

# Peter Kraft, ScD

## List of Publications by Citations

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443  
papers

47,083  
citations

104  
h-index

209  
g-index

476  
ext. papers

56,556  
ext. citations

11.6  
avg, IF

6.32  
L-index

#	Paper	IF	Citations
443	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , <b>2010</b> , 42, 937-48	36.3	2267
442	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , <b>2010</b> , 467, 832-8	50.4	1514
441	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , <b>2012</b> , 44, 981-90	36.3	1482
440	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , <b>2010</b> , 42, 579-89	36.3	1449
439	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , <b>2009</b> , 41, 25-34	36.3	1368
438	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , <b>2007</b> , 39, 870-4	36.3	1240
437	Common variants near MC4R are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , <b>2008</b> , 40, 768-75	36.3	1048
436	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , <b>2007</b> , 39, 645-9	36.3	979
435	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , <b>2008</b> , 40, 310-5	36.3	787
434	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , <b>2014</b> , 46, 234-44	36.3	784
433	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , <b>2010</b> , 42, 949-60	36.3	724
432	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
431	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , <b>2017</b> , 551, 92-94	50.4	643
430	Genome-wide association study of circulating vitamin D levels. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2739-45	5.45	616
429	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , <b>2016</b> , 48, 624-33	36.3	602
428	Causal relationship between obesity and vitamin D status: bi-directional Mendelian randomization analysis of multiple cohorts. <i>PLoS Medicine</i> , <b>2013</b> , 10, e1001383	11.6	592
427	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , <b>2019</b> , 51, 237-244	36.3	516

426	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. <i>Nature Genetics</i> , <b>2009</b> , 41, 986-90	36.3	483
425	Identification of ten loci associated with height highlights new biological pathways in human growth. <i>Nature Genetics</i> , <b>2008</b> , 40, 584-91	36.3	482
424	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. <i>Nature Genetics</i> , <b>2010</b> , 42, 224-8	36.3	463
423	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). <i>Nature Genetics</i> , <b>2009</b> , 41, 579-84	36.3	452
422	Powerful SNP-set analysis for case-control genome-wide association studies. <i>American Journal of Human Genetics</i> , <b>2010</b> , 86, 929-42	11	425
421	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , <b>2017</b> , 66, 2888-2902	29.0	414
420	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. <i>Nature Genetics</i> , <b>2013</b> , 45, 385-91, 391e1-2	36.3	413
419	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , <b>2015</b> , 47, 373-80	36.3	406
418	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , <b>2014</b> , 514, 92-97	50.4	401
417	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , <b>2009</b> , 41, 585-90	36.3	393
416	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. <i>JAMA - Journal of the American Medical Association</i> , <b>2016</b> , 315, 68-76	27.4	391
415	Elevation of circulating branched-chain amino acids is an early event in human pancreatic adenocarcinoma development. <i>Nature Medicine</i> , <b>2014</b> , 20, 1193-1198	50.5	383
414	A genome-wide association study identifies novel alleles associated with hair color and skin pigmentation. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000074	6	373
413	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , <b>2010</b> , 42, 1077-85	36.3	372
412	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , <b>2019</b> , 104, 21-34	11	363
411	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , <b>2018</b> , 50, 928-936	36.3	340
410	Performance of common genetic variants in breast-cancer risk models. <i>New England Journal of Medicine</i> , <b>2010</b> , 362, 986-93	59.2	334
409	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 1103-9	36.3	331

408	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , <b>2013</b> , 45, 392-8, 398e1-2	36.3	327
407	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , <b>2012</b> , 44, 483-9	36.3	326
406	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	324
405	Exploiting gene-environment interaction to detect genetic associations. <i>Human Heredity</i> , <b>2007</b> , 63, 111-9.1		322
404	Integrating functional data to prioritize causal variants in statistical fine-mapping studies. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004722	6	305
403	Genome-wide association studies identify loci associated with age at menarche and age at natural menopause. <i>Nature Genetics</i> , <b>2009</b> , 41, 724-8	36.3	295
402	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , <b>2015</b> , 47, 1415-25	36.3	292
401	Multiple independent loci at chromosome 15q25.1 affect smoking quantity: a meta-analysis and comparison with lung cancer and COPD. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001053	6	291
400	Heterogeneity of breast cancer associations with five susceptibility loci by clinical and pathological characteristics. <i>PLoS Genetics</i> , <b>2008</b> , 4, e1000054	6	280
399	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , <b>2017</b> , 49, 834-841	36.3	257
398	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , <b>2011</b> , 43, 1210-4	36.3	253
397	Methodological challenges in mendelian randomization. <i>Epidemiology</i> , <b>2014</b> , 25, 427-35	3.1	252
396	Anthropometric measures, body mass index, and pancreatic cancer: a pooled analysis from the Pancreatic Cancer Cohort Consortium (PanScan). <i>Archives of Internal Medicine</i> , <b>2010</b> , 170, 791-802		249
395	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , <b>2012</b> , 44, 260-8	36.3	243
394	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , <b>2011</b> , 43, 785-91	36.3	243
393	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , <b>2015</b> , 47, 1294-1303	36.3	226
392	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 994-1000	36.3	226
391	Cigarette smoking and pancreatic cancer: a pooled analysis from the pancreatic cancer cohort consortium. <i>American Journal of Epidemiology</i> , <b>2009</b> , 170, 403-13	3.8	223

