Montserrat Garcia-Closas

List of Publications by Year in Descending Order

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	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
430	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
429	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
428	Measured body size and serum estrogen metabolism in postmenopausal women: the Ghana Breast Health Study.. *Breast Cancer Research*, **2022**, 24, 9	8.3	1
427	Comparison of somatic mutation landscapes in Chinese versus European breast cancer patients.. *Human Genetics and Genomics Advances*, **2022**, 3, 100076	0.8	1
426	A Genome-Wide Gene-Based Gene–Environment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, **2022**, 2, 211-219		0
425	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9	
424	Disinfection By-Products in Drinking Water and Bladder Cancer: Evaluation of Risk Modification by Common Genetic Polymorphisms in Two Case-Control Studies.. *Environmental Health Perspectives*, **2022**, 130, 57006	8.4	1
423	Towards implementation of comprehensive breast cancer risk prediction tools in health care for personalised prevention.. *Preventive Medicine*, **2022**, 107075	4.3	0
422	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
421	The case for increasing diversity in tissue-based functional genomics datasets to understand human disease susceptibility. *Nature Communications*, **2022**, 13,	17.4	1
420	A mixed-model approach for powerful testing of genetic associations with cancer risk incorporating tumor characteristics. *Biostatistics*, **2021**, 22, 772-788	3.7	6
419	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0
418	Racial and Ethnic Disparities in Excess Deaths During the COVID-19 Pandemic, March to December 2020. *Annals of Internal Medicine*, **2021**,	8	19
417	Gene level germline contributions to clinical risk of recurrence scores in Black and White breast cancer patients. *Cancer Research*, **2021**,	10.1	1
416	Evaluating Polygenic Risk Scores for Breast Cancer in Women of African Ancestry. *Journal of the National Cancer Institute*, **2021**, 113, 1168-1176	9.7	9
415	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*, **2021**,	7.8	6

414	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	12.9	3
413	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	4	2
412	Impact of breast cancer risk factors on clinically relevant prognostic biomarkers for primary breast cancer. *Breast Cancer Research and Treatment*, **2021**, 189, 483-495	4.4	3
411	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. *Nature Communications*, **2021**, 12, 4198	17.4	1
410	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	11	1
409	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	9.7	14
408	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. *International Journal of Cancer*, **2021**, 148, 307-319	7.5	13
407	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. *American Journal of Epidemiology*, **2021**, 190, 962-976	3.8	4
406	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	8	18
405	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	8.7	2
404	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	4.4	0
403	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4
402	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. *Genome Medicine*, **2021**, 13, 15	14.4	6
401	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	8.3	12
400	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
399	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	7.5	3
398	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	6.3	5
397	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	8.3	1

396	Discovery of structural deletions in breast cancer predisposition genes using whole genome sequencing data from > 2000 women of African-ancestry. *Human Genetics*, **2021**, 140, 1449-1457	6.3	1
395	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
394	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
393	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	9.8	0
392	Genomic and evolutionary classification of lung cancer in never smokers. *Nature Genetics*, **2021**, 53, 1348-1359	36.3	14
391	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	4	4
390	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
389	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. *Nature Reviews Clinical Oncology*, **2020**, 17, 687-705	19.4	64
388	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
387	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. *Nature Communications*, **2020**, 11, 1217	17.4	16
386	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	5.2	2
385	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. *Nature Communications*, **2020**, 11, 3353	17.4	32
384	iCARE: An R package to build, validate and apply absolute risk models. *PLoS ONE*, **2020**, 15, e0228198	3.7	28
383	Reproductive factors and risk of breast cancer by tumor subtypes among Ghanaian women: A population-based case-control study. *International Journal of Cancer*, **2020**, 147, 1535-1547	7.5	9
382	A framework for transcriptome-wide association studies in breast cancer in diverse study populations. *Genome Biology*, **2020**, 21, 42	18.3	20
381	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
380	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
379	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. *Breast Cancer Research and Treatment*, **2020**, 181, 423-434	4.4	7

