risk of Barrett's Oesophagus and Oesophageal Adenocarcinoma: A Pooled Analysis from the BEACON Consortium. PLoS ONE, 2015, 10, e0138738.	2.5	9
337	Influence of Spirituality and Modesty on Acceptance of Self-Sampling for Cervical Cancer Screening. PLoS ONE, 2015, 10, e0141679.	2.5	20
338	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
339	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
340	PD-L1 protein expression in breast cancer is rare, enriched in basal-like tumours and associated with infiltrating lymphocytes. Annals of Oncology, 2015, 26, 1488-1493.	1.2	234
341	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
342	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	27.0	764

#	ARTICLE	IF	CITATIONS
343	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2015, 1, 18-32.	3.0	24
344	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. <i>EBioMedicine</i> , 2015, 2, 681-689.	6.1	56
345	Germline Mutation in <i>BRCA1</i> or <i>BRCA2</i> and Ten-Year Survival for Women Diagnosed with Epithelial Ovarian Cancer. <i>Clinical Cancer Research</i> , 2015, 21, 652-657.	7.0	138
346	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
347	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. <i>Cancer Discovery</i> , 2015, 5, 368-379.	9.4	56
348	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
349	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015, 36, 256-271.	2.8	14
350	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	4.6	38
351	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	21.4	221
352	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
353	The effect of rare variants on inflation of the test statistics in case-control analyses. <i>BMC Bioinformatics</i> , 2015, 16, 53.	2.6	7
354	Genome-wide significant risk associations for mucinous ovarian carcinoma. <i>Nature Genetics</i> , 2015, 47, 888-897.	21.4	78
355	19. A review of PREDICT using the POSH cohort (women aged 40 years or younger at breast cancer) Tj ETQq1 1 0.784314 rgBT /Over 1.0		
356	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	2.5	28
357	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015, 47, 987-995.	21.4	218
358	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015, 21, 5264-5276.	7.0	33
359	The malignant phenotype in breast cancer is driven by eIF4A1-mediated changes in the translational landscape. <i>Cell Death and Disease</i> , 2015, 6, e1603-e1603.	6.3	136
360	Hereditary Diffuse Gastric Cancer Syndrome. <i>JAMA Oncology</i> , 2015, 1, 23.	7.1	540

#	ARTICLE	IF	CITATIONS
361	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
362	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.	2.5	56
363	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. Gynecologic Oncology, 2015, 136, 542-548.	1.4	15
364	Rare germline copy number deletions of likely functional importance are implicated in endometrial cancer predisposition. Human Genetics, 2015, 134, 269-278.	3.8	13
365	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. Human Genetics, 2015, 134, 231-245.	3.8	34
366	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. International Journal of Cancer, 2015, 136, 1351-1360.	5.1	30
367	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.9	55
368	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. Nature Communications, 2015, 6, 8234.	12.8	63
369	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
370	Common variants at the CHEK2 gene locus and risk of epithelial ovarian cancer. Carcinogenesis, 2015, 36, 1341-1353.	2.8	24
371	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
372	A risk prediction algorithm for ovarian cancer incorporating BRCA1, BRCA2, common alleles and other familial effects. Journal of Medical Genetics, 2015, 52, 465-475.	3.2	52
373	Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel Response. Clinical Cancer Research, 2015, 21, 3094-3094.	7.0	1
374	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	51
375	Rethinking ovarian cancer II: reducing mortality from high-grade serous ovarian cancer. Nature Reviews Cancer, 2015, 15, 668-679.	28.4	839
376	An evaluation of the prognostic model PREDICT using the POSH cohort of women aged ≥ 40 years at breast cancer diagnosis. British Journal of Cancer, 2015, 112, 983-991.	6.4	27
377	Shared genetics underlying epidemiological association between endometriosis and ovarian cancer. Human Molecular Genetics, 2015, 24, 5955-5964.	2.9	68
378	ClinGen and Genetic Testing. New England Journal of Medicine, 2015, 373, 1376-1379.	27.0	5

#	ARTICLE	IF	CITATIONS
379	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
380	Contribution of Germline Mutations in the <i>RAD51B</i> , <i>RAD51C</i> , and <i>RAD51D</i> Genes to Ovarian Cancer in the Population. Journal of Clinical Oncology, 2015, 33, 2901-2907.	1.6	266
381	Reducing overdiagnosis by polygenic risk-stratified screening: findings from the Finnish section of the ERSPC. British Journal of Cancer, 2015, 113, 1086-1093.	6.4	32
382	Dietary intake of minerals and risk of esophageal squamous cell carcinoma: results from the Golestan Cohort Study. American Journal of Clinical Nutrition, 2015, 102, 102-108.	4.7	61
383	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
384	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. Journal of the National Cancer Institute, 2015, 107, .	6.3	311
385	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
386	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.	2.5	24
387	Implications of polygenic risk-stratified screening for prostate cancer on overdiagnosis. Genetics in Medicine, 2015, 17, 789-795.	2.4	87
388	Population Distribution of Lifetime Risk of Ovarian Cancer in the United States. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 671-676.	2.5	82
389	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.	2.9	38
390	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. Human Molecular Genetics, 2015, 24, 1478-1492.	2.9	50
391	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	2.5	22
392	Heart Disease Is Associated With Anthropometric Indices and Change in Body Size Perception Over the Life Course: The Golestan Cohort Study. Global Heart, 2015, 10, 245.	2.3	4
393	Abstract 4684: Assessment of multifactor gene-environment interactions and ovarian cancer risk: SNPs, obesity, and hormone-related risk factors. , 2015, , .		1
394	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407.	1.8	15
395	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
396	Abstract 4633: Evidence that long non-coding RNA variants associate with epithelial ovarian cancer risk. , 2015, , .		0

#	ARTICLE	IF	CITATIONS
397	Abstract 881: Association of adult body mass index and height with risk of ovarian cancer in 39,000 women: Results of a Mendelian randomization study. , 2015, , .		0
398	Abstract POSTER-CTRL-1213: Whole exome and targeted resequencing, of population based ovarian cancer cases and controls, identifies susceptibility genes for ovarian cancer. , 2015, , .		0
399	Abstract 4681: Reducing overdiagnosis by polygenic risk-stratified screening: findings from the Finnish arm of the European randomised study of screening for prostate cancer (ERSPC). , 2015, , .		0
400	Abstract 4634: Variants within super-enhancer regulatory elements associate with epithelial ovarian cancer risk. , 2015, , .		0
401	Abstract 4635: Inherited variants affecting RNA editing may contribute to ovarian cancer susceptibility. Cancer Research, 2015, 75, 4635-4635.	0.9	1
402	Abstract 5570: Heterogeneity of luminal breast cancer characterized by immunohistochemical expression of basal markers. , 2015, , .		0
403	Abstract 4637: The effect of height, BMI and serum lipid levels on ovarian cancer prognosis in over 12,000 women: a Mendelian randomization study. , 2015, , .		0
404	Abstract 2783: Common functional mechanisms underlying pleiotropy at the 19p13.1 breast and ovarian cancer susceptibility locus. , 2015, , .		1
405	Cardiovascular disease mortality and years of life lost attributable to non-optimal systolic blood pressure and hypertension in northeastern Iran. Archives of Iranian Medicine, 2015, 18, 144-52.	0.6	10
406	Determinants of Gastroesophageal Reflux Disease, Including Hookah Smoking and Opium Use—A Cross-Sectional Analysis of 50,000 Individuals. PLoS ONE, 2014, 9, e89256.	2.5	30
407	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
408	Educating doctors and patients about how conflicts of interest can affect healthcare decision making. BMJ, The, 2014, 348, g1384-g1384.	6.0	2
409	Combined image and genomic analysis of high-grade serous ovarian cancer reveals PTEN loss as a common driver event and prognostic classifier. Genome Biology, 2014, 15, 526.	8.8	93
410	Most common “sporadic” cancers have a significant germline genetic component. Human Molecular Genetics, 2014, 23, 6112-6118.	2.9	85
411	Ovarian cancer familial relative risks by tumour subtypes and by known ovarian cancer genetic susceptibility variants. Journal of Medical Genetics, 2014, 51, 108-113.	3.2	58
412	Evidence for a time-dependent association between FOLR1 expression and survival from ovarian carcinoma: implications for clinical testing. An Ovarian Tumour Tissue Analysis consortium study. British Journal of Cancer, 2014, 111, 2297-2307.	6.4	76
413	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
414	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.	3.5	34

