## Fergus J Couch

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2116100/publications.pdf

Version: 2024-02-01

397 papers

41,534 citations

95 h-index 186 g-index

406 all docs

406 docs citations

406 times ranked 33411 citing authors

#	Article	IF	CITATIONS
1	First international workshop of the ATM and cancer risk group (4-5 December 2019). Familial Cancer, 2022, 21, 211-227.	1.9	10
2	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> Alond <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. Journal of the National Cancer Institute, 2022, 114, 109-122.	6.3	19
3	Influence of Cancer Susceptibility Gene Mutations and ABO Blood Group of Pancreatic Cancer Probands on Concomitant Risk to First-Degree Relatives. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 372-381.	2.5	3
4	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants. Genetics in Medicine, 2022, 24, 119-129.	2.4	10
5	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
6	CDK5RAP3, a New BRCA2 Partner That Regulates DNA Repair, Is Associated with Breast Cancer Survival. Cancers, 2022, 14, 353.	3.7	0
7	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362.	2.8	23
8	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
9	Mapping molecular subtype specific alterations in breast cancer brain metastases identifies clinically relevant vulnerabilities. Nature Communications, 2022, 13, 514.	12.8	38
10	Breast Cancer Screening Strategies for Women With <i>ATM, CHEK2</i> , and <i>PALB2</i> Pathogenic Variants. JAMA Oncology, 2022, 8, 587.	7.1	36
11	A clinically compatible drugâ€screening platform based on organotypic cultures identifies vulnerabilities to prevent and treat brain metastasis. EMBO Molecular Medicine, 2022, 14, e14552.	6.9	12
12	Estrogen receptor beta repurposes EZH2 to suppress oncogenic NFκB/p65 signaling in triple negative breast cancer. Npj Breast Cancer, 2022, 8, 20.	5.2	9
13	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27.	5.0	15
14	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	3.3	2
15	Bilateral Oophorectomy and the Risk of Breast Cancer in <i>BRCA1</i> Mutation Carriers: A Reappraisal. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1351-1358.	2.5	3
16	An integrative model for the comprehensive classification of BRCA1 and BRCA2 variants of uncertain clinical significance. Npj Genomic Medicine, 2022, 7, .	3.8	4
17	Classification of <i>BRCA2</i> Variants of Uncertain Significance (VUS) Using an ACMG/AMP Model Incorporating a Homology-Directed Repair (HDR) Functional Assay. Clinical Cancer Research, 2022, 28, 3742-3751.	7.0	7
18	Risk of contralateral breast and other cancers in patients with invasive lobular breast cancer Journal of Clinical Oncology, 2022, 40, 555-555.	1.6	0

#	Article	IF	CITATIONS
19	Methylated DNA markers discriminate ovarian cancer from benign tissue in BRCA carriers Journal of Clinical Oncology, 2022, 40, e17610-e17610.	1.6	0
20	Genetic Risk of Second Primary Cancer in Breast Cancer Survivors: The Multiethnic Cohort Study. Cancer Research, 2022, 82, 3201-3208.	0.9	2
21	Antimullerian Hormone as a Serum Biomarker for Risk of Chemotherapy-Induced Amenorrhea. Journal of the National Cancer Institute, 2021, 113, 1105-1108.	6.3	5
22	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
23	Germline genetic testing in breast cancer: Rationale for the testing of all women diagnosed by the age of 60 years and for riskâ€based testing of those older than 60 years. Cancer, 2021, 127, 828-833.	4.1	20
24	Impact of Personalized Genetic Breast Cancer Risk Estimation With Polygenic Risk Scores on Preventive Endocrine Therapy Intention and Uptake. Cancer Prevention Research, 2021, 14, 175-184.	1.5	11
25	Wholeâ€exome sequencing of non― <i>BRCA1/BRCA2</i> mutation carrier cases at high―isk for hereditary breast/ovarian cancer. Human Mutation, 2021, 42, 290-299.	2.5	32
26	Integration of functional assay data results provides strong evidence for classification of hundreds of BRCA1 variants of uncertain significance. Genetics in Medicine, 2021, 23, 306-315.	2.4	21
27	A clinical calculator to predict disease outcomes in women with triple-negative breast cancer. Breast Cancer Research and Treatment, 2021, 185, 557-566.	2.5	19
28	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
29	Real-World Experiences With Yoga on Cancer-Related Symptoms in Women With Breast Cancer. Global Advances in Health and Medicine, 2021, 10, 216495612098414.	1.6	8
30	Association of mammographic density measures and breast cancer "intrinsic―molecular subtypes. Breast Cancer Research and Treatment, 2021, 187, 215-224.	2.5	11
31	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	27.0	414
32	Genetic Predictors of Chemotherapy-Induced Peripheral Neuropathy from Paclitaxel, Carboplatin and Oxaliplatin: NCCTG/Alliance N08C1, N08CA and N08CB Study. Cancers, 2021, 13, 1084.	3.7	11
33	Strong functional data for pathogenicity or neutrality classify BRCA2 DNA-binding-domain variants of uncertain significance. American Journal of Human Genetics, 2021, 108, 458-468.	6.2	31
34	Germline BRCA1/2 mutations and severe haematological toxicities in patients with breast cancer treated with neoadjuvant chemotherapy. European Journal of Cancer, 2021, 145, 44-52.	2.8	5
35	Germline pathogenic variants in cancer predisposition genes among women with invasive lobular cancer of breast Journal of Clinical Oncology, 2021, 39, 10581-10581.	1.6	0
36	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. Cancers, 2021, 13, 2370.	3.7	4

