

Christopher A Haiman

List of Publications by Year in descending order

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Version: 2024-02-01

590
papers

57,917
citations

2215

99
h-index

1825

210
g-index

610
all docs

610
docs citations

610
times ranked

57675
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Age-Related Clonal Hematopoiesis Associated with Adverse Outcomes. <i>New England Journal of Medicine</i> , 2014, 371, 2488-2498.	27.0	3,474
3	Genome-wide association study identifies novel breast cancer susceptibility loci. <i>Nature</i> , 2007, 447, 1087-1093.	27.8	2,165
4	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
5	Risk of COVID-19 among front-line health-care workers and the general community: a prospective cohort study. <i>Lancet Public Health</i> , The, 2020, 5, e475-e483.	10.0	1,595
6	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
7	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
8	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
9	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. <i>Nature Genetics</i> , 2007, 39, 865-869.	21.4	774
10	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
11	Genetic analyses of diverse populations improves discovery for complex traits. <i>Nature</i> , 2019, 570, 514-518.	27.8	679
12	Ethnic and Racial Differences in the Smoking-Related Risk of Lung Cancer. <i>New England Journal of Medicine</i> , 2006, 354, 333-342.	27.0	668
13	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
14	Multiple regions within 8q24 independently affect risk for prostate cancer. <i>Nature Genetics</i> , 2007, 39, 638-644.	21.4	621
15	The 8q24 cancer risk variant rs6983267 shows long-range interaction with MYC in colorectal cancer. <i>Nature Genetics</i> , 2009, 41, 882-884.	21.4	616
16	Associations of Breast Cancer Risk Factors With Tumor Subtypes: A Pooled Analysis From the Breast Cancer Association Consortium Studies. <i>Journal of the National Cancer Institute</i> , 2011, 103, 250-263.	6.3	596
17	Admixture mapping identifies 8q24 as a prostate cancer risk locus in African-American men. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14068-14073.	7.1	575
18	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012, 44, 651-658.	21.4	519

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19	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
20	Detectable clonal mosaicism from birth to old age and its relationship to cancer. <i>Nature Genetics</i> , 2012, 44, 642-650.	21.4	511
21	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
22	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
23	Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histological subtypes. <i>Nature Genetics</i> , 2017, 49, 1126-1132.	21.4	472
24	Sequence variants in SLC16A11 are a common risk factor for type 2 diabetes in Mexico. <i>Nature</i> , 2014, 506, 97-101.	27.8	439
25	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
26	Common variants on chromosome 5p12 confer susceptibility to estrogen receptor-“positive breast cancer. <i>Nature Genetics</i> , 2008, 40, 703-706.	21.4	412
27	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
28	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. <i>Nature Genetics</i> , 2009, 41, 1116-1121.	21.4	389
29	Choosing Haplotype-Tagging SNPS Based on Unphased Genotype Data Using a Preliminary Sample of Unrelated Subjects with an Example from the Multiethnic Cohort Study. <i>Human Heredity</i> , 2003, 55, 27-36.	0.8	386
30	Genome-wide association studies identify four ER negative-“specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
31	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012, 44, 307-311.	21.4	372
32	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
33	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	21.4	356
34	A common genetic risk factor for colorectal and prostate cancer. <i>Nature Genetics</i> , 2007, 39, 954-956.	21.4	336
35	The landscape of recombination in African Americans. <i>Nature</i> , 2011, 476, 170-175.	27.8	319
36	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	3.5	315

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37	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. <i>Nature Genetics</i> , 2014, 46, 994-1000.	21.4	294
38	Genome-Wide Association Study of Coronary Heart Disease and Its Risk Factors in 8,090 African Americans: The NHLBI CARE Project. <i>PLoS Genetics</i> , 2011, 7, e1001300.	3.5	290
39	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
40	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
41	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
42	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
43	A Genomewide Admixture Map for Latino Populations. <i>American Journal of Human Genetics</i> , 2007, 80, 1024-1036.	6.2	265
44	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
45	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
46	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
47	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
48	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	27.8	248
49	Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. <i>PLoS Biology</i> , 2013, 11, e1001661.	5.6	235
50	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. <i>Nature Genetics</i> , 2013, 45, 690-696.	21.4	232
51	Association of a Low-Frequency Variant in <i>HNFI1A</i> With Type 2 Diabetes in a Latino Population. <i>JAMA - Journal of the American Medical Association</i> , 2014, 311, 2305.	7.4	230
52	Transferability of tag SNPs in genetic association studies in multiple populations. <i>Nature Genetics</i> , 2006, 38, 1298-1303.	21.4	224
53	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009, 41, 1055-1057.	21.4	218
54	Functional Enhancers at the Gene-Poor 8q24 Cancer-Linked Locus. <i>PLoS Genetics</i> , 2009, 5, e1000597.	3.5	214

