

# Fredrick R Schumacher

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3867374/publications.pdf>

Version: 2024-02-01

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	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. <i>International Journal of Epidemiology</i> , 2023, 52, 71-86.	1.9	16
2	The Impact of Race and Sex on Metastatic Bladder Cancer Survival. <i>Urology</i> , 2022, 165, 98-105.	1.0	4
3	Finding a Place for Family History To Inform High-grade Prostate Cancer Risk. <i>European Urology</i> , 2022, , .	1.9	0
4	Abstract 3676: Race-specific methylation profiles and epigenetic age acceleration differentiates estrogen receptor status breast cancer. <i>Cancer Research</i> , 2022, 82, 3676-3676.	0.9	0
5	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.	6.3	45
6	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.	1.0	4
7	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021, 148, 307-319.	5.1	35
8	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.	1.3	36
9	“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.	1.6	3
10	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
11	Genetic architectures of proximal and distal colorectal cancer are partly distinct. <i>Gut</i> , 2021, 70, 1325-1334.	12.1	44
12	Rare Variants in the DNA Repair Pathway and the Risk of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 895-903.	2.5	3
13	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.	3.8	18
14	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.7	6
15	Evaluating the estimation of genetic correlation and heritability using summary statistics. <i>Molecular Genetics and Genomics</i> , 2021, 296, 1221-1234.	2.1	2
16	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.	2.1	2
17	Race and Genetic Alterations in Prostate Cancer. <i>JCO Precision Oncology</i> , 2021, 5, 1650-1653.	3.0	12
18	Gene expression in stress urinary incontinence: a systematic review. <i>International Urogynecology Journal</i> , 2020, 31, 1-14.	1.4	17

#	ARTICLE	IF	CITATIONS
19	Cumulative Burden of Colorectal Cancerâ€“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
20	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.	3.9	10
21	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. <i>Nature Communications</i> , 2020, 11, 3905.	12.8	28
22	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020, 11, 3353.	12.8	75
23	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019, 111, 146-157.	6.3	129
24	Genomeâ€“wide association study of circulating folate oneâ€“carbon metabolites. <i>Genetic Epidemiology</i> , 2019, 43, 1030-1045.	1.3	2
25	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
26	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.	1.4	4
27	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.	2.5	23
28	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
29	Large-Scale Genome-Wide Association Study of East Asians Identifies Loci Associated With Risk for Colorectal Cancer. <i>Gastroenterology</i> , 2019, 156, 1455-1466.	1.3	111
30	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
31	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 208-216.	2.5	21
32	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019, 51, 76-87.	21.4	377
33	Genomeâ€“wide association study and metaâ€“analysis in Northern European populations replicate multiple colorectal cancer risk loci. <i>International Journal of Cancer</i> , 2018, 142, 540-546.	5.1	26
34	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.	2.6	1
35	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , 2018, 9, 4616.	12.8	43
36	Genetic susceptibility markers for a breast-colorectal cancer phenotype: Exploratory results from genome-wide association studies. <i>PLoS ONE</i> , 2018, 13, e0196245.	2.5	9

#	ARTICLE	IF	CITATIONS
37	Comparative Effectiveness of Local and Systemic Therapy for T4 Prostate Cancer. <i>Urology</i> , 2018, 120, 173-179.	1.0	7
38	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	12.8	178
39	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
40	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
41	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.	3.8	31
42	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.	5.1	26
43	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
44	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
45	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.	6.3	20
46	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.	2.5	0
47	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 1427-1435.	2.5	48
48	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
49	Two Novel Susceptibility Loci for Prostate Cancer in Men of African Ancestry. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	57
50	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822.	1.9	45
51	Up For A Challenge (U4C): Stimulating innovation in breast cancer genetic epidemiology. <i>PLoS Genetics</i> , 2017, 13, e1006945.	3.5	3
52	Fine-Mapping of Common Genetic Variants Associated with Colorectal Tumor Risk Identified Potential Functional Variants. <i>PLoS ONE</i> , 2016, 11, e0157521.	2.5	8
53	<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
54	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

