Fredrick R Schumacher

List of Publications by Citations

Source: https://exaly.com/author-pdf/3867374/fredrick-r-schumacher-publications-by-citations.pdf

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
200	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
199	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007 , 39, 645-9	36.3	979
198	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
197	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008 , 40, 310-5	36.3	787
196	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017 , 551, 92-94	50.4	643
195	Identification of ten loci associated with height highlights new biological pathways in human growth. <i>Nature Genetics</i> , 2008 , 40, 584-91	36.3	482
194	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
193	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
192	Detectable clonal mosaicism and its relationship to aging and cancer. <i>Nature Genetics</i> , 2012 , 44, 651-8	36.3	409
191	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
190	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
189	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
188	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
187	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
186	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
185	A genome-wide association meta-analysis identifies new childhood obesity loci. <i>Nature Genetics</i> , 2012 , 44, 526-31	36.3	292

(2011-2011)

184	A common variant at the TERT-CLPTM1L locus is associated with estrogen receptor-negative breast cancer. <i>Nature Genetics</i> , 2011 , 43, 1210-4	36.3	253	
183	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	
182	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011 , 43, 785-91	36.3	243	•
181	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009 , 41, 1055-7	36.3	201	
180	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	
179	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1767-1778	36.3	186	
178	Common variation near CDKN1A, POLD3 and SHROOM2 influences colorectal cancer risk. <i>Nature Genetics</i> , 2012 , 44, 770-6	36.3	184	
177	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	
176	Discovery of common and rare genetic risk variants for colorectal cancer. <i>Nature Genetics</i> , 2019 , 51, 76-	-83 6.3	177	
175	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	
174	Meta-analysis of new genome-wide association studies of colorectal cancer risk. <i>Human Genetics</i> , 2012 , 131, 217-34	6.3	173	
173	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , 2011 , 43, 570-3	36.3	171	
172	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	
171	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	
170	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	
169	Genome-wide association study identifies new prostate cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2011 , 20, 3867-75	5.6	143	
168	Association of aspirin and NSAID use with risk of colorectal cancer according to genetic variants. JAMA - Journal of the American Medical Association, 2015, 313, 1133-42	27.4	135	
167	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, 1252-63	9.7	134	

166	Meta-analysis identifies four new loci associated with testicular germ cell tumor. <i>Nature Genetics</i> , 2013 , 45, 680-5	36.3	132
165	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	6	128
164	A common 8q24 variant in prostate and breast cancer from a large nested case-control study. <i>Cancer Research</i> , 2007 , 67, 2951-6	10.1	127
163	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
162	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
161	Genome-wide association study of colorectal cancer identifies six new susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 7138	17.4	106
160	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
159	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, 1052-6	5 7 4·4	104
158	Evaluation of the 8q24 prostate cancer risk locus and MYC expression. <i>Cancer Research</i> , 2009 , 69, 5568-	-7 4 0.1	102
157	Fatty acid synthase polymorphisms, tumor expression, body mass index, prostate cancer risk, and survival. <i>Journal of Clinical Oncology</i> , 2010 , 28, 3958-64	2.2	94
156	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
155	A model to determine colorectal cancer risk using common genetic susceptibility loci. <i>Gastroenterology</i> , 2015 , 148, 1330-9.e14	13.3	89
154	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
153	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014 , 4, 4999	17.4	87
152	Fine mapping and functional analysis of a common variant in MSMB 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, 7933-8	11.5	85
151	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
150	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
149	Characterization of large structural genetic mosaicism in human autosomes. <i>American Journal of Human Genetics</i> , 2015 , 96, 487-97	11	77

(2018-2014)

148	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
147	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107,	9.7	74
146	Prostate Cancer Susceptibility in Men of African Ancestry at 8q24. <i>Journal of the National Cancer Institute</i> , 2016 , 108,	9.7	72
145	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
144	A large prospective study of SEP15 genetic variation, interaction with plasma selenium levels, and prostate cancer risk and survival. <i>Cancer Prevention Research</i> , 2010 , 3, 604-10	3.2	70
143	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. <i>Journal of the National Cancer Institute</i> , 2019 , 111, 146-157	9.7	67
142	Genome-wide diet-gene interaction analyses for risk of colorectal cancer. PLoS Genetics, 2014, 10, e100	4228	66
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	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016 , 7, 11375	17.4	64
139	Identification of Susceptibility Loci and Genes for Colorectal Cancer Risk. <i>Gastroenterology</i> , 2016 , 150, 1633-1645	13.3	64
138	Fine Mapping and Identification of BMI Loci in African Americans. <i>American Journal of Human Genetics</i> , 2013 , 93, 661-71	11	63
137	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
136	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
135	Female chromosome X mosaicism is age-related and preferentially affects the inactivated X chromosome. <i>Nature Communications</i> , 2016 , 7, 11843	17.4	59
134	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
133	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
132	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
131	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