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55	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
56	Circulating Vitamin D and Colorectal Cancer Risk: An International Pooling Project of 17 Cohorts. <i>Journal of the National Cancer Institute</i> , 2019, 111, 158-169.	6.3	199
57	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , 2011, 43, 570-573.	21.4	198
58	Genome-wide meta-analysis identifies five new susceptibility loci for pancreatic cancer. <i>Nature Communications</i> , 2018, 9, 556.	12.8	188
59	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
60	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
61	Association of Coffee Consumption With Total and Cause-Specific Mortality Among Nonwhite Populations. <i>Annals of Internal Medicine</i> , 2017, 167, 228.	3.9	182
62	Global Patterns of Prostate Cancer Incidence, Aggressiveness, and Mortality in Men of African Descent. <i>Prostate Cancer</i> , 2013, 2013, 1-12.	0.6	180
63	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178
64	<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
65	Phenome-Wide Association Study (PheWAS) for Detection of Pleiotropy within the Population Architecture using Genomics and Epidemiology (PAGE) Network. <i>PLoS Genetics</i> , 2013, 9, e1003087.	3.5	171
66	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	12.8	169
67	Consistent Association of Type 2 Diabetes Risk Variants Found in Europeans in Diverse Racial and Ethnic Groups. <i>PLoS Genetics</i> , 2010, 6, e1001078.	3.5	168
68	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
69	Comprehensive Functional Annotation of 77 Prostate Cancer Risk Loci. <i>PLoS Genetics</i> , 2014, 10, e1004102.	3.5	167
70	The Next PAGE in Understanding Complex Traits: Design for the Analysis of Population Architecture Using Genetics and Epidemiology (PAGE) Study. <i>American Journal of Epidemiology</i> , 2011, 174, 849-859.	3.4	161
71	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011, 20, 3867-3875.	2.9	160
72	Genome-wide physical activity interactions in adiposity • A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	3.5	158

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73	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
74	Low penetrance breast cancer susceptibility loci are associated with specific breast tumor subtypes: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 3289-3303.	2.9	152
75	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
76	Genetic Determinants of Lipid Traits in Diverse Populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. <i>PLoS Genetics</i> , 2011, 7, e1002138.	3.5	146
77	A comprehensive haplotype analysis of CYP19 and breast cancer risk: the Multiethnic Cohort. <i>Human Molecular Genetics</i> , 2003, 12, 2679-2692.	2.9	144
78	Genetic Variation at the <i>CYP19A1</i> Locus Predicts Circulating Estrogen Levels but not Breast Cancer Risk in Postmenopausal Women. <i>Cancer Research</i> , 2007, 67, 1893-1897.	0.9	140
79	The gene, environment association studies consortium (GENEVA): maximizing the knowledge obtained from GWAS by collaboration across studies of multiple conditions. <i>Genetic Epidemiology</i> , 2010, 34, 364-372.	1.3	139
80	The contribution of rare variation to prostate cancer heritability. <i>Nature Genetics</i> , 2016, 48, 30-35.	21.4	139
81	Genome-Wide Association Study in East Asians Identifies Novel Susceptibility Loci for Breast Cancer. <i>PLoS Genetics</i> , 2012, 8, e1002532.	3.5	137
82	A Common 8q24 Variant in Prostate and Breast Cancer from a Large Nested Case-Control Study. <i>Cancer Research</i> , 2007, 67, 2951-2956.	0.9	136
83	Association of Diabetes With Prostate Cancer Risk in the Multiethnic Cohort. <i>American Journal of Epidemiology</i> , 2009, 169, 937-945.	3.4	136
84	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	6.3	129
85	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
86	A tetranucleotide repeat polymorphism in CYP19 and breast cancer risk. <i>International Journal of Cancer</i> , 2000, 87, 204-210.	5.1	127
87	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
88	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
89	Cyclin D1b variant influences prostate cancer growth through aberrant androgen receptor regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 2190-2195.	7.1	123
90	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

