

Peter Kraft, ScD

List of Publications by Year in descending order

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Version: 2024-02-01

438
papers

63,650
citations

906

116
h-index

1158

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. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
2	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	27.8	1,789
3	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
4	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	21.4	1,631
5	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. <i>Nature Genetics</i> , 2009, 41, 25-34.	21.4	1,572
6	A genome-wide association study identifies alleles in <i>FGFR2</i> associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	21.4	1,370
7	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019, 51, 237-244.	21.4	1,307
8	Common variants near <i>MC4R</i> are associated with fat mass, weight and risk of obesity. <i>Nature Genetics</i> , 2008, 40, 768-775.	21.4	1,179
9	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
10	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
11	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007, 39, 645-649.	21.4	1,059
12	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
13	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008, 40, 310-315.	21.4	871
14	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	21.4	870
15	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	21.4	836
16	Causal Relationship between Obesity and Vitamin D Status: Bi-Directional Mendelian Randomization Analysis of Multiple Cohorts. <i>PLoS Medicine</i> , 2013, 10, e1001383.	8.4	753
17	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
18	Genome-wide association study of circulating vitamin D levels. <i>Human Molecular Genetics</i> , 2010, 19, 2739-2745.	2.9	700

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19	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	21.4	652
20	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 68.	7.4	648
21	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
22	Genome-wide association study identifies variants in the ABO locus associated with susceptibility to pancreatic cancer. <i>Nature Genetics</i> , 2009, 41, 986-990.	21.4	597
23	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
24	Powerful SNP-Set Analysis for Case-Control Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2010, 86, 929-942.	6.2	541
25	A genome-wide association study identifies pancreatic cancer susceptibility loci on chromosomes 13q22.1, 1q32.1 and 5p15.33. <i>Nature Genetics</i> , 2010, 42, 224-228.	21.4	539
26	Identification of ten loci associated with height highlights new biological pathways in human growth. <i>Nature Genetics</i> , 2008, 40, 584-591.	21.4	537
27	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
28	Elevation of circulating branched-chain amino acids is an early event in human pancreatic adenocarcinoma development. <i>Nature Medicine</i> , 2014, 20, 1193-1198.	30.7	510
29	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. <i>Nature Genetics</i> , 2013, 45, 385-391.	21.4	492
30	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> , 2009, 41, 579-584.	21.4	487
31	Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies. <i>PLoS Genetics</i> , 2014, 10, e1004722.	3.5	475
32	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	21.4	445
33	A Genome-Wide Association Study Identifies Novel Alleles Associated with Hair Color and Skin Pigmentation. <i>PLoS Genetics</i> , 2008, 4, e1000074.	3.5	439
34	Newly discovered breast cancer susceptibility loci on 3p24 and 17q23.2. <i>Nature Genetics</i> , 2009, 41, 585-590.	21.4	434
35	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	428
36	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> , 2017, 49, 834-841.	21.4	426

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37	A Population-Based Study of Genes Previously Implicated in Breast Cancer. <i>New England Journal of Medicine</i> , 2021, 384, 440-451.	27.0	414
38	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	21.4	408
39	Methodological Challenges in Mendelian Randomization. <i>Epidemiology</i> , 2014, 25, 427-435.	2.7	405
40	Bayesian inference analyses of the polygenic architecture of rheumatoid arthritis. <i>Nature Genetics</i> , 2012, 44, 483-489.	21.4	402
41	Exploiting Gene-Environment Interaction to Detect Genetic Associations. <i>Human Heredity</i> , 2007, 63, 111-119.	0.8	387
42	Performance of Common Genetic Variants in Breast-Cancer Risk Models. <i>New England Journal of Medicine</i> , 2010, 362, 986-993.	27.0	376
43	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
44	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
45	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	21.4	357
46	Genome-wide association studies identify loci associated with age at menarche and age at natural menopause. <i>Nature Genetics</i> , 2009, 41, 724-728.	21.4	348
47	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , 2018, 14, e1007813.	3.5	341
48	Multiple Independent Loci at Chromosome 15q25.1 Affect Smoking Quantity: a Meta-Analysis and Comparison with Lung Cancer and COPD. <i>PLoS Genetics</i> , 2010, 6, e1001053.	3.5	332
49	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> , 2018, 103, 691-706.	6.2	326
50	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	3.5	315
51	Anthropometric Measures, Body Mass Index, and Pancreatic Cancer. <i>Archives of Internal Medicine</i> , 2010, 170, 791.	3.8	314
52	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	21.4	303
53	Cigarette Smoking and Pancreatic Cancer: A Pooled Analysis From the Pancreatic Cancer Cohort Consortium. <i>American Journal of Epidemiology</i> , 2009, 170, 403-413.	3.4	298
54	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	12.8	295