130	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, 721-6	2.8	57
129	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
128	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
127	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-	8 1	54
126	Testicular germ cell tumor susceptibility associated with the UCK2 locus on chromosome 1q23. Human Molecular Genetics, 2013 , 22, 2748-53	5.6	53
125	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	o ^{3.8}	53
124	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
123	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
122	Common genetic variants in prostate cancer risk predictionresults from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 437-44	4	49
121	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, 2237-46	4	49
120	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
119	Characterizing associations and SNP-environment interactions for GWAS-identified prostate cancer risk markersresults from BPC3. <i>PLoS ONE</i> , 2011 , 6, e17142	3.7	49
118	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
117	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
116	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
115	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
114	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, 3089-101	5.6	46
113	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019 , 10, 431	17.4	45

(2011-2009)

112	Evaluation of 8q24 and 17q risk loci and prostate cancer mortality. <i>Clinical Cancer Research</i> , 2009 , 15, 3223-30	12.9	44	
111	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, 2618-27	4	44	
110	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	
109	Prediction of individual genetic risk to prostate cancer using a polygenic score. <i>Prostate</i> , 2015 , 75, 1467	'-7 <u>4</u> 2	43	
108	Genome-wide association study of prostate cancer mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 2869-76	4	42	
107	Genetic variation in RNASEL associated with prostate cancer risk and progression. <i>Carcinogenesis</i> , 2010 , 31, 1597-603	4.6	41	
106	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, 2869-78	5.6	39	
105	Identification of novel genetic markers of breast cancer survival. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	38	
104	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	
103	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. <i>PLoS Genetics</i> , 2014 , 10, e1004285	6	38	
102	Vitamin D receptor genotypes/haplotypes and prostate cancer risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 2549-52	4	38	
101	MicroRNA related polymorphisms and breast cancer risk. <i>PLoS ONE</i> , 2014 , 9, e109973	3.7	37	
100	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015 , 24, 2966-84	5.6	36	
99	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, 3749-57	5.6	36	
98	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	
97	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	
96	Pooled analysis of phosphatidylinositol 3-kinase pathway variants and risk of prostate cancer. <i>Cancer Research</i> , 2010 , 70, 2389-96	10.1	35	
95	Type 2 diabetes risk variants and colorectal cancer risk: the Multiethnic Cohort and PAGE studies. <i>Gut</i> , 2011 , 60, 1703-11	19.2	35	

94	Genome-wide association study of endometrial cancer in E2C2. Human Genetics, 2014, 133, 211-24	6.3	33
93	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. <i>Nature Communications</i> , 2020 , 11, 3353	17.4	32
92	HNF1B and endometrial cancer risk: results from the PAGE study. PLoS ONE, 2012, 7, e30390	3.7	32
91	Association of KLK3 (PSA) genetic variants with prostate cancer risk and PSA levels. <i>Carcinogenesis</i> , 2011 , 32, 853-9	4.6	32
90	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
89	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
88	Comparison of microsatellites, single-nucleotide polymorphisms (SNPs) and composite markers derived from SNPs in linkage analysis. <i>BMC Genetics</i> , 2005 , 6 Suppl 1, S29	2.6	31
87	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
86	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
85	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
84	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , 2018 , 9, 4616	17.4	30
83	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
82	CYP19A1 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, 2734-44	4	29
81	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
80	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
79	Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017 , 46, 1814-1822	7.8	27
78	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
77	Genome-wide association study of colorectal cancer in Hispanics. <i>Carcinogenesis</i> , 2016 , 37, 547-556	4.6	26

(2012-2013)