#	Article	IF	CITATIONS
37	Closing the gap: Trends in inconclusive rates on hereditary cancer testing across racial/ethnic groups Journal of Clinical Oncology, 2021, 39, 10525-10525.	1.6	1
38	Long-term outcomes of patients with node-negative (NO), triple-negative breast cancer (TNBC) who did not receive adjuvant chemotherapy according to stromal TILs (sTILs) Journal of Clinical Oncology, 2021, 39, 548-548.	1.6	0
39	Mutations in $\langle i \rangle$ BRCA1/2 $\langle i \rangle$ and Other Panel Genes in Patients With Metastatic Breast Cancer $\hat{a} \in$ "Association With Patient and Disease Characteristics and Effect on Prognosis. Journal of Clinical Oncology, 2021, 39, 1619-1630.	1.6	39
40	Breast cancer screening for carriers of ATM, CHEK2, and PALB2 pathogenic variants: A comparative modeling analysis Journal of Clinical Oncology, 2021, 39, 10500-10500.	1.6	0
41	The predictive ability of the 313 variant–based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. Genetics in Medicine, 2021, 23, 1726-1737.	2.4	16
42	Characteristics and Spatially Defined Immune (micro)landscapes of Early-stage PD-L1–positive Triple-negative Breast Cancer. Clinical Cancer Research, 2021, 27, 5628-5637.	7.0	32
43	PP2A and E3 ubiquitin ligase deficiencies: Seminal biological drivers in endometrial cancer. Gynecologic Oncology, 2021, 162, 182-189.	1.4	6
44	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
45	N-Terminal Pro Brain Natriuretic Peptide, sST2, and Galectin-3 Levels in Breast Cancer Survivors. Journal of Clinical Medicine, 2021, 10, 3313.	2.4	5
46	Risk of Late-Onset Breast Cancer in Genetically Predisposed Women. Journal of Clinical Oncology, 2021, 39, 3430-3440.	1.6	21
47	A clinical calculator to predict disease outcomes in women with hormone receptor-positive advanced breast cancer treated with first-line endocrine therapy. Breast Cancer Research and Treatment, 2021, 189, 15-23.	2.5	6
48	Clinical effectiveness of olaparib monotherapy in germline BRCA-mutated, HER2-negative metastatic breast cancer in a real-world setting: phase IIIb LUCY interim analysis. European Journal of Cancer, 2021, 152, 68-77.	2.8	18
49	Comparison of the Prevalence of Pathogenic Variants in Cancer Susceptibility Genes in Black Women and Non-Hispanic White Women With Breast Cancer in the United States. JAMA Oncology, 2021, 7, 1045.	7.1	21
50	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
51	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. Journal of Clinical Oncology, 2021, 39, 2564-2573.	1.6	47
52	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
53	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
54	Protein truncating variants in FANCM and risk for ER-negative/triple negative breast cancer. Npj Breast Cancer, 2021, 7, 130.	5.2	6

#	Article	IF	CITATIONS
55	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
56	Association of a novel endometrial cancer biomarker panel with prognostic risk, platinum insensitivity, and targetable therapeutic options. PLoS ONE, 2021, 16, e0245664.	2.5	5
57	Racial and Ethnic Differences in Multigene Hereditary Cancer Panel Test Results for Women With Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 1429-1433.	6.3	18
58	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
59	Germline Pathogenic Variants in Cancer Predisposition Genes Among Women With Invasive Lobular Carcinoma of the Breast. Journal of Clinical Oncology, 2021, 39, 3918-3926.	1.6	22
60	Molecular markers of risk of subsequent invasive breast cancer in women with ductal carcinoma in situ: protocol for a population-based cohort study. BMJ Open, 2021, 11, e053397.	1.9	1
61	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638.	0.9	39
62	Male breast cancer in the United States: Treatment patterns and prognostic factors in the 21st century. Cancer, 2020, 126, 26-36.	4.1	82
63	A clinical guide to hereditary cancer panel testing: evaluation of gene-specific cancer associations and sensitivity of genetic testing criteria in a cohort of 165,000 high-risk patients. Genetics in Medicine, 2020, 22, 407-415.	2.4	136
64	Functional characterization of 84 PALB2 variants of uncertain significance. Genetics in Medicine, 2020, 22, 622-632.	2.4	40
65	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
66	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
67	Classification of variants of uncertain significance in BRCA1 and BRCA2 using personal and family history of cancer from individuals in a large hereditary cancer multigene panel testing cohort. Genetics in Medicine, 2020, 22, 701-708.	2.4	28
68	Recommendations for application of the functional evidence PS3/BS3 criterion using the ACMG/AMP sequence variant interpretation framework. Genome Medicine, 2020, 12, 3.	8.2	312
69	Effect of Germline Mutations in Homologous Recombination Repair Genes on Overall Survival of Patients with Pancreatic Adenocarcinoma. Clinical Cancer Research, 2020, 26, 6505-6512.	7.0	24
70	Breastfeeding and the risk of epithelial ovarian cancer among women with a BRCA1 or BRCA2 mutation. Gynecologic Oncology, 2020, 159, 820-826.	1.4	10
71	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666.	2.4	82
72	A Rare <i>TP53</i> Mutation Predominant in Ashkenazi Jews Confers Risk of Multiple Cancers. Cancer Research, 2020, 80, 3732-3744.	0.9	32

#	Article	IF	Citations
73	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
74	Mutation Rates in Cancer Susceptibility Genes in Patients With Breast Cancer With Multiple Primary Cancers. JCO Precision Oncology, 2020, 4, 916-925.	3.0	9
75	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
76	Contribution of Germline Predisposition Gene Mutations to Breast Cancer Risk in African American Women. Journal of the National Cancer Institute, 2020, 112, 1213-1221.	6.3	51
77	Prediction of the functional impact of missense variants in BRCA1 and BRCA2 with BRCA-ML. Npj Breast Cancer, 2020, 6, 13.	5.2	21
78	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
79	Variants of uncertain clinical significance in hereditary breast and ovarian cancer genes: best practices in functional analysis for clinical annotation. Journal of Medical Genetics, 2020, 57, 509-518.	3.2	33
80	Evaluation of Germline Genetic Testing Criteria in a Hospital-Based Series of Women With Breast Cancer. Journal of Clinical Oncology, 2020, 38, 1409-1418.	1.6	64
81	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1 </i> BRCA2 Pathogenic Variants. JAMA Oncology, 2020, 6, 1218.	7.1	48
82	Folate receptor alpha expression associates with improved disease-free survival in triple negative breast cancer patients. Npj Breast Cancer, 2020, 6, 4.	5.2	49
83	The Contribution of Germline Predisposition Gene Mutations to Clinical Subtypes of Invasive Breast Cancer From a Clinical Genetic Testing Cohort. Journal of the National Cancer Institute, 2020, 112, 1231-1241.	6.3	61
84	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
85	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
86	The Association of Modifiable Breast Cancer Risk Factors and Somatic Genomic Alterations in Breast Tumors: The Cancer Genome Atlas Network. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 599-605.	2.5	7
87	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
88	Reply to On the proportion of male breast cancer among all breast cancers. Cancer, 2020, 126, 2034-2035.	4.1	1
89	Pathogenic Variants in Cancer Predisposition Genes and Prostate Cancer Risk in Men of African Ancestry. JCO Precision Oncology, 2020, 4, 32-43.	3.0	30
90	Real-world experiences with acupuncture among breast cancer survivors: a cross-sectional survey study. Supportive Care in Cancer, 2020, 28, 5833-5838.	2.2	5

