Johanna Schleutker

List of Publications by Year
in descending order

161 papers	11,415 citations	53794 45 h-index	33894 99 g-index
174 all docs	174 docs citations	174 times ranked	15209 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	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
3	Evidence for a prostate cancer susceptibility locus on the X chromosome.. Nature Genetics, 1998, 20, 175-179.	21.4	641
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	Germline mutations in the ribonuclease L gene in families showing linkage with HPC1. Nature Genetics, 2002, 30, 181-184.	21.4	470
6	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
7	A recurrent mutation in PALB2 in Finnish cancer families. Nature, 2007, 446, 316-319.	27.8	402
8	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	21.4	389
9	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	21.4	313
10	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
11	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
12	Germline Alterations of the RNASEL Gene, a Candidate HPC1 Gene at 1q25, in Patients and Families with Prostate Cancer. American Journal of Human Genetics, 2002, 70, 1299-1304.	6.2	202
13	Nonsense-mediated decay microarray analysis identifies mutations of EPHB2 in human prostate cancer. Nature Genetics, 2004, 36, 979-983.	21.4	180
14	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
15	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
16	Exome sequencing identifies FANCM as a susceptibility gene for triple-negative breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15172-15177.	7.1	162
17	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
18	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

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19	Multiple Novel Prostate Cancer Predisposition Loci Confirmed by an International Study: The PRACTICAL Consortium. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2052-2061.	2.5	148
20	Infantile form of neuronal ceroid lipofuscinosis (CLN1) maps to the short arm of chromosome 1. Genomics, 1991, 9, 170-173.	2.9	140
21	A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancerâ€“Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229.	6.2	138
22	CHEK2 variants associate with hereditary prostate cancer. British Journal of Cancer, 2003, 89, 1966-1970.	6.4	124
23	RAD51C is a susceptibility gene for ovarian cancer. Human Molecular Genetics, 2011, 20, 3278-3288.	2.9	124
24	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
25	Biology and Clinical Implications of the 19q13 Aggressive Prostate Cancer Susceptibility Locus. Cell, 2018, 174, 576-589.e18.	28.9	116
26	Screening for BRCA1, BRCA2, CHEK2, PALB2, BRIP1, RAD50, and CDH1 mutations in high-risk Finnish BRCA1/2-founder mutation-negative breast and/or ovarian cancer individuals. Breast Cancer Research, 2011, 13, R20.	5.0	106
27	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 2520-2528.	2.9	100
28	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
29	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
30	Androgen receptor gene mutations in hormone-refractory prostate cancer. Journal of Pathology, 1999, 189, 559-563.	4.5	83
31	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
32	HOXB13 G84E Mutation in Finland: Population-Based Analysis of Prostate, Breast, and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 452-460.	2.5	75
33	Combined Genome-Wide Scan for Prostate Cancer Susceptibility Genes. Journal of the National Cancer Institute, 2004, 96, 1240-1247.	6.3	72
34	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	2.8	68
35	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
36	New Paraoxonase 1 Polymorphism I102V and the Risk of Prostate Cancer in Finnish Men. Journal of the National Cancer Institute, 2003, 95, 812-818.	6.3	62

