Alison Margaret Dunning

List of Publications by Citations

366 papers	29,299 citations	88 h-index	159 g-index
392 ext. papers	34,332 ext. citations	10.5 avg, IF	5.63 L-index

#	Paper	IF	Citations
366	Genome-wide association study identifies novel breast cancer susceptibility loci. *Nature*, **2007**, 447, 1087-93	50.4	1957
365	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
364	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
363	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
362	Genome-wide association study identifies five new breast cancer susceptibility loci. *Nature Genetics* , **2010**, 42, 504-7	36.3	582
361	A common coding variant in CASP8 is associated with breast cancer risk. *Nature Genetics*, **2007**, 39, 352-8	36.3	557
360	Beyond GWASs: illuminating the dark road from association to function. *American Journal of Human Genetics*, **2013**, 93, 779-97	11	515
359	Normal tissue reactions to radiotherapy: towards tailoring treatment dose by genotype. *Nature Reviews Cancer*, **2009**, 9, 134-42	31.3	450
358	Germline mutations of the BRCA1 gene in breast and ovarian cancer families provide evidence for a genotype-phenotype correlation. *Nature Genetics*, **1995**, 11, 428-33	36.3	439
357	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
356	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. *Nature Genetics*, **2013**, 45, 385-91, 391e1-2	36.3	413
355	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
354	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
353	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
352	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. *Nature Genetics*, **2009**, 41, 585-90	36.3	393
351	Association studies for finding cancer-susceptibility genetic variants. *Nature Reviews Cancer*, **2004**, 4, 850-60	31.3	377
350	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936	36.3	340

349	A novel recurrent mutation in MITF predisposes to familial and sporadic melanoma. *Nature*, **2011**, 480, 99-103	50.4	335
348	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
347	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
346	Polymorphisms associated with circulating sex hormone levels in postmenopausal women. *Journal of the National Cancer Institute*, **2004**, 96, 936-45	9.7	291
345	Multiple loci with different cancer specificities within the 8q24 gene desert. *Journal of the National Cancer Institute*, **2008**, 100, 962-6	9.7	283
344	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. *PLoS Genetics*, **2008**, 4, e1000054	6	280
343	A locus on 19p13 modifies risk of breast cancer in BRCA1 mutation carriers and is associated with hormone receptor-negative breast cancer in the general population. *Nature Genetics*, **2010**, 42, 885-92	36.3	276
342	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
341	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. *Nature Genetics*, **2011**, 43, 1210-4	36.3	253
340	Shortened telomere length is associated with increased risk of cancer: a meta-analysis. *PLoS ONE*, **2011**, 6, e20466	3.7	248
339	POT1 loss-of-function variants predispose to familial melanoma. *Nature Genetics*, **2014**, 46, 478-481	36.3	241
338	Differential genetic effects of ESR1 gene polymorphisms on osteoporosis outcomes. *JAMA - Journal of the American Medical Association*, **2004**, 292, 2105-14	27.4	238
337	A transforming growth factorbeta1 signal peptide variant increases secretion in vitro and is associated with increased incidence of invasive breast cancer. *Cancer Research*, **2003**, 63, 2610-5	10.1	238
336	Genome-wide association analysis identifies three new breast cancer susceptibility loci. *Nature Genetics*, **2012**, 44, 312-8	36.3	237
335	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
334	Genome-wide association study in BRCA1 mutation carriers identifies novel loci associated with breast and ovarian cancer risk. *PLoS Genetics*, **2013**, 9, e1003212	6	209
333	DNA repair polymorphisms and cancer risk in non-smokers in a cohort study. *Carcinogenesis*, **2006**, 27, 997-1007	4.6	205
332	Genome-wide association study identifies three new melanoma susceptibility loci. *Nature Genetics*, **2011**, 43, 1108-13	36.3	203

