Alison Margaret Dunning

List of Publications by Year in Descending Order

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	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
365	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
364	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
363	Predicting the Likelihood of Carrying a or Mutation in Asian Patients With Breast Cancer.. *Journal of Clinical Oncology*, **2022**, JCO2101647	2.2	1
362	Overview of health-related quality of life and toxicity of non-small cell lung cancer patients receiving curative-intent radiotherapy in a real-life setting (the REQUITE study).. *Lung Cancer*, **2022**, 166, 228-241	5.9	0
361	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
360	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. *Breast Cancer Research*, **2022**, 24, 27	8.3	1
359	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9	
358	Overlap of high-risk individuals predicted by family history, and genetic and non-genetic breast cancer risk prediction models: implications for risk stratification.. *BMC Medicine*, **2022**, 20, 150	11.4	0
357	Relevance of the MHC region for breast cancer susceptibility in Asians.. *Breast Cancer*, **2022**, 1	3.4	
356	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
355	Cross-Cancer Genome-Wide Association Study of Endometrial Cancer and Epithelial Ovarian Cancer Identifies Genetic Risk Regions Associated with Risk of Both Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 217-228	4	7
354	Body mass index and type 2 diabetes and breast cancer survival: a Mendelian randomization study. *American Journal of Cancer Research*, **2021**, 11, 3921-3934	4.4	
353	Germline breast cancer susceptibility genes, tumor characteristics, and survival. *Genome Medicine*, **2021**, 13, 185	14.4	0
352	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0
351	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
350	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. *Npj Breast Cancer*, **2021**, 7, 46	7.8	1

349	Characterisation of protein-truncating and missense variants in in 15 768 women from Malaysia and Singapore. *Journal of Medical Genetics*, **2021**,	5.8	1
348	First international workshop of the ATM and cancer risk group (4-5 December 2019). *Familial Cancer* , **2021**, 1	3	5
347	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous BRCA1 or BRCA2 pathogenic variant. *Genetics in Medicine*, **2021**, 23, 1726-1737	8.1	2
346	Development of a method for generating SNP interaction-aware polygenic risk scores for radiotherapy toxicity. *Radiotherapy and Oncology*, **2021**, 159, 241-248	5.3	1
345	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. *Nature Communications*, **2021**, 12, 4198	17.4	1
344	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
343	Marital status and prostate cancer incidence: a pooled analysis of 12 case-control studies from the PRACTICAL consortium. *European Journal of Epidemiology*, **2021**, 36, 913-925	12.1	2
342	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
341	Common Susceptibility Loci for Male Breast Cancer. *Journal of the National Cancer Institute*, **2021**, 113, 453-461	9.7	4
340	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
339	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
338	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
337	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
336	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
335	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
334	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
333	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
332	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28

331	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
330	Polygenic risk scores for prediction of breast cancer risk in Asian populations.. *Genetics in Medicine*, **2021**,	8.1	2
329	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
328	Pathogenic Variants in Are Associated With an Adverse Prognosis in Symptomatic Early-Onset Breast Cancer. *JCO Precision Oncology*, **2020**, 4,	3.6	5
327	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
326	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. *Nature Communications*, **2020**, 11, 1217	17.4	16
325	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
324	Candidate Causal Variants at the 8p12 Breast Cancer Risk Locus Regulate. *Cancers*, **2020**, 12,	6.6	3
323	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
322	Non-coding RNAs underlie genetic predisposition to breast cancer. *Genome Biology*, **2020**, 21, 7	18.3	11
321	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
320	Genome-wide association meta-analyses combining multiple risk phenotypes provide insights into the genetic architecture of cutaneous melanoma susceptibility. *Nature Genetics*, **2020**, 52, 494-504	36.3	39
319	External Validation of a Predictive Model for Acute Skin Radiation Toxicity in the REQUITE Breast Cohort. *Frontiers in Oncology*, **2020**, 10, 575909	5.3	5
318	External Validation of a Predictive Model for Acute Skin Radiation Toxicity in the REQUITE Breast Cohort. *Frontiers in Oncology*, **2020**, 10, 575909	5.3	1
317	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
316	Chromatin interactome mapping at 139 independent breast cancer risk signals. *Genome Biology*, **2020**, 21, 8	18.3	12
315	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. *International Journal of Epidemiology*, **2020**, 49, 1117-1131	7.8	17
314	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133