#	Article	IF	CITATIONS
91	Mutation prevalence tables for hereditary cancer derived from multigene panel testing. Human Mutation, 2020, 41, e1-e6.	2.5	19
92	Real-world clinical effectiveness and safety of olaparib monotherapy in HER2-negative gBRCA-mutated metastatic breast cancer: Phase IIIb LUCY interim analysis Journal of Clinical Oncology, 2020, 38, 1087-1087.	1.6	2
93	Uptake of oophorectomy in women with findings on multigene panel testing: Results from the Prospective Registry of Multiplex Testing (PROMPT) Journal of Clinical Oncology, 2020, 38, 1508-1508.	1.6	10
94	N-terminal pro-brain natriuretic peptide levels after receipt of anthracycline for breast cancer Journal of Clinical Oncology, 2020, 38, e24103-e24103.	1.6	0
95	Role of intratumoral NK cells in triple-negative breast cancer in the FinXX trial and Mayo Clinic cohort Journal of Clinical Oncology, 2020, 38, 510-510.	1.6	2
96	Genetic testing experiences and emotional reactions among individuals with variant of uncertain significance results from cancer multiplex genetic testing Journal of Clinical Oncology, 2020, 38, e13680-e13680.	1.6	0
97	Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence-based computational prediction models. Genetics in Medicine, 2019, 21, 71-80.	2.4	52
98	Current Approaches to Cancer Genetic Counseling Services for Spanish-Speaking Patients. Journal of Immigrant and Minority Health, 2019, 21, 434-437.	1.6	13
99	Risk of Different Cancers Among First-degree Relatives of Pancreatic Cancer Patients: Influence of Probandsâ∈™ Susceptibility Gene Mutation Status. Journal of the National Cancer Institute, 2019, 111, 264-271.	6.3	10
100	Genetic predictors of chemotherapy-related amenorrhea inÂwomen with breast cancer. Fertility and Sterility, 2019, 112, 731-739.e1.	1.0	10
101	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
102	Hi-Plex2: a simple and robust approach to targeted sequencing-based genetic screening. BioTechniques, 2019, 67, 118-122.	1.8	11
103	Accuracy of self-reported cancer treatment data in young breast cancer survivors. Journal of Patient-Reported Outcomes, 2019, 3, 24.	1.9	5
104	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
105	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
106	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68.	5.0	31
107	Large scale multifactorial likelihood quantitative analysis of <i>BRCA1</i> and <i>BRCA2</i> variants: An ENIGMA resource to support clinical variant classification. Human Mutation, 2019, 40, 1557-1578.	2.5	102
108	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. British Journal of Cancer, 2019, 121, 180-192.	6.4	19

#	Article	IF	CITATIONS
109	Hereditary Cancer Syndromesâ€"A Primer on Diagnosis and Management, Part 2: Gastrointestinal Cancer Syndromes. Mayo Clinic Proceedings, 2019, 94, 1099-1116.	3.0	33
110	Hereditary Cancer Syndromes—A Primer on Diagnosis and Management. Mayo Clinic Proceedings, 2019, 94, 1084-1098.	3.0	39
111	<i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in women of African origin or ancestry. Human Mutation, 2019, 40, 1781-1796.	2.5	26
112	Germline Genetic Testing for Breast Cancer Risk: The Past, Present, and Future. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2019, 39, 61-74.	3.8	41
113	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
114	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
115	Impact of amino acid substitutions at secondary structures in the BRCT domains of the tumor suppressor BRCA1: Implications for clinical annotation. Journal of Biological Chemistry, 2019, 294, 5980-5992.	3.4	32
116	Oophorectomy and risk of contralateral breast cancer among BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2019, 175, 443-449.	2.5	12
117	Functional analysis of genetic variants in the high-risk breast cancer susceptibility gene PALB2. Nature Communications, 2019, 10, 5296.	12.8	45
118	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
119	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29
120	Cancer susceptibility gene mutations in type I and II endometrial cancer. Gynecologic Oncology, 2019, 152, 20-25.	1.4	32
121	Molecular mechanisms linking high body mass index to breast cancer etiology in post-menopausal breast tumor and tumor-adjacent tissues. Breast Cancer Research and Treatment, 2019, 173, 667-677.	2.5	19
122	Height and Body Mass Index as Modifiers of Breast Cancer Risk in <i>BRCA1</i> / <i>2</i> Mutation Carriers: A Mendelian Randomization Study. Journal of the National Cancer Institute, 2019, 111, 350-364.	6.3	30
123	Clinical validity assessment of genes frequently tested on hereditary breast and ovarian cancer susceptibility sequencing panels. Genetics in Medicine, 2019, 21, 1497-1506.	2.4	52
124	Leptomeningeal carcinomatosis in BRCA-mutated pancreatic cancer Journal of Clinical Oncology, 2019, 37, 239-239.	1.6	3
125	Contribution of Inherited DNA-Repair Gene Mutations to Hormone-Sensitive and Castrate-Resistant Metastatic Prostate Cancer and Implications for Clinical Outcome. JCO Precision Oncology, 2019, 3, 1-12.	3.0	13
126	The <i>BRCA2</i> c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19