331	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
330	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
329	The association between common vitamin D receptor gene variations and osteoporosis: a participant-level meta-analysis. *Annals of Internal Medicine*, **2006**, 145, 255-64	8	185
328	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
327	Germline BRCA mutation and outcome in young-onset breast cancer (POSH): a prospective cohort study. *Lancet Oncology, The*, **2018**, 19, 169-180	21.7	177
326	The extent of linkage disequilibrium in four populations with distinct demographic histories. *American Journal of Human Genetics*, **2000**, 67, 1544-54	11	170
325	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
324	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. *Nature Genetics*, **2015**, 47, 987-995	36.3	162
323	Independent validation of genes and polymorphisms reported to be associated with radiation toxicity: a prospective analysis study. *Lancet Oncology, The*, **2012**, 13, 65-77	21.7	161
322	IGF1 and IGFBP3 tagging polymorphisms are associated with circulating levels of IGF1, IGFBP3 and risk of breast cancer. *Human Molecular Genetics*, **2006**, 15, 1-10	5.6	160
321	Familial defective apolipoprotein B-100: detection in the United Kingdom and Scandinavia, and clinical characteristics of ten cases. *Atherosclerosis*, **1990**, 80, 235-42	3.1	154
320	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
319	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
318	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
317	TP53 and KRAS2 mutations in plasma DNA of healthy subjects and subsequent cancer occurrence: a prospective study. *Cancer Research*, **2006**, 66, 6871-6	10.1	140
316	Air pollution and risk of lung cancer in a prospective study in Europe. *International Journal of Cancer*, **2006**, 119, 169-74	7.5	136
315	A polymorphic stop codon in BRCA2. *Nature Genetics*, **1996**, 14, 253-4	36.3	136
314	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

313	Genetic variation at the CYP19A1 locus predicts circulating estrogen levels but not breast cancer risk in postmenopausal women. *Cancer Research*, **2007**, 67, 1893-7	10.1	134
312	Large-scale evidence for the effect of the COLIA1 Sp1 polymorphism on osteoporosis outcomes: the GENOMOS study. *PLoS Medicine*, **2006**, 3, e90	11.6	134
311	A common variant in BRCA2 is associated with both breast cancer risk and prenatal viability. *Nature Genetics*, **2000**, 26, 362-4	36.3	134
310	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133
309	Telomere length in prospective and retrospective cancer case-control studies. *Cancer Research*, **2010**, 70, 3170-6	10.1	131
308	A common 8q24 variant in prostate and breast cancer from a large nested case-control study. *Cancer Research*, **2007**, 67, 2951-6	10.1	127
307	Errors in the polymerase chain reaction. *Nucleic Acids Research*, **1988**, 16, 10393	20.1	123
306	Genome-wide association study identifies a common variant associated with risk of endometrial cancer. *Nature Genetics*, **2011**, 43, 451-4	36.3	121
305	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
304	Association between common variation in 120 candidate genes and breast cancer risk. *PLoS Genetics*, **2007**, 3, e42	6	118
303	Evidence of gene-environment interactions between common breast cancer susceptibility loci and established environmental risk factors. *PLoS Genetics*, **2013**, 9, e1003284	6	112
302	Polymorphisms in DNA repair genes and epithelial ovarian cancer risk. *International Journal of Cancer*, **2005**, 117, 611-8	7.5	112
301	Red-clover-derived isoflavones and mammographic breast density: a double-blind, randomized, placebo-controlled trial [ISRCTN42940165]. *Breast Cancer Research*, **2004**, 6, R170-9	8.3	111
300	Somatically acquired hypomethylation of IGF2 in breast and colorectal cancer. *Human Molecular Genetics*, **2008**, 17, 2633-43	5.6	110
299	Reproducibility of telomere length assessment: an international collaborative study. *International Journal of Epidemiology*, **2015**, 44, 1673-83	7.8	109
298	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
297	A genome-wide association scan (GWAS) for mean telomere length within the COGS project: identified loci show little association with hormone-related cancer risk. *Human Molecular Genetics*, **2013**, 22, 5056-64	5.6	107
296	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

