Montserrat Garcia-Closas

List of Publications by Citations

431 papers	31,792 citations	85 h-index	165 g-index
472 ext. papers	37,527 ext. citations	9.6 avg, IF	5.97 L-index

#	Paper	IF	Citations
431	Genome-wide association study identifies novel breast cancer susceptibility loci. *Nature*, **2007**, 447, 1087-93	50.4	1957
430	Assessing the probability that a positive report is false: an approach for molecular epidemiology studies. *Journal of the National Cancer Institute*, **2004**, 96, 434-42	9.7	1359
429	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
428	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
427	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
426	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	11.6	616
425	A common coding variant in CASP8 is associated with breast cancer risk. *Nature Genetics*, **2007**, 39, 352-8	36.3	557
424	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, 250-63	9.7	513
423	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, 649-59	40	483
422	Type I and II endometrial cancers: have they different risk factors?. *Journal of Clinical Oncology*, **2013**, 31, 2607-18	2.2	458
421	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, 579-84	36.3	452
420	Association between BRCA1 and BRCA2 mutations and survival in women with invasive epithelial ovarian cancer. *JAMA - Journal of the American Medical Association*, **2012**, 307, 382-90	27.4	427
419	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. *Nature Genetics*, **2013**, 45, 371-84, 384e1-2	36.3	422
418	Detectable clonal mosaicism and its relationship to aging and cancer. *Nature Genetics*, **2012**, 44, 651-8	36.3	409
417	A multi-stage genome-wide association study of bladder cancer identifies multiple susceptibility loci. *Nature Genetics*, **2010**, 42, 978-84	36.3	408
416	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
415	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401

414	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. *Nature Genetics*, **2009**, 41, 585-90	36.3	393
413	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
412	Differences in risk factors for breast cancer molecular subtypes in a population-based study. *Cancer Epidemiology Biomarkers and Prevention*, **2007**, 16, 439-43	4	349
411	Developing and evaluating polygenic risk prediction models for stratified disease prevention. *Nature Reviews Genetics*, **2016**, 17, 392-406	30.1	338
410	Performance of common genetic variants in breast-cancer risk models. *New England Journal of Medicine*, **2010**, 362, 986-93	59.2	334
409	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
408	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
407	Etiology of hormone receptor-defined breast cancer: a systematic review of the literature. *Cancer Epidemiology Biomarkers and Prevention*, **2004**, 13, 1558-68	4	294
406	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. *PLoS Genetics*, **2008**, 4, e1000054	6	280
405	A genome-wide association study identifies susceptibility loci for ovarian cancer at 2q31 and 8q24. *Nature Genetics*, **2010**, 42, 874-9	36.3	277
404	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. *Nature Genetics*, **2013**, 45, 362-70, 370e1-2	36.3	267
403	Hormone-receptor expression and ovarian cancer survival: an Ovarian Tumor Tissue Analysis consortium study. *Lancet Oncology, The*, **2013**, 14, 853-62	21.7	248
402	Critical research gaps and translational priorities for the successful prevention and treatment of breast cancer. *Breast Cancer Research*, **2013**, 15, R92	8.3	248
401	A genome-wide association study identifies a new ovarian cancer susceptibility locus on 9p22.2. *Nature Genetics*, **2009**, 41, 996-1000	36.3	240
400	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
399	Genetic susceptibility to breast cancer. *Molecular Oncology*, **2010**, 4, 174-91	7.9	236
398	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
397	Common variants at 19p13 are associated with susceptibility to ovarian cancer. *Nature Genetics*, **2010**, 42, 880-4	36.3	210

