

Fredrick R Schumacher

List of Publications by Year in Descending Order

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

201 papers	20,676 citations	63 h-index	141 g-index
218 ext. papers	24,840 ext. citations	10.5 avg, IF	4.58 L-index

#	Paper	IF	Citations
201	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 329-337	9.7	14
200	Gender Disparities in Bladder Cancer-Specific Survival in High Poverty Areas Utilizing Ohio Cancer Incidence Surveillance System (OCISS). <i>Urology</i> , 2021 , 151, 163-168	1.6	1
199	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021 , 148, 307-319	7.5	13
198	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. <i>Gastroenterology</i> , 2021 , 160, 1164-1178.e6	13.3	15
197	"Robotic fatigue?" - The impact of case order on positive surgical margins in robotic-assisted laparoscopic prostatectomy. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2021 , 39, 365.e17-365.e23 ¹	2.8	1
196	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	36.3	62
195	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021 , 70, 1325-1334 ¹	19.2	7
194	Rare Variants in the DNA Repair Pathway and the Risk of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021 , 30, 895-903	4	1
193	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. <i>Human Genetics</i> , 2021 , 140, 1353-1365	6.3	5
192	Evaluating the estimation of genetic correlation and heritability using summary statistics. <i>Molecular Genetics and Genomics</i> , 2021 , 296, 1221-1234	3.1	0
191	Data Matching to Support Analysis of Cancer Epidemiology Among Veterans Compared With Non-Veteran Populations-An Exemplar in Brain Tumors. <i>JCO Clinical Cancer Informatics</i> , 2021 , 5, 985-994 ^{5.2}	5.2	0
190	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
189	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	13.3	47
188	Germline genetic variation in prostate susceptibility does not predict outcomes in the chemoprevention trials PCPT and SELECT. <i>Prostate Cancer and Prostatic Diseases</i> , 2020 , 23, 333-342	6.2	5
187	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. <i>Nature Communications</i> , 2020 , 11, 3905	17.4	12
186	Gene expression in stress urinary incontinence: a systematic review. <i>International Urogynecology Journal</i> , 2020 , 31, 1-14	2	8
185	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45

184	Observed racial disparity in the negative predictive value of multi-parametric MRI for the diagnosis for prostate cancer. <i>International Urology and Nephrology</i> , 2019 , 51, 1343-1348	2.3	4
183	Lifetime Occurrence of Brain Metastases Arising from Lung, Breast, and Skin Cancers in the Elderly: A SEER-Medicare Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 917-925	4	16
182	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019 , 120, 647-657	8.7	28
181	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
180	Genome-wide association study of circulating folate one-carbon metabolites. <i>Genetic Epidemiology</i> , 2019 , 43, 1030-1045	2.6	1
179	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019 , 156, 1455-1466	13.3	55
178	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019 , 104, 21-34	11	363
177	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 208-216	4	9
176	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019 , 51, 76-83	36.3	177
175	Genome-wide association study and meta-analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018 , 142, 540-546	7.5	21
174	Comparative Effectiveness of Local and Systemic Therapy for T4 Prostate Cancer. <i>Urology</i> , 2018 , 120, 173-179	1.6	3
173	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
172	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018 , 50, 928-936	36.3	340
171	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018 , 9, 2256	17.4	57
170	Growth factor genes and change in mammographic density after stopping combined hormone therapy in the California Teachers Study. <i>BMC Cancer</i> , 2018 , 18, 1072	4.8	1
169	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , 2018 , 9, 4616	17.4	30
168	Genetic susceptibility markers for a breast-colorectal cancer phenotype: Exploratory results from genome-wide association studies. <i>PLoS ONE</i> , 2018 , 13, e0196245	3.7	2
167	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. <i>Human Genetics</i> , 2017 , 136, 771-800	6.3	23

