Daniel J Weisenberger

List of Publications by Year in descending order

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		6254	12272
147	105,388	80	133
apers	citations	h-index	g-index
151	151	151	104366
ll docs	docs citations	times ranked	citing authors
151 ll docs	151 docs citations	151 times ranked	10436 citing auth

#	Article	IF	CITATIONS
1	Albumin levels predict prognosis in advanced renal cell carcinoma treated with tyrosine kinase inhibitors: a systematic review and meta-analysis. Urologic Oncology: Seminars and Original Investigations, 2022, 40, 12.e13-12.e22.	1.6	6
2	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. Molecular Oncology, 2022, 16, 1913-1930.	4.6	1
3	Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues. Nature Biotechnology, 2022, 40, 720-730.	17.5	22
4	Abstract 3736: SETD2 aberrancy enhanced the synergetic anti-tumor effects of DNA hypomethylating agents and PARP inhibitors in aggressive clear cell renal cell carcinoma. Cancer Research, 2022, 82, 3736-3736.	0.9	0
5	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. Frontiers in Oncology, 2021, 11, 614927.	2.8	5
6	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. Communications Biology, 2021, 4, 769.	4.4	65
7	Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. Genome Medicine, 2021, 13, 130.	8.2	12
8	Racial Disparities in Epigenetic Aging of the Right vs Left Colon. Journal of the National Cancer Institute, 2021, 113, 1779-1782.	6.3	23
9	Immunogenic cell death pathway polymorphisms for predicting oxaliplatin efficacy in metastatic colorectal cancer. , 2020, 8, e001714.		23
10	Cell death and survival pathways in Alzheimer's disease: an integrative hypothesis testing approach utilizing -omic data sets. Neurobiology of Aging, 2020, 95, 15-25.	3.1	23
11	Aberrant DNA methylation of miRNAs in Fuchs endothelial corneal dystrophy. Scientific Reports, 2019, 9, 16385.	3.3	16
12	The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. Genes, 2019, 10, 172.	2.4	134
13	Impact of polymorphisms within genes involved in regulating DNA methylation in patients with metastatic colorectal cancer enrolled in three independent, randomised, open-label clinical trials: a meta-analysis from TRIBE, MAVERICC and FIRE-3. European Journal of Cancer, 2019, 111, 138-147.	2.8	4
14	AMPK variant, a candidate of novel predictor for chemotherapy in metastatic colorectal cancer: A metaâ€analysis using TRIBE, MAVERICC and FIRE3. International Journal of Cancer, 2019, 145, 2082-2090.	5.1	4
15	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. Cancer Prevention Research, 2019, 12, 781-790.	1.5	5
16	Th17 cell pathway-related genetic variants in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC, and FIRE-3 Journal of Clinical Oncology, 2019, 37, 594-594.	1.6	0
17	Genetic variants in RNA binding protein (RBP) to predict outcome in metastatic colorectal cancer (mCRC): Data from FIRE-3, TRIBE, and MAVERICC trials Journal of Clinical Oncology, 2019, 37, 3545-3545.	1.6	0
18	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277

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19	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
20	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
21	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
22	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
23	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
24	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
25	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
26	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
27	IncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic IncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	16.8	400
28	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750
29	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
30	DNA methylation loss in late-replicating domains is linked to mitotic cell division. Nature Genetics, 2018, 50, 591-602.	21.4	258
31	MethyLight and Digital MethyLight. Methods in Molecular Biology, 2018, 1708, 497-513.	0.9	11
32	Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. Theranostics, 2018, 8, 4520-4534.	10.0	40
33	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGIâ€110) in Hepatocellular Carcinoma. Hepatology, 2018, 68, 1412-1428.	7.3	48
34	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
35	Abstract 779: Integrative analysis reveals therapeutic targets to the DNA methyltransferase inhibitor SGI-110 in hepatocellular carcinoma. , 2018, , .		0
36	Abstract 5327: DNA methylation loss in late-replicating domains is linked to mitotic cell division. , 2018,		1