#	ARTICLE	IF	CITATIONS
415	What ethical and legal principles should guide the genotyping of children as part of a personalised screening programme for common cancer?. Journal of Medical Ethics, 2014, 40, 163-167.	1.8	15
416	Variation in NF- κ B Signaling Pathways and Survival in Invasive Epithelial Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1421-1427.	2.5	13
417	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
418	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
419	Association between CD8+ T-cell infiltration and breast cancer survival in 12 439 patients. Annals of Oncology, 2014, 25, 1536-1543.	1.2	610
420	Inclusion of Ki67 significantly improves performance of the PREDICT prognostication and prediction model for early breast cancer. BMC Cancer, 2014, 14, 908.	2.6	42
421	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
422	Risk of Ovarian Cancer and the NF- κ B Pathway: Genetic Association with <i>IL1A</i> and <i>TNFSF10</i> . Cancer Research, 2014, 74, 852-861.	0.9	48
423	Large-Scale Evaluation of Common Variation in Regulatory T Cell-Related Genes and Ovarian Cancer Outcome. Cancer Immunology Research, 2014, 2, 332-340.	3.4	21
424	Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel. Clinical Cancer Research, 2014, 20, 2466-2475.	7.0	91
425	The Effect on Melanoma Risk of Genes Previously Associated With Telomere Length. Journal of the National Cancer Institute, 2014, 106, .	6.3	109
426	Breast cancer susceptibility risk associations and heterogeneity by E-cadherin tumor tissue expression. Breast Cancer Research and Treatment, 2014, 143, 181-187.	2.5	16
427	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
428	Impact of body size and physical activity during adolescence and adult life on overall and cause-specific mortality in a large cohort study from Iran. European Journal of Epidemiology, 2014, 29, 95-109.	5.7	31
429	Genome-wide association study of subtype-specific epithelial ovarian cancer risk alleles using pooled DNA. Human Genetics, 2014, 133, 481-497.	3.8	23
430	A Genome-wide Association Study of Early-Onset Breast Cancer Identifies <i>PFKM</i> as a Novel Breast Cancer Gene and Supports a Common Genetic Spectrum for Breast Cancer at Any Age. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 658-669.	2.5	77
431	The contribution of deleterious germline mutations in BRCA1, BRCA2 and the mismatch repair genes to ovarian cancer in the population. Human Molecular Genetics, 2014, 23, 4703-4709.	2.9	112
432	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Gene-Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28

#	ARTICLE	IF	CITATIONS
433	Kernel canonical correlation analysis for assessing gene-gene interactions and application to ovarian cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 126-131.	2.8	33
434	Consortium analysis of gene and gene-folate interactions in purine and pyrimidine metabolism pathways with ovarian carcinoma risk. <i>Molecular Nutrition and Food Research</i> , 2014, 58, 2023-2035.	3.3	16
435	Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 934-945.	2.5	37
436	Radiogenomics: Radiobiology Enters the Era of Big Data and Team Science. <i>International Journal of Radiation Oncology Biology Physics</i> , 2014, 89, 709-713.	0.8	99
437	FGF receptor genes and breast cancer susceptibility: results from the Breast Cancer Association Consortium. <i>British Journal of Cancer</i> , 2014, 110, 1088-1100.	6.4	21
438	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
439	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	21.4	408
440	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
441	Identification of Single Nucleotide Polymorphisms (SNPs) Associated With Late Toxicity Following Radiation Therapy for Prostate Cancer Through a Meta-Analysis of Genome-Wide Association Studies (GWAS). <i>International Journal of Radiation Oncology Biology Physics</i> , 2014, 90, S55.	0.8	0
442	Long-term erectile function following permanent seed brachytherapy treatment for localized prostate cancer. <i>Radiotherapy and Oncology</i> , 2014, 112, 72-76.	0.6	18
443	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	2.9	12
444	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. <i>Radiotherapy and Oncology</i> , 2014, 111, 178-185.	0.6	128
445	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , 2014, 23, 5294-5302.	2.9	71
446	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	5.0	14
447	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. <i>The Clinical Journal of Pathology</i> , 2014, , n/a-n/a.	0.0	2
448	Abstract 946: Exome genotyping array identifies rare and low-frequency variants that may be associated with ovarian cancer risk. , 2014, , .		0
449	Abstract 3286: Identification of genetic loci associated with ovarian cancer prognosis. , 2014, , .		0
450	Abstract 5545: Rare genetic variation association with neurotoxicity and infection in breast cancer patients enrolled in PG-SNPS. , 2014, , .		0

#	ARTICLE	IF	CITATIONS
451	Abstract 261: Implications of polygenic risk-stratified screening for prostate cancer on overdiagnosis. , 2014, , .		0
452	Abstract 3285: Functional analysis of the 9p22 locus implicates the transcriptional regulation ofBNC2as a mechanism in ovarian cancer predisposition. , 2014, , .		0
453	Abstract 303: Cell Slider: Using crowd sourcing for the scoring of molecular pathology. Cancer Research, 2014, 74, 303-303.	0.9	4
454	Abstract 3288: Integration of GWAS, gene expression and protein interaction data identifies a HOX-centric gene network associated with serous ovarian cancer risk. , 2014, , .		0
455	Gastroesophageal Reflux Disease and overall and Cause-specific Mortality: A Prospective Study of 50000 Individuals. Middle East Journal of Digestive Diseases, 2014, 6, 65-80.	0.4	10
456	Cumulative impact of common genetic variants and other risk factors on colorectal cancer risk in 42â€¹103 individuals. Gut, 2013, 62, 871-881.	12.1	117
457	The admixture maximum likelihood test to test for association between rare variants and disease phenotypes. BMC Bioinformatics, 2013, 14, 177.	2.6	14
458	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	10.7	335
459	Inherited Genetic Susceptibility to Breast Cancer. American Journal of Pathology, 2013, 183, 1038-1051.	3.8	82
460	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	21.4	326
461	Opium Use and Risk of Mortality from Digestive Diseases: A Prospective Cohort Study. American Journal of Gastroenterology, 2013, 108, 1757-1765.	0.4	47
462	Prognosis of early breast cancer by immunohistochemistry defined intrinsic sub-types in patients treated with adjuvant chemotherapy in the NEAT/BR9601 trial. International Journal of Cancer, 2013, 133, 1470-1478.	5.1	15
463	Personalized screening for cancers: should we consider polygenic profiling?. Personalized Medicine, 2013, 10, 511-513.	1.5	10
464	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
465	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
466	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. Breast Cancer Research, 2013, 15, R92.	5.0	320
467	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239.	2.9	2
468	Science is like a vast jigsaw. BMJ, The, 2013, 346, f221-f221.	6.0	0

#	ARTICLE	IF	CITATIONS
469	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
470	Astronomical algorithms for automated analysis of tissue protein expression in breast cancer. British Journal of Cancer, 2013, 108, 602-612.	6.4	31
471	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
472	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
473	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
474	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.	2.9	86
475	Incorporating genomics into breast and prostate cancer screening: assessing the implications. Genetics in Medicine, 2013, 15, 423-432.	2.4	81
476	Smoking water-pipe, chewing nass and prevalence of heart disease: a cross-sectional analysis of baseline data from the Golestan Cohort Study, Iran. Heart, 2013, 99, 272-278.	2.9	42
477	A genome-wide association study identifies new susceptibility loci for esophageal adenocarcinoma and Barrett's esophagus. Nature Genetics, 2013, 45, 1487-1493.	21.4	174
478	Polymorphisms in Inflammation Pathway Genes and Endometrial Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 216-223.	2.5	22
479	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
480	Cost effectiveness of the NHS breast screening programme: life table model. BMJ, The, 2013, 346, f2618-f2618.	6.0	70
481	Evidence of Gene-Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
482	The US Office for Human Research Protections' judgment of the SUPPORT trial seems entirely reasonable. BMJ, The, 2013, 347, f4637-f4637.	6.0	7
483	A genome-wide association scan (GWAS) for mean telomere length within the COGS project: identified loci show little association with hormone-related cancer risk. Human Molecular Genetics, 2013, 22, 5056-5064.	2.9	130
484	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	2.9	100
485	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 880-890.	2.5	54
486	Public health implications from COGS and potential for risk stratification and screening. Nature Genetics, 2013, 45, 349-351.	21.4	108

