## Antoinette S Perry

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Localized hypermutation and associated gene losses in legume chloroplast genomes. Genome Research, 2010, 20, 1700-1710.	5.5	244
2	Nucleotide Substitution Rates in Legume Chloroplast DNA Depend on the Presence of the Inverted Repeat. Journal of Molecular Evolution, 2002, 55, 501-508.	1.8	168
3	The epigenome as a therapeutic target in prostate cancer. Nature Reviews Urology, 2010, 7, 668-680.	3.8	118
4	Long noncoding RNAs and prostate carcinogenesis: the missing â€~linc'?. Trends in Molecular Medicine, 2014, 20, 428-436.	6.7	97
5	Epigenetics of malignant melanoma. Seminars in Cancer Biology, 2018, 51, 80-88.	9.6	95
6	The emerging roles of DNA methylation in the clinical management of prostate cancer. Endocrine-Related Cancer, 2006, 13, 357-377.	3.1	80
7	Noncoding RNAs in Prostate Cancer: The Long and the Short of It. Clinical Cancer Research, 2014, 20, 35-43.	7.0	59
8	Reasons for Discontinuing Active Surveillance: Assessment of 21 Centres in 12 Countries in the Movember GAP3 Consortium. European Urology, 2019, 75, 523-531.	1.9	58
9	The emergence of DNA methylation as a key modulator of aberrant cell death in prostate cancer. Endocrine-Related Cancer, 2008, 15, 11-25.	3.1	51
10	The HIF-1α C1772T polymorphism may be associated with susceptibility to clinically localized prostate cancer but not with elevated expression of hypoxic biomarkers. Cancer Biology and Therapy, 2009, 8, 118-124.	3.4	50
11	In silico mining identifies IGFBP3 as a novel target of methylation in prostate cancer. British Journal of Cancer, 2007, 96, 1587-1594.	6.4	45
12	Integrating biomarkers across omic platforms: an approach to improve stratification of patients with indolent and aggressive prostate cancer. Molecular Oncology, 2018, 12, 1513-1525.	4.6	41
13	Gene expression and epigenetic discovery screen reveal methylation of SFRP2 in prostate cancer. International Journal of Cancer, 2013, 132, 1771-1780.	5.1	40
14	Improving multivariable prostate cancer risk assessment using the Prostate Health Index. BJU International, 2016, 117, 409-417.	2.5	39
15	MicroRNAs as putative mediators of treatment response in prostate cancer. Nature Reviews Urology, 2012, 9, 397-407.	3.8	36
16	Evolutionary Re-organisation of a Large Operon in Adzuki Bean Chloroplast DNA caused by Inverted Repeat Movement. DNA Research, 2002, 9, 157-162.	3.4	33
17	Gemcitabine reactivates epigenetically silenced genes and functions as a DNA methyltransferase inhibitor. International Journal of Molecular Medicine, 2012, 30, 1505-1511.	4.0	31
18	A fourâ€group urine risk classifier for predicting outcomes in patients with prostate cancer. BJU International, 2019, 124, 609-620.	2.5	30

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19	IGFBP7 Promoter Methylation and Gene Expression Analysis in Prostate Cancer. Journal of Urology, 2012, 188, 1354-1360.	0.4	29
20	The role of secreted frizzled-related protein 2 expression in prostate cancer. Histopathology, 2011, 59, 1240-1248.	2.9	27
21	epiCaPture: A Urine DNA Methylation Test for Early Detection of Aggressive Prostate Cancer. JCO Precision Oncology, 2019, 2019, 1-18.	3.0	27
22	A urine-based DNA methylation assay, ProCUrE, to identify clinically significant prostate cancer. Clinical Epigenetics, 2018, 10, 147.	4.1	26
23	Manipulating the epigenome for the treatment of urological malignancies. , 2013, 138, 185-196.		17
24	Development of a multivariable risk model integrating urinary cell DNA methylation and cellâ€free RNA data for the detection of significant prostate cancer. Prostate, 2020, 80, 547-558.	2.3	17
25	Docetaxel maintains its cytotoxic activity under hypoxic conditions in prostate cancer cells. Urologic Oncology: Seminars and Original Investigations, 2012, 30, 912-919.	1.6	16
26	In silico analysis and DHPLC screening strategy identifies novel apoptotic gene targets of aberrant promoter hypermethylation in prostate cancer. Prostate, 2011, 71, 1-17.	2.3	15
27	Longitudinal analysis of individual cfDNA methylome patterns in metastatic prostate cancer. Clinical Epigenetics, 2021, 13, 168.	4.1	14
28	Gene expression analysis in prostate cancer: The importance of the endogenous control. Prostate, 2013, 73, 382-390.	2.3	13
29	Evaluating liquid biopsies for methylomic profiling of prostate cancer. Epigenetics, 2020, 15, 715-727.	2.7	13
30	Discovery of DNA Hypermethylation Using a DHPLC Screening Strategy. Epigenetics, 2007, 2, 43-49.	2.7	11
31	Hypoxia regulates Notch-3 mRNA and receptor activation in prostate cancer cells. Heliyon, 2016, 2, e00104.	3.2	10
32	Analysis of urinary PSA glycosylation is not indicative of high-risk prostate cancer. Clinica Chimica Acta, 2017, 470, 97-102.	1.1	10
33	Expression of the TPα and TPβ isoforms of the thromboxane prostanoid receptor (TP) in prostate cancer: clinical significance and diagnostic potential. Oncotarget, 2016, 7, 73171-73187.	1.8	10
34	MAD2 downregulation in hypoxia is independent of promoter hypermethylation. Cell Cycle, 2010, 9, 2928-2937.	2.6	9
35	Epigenetic Methodologies for the Study of Celiac Disease. Methods in Molecular Biology, 2015, 1326, 131-158.	0.9	8
36	Plant-derived cannabinoids as anticancer agents. Trends in Cancer, 2022, 8, 350-357.	7.4	7

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37	Prostate Cancer Epigenomics. Journal of Urology, 2013, 189, 10-11.	0.4	6
38	Comparative analysis of prostateâ€specific antigen by twoâ€dimensional gel electrophoresis and capillary electrophoresis. Electrophoresis, 2017, 38, 408-416.	2.4	6
39	Assessing DNA Methylation in Cancer Stem Cells. Methods in Molecular Biology, 2018, 1692, 157-178.	0.9	4
40	Mining methylome databases. Trends in Genetics, 2013, 29, 63-65.	6.7	2
41	Multigene Methylation Biomarker Analysis in Prostate Cancer. Epigenetic Diagnosis & Therapy, 2015, 1, 19-27.	0.1	0
42	Holding a MIRror up to the robustness of the prostate cancer urinary transcriptome. Translational Andrology and Urology, 2019, 8, S488-S490.	1.4	0