#	ARTICLE	IF	CITATIONS
55	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
56	Telomere structure and maintenance gene variants and risk of five cancer types. <i>International Journal of Cancer</i> , 2016, 139, 2655-2670.	5.1	43
57	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.	1.9	12
58	Modeling disease risk through analysis of physical interactions between genetic variants within chromatin regulatory circuitry. <i>Nature Genetics</i> , 2016, 48, 1313-1320.	21.4	57
59	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
60	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
61	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016, 7, 11843.	12.8	86
62	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375.	12.8	93
63	Genome-wide association study of colorectal cancer in Hispanics. <i>Carcinogenesis</i> , 2016, 37, 547-556.	2.8	34
64	CYP24A1 variant modifies the association between use of oestrogen plus progestogen therapy and colorectal cancer risk. <i>British Journal of Cancer</i> , 2016, 114, 221-229.	6.4	18
65	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016, 108, djv431.	6.3	111
66	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016, 150, 1633-1645.	1.3	97
67	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, 137-154.	3.8	8
68	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.	8.4	69
69	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
70	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.	5.0	19
71	Prediction of individual genetic risk to prostate cancer using a polygenic score. <i>Prostate</i> , 2015, 75, 1467-1474.	2.3	54
72	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.	2.5	19

#	ARTICLE	IF	CITATIONS
73	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. PLoS ONE, 2015, 10, e0131106.	2.5	2
74	Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. PLoS ONE, 2015, 10, e0143256.	2.5	13
75	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
76	Characterization of Large Structural Genetic Mosaicism in Human Autosomes. American Journal of Human Genetics, 2015, 96, 487-497.	6.2	101
77	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
78	A Model to Determine Colorectal Cancer Risk Using Common Genetic Susceptibility Loci. Gastroenterology, 2015, 148, 1330-1339.e14.	1.3	129
79	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
80	A Genome-wide Pleiotropy Scan for Prostate Cancer Risk. European Urology, 2015, 67, 649-657.	1.9	21
81	Generalizability of established prostate cancer risk variants in men of African ancestry. International Journal of Cancer, 2015, 136, 1210-1217.	5.1	62
82	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
83	Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. Carcinogenesis, 2015, 36, 256-271.	2.8	14
84	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
85	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
86	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. Nature Communications, 2015, 6, 7138.	12.8	138
87	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
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	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

#	ARTICLE	IF	CITATIONS
91	A genome-wide association study for colorectal cancer identifies a risk locus in 14q23.1. Human Genetics, 2015, 134, 1249-1262.	3.8	28
92	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
93	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
94	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
95	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
96	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
97	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
98	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
99	A Genome-Wide â€œPleiotropy Scanâ€•Does Not Identify New Susceptibility Loci for Estrogen Receptor Negative Breast Cancer. PLoS ONE, 2014, 9, e85955.	2.5	8
100	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
101	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
102	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
103	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
104	Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285.	3.5	39
105	Genome-Wide Diet-Gene Interaction Analyses for Risk of Colorectal Cancer. PLoS Genetics, 2014, 10, e1004228.	3.5	81
106	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
107	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
108	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

#	ARTICLE	IF	CITATIONS
109	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051.	12.8	16
110	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, 1018-1027.	3.4	36
111	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
112	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	2.9	53
113	Trans-ethnic genome-wide association study of colorectal cancer identifies a new susceptibility locus in VTIIA. <i>Nature Communications</i> , 2014, 5, 4613.	12.8	72
114	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, 5260-5270.	2.9	37
115	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.	5.0	97
116	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.	5.0	5
117	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, .	6.3	16
118	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, 178-188.	5.1	31
119	Genome-wide association study of endometrial cancer in E2C2. <i>Human Genetics</i> , 2014, 133, 211-224.	3.8	42
120	Identification and characterization of functional risk variants for colorectal cancer mapping to chromosome 11q23.1. <i>Human Molecular Genetics</i> , 2014, 23, 2198-2209.	2.9	36
121	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, 1934-1946.	2.9	32
122	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, 1069-1075.	1.9	75
123	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. <i>Carcinogenesis</i> , 2014, 35, 2068-2073.	2.8	18
124	Large-scale genetic study in East Asians identifies six new loci associated with colorectal cancer risk. <i>Nature Genetics</i> , 2014, 46, 533-542.	21.4	212
125	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
126	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105