#	ARTICLE	IF	CITATIONS
487	Public health genomics and personalized prevention: lessons from the <scp>COGS</scp> project. Journal of Internal Medicine, 2013, 274, 451-456.	6.0	28
488	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	12.8	144
489	Analysis of Over 10,000 Cases Finds No Association between Previously Reported Candidate Polymorphisms and Ovarian Cancer Outcome. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 987-992.	2.5	20
490	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
491	A U-shaped relationship between haematocrit and mortality in a large prospective cohort study. International Journal of Epidemiology, 2013, 42, 601-615.	1.9	22
492	Outside the Box: Proactive care: the patient's right to choose. British Journal of General Practice, 2013, 63, 124.2-124.	1.4	0
493	Prevalence, awareness and risk factors of hypertension in a large cohort of Iranian adult population. Journal of Hypertension, 2013, 31, 1364-1371.	0.5	110
494	Inherited Variants in Regulatory T Cell Genes and Outcome of Ovarian Cancer. PLoS ONE, 2013, 8, e53903.	2.5	20
495	Abstract P108: Associations between Anthropometric Indices and the Prevalence of Heart Disease in Iran: The Golestan Cohort Study. Circulation, 2013, 127, .	1.6	0
496	Abstract 4579: Variants in long non-coding RNAs are associated with epithelial ovarian cancer risk in a pooled analysis of three genome-wide association studies.. , 2013, , .		0
497	Abstract 1352: Epithelial-mesenchymal transition (EMT) gene variants influence epithelial ovarian cancer risk in women of European, African and Asian ancestry.. , 2013, , .		0
498	Abstract 3644: Variation in transmembrane transport genes influence epithelial ovarian cancer risk and histopathologic subtype.. , 2013, , .		0
499	Abstract 2567: Genetic risk stratification for breast cancer based on a polygenic risk score and family history.. , 2013, , .		0
500	Abstract 4850: Variation in circadian rhythm genes influence epithelial ovarian cancer risk and invasiveness.. , 2013, , .		2
501	Abstract 2559: Long non-coding RNAs as functional targets of germline genetic variation at ovarian cancer susceptibility loci.. , 2013, , .		0
502	Abstract 4844: Polymorphisms in regulatory T cell related genes and ovarian cancer survival.. , 2013, , .		0
503	Abstract A27: The ovarian tumor tissue analysis (OTTA) consortium. Clinical Cancer Research, 2013, 19, A27-A27.	7.0	1
504	The gastro-esophageal malignancies in Northern Iran research project: impact on the health research and health care systems in Iran. Archives of Iranian Medicine, 2013, 16, 46-53.	0.6	7

#	ARTICLE	IF	CITATIONS
505	Re: CYP2D6 Genotype and Tamoxifen Response in Postmenopausal Women With Endocrine-Responsive Breast Cancer: The Breast International Group 1-98 Trial and Re: CYP2D6 and UGT2B7 Genotype and Risk of Recurrence in Tamoxifen-Treated Breast Cancer Patients. <i>Journal of the National Cancer Institute</i> , 2012, 104, 1263-1264.	6.3	36
506	Gene Set Analysis of Survival Following Ovarian Cancer Implicates Macrolide Binding and Intracellular Signaling Genes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 529-536.	2.5	7
507	Opium use and mortality in Golestan Cohort Study: prospective cohort study of 50 000 adults in Iran. <i>BMJ, The</i> , 2012, 344, e2502-e2502.	6.0	135
508	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.9	100
509	Population-based screening in the era of genomics. <i>Personalized Medicine</i> , 2012, 9, 451-455.	1.5	21
510	Ovarian Cancer Risk Associated with Inherited Inflammation-Related Variants. <i>Cancer Research</i> , 2012, 72, 1064-1069.	0.9	45
511	Shorter telomere length is associated with increased ovarian cancer risk in both familial and sporadic cases. <i>Journal of Medical Genetics</i> , 2012, 49, 341-344.	3.2	41
512	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. <i>British Journal of Cancer</i> , 2012, 107, 800-807.	6.4	163
513	Adjuvant epirubicin followed by cyclophosphamide, methotrexate and fluorouracil (CMF) vs CMF in early breast cancer: results with over 7 years median follow-up from the randomised phase III NEAT/BR9601 trials. <i>British Journal of Cancer</i> , 2012, 107, 1257-1267.	6.4	14
514	Common Variants at the 19p13.1 and <i>ZNF365</i> Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 645-657.	2.5	47
515	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer-Specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316.	1.6	162
516	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. <i>Twin Research and Human Genetics</i> , 2012, 15, 615-623.	0.6	8
517	Refinement of the associations between risk of colorectal cancer and polymorphisms on chromosomes 1q41 and 12q13.13. <i>Human Molecular Genetics</i> , 2012, 21, 934-946.	2.9	19
518	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	2.9	80
519	The Potential for Risk Stratification in the Management of Ovarian Cancer Risk. <i>International Journal of Gynecological Cancer</i> , 2012, 22, S16-S17.	2.5	9
520	Why the victims were silent. <i>BMJ, The</i> , 2012, 344, e2903-e2903.	6.0	0
521	Any conclusion from this "citizens' jury" will be seriously flawed. <i>BMJ, The</i> , 2012, 345, e8576-e8576.	6.0	0
522	Association Between <i>BRCA1</i> and <i>BRCA2</i> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2012, 307, 382.	7.4	546

#	ARTICLE	IF	CITATIONS
523	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. <i>Nature Genetics</i> , 2012, 44, 1182-1184.	21.4	99
524	Independent validation of genes and polymorphisms reported to be associated with radiation toxicity: a prospective analysis study. <i>Lancet Oncology</i> , The, 2012, 13, 65-77.	10.7	202
525	ABO blood group and risk of epithelial ovarian cancer within the Ovarian Cancer Association Consortium. <i>Cancer Causes and Control</i> , 2012, 23, 1805-1810.	1.8	35
526	Standardized Total Average Toxicity Score: A Scale- and Grade-Independent Measure of Late Radiotherapy Toxicity to Facilitate Pooling of Data From Different Studies. <i>International Journal of Radiation Oncology Biology Physics</i> , 2012, 82, 1065-1074.	0.8	63
527	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012, 44, 770-776.	21.4	210
528	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	21.4	256
529	TGF β 2 induces the formation of tumour-initiating cells in claudinlow breast cancer. <i>Nature Communications</i> , 2012, 3, 1055.	12.8	95
530	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1783-1791.	2.5	17
531	Aurora kinase A outperforms Ki67 as a prognostic marker in ER-positive breast cancer. <i>British Journal of Cancer</i> , 2012, 106, 1798-1806.	6.4	59
532	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	2.9	168
533	Genetic Variants in ER Cofactor Genes and Endometrial Cancer Risk. <i>PLoS ONE</i> , 2012, 7, e42445.	2.5	4
534	Breast Cancer Risk and 6q22.33: Combined Results from Breast Cancer Association Consortium and Consortium of Investigators on Modifiers of BRCA1/2. <i>PLoS ONE</i> , 2012, 7, e35706.	2.5	11
535	Neither off the peg nor made to measure calculations are fit for purpose. <i>BMJ</i> , The, 2012, 345, e6585-e6585.	6.0	0
536	A Ki67/BCL2 index based on immunohistochemistry is highly prognostic in ER α -positive breast cancer. <i>Journal of Pathology</i> , 2012, 226, 97-107.	4.5	70
537	A genome-wide association study identifies a novel susceptibility locus for renal cell carcinoma on 12p11.23. <i>Human Molecular Genetics</i> , 2012, 21, 456-462.	2.9	81
538	Biological and prognostic associations of <i>miR-205</i> and <i>let-7b</i> in breast cancer revealed by <i>in situ</i> hybridization analysis of microRNA expression in arrays of archival tumour tissue. <i>Journal of Pathology</i> , 2012, 227, 306-314.	4.5	68
539	11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132.	2.5	35
540	The prognostic significance of lymphovascular invasion in invasive breast carcinoma. <i>Cancer</i> , 2012, 118, 3670-3680.	4.1	197

#	ARTICLE	IF	CITATIONS
541	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	27.8	1,778
542	Ovarian cancer susceptibility alleles and risk of ovarian cancer in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>Human Mutation</i> , 2012, 33, 690-702.	2.5	34
543	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012, 7, e42380.	2.5	51
544	Abstract 2927: MicroRNA binding site polymorphisms influence ovarian cancer risk in the collaborative oncological gene-environment study. , 2012, , .		0
545	Abstract 2619: Relevance of mismatch repair deficiency in ovarian cancer. , 2012, , .		0
546	Abstract 2928: Functional effects of SNPs in non-coding RNAs at the 3q25 ovarian cancer susceptibility locus. , 2012, , .		0
547	Reducing salt intake in Iran: priorities and challenges. <i>Archives of Iranian Medicine</i> , 2012, 15, 110-2.	0.6	10
548	Advocacy strategies and action plans for reducing salt intake in Iran. <i>Archives of Iranian Medicine</i> , 2012, 15, 320-4.	0.6	8
549	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptorâ€‘Positive, Lower Grade Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2222-2231.	2.5	27
550	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. <i>Journal of the National Cancer Institute</i> , 2011, 103, 250-263.	6.3	596
551	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 3289-3303.	2.9	152
552	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€‘negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
553	Diabetes Mellitus and Its Correlates in an Iranian Adult Population. <i>PLoS ONE</i> , 2011, 6, e26725.	2.5	65
554	Association between KRAS rs61764370 and triple-negative breast cancerâ€‘a false positive?. <i>Lancet Oncology</i> , The, 2011, 12, 723-724.	10.7	2
555	CYP2D6 Gene Variants and Their Association with Breast Cancer Susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1255-1258.	2.5	11
556	Common breast cancer susceptibility alleles are associated with tumour subtypes in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers: results from the Consortium of Investigators of Modifiers of <i>BRCA1/2</i> . <i>Breast Cancer Research</i> , 2011, 13, R110.	5.0	71
557	Cancer stem cell markers in breast cancer: pathological, clinical and prognostic significance. <i>Breast Cancer Research</i> , 2011, 13, R118.	5.0	87
558	Money is the greatest conflict of all. <i>BMJ: British Medical Journal</i> , 2011, 343, d7888-d7888.	2.3	0

