

William B Isaacs

List of Publications by Year in descending order

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Version: 2024-02-01

351
papers

38,458
citations

2795

94
h-index

3394

183
g-index

359
all docs

359
docs citations

359
times ranked

35517
citing authors

#	ARTICLE	IF	CITATIONS
1	Association between pathogenic germline mutations in BRCA2 and ATM and tumor-infiltrating lymphocytes in primary prostate cancer. <i>Cancer Immunology, Immunotherapy</i> , 2022, 71, 943-951.	2.0	9
2	Association of germline rare pathogenic mutations in guideline-recommended genes with prostate cancer progression: A meta-analysis. <i>Prostate</i> , 2022, 82, 107-119.	1.2	4
3	The HOXB13 variant X285K is associated with clinical significance and early age at diagnosis in African American prostate cancer patients. <i>British Journal of Cancer</i> , 2022, 126, 791-796.	2.9	13
4	Health inequity drives disease biology to create disparities in prostate cancer outcomes. <i>Journal of Clinical Investigation</i> , 2022, 132, .	3.9	17
5	KLK3 germline mutation I179T complements DNA repair genes for predicting prostate cancer progression. <i>Prostate Cancer and Prostatic Diseases</i> , 2022, , .	2.0	3
6	Germline <i>BRCA2</i> , <i>ATM</i> and <i>CHEK2</i> alterations shape somatic mutation landscapes in prostate cancer.. <i>Journal of Clinical Oncology</i> , 2022, 40, 148-148.	0.8	0
7	The role of genetic testing in prostate cancer screening, diagnosis, and treatment. <i>Current Opinion in Oncology</i> , 2022, Publish Ahead of Print, .	1.1	0
8	Inherited risk assessment and its clinical utility for predicting prostate cancer from diagnostic prostate biopsies. <i>Prostate Cancer and Prostatic Diseases</i> , 2022, 25, 422-430.	2.0	12
9	Identifying Phased Mutations and Complex Rearrangements in Human Prostate Cancer Cell Lines through Linked-Read Whole-Genome Sequencing. <i>Molecular Cancer Research</i> , 2022, 20, 1013-1020.	1.5	3
10	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. <i>European Urology</i> , 2021, 79, 353-361.	0.9	28
11	Performance of Three Inherited Risk Measures for Predicting Prostate Cancer Incidence and Mortality: A Population-based Prospective Analysis. <i>European Urology</i> , 2021, 79, 419-426.	0.9	36
12	A novel method for detection of exfoliated prostate cancer cells in urine by RNA in situ hybridization. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 220-232.	2.0	3
13	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.	9.4	264
14	Homologous recombination deficiency (HRD) score in germline BRCA2- versus ATM-altered prostate cancer. <i>Modern Pathology</i> , 2021, 34, 1185-1193.	2.9	61
15	Resistance to androgen receptor signaling inhibition does not necessitate development of neuroendocrine prostate cancer. <i>JCI Insight</i> , 2021, 6, .	2.3	22
16	Association of prostate cancer polygenic risk score with number and laterality of tumor cores in active surveillance patients. <i>Prostate</i> , 2021, 81, 703-709.	1.2	11
17	The somatic mutation landscape of germline <i>CHEK2</i> -altered prostate cancer.. <i>Journal of Clinical Oncology</i> , 2021, 39, 5084-5084.	0.8	2
18	Specific Detection of Prostate Cancer Cells in Urine by RNA In Situ Hybridization. <i>Journal of Urology</i> , 2021, 206, 37-43.	0.2	4

