Multiple novel prostate cancer susceptibility signals ide risk loci among Europeans

Human Molecular Genetics

24, 5589-5602

DOI: 10.1093/hmg/ddv203

Citation Report

#	Article	IF	Citations
1	Making sense of GWAS: using epigenomics and genome engineering to understand the functional relevance of SNPs in non-coding regions of the human genome. Epigenetics and Chromatin, 2015, 8, 57.	1.8	277
2	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.	1.4	50
3	Genome-wide association studies in migraine. Current Opinion in Neurology, 2016, 29, 302-308.	1.8	26
4	Biomarkers for prostate cancer: present challenges and future opportunities. Future Science OA, 2016, 2, FSO72.	0.9	35
5	Putative Prostate Cancer Risk SNP in an Androgen Receptorâ€Binding Site of the Melanophilin Gene Illustrates Enrichment of Risk SNPs in Androgen Receptor Target Sites. Human Mutation, 2016, 37, 52-64.	1.1	35
6	Pooled ChIP-Seq Links Variation in Transcription Factor Binding to Complex Disease Risk. Cell, 2016, 165, 730-741.	13.5	107
7	Selenium- or Vitamin Eâ€“Related Gene Variants, Interaction with Supplementation, and Risk of High-Grade Prostate Cancer in SELECT. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1050-1058.	1.1	55
8	Modulation of long noncoding RNAs by risk SNPs underlying genetic predispositions to prostate cancer. Nature Genetics, 2016, 48, 1142-1150.	9.4	196
9	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	1.4	8
10	Rare variants in BRCA2 and CHEK2 are associated with the risk of urinary tract cancers. Scientific Reports, 2016, 6, 33542.	1.6	22
11	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	1.8	37
12	LocusExplorer: a user-friendly tool for integrated visualization of human genetic association data and biological annotations. Bioinformatics, 2016, 32, 949-951.	1.8	13
13	Reducing GWAS Complexity. Cell Cycle, 2016, 15, 22-24.	1.3	16
14	Gene and pathway level analyses of germline DNA-repair gene variants and prostate cancer susceptibility using the iCOGS-genotyping array. British Journal of Cancer, 2016, 114, 945-952.	2.9	17
15	Familial Risk and Heritability of Cancer Among Twins in Nordic Countries. JAMA - Journal of the American Medical Association, 2016, 315, 68.	3.8	648
16	Common cancers share familial susceptibility: implications for cancer genetics and counselling. Journal of Medical Genetics, 2017, 54, 248-253.	1.5	12
17	A multiparametric approach to improve upon existing prostate cancer screening and biopsy recommendations. Current Opinion in Urology, 2017, 27, 475-480.	0.9	3
18	TEX15: A DNA repair gene associated with prostate cancer risk in Han Chinese. Prostate, 2017, 77, 1271-1278.	1.2	9

#	Article	IF	Citations
19	Trans-ethnic meta-regression of genome-wide association studies accounting for ancestry increases power for discovery and improves fine-mapping resolution. Human Molecular Genetics, 2017, 26, 3639-3650.	1.4	170
20	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
21	Potentiating prostate cancer immunotherapy with oncolytic viruses. Nature Reviews Urology, 2018, 15, 235-250.	1.9	46
22	Genetic risk of prostate cancer in Ugandan men. Prostate, 2018, 78, 370-376.	1.2	31
23	Prostate Cancer Germline Variations and Implications for Screening and Treatment. Cold Spring Harbor Perspectives in Medicine, 2018, 8, a030379.	2.9	25
24	Large-scale transcriptome-wide association study identifies new prostate cancer risk regions. Nature Communications, 2018, 9, 4079.	5.8	121
25	CRISPR-mediated deletion of prostate cancer risk-associated CTCF loop anchors identifies repressive chromatin loops. Genome Biology, 2018, 19, 160.	3.8	60
26	High-throughput screening of prostate cancer risk loci by single nucleotide polymorphisms sequencing. Nature Communications, 2018, 9, 2022.	5.8	66
27	Differences in inherited risk among relatives of hereditary prostate cancer patients using genetic risk score. Prostate, 2018, 78, 1063-1068.	1.2	1
28	Family History of Breast or Prostate Cancer and Prostate Cancer Risk. Clinical Cancer Research, 2018, 24, 5910-5917.	3.2	52
29	Prostate Cancer Genomics: Recent Advances and the Prevailing Underrepresentation from Racial and Ethnic Minorities. International Journal of Molecular Sciences, 2018, 19, 1255.	1.8	50
30	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	5.8	88
31	12 new susceptibility loci for prostate cancer identified by genome-wide association study in Japanese population. Nature Communications, 2019, 10, 4422.	5.8	49
32	Genetic associations of breast and prostate cancer are enriched for regulatory elements identified in disease-related tissues. Human Genetics, 2019, 138, 1091-1104.	1.8	7
33	Identification of Novel Susceptibility Loci and Genes for Prostate Cancer Risk: A Transcriptome-Wide Association Study in Over 140,000 European Descendants. Cancer Research, 2019, 79, 3192-3204.	0.4	43
34	An expanded variant list and assembly annotation identifies multiple novel coding and noncoding genes for prostate cancer risk using a normal prostate tissue eQTL data set. PLoS ONE, 2019, 14, e0214588.	1.1	5
35	Post-GWAS in prostate cancer: from genetic association to biological contribution. Nature Reviews Cancer, 2019, 19, 46-59.	12.8	73
36	DNA repair and cancer in colon and rectum: Novel players in genetic susceptibility. International Journal of Cancer, 2020, 146, 363-372.	2.3	40

