

Montserrat Garcia-Closas

List of Publications by Year in descending order

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Version: 2024-02-01

434
papers

41,777
citations

3449

93
h-index

4035

182
g-index

472
all docs

472
docs citations

472
times ranked

42987
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007, 447, 1087-1093.	13.7	2,165
2	Assessing the Probability That a Positive Report is False: An Approach for Molecular Epidemiology Studies. <i>Journal of the National Cancer Institute</i> , 2004, 96, 434-442.	3.0	1,553
3	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
4	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	2.6	1,098
5	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	9.4	960
6	Subtyping of Breast Cancer by Immunohistochemistry to Investigate a Relationship between Subtype and Short and Long Term Survival: A Collaborative Analysis of Data for 10,159 Cases from 12 Studies. <i>PLoS Medicine</i> , 2010, 7, e1000279.	3.9	764
7	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
8	Type I and II Endometrial Cancers: Have They Different Risk Factors?. <i>Journal of Clinical Oncology</i> , 2013, 31, 2607-2618.	0.8	613
9	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. <i>Journal of the National Cancer Institute</i> , 2011, 103, 250-263.	3.0	596
10	A common coding variant in CASP8 is associated with breast cancer risk. <i>Nature Genetics</i> , 2007, 39, 352-358.	9.4	591
11	Developing and evaluating polygenic risk prediction models for stratified disease prevention. <i>Nature Reviews Genetics</i> , 2016, 17, 392-406.	7.7	559
12	NAT2 slow acetylation, GSTM1 null genotype, and risk of bladder cancer: results from the Spanish Bladder Cancer Study and meta-analyses. <i>Lancet, The</i> , 2005, 366, 649-659.	6.3	558
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
14	Association Between <i>BRCA1</i> and <i>BRCA2</i> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. <i>JAMA - Journal of the American Medical Association</i> , 2012, 307, 382.	3.8	546
15	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
16	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012, 44, 651-658.	9.4	519
17	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
18	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. <i>Nature Genetics</i> , 2010, 42, 978-984.	9.4	493

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19	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	9.4	493
20	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). <i>Nature Genetics</i> , 2009, 41, 579-584.	9.4	487
21	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009, 41, 585-590.	9.4	434
22	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
23	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. <i>Genetics in Medicine</i> , 2019, 21, 1708-1718.	1.1	415
24	Differences in Risk Factors for Breast Cancer Molecular Subtypes in a Population-Based Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 439-443.	1.1	394
25	Performance of Common Genetic Variants in Breast-Cancer Risk Models. <i>New England Journal of Medicine</i> , 2010, 362, 986-993.	13.9	376
26	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	9.4	374
27	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. <i>Nature Genetics</i> , 2020, 52, 1219-1226.	9.4	367
28	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
29	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. <i>Lancet Oncology</i> , The, 2013, 14, 853-862.	5.1	335
30	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
31	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. <i>Nature Genetics</i> , 2010, 42, 874-879.	9.4	321
32	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. <i>Breast Cancer Research</i> , 2013, 15, R92.	2.2	320
33	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	1.5	315
34	Etiology of hormone receptor-defined breast cancer: a systematic review of the literature. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2004, 13, 1558-68.	1.1	299
35	Genetic susceptibility to breast cancer. <i>Molecular Oncology</i> , 2010, 4, 174-191.	2.1	291
36	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289

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37	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	3.4	285
38	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. <i>Nature Genetics</i> , 2009, 41, 996-1000.	9.4	276
39	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
40	Genome-wide association analysis identifies three new breast cancer susceptibility loci. <i>Nature Genetics</i> , 2012, 44, 312-318.	9.4	256
41	Risk determination and prevention of breast cancer. <i>Breast Cancer Research</i> , 2014, 16, 446.	2.2	248
42	Common variants at 19p13 are associated with susceptibility to ovarian cancer. <i>Nature Genetics</i> , 2010, 42, 880-884.	9.4	235
43	Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a case-control study. <i>Lancet Oncology</i> , The, 2008, 9, 359-366.	5.1	211
44	Pooled Analysis and Meta-analysis of Glutathione S-Transferase M1 and Bladder Cancer: A HuGE Review. <i>American Journal of Epidemiology</i> , 2002, 156, 95-109.	1.6	209
45	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	2.6	201
46	Polymorphisms in <i>GSTT1</i> , <i>GSTZ1</i> , and <i>CYP2E1</i> , Disinfection By-products, and Risk of Bladder Cancer in Spain. <i>Environmental Health Perspectives</i> , 2010, 118, 1545-1550.	2.8	194
47	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
48	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
49	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
50	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	12.5	178
51	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	1.5	174
52	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. <i>Endocrine-Related Cancer</i> , 2013, 20, 251-262.	1.6	169
53	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , 2012, 21, 5373-5384.	1.4	168
54	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. <i>British Journal of Cancer</i> , 2012, 107, 800-807.	2.9	163