#	ARTICLE	IF	CITATIONS
559	Balancing probabilities. BMJ: British Medical Journal, 2011, 342, d3048-d3048.	2.3	0
560	Functional Polymorphisms in the TERT Promoter Are Associated with Risk of Serous Epithelial Ovarian and Breast Cancers. PLoS ONE, 2011, 6, e24987.	2.5	48
561	Genome-wide association study of renal cell carcinoma identifies two susceptibility loci on 2p21 and 11q13.3. Nature Genetics, 2011, 43, 60-65.	21.4	220
562	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	21.4	141
563	Comparison of methods for handling missing data on immunohistochemical markers in survival analysis of breast cancer. British Journal of Cancer, 2011, 104, 693-699.	6.4	54
564	Polygenic susceptibility to prostate and breast cancer: implications for personalised screening. British Journal of Cancer, 2011, 104, 1656-1663.	6.4	153
565	Patient and tumour characteristics, management, and age-specific survival in women with breast cancer in the East of England. British Journal of Cancer, 2011, 104, 564-570.	6.4	37
566	Endometrial cancer and genetic variation in PTEN, PIK3CA, AKT1, MLH1, and MSH2 within a population-based case-control study. Gynecologic Oncology, 2011, 120, 167-173.	1.4	27
567	Association of KRAS SNP rs61764370 with risk of invasive epithelial ovarian cancer: Implications for clinical testing. Gynecologic Oncology, 2011, 121, S2-S3.	1.4	0
568	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. Journal of Medical Genetics, 2011, 48, 477-484.	3.2	47
569	A combined analysis of genome-wide association studies in breast cancer. Breast Cancer Research and Treatment, 2011, 126, 717-727.	2.5	90
570	Identification of a novel prostate cancer susceptibility variant in the KLK3 gene transcript. Human Genetics, 2011, 129, 687-694.	3.8	83
571	Translating genomics into improved population screening: hype or hope?. Human Genetics, 2011, 130, 19-21.	3.8	7
572	Meta-analysis of 8q24 for seven cancers reveals a locus between NOV and ENPP2 associated with cancer development. BMC Medical Genetics, 2011, 12, 156.	2.1	33
573	A Kallikrein 15 (KLK15) single nucleotide polymorphism located close to a novel exon shows evidence of association with poor ovarian cancer survival. BMC Cancer, 2011, 11, 119.	2.6	20
574	Screening for ovarian cancer in women with varying levels of risk, using annual tests, results in high recall for repeat screening tests. Hereditary Cancer in Clinical Practice, 2011, 9, 11.	1.5	2
575	Vitamin D receptor rs2228570 polymorphism and invasive ovarian carcinoma risk: Pooled analysis in five studies within the Ovarian Cancer Association Consortium. International Journal of Cancer, 2011, 128, 936-943.	5.1	49
576	PSA-detected prostate cancer and the potential for dedifferentiation: estimating the proportion capable of progression. International Journal of Cancer, 2011, 128, 1462-1470.	5.1	14

#	ARTICLE	IF	CITATIONS
577	Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. <i>International Journal of Cancer</i> , 2011, 128, 2063-2074.	5.1	54
578	Validation of a modelling approach for estimating the likely effectiveness of cancer screening using cancer data on prevalence screening and incidence. <i>Cancer Epidemiology</i> , 2011, 35, 139-144.	1.9	4
579	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011, 43, 785-791.	21.4	265
580	Common alleles at 6q25.1 and 1p11.2 are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2011, 20, 3304-3321.	2.9	68
581	Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. <i>Human Molecular Genetics</i> , 2011, 20, 2263-2272.	2.9	22
582	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	2.9	71
583	TGF- β 2 Signaling Pathway and Breast Cancer Susceptibility. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1112-1119.	2.5	49
584	Prostate Cancer Susceptibility Polymorphism rs2660753 Is Not Associated with Invasive Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1028-1031.	2.5	0
585	The Role of KRAS rs61764370 in Invasive Epithelial Ovarian Cancer: Implications for Clinical Testing. <i>Clinical Cancer Research</i> , 2011, 17, 3742-3750.	7.0	47
586	7q21-rs6964587 and breast cancer risk: an extended case-control study by the Breast Cancer Association Consortium. <i>Journal of Medical Genetics</i> , 2011, 48, 698-702.	3.2	5
587	<i>LIN28B</i> Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2011, 71, 3896-3903.	0.9	75
588	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2011, 71, 6240-6249.	0.9	109
589	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. <i>Nature</i> , 2011, 480, 99-103.	27.8	413
590	MicroRNA Processing and Binding Site Polymorphisms Are Not Replicated in the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 1793-1797.	2.5	19
591	Re: Promoting Healthy Skepticism in the News: Helping Journalists Get It Right. <i>Journal of the National Cancer Institute</i> , 2011, 103, 1903-1903.	6.3	1
592	Single nucleotide polymorphism (SNP) analysis demonstrates a significant association of tumour necrosis factor-alpha (<i>TNFA</i>) with primary immune thrombocytopenia among Caucasian adults. <i>Hematology</i> , 2011, 16, 243-248.	1.5	17
593	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. <i>Journal of the National Cancer Institute</i> , 2011, 103, 105-116.	6.3	40
594	KRAS rs61764370 in Epithelial Ovarian Cancer—Response. <i>Clinical Cancer Research</i> , 2011, 17, 6601-6601.	7.0	1

#	ARTICLE	IF	CITATIONS
595	Evaluation of variation in the phosphoinositide-3-kinase catalytic subunit alpha oncogene and breast cancer risk. British Journal of Cancer, 2011, 105, 1934-1939.	6.4	4
596	Breast cancer susceptibility polymorphisms and endometrial cancer risk: a Collaborative Endometrial Cancer Study. Carcinogenesis, 2011, 32, 1862-1866.	2.8	5
597	Multiple Common Susceptibility Variants near BMP Pathway Loci GREM1, BMP4, and BMP2 Explain Part of the Missing Heritability of Colorectal Cancer. PLoS Genetics, 2011, 7, e1002105.	3.5	188
598	Polymorphisms in Stromal Genes and Susceptibility to Serous Epithelial Ovarian Cancer: A Report from the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e19642.	2.5	5
599	Estrogen Receptor Beta rs1271572 Polymorphism and Invasive Ovarian Carcinoma Risk: Pooled Analysis within the Ovarian Cancer Association Consortium. PLoS ONE, 2011, 6, e20703.	2.5	21
600	Hereditary Factors and Pre-invasive Disease. , 2011, , 31-40.		1
601	Abstract 2782: Genetic susceptibility to prostate cancer progression and relationship with PSA level: Case-case study. , 2011, , .		0
602	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. Breast Cancer Research, 2010, 12, R110.	5.0	82
603	Acceptability and accuracy of a non-endoscopic screening test for Barrett's oesophagus in primary care: cohort study. BMJ: British Medical Journal, 2010, 341, c4372-c4372.	2.3	271
604	Variation in genes required for normal mitosis and risk of breast cancer. Breast Cancer Research and Treatment, 2010, 119, 423-430.	2.5	30
605	Vascular endothelial growth factor gene polymorphisms and ovarian cancer survival. Gynecologic Oncology, 2010, 119, 479-483.	1.4	26
606	COGENT (COlorectal cancer GENEtics): an international consortium to study the role of polymorphic variation on the risk of colorectal cancer. British Journal of Cancer, 2010, 102, 447-454.	6.4	43
607	BCL2 in breast cancer: a favourable prognostic marker across molecular subtypes and independent of adjuvant therapy received. British Journal of Cancer, 2010, 103, 668-675.	6.4	259
608	A large-scale meta-analysis to refine colorectal cancer risk estimates associated with MUTYH variants. British Journal of Cancer, 2010, 103, 1875-1884.	6.4	107
609	Genome-wide association study identifies five new breast cancer susceptibility loci. Nature Genetics, 2010, 42, 504-507.	21.4	653
610	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 2010, 42, 880-884.	21.4	235
611	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	21.4	321
612	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. Nature Genetics, 2010, 42, 885-892.	21.4	309

