Peter Kraft, ScD

List of Publications by Year
in descending order

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438 papers	63,650 citations	905 116 h-index	1155 229 g-index
476 all docs	476 docs citations	476 times ranked	58771 citing authors

#	Article	IF	Citations
1	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
2	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
3	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
4	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
5	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
6	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	9.4	1,370
7	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. Nature Genetics, 2019, 51, 237-244.	9.4	1,307
8	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
9	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	13.7	1,099
10	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
11	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	9.4	1,059
12	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
13	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	9.4	871
14	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
15	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
16	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. PLoS Medicine, 2013, 10, e1001383.	3.9	753
17	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	2.6	711
18	Genome-wide association study of circulating vitamin D levels. Human Molecular Genetics, 2010, 19, 2739-2745.	1.4	700

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19	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	9.4	652
20	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. JAMA - Journal of the American Medical Association, 2016, 315, 68.	3.8	648
21	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
22	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. Nature Genetics, 2009, 41, 986-990.	9.4	597
23	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
24	Powerful SNP-Set Analysis for Case-Control Genome-wide Association Studies. American Journal of Human Genetics, 2010, 86, 929-942.	2.6	541
25	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. Nature Genetics, 2010, 42, 224-228.	9.4	539
26	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	9.4	537
27	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	9.4	513
28	Elevation of circulating branched-chain amino acids is an early event in human pancreatic adenocarcinoma development. Nature Medicine, 2014, 20, 1193-1198.	15.2	510
29	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	9.4	492
30	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	9.4	487
31	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. PLoS Genetics, 2014, 10, e1004722.	1.5	475
32	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
33	A Genome-Wide Association Study Identifies Novel Alleles Associated with Hair Color and Skin Pigmentation. PLoS Genetics, 2008, 4, e1000074.	1.5	439
34	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. Nature Genetics, 2009, 41, 585-590.	9.4	434
35	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	3.0	428
36	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.	9.4	426

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37	A Population-Based Study of Genes Previously Implicated in Breast Cancer. New England Journal of Medicine, 2021, 384, 440-451.	13.9	414
38	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	9.4	408
39	Methodological Challenges in Mendelian Randomization. Epidemiology, 2014, 25, 427-435.	1.2	405
40	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. Nature Genetics, 2012, 44, 483-489.	9.4	402
41	Exploiting Gene-Environment Interaction to Detect Genetic Associations. Human Heredity, 2007, 63, 111-119.	0.4	387
42	Performance of Common Genetic Variants in Breast-Cancer Risk Models. New England Journal of Medicine, 2010, 362, 986-993.	13.9	376
43	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	9.4	374
44	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
45	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	9.4	357
46	Genome-wide association studies identify loci associated with age at menarche and age at natural menopause. Nature Genetics, 2009, 41, 724-728.	9.4	348
47	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. PLoS Genetics, 2018, 14, e1007813.	1.5	341
48	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. PLoS Genetics, 2010, 6, e1001053.	1.5	332
49	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706.	2.6	326
50	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. PLoS Genetics, 2008, 4, e1000054.	1.5	315
51	Anthropometric Measures, Body Mass Index, and Pancreatic Cancer. Archives of Internal Medicine, 2010, 170, 791.	4.3	314
52	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
53	Cigarette Smoking and Pancreatic Cancer: A Pooled Analysis From the Pancreatic Cancer Cohort Consortium. American Journal of Epidemiology, 2009, 170, 403-413.	1.6	298
54	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. Nature Communications, 2018, 9, 260.	5.8	295