#	ARTICLE	IF	CITATIONS
127	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
128	Genetic variation across C-reactive protein and risk of prostate cancer. <i>Prostate</i> , 2014, 74, 1034-1042.	2.3	14
129	Fine-Mapping <i>IGF1</i> and Prostate Cancer Risk in African Americans: The Multiethnic Cohort Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 1928-1932.	2.5	7
130	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	2.9	12
131	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. <i>Human Molecular Genetics</i> , 2013, 22, 2748-2753.	2.9	59
132	Fine Mapping and Identification of BMI Loci in African Americans. <i>American Journal of Human Genetics</i> , 2013, 93, 661-671.	6.2	77
133	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
134	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
135	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	24
136	No evidence of interaction between known lipid-associated genetic variants and smoking in the multi-ethnic PAGE population. <i>Human Genetics</i> , 2013, 132, 1427-1431.	3.8	7
137	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.	2.9	2
138	Association of the FTO Obesity Risk Variant rs8050136 With Percentage of Energy Intake From Fat in Multiple Racial/Ethnic Populations. <i>American Journal of Epidemiology</i> , 2013, 178, 780-790.	3.4	59
139	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.	5.1	28
140	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
141	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
142	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
143	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
144	Meta-analysis identifies four new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2013, 45, 680-685.	21.4	154

#	ARTICLE	IF	CITATIONS
145	Identification of Genetic Susceptibility Loci for Colorectal Tumors in a Genome-Wide Meta-analysis. <i>Gastroenterology</i> , 2013, 144, 799-807.e24.	1.3	292
146	Genetic Predictors of Circulating 25-Hydroxyvitamin D and Risk of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 2037-2046.	2.5	30
147	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
148	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
149	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
150	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, 416-425.	0.8	5
151	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, 212-216.	2.5	23
152	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, 926-935.	3.4	16
153	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, 437-444.	2.5	51
154	Incorporating Prior Biologic Information for High-Dimensional Rare Variant Association Studies. <i>Human Heredity</i> , 2012, 74, 184-195.	0.8	19
155	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012, 44, 770-776.	21.4	210
156	A genome-wide association meta-analysis identifies new childhood obesity loci. <i>Nature Genetics</i> , 2012, 44, 526-531.	21.4	352
157	A genome-wide meta-analysis of nodular sclerosing Hodgkin lymphoma identifies risk loci at 6p21.32. <i>Blood</i> , 2012, 119, 469-475.	1.4	66
158	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
159	HNF1B and Endometrial Cancer Risk: Results from the PAGE study. <i>PLoS ONE</i> , 2012, 7, e30390.	2.5	34
160	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.	2.5	71
161	Colorectal Cancer Linkage on Chromosomes 4q21, 8q13, 12q24, and 15q22. <i>PLoS ONE</i> , 2012, 7, e38175.	2.5	24
162	Genetic variation in the toll-like receptor 4 and prostate cancer incidence and mortality. <i>Prostate</i> , 2012, 72, 209-216.	2.3	22

#	ARTICLE	IF	CITATIONS
163	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012, 44, 651-658.	21.4	519
164	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012, 131, 217-234.	3.8	183
165	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
166	Type 2 diabetes risk variants and colorectal cancer risk: the Multiethnic Cohort and PAGE studies. <i>Gut</i> , 2011, 60, 1703-1711.	12.1	43
167	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptorâ€“negative breast cancer. <i>Nature Genetics</i> , 2011, 43, 1210-1214.	21.4	279
168	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.	5.0	15
169	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
170	Meta-analysis of 8q24 for seven cancers reveals a locus between NOV and ENPP2 associated with cancer development. <i>BMC Medical Genetics</i> , 2011, 12, 156.	2.1	33
171	Association of KLK3 (PSA) genetic variants with prostate cancer risk and PSA levels. <i>Carcinogenesis</i> , 2011, 32, 853-859.	2.8	36
172	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
173	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011, 20, 3867-3875.	2.9	160
174	Common Polymorphisms in the Adiponectin and Its Receptor Genes, Adiponectin Levels and the Risk of Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2011, 20, 2618-2627.	2.5	50
175	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. <i>Human Molecular Genetics</i> , 2011, 20, 2869-2878.	2.9	43
176	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. <i>Human Molecular Genetics</i> , 2011, 20, 3322-3329.	2.9	28
177	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
178	Characterizing Associations and SNP-Environment Interactions for GWAS-Identified Prostate Cancer Risk Markersâ€“Results from BPC3. <i>PLoS ONE</i> , 2011, 6, e17142.	2.5	57
179	Fatty Acid Synthase Polymorphisms, Tumor Expression, Body Mass Index, Prostate Cancer Risk, and Survival. <i>Journal of Clinical Oncology</i> , 2010, 28, 3958-3964.	1.6	113
180	Genome-wide Association Study of Prostate Cancer Mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2869-2876.	2.5	46