396	Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a case-control study. *Lancet Oncology, The*, **2008**, 9, 359-66	21.7	193
395	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. *Genetics in Medicine*, **2019**, 21, 1708-1718	8.1	192
394	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. *JAMA Oncology*, **2016**, 2, 1295-1302	13.4	189
393	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
392	Risk determination and prevention of breast cancer. *Breast Cancer Research*, **2014**, 16, 446	8.3	180
391	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	11	167
390	Polymorphisms in GSTT1, GSTZ1, and CYP2E1, disinfection by-products, and risk of bladder cancer in Spain. *Environmental Health Perspectives*, **2010**, 118, 1545-50	8.4	162
389	Pooled analysis and meta-analysis of glutathione S-transferase M1 and bladder cancer: a HuGE review. *American Journal of Epidemiology*, **2002**, 156, 95-109	3.8	159
388	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, 5373-84	5.6	143
387	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
386	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, 3289-303	5.6	140
385	Obesity and risk of ovarian cancer subtypes: evidence from the Ovarian Cancer Association Consortium. *Endocrine-Related Cancer*, **2013**, 20, 251-62	5.7	135
384	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *Journal of Clinical Oncology*, **2012**, 30, 4308-16	2.2	134
383	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, 376-88	6.3	133
382	PREDICT Plus: development and validation of a prognostic model for early breast cancer that includes HER2. *British Journal of Cancer*, **2012**, 107, 800-7	8.7	130
381	Genetic variation in the nucleotide excision repair pathway and bladder cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 536-42	4	128
380	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. *Nature Communications*, **2013**, 4, 1628	17.4	124
379	Genetic polymorphisms in base-excision repair pathway genes and risk of breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 353-8	4	122

378	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. *Nature Genetics*, **2011**, 43, 451-4	36.3	121
377	Intragenic ATM methylation in peripheral blood DNA as a biomarker of breast cancer risk. *Cancer Research*, **2012**, 72, 2304-13	10.1	121
376	Smoking and bladder cancer in Spain: effects of tobacco type, timing, environmental tobacco smoke, and gender. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 1348-54	4	121
375	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
374	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. *PLoS Genetics*, **2013**, 9, e1003284	6	112
373	Established breast cancer risk factors by clinically important tumour characteristics. *British Journal of Cancer*, **2006**, 95, 123-9	8.7	112
372	Large-scale evaluation of candidate genes identifies associations between VEGF polymorphisms and bladder cancer risk. *PLoS Genetics*, **2007**, 3, e29	6	109
371	Intrauterine environments and breast cancer risk: meta-analysis and systematic review. *Breast Cancer Research*, **2008**, 10, R8	8.3	108
370	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
369	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	9.7	107
368	Genetic variation in the base excision repair pathway and bladder cancer risk. *Human Genetics*, **2007** , 121, 233-42	6.3	107
367	Genetic susceptibility loci for breast cancer by estrogen receptor status. *Clinical Cancer Research*, **2008**, 14, 8000-9	12.9	105
366	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	36.3	104
365	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, 1052-67	24.4	104
364	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. *Nature Genetics*, **2020**, 52, 1219-1226	36.3	103
363	Genetic polymorphisms in the one-carbon metabolism pathway and breast cancer risk: a population-based case-control study and meta-analyses. *International Journal of Cancer*, **2007**, 120, 2696-703	7.5	102
362	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
361	Genome-wide association study identifies multiple loci associated with bladder cancer risk. *Human Molecular Genetics*, **2014**, 23, 1387-98	5.6	101