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19	Observed evidence for guideline-recommended genes in predicting prostate cancer risk from a large population-based cohort. <i>Prostate</i> , 2021, 81, 1002-1008.	1.2	10
20	Genetic Susceptibility for Low Testosterone in Men and Its Implications in Biology and Screening: Data from the UK Biobank. <i>European Urology Open Science</i> , 2021, 29, 36-46.	0.2	4
21	Prostate Cancer Predisposition. <i>Urologic Clinics of North America</i> , 2021, 48, 283-296.	0.8	12
22	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. <i>European Urology Oncology</i> , 2021, 4, 570-579.	2.6	38
23	Combined Longitudinal Clinical and Autopsy Phenomic Assessment in Lethal Metastatic Prostate Cancer: Recommendations for Advancing Precision Medicine. <i>European Urology Open Science</i> , 2021, 30, 47-62.	0.2	2
24	Incorporation of Polygenic Risk Score into Guidelines for Inherited Risk Assessment for Prostate Cancer. <i>European Urology</i> , 2021, 80, 139-141.	0.9	4
25	Inherited risk assessment of prostate cancer: it takes three to do it right. <i>Prostate Cancer and Prostatic Diseases</i> , 2020, 23, 59-61.	2.0	8
26	Germline <i>BLM</i> mutations and metastatic prostate cancer. <i>Prostate</i> , 2020, 80, 235-237.	1.2	15
27	Role of androgen receptor splice variant-7 (AR-V7) in prostate cancer resistance to 2nd-generation androgen receptor signaling inhibitors. <i>Oncogene</i> , 2020, 39, 6935-6949.	2.6	60
28	Genomic and Clinicopathologic Characterization of <i>ATM</i> -deficient Prostate Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 4869-4881.	3.2	18
29	Validation of a prostate cancer polygenic risk score. <i>Prostate</i> , 2020, 80, 1314-1321.	1.2	23
30	Feasibility and performance of a novel probe panel to detect somatic DNA copy number alterations in clinical specimens for predicting prostate cancer progression. <i>Prostate</i> , 2020, 80, 1253-1262.	1.2	4
31	Germline HOXB13 G84E mutation carriers and risk to twenty common types of cancer: results from the UK Biobank. <i>British Journal of Cancer</i> , 2020, 123, 1356-1359.	2.9	11
32	A Germline Variant at 8q24 Contributes to Familial Clustering of Prostate Cancer in Men of African Ancestry. <i>European Urology</i> , 2020, 78, 316-320.	0.9	32
33	Implementation of Germline Testing for Prostate Cancer: Philadelphia Prostate Cancer Consensus Conference 2019. <i>Journal of Clinical Oncology</i> , 2020, 38, 2798-2811.	0.8	170
34	Use of Aspirin and Statins in Relation to Inflammation in Benign Prostate Tissue in the Placebo Arm of the Prostate Cancer Prevention Trial. <i>Cancer Prevention Research</i> , 2020, 13, 853-862.	0.7	8
35	Rare Germline Pathogenic Mutations of DNA Repair Genes Are Most Strongly Associated with Grade Group 5 Prostate Cancer. <i>European Urology Oncology</i> , 2020, 3, 224-230.	2.6	41
36	Distinct Genomic Alterations in Prostate Tumors Derived from African American Men. <i>Molecular Cancer Research</i> , 2020, 18, 1815-1824.	1.5	14

