Montserrat Garcia-Closas

List of Publications by Year
in descending order

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434 papers	41,777 citations	2975 93 h-index	3487 182 g-index
472 all docs	472 docs citations	472 times ranked	39486 citing authors

#	Article	IF	Citations
1	Relation of circulating estrogens with hair relaxer and skin lightener use among postmenopausal women in Ghana. Journal of Exposure Science and Environmental Epidemiology, 2023, 33, 301-310.	3.9	3
2	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	1.9	43
3	Gene-Level Germline Contributions to Clinical Risk of Recurrence Scores in Black and White Patients with Breast Cancer. Cancer Research, 2022, 82, 25-35.	0.9	10
4	TP53 Pathway Function, Estrogen Receptor Status, and Breast Cancer Risk Factors in the Carolina Breast Cancer Study. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 124-131.	2.5	2
5	Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65.	4.4	6
6	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
7	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
8	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study. Breast Cancer Research, 2022, 24, 9.	5.0	4
9	A Genome-Wide Gene-Based Geneâ€“Environment Interaction Study of Breast Cancer in More than 90,000 Women. Cancer Research Communications, 2022, 2, 211-219.	1.7	6
10	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
11	Polygenic risk scores for prediction of breast cancer risk in women of African ancestry: a cross-ancestry approach. Human Molecular Genetics, 2022, 31, 3133-3143.	2.9	11
12	Disinfection By-Products in Drinking Water and Bladder Cancer: Evaluation of Risk Modification by Common Genetic Polymorphisms in Two Caseâ€“Control Studies. Environmental Health Perspectives, 2022, 130, 57006.	6.0	5
13	Towards implementation of comprehensive breast cancer risk prediction tools in health care for personalised prevention. Preventive Medicine, 2022, 159, 107075.	3.4	3
14	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
15	The case for increasing diversity in tissue-based functional genomics datasets to understand human disease susceptibility. Nature Communications, 2022, 13, .	12.8	8
16	Distinct Reproductive Risk Profiles for Intrinsic-Like Breast Cancer Subtypes: Pooled Analysis of Population-Based Studies. Journal of the National Cancer Institute, 2022, 114, 1706-1719.	6.3	14
17	Prognostic significance of RNA-based TP53 pathway function among estrogen receptor positive and negative breast cancer cases. Npj Breast Cancer, 2022, 8, .	5.2	1
18	Breast Cancer Risk in Women from Ghana Carrying Rare Germline Pathogenic Mutations. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1593-1601.	2.5	3

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19	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
20	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
21	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. American Journal of Epidemiology, 2021, 190, 962-976.	3.4	16
22	Impact of Population Growth and Aging on Estimates of Excess U.S. Deaths During the COVID-19 Pandemic, March to August 2020. Annals of Internal Medicine, 2021, 174, 437-443.	3.9	40
23	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
24	Browser-based Data Annotation, Active Learning, and Real-Time Distribution of Artificial Intelligence Models: From Tumor Tissue Microarrays to COVID-19 Radiology. Journal of Pathology Informatics, 2021, 12, 38.	1.7	2
25	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078.	12.8	19
26	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. Genome Medicine, 2021, 13, 15.	8.2	15
27	Comparative validation of the BOADICEA and Tyrer-Cuzick breast cancer risk models incorporating classical risk factors and polygenic risk in a population-based prospective cohort of women of European ancestry. Breast Cancer Research, 2021, 23, 22.	5.0	49
28	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	27.0	532
29	Associations of fecal microbial profiles with breast cancer and nonmalignant breast disease in the Ghana Breast Health Study. International Journal of Cancer, 2021, 148, 2712-2723.	5.1	33
30	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. Journal of the National Cancer Institute, 2021, 113, 1168-1176.	6.3	41
31	Targeted Deep Sequencing of Bladder Tumors Reveals Novel Associations between Cancer Gene Mutations and Mutational Signatures with Major Risk Factors. Clinical Cancer Research, 2021, 27, 3725-3733.	7.0	11
32	Tumor-Associated Stromal Cellular Density as a Predictor of Recurrence and Mortality in Breast Cancer: Results from Ethnically Diverse Study Populations. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1397-1407.	2.5	7
33	Impact of breast cancer risk factors on clinically relevant prognostic biomarkers for primary breast cancer. Breast Cancer Research and Treatment, 2021, 189, 483-495.	2.5	6
34	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. Nature Communications, 2021, 12, 4198.	12.8	24
35	Abstract 81: Studying Ghanian Cancer Genomes Using Cell-free DNA. , 2021, , .		0
36	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

