Montserrat Garcia-Closas

List of Publications by Year
in descending order

434 papers	41,777 citations	2963 93 h-index	3476 182 g-index
472 all docs	472 docs citations	472 times ranked	39486 citing authors

#	Article	IF	Citations
1	Genome-wide association study identifies novel breast cancer susceptibility loci. Nature, 2007, 447, 1087-1093.	13.7	2,165
2	Assessing the Probability That a Positive Report is False: An Approach for Molecular Epidemiology Studies. Journal of the National Cancer Institute, 2004, 96, 434-442.	3.0	1,553
3	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
4	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
5	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 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. PLoS Medicine, 2010, 7, e1000279.	3.9	764
7	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
8	Type I and II Endometrial Cancers: Have They Different Risk Factors?. Journal of Clinical Oncology, 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. Journal of the National Cancer Institute, 2011, 103, 250-263.	3.0	596
10	A common coding variant in CASP8 is associated with breast cancer risk. Nature Genetics, 2007, 39, 352-358.	9.4	591
11	Developing and evaluating polygenic risk prediction models for stratified disease prevention. Nature Reviews Genetics, 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. Lancet, The, 2005, 366, 649-659.	6.3	558
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
14	Association Between <emph type="ital">BRCA1</emph> and <emph type="ital">BRCA2</emph> Mutations and Survival in Women With Invasive Epithelial Ovarian Cancer. JAMA - Journal of the American Medical Association, 2012, 307, 382.	3.8	546
15	Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439.	13.9	532
16	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 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. Nature Genetics, 2015, 47, 373-380.	9.4	513
18	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. Nature Genetics, 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. Nature Genetics, 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). Nature Genetics, 2009, 41, 579-584.	9.4	487
21	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
22	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
23	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. Genetics in Medicine, 2019, 21, 1708-1718.	1.1	415
24	Differences in Risk Factors for Breast Cancer Molecular Subtypes in a Population-Based Study. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 439-443.	1.1	394
25	Performance of Common Genetic Variants in Breast-Cancer Risk Models. New England Journal of Medicine, 2010, 362, 986-993.	13.9	376
26	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
27	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. Nature Genetics, 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. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
29	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. Lancet Oncology, The, 2013, 14, 853-862.	5.1	335
30	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. Nature Genetics, 2013, 45, 362-370.	9.4	326
31	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. Nature Genetics, 2010, 42, 874-879.	9.4	321
32	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. Breast Cancer Research, 2013, 15, R92.	2.2	320
33	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
34	Etiology of hormone receptor-defined breast cancer: a systematic review of the literature. Cancer Epidemiology Biomarkers and Prevention, 2004, 13, 1558-68.	1.1	299
35	Genetic susceptibility to breast cancer. Molecular Oncology, 2010, 4, 174-191.	2.1	291
36	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 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. JAMA Oncology, 2016, 2, 1295.	3.4	285
38	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. Nature Genetics, 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. Nature Genetics, 2020, 52, 572-581.	9.4	265
40	Genome-wide association analysis identifies three new breast cancer susceptibility loci. Nature Genetics, 2012, 44, 312-318.	9.4	256
41	Risk determination and prevention of breast cancer. Breast Cancer Research, 2014, 16, 446.	2.2	248
42	Common variants at 19p13 are associated with susceptibility to ovarian cancer. Nature Genetics, 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 caseâ€“control study. Lancet Oncology, 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. American Journal of Epidemiology, 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. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
46	Polymorphisms in GSTT1 , GSTZ1 , and CYP2E1 , Disinfection By-products, and Risk of Bladder Cancer in Spain. Environmental Health Perspectives, 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. Nature Genetics, 2018, 50, 968-978.	9.4	184
48	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
49	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178
50	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. Nature Reviews Clinical Oncology, 2020, 17, 687-705.	12.5	178
51	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
52	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. Endocrine-Related Cancer, 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. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
54	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. British Journal of Cancer, 2012, 107, 800-807.	2.9	163

