

# Peter Kraft

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

301  
papers

16,495  
citations

64  
h-index

120  
g-index

319  
ext. papers

22,009  
ext. citations

10.4  
avg, IF

5.97  
L-index

#	Paper	IF	Citations
301	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
300	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
299	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
298	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , <b>2017</b> , 66, 2888-2902	19.1	414
297	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
296	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
295	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
294	Curses--winner and otherwise--in genetic epidemiology. <i>Epidemiology</i> , <b>2008</b> , 19, 649-51; discussion 657-8	3.1	360
293	Genetic risk prediction--are we there yet?. <i>New England Journal of Medicine</i> , <b>2009</b> , 360, 1701-3	59.2	341
292	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
291	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
290	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
289	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , <b>2012</b> , 44, 483-9	36.3	326
288	Exploiting gene-environment interaction to detect genetic associations. <i>Human Heredity</i> , <b>2007</b> , 63, 111-9.	9.1	322
287	Integrating functional data to prioritize causal variants in statistical fine-mapping studies. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004722	6	305
286	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
285	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

284	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
283	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , <b>2014</b> , 46, 994-1000	36.3	226
282	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , <b>2016</b> , 48, 1462-1472	36.3	198
281	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
280	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
279	Replication in genome-wide association studies. <i>Statistical Science</i> , <b>2009</b> , 24, 561-573	2.4	177
278	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
277	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
276	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
275	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
274	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
273	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
272	Accounting for haplotype uncertainty in matched association studies: a comparison of simple and flexible techniques. <i>Genetic Epidemiology</i> , <b>2005</b> , 28, 261-72	2.6	128
271	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
270	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-462	30.4	119
269	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
268	Beyond odds ratios--communicating disease risk based on genetic profiles. <i>Nature Reviews Genetics</i> , <b>2009</b> , 10, 264-9	30.1	113
267	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

266	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
265	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
264	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , <b>2016</b> , 7, 10494	17.4	107
263	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
262	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
261	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 556	17.4	103
260	The MedSeq Project: a randomized trial of integrating whole genome sequencing into clinical medicine. <i>Trials</i> , <b>2014</b> , 15, 85	2.8	103
259	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
258	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. <i>BMJ, The</i> , <b>2017</b> , 359, j4761	5.9	94
257	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
256	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
255	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
254	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
253	A Pathway Analysis of Hereditary Hemochromatosis-related Genes and Pancreatic Ductal Adenocarcinoma Risk (FS11-05-19). <i>Current Developments in Nutrition</i> , <b>2019</b> , 3,	0.4	78
252	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 487-97	11	77
251	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
250	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
249	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

248	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , <b>2015</b> , 6, 6889	17.4	75
247	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
246	Association of CAV1/CAV2 genomic variants with primary open-angle glaucoma overall and by gender and pattern of visual field loss. <i>Ophthalmology</i> , <b>2014</b> , 121, 508-16	7.3	73
245	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
244	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
243	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 3166	17.4	70
242	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , <b>2021</b> , 591, 211-219	50.4	70
241	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
240	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
239	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
238	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
237	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , <b>2016</b> , 7, 11375	17.4	64
236	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
235	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
234	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
233	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
232	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
231	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

230	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
229	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
228	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , <b>2020</b> , 52, 56-73	36.3	56
227	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
226	Cigarette Smoking and Pancreatic Cancer Survival. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 1822-1828	2.2	55
225	Integrating epidemiology and genetic association: the challenge of gene-environment interaction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2005</b> , 360, 1609-16	5.8	55
224	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
223	Genetic variation in the HSD17B1 gene and risk of prostate cancer. <i>PLoS Genetics</i> , <b>2005</b> , 1, e68	6	54
222	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
221	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
220	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
219	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
218	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , <b>2017</b> , 8, 15724	17.4	50
217	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
216	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
215	A Cross-Cancer Genetic Association Analysis of the DNA Repair and DNA Damage Signaling Pathways for Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2016</b> , 25, 193-200	4	47
214	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
213	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