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37	<i>Trichomonas vaginalis</i> infection and prostate-specific antigen concentration: Insights into prostate involvement and prostate disease risk. <i>Prostate</i> , 2019, 79, 1622-1628.	1.2	11
38	Lactoferrin CpG Island Hypermethylation and Decoupling of mRNA and Protein Expression in the Early Stages of Prostate Carcinogenesis. <i>American Journal of Pathology</i> , 2019, 189, 2311-2322.	1.9	13
39	Concept and benchmarks for assessing narrow-sense validity of genetic risk score values. <i>Prostate</i> , 2019, 79, 1099-1105.	1.2	18
40	Current progress and questions in germline genetics of prostate cancer. <i>Asian Journal of Urology</i> , 2019, 6, 3-9.	0.5	11
41	Molecular Characterization and Clinical Outcomes of Primary Gleason Pattern 5 Prostate Cancer After Radical Prostatectomy. <i>JCO Precision Oncology</i> , 2019, 3, 1-13.	1.5	12
42	Single-Nucleotide Polymorphism-Based Genetic Risk Score and Patient Age at Prostate Cancer Diagnosis. <i>JAMA Network Open</i> , 2019, 2, e1918145.	2.8	20
43	Mannose Receptor-positive Macrophage Infiltration Correlates with Prostate Cancer Onset and Metastatic Castration-resistant Disease. <i>European Urology Oncology</i> , 2019, 2, 429-436.	2.6	46
44	HOXB13 interaction with MEIS1 modifies proliferation and gene expression in prostate cancer. <i>Prostate</i> , 2019, 79, 414-424.	1.2	39
45	Germline Mutations in ATM and BRCA1/2 Are Associated with Grade Reclassification in Men on Active Surveillance for Prostate Cancer. <i>European Urology</i> , 2019, 75, 743-749.	0.9	138
46	A systematic comparison of exercise training protocols on animal models of cardiovascular capacity. <i>Life Sciences</i> , 2019, 217, 128-140.	2.0	32
47	ATM loss in primary prostate cancer: Analysis of >1000 cases using a validated clinical-grade immunohistochemistry (IHC) assay. <i>Journal of Clinical Oncology</i> , 2019, 37, 5069-5069.	0.8	3
48	Updated insights into genetic contribution to prostate cancer predisposition: focus on HOXB13. <i>Canadian Journal of Urology</i> , 2019, 26, 12-13.	0.0	5
49	A comprehensive evaluation of <i>CHEK2</i> germline mutations in men with prostate cancer. <i>Prostate</i> , 2018, 78, 607-615.	1.2	57
50	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	9.4	182
51	Germline DNA-repair Gene Mutations and Outcomes in Men with Metastatic Castration-resistant Prostate Cancer Receiving First-line Abiraterone and Enzalutamide. <i>European Urology</i> , 2018, 74, 218-225.	0.9	140
52	Intraductal/ductal histology and lymphovascular invasion are associated with germline DNA-repair gene mutations in prostate cancer. <i>Prostate</i> , 2018, 78, 401-407.	1.2	105
53	Genetic factors influencing prostate cancer risk in Norwegian men. <i>Prostate</i> , 2018, 78, 186-192.	1.2	11
54	Role of Genetic Testing for Inherited Prostate Cancer Risk: Philadelphia Prostate Cancer Consensus Conference 2017. <i>Journal of Clinical Oncology</i> , 2018, 36, 414-424.	0.8	155