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37	Androgen receptor CAG polymorphism and prostate cancer risk. Human Genetics, 2002, 111, 166-171.	3.8	61
38	Pooled genome linkage scan of aggressive prostate cancer: results from the International Consortium for Prostate Cancer Genetics. Human Genetics, 2006, 120, 471-485.	3.8	57
39	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	9.4	56
40	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
41	Profiling Genetic Variation along the Androgen Biosynthesis and Metabolism Pathways Implicates Several Single Nucleotide Polymorphisms and Their Combinations as Prostate Cancer Risk Factors. Cancer Research, 2006, 66, 743-747.	0.9	54
42	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
43	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
44	Role of the Nijmegen Breakage Syndrome 1 Gene in Familial and Sporadic Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 935-938.	2.5	49
45	A missense substitution A49T in the steroid 5-alpha-reductase gene (SRD5A2) is not associated with prostate cancer in Finland. British Journal of Cancer, 2001, 84, 1344-1347.	6.4	47
46	Genome-wide scan for linkage in finnish hereditary prostate cancer (HPC) families identifies novel susceptibility loci at 11q14 and 3p25-26. Prostate, 2003, 57, 280-289.	2.3	47
47	Germ-line alterations in MSR1 gene and prostate cancer risk. Clinical Cancer Research, 2003, 9, 5252-6.	7.0	45
48	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
49	Relatives of prostate cancer patients have an increased risk of prostate and stomach cancers: a population-based, cancer registry study in Finland. Cancer Causes and Control, 2001, 12, 223-230.	1.8	42
50	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	5.5	42
51	Lactase Persistence, Dietary Intake of Milk, and the Risk for Prostate Cancer in Sweden and Finland. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 956-961.	2.5	41
52	Polymorphisms in Genes Involved in Androgen Pathways as Risk Factors for Prostate Cancer. Journal of Urology, 2009, 181, 1541-1549.	0.4	41
53	A Finnish founder mutation inRAD51D: analysis in breast, ovarian, prostate, and colorectal cancer: Table 1. Journal of Medical Genetics, 2012, 49, 429-432.	3.2	41
54	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	12.8	40

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55	Prostate cancer risk prediction using a polygenic risk score. Scientific Reports, 2020, 10, 17075.	3.3	39
56	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
57	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938.	3.8	37
58	The interaction of CYP3A5 polymorphisms along the androgen metabolism pathway in prostate cancer. International Journal of Cancer, 2008, 122, 2511-2516.	5.1	35
59	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
60	Reducing overdiagnosis by polygenic risk-stratified screening: findings from the Finnish section of the ERSPC. British Journal of Cancer, 2015, 113, 1086-1093.	6.4	32
61	Compelling evidence for a prostate cancer gene at 22q12.3 by the International Consortium for Prostate Cancer Genetics. Human Molecular Genetics, 2007, 16, 1271-1278.	2.9	31
62	ANO7 is associated with aggressive prostate cancer. International Journal of Cancer, 2018, 143, 2479-2487.	5.1	31
63	A major locus for hereditary prostate cancer in Finland: localization by linkage disequilibrium of a haplotype in the HPCX region. Human Genetics, 2005, 117, 307-316.	3.8	30
64	Genetic changes in familial prostate cancer by comparative genomic hybridization. Prostate, 2001, 46, 233-239.	2.3	29
65	KRUPPEL-LIKE FACTOR 6 GERM-LINE MUTATIONS ARE INFREQUENT IN FINNISH HEREDITARY PROSTATE CANCER. Journal of Urology, 2004, 172, 506-507.	0.4	29
66	An Expressed Retrogene of the Master Embryonic Stem Cell Gene POU5F1 Is Associated with Prostate Cancer Susceptibility. American Journal of Human Genetics, 2014, 94, 395-404.	6.2	29
67	Microseminoprotein-Beta Expression in Different Stages of Prostate Cancer. PLoS ONE, 2016, 11, e0150241.	2.5	28
68	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	5.1	28
69	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
70	Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. European Urology, 2021, 79, 353-361.	1.9	28
71	Risk Prediction of Prostate Cancer with Single Nucleotide Polymorphisms and Prostate Specific Antigen. Journal of Urology, 2019, 201, 486-495.	0.4	28
72	Hemochromatosis gene mutations among Finnish male breast and prostate cancer patients. International Journal of Cancer, 2006, 118, 518-520.	5.1	27

