Fredrik Wiklund

List of Publications by Year
in descending order

83 papers	9,101 citations	81900 39 h-index	49909 87 g-index
90 all docs	90 docs citations	90 times ranked	14860 citing authors

#	Article	IF	Citations
1	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. American Journal of Human Genetics, 2016, 99, 877-885.	6.2	1,555
2	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	21.4	738
3	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
4	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
5	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
6	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	21.4	357
7	Prostate cancer screening in men aged 50â€“69 years (STHLM3): a prospective population-based diagnostic study. Lancet Oncology, The, 2015, 16, 1667-1676.	10.7	308
8	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
9	Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75.	21.4	264
10	Two Genome-wide Association Studies of Aggressive Prostate Cancer Implicate Putative Prostate Tumor Suppressor Gene DAB2IP. Journal of the National Cancer Institute, 2007, 99, 1836-1844.	6.3	235
11	A prostate cancer susceptibility allele at 6q22 increases RFX6 expression by modulating HOXB13 chromatin binding. Nature Genetics, 2014, 46, 126-135.	21.4	182
12	<i>PALB2</i>,<i>CHEK2</i>and<i>ATM</i>rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
13	HOXB13 is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2013, 132, 5-14.	3.8	166
14	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
15	Polygenic hazard score to guide screening for aggressive prostate cancer: development and validation in large scale cohorts. BMJ: British Medical Journal, 2018, 360, j5757.	2.3	153
16	Genetic determinants of telomere length and risk of common cancers: a Mendelian randomization study. Human Molecular Genetics, 2015, 24, 5356-5366.	2.9	128
17	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	21.4	120
18	Gene regulatory mechanisms underpinning prostate cancer susceptibility. Nature Genetics, 2016, 48, 387-397.	21.4	119

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19	A meta-analysis of genome-wide association studies to identify prostate cancer susceptibility loci associated with aggressive and non-aggressive disease. Human Molecular Genetics, 2013, 22, 408-415.	2.9	118
20	Polygenic Risk Score Improves Prostate Cancer Risk Prediction: Results from the Stockholm-1 Cohort Study. European Urology, 2011, 60, 21-28.	1.9	117
21	A Population-based Assessment of Germline HOXB13 G84E Mutation and Prostate Cancer Risk. European Urology, 2014, 65, 169-176.	1.9	116
22	Physical Activity and Survival among Men Diagnosed with Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 57-64.	2.5	115
23	H6D Polymorphism in Macrophage-Inhibitory Cytokine-1 Gene Associated With Prostate Cancer. Journal of the National Cancer Institute, 2004, 96, 1248-1254.	6.3	111
24	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. Nature Genetics, 2017, 49, 1141-1147.	21.4	105
25	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
26	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
27	The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. Cancer Causes and Control, 2015, 26, 1603-1616.	1.8	77
28	Assessment of polygenic architecture and risk prediction based on common variants across fourteen cancers. Nature Communications, 2020, 11, 3353.	12.8	75
29	Ten- and 15-yr Prostate Cancer-specific Mortality in Patients with Nonmetastatic Locally Advanced or Aggressive Intermediate Prostate Cancer, Randomized to Lifelong Endocrine Treatment Alone or Combined with Radiotherapy: Final Results of The Scandinavian Prostate Cancer Group-7. European Urology, 2016, 70, 684-691.	1.9	71
30	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	2.8	68
31	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
32	Serum Levels of Human MIC-1/GDF15 Vary in a Diurnal Pattern, Do Not Display a Profile Suggestive of a Satiety Factor and Are Related to BMI. PLoS ONE, 2015, 10, e0133362.	2.5	66
33	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	9.4	56
34	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
35	Atorvastatin prevents ATP-driven invasiveness via P2X7 and EHBP1 signaling in PTEN-expressing prostate cancer cells. Carcinogenesis, 2014, 35, 1547-1555.	2.8	53
36	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

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37	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
38	Two new loci and gene sets related to sex determination and cancer progression are associated with susceptibility to testicular germ cell tumor. Human Molecular Genetics, 2015, 24, 4138-4146.	2.9	49
39	Telomere structure and maintenance gene variants and risk of five cancer types. International Journal of Cancer, 2016, 139, 2655-2670.	5.1	43
40	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
41	Risk of Bilateral Renal Cell Cancer. Journal of Clinical Oncology, 2009, 27, 3737-3741.	1.6	42
42	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	5.5	42
43	The Stockholm-3 (STHLM3) Model can Improve Prostate Cancer Diagnostics in Men Aged 50â€“69 yr Compared with Current Prostate Cancer Testing. European Urology Focus, 2018, 4, 707-710.	3.1	42
44	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	12.8	40
45	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
46	Association of reported prostate cancer risk alleles with PSA levels among men without a diagnosis of prostate cancer. Prostate, 2009, 69, 419-427.	2.3	36
47	Identification of four new susceptibility loci for testicular germ cell tumour. Nature Communications, 2015, 6, 8690.	12.8	36
48	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
49	Oncologic Outcomes After Robot-assisted Radical Prostatectomy: A Large European Single-centre Cohort with Median 10-Year Follow-up. European Urology Focus, 2018, 4, 351-359.	3.1	32
50	Lifetime total physical activity and prostate cancer risk: a population-based caseâ€“control study in Sweden. European Journal of Epidemiology, 2008, 23, 739-746.	5.7	31
51	ANO7 is associated with aggressive prostate cancer. International Journal of Cancer, 2018, 143, 2479-2487.	5.1	31
52	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	5.1	28
53	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
54	A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1731-1738.	2.5	27