378	Toward Risk-Stratified Breast Cancer Screening: Considerations for Changes in Screening Guidelines. *JAMA Oncology*, **2020**, 6, 31-33	13.4	5
377	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
376	Diesel exhaust and bladder cancer risk by pathologic stage and grade subtypes. *Environment International*, **2020**, 135, 105346	12.9	8
375	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	11	20
374	Cancer therapy shapes the fitness landscape of clonal hematopoiesis. *Nature Genetics*, **2020**, 52, 1219-1226	36.3	103
373	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
372	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	7.8	0
371	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. *Journal of the National Cancer Institute*, **2020**, 112, 278-285	9.7	36
370	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	7.8	13
369	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. *International Journal of Cancer*, **2020**, 146, 2130-2138	7.5	9
368	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
367	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
366	Recruiting population controls for case-control studies in sub-Saharan Africa: The Ghana Breast Health Study. *PLoS ONE*, **2019**, 14, e0215347	3.7	5
365	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	9.8	21
364	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. *Breast Cancer Research*, **2019**, 21, 62	8.3	20
363	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
362	Detectible mosaic truncating PPM1D mutations, age and breast cancer risk. *Journal of Human Genetics*, **2019**, 64, 545-550	4.3	3
361	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	9.8	24

360	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
359	Assessment of breast cancer risk: which tools to use?. *Lancet Oncology, The*, **2019**, 20, 463-464	21.7	5
358	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
357	A response to "Personalised medicine and population health: breast and ovarian cancer". *Human Genetics*, **2019**, 138, 287-289	6.3	13
356	Immune gene expression profiling reveals heterogeneity in luminal breast tumors. *Breast Cancer Research*, **2019**, 21, 147	8.3	24
355	Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Research*, **2019**, 21, 144	8.3	11
354	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
353	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. *Genetics in Medicine*, **2019**, 21, 1708-1718	8.1	192
352	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	4.4	16
351	Reply to ‘Mosaic loss of chromosome Y in leukocytes matters’. *Nature Genetics*, **2019**, 51, 7-9	36.3	6
350	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
349	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
348	Etiology of hormone receptor positive breast cancer differs by levels of histologic grade and proliferation. *International Journal of Cancer*, **2018**, 143, 746-757	7.5	9
347	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
346	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	4.9	19
345	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	9.7	1
344	Asthma status is associated with decreased risk of aggressive urothelial bladder cancer. *International Journal of Cancer*, **2018**, 142, 470-476	7.5	8
343	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	5.3	38

342	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
341	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
340	Oncologic Therapy for Solid Tumors Alters the Risk of Clonal Hematopoiesis. *Blood*, **2018**, 132, 747-747	2.2	2
339	Pooled Analysis of Nine Cohorts Reveals Breast Cancer Risk Factors by Tumor Molecular Subtype. *Cancer Research*, **2018**, 78, 6011-6021	10.1	40
338	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
337	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
336	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
335	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
334	Identification and replication of the interplay of four genetic high-risk variants for urinary bladder cancer. *Carcinogenesis*, **2017**, 38, 1167-1179	4.6	9
333	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119	8.3	26
332	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
331	Lessons Learned From Past Gene-Environment Interaction Successes. *American Journal of Epidemiology*, **2017**, 186, 778-786	3.8	42
330	Association between breast cancer genetic susceptibility variants and terminal duct lobular unit involution of the breast. *International Journal of Cancer*, **2017**, 140, 825-832	7.5	9
329	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	8.3	51
328	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
327	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	3.3	7
326	- a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget*, **2017**, 8, 102769-102782	3.3	3
325	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15

324	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	5.6	24
323	rs2735383, located at a microRNA binding site in the 3′UTR of NBS1, is not associated with breast cancer risk. *Scientific Reports*, **2016**, 6, 36874	4.9	2
322	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
321	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
320	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. *Nature Communications*, **2016**, 7, 11843	17.4	59
319	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
318	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
317	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	4.9	16
316	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
315	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
314	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, 341-50	4.4	5
313	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. *Journal of Pathology: Clinical Research*, **2016**, 2, 138-53	5.3	16
312	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. *Human Molecular Genetics*, **2016**, 25, 2612-2620	5.6	15
311	Response. *Journal of the National Cancer Institute*, **2016**, 108,	9.7	
310	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, 1203-14	5.6	20
309	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
308	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
307	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. *British Journal of Cancer*, **2016**, 114, 298-304	8.7	5