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91	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. <i>Nature Communications</i> , 2018, 9, 4079.	12.8	121
92	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
93	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
94	Obesity, body fat distribution, and risk of breast cancer subtypes in African American women participating in the AMBER Consortium. <i>Breast Cancer Research and Treatment</i> , 2015, 150, 655-666.	2.5	118
95	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
96	Characterizing Genetic Risk at Known Prostate Cancer Susceptibility Loci in African Americans. <i>PLoS Genetics</i> , 2011, 7, e1001387.	3.5	117
97	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. <i>PLoS Genetics</i> , 2013, 9, e1003379.	3.5	112
98	A Large Multiethnic Genome-Wide Association Study of Prostate Cancer Identifies Novel Risk Variants and Substantial Ethnic Differences. <i>Cancer Discovery</i> , 2015, 5, 878-891.	9.4	111
99	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv431.	6.3	111
100	FGFR2 variants and breast cancer risk: fine-scale mapping using African American studies and analysis of chromatin conformation. <i>Human Molecular Genetics</i> , 2009, 18, 1692-1703.	2.9	110
101	Enhanced Statistical Tests for GWAS in Admixed Populations: Assessment using African Americans from CARE and a Breast Cancer Consortium. <i>PLoS Genetics</i> , 2011, 7, e1001371.	3.5	110
102	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. <i>Gastroenterology</i> , 2020, 158, 1274-1286.e12.	1.3	110
103	Genome-Wide Association of Body Fat Distribution in African Ancestry Populations Suggests New Loci. <i>PLoS Genetics</i> , 2013, 9, e1003681.	3.5	109
104	Identification of a Functional Genetic Variant at 16q12.1 for Breast Cancer Risk: Results from the Asia Breast Cancer Consortium. <i>PLoS Genetics</i> , 2010, 6, e1001002.	3.5	107
105	IGF-1, IGFBP-1, and IGFBP-3 Polymorphisms Predict Circulating IGF Levels but Not Breast Cancer Risk: Findings from the Breast and Prostate Cancer Cohort Consortium (BPC3). <i>PLoS ONE</i> , 2008, 3, e2578.	2.5	106
106	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	3.5	105
107	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
108	Generalizability of Associations from Prostate Cancer Genome-Wide Association Studies in Multiple Populations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1285-1289.	2.5	102

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109	Common Breast Cancer Susceptibility Variants in <i>LSP1</i> and <i>RAD51L1</i> Are Associated with Mammographic Density Measures that Predict Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1156-1166.	2.5	101
110	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. <i>American Journal of Human Genetics</i> , 2015, 96, 487-497.	6.2	101
111	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
112	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
113	Common variants at 11q12, 10q26 and 3p11.2 are associated with prostate cancer susceptibility in Japanese. <i>Nature Genetics</i> , 2012, 44, 426-429.	21.4	98
114	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
115	High-Quality Diets Associate With Reduced Risk of Colorectal Cancer: Analyses of Diet Quality Indexes in the Multiethnic Cohort. <i>Gastroenterology</i> , 2017, 153, 386-394.e2.	1.3	98
116	Discovery and fine-mapping of adiposity loci using high density imputation of genome-wide association studies in individuals of African ancestry: African Ancestry Anthropometry Genetics Consortium. <i>PLoS Genetics</i> , 2017, 13, e1006719.	3.5	98
117	A Review of Cancer in U.S. Hispanic Populations. <i>Cancer Prevention Research</i> , 2012, 5, 150-163.	1.5	95
118	No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. <i>Journal of Medical Genetics</i> , 2016, 53, 298-309.	3.2	94
119	Identification, Replication, and Fine-Mapping of Loci Associated with Adult Height in Individuals of African Ancestry. <i>PLoS Genetics</i> , 2011, 7, e1002298.	3.5	93
120	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
121	Genome-wide association study identifies breast cancer risk variant at 10q21.2: results from the Asia Breast Cancer Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4991-4999.	2.9	92
122	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> , 2014, 23, 6616-6633.	2.9	90
123	CAUSEL: an epigenome- and genome-editing pipeline for establishing function of noncoding GWAS variants. <i>Nature Medicine</i> , 2015, 21, 1357-1363.	30.7	90
124	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
125	Validation of Genome-Wide Prostate Cancer Associations in Men of African Descent. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 23-32.	2.5	88
126	Two susceptibility loci identified for prostate cancer aggressiveness. <i>Nature Communications</i> , 2015, 6, 6889.	12.8	88