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55	Identification of 22 susceptibility loci associated with testicular germ cell tumors. Nature Communications, 2021, 12, 4487.	12.8	27
56	Assessing the role of insulinâ€like growth factors and binding proteins in prostate cancer using Mendelian randomization: Genetic variants as instruments for circulating levels. International Journal of Cancer, 2016, 139, 1520-1533.	5.1	26
57	Body mass index in relation to serum prostateâ€specific antigen levels and prostate cancer risk. International Journal of Cancer, 2016, 139, 50-57.	5.1	25
58	Prostate cancer genomics: can we distinguish between indolent and fatal disease using genetic markers?. Genome Medicine, 2010, 2, 45.	8.2	23
59	Polyunsaturated fatty acids and prostate cancer risk: a Mendelian randomisation analysis from the PRACTICAL consortium. British Journal of Cancer, 2016, 115, 624-631.	6.4	23
60	A Healthy Lifestyle in Men at Increased Genetic Risk for Prostate Cancer. European Urology, 2023, 83, 343-351.	1.9	23
61	Identification of a Novel Autoimmune Peptide Epitope of Prostein in Prostate Cancer. Journal of Proteome Research, 2017, 16, 204-216.	3.7	21
62	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	2.5	21
63	A differential protein solubility approach for the depletion of highly abundant proteins in plasma using ammonium sulfate. Analyst, The, 2015, 140, 8109-8117.	3.5	20
64	Investigating the possible causal role of coffee consumption with prostate cancer risk and progression using Mendelian randomization analysis. International Journal of Cancer, 2017, 140, 322-328.	5.1	17
65	Synergistic Interaction of <i>HOXB13</i> and <i>CIP2A</i> Predisposes to Aggressive Prostate Cancer. Clinical Cancer Research, 2018, 24, 6265-6276.	7.0	17
66	The roles of stress and social support in prostate cancer mortality. Scandinavian Journal of Urology, 2016, 50, 47-55.	1.0	16
67	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. Cancers, 2020, 12, 3254.	3.7	16
68	Inherited DNA Repair Gene Mutations in Men with Lethal Prostate Cancer. Genes, 2020, 11, 314.	2.4	16
69	Additional SNPs improve risk stratification of a polygenic hazard score for prostate cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 532-541.	3.9	16
70	Circulating insulin-like growth factors and risks of overall, aggressive and early-onset prostate cancer: a collaborative analysis of 20 prospective studies and Mendelian randomization analysis. International Journal of Epidemiology, 2023, 52, 71-86.	1.9	16
71	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
72	Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. Prostate Cancer and Prostatic Diseases, 2022, 25, 755-761.	3.9	14

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73	Identification and Validation of Leucine-rich Î±-2-glycoprotein 1 as a Noninvasive Biomarker for Improved Precision in Prostate Cancer Risk Stratification. European Urology Open Science, 2020, 21, 51-60.	0.4	13
74	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	4.1	11
75	Analysis of plasma from prostate cancer patients links decreased carnosine dipeptidase 1 levels to lymph node metastasis. Translational Proteomics, 2014, 2, 14-24.	1.2	10
76	gsSKAT: Rapid gene set analysis and multiple testing correction for rareâ€variant association studies using weighted linear kernels. Genetic Epidemiology, 2017, 41, 297-308.	1.3	9
77	Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. British Journal of Cancer, 2017, 117, 734-743.	6.4	7
78	Post hoc Analysis for Detecting Individual Rare Variant Risk Associations Using Probit Regression Bayesian Variable Selection Methods in Caseâ€Control Sequencing Studies. Genetic Epidemiology, 2016, 40, 461-469.	1.3	5
79	KLK3 SNPâ€“SNP interactions for prediction of prostate cancer aggressiveness. Scientific Reports, 2021, 11, 9264.	3.3	5
80	E-Science technologies in a workflow for personalized medicine using cancer screening as a case study. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 950-957.	4.4	4
81	Association Study between Polymorphisms in DNA Methylationâ€“Related Genes and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1769-1779.	2.5	4
82	AA9int: SNP interaction pattern search using non-hierarchical additive model set. Bioinformatics, 2018, 34, 4141-4150.	4.1	3
83	Genetically Inferred Telomere Length and Testicular Germ Cell Tumor Risk. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1275-1278.	2.5	2