

Karina Dalsgaard Sørensen

List of Publications by Year in descending order

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Version: 2024-02-01

77
papers

4,946
citations

136950

32
h-index

106344

65
g-index

83
all docs

83
docs citations

83
times ranked

9753
citing authors

#	ARTICLE	IF	CITATIONS
1	Evaluation of Predictors of Biochemical Recurrence in Prostate Cancer Patients, as Detected by 68Ga-PSMA PET/CT. <i>Diagnostics</i> , 2022, 12, 195.	2.6	5
2	Microbiota of the prostate tumor environment investigated by whole-transcriptome profiling. <i>Genome Medicine</i> , 2022, 14, 9.	8.2	14
3	The transcriptional landscape and biomarker potential of circular RNAs in prostate cancer. <i>Genome Medicine</i> , 2022, 14, 8.	8.2	19
4	Dysbiotic microbes and how to find them: a review of microbiome profiling in prostate cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , 2022, 41, 31.	8.6	8
5	Prostate cancer risk stratification improvement across multiple ancestries with new polygenic hazard score. <i>Prostate Cancer and Prostatic Diseases</i> , 2022, 25, 755-761.	3.9	14
6	Independent validation of a pre-specified four-kallikrein marker model for prediction of adverse pathology and biochemical recurrence. <i>British Journal of Cancer</i> , 2022, 126, 1004-1009.	6.4	2
7	FRMD6 has tumor suppressor functions in prostate cancer. <i>Oncogene</i> , 2021, 40, 763-776.	5.9	24
8	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.	21.4	264
9	Additional SNPs improve risk stratification of a polygenic hazard score for prostate cancer. <i>Prostate Cancer and Prostatic Diseases</i> , 2021, 24, 532-541.	3.9	16
10	Polygenic hazard score is associated with prostate cancer in multi-ethnic populations. <i>Nature Communications</i> , 2021, 12, 1236.	12.8	40
11	High-Throughput and Automated Acoustic Trapping of Extracellular Vesicles to Identify microRNAs With Diagnostic Potential for Prostate Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 631021.	2.8	17
12	A polymorphism in the promoter of FRAS1 is a candidate SNP associated with metastatic prostate cancer. <i>Prostate</i> , 2021, 81, 683-693.	2.3	5
13	Risk stratification in men with a negative prostate biopsy: an interim analysis of a prospective cohort study. <i>BJU International</i> , 2021, 128, 702-712.	2.5	0
14	Immune cell analyses of the tumor microenvironment in prostate cancer highlight infiltrating regulatory T cells and macrophages as adverse prognostic factors. <i>Journal of Pathology</i> , 2021, 255, 155-165.	4.5	36
15	⁶⁸ Ga-PSMA PET/CT for Primary Lymph Node and Distant Metastasis NM Staging of High-Risk Prostate Cancer. <i>Journal of Nuclear Medicine</i> , 2021, 62, 214-220.	5.0	64
16	A Nordic initiative for a more personal and accurate diagnostic pathway for prostate cancer. <i>Scandinavian Journal of Primary Health Care</i> , 2020, 38, 249-250.	1.5	2
17	The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. <i>Cancers</i> , 2020, 12, 3254.	3.7	16
18	Epigenetic Analysis of Circulating Tumor DNA in Localized and Metastatic Prostate Cancer: Evaluation of Clinical Biomarker Potential. <i>Cells</i> , 2020, 9, 1362.	4.1	20