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37	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	3.8	18
38	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
39	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data fromâ€‰>â€‰2000 women of African-ancestry. Human Genetics, 2021, 140, 1449-1457.	3.8	4
40	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145.	6.4	9
41	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	27.8	183
42	Circulating tumor DNA is readily detectable among Ghanaian breast cancer patients supporting non-invasive cancer genomic studies in Africa. Npj Precision Oncology, 2021, 5, 83.	5.4	4
43	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	21.4	81
44	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
45	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
46	Racial and Ethnic Disparities in Excess Deaths During the COVID-19 Pandemic, March to December 2020. Annals of Internal Medicine, 2021, 174, 1693-1699.	3.9	93
47	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients. Human Genetics and Genomics Advances, 2021, 3, 100076.	1.7	3
48	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. Journal of the National Cancer Institute, 2020, 112, 278-285.	6.3	61
49	Assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk, in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2020, 49, 216-232.	1.9	21
50	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138.	5.1	13
51	Toward Risk-Stratified Breast Cancer Screening: Considerations for Changes in Screening Guidelines. JAMA Oncology, 2020, 6, 31.	7.1	11
52	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
53	Diesel exhaust and bladder cancer risk by pathologic stage and grade subtypes. Environment International, 2020, 135, 105346.	10.0	25
54	Combined Utility of 25 Disease and Risk Factor Polygenic Risk Scores for Stratifying Risk of All-Cause Mortality. American Journal of Human Genetics, 2020, 107, 418-431.	6.2	55

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55	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 2020, 52, 1219-1226.	21.4	367
56	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848.	6.2	39
57	Polygenic risk score for the prediction of breast cancer is related to lesser terminal duct lobular unit involution of the breast. Npj Breast Cancer, 2020, 6, 41.	5.2	5
58	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
59	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	27.6	178
60	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2
61	A mixed-model approach for powerful testing of genetic associations with cancer risk incorporating tumor characteristics. Biostatistics, 2020, 22, 772-788.	1.5	11
62	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. Nature Communications, 2020, 11, 1217.	12.8	46
63	Cancer Informatics for Cancer Centers (CI4CC): Building a Community Focused on Sharing Ideas and Best Practices to Improve Cancer Care and Patient Outcomes. JCO Clinical Cancer Informatics, 2020, 4, 108-116.	2.1	3
64	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
65	iCARE: An R package to build, validate and apply absolute risk models. PLoS ONE, 2020, 15, e0228198.	2.5	61
66	Reproductive factors and risk of breast cancer by tumor subtypes among Ghanaian women: A populationâ€based caseâ€“control study. International Journal of Cancer, 2020, 147, 1535-1547.	5.1	28
67	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. Genome Biology, 2020, 21, 42.	8.8	60
68	Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468.	1.3	32
69	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
70	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434.	2.5	14
71	Abstract 2320: Evaluating a polygenic risk score for breast cancer in women of African ancestry. , 2020, , .		1
72	Abstract 4613: Cross-ancestry genome-wide association study identifies six new loci for breast cancer in women of African and european ancestry. , 2020, , .		1

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73	The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38.	5.2	28
74	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
75	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
76	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. PLoS ONE, 2019, 14, e0215347.	2.5	14
77	A combination of the immunohistochemical markers CK7 and SATB2 is highly sensitive and specific for distinguishing primary ovarian mucinous tumors from colorectal and appendiceal metastases. Modern Pathology, 2019, 32, 1834-1846.	5.5	54
78	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. Breast Cancer Research, 2019, 21, 62.	5.0	34
79	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	12.8	90
80	Detectible mosaic truncating PPM1D mutations, age and breast cancer risk. Journal of Human Genetics, 2019, 64, 545-550.	2.3	6
81	Combined quantitative measures of ER, PR, HER2, and KI67 provide more prognostic information than categorical combinations in luminal breast cancer. Modern Pathology, 2019, 32, 1244-1256.	5.5	51
82	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
83	Assessment of breast cancer risk: which tools to use?. Lancet Oncology, The, 2019, 20, 463-464.	10.7	9
84	A response to â€œPersonalised medicine and population health: breast and ovarian cancerâ€• Human Genetics, 2019, 138, 287-289.	3.8	14
85	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. Breast Cancer Research, 2019, 21, 147.	5.0	43
86	Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144.	5.0	24
87	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
88	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	2.4	415
89	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
90	Reply to â€˜Mosaic loss of chromosome Y in leukocytes mattersâ€™. Nature Genetics, 2019, 51, 7-9.	21.4	7

