Douglas Easton

List of Publications by Year in Descending Order

412 papers	42,534 citations	96 h-index	199 g-index
454 ext. papers	51,228 ext. citations	12.5 avg, IF	6.13 L-index

#	Paper	IF	Citations
412	Cancer Risks Associated With and Pathogenic Variants.. *Journal of Clinical Oncology*, **2022**, JCO2102112	2.2	7
411	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
410	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
409	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
408	Oral Contraceptive Use in BRCA1 and BRCA2 Mutation Carriers: Absolute Cancer Risks and Benefits.. *Journal of the National Cancer Institute*, **2022**,	9.7	1
407	Predicting the Likelihood of Carrying a or Mutation in Asian Patients With Breast Cancer.. *Journal of Clinical Oncology*, **2022**, JCO2101647	2.2	1
406	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
405	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. *Breast Cancer Research*, **2022**, 24, 27	8.3	1
404	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9	
403	Relevance of the MHC region for breast cancer susceptibility in Asians.. *Breast Cancer*, **2022**, 1	3.4	
402	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
401	CanRisk Tool-A Web Interface for the Prediction of Breast and Ovarian Cancer Risk and the Likelihood of Carrying Genetic Pathogenic Variants. *Cancer Epidemiology Biomarkers and Prevention* , **2021**, 30, 469-473	4	14
400	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	
399	Comprehensive epithelial tubo-ovarian cancer risk prediction model incorporating genetic and epidemiological risk factors. *Journal of Medical Genetics*, **2021**,	5.8	5
398	Germline breast cancer susceptibility genes, tumor characteristics, and survival. *Genome Medicine*, **2021**, 13, 185	14.4	0
397	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0
396	Serum Estradiol and 20 Site-Specific Cancers in Women: Mendelian Randomization Study. *Journal of Clinical Endocrinology and Metabolism*, **2021**,	5.6	2

395	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
394	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
393	Improving reporting standards for polygenic scores in risk prediction studies. *Nature*, **2021**, 591, 211-219	50.4	70
392	Characterisation of PALB2 tumours through whole-exome and whole-transcriptomic analyses. *Npj Breast Cancer*, **2021**, 7, 46	7.8	1
391	Characterisation of protein-truncating and missense variants in in 15 768 women from Malaysia and Singapore. *Journal of Medical Genetics*, **2021**,	5.8	1
390	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. *Npj Breast Cancer*, **2021**, 7, 52	7.8	2
389	Personalized Risk Assessment for Prevention and Early Detection of Breast Cancer: Integration and Implementation (PERSPECTIVE I&I). *Journal of Personalized Medicine*, **2021**, 11,	3.6	13
388	First international workshop of the ATM and cancer risk group (4-5 December 2019). *Familial Cancer* , **2021**, 1	3	5
387	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
386	Cross-ancestry GWAS meta-analysis identifies six breast cancer loci in African and European ancestry women. *Nature Communications*, **2021**, 12, 4198	17.4	1
385	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
384	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
383	Common Susceptibility Loci for Male Breast Cancer. *Journal of the National Cancer Institute*, **2021**, 113, 453-461	9.7	4
382	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
381	Evaluating the role of alcohol consumption in breast and ovarian cancer susceptibility using population-based cohort studies and two-sample Mendelian randomization analyses. *International Journal of Cancer*, **2021**, 148, 1338-1350	7.5	4
380	Epidemiological and ES cell-based functional evaluation of BRCA2 variants identified in families with breast cancer. *Human Mutation*, **2021**, 42, 200-212	4.7	2
379	Detecting rare copy number variants from Illumina genotyping arrays with the CamCNV pipeline: Segmentation of z-scores improves detection and reliability. *Genetic Epidemiology*, **2021**, 45, 237-248	2.6	1
378	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. *Journal of the National Cancer Institute*, **2021**, 113, 434-442	9.7	10