360	A prospective study of NAT2 acetylation genotype, cigarette smoking, and risk of breast cancer. *Carcinogenesis*, **1997**, 18, 2127-32	4.6	101
359	Pathway analysis of breast cancer genome-wide association study highlights three pathways and one canonical signaling cascade. *Cancer Research*, **2010**, 70, 4453-9	10.1	100
358	Mosaic uniparental disomies and aneuploidies as large structural variants of the human genome. *American Journal of Human Genetics*, **2010**, 87, 129-38	11	100
357	Food, nutrient and heterocyclic amine intake and the risk of bladder cancer. *European Journal of Cancer*, **2007**, 43, 1731-40	7.5	99
356	DNA banking for epidemiologic studies: a review of current practices. *Epidemiology*, **2002**, 13, 246-54	3.1	99
355	Polymorphisms in DNA repair genes, smoking, and bladder cancer risk: findings from the international consortium of bladder cancer. *Cancer Research*, **2009**, 69, 6857-64	10.1	94
354	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, 182-9	4.6	94
353	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. *Nature Genetics*, **2016**, 48, 374-86	36.3	93
352	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Research*, **2012**, 72, 1795-803	10.1	93
351	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. *PLoS Genetics*, **2013**, 9, e1003173	6	90
350	Risk of estrogen receptor-positive and -negative breast cancer and single-nucleotide polymorphism 2q35-rs13387042. *Journal of the National Cancer Institute*, **2009**, 101, 1012-8	9.7	90
349	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
348	Mosaic loss of chromosome Y is associated with common variation near TCL1A. *Nature Genetics*, **2016**, 48, 563-8	36.3	87
347	Identification and molecular characterization of a new ovarian cancer susceptibility locus at 17q21.31. *Nature Communications*, **2013**, 4, 1627	17.4	85
346	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. *Nature Genetics*, **2012**, 44, 1182-4	36.3	84
345	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309	5.8	83
344	Evaluation of genetic variation in the double-strand break repair pathway and bladder cancer risk. *Carcinogenesis*, **2007**, 28, 1788-93	4.6	83
343	Common genetic polymorphisms modify the effect of smoking on absolute risk of bladder cancer. *Cancer Research*, **2013**, 73, 2211-20	10.1	82

342	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, 4282-9	5.6	82
341	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, 1046-60	11	80
340	Relationship between serum hormone concentrations, reproductive history, alcohol consumption and genetic polymorphisms in pre-menopausal women. *International Journal of Cancer*, **2002**, 102, 172-8	7.5	80
339	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	11.6	80
338	Epigenome-wide association study reveals decreased average methylation levels years before breast cancer diagnosis. *Clinical Epigenetics*, **2015**, 7, 67	7.7	78
337	Combined associations of genetic and environmental risk factors: implications for prevention of breast cancer. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	78
336	An unusual suspect: an uncommon human-specific synonymous coding variant within the UGT1A6 gene explains a GWAS signal and protects against bladder cancer. *Genome Biology*, **2011**, 12,	18.3	78
335	Reply: Study design and statistics in epidemiology of breast cancer. *British Journal of Cancer*, **2006**, 95, 1302-1303	8.7	78
334	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
333	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, 6616-33	5.6	77
332	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. *Nature Genetics*, **2020**, 52, 572-581	36.3	76
331	Bladder cancer risk and genetic variation in AKR1C3 and other metabolizing genes. *Carcinogenesis*, **2008**, 29, 1955-62	4.6	76
330	Association of ESR1 gene tagging SNPs with breast cancer risk. *Human Molecular Genetics*, **2009**, 18, 1131-9	5.6	75
329	The role of genetic breast cancer susceptibility variants as prognostic factors. *Human Molecular Genetics*, **2012**, 21, 3926-39	5.6	75
328	Tagging single nucleotide polymorphisms in cell cycle control genes and susceptibility to invasive epithelial ovarian cancer. *Cancer Research*, **2007**, 67, 3027-35	10.1	75
327	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
326	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	8.3	74
325	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, 544-53	2.8	74

