Devin C Koestler

List of Publications by Year
in descending order

147 papers	8,209 citations	71102 41 h-index	54911 84 g-index
161 all docs	161 docs citations	161 times ranked	13466 citing authors

#	Article	IF	Citations
1	Variation in placental microRNA expression associates with maternal family history of cardiovascular disease. Journal of Developmental Origins of Health and Disease, 2023, 14, 132-139.	1.4	0
2	Interactions of Age and Blood Immune Factors and Noninvasive Prediction of Glioma Survival. Journal of the National Cancer Institute, 2022, 114, 446-457.	6.3	11
3	Epigenome-wide scan identifies differentially methylated regions for lung cancer using pre-diagnostic peripheral blood. Epigenetics, 2022, 17, 460-472.	2.7	12
4	Selenium-associated differentially expressed microRNAs and their targeted mRNAs across the placental genome in two U.S. birth cohorts. Epigenetics, 2022, 17, 1234-1245.	2.7	3
5	Rates of bone reabsorption and union in mandibular reconstruction using the osteocutaneous radial forearm free flap. Head and Neck, 2022, 44, 420-430.	2.0	5
6	Immune profiles and DNA methylation alterations related with non-muscle-invasive bladder cancer outcomes. Clinical Epigenetics, 2022, 14, 14.	4.1	13
7	shinyOPTIK, a User-Friendly R Shiny Application for Visualizing Cancer Risk Factors and Mortality Across the University of Kansas Cancer Center Catchment Area. JCO Clinical Cancer Informatics, 2022, 6, e2100118.	2.1	4
8	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling. Nature Communications, 2022, 13, 761.	12.8	93
9	A core of differentially methylated CpG loci in gMDSCs isolated from neonatal and adult sources. Clinical Epigenetics, 2022, 14, 27.	4.1	2
10	Human cytomegalovirus alters immune cell profile with potential implications for patient survival in head and neck cancer. Carcinogenesis, 2022, , .	2.8	0
11	A Novel Framework for the Identification of Reference DNA Methylation Libraries for Reference-Based Deconvolution of Cellular Mixtures. Frontiers in Bioinformatics, 2022, 2, .	2.1	6
12	Letter to the Editor: on the stability and internal consistency of component-wise sparse mixture regression-based clustering. Briefings in Bioinformatics, 2022, 23, .	6.5	1
13	Maternal Pre-pregnancy BMI Associates With Sex-Specific Placental microRNA Patterns. Current Developments in Nutrition, 2022, 6, 671.	0.3	0
14	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. Epigenetics, 2021, 16, 770-782.	2.7	12
15	MicroRNA Profiling as a Methodology to Diagnose Ménière's Disease: Potential Application of Machine Learning. Otolaryngology - Head and Neck Surgery, 2021, 164, 399-406.	1.9	11
16	DNA methylation ageing clocks and pancreatic cancer risk: pooled analysis of three prospective nested case-control studies. Epigenetics, 2021, 16, 1306-1316.	2.7	14
17	Comparisons of oral, intestinal, and pancreatic bacterial microbiomes in patients with pancreatic cancer and other gastrointestinal diseases. Journal of Oral Microbiology, 2021, 13, 1887680.	2.7	17
18	A ketogenic diet differentially affects neuron and astrocyte transcription. Journal of Neurochemistry, 2021, 157, 1930-1945.	3.9	15