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55	Differences in inherited risk among relatives of hereditary prostate cancer patients using genetic risk score. <i>Prostate</i> , 2018, 78, 1063-1068.	1.2	1
56	Germline mutations in <i>PPFIBP2</i> are associated with lethal prostate cancer. <i>Prostate</i> , 2018, 78, 1222-1228.	1.2	12
57	Constitutively active androgen receptor splice variants AR-V3, AR-V7 and AR-V9 are co-expressed in castration-resistant prostate cancer metastases. <i>British Journal of Cancer</i> , 2018, 119, 347-356.	2.9	63
58	Germline mutations in DNA repair genes are associated with bladder cancer risk and unfavourable prognosis. <i>BJU International</i> , 2018, 122, 808-813.	1.3	15
59	Sustained influence of infections on prostate-specific antigen concentration: An analysis of changes over 10 years of follow-up. <i>Prostate</i> , 2018, 78, 1024-1034.	1.2	4
60	Effect of germline DNA repair gene mutations on outcomes in men with metastatic castration-resistant prostate cancer receiving first-line abiraterone and enzalutamide.. <i>Journal of Clinical Oncology</i> , 2018, 36, 221-221.	0.8	0
61	Donald S Coffey, a man who meant so much to so many. <i>American Journal of Clinical and Experimental Urology</i> , 2018, 6, 41-42.	0.4	0
62	gsSKAT: Rapid gene set analysis and multiple testing correction for rare variant association studies using weighted linear kernels. <i>Genetic Epidemiology</i> , 2017, 41, 297-308.	0.6	9
63	Analytic, Preanalytic, and Clinical Validation of p53 IHC for Detection of <i>TP53</i> Missense Mutation in Prostate Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 4693-4703.	3.2	62
64	Association between variants in genes involved in the immune response and prostate cancer risk in men randomized to the finasteride arm in the Prostate Cancer Prevention Trial. <i>Prostate</i> , 2017, 77, 908-919.	1.2	21
65	Germline Mutations in ATM and BRCA1/2 Distinguish Risk for Lethal and Indolent Prostate Cancer and are Associated with Early Age at Death. <i>European Urology</i> , 2017, 71, 740-747.	0.9	256
66	Insight into infection-mediated prostate damage: Contrasting patterns of C-reactive protein and prostate-specific antigen levels during infection. <i>Prostate</i> , 2017, 77, 1325-1334.	1.2	8
67	MSH2 Loss in Primary Prostate Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 6863-6874.	3.2	122
68	A genetic variant near <i>GATA3</i> implicated in inherited susceptibility and etiology of benign prostatic hyperplasia (BPH) and lower urinary tract symptoms (LUTS). <i>Prostate</i> , 2017, 77, 1213-1220.	1.2	19
69	What Do Myeloma, Breast Cancer, and Prostate Cancer Have in Common?. <i>European Urology</i> , 2017, 71, 166-167.	0.9	1
70	The expression of AURKA is androgen regulated in castration-resistant prostate cancer. <i>Scientific Reports</i> , 2017, 7, 17978.	1.6	38
71	Appraising the relevance of DNA copy number loss and gain in prostate cancer using whole genome DNA sequence data. <i>PLoS Genetics</i> , 2017, 13, e1007001.	1.5	34
72	Somatic molecular subtyping of prostate tumors from <i>HOXB13</i> G84E carriers. <i>Oncotarget</i> , 2017, 8, 22772-22782.	0.8	9

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73	Post hoc Analysis for Detecting Individual Rare Variant Risk Associations Using Probit Regression Bayesian Variable Selection Methods in Caseâ€Control Sequencing Studies. <i>Genetic Epidemiology</i> , 2016, 40, 461-469.	0.6	5
74	Adding genetic risk score to family history identifies twice as many high-risk men for prostate cancer: Results from the prostate cancer prevention trial. <i>Prostate</i> , 2016, 76, 1120-1129.	1.2	60
75	Genetic variants in cell cycle control pathway confer susceptibility to aggressive prostate carcinoma. <i>Prostate</i> , 2016, 76, 479-490.	1.2	12
76	Key genes involved in the immune response are generally not associated with intraprostatic inflammation in men without a prostate cancer diagnosis: Results from the prostate cancer prevention trial. <i>Prostate</i> , 2016, 76, 565-574.	1.2	5
77	Infectious mononucleosis, other infections and prostate-specific antigen concentration as a marker of prostate involvement during infection. <i>International Journal of Cancer</i> , 2016, 138, 2221-2230.	2.3	11
78	Peripheral Zone Inflammation Is Not Strongly Associated With Lower Urinary Tract Symptom Incidence and Progression in the Placebo Arm of the Prostate Cancer Prevention Trial. <i>Prostate</i> , 2016, 76, 1399-1408.	1.2	6
79	Integrated clinical, whole-genome, and transcriptome analysis of multisampled lethal metastatic prostate cancer. <i>Journal of Physical Education and Sports Management</i> , 2016, 2, a000752.	0.5	24
80	Inflammation, Microbiota, and Prostate Cancer. <i>European Urology Focus</i> , 2016, 2, 374-382.	1.6	40
81	REVEL: An Ensemble Method for Predicting the Pathogenicity of Rare Missense Variants. <i>American Journal of Human Genetics</i> , 2016, 99, 877-885.	2.6	1,555
82	Rare Variation in <i>TET2</i> Is Associated with Clinically Relevant Prostate Carcinoma in African Americans. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1456-1463.	1.1	22
83	DNA-Repair Gene Mutations in Metastatic Prostate Cancer. <i>New England Journal of Medicine</i> , 2016, 375, 1802-1805.	13.9	26
84	Screening for familial and hereditary prostate cancer. <i>International Journal of Cancer</i> , 2016, 138, 2579-2591.	2.3	49
85	Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. <i>Human Genetics</i> , 2016, 135, 923-938.	1.8	37
86	Germline Variants in Asporin Vary by Race, Modulate the Tumor Microenvironment, and Are Differentially Associated with Metastatic Prostate Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 448-458.	3.2	29
87	Identification of miR-30b-3p and miR-30d-5p as direct regulators of androgen receptor signaling in prostate cancer by complementary functional microRNA library screening. <i>Oncotarget</i> , 2016, 7, 72593-72607.	0.8	71
88	Variation in genes involved in the immune response and prostate cancer risk in the placebo arm of the Prostate Cancer Prevention Trial. <i>Prostate</i> , 2015, 75, 1403-1418.	1.2	25
89	Polymorphisms Influencing Prostate-Specific Antigen Concentration May Bias Genome-Wide Association Studies on Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 88-93.	1.1	4
90	Generalizability of established prostate cancer risk variants in men of African ancestry. <i>International Journal of Cancer</i> , 2015, 136, 1210-1217.	2.3	62

