Fredrick R Schumacher

List of Publications by Year
in descending order

207 papers	27,520 citations	11651 70 h-index	6836 155 g-index
218 all docs	218 docs citations	218 times ranked	32654 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
3	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
4	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	21.4	1,059
5	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
6	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	21.4	871
7	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
8	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
9	Identification of ten loci associated with height highlights new biological pathways in human growth. Nature Genetics, 2008, 40, 584-591.	21.4	537
10	Detectable clonal mosaicism and its relationship to aging and cancer. Nature Genetics, 2012, 44, 651-658.	21.4	519
11	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380.	21.4	513
12	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	21.4	493
13	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
14	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
15	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
16	Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87.	21.4	377
17	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
18	A genome-wide association meta-analysis identifies new childhood obesity loci. Nature Genetics, 2012, 44, 526-531.	21.4	352

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19	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. Gastroenterology, 2013, 144, 799-807.e24.	1.3	292
20	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
21	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295.	7.1	285
22	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. Nature Genetics, 2011, 43, 1210-1214.	21.4	279
23	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	2.5	278
24	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
25	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.	21.4	264
26	Generalization and Dilution of Association Results from European GWAS in Populations of Non-European Ancestry: The PAGE Study. PLoS Biology, 2013, 11, e1001661.	5.6	235
27	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	21.4	218
28	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. Nature Genetics, 2014, 46, 533-542.	21.4	212
29	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. Nature Genetics, 2012, 44, 770-776.	21.4	210
30	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.	6.2	201
31	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	21.4	198
32	Meta-analysis of new genome-wide association studies of colorectal cancer risk. Human Genetics, 2012, 131, 217-234.	3.8	183
33	Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166.	12.8	178
34	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
35	Association of Aspirin and NSAID Use With Risk of Colorectal Cancer According to Genetic Variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133.	7.4	171
36	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.	2.9	168

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37	Genome-wide association study identifies new prostate cancer susceptibility loci. Human Molecular Genetics, 2011, 20, 3867-3875.	2.9	160
38	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.	9.4	157
39	Meta-analysis identifies four new loci associated with testicular germ cell tumor. Nature Genetics, 2013, 45, 680-685.	21.4	154
40	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.	6.3	147
41	Genetic Determinants of Lipid Traits in Diverse Populations from the Population Architecture using Genomics and Epidemiology (PAGE) Study. PLoS Genetics, 2011, 7, e1002138.	3.5	146
42	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
43	A Common 8q24 Variant in Prostate and Breast Cancer from a Large Nested Case-Control Study. Cancer Research, 2007, 67, 2951-2956.	0.9	136
44	A Model to Determine Colorectal Cancer Risk Using Common Genetic Susceptibility Loci. Gastroenterology, 2015, 148, 1330-1339.e14.	1.3	129
45	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157.	6.3	129
46	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
47	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.	1.9	124
48	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.	2.9	118
49	Fatty Acid Synthase Polymorphisms, Tumor Expression, Body Mass Index, Prostate Cancer Risk, and Survival. Journal of Clinical Oncology, 2010, 28, 3958-3964.	1.6	113
50	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. Journal of the National Cancer Institute, 2016, 108, djv431.	6.3	111
51	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. Gastroenterology, 2019, 156, 1455-1466.	1.3	111
52	Evaluation of the 8q24 Prostate Cancer Risk Locus and MYC Expression. Cancer Research, 2009, 69, 5568-5574.	0.9	110
53	Cumulative Burden of Colorectal Cancerâ€“Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. Gastroenterology, 2020, 158, 1274-1286.e12.	1.3	110
54	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105

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55	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
56	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	2.9	100
57	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
58	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
59	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
60	Refined histopathological predictors of BRCA1 and BRCA2mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. Breast Cancer Research, 2014, 16, 3419.	5.0	97
61	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. Gastroenterology, 2016, 150, 1633-1645.	1.3	97
62	Fine mapping and functional analysis of a common variant in MSMB on chromosome 10q11.2 associated with prostate cancer susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7933-7938.	7.1	96
63	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	12.8	93
64	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.	2.9	90
65	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
66	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
67	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. Nature Communications, 2016, 7, 11843.	12.8	86
68	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
69	A Large Prospective Study of SEP15 Genetic Variation, Interaction with Plasma Selenium Levels, and Prostate Cancer Risk and Survival. Cancer Prevention Research, 2010, 3, 604-610.	1.5	79
70	Fine Mapping and Identification of BMI Loci in African Americans. American Journal of Human Genetics, 2013, 93, 661-671.	6.2	77
71	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
72	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.	1.9	75