#	Article	IF	Citations
127	Clinical testing of BRCA1 and BRCA2: a worldwide snapshot of technological practices. Npj Genomic Medicine, 2018, 3, 7.	3.8	44
128	The Landscape of Somatic Genetic Alterations in Breast Cancers From ATM Germline Mutation Carriers. Journal of the National Cancer Institute, 2018, 110, 1030-1034.	6.3	90
129	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. International Journal of Cancer, 2018, 143, 746-757.	5.1	19
130	Does mammographic density mediate risk factor associations with breast cancer? An analysis by tumor characteristics. Breast Cancer Research and Treatment, 2018, 170, 129-141.	2.5	11
131	Cardiovascular Concerns in BRCA1 and BRCA2 Mutation Carriers. Current Treatment Options in Cardiovascular Medicine, 2018, 20, 18.	0.9	6
132	Genetic overlap between endometriosis and endometrial cancer: evidence from crossâ€disease genetic correlation and GWAS metaâ€analyses. Cancer Medicine, 2018, 7, 1978-1987.	2.8	62
133	Assessment of the Clinical Relevance of BRCA2 Missense Variants by Functional and Computational Approaches. American Journal of Human Genetics, 2018, 102, 233-248.	6.2	64
134	Common Genetic Variation and Breast Cancer Risk—Past, Present, and Future. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 380-394.	2.5	108
135	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
136	E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. Scientific Reports, 2018, 8, 6574.	3.3	51
137	The <i>BRCA1</i> c. 5096G> A p. Arg1699Gln (R1699Q) intermediate risk variant: breast and ovarian cancer risk estimation and recommendations for clinical management from the ENIGMA consortium. Journal of Medical Genetics, 2018, 55, 15-20.	3.2	50
138	Impact of histopathology, tumor-infiltrating lymphocytes, and adjuvant chemotherapy on prognosis of triple-negative breast cancer. Breast Cancer Research and Treatment, 2018, 167, 89-99.	2.5	74
139	From the laboratory to the clinic: sharing BRCA VUS reclassification tools with practicing genetics professionals. Journal of Community Genetics, 2018, 9, 209-215.	1.2	5
140	BRCA1/2 Mutations and Bevacizumab in the Neoadjuvant Treatment of Breast Cancer: Response and Prognosis Results in Patients With Triple-Negative Breast Cancer From the GeparQuinto Study. Journal of Clinical Oncology, 2018, 36, 2281-2287.	1.6	86
141	Multigene Hereditary Cancer Panels Reveal High-Risk Pancreatic Cancer Susceptibility Genes. JCO Precision Oncology, 2018, 2, 1-28.	3.0	23
142	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. PLoS Genetics, 2018, 14, e1007752.	3.5	148
143	A contemporary review of male breast cancer: current evidence and unanswered questions. Cancer and Metastasis Reviews, 2018, 37, 599-614.	<b>5.</b> 9	63
144	Triple-Negative Breast Cancer Risk Genes Identified by Multigene Hereditary Cancer Panel Testing. Journal of the National Cancer Institute, 2018, 110, 855-862.	6.3	225

#	Article	IF	Citations
145	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430.	0.9	54
146	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
147	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
148	Association Between Inherited Germline Mutations in Cancer Predisposition Genes and Risk of Pancreatic Cancer. JAMA - Journal of the American Medical Association, 2018, 319, 2401.	7.4	375
149	Identification of a pyruvate-to-lactate signature in pancreatic intraductal papillary mucinous neoplasms. Pancreatology, 2018, 18, 46-53.	1.1	9
150	Polygenic risk score for breast cancer in high-risk women Journal of Clinical Oncology, 2018, 36, 1508-1508.	1.6	11
151	Prospective Registry of Multiplex Testing (PROMPT): Feasible and sustainable Journal of Clinical Oncology, 2018, 36, 1543-1543.	1.6	3
152	Breast cancer cell-free DNA (cfDNA) profiles reflect underlying tumor biology: The Circulating Cell-Free Genome Atlas (CCGA) study Journal of Clinical Oncology, 2018, 36, 536-536.	1.6	50
153	Inherited mutations in breast cancer patients with and without multiple primary cancers Journal of Clinical Oncology, 2018, 36, 1503-1503.	1.6	0
154	Expanding BRCA1/2 testing criteria to include other confirmed breast and ovarian cancer susceptibility genes Journal of Clinical Oncology, 2018, 36, 1524-1524.	1.6	0
155	Examining patients' medical and psychosocial experiences following detection of a <i>CDH1</i> variant with multiplex genetic testing Journal of Clinical Oncology, 2018, 36, 1583-1583.	1.6	0
156	Accuracy of self-reported chemotherapy regimens in young breast cancer survivors Journal of Clinical Oncology, 2018, 36, e22143-e22143.	1.6	0
157	Male breast cancer in a multi-gene panel testing cohort: insights and unexpected results. Breast Cancer Research and Treatment, 2017, 161, 575-586.	2.5	116
158	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. European Journal of Human Genetics, 2017, 25, 432-438.	2.8	26
159	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
160	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
161	Associations Between Cancer Predisposition Testing Panel Genes and Breast Cancer. JAMA Oncology, 2017, 3, 1190.	7.1	472
162	Non- BRCA familial breast cancer: review of reported pathology and molecular findings. Pathology, 2017, 49, 363-370.	0.6	32

#	Article	IF	Citations
163	Interaction of mammographic breast density with menopausal status and postmenopausal hormone use in relation to the risk of aggressive breast cancer subtypes. Breast Cancer Research and Treatment, 2017, 165, 421-431.	2.5	11
164	The contribution of pathogenic variants in breast cancer susceptibility genes to familial breast cancer risk. Npj Breast Cancer, 2017, 3, 22.	5.2	108
165	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	21.4	356
166	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
167	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
168	Frequency of mutations in a large series of clinically ascertained ovarian cancer cases tested on multi-gene panels compared to reference controls. Gynecologic Oncology, 2017, 147, 375-380.	1.4	105
169	Gene–environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20
170	Management of Breast Cancer Risk in Women with Ovarian Cancer and Deleterious BRCA1 or BRCA2 Mutations. Annals of Surgical Oncology, 2017, 24, 3107-3109.	1.5	4
171	Clinical Decision-Making in Patients with Variant of Uncertain Significance in BRCA1 or BRCA2 Genes. Annals of Surgical Oncology, 2017, 24, 3067-3072.	1.5	63
172	Germline variation in ADAMTSL1 is associated with prognosis following breast cancer treatment in young women. Nature Communications, 2017, 8, 1632.	12.8	18
173	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. Breast Cancer Research and Treatment, 2017, 161, 117-134.	2.5	18
174	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
175	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2017, 109, .	6.3	242
176	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
177	Evaluation and Adaptation of a Laboratory-Based cDNA Library Preparation Protocol for Retrospective Sequencing of Archived MicroRNAs from up to 35-Year-Old Clinical FFPE Specimens. International Journal of Molecular Sciences, 2017, 18, 627.	4.1	15
178	Alcohol consumption and breast tumor gene expression. Breast Cancer Research, 2017, 19, 108.	5.0	23
179	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
180	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	1.6	152