377	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
376	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
375	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
374	Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut*, **2021**, 70, 1325-1334	19.2	7
373	A multilayered post-GWAS assessment on genetic susceptibility to pancreatic cancer. *Genome Medicine*, **2021**, 13, 15	14.4	6
372	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
371	Potential of polygenic risk scores for improving population estimates of women's breast cancer genetic risks. *Genetics in Medicine*, **2021**, 23, 2114-2121	8.1	3
370	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
369	Oral contraceptive use and ovarian cancer risk for BRCA1/2 mutation carriers: an international cohort study. *American Journal of Obstetrics and Gynecology*, **2021**, 225, 51.e1-51.e17	6.4	9
368	Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. *Journal of the National Cancer Institute*, **2021**,	9.7	3
367	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
366	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
365	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
364	Should Age-Dependent Absolute Risk Thresholds Be Used for Risk Stratification in Risk-Stratified Breast Cancer Screening?. *Journal of Personalized Medicine*, **2021**, 11,	3.6	3
363	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. *Breast Cancer Research*, **2021**, 23, 94	8.3	1
362	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
361	Polygenic risk scores for prediction of breast cancer risk in Asian populations.. *Genetics in Medicine*, **2021**,	8.1	2
360	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

359	The effect of sample size on polygenic hazard models for prostate cancer. *European Journal of Human Genetics*, **2020**, 28, 1467-1475	5.3	5
358	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. *Nature Reviews Clinical Oncology*, **2020**, 17, 687-705	19.4	64
357	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
356	Prostate Cancer Risk by BRCA2 Genomic Regions. *European Urology*, **2020**, 78, 494-497	10.2	2
355	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study. *PLoS ONE*, **2020**, 15, e0229999	3.7	19
354	Identification of novel breast cancer susceptibility loci in meta-analyses conducted among Asian and European descendants. *Nature Communications*, **2020**, 11, 1217	17.4	16
353	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. *Nature Communications*, **2020**, 11, 1536	17.4	12
352	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 1731-1738	4	14
351	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants: Results From the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). *JAMA Oncology*, **2020**, 6, 1218-1230	13.4	25
350	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. *Nature Communications*, **2020**, 11, 3353	17.4	32
349	Ovarian and Breast Cancer Risks Associated With Pathogenic Variants in RAD51C and RAD51D. *Journal of the National Cancer Institute*, **2020**, 112, 1242-1250	9.7	51
348	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
347	Using human genetics to understand the disease impacts of testosterone in men and women. *Nature Medicine*, **2020**, 26, 252-258	50.5	121
346	Letter to the editor: a response to Ming© study on machine learning techniques for personalized breast cancer risk prediction. *Breast Cancer Research*, **2020**, 22, 17	8.3	2
345	Candidate Causal Variants at the 8p12 Breast Cancer Risk Locus Regulate. *Cancers*, **2020**, 12,	6.6	3
344	Alcohol Consumption, Cigarette Smoking, and Risk of Breast Cancer for and Mutation Carriers: Results from The BRCA1 and BRCA2 Cohort Consortium. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 368-378	4	9
343	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
342	Risk-reducing salpingo-oophorectomy, natural menopause, and breast cancer risk: an international prospective cohort of BRCA1 and BRCA2 mutation carriers. *Breast Cancer Research*, **2020**, 22, 8	8.3	22

341	Non-coding RNAs underlie genetic predisposition to breast cancer. *Genome Biology*, **2020**, 21, 7	18.3	11
340	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
339	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
338	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
337	Prostate Cancer Risks for Male BRCA1 and BRCA2 Mutation Carriers: A Prospective Cohort Study. *European Urology*, **2020**, 77, 24-35	10.2	53
336	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
335	Chromatin interactome mapping at 139 independent breast cancer risk signals. *Genome Biology*, **2020**, 21, 8	18.3	12
334	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. *Gastroenterology*, **2020**, 158, 1274-1286.e12	13.3	47
333	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. *International Journal of Epidemiology*, **2020**, 49, 1117-1131	7.8	17
332	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133
331	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. *Genetics in Medicine*, **2020**, 22, 1653-1666	8.1	34
330	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. *Nature Communications*, **2020**, 11, 3905	17.4	12
329	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. *Nature Communications*, **2020**, 11, 3833	17.4	31
328	Identification of 31 loci for mammographic density phenotypes and their associations with breast cancer risk. *Nature Communications*, **2020**, 11, 5116	17.4	9
327	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
326	Association of germline variation with the survival of women with pathogenic variants and breast cancer. *Npj Breast Cancer*, **2020**, 6, 44	7.8	3
325	Identification of Women at High Risk of Breast Cancer Who Need Supplemental Screening. *Radiology*, **2020**, 297, 327-333	20.5	11
324	Comprehensive Functional Characterization and Clinical Interpretation of 20 Splice-Site Variants of the Gene. *Cancers*, **2020**, 12,	6.6	1

