

Dominic J Smiraglia

List of Publications by Year in descending order

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Version: 2024-02-01

80
papers

6,063
citations

81900

39
h-index

76900

74
g-index

88
all docs

88
docs citations

88
times ranked

8552
citing authors

#	ARTICLE	IF	CITATIONS
1	Dynamic patterns of DNA methylation in the normal prostate epithelial differentiation program are targets of aberrant methylation in prostate cancer. <i>Scientific Reports</i> , 2021, 11, 11405.	3.3	3
2	Reduced NCOR2 expression accelerates androgen deprivation therapy failure in prostate cancer. <i>Cell Reports</i> , 2021, 37, 110109.	6.4	19
3	Pharmacological polyamine catabolism upregulation with methionine salvage pathway inhibition as an effective prostate cancer therapy. <i>Nature Communications</i> , 2020, 11, 52.	12.8	37
4	Biomarkers of Exposure and Effect in the Lungs of Smokers, Nonsmokers, and Electronic Cigarette Users. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 443-451.	2.5	43
5	Pan-cancer molecular analysis of the RB tumor suppressor pathway. <i>Communications Biology</i> , 2020, 3, 158.	4.4	50
6	The miR-96 and RAR α signaling axis governs androgen signaling and prostate cancer progression. <i>Oncogene</i> , 2019, 38, 421-444.	5.9	45
7	DNA Methylation and Smoking: Implications for Understanding Effects of Electronic Cigarettes. <i>Current Epidemiology Reports</i> , 2019, 6, 148-161.	2.4	2
8	Pan-cancer analysis of transcriptional metabolic dysregulation using The Cancer Genome Atlas. <i>Nature Communications</i> , 2018, 9, 5330.	12.8	174
9	A methyl-sensitive element induces bidirectional transcription in TATA-less CpG island-associated promoters. <i>PLoS ONE</i> , 2018, 13, e0205608.	2.5	13
10	Dietary Protein Restriction Reprograms Tumor-Associated Macrophages and Enhances Immunotherapy. <i>Clinical Cancer Research</i> , 2018, 24, 6383-6395.	7.0	69
11	Inhibition of the aryl hydrocarbon receptor/polyamine biosynthesis axis suppresses multiple myeloma. <i>Journal of Clinical Investigation</i> , 2018, 128, 4682-4696.	8.2	35
12	Abstract B033: Characterizing the global function of NCOR2 in prostate cancer cells and its contribution to PCa progression. , 2018, , .		0
13	Abstract B052: Leveraging the metabolic stress of polyamine biosynthesis in prostate cancer towards a novel therapeutic approach. , 2018, , .		0
14	The Genomic Impact of DNA CpG Methylation on Gene Expression; Relationships in Prostate Cancer. <i>Biomolecules</i> , 2017, 7, 15.	4.0	92
15	LSD1 dual function in mediating epigenetic corruption of the vitamin D signaling in prostate cancer. <i>Clinical Epigenetics</i> , 2017, 9, 82.	4.1	19
16	Internally ratiometric fluorescent sensors for evaluation of intracellular GTP levels and distribution. <i>Nature Methods</i> , 2017, 14, 1003-1009.	19.0	47
17	Dietary folate levels alter the kinetics and molecular mechanism of prostate cancer recurrence in the CWR22 model. <i>Oncotarget</i> , 2017, 8, 103758-103774.	1.8	13
18	DNA methylation and breast tumor clinicopathological features: The Western New York Exposures and Breast Cancer (WEB) study. <i>Epigenetics</i> , 2016, 11, 643-652.	2.7	17