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91	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
92	The BRCA2 c.68-7TÂ>ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741.	2.5	19
93	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
94	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
95	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
96	RE: Elevated Bladder Cancer in Northern New England: The Role of Drinking Water and Arsenic. Journal of the National Cancer Institute, 2018, 110, 1273-1274.	6.3	1
97	Asthma status is associated with decreased risk of aggressive urothelial bladder cancer. International Journal of Cancer, 2018, 142, 470-476.	5.1	10
98	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. Cancer Research, 2018, 78, 6011-6021.	0.9	67
99	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	3.0	70
100	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
101	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
102	Oncologic Therapy for Solid Tumors Alters the Risk of Clonal Hematopoiesis. Blood, 2018, 132, 747-747.	1.4	3
103	Relationship between crown-like structures and sex-steroid hormones in breast adipose tissue and serum among postmenopausal breast cancer patients. Breast Cancer Research, 2017, 19, 8.	5.0	58
104	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
105	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
106	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
107	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. Carcinogenesis, 2017, 38, 1167-1179.	2.8	18
108	Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840.	5.1	20

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109	Lessons Learned From Past Gene-Environment Interaction Successes. American Journal of Epidemiology, 2017, 186, 778-786.	3.4	53
110	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. International Journal of Cancer, 2017, 140, 825-832.	5.1	9
111	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	2.4	67
112	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
113	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119.	5.0	43
114	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
115	PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782.	1.8	9
116	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
117	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
118	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
119	Association of Active and Sedentary Behaviors with Postmenopausal Estrogen Metabolism. Medicine and Science in Sports and Exercise, 2016, 48, 439-448.	0.4	27
120	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
121	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
122	Patient survival and tumor characteristics associated with CHEK2:p.I157T â€“ findings from the Breast Cancer Association Consortium. Breast Cancer Research, 2016, 18, 98.	5.0	39
123	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
124	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. Breast Cancer Research, 2016, 18, 124.	5.0	52
125	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	7.1	285
126	Inflammatory-Related Genetic Variants in Nonâ€“Muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1144-1150.	2.5	8

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127	Lifetime Number of Ovulatory Cycles and Risks of Ovarian and Endometrial Cancer Among Postmenopausal Women. American Journal of Epidemiology, 2016, 183, 800-814.	3.4	41
128	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
129	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
130	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	21.4	134
131	Developing and evaluating polygenic risk prediction models for stratified disease prevention. Nature Reviews Genetics, 2016, 17, 392-406.	16.3	559
132	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
133	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
134	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. British Journal of Cancer, 2016, 115, 752-760.	6.4	16
135	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
136	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
137	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. Nature Genetics, 2016, 48, 1330-1338.	21.4	161
138	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
139	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
140	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
141	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
142	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
143	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
144	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152

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145	Ages at menarche- and menopause-related genetic variants in relation to terminal duct lobular unit involution in normal breast tissue. Breast Cancer Research and Treatment, 2016, 158, 341-350.	2.5	5
146	Highâ€tthroughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	3.0	19
147	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. Human Molecular Genetics, 2016, 25, ddw092.	2.9	19
148	Response. Journal of the National Cancer Institute, 2016, 108, djv441.	6.3	0
149	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. Human Molecular Genetics, 2016, 25, 1203-1214.	2.9	38
150	No evidence that protein truncating variants inBRIP1are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309.	3.2	94
151	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
152	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304.	6.4	7
153	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
154	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
155	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
156	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	3.5	98
157	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
158	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
159	Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58.	5.0	26
160	Epigenome-wide association study reveals decreased average methylation levels years before breast cancer diagnosis. Clinical Epigenetics, 2015, 7, 67.	4.1	95
161	Analysis of Heritability and Shared Heritability Based on Genome-Wide Association Studies for Thirteen Cancer Types. Journal of the National Cancer Institute, 2015, 107, djv279.	6.3	152
162	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762.	0.4	0

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163	Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. PLoS ONE, 2015, 10, e0143256.	2.5	13
164	SNP-SNP interaction analysis of NF-Î²B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994.	1.8	20
165	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
166	Mitochondrial DNA Copy Number in Peripheral Blood Cells and Risk of Developing Breast Cancer. Cancer Research, 2015, 75, 2844-2850.	0.9	40
167	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
168	Performance of automated scoring of ER, PR, HER2, CK5/6 and EGFR in breast cancer tissue microarrays in the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2015, 1, 18-32.	3.0	24
169	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	6.1	56
170	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
171	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
172	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	2.8	14
173	Infertility and incident endometrial cancer risk: a pooled analysis from the epidemiology of endometrial cancer consortium (E2C2). British Journal of Cancer, 2015, 112, 925-933.	6.4	41
174	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
175	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
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