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19	Identification of a foetal epigenetic compartment in adult human kidney. Epigenetics, 2021, , 1-21.	2.7	0
20	Abstract 774: Methylation-derived biologic age, telomere length, and lung cancer mortality in heavy smokers from CARET. , 2021, , .		0
21	Pre-diagnosis neutrophil-to-lymphocyte ratio and mortality in individuals who develop lung cancer. Cancer Causes and Control, 2021, 32, 1227-1236.	1.8	10
22	Abstract LB086: Methylation-derived neutrophil-to-lymphocyte ratio and lung cancer risk and survival. , 2021, , .		0
23	Low variability in the underlying cellular landscape adversely affects the performance of interaction-based approaches for conducting cell-specific analyses of DNA methylation in bulk samples. Statistical Applications in Genetics and Molecular Biology, 2021, 20, 73-84.	0.6	3
24	Perturbation of BRMS1 interactome reveals pathways that impact metastasis. PLoS ONE, 2021, 16, e0259128.	2.5	0
25	Batch effect reduction of microarray data with dependent samples using an empirical Bayes approach (BRIDGE). Statistical Applications in Genetics and Molecular Biology, 2021, 20, 101-119.	0.6	4
26	Methylation-derived inflammatory measures and lung cancer risk and survival. Clinical Epigenetics, 2021, 13, 222.	4.1	8
27	Epigenome-Wide Association Study Using Prediagnostic Bloods Identifies New Genomic Regions Associated With Pancreatic Cancer Risk. JNCI Cancer Spectrum, 2020, 4, pkaa041.	2.9	8
28	Adherent cell depletion promotes the expansion of renal cell carcinoma infiltrating T cells with optimal characteristics for adoptive transfer. , 2020, 8, e000706.		1
29	Preoperative Risk Factors Predicting Postoperative Complications in Radical Cystectomy for Bladder Cancer. Bladder Cancer, 2020, 6, 151-159.	0.4	2
30	Evolutionary Analysis of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reveals Genomic Divergence with Implications for Universal Vaccine Efficacy. Vaccines, 2020, 8, 591.	4.4	3
31	AHRR methylation in heavy smokers: associations with smoking, lung cancer risk, and lung cancer mortality. BMC Cancer, 2020, 20, 905.	2.6	22
32	Difference in Housing Temperature–Induced Energy Expenditure Elicits Sex–Specific Diet–Induced Metabolic Adaptations in Mice. Obesity, 2020, 28, 1922-1931.	3.0	21
33	Ninety–day ketogenic diet intervention has differential effects on neuronal and astrocytic transcriptional pathways in mouse brain. Alzheimer's and Dementia, 2020, 16, e042387.	0.8	0
34	DNA Methylation–Derived Immune Cell Profiles, CpG Markers of Inflammation, and Pancreatic Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 1577-1585.	2.5	9
35	Randomized Phase IIB Trial of the Lignan Secoisolariciresinol Diglucoside in Premenopausal Women at Increased Risk for Development of Breast Cancer. Cancer Prevention Research, 2020, 13, 623-634.	1.5	16
36	Equivalent change enrichment analysis: assessing equivalent and inverse change in biological pathways between diverse experiments. BMC Genomics, 2020, 21, 180.	2.8	2

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37	Improving the efficiency of clinical trials by standardizing processes for Investigator Initiated Trials. Contemporary Clinical Trials Communications, 2020, 18, 100579.	1.1	3
38	Coexpression of FOXP3 and a Helios isoform enhances the effectiveness of human engineered regulatory T cells. Blood Advances, 2020, 4, 1325-1339.	5.2	23
39	Mitochondrial Haplotype of the Host Stromal Microenvironment Alters Metastasis in a Non-cell Autonomous Manner. Cancer Research, 2020, 80, 1118-1129.	0.9	15
40	Sex and BNIP3 genotype, rather than acute lipid injection, modulate hepatic mitochondrial function and steatosis risk in mice. Journal of Applied Physiology, 2020, 128, 1251-1261.	2.5	12
41	Utilization of Technology to Improve Efficiency in Investigational Drug Management Processes. Journal of Pharmacy Technology, 2020, 36, 84-90.	1.0	0
42	Ewing sarcoma family of tumors-derived small extracellular vesicle proteomics identify potential clinical biomarkers. Oncotarget, 2020, 11, 2995-3012.	1.8	25
43	605. Factors Underlying Antifungal Price Trends in the United States. Open Forum Infectious Diseases, 2020, 7, S364-S364.	0.9	0
44	BIOM-13. DNA METHYLATION MARKS GLUCOCORTICOID PATHWAY RESPONSE IN DEXAMETHASONE-TREATED BRAIN TUMOR PATIENTS. Neuro-Oncology, 2020, 22, ii4-ii4.	1.2	0
45	EPCO-25. AN IMMUNOMETHYLOMIC PLATFORM INTEGRATING SYSTEMIC IMMUNE PROFILES AND EPIGENETIC AGE IN NEURO-ONCOLOGY. Neuro-Oncology, 2020, 22, ii74-ii74.	1.2	0
46	Leveraging cell‐specific differentially methylated regions to identify leukocyte infiltration in adipose tissue. Genetic Epidemiology, 2019, 43, 1018-1029.	1.3	1
47	Relevant Word Order Vectorization for Improved Natural Language Processing in Electronic Health Records. Scientific Reports, 2019, 9, 9253.	3.3	9
48	Absence of an embryonic stem cell DNA methylation signature in human cancer. BMC Cancer, 2019, 19, 711.	2.6	6
49	Serum dioxin and DNA methylation in the sperm of operation ranch hand veterans exposed to Agent Orange. Environmental Health, 2019, 18, 91.	4.0	11
50	Systematic evaluation and validation of reference and library selection methods for deconvolution of cord blood DNA methylation data. Clinical Epigenetics, 2019, 11, 125.	4.1	107
51	Effect of Bazedoxifene and Conjugated Estrogen (Duavee) on Breast Cancer Risk Biomarkers in High-Risk Women: A Pilot Study. Cancer Prevention Research, 2019, 12, 711-720.	1.5	22
52	pwrEWAS: a user-friendly tool for comprehensive power estimation for epigenome wide association studies (EWAS). BMC Bioinformatics, 2019, 20, 218.	2.6	44
53	Sex modulates hepatic mitochondrial adaptations to high-fat diet and physical activity. American Journal of Physiology - Endocrinology and Metabolism, 2019, 317, E298-E311.	3.5	37
54	Improving survival prediction using a novel feature selection and feature reduction framework based on the integration of clinical and molecular data. , 2019, , .		6