295	Effect of germ-line genetic variation on breast cancer survival in a population-based study. *Cancer Research*, **2002**, 62, 3052-7	10.1	103
294	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. *Radiotherapy and Oncology*, **2014**, 111, 178-85	5.3	102
293	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
292	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. *Human Molecular Genetics*, **2009**, 18, 1692-703	5.6	100
291	The effect on melanoma risk of genes previously associated with telomere length. *Journal of the National Cancer Institute*, **2014**, 106,	9.7	97
290	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	96
289	DNA adducts and lung cancer risk: a prospective study. *Cancer Research*, **2005**, 65, 8042-8	10.1	96
288	No association between androgen or vitamin D receptor gene polymorphisms and risk of breast cancer. *Carcinogenesis*, **1999**, 20, 2131-5	4.6	96
287	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
286	19p13.1 is a triple-negative-specific breast cancer susceptibility locus. *Cancer Research*, **2012**, 72, 1795-803	10.1	93
285	A three-stage genome-wide association study identifies a susceptibility locus for late radiotherapy toxicity at 2q24.1. *Nature Genetics*, **2014**, 46, 891-4	36.3	92
284	Life stress, emotional health, and mean telomere length in the European Prospective Investigation into Cancer (EPIC)-Norfolk population study. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2011**, 66, 1152-62	6.4	91
283	Identification of a BRCA2-specific modifier locus at 6p24 related to breast cancer risk. *PLoS Genetics*, **2013**, 9, e1003173	6	90
282	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
281	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. *Nature Genetics*, **2017**, 49, 1133-1140	36.3	89
280	Saliva samples are a viable alternative to blood samples as a source of DNA for high throughput genotyping. *BMC Medical Genomics*, **2012**, 5, 19	3.7	88
279	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. *Human Molecular Genetics*, **2013**, 22, 2520-8	5.6	88
278	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87

277	A combined analysis of genome-wide association studies in breast cancer. *Breast Cancer Research and Treatment*, **2011**, 126, 717-27	4.4	85
276	Amount of DNA in plasma and cancer risk: a prospective study. *International Journal of Cancer*, **2004**, 111, 746-9	7.5	85
275	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
274	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
273	Large-scale analysis of association between polymorphisms in the transforming growth factor beta 1 gene (TGFB1) and osteoporosis: the GENOMOS study. *Bone*, **2008**, 42, 969-81	4.7	83
272	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. *Breast Cancer Research*, **2014**, 16, 3419	8.3	82
271	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
270	Common variants in the ATM, BRCA1, BRCA2, CHEK2 and TP53 cancer susceptibility genes are unlikely to increase breast cancer risk. *Breast Cancer Research*, **2007**, 9, R27	8.3	79
269	Genetic variants in epigenetic genes and breast cancer risk. *Carcinogenesis*, **2006**, 27, 1661-9	4.6	77
268	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
267	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. *Human Molecular Genetics*, **2013**, 22, 2539-50	5.6	75
266	Association of ESR1 gene tagging SNPs with breast cancer risk. *Human Molecular Genetics*, **2009**, 18, 1131-9	5.6	75
265	The role of genetic breast cancer susceptibility variants as prognostic factors. *Human Molecular Genetics*, **2012**, 21, 3926-39	5.6	75
264	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
263	Most common "sporadic" cancers have a significant germline genetic component. *Human Molecular Genetics*, **2014**, 23, 6112-8	5.6	74
262	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
261	CYP2D6 gene variants: association with breast cancer specific survival in a cohort of breast cancer patients from the United Kingdom treated with adjuvant tamoxifen. *Breast Cancer Research*, **2010**, 12, R64	8.3	71
260	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70