390	Pathway analysis by adaptive combination of P-values. <i>Genetic Epidemiology</i> , <b>2009</b> , 33, 700-9	2.6	222
389	Genome-wide and candidate gene association study of cigarette smoking behaviors. <i>PLoS ONE</i> , <b>2009</b> , 4, e4653	3.7	202
388	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , <b>2009</b> , 41, 1055-7	36.3	201
387	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , <b>2016</b> , 48, 1462-1472	36.3	198
386	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. <i>Nature Genetics</i> , <b>2012</b> , 44, 1090-7	36.3	196
385	Joint effects of common genetic variants on the risk for type 2 diabetes in U.S. men and women of European ancestry. <i>Annals of Internal Medicine</i> , <b>2009</b> , 150, 541-50	8	191
384	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , <b>2016</b> , 2, 1295-1302	13.4	189
383	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 1767-1778	36.3	186
382	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2017</b> , 26, 126-135	4	183
381	Vitamin D-related genetic variation, plasma vitamin D, and risk of lethal prostate cancer: a prospective nested case-control study. <i>Journal of the National Cancer Institute</i> , <b>2012</b> , 104, 690-9	9.7	177
380	Replication in genome-wide association studies. <i>Statistical Science</i> , <b>2009</b> , 24, 561-573	2.4	177
379	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , <b>2018</b> , 9, 260	17.4	174
378	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , <b>2012</b> , 131, 217-34	6.3	173
377	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , <b>2015</b> , 20, 647-656	15.1	167
376	Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. <i>American Journal of Human Genetics</i> , <b>2013</b> , 92, 489-503	11	167
375	Meta-analysis of genome-wide association studies identifies 1q22 as a susceptibility locus for intracerebral hemorrhage. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 511-21	11	166
374	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007813	6	166
373	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 2706-15	5.6	164

372	Meta-analysis of 65,734 individuals identifies TSPAN15 and SLC44A2 as two susceptibility loci for venous thromboembolism. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 532-42	11	163
371	The common obesity variant near MC4R gene is associated with higher intakes of total energy and dietary fat, weight change and diabetes risk in women. <i>Human Molecular Genetics</i> , <b>2008</b> , 17, 3502-8	5.6	162
370	Genetic variants in pigmentation genes, pigmentary phenotypes, and risk of skin cancer in Caucasians. <i>International Journal of Cancer</i> , <b>2009</b> , 125, 909-17	7.5	161
369	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. <i>Nature Genetics</i> , <b>2016</b> , 48, 189-94	36.3	159
368	Adjusting for heritable covariates can bias effect estimates in genome-wide association studies. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 329-39	11	155
367	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , <b>2018</b> , 103, 691-706	11	151
366	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , <b>2013</b> , 45, 868-76	36.3	147
365	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 5373-84	5.6	143
364	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 3867-75	5.6	143
363	A genome-wide association search for type 2 diabetes genes in African Americans. <i>PLoS ONE</i> , <b>2012</b> , 7, e29202	3.7	138
362	A genome-wide association study of depressive symptoms. <i>Biological Psychiatry</i> , <b>2013</b> , 73, 667-78	7.9	135
361	Reproducibility of metabolomic profiles among men and women in 2 large cohort studies. <i>Clinical Chemistry</i> , <b>2013</b> , 59, 1657-67	5.5	135
360	Interactions between genetic variants and breast cancer risk factors in the breast and prostate cancer cohort consortium. <i>Journal of the National Cancer Institute</i> , <b>2011</b> , 103, 1252-63	9.7	134
359	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 1856-62	5.6	131
358	Genome-wide significant predictors of metabolites in the one-carbon metabolism pathway. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 4677-87	5.6	127
357	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , <b>2016</b> , 53, 800-811	5.8	121
356	Common variants of FUT2 are associated with plasma vitamin B12 levels. <i>Nature Genetics</i> , <b>2008</b> , 40, 1160-3	9.3	120
355	Characterization of gene-environment interactions for colorectal cancer susceptibility loci. <i>Cancer Research</i> , <b>2012</b> , 72, 2036-44	10.1	119

