

Irene L Andrulis

List of Publications by Year in descending order

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Version: 2024-02-01

211
papers

22,278
citations

11608

70
h-index

10708

138
g-index

222
all docs

222
docs citations

222
times ranked

24790
citing authors

#	ARTICLE	IF	CITATIONS
1	Maternal and prenatal factors and age at thelarche in the LEGACY Girls Study cohort: implications for breast cancer risk. <i>International Journal of Epidemiology</i> , 2023, 52, 272-283.	0.9	1
2	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	3.0	19
3	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in <i>BRCA1</i> and <i>BRCA2</i> compared with those harboring protein truncating variants. <i>Genetics in Medicine</i> , 2022, 24, 119-129.	1.1	10
4	Cancer Risks Associated With <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>Journal of Clinical Oncology</i> , 2022, 40, 1529-1541.	0.8	90
5	Investigating the Potential of Isolating and Expanding Tumour-Infiltrating Lymphocytes from Adult Sarcoma. <i>Cancers</i> , 2022, 14, 548.	1.7	4
6	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	2.0	6
7	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
8	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	2.2	15
9	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744.	3.4	51
10	Weight is More Informative than Body Mass Index for Predicting Postmenopausal Breast Cancer Risk: Prospective Family Study Cohort (ProF-SC). <i>Cancer Prevention Research</i> , 2022, 15, 185-191.	0.7	4
11	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	1.6	2
12	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. <i>Genome Medicine</i> , 2022, 14, 51.	3.6	19
13	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.	1.7	2
14	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.	3.0	45
15	RNA expression profiling reveals PRAME, a potential immunotherapy target, is frequently expressed in solitary fibrous tumors. <i>Modern Pathology</i> , 2021, 34, 951-960.	2.9	14
16	Comparing 5-Year and Lifetime Risks of Breast Cancer Using the Prospective Family Study Cohort. <i>Journal of the National Cancer Institute</i> , 2021, 113, 785-791.	3.0	13
17	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.	2.9	5
18	A case-only study to identify genetic modifiers of breast cancer risk for <i>BRCA1/BRCA2</i> mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19

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19	Breast Cancer Risk Genes " Association Analysis in More than 113,000 Women. <i>New England Journal of Medicine</i> , 2021, 384, 428-439.	13.9	532
20	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. <i>Npj Breast Cancer</i> , 2021, 7, 52.	2.3	7
21	Gene-Environment Interactions Relevant to Estrogen and Risk of Breast Cancer: Can Gene-Environment Interactions Be Detected Only among Candidate SNPs from Genome-Wide Association Studies?. <i>Cancers</i> , 2021, 13, 2370.	1.7	4
22	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&#amp;l). <i>Journal of Personalized Medicine</i> , 2021, 11, 511.	1.1	59
23	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. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	1.1	16
24	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. <i>Nature Communications</i> , 2021, 12, 4496.	5.8	28
25	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203.	2.6	6
26	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. <i>Breast Cancer Research</i> , 2021, 23, 86.	2.2	7
27	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145.	2.9	9
28	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
29	Detection and utility of cell-free and circulating tumour DNA in bone and soft-tissue sarcomas. <i>Bone and Joint Research</i> , 2021, 10, 602-610.	1.3	2
30	Immuno-transcriptomic profiling of extracranial pediatric solid malignancies. <i>Cell Reports</i> , 2021, 37, 110047.	2.9	26
31	Recreational Physical Activity and Outcomes After Breast Cancer in Women at High Familial Risk. <i>JNCI Cancer Spectrum</i> , 2021, 5, pkab090.	1.4	1
32	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.4	39
33	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228,951 Women of European Descent. <i>Journal of the National Cancer Institute</i> , 2020, 112, 295-304.	3.0	35
34	Recreational Physical Activity Is Associated with Reduced Breast Cancer Risk in Adult Women at High Risk for Breast Cancer: A Cohort Study of Women Selected for Familial and Genetic Risk. <i>Cancer Research</i> , 2020, 80, 116-125.	0.4	37
35	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. <i>International Journal of Cancer</i> , 2020, 146, 2130-2138.	2.3	13
36	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120

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37	Cancer Risks Associated With Germline <i>PALB2</i> Pathogenic Variants: An International Study of 524 Families. <i>Journal of Clinical Oncology</i> , 2020, 38, 674-685.	0.8	270
38	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	1.1	82
39	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848.	2.6	39
40	Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 44.	2.3	5
41	Osteosarcoma and soft-tissue sarcomas with an immune infiltrate express PD-L1: relation to clinical outcome and Th1 pathway activation. <i>Oncotarget</i> , 2020, 9, 1737385.	2.1	23
42	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.	9.4	265
43	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	1.6	2
44	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	3.4	48
45	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	0.6	32
46	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers: Results from The BRCA1 and BRCA2 Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 368-378.	1.1	24
47	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	5.8	30
48	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2020, 22, 8.	2.2	41
49	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	2.3	28
50	Two truncating variants in FANCC and breast cancer risk. <i>Scientific Reports</i> , 2019, 9, 12524.	1.6	5
51	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
52	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. <i>British Journal of Cancer</i> , 2019, 121, 180-192.	2.9	19
53	Authors' response: Associations of obesity and circulating insulin and glucose with breast cancer risk. <i>International Journal of Epidemiology</i> , 2019, 48, 1016-1017.	0.9	1
54	<i>BRCA1</i> and <i>BRCA2</i> pathogenic sequence variants in women of African origin or ancestry. <i>Human Mutation</i> , 2019, 40, 1781-1796.	1.1	26