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55	CHEK2*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.	0.8	162
56	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.	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. Cancer Discovery, 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. Human Molecular Genetics, 2011, 20, 3289-3303.	1.4	152
59	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.	3.0	152
60	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	0.8	152
61	Smoking and Bladder Cancer in Spain: Effects of Tobacco Type, Timing, Environmental Tobacco Smoke, and Gender. Cancer Epidemiology Biomarkers and Prevention, 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. Human Genetics, 2006, 119, 376-388.	1.8	144
63	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. Nature Communications, 2013, 4, 1628.	5.8	144
64	Intragenic ATM Methylation in Peripheral Blood DNA as a Biomarker of Breast Cancer Risk. Cancer Research, 2012, 72, 2304-2313.	0.4	142
65	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. Nature Genetics, 2011, 43, 451-454.	9.4	141
66	Genetic Variation in the Nucleotide Excision Repair Pathway and Bladder Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 536-542.	1.1	139
67	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
68	Evidence of Geneâ€“Environment Interactions between Common Breast Cancer Susceptibility Loci and Established Environmental Risk Factors. PLoS Genetics, 2013, 9, e1003284.	1.5	136
69	Mosaic loss of chromosome Y is associated with common variation near TCL1A. Nature Genetics, 2016, 48, 563-568.	9.4	134
70	Genetic Polymorphisms in Base-Excision Repair Pathway Genes and Risk of Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 353-358.	1.1	132
71	Established breast cancer risk factors by clinically important tumour characteristics. British Journal of Cancer, 2006, 95, 123-129.	2.9	127
72	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 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. Carcinogenesis, 1997, 18, 2127-2132.	1.3	122
74	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
75	Large-Scale Evaluation of Candidate Genes Identifies Associations between VEGF Polymorphisms and Bladder Cancer Risk. PLoS Genetics, 2007, 3, e29.	1.5	119
76	Intrauterine environments and breast cancer risk: meta-analysis and systematic review. Breast Cancer Research, 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. PLoS Medicine, 2016, 13, e1002105.	3.9	118
78	Food, nutrient and heterocyclic amine intake and the risk of bladder cancer. European Journal of Cancer, 2007, 43, 1731-1740.	1.3	117
79	Genetic Susceptibility Loci for Breast Cancer by Estrogen Receptor Status. Clinical Cancer Research, 2008, 14, 8000-8009.	3.2	115
80	Genetic variation in the base excision repair pathway and bladder cancer risk. Human Genetics, 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. Cancer Research, 2010, 70, 4453-4459.	0.4	112
82	Mosaic Uniparental Disomies and Aneuploidies as Large Structural Variants of the Human Genome. American Journal of Human Genetics, 2010, 87, 129-138.	2.6	111
83	DNA Banking for Epidemiologic Studies: A Review of Current Practices. Epidemiology, 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. Carcinogenesis, 2011, 32, 182-189.	1.3	110
85	Genetic polymorphisms in the one-carbon metabolism pathway and breast cancer risk: A population-based caseâ€“control study and meta-analyses. International Journal of Cancer, 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. Cancer Research, 2009, 69, 6857-6864.	0.4	107
87	Common Genetic Polymorphisms Modify the Effect of Smoking on Absolute Risk of Bladder Cancer. Cancer Research, 2013, 73, 2211-2220.	0.4	107
88	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
89	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	5.8	105
90	Combined Associations of Genetic and Environmental Risk Factors: Implications for Prevention of Breast Cancer. Journal of the National Cancer Institute, 2014, 106, dju305-dju305.	3.0	101