354	A genome-wide association meta-analysis of circulating sex hormone-binding globulin reveals multiple Loci implicated in sex steroid hormone regulation. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002805	6	116
353	A Population-Based Study of Genes Previously Implicated in Breast Cancer. <i>New England Journal of Medicine</i> , <b>2021</b> , 384, 440-451	59.2	115
352	Heritability in the genome-wide association era. <i>Human Genetics</i> , <b>2012</b> , 131, 1655-64	6.3	113
351	Beyond odds ratios--communicating disease risk based on genetic profiles. <i>Nature Reviews Genetics</i> , <b>2009</b> , 10, 264-9	30.1	113
350	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , <b>2014</b> , 46, 1001-1006	36.3	112
349	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 408-15	5.6	109
348	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , <b>2014</b> , 46, 1233-8	36.3	108
347	Maximizing the power of principal-component analysis of correlated phenotypes in genome-wide association studies. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 662-76	11	108
346	Hyperglycemia, insulin resistance, impaired pancreatic $\beta$ cell function, and risk of pancreatic cancer. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 1027-35	9.7	108
345	Genome-wide joint meta-analysis of SNP and SNP-by-smoking interaction identifies novel loci for pulmonary function. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1003098	6	108
344	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , <b>2016</b> , 7, 10494	17.4	107
343	Challenges and opportunities in genome-wide environmental interaction (GWEI) studies. <i>Human Genetics</i> , <b>2012</b> , 131, 1591-613	6.3	107
342	Melanocortin 1 receptor variants and skin cancer risk. <i>International Journal of Cancer</i> , <b>2006</b> , 119, 1976-84	7.5	106
341	Family history of cancer and risk of pancreatic cancer: a pooled analysis from the Pancreatic Cancer Cohort Consortium (PanScan). <i>International Journal of Cancer</i> , <b>2010</b> , 127, 1421-8	7.5	105
340	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 5356-66	5.6	104
339	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , <b>2016</b> , 6, 1052-67	24.4	104
338	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 556	17.4	103
337	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , <b>2018</b> , 50, 968-978	36.3	101



336	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 1387-98	5.6	101
335	Clinical significance of Philadelphia chromosome positive pediatric acute lymphoblastic leukemia in the context of contemporary intensive therapies. <i>Cancer</i> , <b>1998</b> , 83, 2030-2039	6.4	101
334	Pathway analysis of breast cancer genome-wide association study highlights three pathways and one canonical signaling cascade. <i>Cancer Research</i> , <b>2010</b> , 70, 4453-9	10.1	100
333	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. <i>Cell</i> , <b>2014</b> , 156, 343-58	56.2	96
332	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , <b>2011</b> , 43, 185-7	36.3	96
331	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. <i>BMJ, The</i> , <b>2017</b> , 359, j4761	5.9	94
330	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. <i>International Journal of Epidemiology</i> , <b>2016</b> , 45, 896-908	7.8	92
329	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. <i>Nature Communications</i> , <b>2014</b> , 5, 5260	17.4	89
328	Genome-wide association studies identify several new loci associated with pigmentation traits and skin cancer risk in European Americans. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 2948-59	5.6	89
327	Genome-wide association scans for secondary traits using case-control samples. <i>Genetic Epidemiology</i> , <b>2009</b> , 33, 717-28	2.6	89
326	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 2520-8	5.6	88
325	Gene-environment interactions in genome-wide association studies: a comparative study of tests applied to empirical studies of type 2 diabetes. <i>American Journal of Epidemiology</i> , <b>2012</b> , 175, 191-202	3.8	88
324	Prediagnostic body mass index and pancreatic cancer survival. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 4229-34	2.2	86
323	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , <b>2014</b> , 5, 5303	17.4	84
322	Bias and efficiency in family-based gene-characterization studies: conditional, prospective, retrospective, and joint likelihoods. <i>American Journal of Human Genetics</i> , <b>2000</b> , 66, 1119-31	11	84
321	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , <b>2016</b> , 7, 12048	17.4	82
320	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 1465-72	5.6	82
319	An absolute risk model to identify individuals at elevated risk for pancreatic cancer in the general population. <i>PLoS ONE</i> , <b>2013</b> , 8, e72311	3.7	82



3 <sup>18</sup>	The association of telomere length and genetic variation in telomere biology genes. <i>Human Mutation</i> , <b>2010</b> , 31, 1050-8	4.7	82
3 <sup>17</sup>	Plasma 25-hydroxyvitamin D and risk of pancreatic cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2012</b> , 21, 82-91	4	81
3 <sup>16</sup>	Genome-wide association study identifies novel alleles associated with risk of cutaneous basal cell carcinoma and squamous cell carcinoma. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 3718-24	5.6	80
3 <sup>15</sup>	Genome-wide association study of relative telomere length. <i>PLoS ONE</i> , <b>2011</b> , 6, e19635	3.7	80
3 <sup>14</sup>	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. <i>PLoS Medicine</i> , <b>2016</b> , 13, e1002105	11.6	80
3 <sup>13</sup>	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , <b>2017</b> , 186, 753-761	3.8	78
3 <sup>12</sup>	A prospective study of plasma adiponectin and pancreatic cancer risk in five US cohorts. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 95-103	9.7	78
3 <sup>11</sup>	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 6616-33	5.6	77
3 <sup>10</sup>	Exposure to environmental ozone alters semen quality. <i>Environmental Health Perspectives</i> , <b>2006</b> , 114, 360-5	8.4	77
3 <sup>09</sup>	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , <b>2020</b> , 52, 572-581	36.3	76
3 <sup>08</sup>	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. <i>Depression and Anxiety</i> , <b>2016</b> , 33, 265-80	8.4	76
3 <sup>07</sup>	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , <b>2015</b> , 6, 6889	17.4	75
3 <sup>06</sup>	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	74
3 <sup>05</sup>	Genome-wide association study identifies five susceptibility loci for follicular lymphoma outside the HLA region. <i>American Journal of Human Genetics</i> , <b>2014</b> , 95, 462-71	11	74
3 <sup>04</sup>	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. <i>Nature Genetics</i> , <b>2017</b> , 49, 993-1004	36.3	72
3 <sup>03</sup>	Inclusion of gene-gene and gene-environment interactions unlikely to dramatically improve risk prediction for complex diseases. <i>American Journal of Human Genetics</i> , <b>2012</b> , 90, 962-72	11	71
3 <sup>02</sup>	Genome-wide association study identifies common variants associated with circulating vitamin E levels. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 3876-83	5.6	71
3 <sup>01</sup>	Genomewide meta-analysis identifies loci associated with IGF-I and IGFBP-3 levels with impact on age-related traits. <i>Aging Cell</i> , <b>2016</b> , 15, 811-24	9.9	71