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73	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
74	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
75	Segregation analysis of 1,546 prostate cancer families in Finland shows recessive inheritance. Human Genetics, 2007, 121, 257-267.	3.8	26
76	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
77	FANCM mutation c.5791C>T is a risk factor for triple-negative breast cancer in the Finnish population. Breast Cancer Research and Treatment, 2017, 166, 217-226.	2.5	26
78	Copy Number Variation Analysis in Familial BRCA1/2-Negative Finnish Breast and Ovarian Cancer. PLoS ONE, 2013, 8, e71802.	2.5	26
79	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
80	Hereditary prostate cancer in Finland: fine-mapping validates 3p26 as a major predisposition locus. Human Genetics, 2005, 116, 43-50.	3.8	25
81	Physical and Transcript Map of the Hereditary Prostate Cancer Region at Xq27. Genomics, 2002, 79, 41-50.	2.9	24
82	Association analysis of 9,560 prostate cancer cases from the International Consortium of Prostate Cancer Genetics confirms the role of reported prostate cancer associated SNPs for familial disease. Human Genetics, 2014, 133, 347-356.	3.8	24
83	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
84	Genomeâ€wide linkage analysis of 1,233 prostate cancer pedigrees from the International Consortium for prostate cancer Genetics using novel sumLINK and sumLOD analyses. Prostate, 2010, 70, 735-744.	2.3	22
85	Linkage Disequilibrium Utilized to Establish a Refined Genetic Position of the Salla Disease Locus on 6q14-q15. Genomics, 1995, 27, 286-292.	2.9	21
86	PALB2 variants in hereditary and unselected Finnish Prostate cancer cases. Journal of Negative Results in BioMedicine, 2009, 8, 12.	1.4	21
87	Validation of prostate cancer risk-related loci identified from genome-wide association studies using family-based association analysis: evidence from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics, 2012, 131, 1095-1103.	3.8	21
88	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	2.5	21
89	CHEK2 mutations in primary glioblastomas. Journal of Neuro-Oncology, 2005, 74, 93-95.	2.9	20
90	Case-control analysis of truncating mutations in DNA damage response genes connects TEX15 and FANCD2 with hereditary breast cancer susceptibility. Scientific Reports, 2017, 7, 681.	3.3	20

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91	Whole-exome sequencing of Finnish hereditary breast cancer families. European Journal of Human Genetics, 2017, 25, 85-93.	2.8	20
92	EPHB2 germline variants in patients with colorectal cancer or hyperplastic polyposis. BMC Cancer, 2006, 6, 145.	2.6	19
93	Mutational analysis ofSPANX genes in families with X-Linked prostate cancer. Prostate, 2007, 67, 820-828.	2.3	19
94	A genetic variant nearGATA3implicated in inherited susceptibility and etiology of benign prostatic hyperplasia (BPH) and lower urinary tract symptoms (LUTS). Prostate, 2017, 77, 1213-1220.	2.3	19
95	Recurrent moderateâ€risk mutations in Finnish breast and ovarian cancer patients. International Journal of Cancer, 2019, 145, 2692-2700.	5.1	19
96	Genomeâ€wide linkage scan for prostate cancer susceptibility in Finland: Evidence for a novel locus on 2q37.3 and confirmation of signal on 17q21â€q22. International Journal of Cancer, 2011, 129, 2400-2407.	5.1	18
97	A Physical Map of the 6q14â€“q15 Region Harboring the Locus for the Lysosomal Membrane Sialic Acid Transport Defect. Genomics, 1996, 37, 62-67.	2.9	17
98	Polymorphisms in androgen signaling pathway predisposing to prostate cancer. Molecular and Cellular Endocrinology, 2012, 360, 25-37.	3.2	17
99	Finnish Fanconi anemia mutations and hereditary predisposition to breast and prostate cancer. Clinical Genetics, 2015, 88, 68-73.	2.0	17
100	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.	6.4	17
101	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
102	Synergistic Interaction of HOXB13 and CIP2A Predisposes to Aggressive Prostate Cancer. Clinical Cancer Research, 2018, 24, 6265-6276.	7.0	17
103	Two-locus genome-wide linkage scan for prostate cancer susceptibility genes with an interaction effect. Human Genetics, 2006, 118, 716-724.	3.8	16
104	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
105	Inherited DNA Repair Gene Mutations in Men with Lethal Prostate Cancer. Genes, 2020, 11, 314.	2.4	16
106	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
107	Genetic association analysis of the RTK/ERK pathway with aggressive prostate cancer highlights the potential role of CCND2 in disease progression. Scientific Reports, 2017, 7, 4538.	3.3	15
108	Oligogenic basis of sporadic ALS. Neurology: Genetics, 2019, 5, e335.	1.9	15