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73	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
74	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. Nature Communications, 2014, 5, 4613.	12.8	72
75	Evaluation of the Metabochip Genotyping Array in African Americans and Implications for Fine Mapping of GWAS-Identified Loci: The PAGE Study. PLoS ONE, 2012, 7, e35651.	2.5	71
76	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. PLoS Medicine, 2016, 13, e1002118.	8.4	69
77	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. Human Molecular Genetics, 2015, 24, 5589-5602.	2.9	67
78	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. Blood, 2012, 119, 469-475.	1.4	66
79	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. Journal of the National Cancer Institute, 2015, 107, djv246.	6.3	63
80	Generalizability of established prostate cancer risk variants in men of <scp>A</scp>frican ancestry. International Journal of Cancer, 2015, 136, 1210-1217.	5.1	62
81	Relation of serum insulin-like growth factor-I (IGF-I) and IGF binding protein-3 to risk of prostate cancer (United States). Cancer Causes and Control, 2003, 14, 721-726.	1.8	60
82	Eighteen Insulin-like Growth Factor Pathway Genes, Circulating Levels of IGF-I and Its Binding Protein, and Risk of Prostate and Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2877-2887.	2.5	59
83	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013, 22, 2748-2753.	2.9	59
84	Association of the FTO Obesity Risk Variant rs8050136 With Percentage of Energy Intake From Fat in Multiple Racial/Ethnic Populations. American Journal of Epidemiology, 2013, 178, 780-790.	3.4	59
85	Modeling disease risk through analysis of physical interactions between genetic variants within chromatin regulatory circuitry. Nature Genetics, 2016, 48, 1313-1320.	21.4	57
86	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. Journal of the National Cancer Institute, 2017, 109, .	6.3	57
87	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€"Results from BPC3. PLoS ONE, 2011, 6, e17142.	2.5	57
88	Identification of Novel Genetic Markers of Breast Cancer Survival. Journal of the National Cancer Institute, 2015, 107, .	6.3	56
89	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1121-1129.	2.5	56
90	CYP17 Genetic Variation and Risk of Breast and Prostate Cancer from the National Cancer Institute Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 2237-2246.	2.5	54

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91	Genetic variation in RNASEL associated with prostate cancer risk and progression. Carcinogenesis, 2010, 31, 1597-1603.	2.8	54
92	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
93	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
94	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
95	Common Genetic Variants in Prostate Cancer Risk Predictionâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 437-444.	2.5	51
96	Common Polymorphisms in the Adiponectin and Its Receptor Genes, Adiponectin Levels and the Risk of Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 2618-2627.	2.5	50
97	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. Human Molecular Genetics, 2015, 24, 5603-5618.	2.9	50
98	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
99	Quantifying the Genetic Correlation between Multiple Cancer Types. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 1427-1435.	2.5	48
100	A comprehensive analysis of common IGF1, IGFBP1 and IGFBP3 genetic variation with prospective IGF-I and IGFBP-3 blood levels and prostate cancer risk among Caucasians â€. Human Molecular Genetics, 2010, 19, 3089-3101.	2.9	47
101	Evaluation of 8q24 and 17q Risk Loci and Prostate Cancer Mortality. Clinical Cancer Research, 2009, 15, 3223-3230.	7.0	46
102	Genome-wide Association Study of Prostate Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2869-2876.	2.5	46
103	Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822.	1.9	45
104	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
105	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334.	12.1	44
106	Pooled Analysis of Phosphatidylinositol 3-Kinase Pathway Variants and Risk of Prostate Cancer. Cancer Research, 2010, 70, 2389-2396.	0.9	43
107	Type 2 diabetes risk variants and colorectal cancer risk: the Multiethnic Cohort and PAGE studies. Gut, 2011, 60, 1703-1711.	12.1	43
108	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. Human Molecular Genetics, 2011, 20, 2869-2878.	2.9	43