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91	Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. <i>Human Genetics</i> , 2015, 134, 439-450.	1.8	45
92	The <i>HOXB13</i> G84E Mutation Is Associated with an Increased Risk for Prostate Cancer and Other Malignancies. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1366-1372.	1.1	47
93	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, 5603-5618.	1.4	50
94	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	13.7	1,185
95	Cyclin D1 Loss Distinguishes Prostatic Small-Cell Carcinoma from Most Prostatic Adenocarcinomas. <i>Clinical Cancer Research</i> , 2015, 21, 5619-5629.	3.2	56
96	Large-scale association analysis in Asians identifies new susceptibility loci for prostate cancer. <i>Nature Communications</i> , 2015, 6, 8469.	5.8	51
97	Do Environmental Factors Modify the Genetic Risk of Prostate Cancer?. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 213-220.	1.1	12
98	Understanding the Mechanisms of Androgen Deprivation Resistance in Prostate Cancer at the Molecular Level. <i>European Urology</i> , 2015, 67, 470-479.	0.9	225
99	AR splice variant 7 (AR-V7) and response to taxanes in men with metastatic castration-resistant prostate cancer (mCRPC).. <i>Journal of Clinical Oncology</i> , 2015, 33, 138-138.	0.8	14
100	Genome-Wide Association Scan for Variants Associated with Early-Onset Prostate Cancer. <i>PLoS ONE</i> , 2014, 9, e93436.	1.1	25
101	A Peripheral Circulating TH1 Cytokine Profile Is Inversely Associated with Prostate Cancer Risk in CLUE II. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 2561-2567.	1.1	18
102	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. <i>Human Genetics</i> , 2014, 133, 347-356.	1.8	24
103	Prevalence of the <i>HOXB13</i> G84E prostate cancer risk allele in men treated with radical prostatectomy. <i>BJU International</i> , 2014, 113, 830-835.	1.3	21
104	Leveraging population admixture to characterize the heritability of complex traits. <i>Nature Genetics</i> , 2014, 46, 1356-1362.	9.4	69
105	Rb Loss Is Characteristic of Prostatic Small Cell Neuroendocrine Carcinoma. <i>Clinical Cancer Research</i> , 2014, 20, 890-903.	3.2	275
106	Telomere length as a risk factor for hereditary prostate cancer. <i>Prostate</i> , 2014, 74, 359-364.	1.2	27
107	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251-1253.	6.0	348
108	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408