313	A Deep Learning Approach Validates Genetic Risk Factors for Late Toxicity After Prostate Cancer Radiotherapy in a REQUITE Multi-National Cohort. *Frontiers in Oncology*, **2020**, 10, 541281	5.3	4
312	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. *Nature Communications*, **2020**, 11, 3833	17.4	31
311	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
310	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
309	Radiogenomics Consortium Genome-Wide Association Study Meta-Analysis of Late Toxicity After Prostate Cancer Radiotherapy. *Journal of the National Cancer Institute*, **2020**, 112, 179-190	9.7	32
308	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
307	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
306	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
305	REQUITE: A prospective multicentre cohort study of patients undergoing radiotherapy for breast, lung or prostate cancer. *Radiotherapy and Oncology*, **2019**, 138, 59-67	5.3	26
304	The functional ALDH2 polymorphism is associated with breast cancer risk: A pooled analysis from the Breast Cancer Association Consortium. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e707	2.3	3
303	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
302	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
301	DNA damage and hormone-related cancer: a repair pathway view. *Human Molecular Genetics*, **2019**, 28, R180-R186	5.6	2
300	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
299	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
298	Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Research*, **2019**, 21, 144	8.3	11
297	Prevalence of BRCA1 and BRCA2 pathogenic variants in a large, unselected breast cancer cohort. *International Journal of Cancer*, **2019**, 144, 1195-1204	7.5	18
296	Targeted Resequencing of the Coding Sequence of 38 Genes Near Breast Cancer GWAS Loci in a Large Case-Control Study. *Cancer Epidemiology Biomarkers and Prevention*, **2019**, 28, 822-825	4	4

295	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. *Biological Psychiatry*, **2019**, 85, 946-955	7.9	35
294	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
293	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
292	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
291	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. *Nature Communications*, **2018**, 9, 1340	17.4	39
290	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
289	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
288	Inherited mutations in and in an unselected multiethnic cohort of Asian patients with breast cancer and healthy controls from Malaysia. *Journal of Medical Genetics*, **2018**, 55, 97-103	5.8	24
287	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
286	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936	36.3	340
285	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nature Communications*, **2018**, 9, 2256	17.4	57
284	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
283	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. *Oncotarget*, **2018**, 9, 12630-12638	5.5	6
282	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
281	Differential Burden of Rare and Common Variants on Tumor Characteristics, Survival, and Mode of Detection in Breast Cancer. *Cancer Research*, **2018**, 78, 6329-6338	10.1	13
280	Genome-wide association study implicates immune dysfunction in the development of Hodgkin lymphoma. *Blood*, **2018**, 132, 2040-2052	2.2	10
279	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. *European Urology*, **2018**, 74, 248-252	10.2	13
278	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412

277	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
276	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
275	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. *Carcinogenesis*, **2017**, 38, 511-518	4.6	20
274	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. *Nature Communications*, **2017**, 8, 15034	17.4	26
273	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
272	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
271	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
270	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
269	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
268	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.3	51
267	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
266	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
265	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
264	- a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget*, **2017**, 8, 102769-102782	3.3	3
263	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
262	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
261	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
260	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

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	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
257	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
256	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
255	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
254	A Common Variant at the 14q32 Endometrial Cancer Risk Locus Activates AKT1 through YY1 Binding. *American Journal of Human Genetics*, **2016**, 98, 1159-1169	11	17
253	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
252	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
251	GWAS meta-analysis of 16 852 women identifies new susceptibility locus for endometrial cancer. *Human Molecular Genetics*, **2016**, 25, 2612-2620	5.6	15
250	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
249	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
248	Patients with a High Polygenic Risk of Breast Cancer do not have An Increased Risk of Radiotherapy Toxicity. *Clinical Cancer Research*, **2016**, 22, 1413-20	12.9	11
247	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
246	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
245	Germline TERT promoter mutations are rare in familial melanoma. *Familial Cancer*, **2016**, 15, 139-44	3	34
244	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
243	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
242	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11