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55	A Bayesian framework for identifying consistent patterns of microbial abundance between body sites. Statistical Applications in Genetics and Molecular Biology, 2019, 18, .	0.6	4
56	Optimizing Retrieval of Biospecimens Using the Curated Cancer Clinical Outcomes Database (C3OD). Cancer Informatics, 2019, 18, 117693511988683.	1.9	0
57	The Microbiomes of Pancreatic and Duodenum Tissue Overlap and Are Highly Subject Specific but Differ between Pancreatic Cancer and Noncancer Subjects. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 370-383.	2.5	120
58	O-GlcNAc homeostasis contributes to cell fate decisions during hematopoiesis. Journal of Biological Chemistry, 2019, 294, 1363-1379.	3.4	33
59	A phase Ib trial of cabozantinib in combination with durvalumab (MEDI4736) in previously treated patients with advanced gastroesophageal cancer and other gastrointestinal (GI) malignancies (CAMILLA).. Journal of Clinical Oncology, 2019, 37, TPS56-TPS56.	1.6	5
60	Case Study: Electronic Data Capture System Validation at an Academic Institution. , 2019, 25, 16-22.		0
61	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. Journal of Human Genetics, 2018, 63, 339-348.	2.3	18
62	VaDiR: an integrated approach to Variant Detection in RNA. GigaScience, 2018, 7, .	6.4	16
63	Association of Neutrophil-to-Lymphocyte Ratio With Mortality and Cardiovascular Disease in the Jackson Heart Study and Modification by the Duffy Antigen Variant. JAMA Cardiology, 2018, 3, 455.	6.1	130
64	Subject level clustering using a negative binomial model for small transcriptomic studies. BMC Bioinformatics, 2018, 19, 474.	2.6	8
65	IMMU-07. IMMUNE PROFILES IN THE SAN FRANCISCO ADULT GLIOMA STUDY (AGS) USING IMMUNOMETHYLOMICS. Neuro-Oncology, 2018, 20, vi122-vi122.	1.2	0
66	A Curated Cancer Clinical Outcomes Database (C3OD) for accelerating patient recruitment in cancer clinical trials. JAMIA Open, 2018, 1, 166-171.	2.0	11
67	Methylation-derived Neutrophil-to-Lymphocyte Ratio and Lung Cancer Risk in Heavy Smokers. Cancer Prevention Research, 2018, 11, 727-734.	1.5	28
68	Variation in DNA methylation of human blood over a 1-year period using the Illumina MethylationEPIC array. Epigenetics, 2018, 13, 1056-1071.	2.7	39
69	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. Oral Oncology, 2018, 85, 87-94.	1.5	17
70	Tracing human stem cell lineage during development using DNA methylation. Genome Research, 2018, 28, 1285-1295.	5.5	27
71	An optimized library for reference-based deconvolution of whole-blood biospecimens assayed using the Illumina HumanMethylationEPIC BeadArray. Genome Biology, 2018, 19, 64.	8.8	245
72	Reduced mitochondrial reactive oxygen species production in peripheral nerves of mice fed a ketogenic diet. Experimental Physiology, 2018, 103, 1206-1212.	2.0	23

