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	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
2	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
3	Genetic analysis reveals novel variants for vascular cognitive impairment. Acta Neurologica Scandinavica, 2022, 146, 42-50.	2.1	6
4	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
5	Whole-exome sequencing of Finnish patients with vascular cognitive impairment. European Journal of Human Genetics, 2021, 29, 663-671.	2.8	6
6	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
7	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
8	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. Nature Communications, 2021, 12, 1236.	12.8	40
9	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
10	KLK3 SNPâ€“SNP interactions for prediction of prostate cancer aggressiveness. Scientific Reports, 2021, 11, 9264.	3.3	5
11	Novel prostate cancer susceptibility gene SP6 predisposes patients to aggressive disease. Prostate Cancer and Prostatic Diseases, 2021, 24, 1158-1166.	3.9	5
12	A Rare Variant in ERF (rs144812092) Predisposes to Prostate and Bladder Cancers in an Extended Pedigree. Cancers, 2021, 13, 2399.	3.7	4
13	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
14	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579.	5.4	38
15	BioCPRâ€“A Tool for Correlation Plots. Data, 2021, 6, 97.	2.3	4
16	COL4A1 and COL4A2 Duplication Causes Cerebral Small Vessel Disease With Recurrent Early Onset Ischemic Strokes. Stroke, 2021, 52, e624-e625.	2.0	9
17	An integrative multi-omics analysis to identify candidate DNA methylation biomarkers related to prostate cancer risk. Nature Communications, 2020, 11, 3905.	12.8	28
18	Prostate cancer risk prediction using a polygenic risk score. Scientific Reports, 2020, 10, 17075.	3.3	39

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19	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
20	The effect of sample size on polygenic hazard models for prostate cancer. European Journal of Human Genetics, 2020, 28, 1467-1475.	2.8	14
21	The interactome of the prostate-specific protein Anoctamin 7. Cancer Biomarkers, 2020, 28, 91-100.	1.7	8
22	Inherited DNA Repair Gene Mutations in Men with Lethal Prostate Cancer. Genes, 2020, 11, 314.	2.4	16
23	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
24	ShAn: An easy-to-use tool for interactive and integrated variant annotation. PLoS ONE, 2020, 15, e0235669.	2.5	3
25	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
26	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	12.8	88
27	Oligogenic basis of sporadic ALS. Neurology: Genetics, 2019, 5, e335.	1.9	15
28	Recurrent moderateâ€risk mutations in Finnish breast and ovarian cancer patients. International Journal of Cancer, 2019, 145, 2692-2700.	5.1	19
29	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 208-216.	2.5	21
30	Risk Prediction of Prostate Cancer with Single Nucleotide Polymorphisms and Prostate Specific Antigen. Journal of Urology, 2019, 201, 486-495.	0.4	28
31	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
32	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
33	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. Nature Communications, 2018, 9, 4616.	12.8	43
34	Synergistic Interaction of HOXB13 and CIP2A Predisposes to Aggressive Prostate Cancer. Clinical Cancer Research, 2018, 24, 6265-6276.	7.0	17
35	ANO7 is associated with aggressive prostate cancer. International Journal of Cancer, 2018, 143, 2479-2487.	5.1	31
36	Biology and Clinical Implications of the 19q13 Aggressive Prostate Cancer Susceptibility Locus. Cell, 2018, 174, 576-589.e18.	28.9	116

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37	AA9int: SNP interaction pattern search using non-hierarchical additive model set. Bioinformatics, 2018, 34, 4141-4150.	4.1	3
38	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936.	21.4	652
39	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256.	12.8	88
40	SNP interaction pattern identifier (SIPI): an intensive search for SNPâ€“SNP interaction patterns. Bioinformatics, 2017, 33, 822-833.	4.1	11
41	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
42	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
43	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
44	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
45	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
46	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
47	Whole-exome sequencing of Finnish hereditary breast cancer families. European Journal of Human Genetics, 2017, 25, 85-93.	2.8	20
48	Alcohol consumption and prostate cancer incidence and progression: A Mendelian randomisation study. International Journal of Cancer, 2017, 140, 75-85.	5.1	28
49	Germline EMSY sequence alterations in hereditary breast cancer and ovarian cancer families. BMC Cancer, 2017, 17, 496.	2.6	7
50	Microseminoprotein-Beta Expression in Different Stages of Prostate Cancer. PLoS ONE, 2016, 11, e0150241.	2.5	28
51	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
52	Germline copy number variation analysis in Finnish families with hereditary prostate cancer. Prostate, 2016, 76, 316-324.	2.3	14
53	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
54	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