306	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, 137-54	6.3	6
305	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
304	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
303	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
302	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	3.3	21
301	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
300	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11
299	Association of Active and Sedentary Behaviors with Postmenopausal Estrogen Metabolism. *Medicine and Science in Sports and Exercise*, **2016**, 48, 439-48	1.2	19
298	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317	7.5	26
297	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
296	Patient survival and tumor characteristics associated with CHEK2:p.I157T - findings from the Breast Cancer Association Consortium. *Breast Cancer Research*, **2016**, 18, 98	8.3	26
295	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	8.3	25
294	Prediction of breast cancer risk based on common genetic variants in women of East Asian ancestry. *Breast Cancer Research*, **2016**, 18, 124	8.3	34
293	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
292	Inflammatory-Related Genetic Variants in Non-Muscle-Invasive Bladder Cancer Prognosis: A Multimarker Bayesian Assessment. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 1144-50	4	7
291	Lifetime Number of Ovulatory Cycles and Risks of Ovarian and Endometrial Cancer Among Postmenopausal Women. *American Journal of Epidemiology*, **2016**, 183, 800-14	3.8	29
290	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
289	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93	2.8	15

288	Mosaic loss of chromosome Y is associated with common variation near TCL1A. *Nature Genetics*, **2016**, 48, 563-8	36.3	87
287	Developing and evaluating polygenic risk prediction models for stratified disease prevention. *Nature Reviews Genetics*, **2016**, 17, 392-406	30.1	338
286	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
285	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
284	An investigation of the association of genetic susceptibility risk with somatic mutation burden in breast cancer. *British Journal of Cancer*, **2016**, 115, 752-60	8.7	10
283	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, 256-71	4.6	12
282	Infertility and incident endometrial cancer risk: a pooled analysis from the epidemiology of endometrial cancer consortium (E2C2). *British Journal of Cancer*, **2015**, 112, 925-33	8.7	25
281	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
280	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	11	26
279	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
278	Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. *Breast Cancer Research*, **2015**, 17, 18	8.3	17
277	Integrated analysis of DNA methylation, immunohistochemistry and mRNA expression, data identifies a methylation expression index (MEI) robustly associated with survival of ER-positive breast cancer patients. *Breast Cancer Research and Treatment*, **2015**, 150, 457-466	4.4	6
276	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
275	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
274	Modification of Occupational Exposures on Bladder Cancer Risk by Common Genetic Polymorphisms. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	23
273	Annexin A1 expression in a pooled breast cancer series: association with tumor subtypes and prognosis. *BMC Medicine*, **2015**, 13, 156	11.4	37
272	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
271	Invited commentary: screening and the elusive etiology of prostate cancer. *American Journal of Epidemiology*, **2015**, 182, 390-3	3.8	13

270	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91	4	17
269	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. *Human Molecular Genetics*, **2015**, 24, 285-98	5.6	35
268	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
267	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. *International Journal of Cancer*, **2015**, 136, E685-96	7.5	26
266	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24
265	Epigenome-wide association study reveals decreased average methylation levels years before breast cancer diagnosis. *Clinical Epigenetics*, **2015**, 7, 67	7.7	78
264	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
263	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	2.4	
262	Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. *PLoS ONE*, **2015**, 10, e0143256	3.7	8
261	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
260	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
259	Mitochondrial DNA Copy Number in Peripheral Blood Cells and Risk of Developing Breast Cancer. *Cancer Research*, **2015**, 75, 2844-50	10.1	32
258	Characterization of large structural genetic mosaicism in human autosomes. *American Journal of Human Genetics*, **2015**, 96, 487-97	11	77
257	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	5.3	18
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255	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
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