Suzanne Kolb

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. Nature Genetics, 2013, 45, 385-391.	21.4	492
2	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. Nature Genetics, 2014, 46, 1103-1109.	21.4	408
3	Evidence for a Rare Prostate Cancer–Susceptibility Locus at Chromosome 1p36. American Journal of Human Genetics, 1999, 64, 776-787.	6.2	292
4	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. Nature Genetics, 2011, 43, 785-791.	21.4	265
5	Genome-wide association study of prostate cancer in men of African ancestry identifies a susceptibility locus at 17q21. Nature Genetics, 2011, 43, 570-573.	21.4	198
6	A Combined Genomewide Linkage Scan of 1,233 Families for Prostate Cancer–Susceptibility Genes Conducted by the International Consortium for Prostate Cancer Genetics. American Journal of Human Genetics, 2005, 77, 219-229.	6.2	138
7	Prostate Cancer Specific Mortality and Gleason 7 Disease Differences in Prostate Cancer Outcomes Between Cases With Gleason 4 + 3 and Gleason 3 + 4 Tumors in a Population Based Cohort. Journal of Urology, 2009, 182, 2702-2707.	0.4	133
8	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
9	Characterizing Genetic Risk at Known Prostate Cancer Susceptibility Loci in African Americans. PLoS Genetics, 2011, 7, e1001387.	3.5	117
10	A Genomic Scan of Families with Prostate Cancer Identifies Multiple Regions of Interest. American Journal of Human Genetics, 2000, 67, 100-109.	6.2	88
11	Two susceptibility loci identified for prostate cancer aggressiveness. Nature Communications, 2015, 6, 6889.	12.8	88
12	Analysis of Chromosome 1q42.2-43 in 152 Families with High Risk of Prostate Cancer. American Journal of Human Genetics, 1999, 64, 1087-1095.	6.2	70
13	Genetic Variants in the <i>LEPR</i> , <i>CRY1</i> , <i>RNASEL</i> , <i>IL4</i> , and <i>ARVCF</i> Genes Are Prognostic Markers of Prostate Cancer-Specific Mortality. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1928-1936.	2.5	68
14	Epigenome-Wide Tumor DNA Methylation Profiling Identifies Novel Prognostic Biomarkers of Metastatic-Lethal Progression in Men Diagnosed with Clinically Localized Prostate Cancer. Clinical Cancer Research, 2017, 23, 311-319.	7.0	65
15	Generalizability of established prostate cancer risk variants in men of <scp>A</scp> frican ancestry. International Journal of Cancer, 2015, 136, 1210-1217.	5.1	62
16	Genomic scan of 254 hereditary prostate cancer families. Prostate, 2003, 57, 309-319.	2.3	59
17	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
18	Statin Use in Relation to Prostate Cancer Outcomes in a Population-based Patient Cohort Study. Prostate, 2013, 73, 1214-1222.	2.3	57

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19	Genetic Polymorphisms in Inflammation Pathway Genes and Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 923-933.	2.5	54
20	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
21	Genome-wide Association Study Identifies a Genetic Variant Associated with Risk for More Aggressive Prostate Cancer. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1196-1203.	2.5	48
22	17-Gene Genomic Prostate Score Test Results in the Canary Prostate Active Surveillance Study (PASS) Cohort. Journal of Clinical Oncology, 2020, 38, 1549-1557.	1.6	48
23	Prostate tumor DNA methylation is associated with cigarette smoking and adverse prostate cancer outcomes. Cancer, 2016, 122, 2168-2177.	4.1	47
24	Genetic Linkage Analysis of Prostate Cancer Families to Xq27–28. Human Heredity, 2001, 51, 107-113.	0.8	46
25	Prostate cancer and genetic susceptibility: A genome scan incorporating disease aggressiveness. Prostate, 2006, 66, 317-325.	2.3	45
26	<i>HOXB13</i> mutations in a populationâ€based, case–control study of prostate cancer. Prostate, 2013, 73, 634-641.	2.3	44
27	Linkage analysis of 150 high-risk prostate cancer families at 1q24-25. , 2000, 18, 251-275.		43
28	Germline Missense Variants in the <i>BTNL2</i> Gene Are Associated with Prostate Cancer Susceptibility. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 1520-1528.	2.5	35
29	Gene expression signature of Gleason score is associated with prostate cancer outcomes in a radical prostatectomy cohort. Oncotarget, 2017, 8, 43035-43047.	1.8	35
30	Oligogenic segregation analysis of hereditary prostate cancer pedigrees: Evidence for multiple loci affecting age at onset. International Journal of Cancer, 2003, 105, 630-635.	5.1	34
31	Androgen metabolism and JAK/STAT pathway genes and prostate cancer risk. Cancer Epidemiology, 2012, 36, 347-353.	1.9	34
32	Validation Study of Genes with Hypermethylated Promoter Regions Associated with Prostate Cancer Recurrence. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 1331-1339.	2.5	34
33	Quantitative comparison and reproducibility of pathologist scoring and digital image analysis of estrogen receptor β2 immunohistochemistry in prostate cancer. Diagnostic Pathology, 2016, 11, 63.	2.0	34
34	Circulating levels of 25-hydroxyvitamin D and prostate cancer prognosis. Cancer Epidemiology, 2013, 37, 666-670.	1.9	30
35	DNA methylation profiles in African American prostate cancer patients in relation to disease progression. Genomics, 2019, 111, 10-16.	2.9	30
36	Germline mutations in the p73 gene do not predispose to familial prostate-brain cancer. Prostate, 2001, 48, 292-296.	2.3	29