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37	Identifying aggressive prostate cancer foci using a DNA methylation classifier. Genome Biology, 2017, 18, 3.	8.8	43
38	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
39	A Clinically Distinct and â€~Atypical' Subgroup of Head and Neck Cancers Positive for a CpG Island Methylator Phenotype. EBioMedicine, 2017, 17, 22-23.	6.1	0
40	DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. Epigenetics, 2017, 12, 416-432.	2.7	98
41	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
42	Combination Epigenetic Therapy in Advanced Breast Cancer with 5-Azacitidine and Entinostat: A Phase II National Cancer Institute/Stand Up to Cancer Study. Clinical Cancer Research, 2017, 23, 2691-2701.	7.0	106
43	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
44	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
45	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
46	The genomic landscape of tuberous sclerosis complex. Nature Communications, 2017, 8, 15816.	12.8	154
47	Combination epigenetic therapy in metastatic colorectal cancer (mCRC) with subcutaneous 5-azacitidine and entinostat: a phase 2 consortium/stand Up 2 cancer study. Oncotarget, 2017, 8, 35326-35338.	1.8	66
48	Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. PLoS ONE, 2017, 12, e0175112.	2.5	26
49	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. Oncotarget, 2017, 8, 5439-5448.	1.8	17
50	Genetic and Epigenetic Alterations in Bladder Cancer. International Neurourology Journal, 2016, 20, S84-94.	1.2	49
51	Networks and Consortia for Epigenetic Drug Discovery. , 2016, , 143-166.		1
52	Insights into the Pathogenesis of Anaplastic Large-Cell Lymphoma through Genome-wide DNA Methylation Profiling. Cell Reports, 2016, 17, 596-608.	6.4	55
53	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
54	Promoter methylation of ITF2, but not APC, is associated with microsatellite instability in two populations of colorectal cancer patients. BMC Cancer, 2016, 16, 113.	2.6	7

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55	Identification of DNA Methylation–Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. Cancer Research, 2016, 76, 1954-1964.	0.9	28
56	Effects of folylpolyglutamate synthase modulation on global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. Journal of Nutritional Biochemistry, 2016, 29, 27-35.	4.2	7
57	Promoter Methylation Analysis Reveals That <i>KCNA5</i> Ion Channel Silencing Supports Ewing Sarcoma Cell Proliferation. Molecular Cancer Research, 2016, 14, 26-34.	3.4	22
58	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
59	Clinicopathologic Risk Factor Distributions for <i>MLH1</i> Promoter Region Methylation in CIMP-Positive Tumors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 68-75.	2.5	21
60	Tumor Budding in Colorectal Carcinoma. American Journal of Surgical Pathology, 2015, 39, 1340-1346.	3.7	95
61	Association of the Colorectal CpG Island Methylator Phenotype with Molecular Features, Risk Factors, and Family History. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 512-519.	2.5	71
62	γ-Glutamyl hydrolase modulation significantly influences global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. Genes and Nutrition, 2015, 10, 444.	2.5	10
63	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
64	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
65	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
66	Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. Gastroenterology, 2015, 148, 77-87.e2.	1.3	342
67	Abstract 3288: The KCNA5 promoter is hypermethylated in Ewing sarcoma and silencing contributes to cell proliferation. , 2015, , .		0
68	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
69	Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322.	27.8	2,496
70	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
71	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
72	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	27.8	4,572

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73	Characterizing DNA methylation alterations from The Cancer Genome Atlas. Journal of Clinical Investigation, 2014, 124, 17-23.	8.2	162
74	A Pilot Genome-Scale Profiling of DNA Methylation in Sporadic Pituitary Macroadenomas: Association with Tumor Invasion and Histopathological Subtype. PLoS ONE, 2014, 9, e96178.	2.5	36
75	Molecular subtypes of colorectal cancer in relation to disease survival Journal of Clinical Oncology, 2014, 32, 451-451.	1.6	0
76	Whole-genome bisulfite sequencing of a complex karyotype AML and identification of regulatory aberrations distinct from normal karyotype AML. Journal of Clinical Oncology, 2014, 32, 11075-11075.	1.6	0
77	3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. BMC Pharmacology & Toxicology, 2013, 14, 11.	2.4	21
78	Alterations in Deoxyribonucleic Acid (DNA) Methylation Patterns of Calca, Timp3, Mmp2, and Igf2r Are Associated With Chronic Cystitis in a Cyclophosphamide-induced Mouse Model. Urology, 2013, 82, 253.e9-253.e15.	1.0	4
79	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
80	Associations Between Colorectal Cancer Molecular Markers and Pathways With Clinicopathologic Features in Older Women. Gastroenterology, 2013, 145, 348-356.e2.	1.3	49
81	Integrated analysis of genomeâ€wide copy number alterations and gene expression in microsatellite stable, CpG island methylator phenotypeâ€negative colon cancer. Genes Chromosomes and Cancer, 2013, 52, 450-466.	2.8	51
82	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
83	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
84	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
85	Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. Neurosurgical Focus, 2013, 35, E3.	2.3	28
86	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. Nucleic Acids Research, 2013, 41, e90-e90.	14.5	647
87	DNA Methylation in the Malignant Transformation of Meningiomas. PLoS ONE, 2013, 8, e54114.	2.5	67
88	Tea and Chocolate Consumption and Colorectal Cancer Risk by Molecularly Defined Subtypes in a Prospective Cohort Study of Older Women: Presidential Poster. American Journal of Gastroenterology, 2013, 108, S635-S636.	0.4	1
89	Alterations of immune response of non-small cell lung cancer with Azacytidine. Oncotarget, 2013, 4, 2067-2079.	1.8	336
90	Associations Between Intake of Folate and Related Micronutrients with Molecularly Defined Colorectal Cancer Risks in the Iowa Women's Health Study. Nutrition and Cancer, 2012, 64, 899-910.	2.0	33