300	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , <b>2016</b> , 7, 10933	17.4	70
299	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 3166	17.4	70
298	Obesity susceptibility loci and uncontrolled eating, emotional eating and cognitive restraint behaviors in men and women. <i>Obesity</i> , <b>2014</b> , 22, E135-41	8	70
297	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , <b>2021</b> , 591, 211-219	50.4	70
296	Association of prostate cancer risk variants with gene expression in normal and tumor tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 255-60	4	69
295	Gene-environment interplay in common complex diseases: forging an integrative model—recommendations from an NIH workshop. <i>Genetic Epidemiology</i> , <b>2011</b> , 35, 217-25	2.6	68
294	Improved methods for multi-trait fine mapping of pleiotropic risk loci. <i>Bioinformatics</i> , <b>2017</b> , 33, 248-255	7.2	67
293	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , <b>2016</b> , 7, 66328-66343	3.3	66
292	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , <b>2016</b> , 76, 5103-14	10.1	66
291	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. <i>Nature Communications</i> , <b>2016</b> , 7, 12510	17.4	65
290	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , <b>2016</b> , 7, 11375	17.4	64
289	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , <b>2019</b> , 134, 1645-1657	2.2	63
288	Evaluation of polygenic risk scores for predicting breast and prostate cancer risk. <i>Genetic Epidemiology</i> , <b>2011</b> , 35, 506-514	2.6	63
287	Genome-wide association study identifies polymorphisms in LEPR as determinants of plasma soluble leptin receptor levels. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 1846-55	5.6	63
286	Survival among patients with pancreatic cancer and long-standing or recent-onset diabetes mellitus. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 29-35	2.2	62
285	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , <b>2021</b> , 53, 65-75	36.3	62
284	Expression QTL-based analyses reveal candidate causal genes and loci across five tumor types. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 5294-302	5.6	61
283	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , <b>2016</b> , 7, 11843	17.4	59

282	Prostate cancer (PCa) risk variants and risk of fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>European Urology</i> , <b>2014</b> , 65, 1069-75	10.2	58
281	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , <b>2018</b> , 9, 2256	17.4	57
280	Association of type 2 diabetes susceptibility variants with advanced prostate cancer risk in the Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , <b>2012</b> , 176, 1121-9	3.8	57
279	A genome-wide association study of prognosis in breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2010</b> , 19, 1140-3	4	56
278	Genome-wide association study of circulating retinol levels. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 4724-31	3.6	56
277	Novel genetic markers of breast cancer survival identified by a genome-wide association study. <i>Cancer Research</i> , <b>2012</b> , 72, 1182-9	10.1	56
276	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. <i>PLoS ONE</i> , <b>2017</b> , 12, e0177875	3.7	56
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274	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested case-control study. <i>PLoS Medicine</i> , <b>2018</b> , 15, e1002644	11.6	56
273	CHRNA5 risk variant predicts delayed smoking cessation and earlier lung cancer diagnosis--a meta-analysis. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	55
272	Cigarette Smoking and Pancreatic Cancer Survival. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 1822-1828	2.2	55
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270	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. <i>Nature Communications</i> , <b>2017</b> , 8, 14175	17.4	54
269	Eighteen insulin-like growth factor pathway genes, circulating levels of IGF-I and its binding protein, and risk of prostate and breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2010</b> , 19, 2877-84	8.1	54
268	Genome-wide meta-analysis of joint tests for genetic and gene-environment interaction effects. <i>Human Heredity</i> , <b>2010</b> , 70, 292-300	1.1	54
267	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. <i>Gastroenterology</i> , <b>2016</b> , 151, 351-363.e28	13.3	54
266	Genome-Wide Association Study for Incident Myocardial Infarction and Coronary Heart Disease in Prospective Cohort Studies: The CHARGE Consortium. <i>PLoS ONE</i> , <b>2016</b> , 11, e0144997	3.7	53
265	Consumers report lower confidence in their genetics knowledge following direct-to-consumer personal genomic testing. <i>Genetics in Medicine</i> , <b>2016</b> , 18, 65-72	8.1	52