166	Novel colon cancer susceptibility variants identified from a genome-wide association study in African Americans. <i>International Journal of Cancer</i> , 2017 , 140, 2728-2733	7.5	17
165	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
164	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186
163	Transethnic insight into the genetics of glycaemic traits: fine-mapping results from the Population Architecture using Genomics and Epidemiology (PAGE) consortium. <i>Diabetologia</i> , 2017 , 60, 2384-2398	10.3	16
162	Genome-Wide Testing of Exonic Variants and Breast Cancer Risk in the California Teachers Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1462-1465	4	
161	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1427-1435	4	25
160	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 126-135	4	183
159	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017 , 109,	9.7	38
158	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
157	Common variants in the obesity-associated genes FTO and MC4R are not associated with risk of colorectal cancer. <i>Cancer Epidemiology</i> , 2016 , 44, 1-4	2.8	9
156	Modeling disease risk through analysis of physical interactions between genetic variants within chromatin regulatory circuitry. <i>Nature Genetics</i> , 2016 , 48, 1313-1320	36.3	43
155	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	7.8	92
154	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, 1052-67	24.4	104
153	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016 , 7, 11843	17.4	59
152	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
151	Genome-wide association study of colorectal cancer in Hispanics. <i>Carcinogenesis</i> , 2016 , 37, 547-556	4.6	26
150	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. <i>British Journal of Cancer</i> , 2016 , 114, 221-9	8.7	16
149	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	72

148	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016 , 150, 1633-1645	13.3	64
147	Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. <i>Human Genetics</i> , 2016 , 135, 137-54	6.3	6
146	Association between Adult Height and Risk of Colorectal, Lung, and Prostate Cancer: Results from Meta-analyses of Prospective Studies and Mendelian Randomization Analyses. <i>PLoS Medicine</i> , 2016 , 13, e1002118	11.6	49
145	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
144	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. <i>PLoS ONE</i> , 2016 , 11, e0157521	3.7	5
143	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016 , 53, 800-811	5.8	121
142	Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. <i>JAMA Oncology</i> , 2016 , 2, 1295-1302	13.4	189
141	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
140	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016 , 139, 2655-2670	7.5	30
139	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015 , 36, 256-71	4.6	12
138	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015 , 47, 373-80	36.3	406
137	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. <i>Human Molecular Genetics</i> , 2015 , 24, 5356-66	5.6	104
136	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 7138	17.4	106
135	Integration of multiethnic fine-mapping and genomic annotation to prioritize candidate functional SNPs at prostate cancer susceptibility regions. <i>Human Molecular Genetics</i> , 2015 , 24, 5603-18	5.6	35
134	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38
133	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1121-9	4	46
132	Association of aspirin and NSAID use with risk of colorectal cancer according to genetic variants. <i>JAMA - Journal of the American Medical Association</i> , 2015 , 313, 1133-42	27.4	135
131	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. <i>Human Genetics</i> , 2015 , 134, 1249-1262	6.3	25

130	Multiple novel prostate cancer susceptibility signals identified by fine-mapping of known risk loci among Europeans. <i>Human Molecular Genetics</i> , 2015 , 24, 5589-602	5.6	54
129	Identification of a common variant with potential pleiotropic effect on risk of inflammatory bowel disease and colorectal cancer. <i>Carcinogenesis</i> , 2015 , 36, 999-1007	4.6	21
128	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. <i>Human Molecular Genetics</i> , 2015 , 24, 7406-20	5.6	11
127	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	74
126	Cross Cancer Genomic Investigation of Inflammation Pathway for Five Common Cancers: Lung, Ovary, Prostate, Breast, and Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	47
125	Genome-wide association study of prostate cancer-specific survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1796-800	4	23
124	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015 , 24, 285-98	5.6	35
123	A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. <i>Breast Cancer Research</i> , 2015 , 17, 110	8.3	13
122	Prediction of individual genetic risk to prostate cancer using a polygenic score. <i>Prostate</i> , 2015 , 75, 1467-74	7.4	43
121	Pleiotropic and sex-specific effects of cancer GWAS SNPs on melanoma risk in the population architecture using genomics and epidemiology (PAGE) study. <i>PLoS ONE</i> , 2015 , 10, e0120491	3.7	14
120	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. <i>PLoS ONE</i> , 2015 , 10, e0131106	3.7	2
119	Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. <i>PLoS ONE</i> , 2015 , 10, e0143256	3.7	8
118	Prediction of breast cancer risk based on profiling with common genetic variants. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	324
117	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , 2015 , 96, 487-97	11	77
116	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
115	A model to determine colorectal cancer risk using common genetic susceptibility loci. <i>Gastroenterology</i> , 2015 , 148, 1330-9.e14	13.3	89
114	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36
113	A genome-wide pleiotropy scan for prostate cancer risk. <i>European Urology</i> , 2015 , 67, 649-57	10.2	17