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55	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014, 46, 994-1000.	21.4	294
56	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
57	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016, 2, 1295.	7.1	285
58	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
59	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
60	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 126-135.	2.5	278
61	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011, 43, 785-791.	21.4	265
62	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
63	Improving reporting standards for polygenic scores in risk prediction studies. <i>Nature</i> , 2021, 591, 211-219.	27.8	265
64	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. <i>Nature Genetics</i> , 2021, 53, 65-75.	21.4	264
65	Pathway analysis by adaptive combination of P -values. <i>Genetic Epidemiology</i> , 2009, 33, 700-709.	1.3	248
66	Genome-wide association analyses of esophageal squamous cell carcinoma in Chinese identify multiple susceptibility loci and gene-environment interactions. <i>Nature Genetics</i> , 2012, 44, 1090-1097.	21.4	238
67	Replication in Genome-Wide Association Studies. <i>Statistical Science</i> , 2009, 24, 561-573.	2.8	237
68	Meta-analysis of Genome-wide Association Studies Identifies 1q22 as a Susceptibility Locus for Intracerebral Hemorrhage. <i>American Journal of Human Genetics</i> , 2014, 94, 511-521.	6.2	235
69	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
70	Adjusting for Heritable Covariates Can Bias Effect Estimates in Genome-Wide Association Studies. <i>American Journal of Human Genetics</i> , 2015, 96, 329-339.	6.2	230
71	Genome-Wide and Candidate Gene Association Study of Cigarette Smoking Behaviors. <i>PLoS ONE</i> , 2009, 4, e4653.	2.5	226
72	Meta-analysis of 65,734 Individuals Identifies TSPAN15 and SLC44A2 as Two Susceptibility Loci for Venous Thromboembolism. <i>American Journal of Human Genetics</i> , 2015, 96, 532-542.	6.2	222

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73	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009, 41, 1055-1057.	21.4	218
74	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. <i>Nature Genetics</i> , 2016, 48, 189-194.	21.4	211
75	Joint Effects of Common Genetic Variants on the Risk for Type 2 Diabetes in U.S. Men and Women of European Ancestry. <i>Annals of Internal Medicine</i> , 2009, 150, 541.	3.9	206
76	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> , 2013, 92, 489-503.	6.2	201
77	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. <i>PLoS ONE</i> , 2012, 7, e29202.	2.5	197
78	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> , 2012, 104, 690-699.	6.3	196
79	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. <i>Nature Communications</i> , 2021, 12, 1258.	12.8	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. <i>Human Molecular Genetics</i> , 2008, 17, 3502-3508.	2.9	189
81	Reproducibility of Metabolomic Profiles among Men and Women in 2 Large Cohort Studies. <i>Clinical Chemistry</i> , 2013, 59, 1657-1667.	3.2	189
82	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	12.8	188
83	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	28.9	188
84	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. <i>Nature Genetics</i> , 2018, 50, 968-978.	21.4	184
85	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012, 131, 217-234.	3.8	183
86	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
87	Genetic variants in pigmentation genes, pigmentary phenotypes, and risk of skin cancer in Caucasians. <i>International Journal of Cancer</i> , 2009, 125, 909-917.	5.1	181
88	Genome-wide association study identifies multiple risk loci for chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2013, 45, 868-876.	21.4	179
89	Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 2706-2715.	2.9	178
90	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178