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55	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	5.8	90
56	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	2.9	52
57	The association between weight at birth and breast cancer risk revisited using Mendelian randomisation. <i>European Journal of Epidemiology</i> , 2019, 34, 591-600.	2.5	16
58	10-year performance of four models of breast cancer risk: a validation study. <i>Lancet Oncology</i> , The, 2019, 20, 504-517.	5.1	116
59	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
60	Height and Body Mass Index as Modifiers of Breast Cancer Risk in <i>BRCA1</i> Mutation Carriers: A Mendelian Randomization Study. <i>Journal of the National Cancer Institute</i> , 2019, 111, 350-364.	3.0	30
61	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	0.9	81
62	The <i>BRCA2</i> c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. <i>Human Mutation</i> , 2018, 39, 729-741.	1.1	19
63	Comparison of methods to assess onset of breast development in the LEGACY Girls Study: methodological considerations for studies of breast cancer. <i>Breast Cancer Research</i> , 2018, 20, 33.	2.2	9
64	Identifying actionable variants using next generation sequencing in patients with a historical diagnosis of undifferentiated pleomorphic sarcoma. <i>International Journal of Cancer</i> , 2018, 142, 57-65.	2.3	23
65	Statistical challenges in high-dimensional molecular and genetic epidemiology. <i>Canadian Journal of Statistics</i> , 2018, 46, 24-40.	0.6	0
66	Genome-wide association study identifies the <i>GLDC</i> / <i>L33</i> locus associated with survival of osteosarcoma patients. <i>International Journal of Cancer</i> , 2018, 142, 1594-1601.	2.3	31
67	Age-specific breast cancer risk by body mass index and familial risk: prospective family study cohort (ProF-SC). <i>Breast Cancer Research</i> , 2018, 20, 132.	2.2	51
68	Assessment of PD-L1 expression across breast cancer molecular subtypes, in relation to mutation rate, <i>BRCA1</i> -like status, tumor-infiltrating immune cells and survival. <i>Oncolmmunology</i> , 2018, 7, e1509820.	2.1	80
69	Rearrangement bursts generate canonical gene fusions in bone and soft tissue tumors. <i>Science</i> , 2018, 361, .	6.0	121
70	Genetic susceptibility markers for a breast-colorectal cancer phenotype: Exploratory results from genome-wide association studies. <i>PLoS ONE</i> , 2018, 13, e0196245.	1.1	9
71	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.	0.4	54
72	Tumoral <i>BRD4</i> expression in lymph node-negative breast cancer: association with T-bet+ tumor-infiltrating lymphocytes and disease-free survival. <i>BMC Cancer</i> , 2018, 18, 750.	1.1	13

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73	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.	9.4	184
74	Germline Variation and Breast Cancer Incidence: A Gene-Based Association Study and Whole-Genome Prediction of Early-Onset Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1057-1064.	1.1	9
75	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. <i>Genetics in Medicine</i> , 2017, 19, 30-35.	1.1	53
76	Evaluation of copy-number variants as modifiers of breast and ovarian cancer risk for BRCA1 pathogenic variant carriers. <i>European Journal of Human Genetics</i> , 2017, 25, 432-438.	1.4	26
77	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.	9.4	426
78	Limited influence of germline genetic variation on all-cause mortality in women with early onset breast cancer: evidence from gene-based tests, single-marker regression, and whole-genome prediction. <i>Breast Cancer Research and Treatment</i> , 2017, 164, 707-717.	1.1	4
79	Risks of Breast, Ovarian, and Contralateral Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>JAMA - Journal of the American Medical Association</i> , 2017, 317, 2402.	3.8	1,898
80	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
81	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
82	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
83	Non-invasive optical spectroscopic monitoring of breast development during puberty. <i>Breast Cancer Research</i> , 2017, 19, 12.	2.2	14
84	Pubertal development in girls by breast cancer family history: the LEGACY girls cohort. <i>Breast Cancer Research</i> , 2017, 19, 69.	2.2	18
85	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. <i>Breast Cancer Research and Treatment</i> , 2017, 161, 117-134.	1.1	18
86	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
87	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	0.9	45
88	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. <i>Breast Cancer Research</i> , 2017, 19, 119.	2.2	43
89	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	0.8	152
90	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.	0.8	14