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55	<i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer-Specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316.	0.8	162
56	Association of germline variants in the APOBEC3 region with cancer risk and enrichment with APOBEC-signature mutations in tumors. <i>Nature Genetics</i> , 2016, 48, 1330-1338.	9.4	161
57	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	7.7	157
58	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 3289-3303.	1.4	152
59	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
60	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> 2*1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760.	0.8	152
61	Smoking and Bladder Cancer in Spain: Effects of Tobacco Type, Timing, Environmental Tobacco Smoke, and Gender. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 1348-1354.	1.1	148
62	Polymorphisms in DNA double-strand break repair genes and risk of breast cancer: two population-based studies in USA and Poland, and meta-analyses. <i>Human Genetics</i> , 2006, 119, 376-388.	1.8	144
63	Epigenetic analysis leads to identification of <i>HNF1B</i> as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	5.8	144
64	Intragenic ATM Methylation in Peripheral Blood DNA as a Biomarker of Breast Cancer Risk. <i>Cancer Research</i> , 2012, 72, 2304-2313.	0.4	142
65	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. <i>Nature Genetics</i> , 2011, 43, 451-454.	9.4	141
66	Genetic Variation in the Nucleotide Excision Repair Pathway and Bladder Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 536-542.	1.1	139
67	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014, 23, 1387-1398.	1.4	137
68	Evidence of Gene-Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. <i>PLoS Genetics</i> , 2013, 9, e1003284.	1.5	136
69	Mosaic loss of chromosome Y is associated with common variation near <i>TCL1A</i> . <i>Nature Genetics</i> , 2016, 48, 563-568.	9.4	134
70	Genetic Polymorphisms in Base-Excision Repair Pathway Genes and Risk of Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 353-358.	1.1	132
71	Established breast cancer risk factors by clinically important tumour characteristics. <i>British Journal of Cancer</i> , 2006, 95, 123-129.	2.9	127
72	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

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73	A prospective study of NAT2 acetylation genotype, cigarette smoking, and risk of breast cancer. <i>Carcinogenesis</i> , 1997, 18, 2127-2132.	1.3	122
74	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
75	Large-Scale Evaluation of Candidate Genes Identifies Associations between VEGF Polymorphisms and Bladder Cancer Risk. <i>PLoS Genetics</i> , 2007, 3, e29.	1.5	119
76	Intrauterine environments and breast cancer risk: meta-analysis and systematic review. <i>Breast Cancer Research</i> , 2008, 10, R8.	2.2	118
77	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
78	Food, nutrient and heterocyclic amine intake and the risk of bladder cancer. <i>European Journal of Cancer</i> , 2007, 43, 1731-1740.	1.3	117
79	Genetic Susceptibility Loci for Breast Cancer by Estrogen Receptor Status. <i>Clinical Cancer Research</i> , 2008, 14, 8000-8009.	3.2	115
80	Genetic variation in the base excision repair pathway and bladder cancer risk. <i>Human Genetics</i> , 2007, 121, 233-242.	1.8	113
81	Pathway Analysis of Breast Cancer Genome-Wide Association Study Highlights Three Pathways and One Canonical Signaling Cascade. <i>Cancer Research</i> , 2010, 70, 4453-4459.	0.4	112
82	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. <i>American Journal of Human Genetics</i> , 2010, 87, 129-138.	2.6	111
83	DNA Banking for Epidemiologic Studies: A Review of Current Practices. <i>Epidemiology</i> , 2002, 13, 246-254.	1.2	110
84	GSTM1 null and NAT2 slow acetylation genotypes, smoking intensity and bladder cancer risk: results from the New England bladder cancer study and NAT2 meta-analysis. <i>Carcinogenesis</i> , 2011, 32, 182-189.	1.3	110
85	Genetic polymorphisms in the one-carbon metabolism pathway and breast cancer risk: A population-based case-control study and meta-analyses. <i>International Journal of Cancer</i> , 2007, 120, 2696-2703.	2.3	107
86	Polymorphisms in DNA Repair Genes, Smoking, and Bladder Cancer Risk: Findings from the International Consortium of Bladder Cancer. <i>Cancer Research</i> , 2009, 69, 6857-6864.	0.4	107
87	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. <i>Cancer Research</i> , 2013, 73, 2211-2220.	0.4	107
88	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	1.5	105
89	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	5.8	105
90	Combined Associations of Genetic and Environmental Risk Factors: Implications for Prevention of Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2014, 106, dju305-dju305.	3.0	101