#	Article	IF	CITATIONS
181	TP53-based interaction analysis identifies cis-eQTL variants for TP53BP2, FBXO28, and FAM53A that associate with survival and treatment outcome in breast cancer. Oncotarget, 2017, 8, 18381-18398.	1.8	14
182	$\mbox{\sc i}\mbox{\sc PHIP}\mbox{\sc /i}\mbox{\sc -}\mbox{\sc a}$ a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
183	Association of breast cancer risk with genetic variants showing differential allelic expression: Identification of a novel breast cancer susceptibility locus at 4q21. Oncotarget, 2016, 7, 80140-80163.	1.8	31
184	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	8.4	118
185	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
186	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
187	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
188	<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
189	Functional assays provide a robust tool for the clinical annotation of genetic variants of uncertain significance. Npj Genomic Medicine, 2016, $1$ , .	3.8	70
190	Patient survival and tumor characteristics associated with CHEK2:p.I157T – findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
191	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
192	Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131.	2.5	18
193	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
194	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
195	Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674.	21.4	77
196	Evaluation of ACMG-Guideline-Based Variant Classification of Cancer Susceptibility and Non-Cancer-Associated Genes in Families Affected by Breast Cancer. American Journal of Human Genetics, 2016, 98, 801-817.	6.2	113
197	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2016, 18, 15.	5.0	88
198	Conflicting Interpretation of Genetic Variants and Cancer Risk by Commercial Laboratories as Assessed by the Prospective Registry of Multiplex Testing. Journal of Clinical Oncology, 2016, 34, 4071-4078.	1.6	147

#	Article	IF	Citations
199	A Recurrent <i>ERCC3</i> Truncating Mutation Confers Moderate Risk for Breast Cancer. Cancer Discovery, 2016, 6, 1267-1275.	9.4	41
200	Evidence that the 5p12 Variant rs10941679 Confers Susceptibility to Estrogen-Receptor-Positive Breast Cancer through FGF10 and MRPS30 Regulation. American Journal of Human Genetics, 2016, 99, 903-911.	6.2	59
201	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	2.9	33
202	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1503-1510.	2.5	64
203	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
204	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
205	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. Breast Cancer Research, 2016, 18, 112.	5.0	42
206	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
207	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
208	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). Scientific Reports, 2016, 6, 32512.	3.3	19
209	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	5.0	56
210	The PALB2 p.Leu939Trp mutation is not associated with breast cancer risk. Breast Cancer Research, 2016, 18, 111.	5.0	11
211	Age- and Tumor Subtype–Specific Breast Cancer Risk Estimates for <i>CHEK2</i> *1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
212	Counselling framework for moderate-penetrance cancer-susceptibility mutations. Nature Reviews Clinical Oncology, 2016, 13, 581-588.	27.6	258
213	Impact that Timing of Genetic Mutation Diagnosis has on Surgical Decision Making and Outcome for BRCA1/BRCA2 Mutation Carriers with Breast Cancer. Annals of Surgical Oncology, 2016, 23, 3232-3238.	1.5	46
214	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91.	3.1	62
215	Genomic Biomarkers for Breast Cancer Risk. Advances in Experimental Medicine and Biology, 2016, 882, 1-32.	1.6	42
216	Combined genetic and splicing analysis of BRCA1 c.[594-2A>C; 641A>G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268.	2.9	106

#	Article	IF	CITATIONS
217	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
218	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
219	Integrated Genomic Analysis of Pancreatic Ductal Adenocarcinomas Reveals Genomic Rearrangement Events as Significant Drivers of Disease. Cancer Research, 2016, 76, 749-761.	0.9	27
220	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
221	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
222	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
223	Prevalence of Pathogenic Mutations in Cancer Predisposition Genes among Pancreatic Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 207-211.	2.5	116
224	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
225	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
226	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
227	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
228	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. Breast Cancer Research, 2015, 17, 61.	5.0	26
229	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
230	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
231	Disseminated Medulloblastoma in a Child with Germline BRCA2 6174delT Mutation and without Fanconi Anemia. Frontiers in Oncology, 2015, 5, 191.	2.8	16
232	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	2.5	34
233	Transcriptomic and Immunohistochemical Profiling of SLC6A14 in Pancreatic Ductal Adenocarcinoma.  BioMed Research International, 2015, 2015, 1-10.	1.9	22
234	SNP-SNP interaction analysis of NF-l <sup>o</sup> B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20

#	Article	IF	CITATIONS
235	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
236	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	2.9	40
237	Gene-Panel Sequencing and the Prediction of Breast-Cancer Risk. New England Journal of Medicine, 2015, 372, 2243-2257.	27.0	764
238	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
239	Inherited Mutations in 17 Breast Cancer Susceptibility Genes Among a Large Triple-Negative Breast Cancer Cohort Unselected for Family History of Breast Cancer. Journal of Clinical Oncology, 2015, 33, 304-311.	1.6	521
240	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
241	BRCA1 Circos: a visualisation resource for functional analysis of missense variants. Journal of Medical Genetics, 2015, 52, 224-230.	3.2	32
242	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
243	A preliminary investigation of genetic counselors' information needs when receiving a variant of uncertain significance result: a mixed methods study. Genetics in Medicine, 2015, 17, 739-746.	2.4	24
244	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	21.4	221
245	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
246	The Contributions of Breast Density and Common Genetic Variation to Breast Cancer Risk. Journal of the National Cancer Institute, 2015, 107, .	6.3	174
247	<i>FANCM</i> c.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	2.9	91
248	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. American Journal of Human Genetics, 2015, 97, 22-34.	6.2	37
249	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
250	Association of Type and Location of <i>BRCA1</i> BRCA2Mutations With Risk of Breast and Ovarian Cancer. JAMA - Journal of the American Medical Association, 2015, 313, 1347.	7.4	390
251	Dense and Nondense Mammographic Area and Risk of Breast Cancer by Age and Tumor Characteristics. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 798-809.	2.5	42
252	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. Cancer Research, 2015, 75, 2457-2467.	0.9	55