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109	AR-V7 and Resistance to Enzalutamide and Abiraterone in Prostate Cancer. <i>New England Journal of Medicine</i> , 2014, 371, 1028-1038.	13.9	2,233
110	Genome-wide Scan of 29,141 African Americans Finds No Evidence of Directional Selection since Admixture. <i>American Journal of Human Genetics</i> , 2014, 95, 437-444.	2.6	69
111	Identification of a novel germline <i>SPOP</i> mutation in a family with hereditary prostate cancer. <i>Prostate</i> , 2014, 74, 983-990.	1.2	18
112	Androgen receptor splice variant, AR-V7, and resistance to enzalutamide and abiraterone in men with metastatic castration-resistant prostate cancer (mCRPC). <i>Journal of Clinical Oncology</i> , 2014, 32, 5001-5001.	0.8	20
113	Association of the <i>HOXB13 G84E</i> mutation with increased risk for prostate cancer and other malignancies. <i>Journal of Clinical Oncology</i> , 2014, 32, 1558-1558.	0.8	0
114	Genome-wide Association Study Identifies Loci at <i>ATF7IP</i> and <i>KLK2</i> Associated with Percentage of Circulating Free PSA. <i>Neoplasia</i> , 2013, 15, 95-IN30.	2.3	11
115	Loss of PTEN Is Associated with Aggressive Behavior in ERG-Positive Prostate Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 2333-2344.	1.1	121
116	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. <i>Science Translational Medicine</i> , 2013, 5, 169ra10.	5.8	231
117	<i>HOXB13</i> is a susceptibility gene for prostate cancer: results from the International Consortium for Prostate Cancer Genetics (ICPCG). <i>Human Genetics</i> , 2013, 132, 5-14.	1.8	166
118	Genome-wide Association Study Identifies Genetic Determinants of Urine PCA3 Levels in Men. <i>Neoplasia</i> , 2013, 15, 448-IN26.	2.3	7
119	Genetic markers associated with early cancer-specific mortality following prostatectomy. <i>Cancer</i> , 2013, 119, 2405-2412.	2.0	81
120	Nucleotide resolution analysis of <i>TMPRSS2</i> and <i>ERG</i> rearrangements in prostate cancer. <i>Journal of Pathology</i> , 2013, 230, 174-183.	2.1	41
121	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, 408-415.	1.4	118
122	The G84E mutation of <i>HOXB13</i> is associated with increased risk for prostate cancer: results from the REDUCE trial. <i>Carcinogenesis</i> , 2013, 34, 1260-1264.	1.3	50
123	Global Patterns of Prostate Cancer Incidence, Aggressiveness, and Mortality in Men of African Descent. <i>Prostate Cancer</i> , 2013, 2013, 1-12.	0.4	180
124	A Genome-Wide Assessment of Variability in Human Serum Metabolism. <i>Human Mutation</i> , 2013, 34, 515-524.	1.1	42
125	Tracking the clonal origin of lethal prostate cancer. <i>Journal of Clinical Investigation</i> , 2013, 123, 4918-4922.	3.9	440
126	Infections and inflammation in prostate cancer. <i>American Journal of Clinical and Experimental Urology</i> , 2013, 1, 3-11.	0.4	42