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91	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174
92	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> , 2012, 21, 5373-5384.	2.9	168
93	Genetic variants in ABO blood group region, plasma soluble E-selectin levels and risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010, 19, 1856-1862.	2.9	165
94	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	1.4	162
95	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011, 20, 3867-3875.	2.9	160
96	Genome-wide significant predictors of metabolites in the one-carbon metabolism pathway. <i>Human Molecular Genetics</i> , 2009, 18, 4677-4687.	2.9	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. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
98	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
99	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> , 2012, 8, e1002805.	3.5	151
100	Current Challenges and New Opportunities for Gene-Environment Interaction Studies of Complex Diseases. <i>American Journal of Epidemiology</i> , 2017, 186, 753-761.	3.4	150
101	A Genome-Wide Association Study of Depressive Symptoms. <i>Biological Psychiatry</i> , 2013, 73, 667-678.	1.3	149
102	Maximizing the Power of Principal-Component Analysis of Correlated Phenotypes in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2014, 94, 662-676.	6.2	149
103	Joint analysis of three genome-wide association studies of esophageal squamous cell carcinoma in Chinese populations. <i>Nature Genetics</i> , 2014, 46, 1001-1006.	21.4	148
104	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> , 2011, 103, 1252-1263.	6.3	147
105	Genome-wide association study identifies multiple susceptibility loci for diffuse large B cell lymphoma. <i>Nature Genetics</i> , 2014, 46, 1233-1238.	21.4	147
106	Hyperglycemia, Insulin Resistance, Impaired Pancreatic Î²-Cell Function, and Risk of Pancreatic Cancer. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1027-1035.	6.3	146
107	Common variants of <i>FUT2</i> are associated with plasma vitamin B12 levels. <i>Nature Genetics</i> , 2008, 40, 1160-1162.	21.4	142
108	Heritability in the genome-wide association era. <i>Human Genetics</i> , 2012, 131, 1655-1664.	3.8	142

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109	Characterization of Gene-Environment Interactions for Colorectal Cancer Susceptibility Loci. <i>Cancer Research</i> , 2012, 72, 2036-2044.	0.9	140
110	Genome-wide association study identifies multiple loci associated with bladder cancer risk. <i>Human Molecular Genetics</i> , 2014, 23, 1387-1398.	2.9	137
111	Beyond odds ratios – communicating disease risk based on genetic profiles. <i>Nature Reviews Genetics</i> , 2009, 10, 264-269.	16.3	131
112	Genome-Wide Joint Meta-Analysis of SNP and SNP-by-Smoking Interaction Identifies Novel Loci for Pulmonary Function. <i>PLoS Genetics</i> , 2012, 8, e1003098.	3.5	130
113	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> , 2010, 127, 1421-1428.	5.1	128
114	Challenges and opportunities in genome-wide environmental interaction (GWEI) studies. <i>Human Genetics</i> , 2012, 131, 1591-1613.	3.8	128
115	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015, 24, 5356-5366.	2.9	128
116	Circulating vitamin D concentration and risk of seven cancers: Mendelian randomisation study. <i>BMJ: British Medical Journal</i> , 2017, 359, j4761.	2.3	126
117	Mendelian randomization study of adiposity-related traits and risk of breast, ovarian, prostate, lung and colorectal cancer. <i>International Journal of Epidemiology</i> , 2016, 45, 896-908.	1.9	124
118	Melanocortin 1 receptor variants and skin cancer risk. <i>International Journal of Cancer</i> , 2006, 119, 1976-1984.	5.1	123
119	Genome-wide association study of breast cancer in Latinas identifies novel protective variants on 6q25. <i>Nature Communications</i> , 2014, 5, 5260.	12.8	123
120	An Absolute Risk Model to Identify Individuals at Elevated Risk for Pancreatic Cancer in the General Population. <i>PLoS ONE</i> , 2013, 8, e72311.	2.5	120
121	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
122	Improved methods for multi-trait fine mapping of pleiotropic risk loci. <i>Bioinformatics</i> , 2017, 33, 248-255.	4.1	119
123	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> , 2013, 22, 408-415.	2.9	118
124	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> , 2016, 13, e1002105.	8.4	118
125	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2016, 7, 12048.	12.8	117
126	Prediagnostic Body Mass Index and Pancreatic Cancer Survival. <i>Journal of Clinical Oncology</i> , 2013, 31, 4229-4234.	1.6	115