241	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
240	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
239	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
238	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
237	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
236	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
235	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
234	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
233	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
232	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
231	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
230	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
229	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
228	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
227	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. *Nature Genetics*, **2015**, 47, 987-995	36.3	162
226	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
225	Identification of novel genetic markers of breast cancer survival. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	38
224	Rare germline copy number deletions of likely functional importance are implicated in endometrial cancer predisposition. *Human Genetics*, **2015**, 134, 269-78	6.3	12

223	Candidate locus analysis of the TERT-CLPTM1L cancer risk region on chromosome 5p15 identifies multiple independent variants associated with endometrial cancer risk. *Human Genetics*, **2015**, 134, 231-45	6.3	30
222	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
221	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
220	Fine mapping of genetic susceptibility loci for melanoma reveals a mixture of single variant and multiple variant regions. *International Journal of Cancer*, **2015**, 136, 1351-60	7.5	26
219	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. *Cancer Research*, **2015**, 75, 2457-67	10.1	45
218	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
217	Is Southern blotting necessary to measure telomere length reproducibly? AuthorsQResponse to: Commentary: The reliability of telomere length measurements. *International Journal of Epidemiology*, **2015**, 44, 1686-7	7.8	7
216	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
215	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
214	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocrine-Related Cancer*, **2015**, 22, 851-61	5.7	19
213	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
212	Reproducibility of telomere length assessment: an international collaborative study. *International Journal of Epidemiology*, **2015**, 44, 1673-83	7.8	109
211	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
210	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
209	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
208	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. *Scientific Reports*, **2015**, 5, 17369	4.9	27
207	A polymorphism in the base excision repair gene PARP2 is associated with differential prognosis by chemotherapy among postmenopausal breast cancer patients. *BMC Cancer*, **2015**, 15, 978	4.8	6
206	Common germline polymorphisms associated with breast cancer-specific survival. *Breast Cancer Research*, **2015**, 17, 58	8.3	24

205	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
204	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	
203	Assessing associations between the AURKA-HMMR-TPX2-TUBG1 functional module and breast cancer risk in BRCA1/2 mutation carriers. *PLoS ONE*, **2015**, 10, e0120020	3.7	26
202	SNP-SNP interaction analysis of NF-B signaling pathway on breast cancer survival. *Oncotarget*, **2015**, 6, 37979-94	3.3	19
201	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
200	Telomere length and common disease: study design and analytical challenges. *Human Genetics*, **2015**, 134, 679-89	6.3	55
199	Reproducibility of telomere length assessment: AuthorsQ Response to Damjan Krstajic and Ljubomir Buturovic. *International Journal of Epidemiology*, **2015**, 44, 1739-41	7.8	8
198	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
197	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. *Human Molecular Genetics*, **2015**, 24, 2966-84	5.6	36
196	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
195	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46,450 cases and 42,461 controls from the breast cancer association consortium. *Human Molecular Genetics*, **2014**, 23, 1934-46	5.6	28
194	POT1 loss-of-function variants predispose to familial melanoma. *Nature Genetics*, **2014**, 46, 478-481	36.3	241
193	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
192	Identification of new genetic susceptibility loci for breast cancer through consideration of gene-environment interactions. *Genetic Epidemiology*, **2014**, 38, 84-93	2.6	24
191	STROGAR - STrengthening the Reporting Of Genetic Association studies in Radiogenomics. *Radiotherapy and Oncology*, **2014**, 110, 182-8	5.3	47
190	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
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6	High-Throughput Techniques Genotyping and Genomics141-154		
5	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
4	Chromatin interactome mapping at 139 independent breast cancer risk signals		3
3	High-throughput allelic expression imbalance analyses identify candidate breast cancer risk genes		3
2	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses		2
1	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1