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109	KLF6 IVS1 -27G>A Variant and the Risk of Prostate Cancer in Finland. European Urology, 2007, 52, 1076-1081.	1.9	14
110	Chromosomes 4 and 8 implicated in a genome wide SNP linkage scan of 762 prostate cancer families collected by the ICPCG. Prostate, 2012, 72, 410-426.	2.3	14
111	Germline copy number variation analysis in Finnish families with hereditary prostate cancer. Prostate, 2016, 76, 316-324.	2.3	14
112	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
113	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
114	C-reactive protein haplotype is associated with high PSA as a marker of metastatic prostate cancer but not with overall cancer risk. British Journal of Cancer, 2009, 100, 1846-1851.	6.4	13
115	Identification of an aggressive prostate cancer predisposing variant at 11q13. International Journal of Cancer, 2011, 129, 599-606.	5.1	13
116	Germline Mutation Analysis of the Androgen Receptor Gene in Finnish Patients With Prostate Cancer. Journal of Urology, 2004, 171, 431-433.	0.4	12
117	ARLTS1 germline variants and the risk for breast, prostate, and colorectal cancer. European Journal of Human Genetics, 2008, 16, 983-991.	2.8	12
118	ARLTS1 and Prostate Cancer Risk - Analysis of Expression and Regulation. PLoS ONE, 2013, 8, e72040.	2.5	12
119	Fineâ€mapping the 2q37 and 17q11.2â€q22 loci for novel genes and sequence variants associated with a genetic predisposition to prostate cancer. International Journal of Cancer, 2015, 136, 2316-2327.	5.1	12
120	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	4.1	11
121	Haplotype analysis in prenatal diagnosis and carrier identification of Salla disease.. Journal of Medical Genetics, 1996, 33, 36-41.	3.2	10
122	Generalized Mannâ€“Whitney Type Tests for Microarray Experiments. Scandinavian Journal of Statistics, 2014, 41, 672-692.	1.4	10
123	MiRNA Profiles in Lymphoblastoid Cell Lines of Finnish Prostate Cancer Families. PLoS ONE, 2015, 10, e0127427.	2.5	9
124	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
125	COL4A1 and COL4A2 Duplication Causes Cerebral Small Vessel Disease With Recurrent Early Onset Ischemic Strokes. Stroke, 2021, 52, e624-e625.	2.0	9
126	Contribution of ARLTS1 Cys148Arg (T442C) Variant with Prostate Cancer Risk and ARLTS1 Function in Prostate Cancer Cells. PLoS ONE, 2011, 6, e26595.	2.5	8

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127	NMD and microRNA expression profiling of the HPCX1 locus reveal MAGEC1 as a candidate prostate cancer predisposition gene. BMC Cancer, 2011, 11, 327.	2.6	8
128	Screening of Finnish RAD51Cfounder mutations in prostate and colorectal cancer patients. BMC Cancer, 2012, 12, 552.	2.6	8
129	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	2.9	8
130	Germline variants in IL4, MGMT and AKT1 are associated with prostate cancer-specific mortality: An analysis of 12,082 prostate cancer cases. Prostate Cancer and Prostatic Diseases, 2018, 21, 228-237.	3.9	8
131	The interactome of the prostate-specific protein Anoctamin 7. Cancer Biomarkers, 2020, 28, 91-100.	1.7	8
132	Exclusion of the 750â€kb genetically unstable region at Xq27 as a candidate locus for prostate malignancy in HPCX1â€linked families. Genes Chromosomes and Cancer, 2012, 51, 933-948.	2.8	7
133	Clinical and histopathological characteristics of familial prostate cancer in Finland. BJU International, 2012, 109, 557-563.	2.5	7
134	Assessing Interactions of Two Loci (rs4242382 and rs10486567) in Familial Prostate Cancer: Statistical Evaluation of Epistasis. PLoS ONE, 2014, 9, e89508.	2.5	7
135	Polymorphisms of Genes Involved in Glucose and Energy Metabolic Pathways and Prostate Cancer: Interplay with Metformin. European Urology, 2015, 68, 1089-1097.	1.9	7
136	Germline EMSY sequence alterations in hereditary breast cancer and ovarian cancer families. BMC Cancer, 2017, 17, 496.	2.6	7
137	ANO7 rs77559646 Is Associated With First-line Docetaxel Treatment Response in Metastatic Castration-resistant Prostate Cancer. Anticancer Research, 2019, 39, 5353-5359.	1.1	7
138	The variant rs77559646 associated with aggressive prostate cancer disrupts ANO7 mRNA splicing and protein expression. Human Molecular Genetics, 2022, 31, 2063-2077.	2.9	7
139	Nationwide cancer family ascertainment using Finnish cancer registry data on family names and places of birth for 35,761 prostate cancer patients. International Journal of Cancer, 2000, 88, 307-312.	5.1	6
140	Whole-exome sequencing of Finnish patients with vascular cognitive impairment. European Journal of Human Genetics, 2021, 29, 663-671.	2.8	6
141	Genetic analysis reveals novel variants for vascular cognitive impairment. Acta Neurologica Scandinavica, 2022, 146, 42-50.	2.1	6
142	Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. BMC Medical Genetics, 2012, 13, 46.	2.1	5
143	Fine mapping of 11q13.5 identifies regions associated with prostate cancer and prostate cancer death. European Journal of Cancer, 2013, 49, 3335-3343.	2.8	5
144	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