#	Article	IF	Citations
37	Disparities in prostate cancer incidence and mortality rates: Solvable or not?. Prostate, 2020, 80, 3-16.	1.2	30
38	Survival outcomes in men with a positive family history of prostate cancer: a registry based study. BMC Cancer, 2020, 20, 894.	1.1	11
39	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
40	DNA methylation and cis-regulation of gene expression by prostate cancer risk SNPs. PLoS Genetics, 2020, 16, e1008667.	1.5	15
41	Whole-exome Sequencing of Prostate Cancer in Sardinian Identify Recurrent UDP-glucuronosyltransferase Amplifications. Journal of Cancer, 2021, 12, 438-450.	1.2	5
42	Hepatocyte nuclear factor 1 beta: A perspective in cancer. Cancer Medicine, 2021, 10, 1791-1804.	1.3	15
43	Identification of Germline Genetic Variants that Increase Prostate Cancer Risk and Influence Development of Aggressive Disease. Cancers, 2021, 13, 760.	1.7	22
44	The Etiology of Prostate Cancer. , 0, , 17-28.		1
45	Parallel Reporter Assays Identify Altered Regulatory Role of rs684232 in Leading to Prostate Cancer Predisposition. International Journal of Molecular Sciences, 2021, 22, 8792.	1.8	9
46	Evolutionary selection of alleles in the melanophilin gene that impacts on prostate organ function and cancer risk. Evolution, Medicine and Public Health, 2021, 9, 311-321.	1.1	3
48	Exome-based genome-wide association study and risk assessment using genetic risk score to prostate cancer in the Korean population. Oncotarget, 2017, 8, 43934-43943.	0.8	7
49	Network-directed cis-mediator analysis of normal prostate tissue expression profiles reveals downstream regulatory associations of prostate cancer susceptibility loci. Oncotarget, 2017, 8, 85896-85908.	0.8	2
50	Active monitoring, radical prostatectomy and radical radiotherapy in PSA-detected clinically localised prostate cancer: the ProtecT three-arm RCT. Health Technology Assessment, 2020, 24, 1-176.	1.3	22
51	Racial Differences in the Diagnosis and Treatment of Prostate Cancer. International Neurourology Journal, 2016, 20, S112-119.	0.5	63
56	Building a Prostate Cancer Lifestyle Medicine Program. , 2020, , 327-333.		0
57	Novel role of prostate cancer risk variant rs7247241 on PPP1R14A isoform transition through allelic TF binding and CpG methylation. Human Molecular Genetics, 2022, 31, 1610-1621.	1.4	5
58	H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility. American Journal of Human Genetics, 2021, 108, 2284-2300.	2.6	31
59	A microRNA Transcriptome-wide Association Study of Prostate Cancer Risk. Frontiers in Genetics, 2022, 13, 836841.	1.1	3

#	Article	IF	Citations
61	Association between obesity and frequency of highâ€‘grade prostate cancer on biopsy in men: A singleâ€‘center retrospective study. Molecular and Clinical Oncology, 2022, 17, .	0.4	8
65	Characterizing prostate cancer risk through multi-ancestry genome-wide discovery of 187 novel risk variants. Nature Genetics, 2023, 55, 2065-2074.	9.4	4