#	Article	IF	CITATIONS
253	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
254	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. BMC Medicine, 2015, 13, 156.	5.5	51
255	The association of copy number variation and percent mammographic density. BMC Research Notes, 2015, 8, 297.	1.4	2
256	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
257	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861.	3.1	25
258	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
259	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
260	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
261	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
262	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
263	A Genome Wide Meta-Analysis Study for Identification of Common Variation Associated with Breast Cancer Prognosis. PLoS ONE, 2014, 9, e101488.	2.5	42
264	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
265	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
266	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	3.5	47
267	The Oncogenic STP Axis Promotes Triple-Negative Breast Cancer via Degradation of the REST Tumor Suppressor. Cell Reports, 2014, 9, 1318-1332.	6.4	24
268	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
269	Associations of common breast cancer susceptibility alleles with risk of breast cancer subtypes in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research, 2014, 16, 3416.	5.0	57
270	Functional Assays for Analysis of Variants of Uncertain Significance in <i>BRCA2</i> . Human Mutation, 2014, 35, 151-164.	2.5	107

#	Article	IF	Citations
271	Two Decades After <i>BRCA:</i> Setting Paradigms in Personalized Cancer Care and Prevention. Science, 2014, 343, 1466-1470.	12.6	300
272	Identification of New Genetic Susceptibility Loci for Breast Cancer Through Consideration of Geneâ€Environment Interactions. Genetic Epidemiology, 2014, 38, 84-93.	1.3	28
273	Genome-wide association study identifies 25 known breast cancer susceptibility loci as risk factors for triple-negative breast cancer. Carcinogenesis, 2014, 35, 1012-1019.	2.8	145
274	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	12.8	109
275	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer.  Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	7.1	162
276	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
277	Breast-Cancer Risk in Families with Mutations in <i>PALB2</i> . New England Journal of Medicine, 2014, 371, 497-506.	27.0	745
278	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
279	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
280	Fibroblast growth factor receptor 2 translocations in intrahepatic cholangiocarcinoma. Human Pathology, 2014, 45, 1630-1638.	2.0	235
281	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
282	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. The Clinical Journal of Pathology, 2014, , n/a-n/a.	0.0	2
283	A Classification Model for <i>BRCA2</i> DNA Binding Domain Missense Variants Based on Homology-Directed Repair Activity. Cancer Research, 2013, 73, 265-275.	0.9	103
284	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
285	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
286	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
287	Genetic Alterations Associated With Progression From Pancreatic Intraepithelial Neoplasia to Invasive Pancreatic Tumor. Gastroenterology, 2013, 145, 1098-1109.e1.	1.3	166
288	Genome-wide association studies identify four ER negative–specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374

#	Article	IF	CITATIONS
289	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
290	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. Breast Cancer Research and Treatment, 2013, 138, 529-542.	2.5	18
291	Genetic modifiers of menopausal hormone replacement therapy and breast cancer risk: a genome–wide interaction study. Endocrine-Related Cancer, 2013, 20, 875-887.	3.1	26
292	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
293	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	3.5	244
294	Evidence of Gene–Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	3.5	136
295	Biallelic Deleterious <i>BRCA1</i> Mutations in a Woman with Early-Onset Ovarian Cancer. Cancer Discovery, 2013, 3, 399-405.	9.4	124
296	BRCA1/2 Sequence Variants of Uncertain Significance: A Primer for Providers to Assist in Discussions and in Medical Management. Oncologist, 2013, 18, 518-524.	3.7	76
297	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 2013, 4, 1627.	12.8	98
298	SoftSearch: Integration of Multiple Sequence Features to Identify Breakpoints of Structural Variations. PLoS ONE, 2013, 8, e83356.	2.5	37
299	A Nonsynonymous Polymorphism in <i>IRS1</i> Modifies Risk of Developing Breast and Ovarian Cancers in <i>BRCA1</i> BRCA1 BRCA1 Biomarkers and Prevention, 2012, 21, 1362-1370.	2.5	23
300	Common Breast Cancer Susceptibility Variants in <i>LSP1</i> and <i>RAD51L1</i> Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1156-1166.	2.5	101
301	BRCA1 R1699Q variant displaying ambiguous functional abrogation confers intermediate breast and ovarian cancer risk. Journal of Medical Genetics, 2012, 49, 525-532.	3.2	97
302	Identification of a novel percent mammographic density locus at 12q24. Human Molecular Genetics, 2012, 21, 3299-3305.	2.9	31
303	19p13.1 Is a Triple-Negative–Specific Breast Cancer Susceptibility Locus. Cancer Research, 2012, 72, 1795-1803.	0.9	100
304	Mammographic Breast Density and Breast Cancer: Evidence of a Shared Genetic Basis. Cancer Research, 2012, 72, 1478-1484.	0.9	54
305	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. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	2.5	47
306	Pathology of Breast and Ovarian Cancers among <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from the Consortium of Investigators of Modifiers of <i>BRCA1</i> / <i> 2</i> (CIMBA). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 134-147.	2.5	513

#	Article	IF	Citations
307	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancerâ€"Specific Death, and Increased Risk of a Second Breast Cancer. Journal of Clinical Oncology, 2012, 30, 4308-4316.	1.6	162
308	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	2.9	80
309	The influence of mammogram acquisition on the mammographic density and breast cancer association in the mayo mammography health study cohort. Breast Cancer Research, 2012, 14, R147.	5.0	47
310	Evaluation of chromosome 6p22 as a breast cancer risk modifier locus in a follow-up study of BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2012, 136, 295-302.	2.5	4
311	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	21.4	256
312	Mutation screening of RAD51C in high-risk breast and ovarian cancer families. Familial Cancer, 2012, 11, 381-385.	1.9	18
313	BRCA2 Localization to the Midbody by Filamin A Regulates CEP55 Signaling and Completion of Cytokinesis. Developmental Cell, 2012, 23, 137-152.	7.0	74
314	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	2.9	168
315	11q13 is a susceptibility locus for hormone receptor positive breast cancer. Human Mutation, 2012, 33, 1123-1132.	2.5	35
316	A guide for functional analysis of <i>BRCA1</i> variants of uncertain significance. Human Mutation, 2012, 33, 1526-1537.	2.5	117
317	Common variants at $12p11$ , $12q24$ , $9p21$ , $9q31.2$ and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2mutation carriers. Breast Cancer Research, 2012, 14, R33.	5.0	78
318	A review of a multifactorial probability-based model for classification of BRCA1 and BRCA2 variants of uncertain significance (VUS). Human Mutation, 2012, 33, 8-21.	2.5	190
319	ENIGMA-Evidence-based network for the interpretation of germline mutant alleles: An international initiative to evaluate risk and clinical significance associated with sequence variation in BRCA1 and BRCA2 genes. Human Mutation, 2012, 33, 2-7.	2.5	269
320	Classification of missense substitutions in the BRCA genes: A database dedicated to Ex-UVs. Human Mutation, 2012, 33, 22-28.	2.5	65
321	Ovarian cancer susceptibility alleles and risk of ovarian cancer in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. Human Mutation, 2012, 33, 690-702.	2.5	34
322	Confirmation of 5p12 As a Susceptibility Locus for Progesterone-Receptor–Positive, Lower Grade Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2222-2231.	2.5	27
323	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. Journal of the National Cancer Institute, 2011, 103, 250-263.	6.3	596
324	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2011, 20, 3289-3303.	2.9	152