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55	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
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	Blood lipids and prostate cancer: a Mendelian randomization analysis. Cancer Medicine, 2016, 5, 1125-1136.	2.8	68
58	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
59	Prostate cancer risk regions at 8q24 and 17q24 are differentially associated with somaticTMPRSS2:ERGfusion status. Human Molecular Genetics, 2016, 25, ddw349.	2.9	8
60	Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979.	12.8	50
61	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
62	Pubertal development and prostate cancer risk: Mendelian randomization study in a population-based cohort. BMC Medicine, 2016, 14, 66.	5.5	42
63	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
64	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
65	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
66	Prostate cancer screening using risk stratification based on a multiâ€state model of genetic variants. Prostate, 2015, 75, 825-835.	2.3	2
67	Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474.	2.3	54
68	MiRNA Profiles in Lymphoblastoid Cell Lines of Finnish Prostate Cancer Families. PLoS ONE, 2015, 10, e0127427.	2.5	9
69	A Large-Scale Analysis of Genetic Variants within Putative miRNA Binding Sites in Prostate Cancer. Cancer Discovery, 2015, 5, 368-379.	9.4	56
70	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
71	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
72	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

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73	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
74	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
75	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
76	Genome-Wide Association Study of Prostate Cancerâ€“Specific Survival. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1796-1800.	2.5	27
77	Finnish Fanconi anemia mutations and hereditary predisposition to breast and prostate cancer. Clinical Genetics, 2015, 88, 68-73.	2.0	17
78	Assessing Interactions of Two Loci (rs4242382 and rs10486567) in Familial Prostate Cancer: Statistical Evaluation of Epistasis. PLoS ONE, 2014, 9, e89508.	2.5	7
79	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
80	Generalized Mannâ€“Whitney Type Tests for Microarray Experiments. Scandinavian Journal of Statistics, 2014, 41, 672-692.	1.4	10
81	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
82	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
83	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
84	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
85	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
86	Genetic heterogeneity in Finnish hereditary prostate cancer using ordered subset analysis. European Journal of Human Genetics, 2013, 21, 437-443.	2.8	4
87	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
88	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
89	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
90	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492

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91	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
92	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
93	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
94	ARLTS1 and Prostate Cancer Risk - Analysis of Expression and Regulation. PLoS ONE, 2013, 8, e72040.	2.5	12
95	Copy Number Variation Analysis in Familial BRCA1/2-Negative Finnish Breast and Ovarian Cancer. PLoS ONE, 2013, 8, e71802.	2.5	26
96	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
97	Analysis of Xq27-28 linkage in the international consortium for prostate cancer genetics (ICPCG) families. BMC Medical Genetics, 2012, 13, 46.	2.1	5
98	Screening of Finnish RAD51Cfounder mutations in prostate and colorectal cancer patients. BMC Cancer, 2012, 12, 552.	2.6	8
99	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
100	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
101	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
102	Polymorphisms in androgen signaling pathway predisposing to prostate cancer. Molecular and Cellular Endocrinology, 2012, 360, 25-37.	3.2	17
103	Clinical and histopathological characteristics of familial prostate cancer in Finland. BJU International, 2012, 109, 557-563.	2.5	7
104	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
105	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
106	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
107	Identification of an aggressive prostate cancer predisposing variant at 11q13. International Journal of Cancer, 2011, 129, 599-606.	5.1	13
108	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