#	ARTICLE	IF	CITATIONS
181	A Large Prospective Study of <i>SEP15</i> Genetic Variation, Interaction with Plasma Selenium Levels, and Prostate Cancer Risk and Survival. <i>Cancer Prevention Research</i> , 2010, 3, 604-610.	1.5	79
182	Eighteen Insulin-like Growth Factor Pathway Genes, Circulating Levels of IGF-I and Its Binding Protein, and Risk of Prostate and Breast Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2877-2887.	2.5	59
183	Pooled Analysis of Phosphatidylinositol 3-Kinase Pathway Variants and Risk of Prostate Cancer. <i>Cancer Research</i> , 2010, 70, 2389-2396.	0.9	43
184	Refining the Prostate Cancer Genetic Association within the <i>JAZF1</i> Gene on Chromosome 7p15.2. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 1349-1355.	2.5	26
185	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. <i>Human Molecular Genetics</i> , 2010, 19, 3089-3101.	2.9	47
186	Genetic variation in RNASEL associated with prostate cancer risk and progression. <i>Carcinogenesis</i> , 2010, 31, 1597-1603.	2.8	54
187	Fine mapping and functional analysis of a common variant in <i>MSMB</i> on chromosome 10q11.2 associated with prostate cancer susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7933-7938.	7.1	96
188	Evaluation of 8q24 and 17q Risk Loci and Prostate Cancer Mortality. <i>Clinical Cancer Research</i> , 2009, 15, 3223-3230.	7.0	46
189	Copy number variation in the Framingham Heart Study. <i>BMC Proceedings</i> , 2009, 3, S133.	1.6	6
190	Quantitative trait loci predicting circulating sex steroid hormones in men from the NCI-Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Human Molecular Genetics</i> , 2009, 18, 3749-3757.	2.9	37
191	<i>CYP19A1</i> Genetic Variation in Relation to Prostate Cancer Risk and Circulating Sex Hormone Concentrations in Men from the Breast and Prostate Cancer Cohort Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 2734-2744.	2.5	33
192	Evaluation of the 8q24 Prostate Cancer Risk Locus and <i>MYC</i> Expression. <i>Cancer Research</i> , 2009, 69, 5568-5574.	0.9	110
193	Polymorphism in endostatin, an angiogenesis inhibitor, and prostate cancer risk and survival: A prospective study. <i>International Journal of Cancer</i> , 2009, 125, 1143-1146.	5.1	9
194	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009, 41, 1055-1057.	21.4	218
195	Toll-like Receptor Signaling Pathway Variants and Prostate Cancer Mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 1859-1863.	2.5	25
196	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
197	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008, 40, 310-315.	21.4	871
198	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

#	ARTICLE	IF	CITATIONS
199	trans-Fatty acid intake and increased risk of advanced prostate cancer: modification by RNASEL R462Q variant. <i>Carcinogenesis</i> , 2007, 28, 1232-1236.	2.8	30
200	CYP17 Genetic Variation and Risk of Breast and Prostate Cancer from the National Cancer Institute Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 2237-2246.	2.5	54
201	A Bayesian latent class analysis for whole-genome association analyses: an illustration using the GAW15 simulated rheumatoid arthritis dense scan data. <i>BMC Proceedings</i> , 2007, 1, S112.	1.6	8
202	Model selection and Bayesian methods in statistical genetics: Summary of Group 11 contributions to Genetic Analysis Workshop 15. <i>Genetic Epidemiology</i> , 2007, 31, S96-S102.	1.3	7
203	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
204	Vitamin D Receptor Genotypes/Haplotypes and Prostate Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006, 15, 2549-2552.	2.5	41
205	Comparison of microsatellites, single-nucleotide polymorphisms (SNPs) and composite markers derived from SNPs in linkage analysis. <i>BMC Genetics</i> , 2005, 6, S29.	2.7	33
206	Relation of serum insulin-like growth factor-I (IGF-I) and IGF binding protein-3 to risk of prostate cancer (United States). <i>Cancer Causes and Control</i> , 2003, 14, 721-726.	1.8	60
207	Comparison of missing data approaches in linkage analysis. <i>BMC Genetics</i> , 2003, 4, S44.	2.7	3