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91	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 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. Human Molecular Genetics, 2011, 20, 4282-4289.	1.4	100
93	19p13.1 Is a Triple-Negativeâ€“Specific Breast Cancer Susceptibility Locus. Cancer Research, 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. Cancer Research, 2016, 76, 5103-5114.	0.4	100
95	Risk of Estrogen Receptorâ€“Positive and â€“Negative Breast Cancer and Singleâ€“Nucleotide Polymorphism 2q35-rs13387042. Journal of the National Cancer Institute, 2009, 101, 1012-1018.	3.0	99
96	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	9.4	99
97	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 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. American Journal of Human Genetics, 2013, 93, 1046-1060.	2.6	98
99	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. Nature Communications, 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. PLoS Genetics, 2016, 12, e1006493.	1.5	98
101	Epigenome-wide association study reveals decreased average methylation levels years before breast cancer diagnosis. Clinical Epigenetics, 2015, 7, 67.	1.8	95
102	Relationship between serum hormone concentrations, reproductive history, alcohol consumption and genetic polymorphisms in pre-menopausal women. International Journal of Cancer, 2002, 102, 172-178.	2.3	94
103	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.	1.5	94
104	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
105	Racial and Ethnic Disparities in Excess Deaths During the COVID-19 Pandemic, March to December 2020. Annals of Internal Medicine, 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. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
107	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
108	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. Carcinogenesis, 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. International Journal of Epidemiology, 2018, 47, 526-536.	0.9	88
110	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
111	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. Carcinogenesis, 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). Cancer Causes and Control, 1997, 8, 544-553.	0.8	86
113	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 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?. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 1595-1600.	1.1	85
115	Association of ESR1 gene tagging SNPs with breast cancer risk. Human Molecular Genetics, 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. Breast Cancer Research, 2010, 12, R110.	2.2	82
117	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
118	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	9.4	81
119	Glutathione S-Transferase Mu and Theta Polymorphisms and Breast Cancer Susceptibility. Journal of the National Cancer Institute, 1999, 91, 1960-1964.	3.0	80
120	The role of genetic breast cancer susceptibility variants as prognostic factors. Human Molecular Genetics, 2012, 21, 3926-3939.	1.4	80
121	Common genetic variants in the PSCA gene influence gene expression and bladder cancer risk. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4974-4979.	3.3	79
122	Differential Misclassification and the Assessment of Gene-Environment Interactions in Case-Control Studies. American Journal of Epidemiology, 1998, 147, 426-433.	1.6	78
123	Tagging Single Nucleotide Polymorphisms in Cell Cycle Control Genes and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2007, 67, 3027-3035.	0.4	78
124	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	5.8	78
125	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 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. American Journal of Human Genetics, 2015, 96, 5-20.	2.6	76

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127	ESR1/SYNE1 Polymorphism and Invasive Epithelial Ovarian Cancer Risk: An Ovarian Cancer Association Consortium Study. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 245-250.	1.1	75
128	LIN28B Polymorphisms Influence Susceptibility to Epithelial Ovarian Cancer. Cancer Research, 2011, 71, 3896-3903.	0.4	75
129	Genetic and Non-genetic Predictors of LINE-1 Methylation in Leukocyte DNA. Environmental Health Perspectives, 2013, 121, 650-656.	2.8	75
130	BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.4	75
131	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
132	Cigarette Smoking and Cancer Risk: Modeling Total Exposure and Intensity. American Journal of Epidemiology, 2007, 166, 479-489.	1.6	73
133	Consortium analysis of 7 candidate SNPs for ovarian cancer. International Journal of Cancer, 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 Consortiumâ€. Human Molecular Genetics, 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. Cancer Research, 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. Human Molecular Genetics, 2012, 21, 1918-1930.	1.4	71
137	Genetic variation in five genes important in telomere biology and risk for breast cancer. British Journal of Cancer, 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. Journal of Pathology: Clinical Research, 2018, 4, 250-261.	1.3	70
139	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603.	1.1	67
140	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. Cancer Research, 2018, 78, 6011-6021.	0.4	67
141	Comparison of yield and genotyping performance of multiple displacement amplification and OmniPlexâ„¢ whole genome amplified DNA generated from multiple DNA sources. Human Mutation, 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. Environmental Health Perspectives, 2007, 115, 1569-1572.	2.8	63
143	Single Nucleotide Polymorphisms in the TP53 Region and Susceptibility to Invasive Epithelial Ovarian Cancer. Cancer Research, 2009, 69, 2349-2357.	0.4	63
144	Genetic Susceptibility to Distinct Bladder Cancer Subphenotypes. European Urology, 2010, 57, 283-292.	0.9	63