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19	Metastatic phenotype in CWR22 prostate cancer xenograft following castration. <i>Prostate</i> , 2016, 76, 359-368.	2.3	8
20	The essential role of methylthioadenosine phosphorylase in prostate cancer. <i>Oncotarget</i> , 2016, 7, 14380-14393.	1.8	29
21	KLLN epigenotypeâ€“phenotype associations in Cowden syndrome. <i>European Journal of Human Genetics</i> , 2015, 23, 1538-1543.	2.8	19
22	Hormone stimulation of androgen receptor mediates dynamic changes in DNA methylation patterns at regulatory elements. <i>Oncotarget</i> , 2015, 6, 42575-42589.	1.8	30
23	Gene Silencing Associated with SWI/SNF Complex Loss during NSCLC Development. <i>Molecular Cancer Research</i> , 2014, 12, 560-570.	3.4	23
24	Epigenetic DNA Methylation of Antioxidative Stress Regulator <i>NRF2</i> in Human Prostate Cancer. <i>Cancer Prevention Research</i> , 2014, 7, 1186-1197.	1.5	69
25	Abstract 1383: Evolution of the NCOR1 and NCOR2/SMRT cistromes in prostate cancer progression. , 2014, , .		0
26	Abstract 3390: Epigenetic corruption of the Vitamin D signaling in prostate cancer. , 2014, , .		0
27	Recruitment of NCOR1 to VDR target genes is enhanced in prostate cancer cells and associates with altered DNA methylation patterns. <i>Carcinogenesis</i> , 2013, 34, 248-256.	2.8	50
28	Epigenetic distortion to VDR transcriptional regulation in prostate cancer cells. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2013, 136, 258-263.	2.5	12
29	Gene silencing of SLC5A8 identified by genome-wide methylation profiling in lung cancer. <i>Lung Cancer</i> , 2013, 79, 198-204.	2.0	26
30	Developmental programming in skeletal muscle in response to overnourishment in the immediate postnatal life in rats. <i>Journal of Nutritional Biochemistry</i> , 2013, 24, 1859-1869.	4.2	39
31	Epigenetic changes in hypothalamic appetite regulatory genes may underlie the developmental programming for obesity in rat neonates subjected to a high-carbohydrate dietary modification. <i>Journal of Developmental Origins of Health and Disease</i> , 2013, 4, 479-490.	1.4	34
32	Adult-onset obesity induced by early life overnutrition could be reversed by moderate caloric restriction. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2013, 305, E785-E794.	3.5	12
33	Adultâ€“onset obesity induced by early life overnutrition could be reversed by caloric restriction. <i>FASEB Journal</i> , 2013, 27, 640.2.	0.5	0
34	IMA: an R package for high-throughput analysis of Illumina's 450K Infinium methylation data. <i>Bioinformatics</i> , 2012, 28, 729-730.	4.1	275
35	Dietary Folate Deficiency Blocks Prostate Cancer Progression in the TRAMP Model. <i>Cancer Prevention Research</i> , 2011, 4, 1825-1834.	1.5	39
36	Mild folate deficiency induces genetic and epigenetic instability and phenotype changes in prostate cancer cells. <i>BMC Biology</i> , 2010, 8, 6.	3.8	68

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37	Tissue specific DNA methylation of CpG islands in normal human adult somatic tissues distinguishes neural from non-neural tissues. <i>Epigenetics</i> , 2010, 5, 527-538.	2.7	76
38	Polyamine biosynthesis impacts cellular folate requirements necessary to maintain <i>S-adenosylmethionine</i> and nucleotide pools. <i>FASEB Journal</i> , 2009, 23, 2888-2897.	0.5	51
39	Epigenetic silencing of the kinase tumor suppressor WNK2 is tumor-type and tumor-grade specific. <i>Neuro-Oncology</i> , 2009, 11, 414-422.	1.2	50
40	Loss of the SMRT/NCoR2 Corepressor Correlates with JAG2 Overexpression in Multiple Myeloma. <i>Cancer Research</i> , 2009, 69, 4380-4387.	0.9	64
41	Tissue specific differentially methylated regions (TDMR): Changes in DNA methylation during development. <i>Genomics</i> , 2009, 93, 130-139.	2.9	116
42	Restriction Landmark Genomic Scanning: Analysis of CpG Islands in Genomes by 2D Gel Electrophoresis. <i>Methods in Molecular Biology</i> , 2009, 507, 131-148.	0.9	17
43	Phenotype-Specific CpG Island Methylation Events in a Murine Model of Prostate Cancer. <i>Cancer Research</i> , 2008, 68, 4173-4182.	0.9	18
44	Frequently Methylated Tumor Suppressor Genes in Head and Neck Squamous Cell Carcinoma. <i>Cancer Research</i> , 2008, 68, 4494-4499.	0.9	115
45	Prostate-Specific Membrane Antigen Expression Is a Potential Prognostic Marker in Endometrial Adenocarcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 571-577.	2.5	21
46	A novel role for mitochondria in regulating epigenetic modifications in the nucleus. <i>Cancer Biology and Therapy</i> , 2008, 7, 1182-1190.	3.4	189
47	Identification of Novel Methylation Markers in Cervical Cancer Using Restriction Landmark Genomic Scanning. <i>Cancer Research</i> , 2008, 68, 2489-2497.	0.9	63
48	Stage-Specific Alterations of DNA Methyltransferase Expression, DNA Hypermethylation, and DNA Hypomethylation during Prostate Cancer Progression in the Transgenic Adenocarcinoma of Mouse Prostate Model. <i>Molecular Cancer Research</i> , 2008, 6, 1365-1374.	3.4	68
49	A unique configuration of genome-wide DNA methylation patterns in the testis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 228-233.	7.1	149
50	Identification of DNA Methylation in 3' Genomic Regions that are Associated with Upregulation of Gene Expression in Colorectal Cancer. <i>Epigenetics</i> , 2007, 2, 161-172.	2.7	35
51	Developmental acquisition of genome-wide DNA methylation occurs prior to meiosis in male germ cells. <i>Developmental Biology</i> , 2007, 307, 368-379.	2.0	210
52	Restriction Landmark Genomic Scanning (RLGS) spot identification by second generation virtual RLGS in multiple genomes with multiple enzyme combinations. <i>BMC Genomics</i> , 2007, 8, 446.	2.8	37
53	SMRT; Not So Smart in Multiple Myeloma. <i>Blood</i> , 2007, 110, 4137-4137.	1.4	1
54	DNA copy number gains in head and neck squamous cell carcinoma. <i>Oncogene</i> , 2006, 25, 1424-1433.	5.9	49