324	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
323	LIN28B polymorphisms influence susceptibility to epithelial ovarian cancer. *Cancer Research*, **2011**, 71, 3896-903	10.1	70
322	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, 1595-600	4	70
321	Glutathione S-transferase mu and theta polymorphisms and breast cancer susceptibility. *Journal of the National Cancer Institute*, **1999**, 91, 1960-4	9.7	70
320	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, 4974-9	11.5	69
319	Winner© 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	6	67
318	Genetic and non-genetic predictors of LINE-1 methylation in leukocyte DNA. *Environmental Health Perspectives*, **2013**, 121, 650-6	8.4	66
317	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. *Human Molecular Genetics*, **2011**, 20, 4693-706	5.6	66
316	Consortium analysis of 7 candidate SNPs for ovarian cancer. *International Journal of Cancer*, **2008**, 123, 380-388	7.5	66
315	Differential misclassification and the assessment of gene-environment interactions in case-control studies. *American Journal of Epidemiology*, **1998**, 147, 426-33	3.8	66
314	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. *Cancer Research*, **2016**, 76, 5103-14	10.1	66
313	BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	65
312	Genetic variation in five genes important in telomere biology and risk for breast cancer. *British Journal of Cancer*, **2007**, 97, 832-6	8.7	65
311	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. *Nature Reviews Clinical Oncology*, **2020**, 17, 687-705	19.4	64
310	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
309	ESR1/SYNE1 polymorphism and invasive epithelial ovarian cancer risk: an Ovarian Cancer Association Consortium study. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 245-50	4	64
308	Cigarette smoking and cancer risk: modeling total exposure and intensity. *American Journal of Epidemiology*, **2007**, 166, 479-89	3.8	62
307	Comparison of yield and genotyping performance of multiple displacement amplification and OmniPlex whole genome amplified DNA generated from multiple DNA sources. *Human Mutation*, **2005**, 26, 262-70	4.7	61

306	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, 1344-55	10.1	60
305	Genetic variation in tumor necrosis factor and lymphotoxin-alpha (TNF-LTA) and breast cancer risk. *Human Genetics*, **2007**, 121, 483-90	6.3	60
304	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
303	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	11	59
302	Mapping of the UGT1A locus identifies an uncommon coding variant that affects mRNA expression and protects from bladder cancer. *Human Molecular Genetics*, **2012**, 21, 1918-30	5.6	58
301	DNA hypermethylation of ESR1 and PGR in breast cancer: pathologic and epidemiologic associations. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 3036-43	4	56
300	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
299	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, 242-7	4	55
298	Leukocyte telomere length in a population-based case-control study of ovarian cancer: a pilot study. *Cancer Causes and Control*, **2010**, 21, 77-82	2.8	55
297	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	7.8	53
296	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
295	Five polymorphisms and breast cancer risk: results from the Breast Cancer Association Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 1610-6	4	53
294	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, 1569-72	8.4	53
293	Polymorphisms in one-carbon metabolism and trans-sulfuration pathway genes and susceptibility to bladder cancer. *International Journal of Cancer*, **2007**, 120, 2452-8	7.5	53
292	Single nucleotide polymorphisms in the TP53 region and susceptibility to invasive epithelial ovarian cancer. *Cancer Research*, **2009**, 69, 2349-57	10.1	52
291	Genetic susceptibility to distinct bladder cancer subphenotypes. *European Urology*, **2010**, 57, 283-92	10.2	52
290	The ATM missense mutation p.Ser49Cys (c.146C>G) and the risk of breast cancer. *Human Mutation*, **2006**, 27, 538-44	4.7	52
289	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52