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145	Genetic variation in tumor necrosis factor and lymphotoxin-alpha (TNFâ€“LTA) and breast cancer risk. Human Genetics, 2007, 121, 483-490.	1.8	62
146	Discovery and validation of methylation markers for endometrial cancer. International Journal of Cancer, 2014, 135, 1860-1868.	2.3	62
147	Two Estrogen-Related Variants in CYP19A1 and Endometrial Cancer Risk: A Pooled Analysis in the Epidemiology of Endometrial Cancer Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 242-247.	1.1	61
148	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. Journal of the National Cancer Institute, 2020, 112, 278-285.	3.0	61
149	iCARE: An R package to build, validate and apply absolute risk models. PLoS ONE, 2020, 15, e0228198.	1.1	61
150	Polymorphisms in one-carbon metabolism and trans-sulfuration pathway genes and susceptibility to bladder cancer. International Journal of Cancer, 2007, 120, 2452-2458.	2.3	60
151	DNA Hypermethylation ofESR1andPGRin Breast Cancer: Pathologic and Epidemiologic Associations. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3036-3043.	1.1	60
152	Temporal Stability and Determinants of White Blood Cell DNA Methylation in the Breakthrough Generations Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 221-229.	1.1	60
153	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. Genome Biology, 2020, 21, 42.	3.8	60
154	A single nucleotide polymorphism tags variation in the arylamine N-acetyltransferase 2 phenotype in populations of European background. Pharmacogenetics and Genomics, 2011, 21, 231-236.	0.7	60
155	Leukocyte telomere length in a population-based caseâ€“control study of ovarian cancer: a pilot study. Cancer Causes and Control, 2010, 21, 77-82.	0.8	59
156	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.	2.6	59
157	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. Journal of Medical Genetics, 2012, 49, 601-608.	1.5	58
158	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.	2.2	58
159	The Obesity-Associated Polymorphisms FTO rs9939609 and MC4R rs17782313 and Endometrial Cancer Risk in Non-Hispanic White Women. PLoS ONE, 2011, 6, e16756.	1.1	58
160	Five Polymorphisms and Breast Cancer Risk: Results from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1610-1616.	1.1	57
161	TheATMmissense mutation p.Ser49Cys (c.146C>G) and the risk of breast cancer. Human Mutation, 2006, 27, 538-544.	1.1	56
162	Adulthood Lifetime Physical Activity and Breast Cancer. Epidemiology, 2008, 19, 226-236.	1.2	56

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163	DNA mismatch repair gene MSH6 implicated in determining age at natural menopause. Human Molecular Genetics, 2014, 23, 2490-2497.	1.4	56
164	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. EBioMedicine, 2015, 2, 681-689.	2.7	56
165	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	3.0	56
166	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.	2.2	56
167	Common genetic variants in the 9p21 region and their associations with multiple tumours. British Journal of Cancer, 2013, 108, 1378-1386.	2.9	55
168	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.	2.6	55
169	Assessment of Automated Image Analysis of Breast Cancer Tissue Microarrays for Epidemiologic Studies. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 992-999.	1.1	54
170	Combined and Interactive Effects of Environmental and GWAS-Identified Risk Factors in Ovarian Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 880-890.	1.1	54
171	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.	2.9	54
172	Genetic variation in TP53 and risk of breast cancer in a population-based caseâ€“control study. Carcinogenesis, 2007, 28, 1680-1686.	1.3	53
173	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	1.4	53
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