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55	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294
56	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
57	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	3.4	285
58	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	9.4	284
59	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	9.4	279
60	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
61	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	9.4	265
62	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	9.4	265
63	Improving reporting standards for polygenic scores in risk prediction studies. Nature, 2021, 591, 211-219.	13.7	265
64	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.	9.4	264
65	Pathway analysis by adaptive combination of Pâ€values. Genetic Epidemiology, 2009, 33, 700-709.	0.6	248
66	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. Nature Genetics, 2012, 44, 1090-1097.	9.4	238
67	Replication in Genome-Wide Association Studies. Statistical Science, 2009, 24, 561-573.	1.6	237
68	Meta-analysis of Genome-wide Association Studies Identifies 1q22 as a Susceptibility Locus for Intracerebral Hemorrhage. American Journal of Human Genetics, 2014, 94, 511-521.	2.6	235
69	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	4.1	235
70	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. American Journal of Human Genetics, 2015, 96, 329-339.	2.6	230
71	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. PLoS ONE, 2009, 4, e4653.	1.1	226
72	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. American Journal of Human Genetics, 2015, 96, 532-542.	2.6	222

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73	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	9.4	218
74	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	9.4	211
75	Joint Effects of Common Genetic Variants on the Risk for Type 2 Diabetes in U.S. Men and Women of European Ancestry. Annals of Internal Medicine, 2009, 150, 541.	2.0	206
76	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	2.6	201
77	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
78	Vitamin Dâ€“Related Genetic Variation, Plasma Vitamin D, and Risk of Lethal Prostate Cancer: A Prospective Nested Caseâ€“Control Study. Journal of the National Cancer Institute, 2012, 104, 690-699.	3.0	196
79	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
80	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. Human Molecular Genetics, 2008, 17, 3502-3508.	1.4	189
81	Reproducibility of Metabolomic Profiles among Men and Women in 2 Large Cohort Studies. Clinical Chemistry, 2013, 59, 1657-1667.	1.5	189
82	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. Nature Communications, 2018, 9, 556.	5.8	188
83	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
84	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	9.4	184
85	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	1.8	183
86	Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397.	13.7	183
87	Genetic variants in pigmentation genes, pigmentary phenotypes, and risk of skin cancer in Caucasians. International Journal of Cancer, 2009, 125, 909-917.	2.3	181
88	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. Nature Genetics, 2013, 45, 868-876.	9.4	179
89	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. Human Molecular Genetics, 2010, 19, 2706-2715.	1.4	178
90	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	5.8	178

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91	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	1.5	174
92	A meta-analysis of genome-wide association studies of breast cancer identifies two novel susceptibility loci at 6q14 and 20q11. Human Molecular Genetics, 2012, 21, 5373-5384.	1.4	168
93	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 1856-1862.	1.4	165
94	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	0.6	162
95	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	1.4	160
96	Genome-wide significant predictors of metabolites in the one-carbon metabolism pathway. Human Molecular Genetics, 2009, 18, 4677-4687.	1.4	157
97	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	7.7	157
98	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
99	A Genome-Wide Association Meta-Analysis of Circulating Sex Hormoneâ€“Binding Globulin Reveals Multiple Loci Implicated in Sex Steroid Hormone Regulation. PLoS Genetics, 2012, 8, e1002805.	1.5	151
100	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. American Journal of Epidemiology, 2017, 186, 753-761.	1.6	150
101	A Genome-Wide Association Study of Depressive Symptoms. Biological Psychiatry, 2013, 73, 667-678.	0.7	149
102	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. American Journal of Human Genetics, 2014, 94, 662-676.	2.6	149
103	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. Nature Genetics, 2014, 46, 1001-1006.	9.4	148
104	Interactions Between Genetic Variants and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. Journal of the National Cancer Institute, 2011, 103, 1252-1263.	3.0	147
105	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. Nature Genetics, 2014, 46, 1233-1238.	9.4	147
106	Hyperglycemia, Insulin Resistance, Impaired Pancreatic Î²-Cell Function, and Risk of Pancreatic Cancer. Journal of the National Cancer Institute, 2013, 105, 1027-1035.	3.0	146
107	Common variants of FUT2 are associated with plasma vitamin B12 levels. Nature Genetics, 2008, 40, 1160-1162.	9.4	142
108	Heritability in the genome-wide association era. Human Genetics, 2012, 131, 1655-1664.	1.8	142