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145	Expressional profiling of prostate cancer risk SNPs at 11q13.5 identifies DGAT2 as a new target gene. Genes Chromosomes and Cancer, 2016, 55, 661-673.	2.8	5
146	KLK3 SNPâ€“SNP interactions for prediction of prostate cancer aggressiveness. Scientific Reports, 2021, 11, 9264.	3.3	5
147	Novel prostate cancer susceptibility gene SP6 predisposes patients to aggressive disease. Prostate Cancer and Prostatic Diseases, 2021, 24, 1158-1166.	3.9	5
148	Confirmation of the chromosomal localization of human lamp genes and their exclusion as candidate genes for Salla disease. Human Genetics, 1991, 88, 95-97.	3.8	4
149	Genetic heterogeneity in Finnish hereditary prostate cancer using ordered subset analysis. European Journal of Human Genetics, 2013, 21, 437-443.	2.8	4
150	A Rare Variant in ERF (rs144812092) Predisposes to Prostate and Bladder Cancers in an Extended Pedigree. Cancers, 2021, 13, 2399.	3.7	4
151	BioCPRâ€“A Tool for Correlation Plots. Data, 2021, 6, 97.	2.3	4
152	Androgen receptor gene mutations in hormoneâ€refractory prostate cancer. Journal of Pathology, 1999, 189, 559-563.	4.5	4
153	AA9int: SNP interaction pattern search using non-hierarchical additive model set. Bioinformatics, 2018, 34, 4141-4150.	4.1	3
154	ShAn: An easy-to-use tool for interactive and integrated variant annotation. PLoS ONE, 2020, 15, e0235669.	2.5	3
155	Incidence of Cancer in Finnish Families with Clinically Aggressive and Nonaggressive Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3049-3056.	2.5	2
156	Fine-mapping identifies multiple prostate cancer risk loci at 5p15, one of which associates with TERT expression. Human Molecular Genetics, 2013, 22, 4239-4239.	2.9	2
157	Prostate cancer screening using risk stratification based on a multiâ€state model of genetic variants. Prostate, 2015, 75, 825-835.	2.3	2
158	PHACTR1 genetic variability is not critical in small vessel ischemic disease patients and PcomA recruitment in C57BL/6J mice. Scientific Reports, 2021, 11, 6072.	3.3	2
159	Evaluation of the RHINO gene for breast cancer predisposition in Finnish breast cancer families. Breast Cancer Research and Treatment, 2014, 144, 437-441.	2.5	1
160	Multisite Evaluation and Validation of a Sensitive Diagnostic and Screening System for Spinal Muscular Atrophy that Reports SMN1 and SMN2 Copy Number, along with Disease Modifier and Gene Duplication Variants. Journal of Molecular Diagnostics, 2021, 23, 753-764.	2.8	1
161	Molecular genetics of human prostate cancer. Current Opinion in Urology, 1997, 7, 259-262.	1.8	0