259	Individual patient data meta-analysis shows a significant association between the ATM rs1801516 SNP and toxicity after radiotherapy in 5456 breast and prostate cancer patients. *Radiotherapy and Oncology*, **2016**, 121, 431-439	5.3	69
258	Do MDM2 SNP309 and TP53 R72P interact in breast cancer susceptibility? A large pooled series from the breast cancer association consortium. *Cancer Research*, **2007**, 67, 9584-90	10.1	69
257	Tagging single-nucleotide polymorphisms in antioxidant defense enzymes and susceptibility to breast cancer. *Cancer Research*, **2006**, 66, 1225-33	10.1	69
256	Prevalence of the HOXB13 G84E germline mutation in British men and correlation with prostate cancer risk, tumour characteristics and clinical outcomes. *Annals of Oncology*, **2015**, 26, 756-761	10.3	67
255	Polymorphisms in the initiators of RET (rearranged during transfection) signaling pathway and susceptibility to sporadic medullary thyroid carcinoma. *Journal of Clinical Endocrinology and Metabolism*, **2005**, 90, 6268-74	5.6	67
254	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
253	From candidate gene studies to GWAS and post-GWAS analyses in breast cancer. *Current Opinion in Genetics and Development*, **2015**, 30, 32-41	4.9	65
252	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
251	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
250	Allelic association of the human homologue of the mouse modifier Ptprj with breast cancer. *Human Molecular Genetics*, **2005**, 14, 2349-56	5.6	64
249	A genome-wide association study of early-onset breast cancer identifies PFKM as a novel breast cancer gene and supports a common genetic spectrum for breast cancer at any age. *Cancer Epidemiology Biomarkers and Prevention*, **2014**, 23, 658-69	4	63
248	Multi-factor dimensionality reduction applied to a large prospective investigation on gene-gene and gene-environment interactions. *Carcinogenesis*, **2007**, 28, 414-22	4.6	62
247	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. *Nature Genetics*, **2021**, 53, 65-75	36.3	62
246	Polymorphisms in the human aromatase cytochrome P450 gene (CYP19) and breast cancer risk. *Carcinogenesis*, **2000**, 21, 189-93	4.6	60
245	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
244	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nature Communications*, **2018**, 9, 2256	17.4	57
243	Fine scale mapping of the breast cancer 16q12 locus. *Human Molecular Genetics*, **2010**, 19, 2507-15	5.6	57
242	The patched polymorphism Pro1315Leu (C3944T) may modulate the association between use of oral contraceptives and breast cancer risk. *International Journal of Cancer*, **2003**, 103, 779-83	7.5	57

241	Common variants associated with breast cancer in genome-wide association studies are modifiers of breast cancer risk in BRCA1 and BRCA2 mutation carriers. *Human Molecular Genetics*, **2010**, 19, 2886-97	5.6	56
240	Association of single-nucleotide polymorphisms in the cell cycle genes with breast cancer in the British population. *Carcinogenesis*, **2008**, 29, 333-41	4.6	56
239	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
238	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
237	Telomere length and common disease: study design and analytical challenges. *Human Genetics*, **2015**, 134, 679-89	6.3	55
236	A replicated association between polymorphisms near TNFβ and risk for adverse reactions to radiotherapy. *British Journal of Cancer*, **2012**, 107, 748-53	8.7	55
235	Prognostic value of PAI1 in invasive breast cancer: evidence that tumor-specific factors are more important than genetic variation in regulating PAI1 expression. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 2107-14	4	55
234	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. *Human Molecular Genetics*, **2015**, 24, 5589-602	5.6	54
233	Radiogenomics: the search for genetic predictors of radiotherapy response. *Future Oncology*, **2014**, 10, 2391-406	3.6	54
232	Genetic variation in the HSD17B1 gene and risk of prostate cancer. *PLoS Genetics*, **2005**, 1, e68	6	54
231	XRCC1 Polymorphism Associated With Late Toxicity After Radiation Therapy in Breast Cancer Patients. *International Journal of Radiation Oncology Biology Physics*, **2015**, 92, 1084-1092	4	53
230	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
229	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
228	Five polymorphisms and breast cancer risk: results from the Breast Cancer Association Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 1610-6	4	53
227	Rat Mcs5a is a compound quantitative trait locus with orthologous human loci that associate with breast cancer risk. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 6299-304	11.5	53
226	Individual patient data meta-analysis shows no association between the SNP rs1800469 in TGFB and late radiotherapy toxicity. *Radiotherapy and Oncology*, **2012**, 105, 289-95	5.3	52
225	Phytoestrogen exposure is associated with circulating sex hormone levels in postmenopausal women and interact with ESR1 and NR1I2 gene variants. *Cancer Epidemiology Biomarkers and Prevention*, **2007**, 16, 1009-16	4	52
224	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