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109	Characterization of Geneâ€“Environment Interactions for Colorectal Cancer Susceptibility Loci. Cancer Research, 2012, 72, 2036-2044.	0.4	140
110	Genome-wide association study identifies multiple loci associated with bladder cancer risk. Human Molecular Genetics, 2014, 23, 1387-1398.	1.4	137
111	Beyond odds ratios â€" communicating disease risk based on genetic profiles. Nature Reviews Genetics, 2009, 10, 264-269.	7.7	131
112	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. PLoS Genetics, 2012, 8, e1003098.	1.5	130
113	Family history of cancer and risk of pancreatic cancer: A pooled analysis from the Pancreatic Cancer Cohort Consortium (PanScan). International Journal of Cancer, 2010, 127, 1421-1428.	2.3	128
114	Challenges and opportunities in genome-wide environmental interaction (GWEI) studies. Human Genetics, 2012, 131, 1591-1613.	1.8	128
115	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	1.4	128
116	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. BMJ: British Medical Journal, 2017, 359, j4761.	2.4	126
117	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. International Journal of Epidemiology, 2016, 45, 896-908.	0.9	124
118	Melanocortin 1 receptor variants and skin cancer risk. International Journal of Cancer, 2006, 119, 1976-1984.	2.3	123
119	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. Nature Communications, 2014, 5, 5260.	5.8	123
120	An Absolute Risk Model to Identify Individuals at Elevated Risk for Pancreatic Cancer in the General Population. PLoS ONE, 2013, 8, e72311.	1.1	120
121	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	9.4	120
122	Improved methods for multi-trait fine mapping of pleiotropic risk loci. Bioinformatics, 2017, 33, 248-255.	1.8	119
123	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	1.4	118
124	Genetically Predicted Body Mass Index and Breast Cancer Risk: Mendelian Randomization Analyses of Data from 145,000 Women of European Descent. PLoS Medicine, 2016, 13, e1002105.	3.9	118
125	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2016, 7, 12048.	5.8	117
126	Prediagnostic Body Mass Index and Pancreatic Cancer Survival. Journal of Clinical Oncology, 2013, 31, 4229-4234.	0.8	115

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127	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
128	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
129	Pathway Analysis of Breast Cancer Genome-Wide Association Study Highlights Three Pathways and One Canonical Signaling Cascade. Cancer Research, 2010, 70, 4453-4459.	0.4	112
130	Clinical significance of Philadelphia chromosome positive pediatric acute lymphoblastic leukemia in the context of contemporary intensive therapies. Cancer, 1998, 83, 2030-2039.	2.0	111
131	Genomeâ€wide association scans for secondary traits using caseâ€control samples. Genetic Epidemiology, 2009, 33, 717-728.	0.6	110
132	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. Nature Genetics, 2011, 43, 185-187.	9.4	109
133	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. Nature Communications, 2014, 5, 5303.	5.8	109
134	A genome-wide association study of bitter and sweet beverage consumption. Human Molecular Genetics, 2019, 28, 2449-2457.	1.4	108
135	Exposure to Environmental Ozone Alters Semen Quality. Environmental Health Perspectives, 2006, 114, 360-365.	2.8	107
136	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. Nature Communications, 2017, 8, 15724.	5.8	106
137	Genome-wide association studies identify several new loci associated with pigmentation traits and skin cancer risk in European Americans. Human Molecular Genetics, 2013, 22, 2948-2959.	1.4	104
138	A genome-wide association study of early menopause and the combined impact of identified variants. Human Molecular Genetics, 2013, 22, 1465-1472.	1.4	104
139	Genome-wide association study identifies common variants associated with circulating vitamin E levels. Human Molecular Genetics, 2011, 20, 3876-3883.	1.4	102
140	Gene-Environment Interactions in Genome-Wide Association Studies: A Comparative Study of Tests Applied to Empirical Studies of Type 2 Diabetes. American Journal of Epidemiology, 2012, 175, 191-202.	1.6	102
141	A Prospective Study of Plasma Adiponectin and Pancreatic Cancer Risk in Five US Cohorts. Journal of the National Cancer Institute, 2013, 105, 95-103.	3.0	101
142	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	1.4	100
143	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.4	100
144	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	3.0	99