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127	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. <i>Nature Genetics</i> , 2017, 49, 993-1004.	21.4	114
128	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. <i>Cell</i> , 2014, 156, 343-358.	28.9	113
129	Pathway Analysis of Breast Cancer Genome-Wide Association Study Highlights Three Pathways and One Canonical Signaling Cascade. <i>Cancer Research</i> , 2010, 70, 4453-4459.	0.9	112
130	Clinical significance of Philadelphia chromosome positive pediatric acute lymphoblastic leukemia in the context of contemporary intensive therapies. <i>Cancer</i> , 1998, 83, 2030-2039.	4.1	111
131	Genome-wide association scans for secondary traits using case-control samples. <i>Genetic Epidemiology</i> , 2009, 33, 717-728.	1.3	110
132	Common variants in ZNF365 are associated with both mammographic density and breast cancer risk. <i>Nature Genetics</i> , 2011, 43, 185-187.	21.4	109
133	Genome-wide association study identifies multiple loci associated with both mammographic density and breast cancer risk. <i>Nature Communications</i> , 2014, 5, 5303.	12.8	109
134	A genome-wide association study of bitter and sweet beverage consumption. <i>Human Molecular Genetics</i> , 2019, 28, 2449-2457.	2.9	108
135	Exposure to Environmental Ozone Alters Semen Quality. <i>Environmental Health Perspectives</i> , 2006, 114, 360-365.	6.0	107
136	Genome-wide association study identifies multiple risk loci for renal cell carcinoma. <i>Nature Communications</i> , 2017, 8, 15724.	12.8	106
137	Genome-wide association studies identify several new loci associated with pigmentation traits and skin cancer risk in European Americans. <i>Human Molecular Genetics</i> , 2013, 22, 2948-2959.	2.9	104
138	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013, 22, 1465-1472.	2.9	104
139	Genome-wide association study identifies common variants associated with circulating vitamin E levels. <i>Human Molecular Genetics</i> , 2011, 20, 3876-3883.	2.9	102
140	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> , 2012, 175, 191-202.	3.4	102
141	A Prospective Study of Plasma Adiponectin and Pancreatic Cancer Risk in Five US Cohorts. <i>Journal of the National Cancer Institute</i> , 2013, 105, 95-103.	6.3	101
142	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , 2013, 22, 2520-2528.	2.9	100
143	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.9	100
144	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	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. <i>Depression and Anxiety</i> , 2016, 33, 265-280.	4.1	99
146	Bias and Efficiency in Family-Based Gene-Characterization Studies: Conditional, Prospective, Retrospective, and Joint Likelihoods. <i>American Journal of Human Genetics</i> , 2000, 66, 1119-1131.	6.2	98
147	Plasma 25-Hydroxyvitamin D and Risk of Pancreatic Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 82-91.	2.5	97
148	Association of Prostate Cancer Risk Variants with Gene Expression in Normal and Tumor Tissue. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 255-260.	2.5	97
149	Genome-Wide Association Study of Relative Telomere Length. <i>PLoS ONE</i> , 2011, 6, e19635.	2.5	97
150	Inclusion of Gene-Gene and Gene-Environment Interactions Unlikely to Dramatically Improve Risk Prediction for Complex Diseases. <i>American Journal of Human Genetics</i> , 2012, 90, 962-972.	6.2	96
151	Genome-wide Association Study Identifies Five Susceptibility Loci for Follicular Lymphoma outside the HLA Region. <i>American Journal of Human Genetics</i> , 2014, 95, 462-471.	6.2	96
152	Gene-Environment interplay in common complex diseases: forging an integrative model—recommendations from an NIH workshop. <i>Genetic Epidemiology</i> , 2011, 35, 217-225.	1.3	95
153	Meta-analysis of genome-wide association studies discovers multiple loci for chronic lymphocytic leukemia. <i>Nature Communications</i> , 2016, 7, 10933.	12.8	94
154	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. <i>Nature Communications</i> , 2016, 7, 12510.	12.8	94
155	The association of telomere length and genetic variation in telomere biology genes. <i>Human Mutation</i> , 2010, 31, 1050-1058.	2.5	93
156	Genome-wide association study of circulating retinol levels. <i>Human Molecular Genetics</i> , 2011, 20, 4724-4731.	2.9	93
157	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
158	Genome-wide association study identifies novel alleles associated with risk of cutaneous basal cell carcinoma and squamous cell carcinoma. <i>Human Molecular Genetics</i> , 2011, 20, 3718-3724.	2.9	92
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