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91	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	2.6	101
92	A genome-wide association study of bladder cancer identifies a new susceptibility locus within SLC14A1, a urea transporter gene on chromosome 18q12.3. <i>Human Molecular Genetics</i> , 2011, 20, 4282-4289.	1.4	100
93	19p13.1 Is a Triple-Negative-Specific Breast Cancer Susceptibility Locus. <i>Cancer Research</i> , 2012, 72, 1795-1803.	0.4	100
94	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.4	100
95	Risk of Estrogen Receptor-Positive and -Negative Breast Cancer and Single-Nucleotide Polymorphism 2q35-rs13387042. <i>Journal of the National Cancer Institute</i> , 2009, 101, 1012-1018.	3.0	99
96	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. <i>Nature Genetics</i> , 2012, 44, 1182-1184.	9.4	99
97	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
98	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	98
99	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. <i>Nature Communications</i> , 2013, 4, 1627.	5.8	98
100	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. <i>PLoS Genetics</i> , 2016, 12, e1006493.	1.5	98
101	Epigenome-wide association study reveals decreased average methylation levels years before breast cancer diagnosis. <i>Clinical Epigenetics</i> , 2015, 7, 67.	1.8	95
102	Relationship between serum hormone concentrations, reproductive history, alcohol consumption and genetic polymorphisms in pre-menopausal women. <i>International Journal of Cancer</i> , 2002, 102, 172-178.	2.3	94
103	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
104	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	5.8	93
105	Racial and Ethnic Disparities in Excess Deaths During the COVID-19 Pandemic, March to December 2020. <i>Annals of Internal Medicine</i> , 2021, 174, 1693-1699.	2.0	93
106	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	1.4	90
107	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
108	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. <i>Carcinogenesis</i> , 2008, 29, 1955-1962.	1.3	88

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109	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 526-536.	0.9	88
110	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
111	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. <i>Carcinogenesis</i> , 2007, 28, 1788-1793.	1.3	87
112	A case-control study of cytochrome P450 1A1, glutathione S-transferase M1, cigarette smoking and lung cancer susceptibility (Massachusetts, United States). <i>Cancer Causes and Control</i> , 1997, 8, 544-553.	0.8	86
113	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	5.8	86
114	Risk of Bladder Cancer Associated with Family History of Cancer: Do Low-Penetrance Polymorphisms Account for the Increase in Risk?. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 1595-1600.	1.1	85
115	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139.	1.4	84
116	Assessing interactions between the associations of common genetic susceptibility variants, reproductive history and body mass index with breast cancer risk in the breast cancer association consortium: a combined case-control study. <i>Breast Cancer Research</i> , 2010, 12, R110.	2.2	82
117	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
118	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021, 53, 1348-1359.	9.4	81
119	Glutathione S-Transferase Mu and Theta Polymorphisms and Breast Cancer Susceptibility. <i>Journal of the National Cancer Institute</i> , 1999, 91, 1960-1964.	3.0	80
120	The role of genetic breast cancer susceptibility variants as prognostic factors. <i>Human Molecular Genetics</i> , 2012, 21, 3926-3939.	1.4	80
121	Common genetic variants in the <i>PSCA</i> gene influence gene expression and bladder cancer risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4974-4979.	3.3	79
122	Differential Misclassification and the Assessment of Gene-Environment Interactions in Case-Control Studies. <i>American Journal of Epidemiology</i> , 1998, 147, 426-433.	1.6	78
123	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2007, 67, 3027-3035.	0.4	78
124	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
125	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
126	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