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73	Licofelone Enhances the Efficacy of Paclitaxel in Ovarian Cancer by Reversing Drug Resistance and Tumor Stem-like Properties. Cancer Research, 2018, 78, 4370-4385.	0.9	38
74	Developing a genetic signature to predict drug response in ovarian cancer. Oncotarget, 2018, 9, 14828-14848.	1.8	14
75	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. Nature Methods, 2017, 14, 216-217.	19.0	59
76	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. Clinical Epigenetics, 2017, 9, 10.	4.1	60
77	Integrative epigenetic and genetic pan-cancer somatic alteration portraits. Epigenetics, 2017, 12, 561-574.	2.7	18
78	DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio: An Epigenetic Tool to Explore Cancer Inflammation and Outcomes. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 328-338.	2.5	62
79	Mitochondrial Haplotype Alters Mammary Cancer Tumorigenicity and Metastasis in an Oncogenic Driver–Dependent Manner. Cancer Research, 2017, 77, 6941-6949.	0.9	28
80	Maternal serum PFOA concentration and DNA methylation in cord blood: A pilot study. Environmental Research, 2017, 158, 174-178.	7.5	28
81	The aquaglyceroporin AQP9 contributes to the sex-specific effects of in utero arsenic exposure on placental gene expression. Environmental Health, 2017, 16, 59.	4.0	16
82	Mitochondrial Genomic Backgrounds Affect Nuclear DNA Methylation and Gene Expression. Cancer Research, 2017, 77, 6202-6214.	0.9	51
83	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124
84	Sustained O-GlcNAcylation reprograms mitochondrial function to regulate energy metabolism. Journal of Biological Chemistry, 2017, 292, 14940-14962.	3.4	79
85	digit–a tool fordetection andidentification ofgenomicinterchromosomaltranslocations. Nucleic Acids Research, 2017, 45, gkx010.	14.5	0
86	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. JCO Clinical Cancer Informatics, 2017, 1, 1-15.	2.1	12
87	Preoperative risk factors predicting postoperative complications in radical cystectomy for bladder cancer.. Journal of Clinical Oncology, 2017, 35, 395-395.	1.6	0
88	An ensemble-based Cox proportional hazards regression framework for predicting survival in metastatic castration-resistant prostate cancer (mCRPC) patients. F1000Research, 2016, 5, 2677.	1.6	1
89	Prenatal Programming of Infant Neurobehaviour in a Healthy Population. Paediatric and Perinatal Epidemiology, 2016, 30, 367-375.	1.7	34
90	Epigenetic and genetic burden measures are associated with tumor characteristics in invasive breast carcinoma. Epigenetics, 2016, 11, 344-353.	2.7	14