288	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.1	51
287	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
286	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. *Journal of Medical Genetics*, **2012**, 49, 601-8	5.8	49
285	Comparison of 6q25 breast cancer hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). *PLoS ONE*, **2012**, 7, e42380	3.7	49
284	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. *Human Molecular Genetics*, **2014**, 23, 6096-111	5.6	48
283	Adulthood lifetime physical activity and breast cancer. *Epidemiology*, **2008**, 19, 226-36	3.1	48
282	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
281	Genetic variation in TP53 and risk of breast cancer in a population-based case control study. *Carcinogenesis*, **2007**, 28, 1680-6	4.6	47
280	Hormonal markers in breast cancer: coexpression, relationship with pathologic characteristics, and risk factor associations in a population-based study. *Cancer Research*, **2007**, 67, 10608-17	10.1	46
279	The obesity-associated polymorphisms FTO rs9939609 and MC4R rs17782313 and endometrial cancer risk in non-Hispanic white women. *PLoS ONE*, **2011**, 6, e16756	3.7	46
278	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
277	Association between a germline OCA2 polymorphism at chromosome 15q13.1 and estrogen receptor-negative breast cancer survival. *Journal of the National Cancer Institute*, **2010**, 102, 650-62	9.7	45
276	Expression of TGF-beta signaling factors in invasive breast cancers: relationships with age at diagnosis and tumor characteristics. *Breast Cancer Research and Treatment*, **2010**, 121, 727-35	4.4	45
275	Estimating age-specific breast cancer risks: a descriptive tool to identify age interactions. *Cancer Causes and Control*, **2007**, 18, 439-47	2.8	45
274	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	8.3	44
273	Crowdsourcing the General Public for Large Scale Molecular Pathology Studies in Cancer. *EBioMedicine*, **2015**, 2, 681-9	8.8	44
272	A single nucleotide polymorphism tags variation in the arylamine N-acetyltransferase 2 phenotype in populations of European background. *Pharmacogenetics and Genomics*, **2011**, 21, 231-6	1.9	44
271	Temporal stability and determinants of white blood cell DNA methylation in the breakthrough generations study. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 221-9	4	43

270	Discovery and validation of methylation markers for endometrial cancer. *International Journal of Cancer*, **2014**, 135, 1860-8	7.5	43
269	Assessment of automated image analysis of breast cancer tissue microarrays for epidemiologic studies. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 992-9	4	43
268	Epidemiologic determinants of vaginal pH. *American Journal of Obstetrics and Gynecology*, **1999**, 180, 1060-6	6.4	43
267	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	11	43
266	Lessons Learned From Past Gene-Environment Interaction Successes. *American Journal of Epidemiology*, **2017**, 186, 778-786	3.8	42
265	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. *Journal of Medical Genetics*, **2011**, 48, 477-84	5.8	42
264	Genetic variations in the sonic hedgehog pathway affect clinical outcomes in non-muscle-invasive bladder cancer. *Cancer Prevention Research*, **2010**, 3, 1235-45	3.2	42
263	Evaluation of candidate stromal epithelial cross-talk genes identifies association between risk of serous ovarian cancer and TERT, a cancer susceptibility "hot-spot". *PLoS Genetics*, **2010**, 6, e1001016	6	42
262	Progesterone receptor variation and risk of ovarian cancer is limited to the invasive endometrioid subtype: results from the Ovarian Cancer Association Consortium pooled analysis. *British Journal of Cancer*, **2008**, 98, 282-8	8.7	42
261	Common genetic variation in TP53 and its flanking genes, WDR79 and ATP1B2, and susceptibility to breast cancer. *International Journal of Cancer*, **2007**, 121, 2532-8	7.5	42
260	Hair dye use is not associated with risk for bladder cancer: evidence from a case-control study in Spain. *European Journal of Cancer*, **2006**, 42, 1448-54	7.5	42
259	Loss of antigenicity in stored sections of breast cancer tissue microarrays. *Cancer Epidemiology Biomarkers and Prevention*, **2004**, 13, 667-72	4	42
258	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	8.3	41
257	TGFB1 and TGFBR1 polymorphic variants in relationship to bladder cancer risk and prognosis. *International Journal of Cancer*, **2009**, 124, 608-13	7.5	41
256	Variation in breast cancer hormone receptor and HER2 levels by etiologic factors: a population-based analysis. *International Journal of Cancer*, **2007**, 121, 1079-85	7.5	41
255	Use of analgesics and nonsteroidal anti-inflammatory drugs, genetic predisposition, and bladder cancer risk in Spain. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 1696-702	4	41
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