#	ARTICLE	IF	CITATIONS
613	Meta-analysis of three genome-wide association studies identifies susceptibility loci for colorectal cancer at 1q41, 3q26.2, 12q13.13 and 20q13.33. <i>Nature Genetics</i> , 2010, 42, 973-977.	21.4	335
614	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
615	Verbal Autopsy: Reliability and Validity Estimates for Causes of Death in the Golestan Cohort Study in Iran. <i>PLoS ONE</i> , 2010, 5, e11183.	2.5	72
616	Risk Factors for Breast Cancer. <i>Epidemiology</i> , 2010, 21, 566-572.	2.7	30
617	Common variants associated with breast cancer in genome-wide association studies are modifiers of breast cancer risk in BRCA1 and BRCA2 mutation carriers. <i>Human Molecular Genetics</i> , 2010, 19, 2886-2897.	2.9	60
618	A Genome-Wide Association Study of Prognosis in Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 1140-1143.	2.5	57
619	Polymorphism in the <i>GALNT1</i> Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women: The Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 600-604.	2.5	23
620	No Association between TERT-CLPTM1L Single Nucleotide Polymorphism rs401681 and Mean Telomere Length or Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 1862-1865.	2.5	40
621	Genetic Variation in <i>TYMS</i> in the One-Carbon Transfer Pathway Is Associated with Ovarian Carcinoma Types in the Ovarian Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 1822-1830.	2.5	24
622	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 992-999.	2.5	54
623	Telomere Length in Prospective and Retrospective Cancer Case-Control Studies. <i>Cancer Research</i> , 2010, 70, 3170-3176.	0.9	142
624	How to validate a breast cancer prognostic signature. <i>Nature Reviews Clinical Oncology</i> , 2010, 7, 615-616.	27.6	8
625	Missense Variants in <i>ATM</i> in 26,101 Breast Cancer Cases and 29,842 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2143-2151.	2.5	33
626	Evaluation of Candidate Stromal Epithelial Cross-Talk Genes Identifies Association between Risk of Serous Ovarian Cancer and TERT, a Cancer Susceptibility "Hot-Spot". <i>PLoS Genetics</i> , 2010, 6, e1001016.	3.5	48
627	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. <i>PLoS Medicine</i> , 2010, 7, e1000279.	8.4	764
628	<i>ESR1/SYNE1</i> Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 245-250.	2.5	75
629	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptor- "Negative Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2010, 102, 650-662.	6.3	48
630	Molecular Pathology in Epidemiologic Studies: A Primer on Key Considerations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 966-972.	2.5	28

#	ARTICLE	IF	CITATIONS
631	A genome-wide association scan on estrogen receptor-negative breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R93.	5.0	35
632	A Prospective, Multicenter Study to Evaluate a Novel, Nonendoscopic Screening Device for Barrett's Esophagus in the Community Setting. <i>Gastroenterology</i> , 2010, 139, e17.	1.3	0
633	Fine scale mapping of the breast cancer 16q12 locus. <i>Human Molecular Genetics</i> , 2010, 19, 2507-2515.	2.9	68
634	The inherited genetics of ovarian and endometrial cancer. <i>Current Opinion in Genetics and Development</i> , 2010, 20, 231-238.	3.3	64
635	Common germ-line polymorphism of C1QA and breast cancer survival. <i>British Journal of Cancer</i> , 2010, 102, 1294-1299.	6.4	19
636	No association between SNPs regulating TGF- β 1 secretion and late radiotherapy toxicity to the breast: Results from the RAPPER study. <i>Radiotherapy and Oncology</i> , 2010, 97, 9-14.	0.6	54
637	Predictive markers of anthracycline benefit: a prospectively planned analysis of the UK National Epirubicin Adjuvant Trial (NEAT/BR9601). <i>Lancet Oncology</i> , The, 2010, 11, 266-274.	10.7	122
638	CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. <i>Breast Cancer Research</i> , 2010, 12, R64.	5.0	76
639	PREDICT: a new UK prognostic model that predicts survival following surgery for invasive breast cancer. <i>Breast Cancer Research</i> , 2010, 12, R1.	5.0	285
640	Familial relative risks for breast cancer by pathological subtype: a population-based cohort study. <i>Breast Cancer Research</i> , 2010, 12, R10.	5.0	33
641	Common Genetic Susceptibility Loci. , 2010, , 301-320.		0
642	A polymorphism in the GALNT2 gene and ovarian cancer risk in four population based case-control studies. <i>International Journal of Molecular Epidemiology and Genetics</i> , 2010, 1, 272-7.	0.4	8
643	Polygenic susceptibility to breast cancer: current state-of-the-art. <i>Future Oncology</i> , 2009, 5, 689-701.	2.4	35
644	Mean sojourn time, overdiagnosis, and reduction in advanced stage prostate cancer due to screening with PSA: implications of sojourn time on screening. <i>British Journal of Cancer</i> , 2009, 100, 1198-1204.	6.4	58
645	Association between invasive ovarian cancer susceptibility and 11 best candidate SNPs from breast cancer genome-wide association study. <i>Human Molecular Genetics</i> , 2009, 18, 2297-2304.	2.9	42
646	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139.	2.9	84
647	Genetic Variation in the Chromosome 17q23 Amplicon and Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1864-1868.	2.5	34
648	Common Polymorphisms in the Prostaglandin Pathway Genes and Their Association with Breast Cancer Susceptibility and Survival. <i>Clinical Cancer Research</i> , 2009, 15, 2181-2191.	7.0	51

#	ARTICLE	IF	CITATIONS
649	Stage Shift in Psa-detected Prostate Cancers – Effect Modification by Gleason Score. Journal of Medical Screening, 2009, 16, 98-101.	2.3	19
650	Risk of Estrogen Receptor–Positive and –Negative Breast Cancer and Single–Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	6.3	99
651	Functional complementation studies identify candidate genes and common genetic variants associated with ovarian cancer survival. Human Molecular Genetics, 2009, 18, 1869-1878.	2.9	17
652	Single Nucleotide Polymorphisms in the <i>TP53</i> Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.9	63
653	Common Genetic Variation in Candidate Genes and Susceptibility to Subtypes of Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 255-259.	2.5	50
654	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. Human Molecular Genetics, 2009, 18, 1692-1703.	2.9	110
655	Seq4SNPs: new software for retrieval of multiple, accurately annotated DNA sequences, ready formatted for SNP assay design. BMC Bioinformatics, 2009, 10, 180.	2.6	4
656	Genetic variation in SIPA1 in relation to breast cancer risk and survival after breast cancer diagnosis. International Journal of Cancer, 2009, 124, 1716-1720.	5.1	22
657	Common germline variation in mismatch repair genes and survival after a diagnosis of colorectal cancer. International Journal of Cancer, 2009, 124, 1887-1891.	5.1	17
658	Common germline polymorphisms in <i>COMT</i> , <i>CYP19A1</i> , <i>ESR1</i> , <i>PGR</i> , <i>SULT1E1</i> and <i>STS</i> and survival after a diagnosis of breast cancer. International Journal of Cancer, 2009, 125, 2687-2696.	5.1	34
659	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
660	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 2009, 41, 996-1000.	21.4	276
661	p53 polymorphisms: cancer implications. Nature Reviews Cancer, 2009, 9, 95-107.	28.4	564
662	Normal tissue reactions to radiotherapy: towards tailoring treatment dose by genotype. Nature Reviews Cancer, 2009, 9, 134-142.	28.4	593
663	Validating genetic risk associations for ovarian cancer through the international Ovarian Cancer Association Consortium. British Journal of Cancer, 2009, 100, 412-420.	6.4	47
664	Tagging single-nucleotide polymorphisms in candidate oncogenes and susceptibility to ovarian cancer. British Journal of Cancer, 2009, 100, 993-1001.	6.4	24
665	Prevalent cases in observational studies of cancer survival: do they bias hazard ratio estimates?. British Journal of Cancer, 2009, 100, 1806-1811.	6.4	60
666	Molecular characteristics of screen-detected vs symptomatic breast cancers and their impact on survival. British Journal of Cancer, 2009, 101, 1338-1344.	6.4	77