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37	Association of variants in estrogenâ€related pathway genes with prostate cancer risk. Prostate, 2013, 73, 1-10.	2.3	28
38	A polymorphism in the CYP17 gene and risk of prostate cancer. Cancer Epidemiology Biomarkers and Prevention, 2002, 11, 243-7.	2.5	28
39	Investigation of the Relationship Between Prostate Cancer and <i>MSMB</i> and <i>NCOA4</i> Genetic Variants and Protein Expression. Human Mutation, 2013, 34, 149-156.	2.5	26
40	<i>CYP17</i> polymorphisms and prostate cancer outcomes. Prostate, 2010, 70, 1094-1101.	2.3	25
41	Gene expression panel predicts metastaticâ€lethal prostate cancer outcomes in men diagnosed with clinically localized prostate cancer. Molecular Oncology, 2017, 11, 140-150.	4.6	24
42	Identification of a prostate cancer susceptibility locus on chromosome 7q11–21 in Jewish families. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 1939-1944.	7.1	23
43	<i>Trichomonas vaginalis</i> infection and risk of advanced prostate cancer. Prostate, 2016, 76, 620-623.	2.3	22
44	Vigorous Physical Activity Is Associated with Lower Risk of Metastatic–Lethal Progression in Prostate Cancer and Hypomethylation in the <i>CRACR2A</i> Gene. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 258-264.	2.5	20
45	Identification and characterization of novel SNPs in CHEK2 in Ashkenazi Jewish men with prostate cancer. Cancer Letters, 2008, 270, 173-180.	7.2	19
46	A Meta-analysis of Multiple Myeloma Risk Regions in African and European Ancestry Populations Identifies Putatively Functional Loci. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1609-1618.	2.5	18
47	Discovery and fine-mapping of height loci via high-density imputation of GWASs in individuals of African ancestry. American Journal of Human Genetics, 2021, 108, 564-582.	6.2	18
48	Expression of cell cycle-regulated genes and prostate cancer prognosis in a population-based cohort. Prostate, 2015, 75, 1354-1362.	2.3	16
49	A five pG DNA methylation score to predict metastaticâ€lethal outcomes in men treated with radical prostatectomy for localized prostate cancer. Prostate, 2018, 78, 1084-1091.	2.3	16
50	Prostate Cancer Expression Profiles of Cytoplasmic ERβ1 and Nuclear ERβ2 are Associated with Poor Outcomes following Radical Prostatectomy. Journal of Urology, 2016, 195, 1760-1766.	0.4	12
51	Copy number alterations are associated with metastatic-lethal progression in prostate cancer. Prostate Cancer and Prostatic Diseases, 2020, 23, 494-506.	3.9	12
52	Whole exome sequencing in 75 high-risk families with validation and replication in independent case-control studies identifies <i>TANGO2</i> , <i>OR5H14</i> , and <i>CHAD</i> as new prostate cancer susceptibility genes. Oncotarget, 2017, 8, 1495-1507.	1.8	11
53	Genetic factors associated with prostate cancer conversion from active surveillance to treatment. Human Genetics and Genomics Advances, 2022, 3, 100070.	1.7	10
54	Confirmation of Prostate Cancer Susceptibility Genes Using High-Risk Families. Journal of the National Cancer Institute Monographs, 1999, 1999, 81-87.	2.1	9

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55	A fourâ€gene transcript score to predict metastaticâ€lethal progression in men treated for localized prostate cancer: Development and validation studies. Prostate, 2019, 79, 1589-1596.	2.3	8
56	Methodological Considerations in Estimation of Phenotype Heritability Using Genome-Wide SNP Data, Illustrated by an Analysis of the Heritability of Height in a Large Sample of African Ancestry Adults. PLoS ONE, 2015, 10, e0131106.	2.5	2
57	CYP17 POLYMORPHISMS AND PROSTATE CANCER OUTCOMES. Journal of Urology, 2009, 181, 777-777.	0.4	0
58	PD47-03 EXPRESSION OF CYTOPLASMIC ERÎ ² 1 AND NUCLEAR ERÎ ² 2 IS ASSOCIATED WITH POOR OUTCOMES FOLLOWING RADICAL PROSTATECTOMY FOR LOCALIZED PROSTATE CANCER. Journal of Urology, 2015, 193, .	0.4	0
59	Abstract 5066: Generalizability of established prostate cancer risk variants in men of African ancestry. , 2014, , .		0