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91	<i>PHIP</i> - a novel candidate breast cancer susceptibility locus on 6q14.1. <i>Oncotarget</i> , 2017, 8, 102769-102782.	0.8	9
92	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.	0.8	31
93	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.	3.9	118
94	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. <i>PLoS ONE</i> , 2016, 11, e0158801.	1.1	10
95	ABRAXAS (FAM175A) and Breast Cancer Susceptibility: No Evidence of Association in the Breast Cancer Family Registry. <i>PLoS ONE</i> , 2016, 11, e0156820.	1.1	5
96	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	1.1	12
97	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	2.3	51
98	Patient survival and tumor characteristics associated with CHEK2:p.I157T findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98.	2.2	39
99	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , 2016, 18, 64.	2.2	31
100	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	2.2	43
101	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. <i>Cancer Causes and Control</i> , 2016, 27, 679-693.	0.8	21
102	Male breast cancer in BRCA1 and BRCA2 mutation carriers: pathology data from the Consortium of Investigators of Modifiers of BRCA1/2. <i>Breast Cancer Research</i> , 2016, 18, 15.	2.2	88
103	Histone H3K36 mutations promote sarcomagenesis through altered histone methylation landscape. <i>Science</i> , 2016, 352, 844-849.	6.0	327
104	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.	2.6	59
105	The genomic landscape of epithelioid sarcoma cell lines and tumours. <i>Journal of Pathology</i> , 2016, 238, 63-73.	2.1	43
106	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.	1.4	33
107	rs2735383, located at a microRNA binding site in the 3'UTR of NBS1, is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	1.6	2
108	Inheritance of deleterious mutations at both BRCA1 and BRCA2 in an international sample of 32,295 women. <i>Breast Cancer Research</i> , 2016, 18, 112.	2.2	42

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109	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
110	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
111	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.	1.6	19
112	Integrative analyses reveal signaling pathways underlying familial breast cancer susceptibility. <i>Molecular Systems Biology</i> , 2016, 12, 860.	3.2	14
113	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> <i>2</i> *110delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	152
114	Cohort Profile: The Breast Cancer Prospective Family Study Cohort (ProF-SC). <i>International Journal of Epidemiology</i> , 2016, 45, 683-692.	0.9	48
115	Validation of Intratumoral T-bet+ Lymphoid Cells as Predictors of Disease-Free Survival in Breast Cancer. <i>Cancer Immunology Research</i> , 2016, 4, 41-48.	1.6	25
116	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. <i>Human Molecular Genetics</i> , 2016, 25, 2256-2268.	1.4	106
117	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.	1.5	94
118	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.	9.4	125
119	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. <i>Human Genetics</i> , 2016, 135, 137-154.	1.8	8
120	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv315.	3.0	77
121	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	0.6	18
122	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	1.1	26
123	Gene-expression patterns in peripheral blood classify familial breast cancer susceptibility. <i>BMC Medical Genomics</i> , 2015, 8, 72.	0.7	13
124	An original phylogenetic approach identified mitochondrial haplogroup T1a1 as inversely associated with breast cancer risk in BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2015, 17, 61.	2.2	26
125	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	2.2	26
126	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. <i>Breast Cancer Research</i> , 2015, 17, 110.	2.2	19

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127	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv279.	3.0	152
128	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. <i>PLoS ONE</i> , 2015, 10, e0120020.	1.1	34
129	Atypical Protein Kinase C Zeta: Potential Player in Cell Survival and Cell Migration of Ovarian Cancer. <i>PLoS ONE</i> , 2015, 10, e0123528.	1.1	19
130	SNP-SNP interaction analysis of NF- κ B signaling pathway on breast cancer survival. <i>Oncotarget</i> , 2015, 6, 37979-37994.	0.8	20
131	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
132	Psychosocial Adjustment in School-age Girls With a Family History of Breast Cancer. <i>Pediatrics</i> , 2015, 136, 927-937.	1.0	13
133	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	1.4	40
134	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.	2.6	76
135	A high-resolution copy-number variation resource for clinical and population genetics. <i>Genetics in Medicine</i> , 2015, 17, 747-752.	1.1	73
136	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.	1.3	14
137	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221
138	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.	9.4	513
139	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	1.4	128
140	Polymorphisms in a Putative Enhancer at the 10q21.2 Breast Cancer Risk Locus Regulate NRBF2 Expression. <i>American Journal of Human Genetics</i> , 2015, 97, 22-34.	2.6	37
141	A Genome-Wide Scan Identifies Variants in <i>NFIB</i> Associated with Metastasis in Patients with Osteosarcoma. <i>Cancer Discovery</i> , 2015, 5, 920-931.	7.7	88
142	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
143	Germline TP53 Variants and Susceptibility to Osteosarcoma. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	109
144	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. <i>Cancer Research</i> , 2015, 75, 2457-2467.	0.4	55

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145	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
146	Menacalc, a quantitative method of metastasis assessment, as a prognostic marker for axillary node-negative breast cancer. <i>BMC Cancer</i> , 2015, 15, 483.	1.1	27
147	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	3.0	99
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