76	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
<i>75</i>	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	26
74	Trans-fatty acid intake and increased risk of advanced prostate cancer: modification by RNASEL R462Q variant. <i>Carcinogenesis</i> , 2007 , 28, 1232-6	4.6	26
73	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
72	Quantifying the Genetic Correlation between Multiple Cancer Types. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017 , 26, 1427-1435	4	25
71	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
70	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
69	Genome-wide association study of prostate cancer-specific survival. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1796-800	4	23
68	Colorectal cancer linkage on chromosomes 4q21, 8q13, 12q24, and 15q22. <i>PLoS ONE</i> , 2012 , 7, e38175	3.7	23
67	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
66	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
65	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. <i>Human Molecular Genetics</i> , 2011 , 20, 3322-9	5.6	22
64	Toll-like receptor signaling pathway variants and prostate cancer mortality. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 1859-63	4	22
63	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
62	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
61	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
60	Refining the prostate cancer genetic association within the JAZF1 gene on chromosome 7p15.2. Cancer Epidemiology Biomarkers and Prevention, 2010 , 19, 1349-55	4	21
59	Replication of five prostate cancer loci identified in an Asian populationresults from the NCI Breast and Prostate Cancer Cohort Consortium (BPC3). Cancer Epidemiology Biomarkers and Prevention 2012 21 212-6	4	21

58	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
57	RAD51B in Familial Breast Cancer. <i>PLoS ONE</i> , 2016 , 11, e0153788	3.7	18
56	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
55	Cross-cancer pleiotropic analysis of endometrial cancer: PAGE and E2C2 consortia. <i>Carcinogenesis</i> , 2014 , 35, 2068-73	4.6	17
54	A genome-wide pleiotropy scan for prostate cancer risk. <i>European Urology</i> , 2015 , 67, 649-57	10.2	17
53	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
52	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
51	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
50	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-	2032	16
49	Genetic variation in the toll-like receptor 4 and prostate cancer incidence and mortality. <i>Prostate</i> , 2012 , 72, 209-16	4.2	16
48	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</i>	3.8	15
47	of Epidemiology, 2012 , 175, 926-35 Incorporating prior biologic information for high-dimensional rare variant association studies. Human Heredity, 2012 , 74, 184-95	1.1	15
46	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
45	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
44	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
43	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	9.7	14
42	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
41	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

(2007-2011)

40	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
39	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
38	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
37	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
36	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
35	Genetic variation across C-reactive protein and risk of prostate cancer. <i>Prostate</i> , 2014 , 74, 1034-42	4.2	11
34	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
33	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
32	Polymorphism in endostatin, an angiogenesis inhibitor, and prostate cancer risk and survival: A prospective study. <i>International Journal of Cancer</i> , 2009 , 125, 1143-6	7.5	9
31	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
30	Body Mass Index Genetic Risk Score and Endometrial Cancer Risk. <i>PLoS ONE</i> , 2015 , 10, e0143256	3.7	8
29	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 Suppl 1, S112	2.3	8
28	Gene expression in stress urinary incontinence: a systematic review. <i>International Urogynecology Journal</i> , 2020 , 31, 1-14	2	8
27	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
26	Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-13	34 9.2	7
25	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
24	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
23	Model selection and Bayesian methods in statistical genetics: summary of group 11 contributions to Genetic Analysis Workshop 15. <i>Genetic Epidemiology</i> , 2007 , 31 Suppl 1, S96-102	2.6	6

22	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
21	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
20	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
19	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
18	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
17	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
16	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
15	Copy number variation in the Framingham Heart Study. <i>BMC Proceedings</i> , 2009 , 3 Suppl 7, S133	2.3	4
14	Comparative Effectiveness of Local and Systemic Therapy for T4 Prostate Cancer. <i>Urology</i> , 2018 , 120, 173-179	1.6	3
13	Comparison of missing data approaches in linkage analysis. <i>BMC Genetics</i> , 2003 , 4 Suppl 1, S44	2.6	3
12	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
11	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
10	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
9	Genome-wide association study of circulating folate one-carbon metabolites. <i>Genetic Epidemiology</i> , 2019 , 43, 1030-1045	2.6	1
8	Assessment of Polygenic Architecture and Risk Prediction based on Common Variants Across Fourteen Cancers		1
7	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
6	"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	7-365.e	23 ¹
5	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

LIST OF PUBLICATIONS

4	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
3	Evaluating the estimation of genetic correlation and heritability using summary statistics. <i>Molecular Genetics and Genomics</i> , 2021 , 296, 1221-1234	3.1	O
2	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	
1	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, 985-9	94 ^{5.2}	