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19	FcRn overexpression in human cancer drives albumin recycling and cell growth; a mechanistic basis for exploitation in targeted albumin-drug designs. <i>Journal of Controlled Release</i> , 2020, 322, 53-63.	9.9	29
20	Validation of the four-miRNA biomarker panel MiCaP for prediction of long-term prostate cancer outcome. <i>Scientific Reports</i> , 2020, 10, 10704.	3.3	8
21	The effect of assessing genetic risk of prostate cancer on the use of PSA tests in primary care: A cluster randomized controlled trial. <i>PLoS Medicine</i> , 2020, 17, e1003033.	8.4	6
22	Profiling of Circulating microRNAs in Prostate Cancer Reveals Diagnostic Biomarker Potential. <i>Diagnostics</i> , 2020, 10, 188.	2.6	22
23	A genetic risk assessment for prostate cancer influences patients' risk perception and use of repeat PSA testing: a cross-sectional study in Danish general practice. <i>BJGP Open</i> , 2020, 4, bjgpopen20X101039.	1.8	1
24	Epigenetic silencing of MEIS2 in prostate cancer recurrence. <i>Clinical Epigenetics</i> , 2019, 11, 147.	4.1	20
25	Elevated miR-615-3p Expression Predicts Adverse Clinical Outcome and Promotes Proliferation and Migration of Prostate Cancer Cells. <i>American Journal of Pathology</i> , 2019, 189, 2377-2388.	3.8	16
26	Epigenetics of Urological Cancers. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4775.	4.1	7
27	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
28	A novel combined miRNA and methylation marker panel (miMe) for prediction of prostate cancer outcome after radical prostatectomy. <i>International Journal of Cancer</i> , 2019, 145, 3445-3452.	5.1	12
29	A five-microRNA model (pCaP) for predicting prostate cancer aggressiveness using cell-free urine. <i>International Journal of Cancer</i> , 2019, 145, 2558-2567.	5.1	36
30	5hmC Level Predicts Biochemical Failure Following Radical Prostatectomy in Prostate Cancer Patients with ERG Negative Tumors. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1025.	4.1	4
31	Aberrant DOCK2, GRASP, HIF3A and PKFP Hypermethylation has Potential as a Prognostic Biomarker for Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1173.	4.1	28
32	Independent Validation of a Diagnostic Noninvasive 3-MicroRNA Ratio Model (uCaP) for Prostate Cancer in Cell-Free Urine. <i>Clinical Chemistry</i> , 2019, 65, 540-548.	3.2	20
33	Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 208-216.	2.5	21
34	Biomarker potential of STG and GALNAC3 and ZNF660 promoter hypermethylation in prostate cancer tissue and liquid biopsies. <i>Molecular Oncology</i> , 2018, 12, 545-560.	4.6	49
35	Diagnostic and Prognostic MicroRNA Biomarkers for Prostate Cancer in Cell-free Urine. <i>European Urology Focus</i> , 2018, 4, 825-833.	3.1	86
36	Exploring the transcriptome of hormone-naïve multifocal prostate cancer and matched lymph node metastases. <i>British Journal of Cancer</i> , 2018, 119, 1527-1537.	6.4	10

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37	Germline variation at 8q24 and prostate cancer risk in men of European ancestry. <i>Nature Communications</i> , 2018, 9, 4616.	12.8	43
38	Picomolar sensitive and SNP-selective “Off-On” hairpin genosensor based on structure-tunable redox indicator signals. <i>Biosensors and Bioelectronics</i> , 2018, 117, 444-449.	10.1	11
39	Training and validation of a novel 4-miRNA ratio model (MiCaP) for prediction of postoperative outcome in prostate cancer patients. <i>Annals of Oncology</i> , 2018, 29, 2003-2009.	1.2	29
40	Perceptions about screening for prostate cancer using genetic lifetime risk assessment: a qualitative study. <i>BMC Family Practice</i> , 2018, 19, 32.	2.9	5
41	Dysregulation and prognostic potential of 5-methylcytosine (5mC), 5-hydroxymethylcytosine (5hmC), 5-formylcytosine (5fC), and 5-carboxylcytosine (5caC) levels in prostate cancer. <i>Clinical Epigenetics</i> , 2018, 10, 105.	4.1	36
42	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	21.4	652
43	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. <i>Nature Communications</i> , 2018, 9, 2256.	12.8	88
44	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3.	8.8	43
45	Heterogeneous patterns of DNA methylation-based field effects in histologically normal prostate tissue from cancer patients. <i>Scientific Reports</i> , 2017, 7, 40636.	3.3	35
46	miRNAs associated with prostate cancer risk and progression. <i>BMC Urology</i> , 2017, 17, 18.	1.4	79
47	An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes. <i>Cell Systems</i> , 2017, 4, 587-599.e4.	6.2	413
48	epiG: statistical inference and profiling of DNA methylation from whole-genome bisulfite sequencing data. <i>Genome Biology</i> , 2017, 18, 38.	8.8	6
49	RHCG and TCAF1 promoter hypermethylation predicts biochemical recurrence in prostate cancer patients treated by radical prostatectomy. <i>Oncotarget</i> , 2017, 8, 5774-5788.	1.8	22
50	Comprehensive Evaluation of TFF3 Promoter Hypomethylation and Molecular Biomarker Potential for Prostate Cancer Diagnosis and Prognosis. <i>International Journal of Molecular Sciences</i> , 2017, 18, 2017.	4.1	20
51	Bivalent Regions of Cytosine Methylation and H3K27 Acetylation Suggest an Active Role for DNA Methylation at Enhancers. <i>Molecular Cell</i> , 2016, 62, 422-431.	9.7	106
52	Prevalence of the HOXB13 G84E mutation in Danish men undergoing radical prostatectomy and its correlations with prostate cancer risk and aggressiveness. <i>BJU International</i> , 2016, 118, 646-653.	2.5	31
53	The Potential of MicroRNAs as Prostate Cancer Biomarkers. <i>European Urology</i> , 2016, 70, 312-322.	1.9	243
54	Large-scale evaluation of SLC18A2 in prostate cancer reveals diagnostic and prognostic biomarker potential at three molecular levels. <i>Molecular Oncology</i> , 2016, 10, 825-837.	4.6	20