212	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
211	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , <b>2019</b> , 10, 431	17.4	45
210	Novel Associations between Common Breast Cancer Susceptibility Variants and Risk-Predicting Mammographic Density Measures. <i>Cancer Research</i> , <b>2015</b> , 75, 2457-67	10.1	45
209	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
208	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
207	Circulating vitamin D, vitamin D-related genetic variation, and risk of fatal prostate cancer in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>Cancer</i> , <b>2015</b> , 121, 1949-56	6.4	43
206	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
205	Precision Prevention and Early Detection of Cancer: Fundamental Principles. <i>Cancer Discovery</i> , <b>2018</b> , 8, 803-811	24.4	40
204	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , <b>2019</b> , 10, 4957	17.4	40
203	Study designs for genome-wide association studies. <i>Advances in Genetics</i> , <b>2008</b> , 60, 465-504	3.3	40
202	Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 1663-76	5.6	39
201	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,	9.7	38
200	Identification of a melanoma susceptibility locus and somatic mutation in TET2. <i>Carcinogenesis</i> , <b>2014</b> , 35, 2097-101	4.6	38
199	Genome-wide association study of selenium concentrations. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 1469-77	3.6	37
198	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. <i>Nature Communications</i> , <b>2016</b> , 7, 10979	17.4	37
197	Impact of Pre-analytic Blood Sample Collection Factors on Metabolomics. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2016</b> , 25, 823-829	4	37
196	Transcriptome-wide association studies accounting for colocalization using Egger regression. <i>Genetic Epidemiology</i> , <b>2018</b> , 42, 418-433	2.6	37
195	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 5603-18	5.6	35

194	Genome-wide interaction study of smoking and bladder cancer risk. <i>Carcinogenesis</i> , <b>2014</b> , 35, 1737-44	4.6	33
193	Using genetics to test the causal relationship of total adiposity and periodontitis: Mendelian randomization analyses in the Gene-Lifestyle Interactions and Dental Endpoints (GLIDE) Consortium. <i>International Journal of Epidemiology</i> , <b>2015</b> , 44, 638-50	7.8	33
192	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
191	Red meat intake, NAT2, and risk of colorectal cancer: a pooled analysis of 11 studies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 198-205	4	32
190	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , <b>2020</b> , 11, 3353	17.4	32
189	Genetic Predictors of Cardiovascular Mortality During Intensive Glycemic Control in Type 2 Diabetes: Findings From the ACCORD Clinical Trial. <i>Diabetes Care</i> , <b>2016</b> , 39, 1915-1924	14.6	32
188	Pancreatic Cancer Risk Associated with Prediagnostic Plasma Levels of Leptin and Leptin Receptor Genetic Polymorphisms. <i>Cancer Research</i> , <b>2016</b> , 76, 7160-7167	10.1	32
187	Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. <i>Genetics in Medicine</i> , <b>2017</b> , 19, 30-35	8.1	31
186	Integration of Metabolomic and Other Omics Data in Population-Based Study Designs: An Epidemiological Perspective. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	31
185	Summarizing polygenic risks for complex diseases in a clinical whole-genome report. <i>Genetics in Medicine</i> , <b>2015</b> , 17, 536-44	8.1	30
184	Prediagnostic Plasma 25-Hydroxyvitamin D and Pancreatic Cancer Survival. <i>Journal of Clinical Oncology</i> , <b>2016</b> , 34, 2899-905	2.2	30
183	Fine-mapping the HOXB region detects common variants tagging a rare coding allele: evidence for synthetic association in prostate cancer. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004129	6	30
182	Post-GWAS gene-environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79,000 women. <i>Human Molecular Genetics</i> , <b>2014</b> , 23, 5260-70	5.6	30
181	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , <b>2016</b> , 139, 2655-2670	7.5	30
180	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , <b>2018</b> , 9, 4616	17.4	30
179	Prescription medication changes following direct-to-consumer personal genomic testing: findings from the Impact of Personal Genomics (PGen) Study. <i>Genetics in Medicine</i> , <b>2017</b> , 19, 537-545	8.1	29
178	Assessing the Association of Mitochondrial Genetic Variation With Primary Open-Angle Glaucoma Using Gene-Set Analyses <b>2016</b> , 57, 5046-5052		29
177	Gain-of-function mutations in SMAD4 cause a distinctive repertoire of cardiovascular phenotypes in patients with Myhre syndrome. <i>American Journal of Medical Genetics, Part A</i> , <b>2016</b> , 170, 2617-31	2.5	29