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91	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. Genome Research, 2012, 22, 271-282.	5.5	527
92	Cancer Risks for the Relatives of Colorectal Cancer Cases with a Methylated <i>MLH1</i> Promoter Region: Data from the Colorectal Cancer Family Registry. Cancer Prevention Research, 2012, 5, 328-335.	1.5	12
93	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. Gut, 2012, 61, 1299-1305.	12.1	36
94	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
95	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
96	cis-Expression QTL Analysis of Established Colorectal Cancer Risk Variants in Colon Tumors and Adjacent Normal Tissue. PLoS ONE, 2012, 7, e30477.	2.5	55
97	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina–associated domains. Nature Genetics, 2012, 44, 40-46.	21.4	588
98	Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. PLoS ONE, 2012, 7, e50266.	2.5	103
99	Abstract 5518: Clinicopathologic associations with colorectal cancer molecular pathways in a cohort study of older women. , 2012, , .		0
100	Abstract 4492: Colorectal cancer survival by molecular subtypes in a population-based cohort of older women. , 2012, , .		0
101	Frequency of Deletions of EPCAM (TACSTD1) in MSH2-Associated Lynch Syndrome Cases. Journal of Molecular Diagnostics, 2011, 13, 93-99.	2.8	79
102	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. Nature Biotechnology, 2011, 29, 1132-1144.	17.5	509
103	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	27.8	6,541
104	Alcohol Intake and Colorectal Cancer Risk by Molecularly Defined Subtypes in a Prospective Study of Older Women. Cancer Prevention Research, 2011, 4, 2035-2043.	1.5	17
105	Epigenetic Subgroups of Esophageal and Gastric Adenocarcinoma with Differential GATA5 DNA Methylation Associated with Clinical and Lifestyle Factors. PLoS ONE, 2011, 6, e25985.	2.5	10
106	Modeling measurement error in tumor characterization studies. BMC Bioinformatics, 2011, 12, 284.	2.6	3
107	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer. , 2011, , .		5
108	Abstract 1620: Effects of Î ³ -glutamyl hydrolase and folylpolyglutamyl synthase modulation on		0

gene-specific promoter CpG island methylation. , 2011, , .

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109	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	16.8	2,078
110	Cigarette Smoking and Colorectal Cancer Risk by Molecularly Defined Subtypes. Journal of the National Cancer Institute, 2010, 102, 1012-1022.	6.3	261
111	Unique DNA Methylation Patterns Distinguish Noninvasive and Invasive Urothelial Cancers and Establish an Epigenetic Field Defect in Premalignant Tissue. Cancer Research, 2010, 70, 8169-8178.	0.9	148
112	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. Genome Research, 2010, 20, 440-446.	5.5	740
113	Abstract 155: A comparison of DNA methylation in identical twins discordant for Hodgkin lymphoma. , 2010, , .		0
114	The Relationship of DNA Methylation with Age, Gender and Genotype in Twins and Healthy Controls. PLoS ONE, 2009, 4, e6767.	2.5	311
115	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. Human Molecular Genetics, 2009, 18, 4808-4817.	2.9	230
116	<i>LINE-1</i> methylation in plasma DNA as a biomarker of activity of DNA methylation inhibitors in patients with solid tumors. Epigenetics, 2009, 4, 176-184.	2.7	53
117	The methylenetetrahydrofolate reductase C677T mutation induces cellâ€specific changes in genomic DNA methylation and uracil misincorporation: A possible molecular basis for the siteâ€specific cancer risk modification. International Journal of Cancer, 2009, 124, 1999-2005.	5.1	80
118	Locking in on the human methylome. Nature Biotechnology, 2009, 27, 341-342.	17.5	19
119	MethyLight. Methods in Molecular Biology, 2009, 507, 325-337.	0.9	106
120	Analysis of the Association between CIMP and BRAFV600E in Colorectal Cancer by DNA Methylation Profiling. PLoS ONE, 2009, 4, e8357.	2.5	133
121	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. Laboratory Investigation, 2008, 88, 161-170.	3.7	156
122	DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. Leukemia, 2008, 22, 1035-1043.	7.2	83
123	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	27.8	6,879
124	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. Molecular Cancer, 2008, 7, 62.	19.2	114
125	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. Nucleic Acids Research, 2008, 36, 4689-4698.	14.5	133
126	Molecular Characterization of MSI-H Colorectal Cancer by <i>MLHI</i> Promoter Methylation, Immunohistochemistry, and Mismatch Repair Germline Mutation Screening. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3208-3215.	2.5	207