#	ARTICLE	IF	CITATIONS
667	Role of genetic polymorphisms and ovarian cancer susceptibility. <i>Molecular Oncology</i> , 2009, 3, 171-181.	4.6	69
668	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1610-1616.	2.5	57
669	Combined effects of single nucleotide polymorphisms TP53 R72P and MDM2 SNP309, and p53 expression on survival of breast cancer patients. <i>Breast Cancer Research</i> , 2009, 11, R89.	5.0	35
670	Association between Common Germline Genetic Variation in 94 Candidate Genes or Regions and Risks of Invasive Epithelial Ovarian Cancer. <i>PLoS ONE</i> , 2009, 4, e5983.	2.5	38
671	High-Frequency Low-Penetrance Alleles. , 2009, , 249-262.		0
672	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. <i>Breast Cancer Research and Treatment</i> , 2008, 111, 139-144.	2.5	50
673	Haplotypes of the estrogen receptor beta gene and breast cancer risk. <i>International Journal of Cancer</i> , 2008, 122, 387-392.	5.1	38
674	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008, 123, 380-388.	5.1	73
675	Common Single-Nucleotide Polymorphisms in DNA Double-Strand Break Repair Genes and Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 3482-3489.	2.5	32
676	Progesterone receptor variation and risk of ovarian cancer is limited to the invasive endometrioid subtype: results from the ovarian cancer association consortium pooled analysis. <i>British Journal of Cancer</i> , 2008, 98, 282-288.	6.4	49
677	The BOADICEA model of genetic susceptibility to breast and ovarian cancers: updates and extensions. <i>British Journal of Cancer</i> , 2008, 98, 1457-1466.	6.4	461
678	A genome-wide association study identifies colorectal cancer susceptibility loci on chromosomes 10p14 and 8q23.3. <i>Nature Genetics</i> , 2008, 40, 623-630.	21.4	514
679	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. <i>Nature Genetics</i> , 2008, 40, 631-637.	21.4	542
680	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. <i>Nature Genetics</i> , 2008, 40, 1426-1435.	21.4	498
681	Shedding light on skin cancer. <i>Nature Genetics</i> , 2008, 40, 817-818.	21.4	12
682	Meta-analysis confirms BCL2 is an independent prognostic marker in breast cancer. <i>BMC Cancer</i> , 2008, 8, 153.	2.6	159
683	Proliferation markers and survival in early breast cancer: A systematic review and meta-analysis of 85 studies in 32,825 patients. <i>Breast</i> , 2008, 17, 323-334.	2.2	353
684	Genetic variation in stromal proteins decorin and lumican with breast cancer: investigations in two case-control studies. <i>Breast Cancer Research</i> , 2008, 10, R98.	5.0	41

#	ARTICLE	IF	CITATIONS
685	Effects of common germline genetic variation in cell cycle control genes on breast cancer survival: results from a population-based cohort. <i>Breast Cancer Research</i> , 2008, 10, R47.	5.0	33
686	Mismatch repair gene polymorphisms and survival in invasive ovarian cancer patients. <i>European Journal of Cancer</i> , 2008, 44, 2259-2265.	2.8	20
687	<i>Hyaluronan-Mediated Motility Receptor</i> Gene Single Nucleotide Polymorphisms and Risk of Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 3618-3620.	2.5	21
688	Cell type-specific DNA methylation patterns in the human breast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14076-14081.	7.1	210
689	Common variants in mismatch repair genes and risk of colorectal cancer. <i>Gut</i> , 2008, 57, 1097-1101.	12.1	45
690	Somatically acquired hypomethylation of IGF2 in breast and colorectal cancer. <i>Human Molecular Genetics</i> , 2008, 17, 2633-2643.	2.9	124
691	Association of a Common AKAP9 Variant With Breast Cancer Risk: A Collaborative Analysis. <i>Journal of the National Cancer Institute</i> , 2008, 100, 437-442.	6.3	44
692	Identification of Common Variants in the SHBG Gene Affecting Sex Hormone-Binding Globulin Levels and Breast Cancer Risk in Postmenopausal Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 3490-3498.	2.5	50
693	Polygenes, Risk Prediction, and Targeted Prevention of Breast Cancer. <i>New England Journal of Medicine</i> , 2008, 358, 2796-2803.	27.0	558
694	Effects of Common Germ-Line Genetic Variation in Cell Cycle Genes on Ovarian Cancer Survival. <i>Clinical Cancer Research</i> , 2008, 14, 1090-1095.	7.0	29
695	Risk Factors for the Incidence of Breast Cancer: Do They Affect Survival From the Disease?. <i>Journal of Clinical Oncology</i> , 2008, 26, 3310-3316.	1.6	174
696	The Effects of Common Genetic Variants in Oncogenes on Ovarian Cancer Survival. <i>Clinical Cancer Research</i> , 2008, 14, 5833-5839.	7.0	32
697	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	3.5	315
698	Association of single-nucleotide polymorphisms in the cell cycle genes with breast cancer in the British population. <i>Carcinogenesis</i> , 2008, 29, 333-341.	2.8	68
699	<i>HSD17B1</i> Genetic Variants and Hormone Receptor-Defined Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 2766-2772.	2.5	11
700	Association Study of Prostate Cancer Susceptibility Variants with Risks of Invasive Ovarian, Breast, and Colorectal Cancer. <i>Cancer Research</i> , 2008, 68, 8837-8842.	0.9	14
701	Multiple Loci With Different Cancer Specificities Within the 8q24 Gene Desert. <i>Journal of the National Cancer Institute</i> , 2008, 100, 962-966.	6.3	306
702	Polymorphism in the <i>IL18</i> Gene and Epithelial Ovarian Cancer in Non-Hispanic White Women. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 3567-3572.	2.5	18

#	ARTICLE	IF	CITATIONS
703	Breast Cancer Risk Polymorphisms and Interaction with Ionizing Radiation among U.S. Radiologic Technologists. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 2007-2011.	2.5	32
704	Predicting the likelihood of carrying a BRCA1 or BRCA2 mutation: validation of BOADICEA, BRCAPRO, IBIS, Myriad and the Manchester scoring system using data from UK genetics clinics. <i>Journal of Medical Genetics</i> , 2008, 45, 425-431.	3.2	167
705	Role of Genetic Polymorphisms in Ovarian Cancer Susceptibility: Development of an International Ovarian Cancer Association Consortium. , 2008, 622, 53-67.		19
706	Association between Common Variation in 120 Candidate Genes and Breast Cancer Risk. <i>PLoS Genetics</i> , 2007, 3, e42.	3.5	134
707	Association Between Single-Nucleotide Polymorphisms in Hormone Metabolism and DNA Repair Genes and Epithelial Ovarian Cancer: Results from Two Australian Studies and an Additional Validation Set. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 2557-2565.	2.5	65
708	Germline genetic variation and breast cancer survival: prognostic and therapeutic implications. <i>Future Oncology</i> , 2007, 3, 491-495.	2.4	4
709	Founder and Recurrent CDH1 Mutations in Families With Hereditary Diffuse Gastric Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2007, 297, 2360.	7.4	394
710	Cancer genetics of epigenetic genes. <i>Human Molecular Genetics</i> , 2007, 16, R28-R49.	2.9	223
711	How Not to Interpret a P Value?. <i>Journal of the National Cancer Institute</i> , 2007, 99, 332-333.	6.3	11
712	Common Germline Genetic Variation in Antioxidant Defense Genes and Survival After Diagnosis of Breast Cancer. <i>Journal of Clinical Oncology</i> , 2007, 25, 3015-3023.	1.6	102
713	Turning the Pump Handle: Evolving Methods for Integrating the Evidence on Gene-Disease Association. <i>American Journal of Epidemiology</i> , 2007, 166, 863-866.	3.4	25
714	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2007, 67, 3027-3035.	0.9	78
715	Rat Mcs5a is a compound quantitative trait locus with orthologous human loci that associate with breast cancer risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6299-6304.	7.1	64
716	Response: Re: Commonly Studied Single-Nucleotide Polymorphisms and Breast Cancer: Results From the Breast Cancer Association Consortium. <i>Journal of the National Cancer Institute</i> , 2007, 99, 488-489.	6.3	6
717	Common variants in the ATM, BRCA1, BRCA2, CHEK2 and TP53 cancer susceptibility genes are unlikely to increase breast cancer risk. <i>Breast Cancer Research</i> , 2007, 9, R27.	5.0	94
718	Do MDM2 SNP309 and TP53 R72P Interact in Breast Cancer Susceptibility? A Large Pooled Series from the Breast Cancer Association Consortium. <i>Cancer Research</i> , 2007, 67, 9584-9590.	0.9	80
719	Tagging Single Nucleotide Polymorphisms in the BRIP1 Gene and Susceptibility to Breast and Ovarian Cancer. <i>PLoS ONE</i> , 2007, 2, e268.	2.5	54
720	Contribution of <i>BRCA1</i> and <i>BRCA2</i> mutations to inherited ovarian cancer. <i>Human Mutation</i> , 2007, 28, 1207-1215.	2.5	76