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127	Variation in <i>IL10</i> and Other Genes Involved in the Immune Response and in Oxidation and Prostate Cancer Recurrence. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1774-1782.	1.1	49
128	A genome-wide search for loci interacting with known prostate cancer risk-associated genetic variants. <i>Carcinogenesis</i> , 2012, 33, 598-603.	1.3	38
129	Genome-wide association study identifies a new locus JMJD1C at 10q21 that may influence serum androgen levels in men. <i>Human Molecular Genetics</i> , 2012, 21, 5222-5228.	1.4	79
130	The Role of Genetic Markers in the Management of Prostate Cancer. <i>European Urology</i> , 2012, 62, 577-587.	0.9	92
131	Distinct Transcriptional Programs Mediated by the Ligand-Dependent Full-Length Androgen Receptor and Its Splice Variants in Castration-Resistant Prostate Cancer. <i>Cancer Research</i> , 2012, 72, 3457-3462.	0.4	518
132	Potential Impact of Adding Genetic Markers to Clinical Parameters in Predicting Prostate Biopsy Outcomes in Men Following an Initial Negative Biopsy: Findings from the REDUCE Trial. <i>European Urology</i> , 2012, 62, 953-961.	0.9	85
133	Identification of a novel NBN truncating mutation in a family with hereditary prostate cancer. <i>Familial Cancer</i> , 2012, 11, 595-600.	0.9	15
134	Germline Mutations in <i>HOXB13</i> and Prostate-Cancer Risk. <i>New England Journal of Medicine</i> , 2012, 366, 141-149.	13.9	566
135	Association of prostate cancer risk with snps in regions containing androgen receptor binding sites captured by ChIP-on-chip analyses. <i>Prostate</i> , 2012, 72, 376-385.	1.2	15
136	Chromosomes 4 and 8 implicated in a genome wide SNP linkage scan of 762 prostate cancer families collected by the ICPCG. <i>Prostate</i> , 2012, 72, 410-426.	1.2	14
137	DIAPH3 governs the cellular transition to the amoeboid tumour phenotype. <i>EMBO Molecular Medicine</i> , 2012, 4, 743-760.	3.3	92
138	Genome-wide two-locus epistasis scans in prostate cancer using two European populations. <i>Human Genetics</i> , 2012, 131, 1225-1234.	1.8	17
139	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). <i>Human Genetics</i> , 2012, 131, 1095-1103.	1.8	21
140	Inherited susceptibility for aggressive prostate cancer. <i>Asian Journal of Andrology</i> , 2012, 14, 415-418.	0.8	6
141	Identification of New Differentially Methylated Genes That Have Potential Functional Consequences in Prostate Cancer. <i>PLoS ONE</i> , 2012, 7, e48455.	1.1	65
142	Evaluation of PPP2R2A as a prostate cancer susceptibility gene: a comprehensive germline and somatic study. <i>Cancer Genetics</i> , 2011, 204, 375-381.	0.2	51
143	GENETIC BASIS FOR PROSTATE CANCER. , 2011, , 39-52.		0
144	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. <i>Nature Genetics</i> , 2011, 43, 570-573.	9.4	198

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145	Polygenic Risk Score Improves Prostate Cancer Risk Prediction: Results from the Stockholm-1 Cohort Study. <i>European Urology</i> , 2011, 60, 21-28.	0.9	117
146	Inherited genetic markers discovered to date are able to identify a significant number of men at considerably elevated risk for prostate cancer. <i>Prostate</i> , 2011, 71, 421-430.	1.2	38
147	Functional annotation of risk loci identified through genome-wide association studies for prostate cancer. <i>Prostate</i> , 2011, 71, 955-963.	1.2	25
148	A snapshot of the expression signature of androgen receptor splicing variants and their distinctive transcriptional activities. <i>Prostate</i> , 2011, 71, 1656-1667.	1.2	177
149	Immunomodulatory IL-18 binding protein is produced by prostate cancer cells and its levels in urine and serum correlate with tumor status. <i>International Journal of Cancer</i> , 2011, 129, 424-432.	2.3	42
150	Genome-wide copy-number variation analysis identifies common genetic variants at 20p13 associated with aggressiveness of prostate cancer. <i>Carcinogenesis</i> , 2011, 32, 1057-1062.	1.3	33
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