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109	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	5.1	43
110	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
111	Genome-wide association study of endometrial cancer in E2C2. Human Genetics, 2014, 133, 211-224.	3.8	42
112	Vitamin D Receptor Genotypes/Haplotypes and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2549-2552.	2.5	41
113	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
114	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
115	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
116	Quantitative trait loci predicting circulating sex steroid hormones in men from the NCI-Breast and Prostate Cancer Cohort Consortium (BPC3). Human Molecular Genetics, 2009, 18, 3749-3757.	2.9	37
117	Post-GWAS geneâ€“environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79 000 women. Human Molecular Genetics, 2014, 23, 5260-5270.	2.9	37
118	Association of KLK3 (PSA) genetic variants with prostate cancer risk and PSA levels. Carcinogenesis, 2011, 32, 853-859.	2.8	36
119	Additive Interactions Between Susceptibility Single-Nucleotide Polymorphisms Identified in Genome-Wide Association Studies and Breast Cancer Risk Factors in the Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2014, 180, 1018-1027.	3.4	36
120	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. Human Molecular Genetics, 2014, 23, 2198-2209.	2.9	36
121	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6.	1.3	36
122	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. Gut, 2014, 63, 800-807.	12.1	35
123	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319.	5.1	35
124	HNF1B and Endometrial Cancer Risk: Results from the PAGE study. PLoS ONE, 2012, 7, e30390.	2.5	34
125	Fine-Mapping the HOXB Region Detects Common Variants Tagging a Rare Coding Allele: Evidence for Synthetic Association in Prostate Cancer. PLoS Genetics, 2014, 10, e1004129.	3.5	34
126	Genome-wide association study of colorectal cancer in Hispanics. Carcinogenesis, 2016, 37, 547-556.	2.8	34

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127	Comparison of microsatellites, single-nucleotide polymorphisms (SNPs) and composite markers derived from SNPs in linkage analysis. BMC Genetics, 2005, 6, S29.	2.7	33
128	CYP19A1 Genetic Variation in Relation to Prostate Cancer Risk and Circulating Sex Hormone Concentrations in Men from the Breast and Prostate Cancer Cohort Consortium. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 2734-2744.	2.5	33
129	Meta-analysis of 8q24 for seven cancers reveals a locus between NOV and ENPP2 associated with cancer development. BMC Medical Genetics, 2011, 12, 156.	2.1	33
130	Insulin-like Growth Factor Pathway Genetic Polymorphisms, Circulating IGF1 and IGFBP3, and Prostate Cancer Survival. Journal of the National Cancer Institute, 2014, 106, dju085.	6.3	33
131	A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. Human Molecular Genetics, 2014, 23, 1934-1946.	2.9	32
132	Multiancestral Analysis of Inflammation-Related Genetic Variants and C-Reactive Protein in the Population Architecture Using Genomics and Epidemiology Study. Circulation: Cardiovascular Genetics, 2014, 7, 178-188.	5.1	31
133	Trans-ethnic fine-mapping of genetic loci for body mass index in the diverse ancestral populations of the Population Architecture using Genomics and Epidemiology (PAGE) Study reveals evidence for multiple signals at established loci. Human Genetics, 2017, 136, 771-800.	3.8	31
134	trans-Fatty acid intake and increased risk of advanced prostate cancer: modification by RNASEL R462Q variant. Carcinogenesis, 2007, 28, 1232-1236.	2.8	30
135	Genetic Predictors of Circulating 25-Hydroxyvitamin D and Risk of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 2037-2046.	2.5	30
136	A novel colorectal cancer risk locus at 4q32.2 identified from an international genome-wide association study. Carcinogenesis, 2014, 35, 2512-2519.	2.8	30
137	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	2.9	28
138	Insulinâ€like growth factor pathway genes and blood concentrations, dietary protein and risk of prostate cancer in the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). International Journal of Cancer, 2013, 133, 495-504.	5.1	28
139	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. Human Genetics, 2015, 134, 1249-1262.	3.8	28
140	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. Carcinogenesis, 2015, 36, 999-1007.	2.8	28
141	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
142	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
143	Refining the Prostate Cancer Genetic Association within the JAZF1 Gene on Chromosome 7p15.2. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 1349-1355.	2.5	26
144	Novel colon cancer susceptibility variants identified from a genomeâ€wide association study in African Americans. International Journal of Cancer, 2017, 140, 2728-2733.	5.1	26

