

Antoinette S Perry

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5319237/publications.pdf>

Version: 2024-02-01

42
papers

1,650
citations

279798

23
h-index

289244

40
g-index

44
all docs

44
docs citations

44
times ranked

2832
citing authors

#	ARTICLE	IF	CITATIONS
1	Plant-derived cannabinoids as anticancer agents. <i>Trends in Cancer</i> , 2022, 8, 350-357.	7.4	7
2	Longitudinal analysis of individual cfDNA methylome patterns in metastatic prostate cancer. <i>Clinical Epigenetics</i> , 2021, 13, 168.	4.1	14
3	Development of a multivariable risk model integrating urinary cell DNA methylation and cell-free RNA data for the detection of significant prostate cancer. <i>Prostate</i> , 2020, 80, 547-558.	2.3	17
4	Evaluating liquid biopsies for methylomic profiling of prostate cancer. <i>Epigenetics</i> , 2020, 15, 715-727.	2.7	13
5	A four-group urine risk classifier for predicting outcomes in patients with prostate cancer. <i>BJU International</i> , 2019, 124, 609-620.	2.5	30
6	epiCaPture: A Urine DNA Methylation Test for Early Detection of Aggressive Prostate Cancer. <i>JCO Precision Oncology</i> , 2019, 2019, 1-18.	3.0	27
7	Holding a MIRror up to the robustness of the prostate cancer urinary transcriptome. <i>Translational Andrology and Urology</i> , 2019, 8, S488-S490.	1.4	0
8	Reasons for Discontinuing Active Surveillance: Assessment of 21 Centres in 12 Countries in the Movember GAP3 Consortium. <i>European Urology</i> , 2019, 75, 523-531.	1.9	58
9	Epigenetics of malignant melanoma. <i>Seminars in Cancer Biology</i> , 2018, 51, 80-88.	9.6	95
10	Assessing DNA Methylation in Cancer Stem Cells. <i>Methods in Molecular Biology</i> , 2018, 1692, 157-178.	0.9	4
11	A urine-based DNA methylation assay, ProCUrE, to identify clinically significant prostate cancer. <i>Clinical Epigenetics</i> , 2018, 10, 147.	4.1	26
12	Integrating biomarkers across omic platforms: an approach to improve stratification of patients with indolent and aggressive prostate cancer. <i>Molecular Oncology</i> , 2018, 12, 1513-1525.	4.6	41
13	Analysis of urinary PSA glycosylation is not indicative of high-risk prostate cancer. <i>Clinica Chimica Acta</i> , 2017, 470, 97-102.	1.1	10
14	Comparative analysis of prostate-specific antigen by two-dimensional gel electrophoresis and capillary electrophoresis. <i>Electrophoresis</i> , 2017, 38, 408-416.	2.4	6
15	Hypoxia regulates Notch-3 mRNA and receptor activation in prostate cancer cells. <i>Heliyon</i> , 2016, 2, e00104.	3.2	10
16	Improving multivariable prostate cancer risk assessment using the Prostate Health Index. <i>BJU International</i> , 2016, 117, 409-417.	2.5	39
17	Expression of the TP1± and TP1² isoforms of the thromboxane prostanoid receptor (TP) in prostate cancer: clinical significance and diagnostic potential. <i>Oncotarget</i> , 2016, 7, 73171-73187.	1.8	10
18	Multigene Methylation Biomarker Analysis in Prostate Cancer. <i>Epigenetic Diagnosis & Therapy</i> , 2015, 1, 19-27.	0.1	0

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19	Epigenetic Methodologies for the Study of Celiac Disease. <i>Methods in Molecular Biology</i> , 2015, 1326, 131-158.	0.9	8
20	Long noncoding RNAs and prostate carcinogenesis: the missing link?. <i>Trends in Molecular Medicine</i> , 2014, 20, 428-436.	6.7	97
21	Noncoding RNAs in Prostate Cancer: The Long and the Short of It. <i>Clinical Cancer Research</i> , 2014, 20, 35-43.	7.0	59
22	Gene expression and epigenetic discovery screen reveal methylation of SFRP2 in prostate cancer. <i>International Journal of Cancer</i> , 2013, 132, 1771-1780.	5.1	40
23	Prostate Cancer Epigenomics. <i>Journal of Urology</i> , 2013, 189, 10-11.	0.4	6
24	Mining methylome databases. <i>Trends in Genetics</i> , 2013, 29, 63-65.	6.7	2
25	Manipulating the epigenome for the treatment of urological malignancies. , 2013, 138, 185-196.		17
26	Gene expression analysis in prostate cancer: The importance of the endogenous control. <i>Prostate</i> , 2013, 73, 382-390.	2.3	13
27	Gemcitabine reactivates epigenetically silenced genes and functions as a DNA methyltransferase inhibitor. <i>International Journal of Molecular Medicine</i> , 2012, 30, 1505-1511.	4.0	31
28	Docetaxel maintains its cytotoxic activity under hypoxic conditions in prostate cancer cells. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2012, 30, 912-919.	1.6	16
29	IGFBP7 Promoter Methylation and Gene Expression Analysis in Prostate Cancer. <i>Journal of Urology</i> , 2012, 188, 1354-1360.	0.4	29
30	MicroRNAs as putative mediators of treatment response in prostate cancer. <i>Nature Reviews Urology</i> , 2012, 9, 397-407.	3.8	36
31	The role of secreted frizzled-related protein 2 expression in prostate cancer. <i>Histopathology</i> , 2011, 59, 1240-1248.	2.9	27
32	In silico analysis and DHPLC screening strategy identifies novel apoptotic gene targets of aberrant promoter hypermethylation in prostate cancer. <i>Prostate</i> , 2011, 71, 1-17.	2.3	15
33	Localized hypermutation and associated gene losses in legume chloroplast genomes. <i>Genome Research</i> , 2010, 20, 1700-1710.	5.5	244
34	MAD2 downregulation in hypoxia is independent of promoter hypermethylation. <i>Cell Cycle</i> , 2010, 9, 2928-2937.	2.6	9
35	The epigenome as a therapeutic target in prostate cancer. <i>Nature Reviews Urology</i> , 2010, 7, 668-680.	3.8	118
36	The HIF-1 α C1772T polymorphism may be associated with susceptibility to clinically localized prostate cancer but not with elevated expression of hypoxic biomarkers. <i>Cancer Biology and Therapy</i> , 2009, 8, 118-124.	3.4	50

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37	The emergence of DNA methylation as a key modulator of aberrant cell death in prostate cancer. <i>Endocrine-Related Cancer</i> , 2008, 15, 11-25.	3.1	51
38	Discovery of DNA Hypermethylation Using a DHPLC Screening Strategy. <i>Epigenetics</i> , 2007, 2, 43-49.	2.7	11
39	In silico mining identifies IGFBP3 as a novel target of methylation in prostate cancer. <i>British Journal of Cancer</i> , 2007, 96, 1587-1594.	6.4	45
40	The emerging roles of DNA methylation in the clinical management of prostate cancer. <i>Endocrine-Related Cancer</i> , 2006, 13, 357-377.	3.1	80
41	Evolutionary Re-organisation of a Large Operon in Adzuki Bean Chloroplast DNA caused by Inverted Repeat Movement. <i>DNA Research</i> , 2002, 9, 157-162.	3.4	33
42	Nucleotide Substitution Rates in Legume Chloroplast DNA Depend on the Presence of the Inverted Repeat. <i>Journal of Molecular Evolution</i> , 2002, 55, 501-508.	1.8	168