264	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , <b>2019</b> , 48, 795-806	7.8	52
263	Genome-wide association study of circulating estradiol, testosterone, and sex hormone-binding globulin in postmenopausal women. <i>PLoS ONE</i> , <b>2012</b> , 7, e37815	3.7	51
262	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 1307-1318	8.3	50
261	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , <b>2017</b> , 8, 15724	17.4	50
260	Prediction of breast cancer risk by genetic risk factors, overall and by hormone receptor status. <i>Journal of Medical Genetics</i> , <b>2012</b> , 49, 601-8	5.8	49
259	Common genetic variants in prostate cancer risk prediction--results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2012</b> , 21, 437-44	4	49
258	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. <i>PLoS Medicine</i> , <b>2016</b> , 13, e1002118	11.6	49
257	Characterizing associations and SNP-environment interactions for GWAS-identified prostate cancer risk markers--results from BPC3. <i>PLoS ONE</i> , <b>2011</b> , 6, e17142	3.7	49
256	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 1741	17.4	47
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253	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , <b>2021</b> , 12, 1258	17.4	47
252	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. <i>Nature Communications</i> , <b>2018</b> , 9, 4774	17.4	47
251	TERT gene harbors multiple variants associated with pancreatic cancer susceptibility. <i>International Journal of Cancer</i> , <b>2015</b> , 137, 2175-83	7.5	46
250	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. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 3089-101	5.6	46
249	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , <b>2019</b> , 10, 431	17.4	45
248	A genome-wide association study of bitter and sweet beverage consumption. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 2449-2457	5.6	45
247	Inclusion of endogenous hormone levels in risk prediction models of postmenopausal breast cancer. <i>Journal of Clinical Oncology</i> , <b>2014</b> , 32, 3111-7	2.2	45

246	Circadian genes and breast cancer susceptibility in rotating shift workers. <i>International Journal of Cancer</i> , <b>2012</b> , 131, 2547-52	7.5	45
245	A genome-wide association study of marginal zone lymphoma shows association to the HLA region. <i>Nature Communications</i> , <b>2015</b> , 6, 5751	17.4	44
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243	Genome-wide association study identifies nidogen 1 (NID1) as a susceptibility locus to cutaneous nevi and melanoma risk. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 2673-9	5.6	43
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241	Aggregate penetrance of genomic variants for actionable disorders in European and African Americans. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 364ra151	17.5	41
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225	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , <b>2021</b> , 5, 59-70	12.8	33
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157	Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. <i>Breast Cancer Research</i> , <b>2019</b> , 21, 68	8.3	18

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149	A Mendelian randomization analysis of circulating lipid traits and breast cancer risk. <i>International Journal of Epidemiology</i> , <b>2020</b> , 49, 1117-1131	7.8	17
148	The genetic interplay between body mass index, breast size and breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , <b>2019</b> , 48, 781-794	7.8	16
147	Agnostic Pathway/Gene Set Analysis of Genome-Wide Association Data Identifies Associations for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , <b>2019</b> , 111, 557-567	9.7	16
146	Genetic Tools for Coronary Risk Assessment in Type 2 Diabetes: A Cohort Study From the ACCORD Clinical Trial. <i>Diabetes Care</i> , <b>2018</b> , 41, 2404-2413	14.6	16
145	Use of deep whole-genome sequencing data to identify structure risk variants in breast cancer susceptibility genes. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 853-859	5.6	15
144	Quantifying the Polygenic Contribution to Cutaneous Squamous Cell Carcinoma Risk. <i>Journal of Investigative Dermatology</i> , <b>2018</b> , 138, 1507-1510	4.3	15
143	Genetic overlap between autoimmune diseases and non-Hodgkin lymphoma subtypes. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 844-863	2.6	15
142	Association of a Primary Open-Angle Glaucoma Genetic Risk Score With Earlier Age at Diagnosis. <i>JAMA Ophthalmology</i> , <b>2019</b> , 137, 1190-1194	3.9	15
141	Sex specific associations in genome wide association analysis of renal cell carcinoma. <i>European Journal of Human Genetics</i> , <b>2019</b> , 27, 1589-1598	5.3	15
140	Interactions between genome-wide significant genetic variants and circulating concentrations of insulin-like growth factor 1, sex hormones, and binding proteins in relation to prostate cancer risk in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , <b>2012</b> , 175, 926-35	3.8	15
139	Circulating Lysophosphatidylcholines, Phosphatidylcholines, Ceramides, and Sphingomyelins and Ovarian Cancer Risk: A 23-Year Prospective Study. <i>Journal of the National Cancer Institute</i> , <b>2020</b> , 112, 628-636	9.7	15