#	Article	IF	Citations
325	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor–negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
326	Inactivation of Brca2 Promotes Trp53-Associated but Inhibits KrasG12D-Dependent Pancreatic Cancer Development in Mice. Gastroenterology, 2011, 140, 1303-1313.e3.	1.3	65
327	Modification of <i>BRCA1</i> -Associated Breast and Ovarian Cancer Risk by <ibrca1< i="">-Interacting Genes. Cancer Research, 2011, 71, 5792-5805.</ibrca1<>	0.9	49
328	Common breast cancer susceptibility alleles are associated with tumour subtypes in BRCA1 and BRCA2 mutation carriers: results from the Consortium of Investigators of Modifiers of BRCA1/2. Breast Cancer Research, 2011, 13, R110.	5.0	71
329	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. Nature Genetics, 2011, 43, 185-187.	21.4	109
330	Evaluation of associations between common variation in mitotic regulatory pathways and risk of overall and high grade breast cancer. Breast Cancer Research and Treatment, 2011, 129, 617-622.	2.5	25
331	Splicing and multifactorial analysis of intronic BRCA1 and BRCA2 sequence variants identifies clinically significant splicing aberrations up to 12 nucleotides from the intron/exon boundary. Human Mutation, 2011, 32, 678-687.	2.5	74
332	Common alleles at $6q25.1$ and $1p11.2$ are associated with breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2011, 20, 3304-3321.	2.9	68
333	Assessment of Hepatocyte Growth Factor in Ovarian Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1638-1648.	2.5	31
334	A Computational Method to Classify Variants of Uncertain Significance Using Functional Assay Data with Application to <i>BRCA1</i> . Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1078-1088.	2.5	54
335	Common Breast Cancer Susceptibility Loci Are Associated with Triple-Negative Breast Cancer. Cancer Research, 2011, 71, 6240-6249.	0.9	109
336	Genetic Variation at 9p22.2 and Ovarian Cancer Risk for BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2011, 103, 105-116.	6.3	40
337	Association of genetic variation in mitotic kinases with breast cancer risk. Breast Cancer Research and Treatment, 2010, 119, 453-462.	2.5	22
338	Predicting BRCA1 and BRCA2 gene mutation carriers: comparison of PENN II model to previous study. Familial Cancer, 2010, 9, 495-502.	1.9	45
339	Detection of splicing aberrations caused by BRCA1 and BRCA2 sequence variants encoding missense substitutions: implications for prediction of pathogenicity. Human Mutation, 2010, 31, E1484-E1505.	2.5	86
340	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
341	Common Breast Cancer Susceptibility Alleles and the Risk of Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Implications for Risk Prediction. Cancer Research, 2010, 70, 9742-9754.	0.9	169
342	Common variants associated with breast cancer in genome-wide association studies are modifiers of breast cancer risk in BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2010, 19, 2886-2897.	2.9	60

#	Article	IF	CITATIONS
343	Association of Mitotic Regulation Pathway Polymorphisms with Pancreatic Cancer Risk and Outcome. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 251-257.	2.5	23
344	Association of Risk-Reducing Surgery in <emph type="ital">BRCA1</emph> or <emph type="ital">BRCA2</emph> Mutation Carriers With Cancer Risk and Mortality. JAMA - Journal of the American Medical Association, 2010, 304, 967.	7.4	1,241
345	Association of the Variants <i>CASP8 </i> D302H and <i>CASP10 </i> V410I with Breast and Ovarian Cancer Risk in <i>BRCA1 </i> BRCA2  Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2859-2868.	2.5	37
346	Common Genetic Variants and Modification of Penetrance of BRCA2-Associated Breast Cancer. PLoS Genetics, 2010, 6, e1001183.	3.5	85
347	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptor–Negative Breast Cancer Survival. Journal of the National Cancer Institute, 2010, 102, 650-662.	6.3	48
348	Evidence for SMAD3 as a modifier of breast cancer risk in BRCA2mutation carriers. Breast Cancer Research, 2010, 12, R102.	5.0	25
349	Association of Breast Cancer Susceptibility Variants with Risk of Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3044-3048.	2.5	23
350	Genetic Variation in the Chromosome 17q23 Amplicon and Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1864-1868.	2.5	34
351	Common variants in LSP1, 2q35 and 8q24 and breast cancer risk for BRCA1 and BRCA2 mutation carriers. Human Molecular Genetics, 2009, 18, 4442-4456.	2.9	99
352	Polymorphic Variants in Hereditary Pancreatic Cancer Genes Are Not Associated with Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2549-2552.	2.5	9
353	Genome-wide association studies identify new breast cancer susceptibility genes. Current Breast Cancer Reports, 2009, 1, 131-138.	1.0	3
354	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	21.4	434
355	Assessment of functional effects of unclassified genetic variants. Human Mutation, 2008, 29, 1314-1326.	2.5	93
356	Prediction and assessment of splicing alterations: implications for clinical testing. Human Mutation, 2008, 29, 1304-1313.	2.5	108
357	International variation in rates of uptake of preventive options in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. International Journal of Cancer, 2008, 122, 2017-2022.	5.1	306
358	Common Breast Cancer-Predisposition Alleles Are Associated with Breast Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. American Journal of Human Genetics, 2008, 82, 937-948.	6.2	257
359	Secondary mutations as a mechanism of cisplatin resistance in BRCA2-mutated cancers. Nature, 2008, 451, 1116-1120.	27.8	934
360	Genetic variation in stromal proteins decorin and lumican with breast cancer: investigations in two case-control studies. Breast Cancer Research, 2008, 10, R98.	5.0	41