112	Generalizability of established prostate cancer risk variants in men of African ancestry. <i>International Journal of Cancer</i> , 2015 , 136, 1210-7	7.5	51
111	Fine-scale mapping of the 5q11.2 breast cancer locus reveals at least three independent risk variants regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015 , 96, 5-20	11	59
110	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014 , 23, 2198-209	5.6	31
109	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. <i>Human Molecular Genetics</i> , 2014 , 23, 1934-46	5.6	28
108	Prostate cancer (PCa) risk variants and risk of fatal PCa in the National Cancer Institute Breast and Prostate Cancer Cohort Consortium. <i>European Urology</i> , 2014 , 65, 1069-75	10.2	58
107	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. <i>Carcinogenesis</i> , 2014 , 35, 2068-73	4.6	17
106	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014 , 46, 533-42	36.3	175
105	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014 , 46, 1103-9	36.3	331
104	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
103	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014 , 46, 1173-86	36.3	1339
102	Genetic variation across C-reactive protein and risk of prostate cancer. <i>Prostate</i> , 2014 , 74, 1034-42	4.2	11
101	Fine-mapping IGF1 and prostate cancer risk in African Americans: the multiethnic cohort study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 1928-32	4	5
100	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014 , 23, 6034-46	5.6	11
99	A genome-wide "pleiotropy scan" does not identify new susceptibility loci for estrogen receptor negative breast cancer. <i>PLoS ONE</i> , 2014 , 9, e85955	3.7	7
98	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37
97	A novel colorectal cancer risk locus at 4q32.2 identified from an international genome-wide association study. <i>Carcinogenesis</i> , 2014 , 35, 2512-9	4.6	25
96	Pleiotropic effects of genetic risk variants for other cancers on colorectal cancer risk: PAGE, GECCO and CCFR consortia. <i>Gut</i> , 2014 , 63, 800-7	19.2	27
95	Replication of associations between GWAS SNPs and melanoma risk in the Population Architecture Using Genomics and Epidemiology (PAGE) Study. <i>Journal of Investigative Dermatology</i> , 2014 , 134, 2049-2052	4.3	16

94	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38
93	Genome-wide diet-gene interaction analyses for risk of colorectal cancer. <i>PLoS Genetics</i> , 2014 , 10, e1004228	6	66
92	Insulin-like growth factor pathway genetic polymorphisms, circulating IGF1 and IGFBP3, and prostate cancer survival. <i>Journal of the National Cancer Institute</i> , 2014 , 106, dju085	9.7	31
91	Association of cancer susceptibility variants with risk of multiple primary cancers: The population architecture using genomics and epidemiology study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014 , 23, 2568-78	4	21
90	Fine-mapping the HOXB region detects common variants tagging a rare coding allele: evidence for synthetic association in prostate cancer. <i>PLoS Genetics</i> , 2014 , 10, e1004129	6	30
89	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014 , 5, 4051	17.4	13
88	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. <i>American Journal of Epidemiology</i> , 2014 , 180, 1018-27	3.8	29
87	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, 6616-33	5.6	77
86	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014 , 23, 6096-111	5.6	48
85	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTI1A. <i>Nature Communications</i> , 2014 , 5, 4613	17.4	62
84	Post-GWAS gene-environment interplay in breast cancer: results from the Breast and Prostate Cancer Cohort Consortium and a meta-analysis on 79,000 women. <i>Human Molecular Genetics</i> , 2014 , 23, 5260-70	5.6	30
83	Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014 , 16, 3419	8.3	82
82	Hormone metabolism pathway genes and mammographic density change after quitting estrogen and progestin combined hormone therapy in the California Teachers Study. <i>Breast Cancer Research</i> , 2014 , 16, 477	8.3	4
81	Insulin-like Growth Factor Pathway Genetic Polymorphisms, Circulating IGF1 and IGFBP3, and Prostate Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2014 , 106,	9.7	14
80	Multiancestral analysis of inflammation-related genetic variants and C-reactive protein in the population architecture using genomics and epidemiology study. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 178-88		22
79	Genome-wide association study of endometrial cancer in E2C2. <i>Human Genetics</i> , 2014 , 133, 211-24	6.3	33
78	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. <i>Human Molecular Genetics</i> , 2013 , 22, 2748-53	5.6	53
77	Fine Mapping and Identification of BMI Loci in African Americans. <i>American Journal of Human Genetics</i> , 2013 , 93, 661-71	11	63