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127	<i>ESR1/SYNE1</i> Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 245-250.	1.1	75
128	<i>LIN28B</i> Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2011, 71, 3896-3903.	0.4	75
129	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. <i>Environmental Health Perspectives</i> , 2013, 121, 650-656.	2.8	75
130	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. <i>Cancer Research</i> , 2017, 77, 2789-2799.	0.4	75
131	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	5.8	75
132	Cigarette Smoking and Cancer Risk: Modeling Total Exposure and Intensity. <i>American Journal of Epidemiology</i> , 2007, 166, 479-489.	1.6	73
133	Consortium analysis of 7 candidate SNPs for ovarian cancer. <i>International Journal of Cancer</i> , 2008, 123, 380-388.	2.3	73
134	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	1.4	71
135	Replication and Functional Genomic Analyses of the Breast Cancer Susceptibility Locus at 6q25.1 Generalize Its Importance in Women of Chinese, Japanese, and European Ancestry. <i>Cancer Research</i> , 2011, 71, 1344-1355.	0.4	71
136	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. <i>Human Molecular Genetics</i> , 2012, 21, 1918-1930.	1.4	71
137	Genetic variation in five genes important in telomere biology and risk for breast cancer. <i>British Journal of Cancer</i> , 2007, 97, 832-836.	2.9	70
138	Association of p16 expression with prognosis varies across ovarian carcinoma histotypes: an Ovarian Tumor Tissue Analysis consortium study. <i>Journal of Pathology: Clinical Research</i> , 2018, 4, 250-261.	1.3	70
139	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603.	1.1	67
140	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. <i>Cancer Research</i> , 2018, 78, 6011-6021.	0.4	67
141	Comparison of yield and genotyping performance of multiple displacement amplification and OmniPlex, whole genome amplified DNA generated from multiple DNA sources. <i>Human Mutation</i> , 2005, 26, 262-270.	1.1	63
142	Total Fluid and Water Consumption and the Joint Effect of Exposure to Disinfection By-Products on Risk of Bladder Cancer. <i>Environmental Health Perspectives</i> , 2007, 115, 1569-1572.	2.8	63
143	Single Nucleotide Polymorphisms in the <i>TP53</i> Region and Susceptibility to Invasive Epithelial Ovarian Cancer. <i>Cancer Research</i> , 2009, 69, 2349-2357.	0.4	63
144	Genetic Susceptibility to Distinct Bladder Cancer Subphenotypes. <i>European Urology</i> , 2010, 57, 283-292.	0.9	63

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145	Genetic variation in tumor necrosis factor and lymphotoxin-alpha (TNF- α -LTA) and breast cancer risk. <i>Human Genetics</i> , 2007, 121, 483-490.	1.8	62
146	Discovery and validation of methylation markers for endometrial cancer. <i>International Journal of Cancer</i> , 2014, 135, 1860-1868.	2.3	62
147	Two Estrogen-Related Variants in <i>CYP19A1</i> and Endometrial Cancer Risk: A Pooled Analysis in the Epidemiology of Endometrial Cancer Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 242-247.	1.1	61
148	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. <i>Journal of the National Cancer Institute</i> , 2020, 112, 278-285.	3.0	61
149	iCARE: An R package to build, validate and apply absolute risk models. <i>PLoS ONE</i> , 2020, 15, e0228198.	1.1	61
150	Polymorphisms in one-carbon metabolism and trans-sulfuration pathway genes and susceptibility to bladder cancer. <i>International Journal of Cancer</i> , 2007, 120, 2452-2458.	2.3	60
151	DNA Hypermethylation of <i>ESR1</i> and <i>PGR</i> in Breast Cancer: Pathologic and Epidemiologic Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 3036-3043.	1.1	60
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