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137	A genome-wide association study to identify genetic susceptibility loci that modify ductal and lobular postmenopausal breast cancer risk associated with menopausal hormone therapy use: a two-stage design with replication. <i>Breast Cancer Research and Treatment</i> , <b>2013</b> , 138, 529-542	4.4	14
136	Association of Prostate Cancer Risk Variants with TMPRSS2:ERG Status: Evidence for Distinct Molecular Subtypes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2016</b> , 25, 745-9	4	14
135	Genetic associations with neuroendocrine tumor risk: results from a genome-wide association study. <i>Endocrine-Related Cancer</i> , <b>2016</b> , 23, 587-94	5.7	14
134	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , <b>2021</b> , 113, 329-337	9.7	14
133	Biomarker correlation network in colorectal carcinoma by tumor anatomic location. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 304	3.6	13
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131	Interaction of a genetic risk score with physical activity, physical inactivity, and body mass index in relation to venous thromboembolism risk. <i>Genetic Epidemiology</i> , <b>2018</b> , 42, 354-365	2.6	13
130	Incorporation of Biological Knowledge Into the Study of Gene-Environment Interactions. <i>American Journal of Epidemiology</i> , <b>2017</b> , 186, 771-777	3.8	13
129	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. <i>Scientific Reports</i> , <b>2017</b> , 7, 11380	4.9	13
128	Genome-wide meta-analysis identifies eight new susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , <b>2020</b> , 11, 820	17.4	13
127	A response to "Personalised medicine and population health: breast and ovarian cancer". <i>Human Genetics</i> , <b>2019</b> , 138, 287-289	6.3	13
126	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. <i>International Journal of Epidemiology</i> , <b>2020</b> , 49, 216-232	7.8	13
125	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , <b>2021</b> , 148, 307-319	7.5	13
124	Polymorphism Influences the Cardiovascular Benefit of Fenofibrate in Type 2 Diabetes: Findings From ACCORD-Lipid. <i>Diabetes</i> , <b>2020</b> , 69, 771-783	0.9	12
123	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , <b>2019</b> , 5, 38	7.8	12
122	Genomics, Telomere Length, Epigenetics, and Metabolomics in the Nurses' Health Studies. <i>American Journal of Public Health</i> , <b>2016</b> , 106, 1663-8	5.1	12
121	Targeted sequencing to identify novel genetic risk factors for deep vein thrombosis: a study of 734 genes. <i>Journal of Thrombosis and Haemostasis</i> , <b>2018</b> , 16, 2432-2441	15.4	12

120	Risk of Breast Cancer Among Carriers of Pathogenic Variants in Breast Cancer Predisposition Genes Varies by Polygenic Risk Score. <i>Journal of Clinical Oncology</i> , <b>2021</b> , 39, 2564-2573	2.2	12
119	A large-scale exome array analysis of venous thromboembolism. <i>Genetic Epidemiology</i> , <b>2019</b> , 43, 449-457.	2.6	11
118	Joint effects of colorectal cancer susceptibility loci, circulating 25-hydroxyvitamin D and risk of colorectal cancer. <i>PLoS ONE</i> , <b>2014</b> , 9, e92212	3.7	11
117	Associations between smoking behavior-related alleles and the risk of melanoma. <i>Oncotarget</i> , <b>2016</b> , 7, 47366-47375	3.3	11
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115	Metabolome-Wide Association Study of the Relationship Between Habitual Physical Activity and Plasma Metabolite Levels. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1932-1943	3.8	10
114	Lupus-related single nucleotide polymorphisms and risk of diffuse large B-cell lymphoma. <i>Lupus Science and Medicine</i> , <b>2017</b> , 4, e000187	4.6	10
113	Residential particulate matter and distance to roadways in relation to mammographic density: results from the Nurses' Health Studies. <i>Breast Cancer Research</i> , <b>2017</b> , 19, 124	8.3	10
112	Prediagnostic Leukocyte Telomere Length and Pancreatic Cancer Survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2019</b> , 28, 1868-1875	4	10
111	Personalizing Breast Cancer Screening Based on Polygenic Risk and Family History. <i>Journal of the National Cancer Institute</i> , <b>2021</b> , 113, 434-442	9.7	10
110	Modulation of GLP-1 Levels by a Genetic Variant That Regulates the Cardiovascular Effects of Intensive Glycemic Control in ACCORD. <i>Diabetes Care</i> , <b>2018</b> , 41, 348-355	14.6	10
109	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. <i>EBioMedicine</i> , <b>2019</b> , 48, 203-211	8.8	9
108	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. <i>Genetic Epidemiology</i> , <b>2020</b> , 44, 442-468	2.6	9
107	A genome-wide association study of energy intake and expenditure. <i>PLoS ONE</i> , <b>2018</b> , 13, e0201555	3.7	9
106	Testosterone Pathway Genetic Polymorphisms in Relation to Primary Open-Angle Glaucoma: An Analysis in Two Large Datasets <b>2018</b> , 59, 629-636		9
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104	Joint Effects of PON1 Polymorphisms and Vegetable Intake on Ischemic Stroke: A Family-Based Case Control Study. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	9
103	A lipid-related metabolomic pattern of diet quality. <i>American Journal of Clinical Nutrition</i> , <b>2020</b> , 112, 1613-1630	7	9