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145	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. Depression and Anxiety, 2016, 33, 265-280.	2.0	99
146	Bias and Efficiency in Family-Based Gene-Characterization Studies: Conditional, Prospective, Retrospective, and Joint Likelihoods. American Journal of Human Genetics, 2000, 66, 1119-1131.	2.6	98
147	Plasma 25-Hydroxyvitamin D and Risk of Pancreatic Cancer. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 82-91.	1.1	97
148	Association of Prostate Cancer Risk Variants with Gene Expression in Normal and Tumor Tissue. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 255-260.	1.1	97
149	Genome-Wide Association Study of Relative Telomere Length. PLoS ONE, 2011, 6, e19635.	1.1	97
150	Inclusion of Gene-Gene and Gene-Environment Interactions Unlikely to Dramatically Improve Risk Prediction for Complex Diseases. American Journal of Human Genetics, 2012, 90, 962-972.	2.6	96
151	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. American Journal of Human Genetics, 2014, 95, 462-471.	2.6	96
152	Geneâ€environment interplay in common complex diseases: forging an integrative modelâ€"recommendations from an NIH workshop. Genetic Epidemiology, 2011, 35, 217-225.	0.6	95
153	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. Nature Communications, 2016, 7, 10933.	5.8	94
154	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. Nature Communications, 2016, 7, 12510.	5.8	94
155	The association of telomere length and genetic variation in telomere biology genesa. Human Mutation, 2010, 31, 1050-1058.	1.1	93
156	Genome-wide association study of circulating retinol levels. Human Molecular Genetics, 2011, 20, 4724-4731.	1.4	93
157	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
158	Genome-wide association study identifies novel alleles associated with risk of cutaneous basal cell carcinoma and squamous cell carcinoma. Human Molecular Genetics, 2011, 20, 3718-3724.	1.4	92
159	Obesity susceptibility loci and uncontrolled eating, emotional eating and cognitive restraint behaviors in men and women. Obesity, 2014, 22, E135-41.	1.5	92
160	Addition of a polygenic risk score, mammographic density, and endogenous hormones to existing breast cancer risk prediction models: A nested caseâ€"control study. PLoS Medicine, 2018, 15, e1002644.	3.9	91
161	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	1.4	90
162	Selection in Europeans on Fatty Acid Desaturases Associated with Dietary Changes. Molecular Biology and Evolution, 2017, 34, 1307-1318.	3.5	90

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163	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741.	5.8	90
164	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	5.8	88
165	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. Oncotarget, 2016, 7, 66328-66343.	0.8	88
166	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
167	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
168	Novel pleiotropic risk loci for melanoma and nevus density implicate multiple biological pathways. Nature Communications, 2018, 9, 4774.	5.8	87
169	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	5.8	86
170	Survival Among Patients With Pancreatic Cancer and Long-Standing or Recent-Onset Diabetes Mellitus. Journal of Clinical Oncology, 2015, 33, 29-35.	0.8	83
171	Genomewide metaâ€analysis identifies loci associated with <scp>IGF</scp> â€I and <scp>IGFBP</scp> â€3 levels with impact on ageâ€related traits. Aging Cell, 2016, 15, 811-824.	3.0	83
172	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	0.9	81
173	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
174	Obesity, metabolic factors and risk of different histological types of lung cancer: A Mendelian randomization study. PLoS ONE, 2017, 12, e0177875.	1.1	79
175	Cigarette Smoking and Pancreatic Cancer Survival. Journal of Clinical Oncology, 2017, 35, 1822-1828.	0.8	78
176	Prostate Cancer (PCa) Risk Variants and Risk of Fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. European Urology, 2014, 65, 1069-1075.	0.9	75
177	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. Nature Communications, 2017, 8, 14175.	5.8	75
178	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	5.8	75
179	Genome-wide association study identifies polymorphisms in LEPR as determinants of plasma soluble leptin receptor levels. Human Molecular Genetics, 2010, 19, 1846-1855.	1.4	74
180	Evaluation of polygenic risk scores for predicting breast and prostate cancer risk. Genetic Epidemiology, 2011, 35, n/a-n/a.	0.6	74

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181	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	0.6	74
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