323	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
322	Genetically Predicted Levels of DNA Methylation Biomarkers and Breast Cancer Risk: Data From 228 951 Women of European Descent. *Journal of the National Cancer Institute*, **2020**, 112, 295-304	9.7	18
321	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
320	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. *International Journal of Cancer*, **2020**, 146, 2130-2138	7.5	9
319	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study **2020**, 15, e0229999		
318	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study **2020**, 15, e0229999		
317	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study **2020**, 15, e0229999		
316	Evaluating clinician acceptability of the prototype CanRisk tool for predicting risk of breast and ovarian cancer: A multi-methods study **2020**, 15, e0229999		
315	Re-evaluating genetic variants identified in candidate gene studies of breast cancer risk using data from nearly 280,000 women of Asian and European ancestry. *EBioMedicine*, **2019**, 48, 203-211	8.8	9
314	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
313	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
312	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. *Breast Cancer Research*, **2019**, 21, 68	8.3	18
311	Mendelian randomisation study of height and body mass index as modifiers of ovarian cancer risk in 22,588 BRCA1 and BRCA2 mutation carriers. *British Journal of Cancer*, **2019**, 121, 180-192	8.7	13
310	AuthorsÕresponse: Associations of obesity and circulating insulin and glucose with breast cancer risk. *International Journal of Epidemiology*, **2019**, 48, 1016-1017	7.8	
309	BRCA1 and BRCA2 pathogenic sequence variants in women of African origin or ancestry. *Human Mutation*, **2019**, 40, 1781-1796	4.7	16
308	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
307	Association analyses identify 31 new risk loci for colorectal cancer susceptibility. *Nature Communications*, **2019**, 10, 2154	17.4	81
306	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47

305	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
304	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
303	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
302	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 781-794	7.8	16
301	Sex specific associations in genome wide association analysis of renal cell carcinoma. *European Journal of Human Genetics*, **2019**, 27, 1589-1598	5.3	15
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	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. *Human Genetics*, **2019**, 138, 307-326	6.3	17
298	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
297	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
296	Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Research*, **2019**, 21, 144	8.3	11
295	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
294	The influence of obesity-related factors in the etiology of renal cell carcinoma-A mendelian randomization study. *PLoS Medicine*, **2019**, 16, e1002724	11.6	38
293	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. *Blood*, **2019**, 133, 1130-1139	2.2	17
292	Is Schizophrenia a Risk Factor for Breast Cancer?-Evidence From Genetic Data. *Schizophrenia Bulletin*, **2019**, 45, 1251-1256	1.3	11
291	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. *International Journal of Epidemiology*, **2019**, 48, 767-780	7.8	18
290	BOADICEA: a comprehensive breast cancer risk prediction model incorporating genetic and nongenetic risk factors. *Genetics in Medicine*, **2019**, 21, 1708-1718	8.1	192
289	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
288	Height and Body Mass Index as Modifiers of Breast Cancer Risk in BRCA1/2 Mutation Carriers: A Mendelian Randomization Study. *Journal of the National Cancer Institute*, **2019**, 111, 350-364	9.7	22

287	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
286	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
285	CliniciansQuse of breast cancer risk assessment tools according to their perceived importance of breast cancer risk factors: an international survey. *Journal of Community Genetics*, **2019**, 10, 61-71	2.5	5
284	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
283	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
282	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. *Nature Genetics*, **2018**, 50, 682-692	36.3	112
281	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
280	Genome-wide association study identifies susceptibility loci for B-cell childhood acute lymphoblastic leukemia. *Nature Communications*, **2018**, 9, 1340	17.4	39
279	Mutational spectrum in a worldwide study of 29,700 families with BRCA1 or BRCA2 mutations. *Human Mutation*, **2018**, 39, 593-620	4.7	138
278	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
277	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. *Human Molecular Genetics*, **2018**, 27, 853-859	5.6	15
276	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
275	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. *BMJ, The*, **2018**, 360, j5757	5.9	85
274	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
273	pedigreejs: a web-based graphical pedigree editor. *Bioinformatics*, **2018**, 34, 1069-1071	7.2	5
272	Risks of breast or ovarian cancer in BRCA1 or BRCA2 predictive test negatives: findings from the EMBRACE study. *Genetics in Medicine*, **2018**, 20, 1575-1582	8.1	12
271	Use of the BOADICEA Web Application in clinical practice: appraisals by clinicians from various countries. *Familial Cancer*, **2018**, 17, 31-41	3	6
270	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