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145	Genomeâ€wide association study and metaâ€analysis in Northern European populations replicate multiple colorectal cancer risk loci. International Journal of Cancer, 2018, 142, 540-546.	5.1	26
146	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
147	Toll-like Receptor Signaling Pathway Variants and Prostate Cancer Mortality. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 1859-1863.	2.5	25
148	Colorectal Cancer Linkage on Chromosomes 4q21, 8q13, 12q24, and 15q22. PLoS ONE, 2012, 7, e38175.	2.5	24
149	Genetic variants associated with fasting glucose and insulin concentrations in an ethnically diverse population: results from the Population Architecture using Genomics and Epidemiology (PAGE) study. BMC Medical Genetics, 2013, 14, 98.	2.1	24
150	Replication of Five Prostate Cancer Loci Identified in an Asian Populationâ€"Results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 212-216.	2.5	23
151	Association of Cancer Susceptibility Variants with Risk of Multiple Primary Cancers: The Population Architecture using Genomics and Epidemiology Study. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 2568-2578.	2.5	23
152	Lifetime Occurrence of Brain Metastases Arising from Lung, Breast, and Skin Cancers in the Elderly: A SEER-Medicare Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 917-925.	2.5	23
153	Genetic variation in the tollâ€like receptor 4 and prostate cancer incidence and mortality. Prostate, 2012, 72, 209-216.	2.3	22
154	Replication of Associations between GWAS SNPs and Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. Journal of Investigative Dermatology, 2014, 134, 2049-2052.	0.7	21
155	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657.	1.9	21
156	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	2.5	21
157	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. Diabetologia, 2017, 60, 2384-2398.	6.3	20
158	Incorporating Prior Biologic Information for High-Dimensional Rare Variant Association Studies. Human Heredity, 2012, 74, 184-195.	0.8	19
159	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110.	5.0	19
160	Pleiotropic and Sex-Specific Effects of Cancer GWAS SNPs on Melanoma Risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. PLoS ONE, 2015, 10, e0120491.	2.5	19
161	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. Carcinogenesis, 2014, 35, 2068-2073.	2.8	18
162	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. British Journal of Cancer, 2016, 114, 221-229.	6.4	18

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163	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	3.8	18
164	Identification of shared and unique susceptibility pathways among cancers of the lung, breast, and prostate from genome-wide association studies and tissue-specific protein interactions. Human Molecular Genetics, 2015, 24, 7406-7420.	2.9	17
165	Gene expression in stress urinary incontinence: a systematic review. International Urogynecology Journal, 2020, 31, 1-14.	1.4	17
166	Interactions Between Genome-wide Significant Genetic Variants and Circulating Concentrations of Insulin-like Growth Factor 1, Sex Hormones, and Binding Proteins in Relation to Prostate Cancer Risk in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. American Journal of Epidemiology, 2012, 175, 926-935.	3.4	16
167	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	12.8	16
168	Insulin-like Growth Factor Pathway Genetic Polymorphisms, Circulating IGF1 and IGFBP3, and Prostate Cancer Survival. Journal of the National Cancer Institute, 2014, 106, .	6.3	16
169	Circulating insulin-like growth factors and risks of overall, aggressive and early-onset prostate cancer: a collaborative analysis of 20 prospective studies and Mendelian randomization analysis. International Journal of Epidemiology, 2023, 52, 71-86.	1.9	16
170	The association of polymorphisms in hormone metabolism pathway genes, menopausal hormone therapy, and breast cancer risk: a nested case-control study in the California Teachers Study cohort. Breast Cancer Research, 2011, 13, R37.	5.0	15
171	Genetic variation across C-reactive protein and risk of prostate cancer. Prostate, 2014, 74, 1034-1042.	2.3	14
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