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100	A whole genome approach for discovering the genetic basis of blood group antigens: independent confirmation for P1 and Xg. <i>Transfusion</i> , <b>2019</b> , 59, 908-915	2.9	9
99	Genome-wide association study of anti-Müllerian hormone levels in pre-menopausal women of late reproductive age and relationship with genetic determinants of reproductive lifespan. <i>Human Molecular Genetics</i> , <b>2019</b> , 28, 1392-1401	5.6	9
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97	Interactions Between Genome-Wide Significant Genetic Variants and Circulating Concentrations of 25-Hydroxyvitamin D in Relation to Prostate Cancer Risk in the National Cancer Institute BPC3. <i>American Journal of Epidemiology</i> , <b>2017</b> , 185, 452-464	3.8	8
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92	Two high-risk susceptibility loci at 6p25.3 and 14q32.13 for Waldenström macroglobulinemia. <i>Nature Communications</i> , <b>2018</b> , 9, 4182	17.4	8
91	Polygenic risk score of shorter telomere length and risk of depression and anxiety in women. <i>Journal of Psychiatric Research</i> , <b>2018</b> , 103, 182-188	5.2	8
90	Variation in predictive ability of common genetic variants by established strata: the example of breast cancer and age. <i>Epidemiology</i> , <b>2015</b> , 26, 51-8	3.1	7
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82	The case-only test for gene-environment interaction is not uniformly powerful: an empirical example. <i>Genetic Epidemiology</i> , <b>2013</b> , 37, 402-7	2.6	7
81	A targeted genetic association study of epithelial ovarian cancer susceptibility. <i>Oncotarget</i> , <b>2016</b> , 7, 7381-9	3.9	7
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79	Colorectal cancer susceptibility variants and risk of conventional adenomas and serrated polyps: results from three cohort studies. <i>International Journal of Epidemiology</i> , <b>2020</b> , 49, 259-269	7.8	7
78	Genetic Correlations Between Diabetes and Glaucoma: An Analysis of Continuous and Dichotomous Phenotypes. <i>American Journal of Ophthalmology</i> , <b>2019</b> , 206, 245-255	4.9	6
77	Joint effects of fatty acid desaturase 1 polymorphisms and dietary polyunsaturated fatty acid intake on circulating fatty acid proportions. <i>American Journal of Clinical Nutrition</i> , <b>2018</b> , 107, 826-833	7	6
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70	Additive and Multiplicative Interactions Between Genetic Risk Score and Family History and Lifestyle in Relation to Risk of Type 2 Diabetes. <i>American Journal of Epidemiology</i> , <b>2020</b> , 189, 445-460	3.8	6
69	Circulating carotenoids and breast cancer among high-risk individuals. <i>American Journal of Clinical Nutrition</i> , <b>2021</b> , 113, 525-533	7	6
68	Analysis of epidemiologic studies of genetic effects and gene-environment interactions. <i>Iarc (international Agency for Research on Cancer) Scientific Publications</i> , <b>2011</b> , 281-301		6
67	Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. <i>British Journal of Cancer</i> , <b>2016</b> , 114, 298-304	8.7	5



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65	Distinct in vivo engraftment and growth patterns of t(1;19)+/E2A-PBX1+ and t(9;22)+/BCR-ABL+ human leukemia cells in SCID mice. <i>Leukemia and Lymphoma</i> , <b>1998</b> , 32, 77-87	1.9	5
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63	Joint Analysis of Multiple Interaction Parameters in Genetic Association Studies. <i>Genetics</i> , <b>2019</b> , 211, 483-494	4	5
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53	Genome-Wide Association Study for Urinary and Fecal Incontinence in Women. <i>Journal of Urology</i> , <b>2020</b> , 203, 978-983	2.5	4
52	A large cross-ancestry meta-analysis of genome-wide association studies identifies 69 novel risk loci for primary open-angle glaucoma and includes a genetic link with Alzheimer's disease		4
51	Improving reporting standards for polygenic scores in risk prediction studies		4
50	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , <b>2021</b> , 12, 1078	17.4	4
49	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. <i>Breast Cancer Research</i> , <b>2022</b> , 24, 2	8.3	3