#	Article	IF	CITATIONS
361	Association of Genetic Variation in Genes Implicated in the $\hat{l}^2$ -Catenin Destruction Complex with Risk of Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2101-2108.	2.5	67
362	Clinically Applicable Models to Characterize <i>BRCA1 </i> Significance. Journal of Clinical Oncology, 2008, 26, 5393-5400.	1.6	77
363	Mutational Analysis of Thirty-two Double-Strand DNA Break Repair Genes in Breast and Pancreatic Cancers. Cancer Research, 2008, 68, 971-975.	0.9	45
364	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	3.5	315
365	Functional Assays for Classification of <i>BRCA2</i> Variants of Uncertain Significance. Cancer Research, 2008, 68, 3523-3531.	0.9	108
366	Classifying Variants of Undetermined Significance in BRCA2 with Protein Likelihood Ratios. Cancer Informatics, 2008, 6, CIN.S618.	1.9	45
367	The Prevalence of BRCA2 Mutations in Familial Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 342-346.	2.5	255
368	<i>AURKA</i> F31I Polymorphism and Breast Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: A Consortium of Investigators of Modifiers of BRCA1/2 Study. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1416-1421.	2.5	30
369	Determination of Cancer Risk Associated with Germ Line BRCA1 Missense Variants by Functional Analysis. Cancer Research, 2007, 67, 1494-1501.	0.9	110
370	Strong Evidence of a Genetic Determinant for Mammographic Density, a Major Risk Factor for Breast Cancer. Cancer Research, 2007, 67, 8412-8418.	0.9	69
371	A Systematic Genetic Assessment of 1,433 Sequence Variants of Unknown Clinical Significance in the BRCA1 and BRCA2 Breast Cancer–Predisposition Genes. American Journal of Human Genetics, 2007, 81, 873-883.	6.2	416
372	RAD51 135Gâ†'C Modifies Breast Cancer Risk among BRCA2 Mutation Carriers: Results from a Combined Analysis of 19 Studies. American Journal of Human Genetics, 2007, 81, 1186-1200.	6.2	217
373	Identification of BRCA1 missense substitutions that confer partial functional activity: potential moderate risk variants?. Breast Cancer Research, 2007, 9, R82.	5.0	58
374	An international initiative to identify genetic modifiers of cancer risk in BRCA1 and BRCA2 mutation carriers: the Consortium of Investigators of Modifiers of BRCA1 and BRCA2 (CIMBA). Breast Cancer Research, 2007, 9, 104.	5.0	136
375	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	21.4	591
376	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	27.8	2,165
377	Control of BRCA2 Cellular and Clinical Functions by a Nuclear Partner, PALB2. Molecular Cell, 2006, 22, 719-729.	9.7	724
378	Cancer Risk Assessment at the Atomic Level. Cancer Research, 2006, 66, 1897-1899.	0.9	15

#	Article	IF	CITATIONS
379	Salpingo-oophorectomy and the Risk of Ovarian, Fallopian Tube, and Peritoneal Cancers in Women With a <emph type="ITAL">BRCA1</emph> or <emph type="ITAL">BRCA2</emph> Mutation. JAMA - Journal of the American Medical Association, 2006, 296, 185.	7.4	544
380	Increased prevalence of the BRCA2 polymorphic stop codon K3326X among individuals with familial pancreatic cancer. Oncogene, 2005, 24, 3652-3656.	5.9	68
381	Reply to Palacios et al., ?ERBB2 and MYC alterations in BRCA1- and BRCA2-associated cancers?. Genes Chromosomes and Cancer, 2005, 42, 206-206.	2.8	0
382	Targeted therapy for BRCA2 deficient tumors. Cancer Biology and Therapy, 2005, 4, 707-708.	3.4	2
383	Germ line Fanconi anemia complementation group C mutations and pancreatic cancer. Cancer Research, 2005, 65, 383-6.	0.9	89
384	Functional evaluation and cancer risk assessment of BRCA2 unclassified variants. Cancer Research, 2005, 65, 417-26.	0.9	97
385	Genetic Epidemiology of BRCA1. Cancer Biology and Therapy, 2004, 3, 509-514.	3.4	19
386	The Role of Tbx2 and Tbx3 in Mammary Development and Tumorigenesis. Journal of Mammary Gland Biology and Neoplasia, 2004, 9, 109-118.	2.7	85
387	Integrated Evaluation of DNA Sequence Variants of Unknown Clinical Significance: Application to BRCA1 and BRCA2. American Journal of Human Genetics, 2004, 75, 535-544.	6.2	351
388	Is BRCA1 Associated with Familial Breast Cancer in India?. Cancer Biology and Therapy, 2002, 1, 22-23.	3 <b>.</b> 4	1
389	Oral Contraceptives and the Risk of Breast Cancer in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2002, 94, 1773-1779.	6.3	318
390	BRCA2 and Pancreatic Cancer. International Journal of Gastrointestinal Cancer, 2002, 31, 99-106.	0.4	43
391	TBX2 is preferentially amplified in BRCA1- and BRCA2-related breast tumors. Cancer Research, 2002, 62, 3587-91.	0.9	69
392	Genetic heterogeneity in Peutz-Jeghers syndrome. Human Mutation, 2000, 16, 23-30.	2.5	125
393	p73 mutations are not detected in sporadic and hereditary breast cancer. Breast Cancer Research and Treatment, 1999, 58, 25-29.	2.5	16
394	I1307KAPC variant in non-Ashkenazi Jewish women affected with breast cancer., 1999, 85, 189-190.		5
395	<i>BRCA1</i> Mutations in Women Attending Clinics That Evaluate the Risk of Breast Cancer. New England Journal of Medicine, 1997, 336, 1409-1415.	27.0	660
396	Localization of the human homolog of the yeast cell division control 27 gene (CDC27) proximal to ITGB3 on human chromosome 17q21.3. Somatic Cell and Molecular Genetics, 1995, 21, 351-355.	0.7	1

#	Article	IF	CITATIONS
397	Mutations in the BRCA1 gene in families with early-onset breast and ovarian cancer. Nature Genetics, 1994, 8, 387-391.	21.4	384