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109	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
110	RAD51C is a susceptibility gene for ovarian cancer. Human Molecular Genetics, 2011, 20, 3278-3288.	2.9	124
111	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
112	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
113	PALB2 variants in hereditary and unselected Finnish Prostate cancer cases. Journal of Negative Results in BioMedicine, 2009, 8, 12.	1.4	21
114	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	21.4	313
115	Identification of seven new prostate cancer susceptibility loci through a genome-wide association study. Nature Genetics, 2009, 41, 1116-1121.	21.4	389
116	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
117	Polymorphisms in Genes Involved in Androgen Pathways as Risk Factors for Prostate Cancer. Journal of Urology, 2009, 181, 1541-1549.	0.4	41
118	The interaction of CYP3A5 polymorphisms along the androgen metabolism pathway in prostate cancer. International Journal of Cancer, 2008, 122, 2511-2516.	5.1	35
119	ARLTS1 germline variants and the risk for breast, prostate, and colorectal cancer. European Journal of Human Genetics, 2008, 16, 983-991.	2.8	12
120	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
121	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
122	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
123	Mutational analysis ofSPANX genes in families with X-Linked prostate cancer. Prostate, 2007, 67, 820-828.	2.3	19
124	A recurrent mutation in PALB2 in Finnish cancer families. Nature, 2007, 446, 316-319.	27.8	402
125	KLF6 IVS1 -27G>A Variant and the Risk of Prostate Cancer in Finland. European Urology, 2007, 52, 1076-1081.	1.9	14
126	Segregation analysis of 1,546 prostate cancer families in Finland shows recessive inheritance. Human Genetics, 2007, 121, 257-267.	3.8	26

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127	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
128	Two-locus genome-wide linkage scan for prostate cancer susceptibility genes with an interaction effect. Human Genetics, 2006, 118, 716-724.	3.8	16
129	EPHB2 germline variants in patients with colorectal cancer or hyperplastic polyposis. BMC Cancer, 2006, 6, 145.	2.6	19
130	Hemochromatosis gene mutations among Finnish male breast and prostate cancer patients. International Journal of Cancer, 2006, 118, 518-520.	5.1	27
131	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
132	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
133	Hereditary prostate cancer in Finland: fine-mapping validates 3p26 as a major predisposition locus. Human Genetics, 2005, 116, 43-50.	3.8	25
134	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
135	CHEK2 mutations in primary glioblastomas. Journal of Neuro-Oncology, 2005, 74, 93-95.	2.9	20
136	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
137	Combined Genome-Wide Scan for Prostate Cancer Susceptibility Genes. Journal of the National Cancer Institute, 2004, 96, 1240-1247.	6.3	72
138	Nonsense-mediated decay microarray analysis identifies mutations of EPHB2 in human prostate cancer. Nature Genetics, 2004, 36, 979-983.	21.4	180
139	Germline Mutation Analysis of the Androgen Receptor Gene in Finnish Patients With Prostate Cancer. Journal of Urology, 2004, 171, 431-433.	0.4	12
140	KRUPPEL-LIKE FACTOR 6 GERM-LINE MUTATIONS ARE INFREQUENT IN FINNISH HEREDITARY PROSTATE CANCER. Journal of Urology, 2004, 172, 506-507.	0.4	29
141	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
142	CHEK2 variants associate with hereditary prostate cancer. British Journal of Cancer, 2003, 89, 1966-1970.	6.4	124
143	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
144	Germ-line alterations in MSR1 gene and prostate cancer risk. Clinical Cancer Research, 2003, 9, 5252-6.	7.0	45

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145	Physical and Transcript Map of the Hereditary Prostate Cancer Region at Xq27. Genomics, 2002, 79, 41-50.	2.9	24
146	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
147	Androgen receptor CAG polymorphism and prostate cancer risk. Human Genetics, 2002, 111, 166-171.	3.8	61
148	Germline mutations in the ribonuclease L gene in families showing linkage with HPC1. Nature Genetics, 2002, 30, 181-184.	21.4	470
149	Genetic changes in familial prostate cancer by comparative genomic hybridization. Prostate, 2001, 46, 233-239.	2.3	29
150	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
151	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
152	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
153	Androgen receptor gene mutations in hormone-refractory prostate cancer. Journal of Pathology, 1999, 189, 559-563.	4.5	83
154	Androgen receptor gene mutations in hormoneâ€refractory prostate cancer. Journal of Pathology, 1999, 189, 559-563.	4.5	4
155	Evidence for a prostate cancer susceptibility locus on the X chromosome.. Nature Genetics, 1998, 20, 175-179.	21.4	641
156	Molecular genetics of human prostate cancer. Current Opinion in Urology, 1997, 7, 259-262.	1.8	0
157	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
158	Haplotype analysis in prenatal diagnosis and carrier identification of Salla disease.. Journal of Medical Genetics, 1996, 33, 36-41.	3.2	10
159	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
160	Infantile form of neuronal ceroid lipofuscinosis (CLN1) maps to the short arm of chromosome 1. Genomics, 1991, 9, 170-173.	2.9	140
161	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