#	ARTICLE	IF	CITATIONS
721	Screening for theBRCA1-ins6kbEx13mutation: potential for misdiagnosis. Human Mutation, 2007, 28, 525-526.	2.5	8
722	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
723	Common variants in WFS1 confer risk of type 2 diabetes. Nature Genetics, 2007, 39, 951-953.	21.4	333
724	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
725	A common variant of the p16INK4a genetic region is associated with physical function in older people. Mechanisms of Ageing and Development, 2007, 128, 370-377.	4.6	80
726	Commonly Studied Single-Nucleotide Polymorphisms and Breast Cancer: Results From the Breast Cancer Association Consortium. Journal of the National Cancer Institute, 2006, 98, 1382-1396.	6.3	238
727	Relative and absolute risk of colorectal cancer for individuals with a family history: A meta-analysis. European Journal of Cancer, 2006, 42, 216-227.	2.8	377
728	BRCA1, BRCA2 and TP53 mutations in very early-onset breast cancer with associated risks to relatives. European Journal of Cancer, 2006, 42, 1143-1150.	2.8	139
729	Interactions between genes involved in the antioxidant defence system and breast cancer risk. British Journal of Cancer, 2006, 95, 525-531.	6.4	30
730	HapMap-based study of the 17q21 ERBB2 amplicon in susceptibility to breast cancer. British Journal of Cancer, 2006, 95, 1689-1695.	6.4	35
731	Evaluation of an algorithm of tagging SNPs selection by linkage disequilibrium. Clinical Biochemistry, 2006, 39, 240-243.	1.9	11
732	Pharmacogenetics of cancer chemotherapy. Biochimica Et Biophysica Acta: Reviews on Cancer, 2006, 1766, 168-183.	7.4	19
733	The admixture maximum likelihood test: a novel experimentâ€wise test of association between disease and multiple SNPs. Genetic Epidemiology, 2006, 30, 636-643.	1.3	31
734	Common Variants in RB1 Gene and Risk of Invasive Ovarian Cancer. Cancer Research, 2006, 66, 10220-10226.	0.9	39
735	IGF1 and IGFBP3 tagging polymorphisms are associated with circulating levels of IGF1, IGFBP3 and risk of breast cancer. Human Molecular Genetics, 2006, 15, 1-10.	2.9	181
736	BRCA1 and BRCA2 Cancer Risks. Journal of Clinical Oncology, 2006, 24, 3312-3313.	1.6	26
737	Common variants in mismatch repair genes and risk of invasive ovarian cancer. Carcinogenesis, 2006, 27, 2235-2242.	2.8	67
738	Bcl-2 Is a Prognostic Marker in Breast Cancer Independently of the Nottingham Prognostic Index. Clinical Cancer Research, 2006, 12, 2468-2475.	7.0	188

#	ARTICLE	IF	CITATIONS
739	Polymorphisms in RET and Its Coreceptors and Ligands as Genetic Modifiers of Multiple Endocrine Neoplasia Type 2A. <i>Cancer Research</i> , 2006, 66, 1177-1180.	0.9	52
740	Prognostic Value of PAI1 in Invasive Breast Cancer: Evidence That Tumor-Specific Factors Are More Important Than Genetic Variation in Regulating PAI1 Expression. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 2107-2114.	2.5	63
741	BRCA1 Suppresses Osteopontin-mediated Breast Cancer. <i>Journal of Biological Chemistry</i> , 2006, 281, 26587-26601.	3.4	28
742	Single-nucleotide polymorphisms in the RB1 gene and association with breast cancer in the British population. <i>British Journal of Cancer</i> , 2006, 94, 1921-1926.	6.4	10
743	Genetic variants in epigenetic genes and breast cancer risk. <i>Carcinogenesis</i> , 2006, 27, 1661-1669.	2.8	85
744	Tagging Single-Nucleotide Polymorphisms in Antioxidant Defense Enzymes and Susceptibility to Breast Cancer. <i>Cancer Research</i> , 2006, 66, 1225-1233.	0.9	76
745	Association of the Progesterone Receptor Gene with Breast Cancer Risk: A Single-Nucleotide Polymorphism Tagging Approach. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 675-682.	2.5	55
746	Five Glutathione S-Transferase Gene Variants in 23,452 Cases of Lung Cancer and 30,397 Controls: Meta-Analysis of 130 Studies. <i>PLoS Medicine</i> , 2006, 3, e91.	8.4	124
747	Polygenic Inherited Predisposition to Breast Cancer. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2005, 70, 35-41.	1.1	27
748	Reply: Remarks on the BOADICEA model of genetic susceptibility to breast and ovarian Cancer Research UK. <i>British Journal of Cancer</i> , 2005, 92, 1337-1338.	6.4	1
749	Sipa1 is a candidate for underlying the metastasis efficiency modifier locus Mtes1. <i>Nature Genetics</i> , 2005, 37, 1055-1062.	21.4	169
750	Genetic Epidemiology of Cancer: Relatively risky relatives. <i>European Journal of Human Genetics</i> , 2005, 13, 519-520.	2.8	3
751	Common variation in EMSY and risk of breast and ovarian cancer: a case-control study using HapMap tagging SNPs. <i>BMC Cancer</i> , 2005, 5, 81.	2.6	14
752	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. <i>International Journal of Cancer</i> , 2005, 117, 611-618.	5.1	123
753	Identification and validation of prognostic markers in breast cancer with the complementary use of array-CGH and tissue microarrays. <i>Journal of Pathology</i> , 2005, 205, 388-396.	4.5	137
754	Genetic Variation in the HSD17B1 Gene and Risk of Prostate Cancer. <i>PLoS Genetics</i> , 2005, 1, e68.	3.5	66
755	Genetic variation in the HSD17B1 gene and risk of prostate cancer. <i>PLoS Genetics</i> , 2005, preprint, e68.	3.5	6
756	Common Polymorphisms in ERCC2 (Xeroderma pigmentosum D) are not Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 1828-1831.	2.5	23

#	ARTICLE	IF	CITATIONS
757	Reply: a bias in genotyping of the ERBB2 (HER2) Ile655Val variant. <i>Carcinogenesis</i> , 2005, 26, 2213-2213.	2.8	1
758	RESPONSE: Re: Polymorphisms Associated With Circulating Sex Hormone Levels in Postmenopausal Women. <i>Journal of the National Cancer Institute</i> , 2005, 97, 153-154.	6.3	7
759	Evidence that both genetic instability and selection contribute to the accumulation of chromosome alterations in cancer. <i>Carcinogenesis</i> , 2005, 26, 923-930.	2.8	39
760	Allelic association of the human homologue of the mouse modifier Ptp ^{trj} with breast cancer. <i>Human Molecular Genetics</i> , 2005, 14, 2349-2356.	2.9	70
761	Polymorphisms in the Initiators of RET (Rearranged during Transfection) Signaling Pathway and Susceptibility to Sporadic Medullary Thyroid Carcinoma. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 6268-6274.	3.6	74
762	Breast and ovarian cancer risks to carriers of the BRCA1 5382insC and 185delAG and BRCA2 6174delT mutations: a combined analysis of 22 population based studies. <i>Journal of Medical Genetics</i> , 2005, 42, 602-603.	3.2	121
763	The Reliable Identification of Disease-Gene Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 1362-1362.	2.5	18
764	Common ERBB2 polymorphisms and risk of breast cancer in a white British population: a case-control study. <i>Breast Cancer Research</i> , 2005, 7, R204-9.	5.0	55
765	Breast Cancer Risks for <i>BRCA1/2</i> Carriers. <i>Science</i> , 2004, 306, 2187-2191.	12.6	44
766	Pathology of Ovarian Cancers in BRCA1 and BRCA2 Carriers. <i>Clinical Cancer Research</i> , 2004, 10, 2473-2481.	7.0	224
767	Oral contraceptive use and ovarian cancer risk among carriers of BRCA1 or BRCA2 mutations. <i>British Journal of Cancer</i> , 2004, 91, 1911-1915.	6.4	138
768	Polymorphisms Associated With Circulating Sex Hormone Levels in Postmenopausal Women. <i>Journal of the National Cancer Institute</i> , 2004, 96, 936-945.	6.3	308
769	Association studies for finding cancer-susceptibility genetic variants. <i>Nature Reviews Cancer</i> , 2004, 4, 850-860.	28.4	417
770	The BOADICEA model of genetic susceptibility to breast and ovarian cancer. <i>British Journal of Cancer</i> , 2004, 91, 1580-1590.	6.4	411
771	Model of the early development of diffuse gastric cancer in E-cadherin mutation carriers and its implications for patient screening. <i>Journal of Pathology</i> , 2004, 203, 681-687.	4.5	242
772	Role of CHEK2*1100delC in unselected series of non-BRCA1/2 male breast cancers. <i>International Journal of Cancer</i> , 2004, 108, 477-478.	5.1	47
773	Association of a Common Variant of the CASP8 Gene With Reduced Risk of Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2004, 96, 1866-1869.	6.3	188
774	STK15 polymorphisms and association with risk of invasive ovarian cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2004, 13, 1589-94.	2.5	24