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91	Enlarged leukocyte referent libraries can explain additional variance in blood-based epigenome-wide association studies. Epigenomics, 2016, 8, 1185-1192.	2.1	14
92	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). BMC Bioinformatics, 2016, 17, 120.	2.6	142
93	Fetal exposures and perinatal influences on the stool microbiota of premature infants. Journal of Maternal-Fetal and Neonatal Medicine, 2016, 29, 99-105.	1.5	42
94	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. Clinical Epigenetics, 2015, 7, 75.	4.1	49
95	CpG island methylation profile in non-invasive oral rinse samples is predictive of oral and pharyngeal carcinoma. Clinical Epigenetics, 2015, 7, 125.	4.1	19
96	Targeted or whole genome sequencing of formalin fixed tissue samples: potential applications in cancer genomics. Oncotarget, 2015, 6, 25943-25961.	1.8	53
97	Genome Wide DNA Methylation Profiles Provide Clues to the Origin and Pathogenesis of Germ Cell Tumors. PLoS ONE, 2015, 10, e0122146.	2.5	63
98	Placental DNA Methylation Related to Both Infant Toenail Mercury and Adverse Neurobehavioral Outcomes. Environmental Health Perspectives, 2015, 123, 723-729.	6.0	80
99	GLI3 Links Environmental Arsenic Exposure and Human Fetal Growth. EBioMedicine, 2015, 2, 536-543.	6.1	15
100	DNA methylation changes in the placenta are associated with fetal manganese exposure. Reproductive Toxicology, 2015, 57, 43-49.	2.9	43
101	Associations between Gut Microbial Colonization in Early Life and Respiratory Outcomes in Cystic Fibrosis. Journal of Pediatrics, 2015, 167, 138-147.e3.	1.8	131
102	Differential DNA methylation in umbilical cord blood of infants exposed to mercury and arsenic *in utero*. Epigenetics, 2015, 10, 508-515.	2.7	111
103	Model-Based Clustering of DNA Methylation Array Data. Translational Bioinformatics, 2015, , 91-123.	0.0	1
104	Leukocyte-adjusted epigenome-wide association studies of blood from solid tumor patients. Epigenetics, 2014, 9, 884-895.	2.7	35
105	Individualizing Care for Ovarian Cancer Patients Using Big Data. Journal of the National Cancer Institute, 2014, 106, .	6.3	1
106	The era of integrative genomics: more data or better methods?. Epigenomics, 2014, 6, 463-467.	2.1	2
107	Age-related DNA methylation in normal breast tissue and its relationship with invasive breast tumor methylation. Epigenetics, 2014, 9, 268-275.	2.7	67
108	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. Modern Pathology, 2014, 27, 145-155.	5.5	40

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109	Integrative genomic analysis identifies epigenetic marks that mediate genetic risk for epithelial ovarian cancer. BMC Medical Genomics, 2014, 7, 8.	1.5	32
110	Sex-specific associations between placental leptin promoter DNA methylation and infant neurobehavior. Psychoneuroendocrinology, 2014, 40, 1-9.	2.7	54
111	In utero arsenic exposure and fetal immune repertoire in a US pregnancy cohort. Clinical Immunology, 2014, 155, 188-197.	3.2	74
112	Methylation of leukocyte DNA and ovarian cancer: relationships with disease status and outcome. BMC Medical Genomics, 2014, 7, 21.	1.5	21
113	Placental FKBP5 Genetic and Epigenetic Variation Is Associated with Infant Neurobehavioral Outcomes in the RICHS Cohort. PLoS ONE, 2014, 9, e104913.	2.5	97
114	A recursively partitioned mixture model for clustering time-course gene expression data. Translational Cancer Research, 2014, 3, 217-232.	1.0	4
115	Integrative clustering methods for high-dimensional molecular data. Translational Cancer Research, 2014, 3, 202-216.	1.0	32
116	Ensemble-based methods for forecasting census in hospital units. BMC Medical Research Methodology, 2013, 13, 67.	3.1	12
117	Placental DNA methylation alterations associated with maternal tobacco smoking at the *RUNX3* gene are also associated with gestational age. Epigenomics, 2013, 5, 619-630.	2.1	89
118	Review of processing and analysis methods for DNA methylation array data. British Journal of Cancer, 2013, 109, 1394-1402.	6.4	164
119	Association between In Utero arsenic exposure, placental gene expression, and infant birth weight: a US birth cohort study. Environmental Health, 2013, 12, 58.	4.0	68
120	Tissue-specific Leptin promoter DNA methylation is associated with maternal and infant perinatal factors. Molecular and Cellular Endocrinology, 2013, 381, 160-167.	3.2	97
121	Semisupervised Methods for Analyzing High-dimensional Genomic Data. , 2013, , 93-106.		0
122	Recursively partitioned mixture model clustering of DNA methylation data using biologically informed correlation structures. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 225-40.	0.6	13
123	Epigenome-wide ovarian cancer analysis identifies a methylation profile differentiating clear-cell histology with epigenetic silencing of the HERG K+ channel. Human Molecular Genetics, 2013, 22, 3038-3047.	2.9	60
124	Differential DNA Methylation in Umbilical Cord Blood of Infants Exposed to Low Levels of Arsenic *in Utero*. Environmental Health Perspectives, 2013, 121, 971-977.	6.0	166
125	Placental *HTR2A* methylation is associated with infant neurobehavioral outcomes. Epigenetics, 2013, 8, 796-801.	2.7	61
126	Blood-based profiles of DNA methylation predict the underlying distribution of cell types. Epigenetics, 2013, 8, 816-826.	2.7	213