176	Leucocyte telomere length, genetic variants at the gene region and risk of pancreatic cancer. <i>Gut</i> , <b>2017</b> , 66, 1116-1122	19.2	28
175	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , <b>2019</b> , 120, 647-657	8.7	28
174	A Genome-Wide Association Study of Cutaneous Squamous Cell Carcinoma among European Descendants. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2016</b> , 25, 714-20	4	28
173	Association of breast cancer risk loci with breast cancer survival. <i>International Journal of Cancer</i> , <b>2015</b> , 137, 2837-45	7.5	28
172	Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. <i>Carcinogenesis</i> , <b>2016</b> , 37, 96-105	4.6	27
171	Genetic Variants Related to Longer Telomere Length are Associated with Increased Risk of Renal Cell Carcinoma. <i>European Urology</i> , <b>2017</b> , 72, 747-754	10.2	27
170	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , <b>2017</b> , 46, 1814-1822	7.8	27
169	A comprehensive survey of genetic variation in 20,691 subjects from four large cohorts. <i>PLoS ONE</i> , <b>2017</b> , 12, e0173997	3.7	27
168	A genome-wide investigation of food addiction. <i>Obesity</i> , <b>2016</b> , 24, 1336-41	8	27
167	Associations of dairy intake with risk of mortality in women and men: three prospective cohort studies. <i>BMJ, The</i> , <b>2019</b> , 367, l6204	5.9	27
166	The genetics of vitamin D. <i>Bone</i> , <b>2019</b> , 126, 59-77	4.7	27
165	Functional characterization of a multi-cancer risk locus on chr5p15.33 reveals regulation of TERT by ZNF148. <i>Nature Communications</i> , <b>2017</b> , 8, 15034	17.4	26
164	Complex diseases, complex genes: keeping pathways on the right track. <i>Epidemiology</i> , <b>2009</b> , 20, 508-11	3.1	26
163	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , <b>2017</b> , 46, 894-904	7.8	25
162	Efficient cross-trait penalized regression increases prediction accuracy in large cohorts using secondary phenotypes. <i>Nature Communications</i> , <b>2019</b> , 10, 569	17.4	25
161	Investigating the genetic relationship between Alzheimer's disease and cancer using GWAS summary statistics. <i>Human Genetics</i> , <b>2017</b> , 136, 1341-1351	6.3	25
160	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2017</b> , 26, 1427-1435	4	25
159	Finding the missing gene-environment interactions. <i>European Journal of Epidemiology</i> , <b>2015</b> , 30, 353-5	12.1	25

158	A Transcriptome-Wide Association Study Identifies Novel Candidate Susceptibility Genes for Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , <b>2020</b> , 112, 1003-1012	9.7	25
157	De Novo Variants in the ATPase Module of MORC2 Cause a Neurodevelopmental Disorder with Growth Retardation and Variable Craniofacial Dysmorphism. <i>American Journal of Human Genetics</i> , <b>2020</b> , 107, 352-363	11	25
156	Identification of independent association signals and putative functional variants for breast cancer risk through fine-scale mapping of the 12p11 locus. <i>Breast Cancer Research</i> , <b>2016</b> , 18, 64	8.3	25
155	Statin use and pancreatic cancer risk in two prospective cohort studies. <i>Journal of Gastroenterology</i> , <b>2018</b> , 53, 959-966	6.9	24
154	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , <b>2015</b> , 17, 58	8.3	24
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21	Prediagnostic 25-Hydroxyvitamin D Concentrations in Relation to Tumor Molecular Alterations and Risk of Breast Cancer Recurrence. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2020</b> , 29, 1253-1263	4	1
20	A Genome-Wide Association Study of Childhood Body Fatness. <i>Obesity</i> , <b>2021</b> , 29, 446-453	8	1
19	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
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