#	ARTICLE	IF	CITATIONS
775	BRCA2 arg372hispolymorphism and epithelial ovarian cancer risk. International Journal of Cancer, 2003, 103, 427-430.	5.1	37
776	The patched polymorphism Pro1315Leu (C3944T) may modulate the association between use of oral contraceptives and breast cancer risk. International Journal of Cancer, 2003, 103, 779-783.	5.1	65
777	A proinflammatory genetic profile increases the risk for chronic atrophic gastritis and gastric carcinoma. Gastroenterology, 2003, 125, 364-371.	1.3	450
778	Prediction of pathogenic mutations in patients with early-onset breast cancer by family history. Lancet, The, 2003, 361, 1101-1102.	13.7	200
779	Average Risks of Breast and Ovarian Cancer Associated with BRCA1 or BRCA2 Mutations Detected in Case Series Unselected for Family History: A Combined Analysis of 22 Studies. American Journal of Human Genetics, 2003, 72, 1117-1130.	6.2	3,105
780	Issues of consent and feedback in a genetic epidemiological study of women with breast cancer. Journal of Medical Ethics, 2003, 29, 93-96.	1.8	51
781	Re: On the Use of Familial Aggregation in Population-Based Case Probands for Calculating Penetrance. Journal of the National Cancer Institute, 2003, 95, 75-76.	6.3	7
782	Molecular Classification of Breast Carcinomas Using Tissue Microarrays. Diagnostic Molecular Pathology, 2003, 12, 27-34.	2.1	153
783	Genetic Susceptibility, Predicting Risk and Preventing Cancer. Recent Results in Cancer Research, 2003, 163, 7-18.	1.8	8
784	BRCA1/2 mutation status influences somatic genetic progression in inherited and sporadic epithelial ovarian cancer cases. Cancer Research, 2003, 63, 417-23.	0.9	33
785	A transforming growth factorbeta1 signal peptide variant increases secretion in vitro and is associated with increased incidence of invasive breast cancer. Cancer Research, 2003, 63, 2610-5.	0.9	265
786	Common polymorphisms in checkpoint kinase 2 are not associated with breast cancer risk. Cancer Epidemiology Biomarkers and Prevention, 2003, 12, 809-12.	2.5	8
787	A comprehensive model for familial breast cancer incorporating BRCA1, BRCA2 and other genes. British Journal of Cancer, 2002, 86, 76-83.	6.4	422
788	Helicobacter pylori and Interleukin 1 Genotyping: An Opportunity to Identify High-Risk Individuals for Gastric Carcinoma. Journal of the National Cancer Institute, 2002, 94, 1680-1687.	6.3	563
789	Variants in DNA double-strand break repair genes and breast cancer susceptibility. Human Molecular Genetics, 2002, 11, 1399-1407.	2.9	331
790	The genetics of ovarian cancer. Best Practice and Research in Clinical Obstetrics and Gynaecology, 2002, 16, 449-468.	2.8	62
791	BRCA1 and BRCA2 mutations in Russian familial breast cancer. Human Mutation, 2002, 19, 184-184.	2.5	34
792	CDH1 c-160a promotor polymorphism is not associated with risk of stomach cancer. International Journal of Cancer, 2002, 101, 196-197.	5.1	50

#	ARTICLE	IF	CITATIONS
793	Polygenic susceptibility to breast cancer and implications for prevention. <i>Nature Genetics</i> , 2002, 31, 33-36.	21.4	874
794	Interleukin 1B and interleukin 1RN polymorphisms are associated with increased risk of gastric carcinoma. <i>Gastroenterology</i> , 2001, 121, 823-829.	1.3	402
795	Incidence of gastric cancer and breast cancer in CDH1 (E-cadherin) mutation carriers from hereditary diffuse gastric cancer families. <i>Gastroenterology</i> , 2001, 121, 1348-1353.	1.3	579
796	BRCA1 and BRCA2 mutations in a population-based study of male breast cancer. <i>Breast Cancer Research</i> , 2001, 4, R2.	5.0	152
797	Degenerate Oligonucleotide Primed-Polymerase Chain Reaction-Based Array Comparative Genomic Hybridization for Extensive Amplicon Profiling of Breast Cancers. <i>American Journal of Pathology</i> , 2001, 158, 1623-1631.	3.8	98
798	Fundamentals of genetic epidemiology. , 2001, , 65-105.		0
799	Genetic science and technology. , 2001, , 23-64.		0
800	Genetics in medicine. , 2001, , 106-155.		0
801	Genetics in health services. , 2001, , 156-185.		0
802	Ethical, legal and social implications of genetics. , 2001, , 186-224.		0
803	Apparent humanBRCA1 knockout caused by mispriming during polymerase chain reaction: Implications for genetic testing. <i>Genes Chromosomes and Cancer</i> , 2001, 31, 96-98.	2.8	29
804	Evidence for further breast cancer susceptibility genes in addition to <i>BRCA1</i> and <i>BRCA2</i> in a population-based study. <i>Genetic Epidemiology</i> , 2001, 21, 1-18.	1.3	263
805	Polymorphisms in CYP1A1 and smoking: no association with breast cancer risk. <i>Carcinogenesis</i> , 2001, 22, 1797-1800.	2.8	48
806	Ovarian and breast cancer risks to women in families with two or more cases of ovarian cancer. <i>International Journal of Cancer</i> , 2000, 87, 110-117.	5.1	68
807	Frequent loss of BRCA1 mRNA and protein expression in sporadic ovarian cancers. <i>International Journal of Cancer</i> , 2000, 87, 317-321.	5.1	84
808	An analysis of ovarian tumor diameter and survival. <i>International Journal of Gynecological Cancer</i> , 2000, 10, 449-451.	2.5	7
809	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. <i>Nature Genetics</i> , 2000, 26, 362-364.	21.4	152
810	Prevalence and penetrance of BRCA1 and BRCA2 mutations in a population-based series of breast cancer cases. <i>British Journal of Cancer</i> , 2000, 83, 1301-1308.	6.4	573

#	ARTICLE	IF	CITATIONS
811	Polymorphisms in the human aromatase cytochrome P450 gene (CYP19) and breast cancer risk. Carcinogenesis, 2000, 21, 189-193.	2.8	74
812	No association between androgen or vitamin D receptor gene polymorphisms and risk of breast cancer. Carcinogenesis, 1999, 20, 2131-2135.	2.8	103
813	Somatic mutations in the p53 gene and prognosis in breast cancer: a meta-analysis. British Journal of Cancer, 1999, 80, 1968-1973.	6.4	268
814	Increased frequency of TP53 mutations in BRCA1 and BRCA2 ovarian tumours. , 1999, 25, 91-96.		68
815	The genetics of inherited breast cancer. Journal of Mammary Gland Biology and Neoplasia, 1998, 3, 365-376.	2.7	33
816	A systematic review and meta-analysis of family history and risk of ovarian cancer. BJOG: an International Journal of Obstetrics and Gynaecology, 1998, 105, 493-499.	2.3	209
817	Absolute risk of breast cancer in women at increased risk: a more useful clinical measure than relative risk?. Breast, 1998, 7, 255-259.	2.2	17
818	No association between a polymorphism in the steroid metabolism gene CYP17 and risk of breast cancer. British Journal of Cancer, 1998, 77, 2045-2047.	6.4	88
819	Screening for breast and ovarian cancer: the relevance of family history. British Medical Bulletin, 1998, 54, 823-838.	6.9	27
820	Family history and the risk of breast cancer: A systematic review and meta-analysis. International Journal of Cancer, 1997, 71, 800-809.	5.1	494
821	Family history and the risk of breast cancer: A systematic review and meta-analysis. International Journal of Cancer, 1997, 71, 800-809.	5.1	8
822	Selective or universal neonatal BCG immunization: what policy for a district with a high incidence of tuberculosis?. Public Health, 1996, 110, 179-183.	2.9	11
823	Health promotion in primary care: modelling the impact of intervention on coronary heart disease and stroke. Journal of Public Health, 1995, 17, 150-156.	1.8	10
824	Vitamin A supplementation in preschool children with acute diarrhoea. BMJ: British Medical Journal, 1995, 310, 530-530.	2.3	0
825	Health promotion in general practice. BMJ: British Medical Journal, 1994, 308, 852-853.	2.3	1
826	Erythromelalgia—the role of hypnotherapy. Postgraduate Medical Journal, 1992, 68, 44-46.	1.8	23
827	Role of Gonadal and Adrenal Steroids in the Impairment of the Male Rat's Sexual Behaviour by Hyperprolactinaemia. Neuroendocrinology, 1984, 39, 555-562.	2.5	16
828	The polygenic basis of breast cancer. , 0, , 224-232.		1

#	ARTICLE	IF	CITATIONS
829	eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. Cancer Epidemiology Biomarkers and Prevention, 0, , .	2.5	1