76	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, 1046-60	11	80
75	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, 371-84, 384e1-2	36.3	422
74	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. <i>BMC Medical Genetics</i> , 2013 , 14, 98	2.1	22
73	No evidence of interaction between known lipid-associated genetic variants and smoking in the multi-ethnic PAGE population. <i>Human Genetics</i> , 2013 , 132, 1427-31	6.3	6
72	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , 2013 , 22, 4239-4239	5.6	2
71	Association of the FTO obesity risk variant rs8050136 with percentage of energy intake from fat in multiple racial/ethnic populations: the PAGE study. <i>American Journal of Epidemiology</i> , 2013 , 178, 780-90	3.8	53
70	Insulin-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). <i>International Journal of Cancer</i> , 2013 , 133, 495-504	7.5	19
69	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	11	167
68	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013 , 45, 392-8, 398e1-2	36.3	327
67	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. <i>Nature Genetics</i> , 2013 , 45, 385-91, 391e1-2	36.3	413
66	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013 , 45, 353-61, 361e1-2	36.3	813
65	Meta-analysis identifies four new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2013 , 45, 680-5	36.3	132
64	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. <i>Gastroenterology</i> , 2013 , 144, 799-807.e24	13.3	250
63	Genetic predictors of circulating 25-hydroxyvitamin d and risk of colorectal cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 2037-46	4	26
62	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, 408-15	5.6	109
61	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	9.7	155
60	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. <i>Human Molecular Genetics</i> , 2013 , 22, 2520-8	5.6	88
59	Post-genome-wide association study challenges for lipid traits: describing age as a modifier of gene-lipid associations in the Population Architecture using Genomics and Epidemiology (PAGE) study. <i>Annals of Human Genetics</i> , 2013 , 77, 416-25	2.2	4

58	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012 , 131, 217-34	6.3	173
57	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012 , 44, 770-6	36.3	184
56	A genome-wide association meta-analysis identifies new childhood obesity loci. <i>Nature Genetics</i> , 2012 , 44, 526-31	36.3	292
55	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. <i>Blood</i> , 2012 , 119, 469-75	2.2	52
54	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, 5373-84	5.6	143
53	HNF1B and endometrial cancer risk: results from the PAGE study. <i>PLoS ONE</i> , 2012 , 7, e30390	3.7	32
52	Evaluation of the metabochip genotyping array in African Americans and implications for fine mapping of GWAS-identified loci: the PAGE study. <i>PLoS ONE</i> , 2012 , 7, e35651	3.7	59
51	Colorectal cancer linkage on chromosomes 4q21, 8q13, 12q24, and 15q22. <i>PLoS ONE</i> , 2012 , 7, e38175	3.7	23
50	Genetic variation in the toll-like receptor 4 and prostate cancer incidence and mortality. <i>Prostate</i> , 2012 , 72, 209-16	4.2	16
49	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012 , 44, 651-8	36.3	409
48	Replication of five prostate cancer loci identified in an Asian population--results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 212-6	4	21
47	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. <i>American Journal of Epidemiology</i> , 2012 , 175, 826-37	3.8	15
46	Common genetic variants in prostate cancer risk prediction--results from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 437-44	4	49
45	Incorporating prior biologic information for high-dimensional rare variant association studies. <i>Human Heredity</i> , 2012 , 74, 184-95	1.1	15
44	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. <i>Breast Cancer Research</i> , 2011 , 13, R37	8.3	13
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1	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1