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47	Mixed-model admixture mapping identifies smoking-dependent loci of lung function in African Americans. <i>European Journal of Human Genetics</i> , <b>2020</b> , 28, 656-668	5.3	3
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42	Leveraging Methylome-Environment Interaction to Detect Genetic Determinants of Disease. <i>Human Heredity</i> , <b>2016</b> , 81, 26-34	1.1	2
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40	VEXOR: an integrative environment for prioritization of functional variants in fine-mapping analysis. <i>Bioinformatics</i> , <b>2017</b> , 33, 1389-1391	7.2	2
39	Estimating the effective sample size in association studies of quantitative traits		2
38	Prospective Evaluation of a Breast Cancer Risk Model Integrating Classical Risk Factors and Polygenic Risk in 15 Cohorts from Six Countries		2
37	Combining genome-wide studies of breast, prostate, ovarian and endometrial cancers maps cross-cancer susceptibility loci and identifies new genetic associations		2
36	Circulating Lysophosphatidylcholines, Phosphatidylcholines, Ceramides, and Sphingomyelins and Ovarian Cancer Risk: a 23-year Prospective Study		2
35	A prospective analysis of circulating plasma metabolomics and ovarian cancer risk		2
34	Hepcidin-regulating iron metabolism genes and pancreatic ductal adenocarcinoma: a pathway analysis of genome-wide association studies. <i>American Journal of Clinical Nutrition</i> , <b>2021</b> , 114, 1408-1417		2
33	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , <b>2021</b> , 124, 842-854	8.7	2
32	Smoking Modifies Pancreatic Cancer Risk Loci on 2q21.3. <i>Cancer Research</i> , <b>2021</b> , 81, 3134-3143	10.1	2
31	Hierarchical modeling of melanocortin 1 receptor variants with skin cancer risk. <i>Genetic Epidemiology</i> , <b>2018</b> , 42, 571-586	2.6	2

30	Polygenic risk scores for prediction of breast cancer risk in Asian populations.. <i>Genetics in Medicine</i> , <b>2021</b> ,	8.1	2
29	Polygenic scores, diet quality, and type 2 diabetes risk: An observational study among 35,759 adults from 3 US cohorts.. <i>PLoS Medicine</i> , <b>2022</b> , 19, e1003972	11.6	2
28	Cross-Cancer Analysis Reveals Novel Pleiotropic Associations-Response. <i>Cancer Research</i> , <b>2017</b> , 77, 6045-6046	10.4	1
27	Response to Day et al. <i>American Journal of Human Genetics</i> , <b>2016</b> , 98, 394-5	11	1
26	Genomic correlation, shared loci, and causal relationship between obesity and polycystic ovary syndrome: a large-scale genome-wide cross-trait analysis.. <i>BMC Medicine</i> , <b>2022</b> , 20, 66	11.4	1
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24	Common variants in breast cancer risk loci predispose to distinct tumor subtypes		1
23	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts		1
22	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1
21	Playing Musical Chairs in Big Data to Reveal Variables Associations		1
20	Genomic analyses for age at menarche identify 389 independent signals and indicate BMI-independent effects of puberty timing on cancer susceptibility		1
19	Prediagnostic Inflammation and Pancreatic Cancer Survival. <i>Journal of the National Cancer Institute</i> , <b>2021</b> , 113, 1186-1193	9.7	1
18	Obesity, Adiposity, and Risk of Symptomatic Gallstone Disease According to Genetic Susceptibility. <i>Clinical Gastroenterology and Hepatology</i> , <b>2021</b> ,	6.9	1
17	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1190-1203	11	1
16	A Genome-Wide Association Study of Childhood Body Fatness. <i>Obesity</i> , <b>2021</b> , 29, 446-453	8	1
15	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. <i>Breast Cancer Research</i> , <b>2021</b> , 23, 86	8.3	1
14	Multitrait GWAS to connect disease variants and biological mechanisms. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009763	13	1
13	A 584bp deletion in CTRB2 inhibits chymotrypsin B2 activity and secretion and confers risk of pancreatic cancer. <i>American Journal of Human Genetics</i> , <b>2021</b> , 108, 1852-1865	11	1

12	Rare germline copy number variants (CNVs) and breast cancer risk.. <i>Communications Biology</i> , <b>2022</b> , 5, 65	6.7	o
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9	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , <b>2021</b> , 11, 19787	4.9	o
8	Multitrait transcriptome-wide association study (TWAS) tests. <i>Genetic Epidemiology</i> , <b>2021</b> , 45, 563-576	2.6	o
7	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , <b>2021</b> , 125, 1135-1145	8.7	o
6	Height, nevus count, and risk of cutaneous malignant melanoma: Results from 2 large cohorts of US women. <i>Journal of the American Academy of Dermatology</i> , <b>2020</b> , 83, 1049-1056	4.5	
5	Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. <i>Obstetrical and Gynecological Survey</i> , <b>2015</b> , 70, 758-762 <sup>2,4</sup>		
4	Involvement of fine particulate matter exposure with gene expression pathways in breast tumor and adjacent-normal breast tissue. <i>Environmental Research</i> , <b>2020</b> , 186, 109535	7.9	
3	A comprehensive analysis of polymorphic variants in steroid hormone and insulin-like growth factor-1 metabolism and risk of in situ breast cancer: Results from the Breast and Prostate Cancer Cohort Consortium. <i>International Journal of Cancer</i> , <b>2018</b> , 142, 1182-1188	7.5	
2	Reply to 'Misestimation of heritability and prediction accuracy of male-pattern baldness'. <i>Nature Communications</i> , <b>2018</b> , 9, 2538	17.4	
1	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. <i>Scientific Reports</i> , <b>2022</b> , 12, 6199	4.9	