223	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	8.3	51
222	Genetic susceptibility according to three metabolic pathways in cancers of the lung and bladder and in myeloid leukemias in nonsmokers. *Annals of Oncology*, **2007**, 18, 1230-42	10.3	51
221	Common ERBB2 polymorphisms and risk of breast cancer in a white British population: a case-control study. *Breast Cancer Research*, **2005**, 7, R204-9	8.3	51
220	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. *EBioMedicine*, **2016**, 10, 150-63	8.8	50
219	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
218	Standardized Total Average Toxicity score: a scale- and grade-independent measure of late radiotherapy toxicity to facilitate pooling of data from different studies. *International Journal of Radiation Oncology Biology Physics*, **2012**, 82, 1065-74	4	49
217	Phytoestrogen exposure, polymorphisms in COMT, CYP19, ESR1, and SHBG genes, and their associations with prostate cancer risk. *Nutrition and Cancer*, **2006**, 56, 31-9	2.8	49
216	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
215	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
214	The CASP8 -652 6N del promoter polymorphism and breast cancer risk: a multicenter study. *Breast Cancer Research and Treatment*, **2008**, 111, 139-44	4.4	48
213	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
212	STROGAR - STrengthening the Reporting Of Genetic Association studies in Radiogenomics. *Radiotherapy and Oncology*, **2014**, 110, 182-8	5.3	47
211	Rare, protein-truncating variants in , and , but not , are associated with increased breast cancer risks. *Journal of Medical Genetics*, **2017**, 54, 732-741	5.8	47
210	No association between SNPs regulating TGF-1 secretion and late radiotherapy toxicity to the breast: results from the RAPPER study. *Radiotherapy and Oncology*, **2010**, 97, 9-14	5.3	47
209	Identification of common variants in the SHBG gene affecting sex hormone-binding globulin levels and breast cancer risk in postmenopausal women. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 3490-8	4	47
208	Tagging single nucleotide polymorphisms in the BRIP1 gene and susceptibility to breast and ovarian cancer. *PLoS ONE*, **2007**, 2, e268	3.7	47
207	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. *Human Molecular Genetics*, **2015**, 24, 1478-92	5.6	46
206	A comprehensive analysis of common IGF1, IGFBP1 and IGFBP3 genetic variation with prospective IGF-I and IGFBP-3 blood levels and prostate cancer risk among Caucasians. *Human Molecular Genetics*, **2010**, 19, 3089-101	5.6	46

205	Common polymorphisms in the prostaglandin pathway genes and their association with breast cancer susceptibility and survival. *Clinical Cancer Research*, **2009**, 15, 2181-91	12.9	46
204	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
203	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Research*, **2015**, 75, 2457-67	10.1	45
202	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
201	Polymorphisms in CYP1A1 and smoking: no association with breast cancer risk. *Carcinogenesis*, **2001**, 22, 1797-800	4.6	44
200	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
199	Association of the progesterone receptor gene with breast cancer risk: a single-nucleotide polymorphism tagging approach. *Cancer Epidemiology Biomarkers and Prevention*, **2006**, 15, 675-82	4	43
198	Polymorphisms in the CYP19 gene may affect the positive correlations between serum and urine phytoestrogen metabolites and plasma androgen concentrations in men. *Journal of Nutrition*, **2005**, 135, 2680-6	4.1	43
197	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
196	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 1503-1510	4	42
195	A role for XRCC2 gene polymorphisms in breast cancer risk and survival. *Journal of Medical Genetics*, **2011**, 48, 477-84	5.8	42
194	A large study of androgen receptor germline variants and their relation to sex hormone levels and prostate cancer risk. Results from the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. *Journal of Clinical Endocrinology and Metabolism*, **2010**, 95, E121-7	5.6	42
193	Common genetic variation in candidate genes and susceptibility to subtypes of breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 255-9	4	42
192	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
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