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55	Contour Area Filtering of two-dimensional electrophoresis images. <i>Medical Image Analysis</i> , 2006, 10, 353-365.	11.6	9
56	DNA Methylation Pathway Alterations in an Autochthonous Murine Model of Prostate Cancer. <i>Cancer Research</i> , 2006, 66, 11659-11667.	0.9	49
57	Epigenetic regulation of the tumor suppressor gene TCF21 on 6q23-q24 in lung and head and neck cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 982-987.	7.1	150
58	Genome-wide Analysis of DNA Methylation Changes in Human Malignancies. , 2006, 310, 179-198.		20
59	Discovering DNA Methylation Differences with Restriction Landmark Genomic Scanning. , 2004, , 95-112.		0
60	The Development of CpG Island Methylation Biomarkers Using Restriction Landmark Genomic Scanning. <i>Annals of the New York Academy of Sciences</i> , 2003, 983, 110-119.	3.8	13
61	SLC5A8, a sodium transporter, is a tumor suppressor gene silenced by methylation in human colon aberrant crypt foci and cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 8412-8417.	7.1	264
62	A comprehensive search for DNA amplification in lung cancer identifies inhibitors of apoptosis cIAP1 and cIAP2 as candidate oncogenes. <i>Human Molecular Genetics</i> , 2003, 12, 791-801.	2.9	141
63	Ageing results in hypermethylation of ribosomal DNA in sperm and liver of male rats. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1775-1780.	7.1	177
64	Differential targets of CpG island hypermethylation in primary and metastatic head and neck squamous cell carcinoma (HNSCC). <i>Journal of Medical Genetics</i> , 2003, 40, 25-33.	3.2	53
65	HLTF gene silencing in human colon cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4562-4567.	7.1	145
66	An Ascl Boundary Library for the Studies of Genetic and Epigenetic Alterations in CpG Islands. <i>Genome Research</i> , 2002, 12, 1591-1598.	5.5	24
67	Restriction landmark genome scanning. <i>Methods</i> , 2002, 27, 144-149.	3.8	51
68	Distinct epigenetic phenotypes in seminomatous and nonseminomatous testicular germ cell tumors. <i>Oncogene</i> , 2002, 21, 3909-3916.	5.9	161
69	The study of aberrant methylation in cancer via restriction landmark genomic scanning. <i>Oncogene</i> , 2002, 21, 5414-5426.	5.9	76
70	Global Methylation Profiling of Lung Cancer Identifies Novel Methylated Genes. <i>Neoplasia</i> , 2001, 3, 314-323.	5.3	76
71	Novel methylation targets in de novo acute myeloid leukemia with prevalence of chromosome 11 loci. <i>Blood</i> , 2001, 97, 3226-3233.	1.4	91
72	Aberrant hypermethylation of the major breakpoint cluster region in 17p11.2 in medulloblastomas but not supratentorial PNETs. <i>Genes Chromosomes and Cancer</i> , 2001, 30, 38-47.	2.8	57

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73	Excessive CpG island hypermethylation in cancer cell lines versus primary human malignancies. <i>Human Molecular Genetics</i> , 2001, 10, 1413-1419.	2.9	198
74	Aberrant hypermethylation of the major breakpoint cluster region in 17p11.2 in medulloblastomas but not supratentorial PNETs. <i>Genes Chromosomes and Cancer</i> , 2001, 30, 38-47.	2.8	18
75	Aberrant CpG-island methylation has non-random and tumour-type-specific patterns. <i>Nature Genetics</i> , 2000, 24, 132-138.	21.4	1,292
76	Methylation of the estrogen receptor- α gene promoter is selectively increased in proliferating human aortic smooth muscle cells. <i>Cardiovascular Research</i> , 2000, 46, 172-179.	3.8	115
77	Gene amplification in PNETs/medulloblastomas: mapping of a novel amplified gene within the MYCN amplicon. <i>Journal of Medical Genetics</i> , 2000, 37, 501-509.	3.2	46
78	A New Tool for the Rapid Cloning of Amplified and Hypermethylated Human DNA Sequences from Restriction Landmark Genome Scanning Gels. <i>Genomics</i> , 1999, 58, 254-262.	2.9	74
79	Physical Characterization of the Chromosomal Rearrangements That Accompany the Transgene Insertion in the Chakragati Mouse Mutant. <i>Genomics</i> , 1997, 45, 562-571.	2.9	10
80	Genetic Characterization of the Chromosomal Rearrangements That Accompany the Transgene Insertion in the Chakragati Mouse Mutant. <i>Genomics</i> , 1997, 45, 572-579.	2.9	9