269	Exome array analysis identifies ETFB as a novel susceptibility gene for anthracycline-induced cardiotoxicity in cancer patients. *Breast Cancer Research and Treatment*, **2018**, 167, 249-256	4.4	15
268	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. *Cancer Research*, **2018**, 78, 5419-5430	10.1	32
267	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9
266	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
265	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936	36.3	340
264	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nature Communications*, **2018**, 9, 2256	17.4	57
263	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
262	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. *Oncotarget*, **2018**, 9, 12630-12638	5.3	6
261	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
260	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. *Nature Communications*, **2018**, 9, 4616	17.4	30
259	BRCA Challenge: BRCA Exchange as a global resource for variants in BRCA1 and BRCA2. *PLoS Genetics*, **2018**, 14, e1007752	6	90
258	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. *JNCI Cancer Spectrum*, **2018**, 2, pky023	4.6	13
257	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
256	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. *Nature Communications*, **2018**, 9, 3707	17.4	57
255	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. *European Urology*, **2018**, 74, 248-252	10.2	13
254	A somatic-mutational process recurrently duplicates germline susceptibility loci and tissue-specific super-enhancers in breast cancers. *Nature Genetics*, **2017**, 49, 341-348	36.3	54
253	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
252	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49

251	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
250	Evaluating genetic variants associated with breast cancer risk in high and moderate-penetrance genes in Asians. *Carcinogenesis*, **2017**, 38, 511-518	4.6	20
249	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. *JAMA - Journal of the American Medical Association*, **2017**, 317, 2402-2416	27.4	1140
248	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. *Nature Communications*, **2017**, 8, 15724	17.4	50
247	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
246	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. *Nature Genetics*, **2017**, 49, 680-691	36.3	190
245	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
244	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
243	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. *Journal of Clinical Oncology*, **2017**, 35, 2240-2250	2.2	101
242	Gene-environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. *International Journal of Cancer*, **2017**, 141, 1830-1840	7.5	13
241	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. *British Journal of Cancer*, **2017**, 117, 734-743	8.7	5
240	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
239	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. *European Urology*, **2017**, 72, 747-754	10.2	27
238	Genome-wide association study of classical Hodgkin lymphoma identifies key regulators of disease susceptibility. *Nature Communications*, **2017**, 8, 1892	17.4	24
237	Quantifying the Genetic Correlation between Multiple Cancer Types. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 1427-1435	4	25
236	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. *Bioinformatics*, **2017**, 33, 1389-1391	7.2	2
235	Association of breast cancer risk in BRCA1 and BRCA2 mutation carriers with genetic variants showing differential allelic expression: identification of a modifier of breast cancer risk at locus 11q22.3. *Breast Cancer Research and Treatment*, **2017**, 161, 117-134	4.4	15
234	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	6.3	51

233	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. *Cancer Epidemiology Biomarkers and Prevention*, **2017**, 26, 126-135	4	183
232	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	153
231	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. *Journal of the National Cancer Institute*, **2017**, 109,	9.7	38
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9	Enhancing the BOADICEA cancer risk prediction model to incorporate new data on RAD51C, RAD51D, BARD1, updates to tumour pathology and cancer incidences		1
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7	Prospective Evaluation of a Breast Cancer Risk Model Integrating Classical Risk Factors and Polygenic Risk in 15 Cohorts from Six Countries		2
6	Improving reporting standards for polygenic scores in risk prediction studies		4
5	Combining genome-wide studies of breast, prostate, ovarian and endometrial cancers maps cross-cancer susceptibility loci and identifies new genetic associations		2
4	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers		5
3	Chromatin interactome mapping at 139 independent breast cancer risk signals		3
2	High-throughput allelic expression imbalance analyses identify candidate breast cancer risk genes		3
1	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1