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127	Epigenetic stem cell signature in cancer. Nature Genetics, 2007, 39, 157-158.	21.4	1,023
128	DNA Methylation in the Human Cerebral Cortex Is Dynamically Regulated throughout the Life Span and Involves Differentiated Neurons. PLoS ONE, 2007, 2, e895.	2.5	375
129	Precision and Performance Characteristics of Bisulfite Conversion and Real-Time PCR (MethyLight) for Quantitative DNA Methylation Analysis. Journal of Molecular Diagnostics, 2006, 8, 209-217.	2.8	361
130	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. Nature Genetics, 2006, 38, 787-793.	21.4	1,715
131	Quantitative analysis of associations between DNA hypermethylation, hypomethylation, and DNMT RNA levels in ovarian tumors. Oncogene, 2006, 25, 2636-2645.	5.9	129
132	CpG island methylator phenotype (CIMP) of colorectal cancer is best characterised by quantitative DNA methylation analysis and prospective cohort studies. Gut, 2006, 55, 1000-1006.	12.1	308
133	Gene-Specific Methylation and Subsequent Risk of Colorectal Adenomas among Participants of the Polyp Prevention Trial. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1219-1223.	2.5	17
134	Footprinting of mammalian promoters: use of a CpG DNA methyltransferase revealing nucleosome positions at a single molecule level. Nucleic Acids Research, 2005, 33, e176-e176.	14.5	185
135	Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. European Journal of Cancer, 2005, 41, 2769-2778.	2.8	109
136	Analysis of repetitive element DNA methylation by MethyLight. Nucleic Acids Research, 2005, 33, 6823-6836.	14.5	636
137	Continuous Zebularine Treatment Effectively Sustains Demethylation in Human Bladder Cancer Cells. Molecular and Cellular Biology, 2004, 24, 1270-1278.	2.3	205
138	Detection of Methylated Apoptosis-Associated Genes in Urine Sediments of Bladder Cancer Patients. Clinical Cancer Research, 2004, 10, 7457-7465.	7.0	202
139	Distinct localization of histone H3 acetylation and H3-K4 methylation to the transcription start sites in the human genome. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7357-7362.	7.1	435
140	Preferential response of cancer cells to zebularine. Cancer Cell, 2004, 6, 151-158.	16.8	282
141	DNA Demethylating Agents. , 2004, , 151-167.		2
142	Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. Molecular Cancer Research, 2004, 2, 62-72.	3.4	74
143	Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. Molecular Cancer Research, 2004, 2, 62-72.	3.4	151
144	Identification and characterization of alternatively spliced variants of DNA methyltransferase 3a in mammalian cells. Gene, 2002, 298, 91-99.	2.2	51

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145	Cell division is required for de novo methylation of CpG islands in bladder cancer cells. Cancer Research, 2002, 62, 2378-84.	0.9	72
146	Histone H3-lysine 9 methylation is associated with aberrant gene silencing in cancer cells and is rapidly reversed by 5-aza-2'-deoxycytidine. Cancer Research, 2002, 62, 6456-61.	0.9	310
147	Cytosine Methylation in a CpG Sequence Leads to Enhanced Reactivity with Benzo[a]pyrene Diol Epoxide That Correlates with a Conformational Change. Journal of Biological Chemistry, 1999, 274, 23948-23955.	3.4	61