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127	Neonatal intensive care unit: predictive models for length of stay. Journal of Perinatology, 2013, 33, 147-153.	2.0	38
128	Developmental genes targeted for epigenetic variation between twin-twin transfusion syndrome children. Clinical Epigenetics, 2013, 5, 18.	4.1	6
129	Abstract 3640: Age-related DNA methylation in normal breast tissues.. , 2013, , .		0
130	Abstract 3642: Profiles of DNA methylation in peripheral blood are associated with bladder cancer survival.. , 2013, , .		0
131	Epigenetic biomarkers of T-cells in human glioma. Epigenetics, 2012, 7, 1391-1402.	2.7	31
132	Peripheral Blood Immune Cell Methylation Profiles Are Associated with Nonhematopoietic Cancers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1293-1302.	2.5	103
133	DNA methylation arrays as surrogate measures of cell mixture distribution. BMC Bioinformatics, 2012, 13, 86.	2.6	2,563
134	Peripheral blood DNA methylation profiles are indicative of head and neck squamous cell carcinoma: An epigenome-wide association study. Epigenetics, 2012, 7, 291-299.	2.7	84
135	<i>In Utero</i> Exposures, Infant Growth, and DNA Methylation of Repetitive Elements and Developmentally Related Genes in Human Placenta. Environmental Health Perspectives, 2012, 120, 296-302.	6.0	174
136	Placenta-Imprinted Gene Expression Association of Infant Neurobehavior. Journal of Pediatrics, 2012, 160, 854-860.e2.	1.8	36
137	Nonfilter and filter cigarette consumption and the incidence of lung cancer by histological type in Japan and the United States: Analysis of 30â€year data from populationâ€based cancer registries. International Journal of Cancer, 2011, 128, 1918-1928.	5.1	59
138	Association of secondhand smoke exposures with DNA methylation in bladder carcinomas. Cancer Causes and Control, 2011, 22, 1205-1213.	1.8	38
139	DNA Methylation, Isocitrate Dehydrogenase Mutation, and Survival in Glioma. Journal of the National Cancer Institute, 2011, 103, 143-153.	6.3	224
140	DNA Methylation Array Analysis Identifies Profiles of Blood-Derived DNA Methylation Associated With Bladder Cancer. Journal of Clinical Oncology, 2011, 29, 1133-1139.	1.6	118
141	Infant growth restriction is associated with distinct patterns of DNA methylation in human placentas. Epigenetics, 2011, 6, 920-927.	2.7	133
142	Polycomb group genes are targets of aberrant DNA methylation in renal cell carcinoma. Epigenetics, 2011, 6, 703-709.	2.7	27
143	Birthweight is associated with DNA promoter methylation of the glucocorticoid receptor in human placenta. Epigenetics, 2011, 6, 566-572.	2.7	148
144	Downregulated microRNAs in the differential diagnosis of malignant pleural mesothelioma. International Journal of Cancer, 2010, 127, 2859-2869.	5.1	93

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145	DNA methylation profiles delineate etiologic heterogeneity and clinically important subgroups of bladder cancer. Carcinogenesis, 2010, 31, 1972-1976.	2.8	29
146	Semi-supervised recursively partitioned mixture models for identifying cancer subtypes. Bioinformatics, 2010, 26, 2578-2585.	4.1	114
147	Patients with type 2 diabetes and elevated fibrosisâ€4 are underâ€referred to hepatology and have unrecognized hepatic decompensation. Journal of Gastroenterology and Hepatology (Australia), 0, , .	2.8	2