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127	Three new pancreatic cancer susceptibility signals identified on chromosomes 1q32.1, 5p15.33 and 8q24.21. <i>Oncotarget</i> , 2016, 7, 66328-66343.	1.8	88
128	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018, 9, 2256.	12.8	88
129	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
130	Common genetic determinants of breast-cancer risk in East Asian women: a collaborative study of 23 637 breast cancer cases and 25 579 controls. <i>Human Molecular Genetics</i> , 2013, 22, 2539-2550.	2.9	86
131	A sequence repeat in the insulin-like growth factor-1 gene and risk of breast cancer. <i>International Journal of Cancer</i> , 2002, 100, 332-336.	5.1	84
132	Association of ESR1 gene tagging SNPs with breast cancer risk. <i>Human Molecular Genetics</i> , 2009, 18, 1131-1139.	2.9	84
133	Cyclin D1 Splice Variants: Polymorphism, Risk, and Isoform-Specific Regulation in Prostate Cancer. <i>Clinical Cancer Research</i> , 2009, 15, 5338-5349.	7.0	84
134	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
135	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
136	Fine mapping of the association with obesity at the FTO locus in African-derived populations. <i>Human Molecular Genetics</i> , 2010, 19, 2907-2916.	2.9	82
137	Racial/Ethnic Differences in Postmenopausal Endogenous Hormones: The Multiethnic Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 1849-1855.	2.5	79
138	Polymorphisms in Steroid Hormone Pathway Genes and Mammographic Density. <i>Breast Cancer Research and Treatment</i> , 2003, 77, 27-36.	2.5	78
139	Informed Conditioning on Clinical Covariates Increases Power in Case-Control Association Studies. <i>PLoS Genetics</i> , 2012, 8, e1003032.	3.5	78
140	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
141	Admixture Mapping of 15,280 African Americans Identifies Obesity Susceptibility Loci on Chromosomes 5 and X. <i>PLoS Genetics</i> , 2009, 5, e1000490.	3.5	78
142	Fine Mapping and Identification of BMI Loci in African Americans. <i>American Journal of Human Genetics</i> , 2013, 93, 661-671.	6.2	77
143	Genetic Variants Associated With Quantitative Glucose Homeostasis Traits Translate to Type 2 Diabetes in Mexican Americans: The GUARDIAN (Genetics Underlying Diabetes in Hispanics) Consortium. <i>Diabetes</i> , 2015, 64, 1853-1866.	0.6	77
144	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. <i>Cancer Causes and Control</i> , 2015, 26, 1603-1616.	1.8	77

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145	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. American Journal of Human Genetics, 2015, 96, 5-20.	6.2	76
146	Genetic and functional analysis of <i>CHEK2</i> (<i>CHK2</i>) variants in multiethnic cohorts. International Journal of Cancer, 2007, 121, 2661-2667.	5.1	75
147	<i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799.	0.9	75
148	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
149	Racial/Ethnic Differences in Lung Cancer Incidence in the Multiethnic Cohort Study: An Update. Journal of the National Cancer Institute, 2019, 111, 811-819.	6.3	74
150	Generalizability and Epidemiologic Characterization of Eleven Colorectal Cancer GWAS Hits in Multiple Populations. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 70-81.	2.5	73
151	The Dietary Inflammatory Index Is Associated with Colorectal Cancer Risk in the Multiethnic Cohort. Journal of Nutrition, 2017, 147, jn242529.	2.9	73
152	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. Nature Communications, 2014, 5, 4613.	12.8	72
153	A genome-wide association study of prostate cancer in West African men. Human Genetics, 2014, 133, 509-521.	3.8	72
154	Strategies for Enriching Variant Coverage in Candidate Disease Loci on a Multiethnic Genotyping Array. PLoS ONE, 2016, 11, e0167758.	2.5	72
155	Replication and Functional Genomic Analyses of the Breast Cancer Susceptibility Locus at 6q25.1 Generalize Its Importance in Women of Chinese, Japanese, and European Ancestry. Cancer Research, 2011, 71, 1344-1355.	0.9	71
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