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55	PINCAGE: probabilistic integration of cancer genomics data for perturbed gene identification and sample classification. <i>Bioinformatics</i> , 2016, 32, 1353-1365.	4.1	12
56	<i>HNF1B</i> variants associate with promoter methylation and regulate gene networks activated in prostate and ovarian cancer. <i>Oncotarget</i> , 2016, 7, 74734-74746.	1.8	38
57	Novel diagnostic and prognostic classifiers for prostate cancer identified by genome-wide microRNA profiling. <i>Oncotarget</i> , 2016, 7, 30760-30771.	1.8	70
58	Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy. <i>Scientific Reports</i> , 2015, 5, 16018.	3.3	108
59	High levels of 5-hydroxymethylcytosine (5hmC) is an adverse predictor of biochemical recurrence after prostatectomy in ERG-negative prostate cancer. <i>Clinical Epigenetics</i> , 2015, 7, 111.	4.1	26
60	SMAP: a streamlined methylation analysis pipeline for bisulfite sequencing. <i>GigaScience</i> , 2015, 4, 29.	6.4	13
61	Risk Analysis of Prostate Cancer in PRACTICAL, a Multinational Consortium, Using 25 Known Prostate Cancer Susceptibility Loci. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1121-1129.	2.5	56
62	BS-SNPer: SNP calling in bisulfite-seq data. <i>Bioinformatics</i> , 2015, 31, 4006-4008.	4.1	61
63	Next-Generation Sequencing of RNA and DNA Isolated from Paired Fresh-Frozen and Formalin-Fixed Paraffin-Embedded Samples of Human Cancer and Normal Tissue. <i>PLoS ONE</i> , 2014, 9, e98187.	2.5	284
64	Prognostic DNA Methylation Markers for Prostate Cancer. <i>International Journal of Molecular Sciences</i> , 2014, 15, 16544-16576.	4.1	90
65	Profiling of circulating microRNAs for prostate cancer biomarker discovery. <i>Drug Delivery and Translational Research</i> , 2014, 4, 19-30.	5.8	84
66	Hypermethylation of the <i>GABRE</i> 4miR-452 4miR-224 Promoter in Prostate Cancer Predicts Biochemical Recurrence after Radical Prostatectomy. <i>Clinical Cancer Research</i> , 2014, 20, 2169-2181.	7.0	86
67	A Dual Program for Translation Regulation in Cellular Proliferation and Differentiation. <i>Cell</i> , 2014, 158, 1281-1292.	28.9	414
68	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.	2.9	118
69	DNA Methylation Signatures for Prediction of Biochemical Recurrence After Radical Prostatectomy of Clinically Localized Prostate Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 3250-3258.	1.6	117
70	Research Highlights: New insights into prostate cancer susceptibility. <i>Personalized Medicine</i> , 2013, 10, 427-430.	1.5	0
71	Research Highlights: The search for better prostate cancer biomarkers continues. <i>Personalized Medicine</i> , 2012, 9, 471-474.	1.5	0
72	Seven prostate cancer susceptibility loci identified by a multi-stage genome-wide association study. <i>Nature Genetics</i> , 2011, 43, 785-791.	21.4	265

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73	Promoter hypomethylation and upregulation of trefoil factors in prostate cancer. International Journal of Cancer, 2010, 127, 1857-1865.	5.1	48
74	Discovery of prostate cancer biomarkers by microarray gene expression profiling. Expert Review of Molecular Diagnostics, 2010, 10, 49-64.	3.1	60
75	Genetic and Epigenetic <i>SLC18A2</i> Silencing in Prostate Cancer Is an Independent Adverse Predictor of Biochemical Recurrence after Radical Prostatectomy. Clinical Cancer Research, 2009, 15, 1400-1410.	7.0	26
76	Chromosomal deletion, promoter hypermethylation and downregulation of <i>FYN</i> in prostate cancer. International Journal of Cancer, 2008, 122, 509-519.	5.1	22
77	Ethical Principles in the Analysis of Prostate Cancer Diagnostics. Cancer Investigation, 0, , 1-15.	1.3	0