

Devin C Koestler

List of Publications by Year in descending order

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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	DNA methylation arrays as surrogate measures of cell mixture distribution. BMC Bioinformatics, 2012, 13, 86.	2.6	2,563
2	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
3	DNA Methylation, Isocitrate Dehydrogenase Mutation, and Survival in Glioma. Journal of the National Cancer Institute, 2011, 103, 143-153.	6.3	224
4	Blood-based profiles of DNA methylation predict the underlying distribution of cell types. Epigenetics, 2013, 8, 816-826.	2.7	213
5	<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
6	Differential DNA Methylation in Umbilical Cord Blood of Infants Exposed to Low Levels of Arsenic <i>in Utero</i> . Environmental Health Perspectives, 2013, 121, 971-977.	6.0	166
7	Review of processing and analysis methods for DNA methylation array data. British Journal of Cancer, 2013, 109, 1394-1402.	6.4	164
8	Birthweight is associated with DNA promoter methylation of the glucocorticoid receptor in human placenta. Epigenetics, 2011, 6, 566-572.	2.7	148
9	Improving cell mixture deconvolution by identifying optimal DNA methylation libraries (IDOL). BMC Bioinformatics, 2016, 17, 120.	2.6	142
10	Infant growth restriction is associated with distinct patterns of DNA methylation in human placentas. Epigenetics, 2011, 6, 920-927.	2.7	133
11	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
12	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
13	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
14	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
15	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
16	Semi-supervised recursively partitioned mixture models for identifying cancer subtypes. Bioinformatics, 2010, 26, 2578-2585.	4.1	114
17	Differential DNA methylation in umbilical cord blood of infants exposed to mercury and arsenic <i>in utero</i> . Epigenetics, 2015, 10, 508-515.	2.7	111
18	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

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19	Peripheral Blood Immune Cell Methylation Profiles Are Associated with Nonhematopoietic Cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1293-1302.	2.5	103
20	Tissue-specific Leptin promoter DNA methylation is associated with maternal and infant perinatal factors. <i>Molecular and Cellular Endocrinology</i> , 2013, 381, 160-167.	3.2	97
21	Placental FKBP5 Genetic and Epigenetic Variation Is Associated with Infant Neurobehavioral Outcomes in the RICHs Cohort. <i>PLoS ONE</i> , 2014, 9, e104913.	2.5	97
22	Downregulated microRNAs in the differential diagnosis of malignant pleural mesothelioma. <i>International Journal of Cancer</i> , 2010, 127, 2859-2869.	5.1	93
23	Enhanced cell deconvolution of peripheral blood using DNA methylation for high-resolution immune profiling. <i>Nature Communications</i> , 2022, 13, 761.	12.8	93
24	Placental DNA methylation alterations associated with maternal tobacco smoking at the <i>RUNX3</i> gene are also associated with gestational age. <i>Epigenomics</i> , 2013, 5, 619-630.	2.1	89
25	Peripheral blood DNA methylation profiles are indicative of head and neck squamous cell carcinoma: An epigenome-wide association study. <i>Epigenetics</i> , 2012, 7, 291-299.	2.7	84
26	Placental DNA Methylation Related to Both Infant Toenail Mercury and Adverse Neurobehavioral Outcomes. <i>Environmental Health Perspectives</i> , 2015, 123, 723-729.	6.0	80
27	Sustained O-GlcNAcylation reprograms mitochondrial function to regulate energy metabolism. <i>Journal of Biological Chemistry</i> , 2017, 292, 14940-14962.	3.4	79
28	In utero arsenic exposure and fetal immune repertoire in a US pregnancy cohort. <i>Clinical Immunology</i> , 2014, 155, 188-197.	3.2	74
29	Association between In Utero arsenic exposure, placental gene expression, and infant birth weight: a US birth cohort study. <i>Environmental Health</i> , 2013, 12, 58.	4.0	68
30	Age-related DNA methylation in normal breast tissue and its relationship with invasive breast tumor methylation. <i>Epigenetics</i> , 2014, 9, 268-275.	2.7	67
31	Genome Wide DNA Methylation Profiles Provide Clues to the Origin and Pathogenesis of Germ Cell Tumors. <i>PLoS ONE</i> , 2015, 10, e0122146.	2.5	63
32	DNA Methylation-Derived Neutrophil-to-Lymphocyte Ratio: An Epigenetic Tool to Explore Cancer Inflammation and Outcomes. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 328-338.	2.5	62
33	Placental <i>HTR2A</i> methylation is associated with infant neurobehavioral outcomes. <i>Epigenetics</i> , 2013, 8, 796-801.	2.7	61
34	Epigenome-wide ovarian cancer analysis identifies a methylation profile differentiating clear-cell histology with epigenetic silencing of the HERG K ⁺ channel. <i>Human Molecular Genetics</i> , 2013, 22, 3038-3047.	2.9	60
35	Immunomethylomic approach to explore the blood neutrophil lymphocyte ratio (NLR) in glioma survival. <i>Clinical Epigenetics</i> , 2017, 9, 10.	4.1	60
36	Nonfilter and filter cigarette consumption and the incidence of lung cancer by histological type in Japan and the United States: Analysis of 30-year data from population-based cancer registries. <i>International Journal of Cancer</i> , 2011, 128, 1918-1928.	5.1	59

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37	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	19.0	59
38	Sex-specific associations between placental leptin promoter DNA methylation and infant neurobehavior. <i>Psychoneuroendocrinology</i> , 2014, 40, 1-9.	2.7	54
39	Targeted or whole genome sequencing of formalin fixed tissue samples: potential applications in cancer genomics. <i>Oncotarget</i> , 2015, 6, 25943-25961.	1.8	53
40	Mitochondrial Genomic Backgrounds Affect Nuclear DNA Methylation and Gene Expression. <i>Cancer Research</i> , 2017, 77, 6202-6214.	0.9	51
41	DNA methylation in ductal carcinoma in situ related with future development of invasive breast cancer. <i>Clinical Epigenetics</i> , 2015, 7, 75.	4.1	49
42	pwrEWAS: a user-friendly tool for comprehensive power estimation for epigenome wide association studies (EWAS). <i>BMC Bioinformatics</i> , 2019, 20, 218.	2.6	44
43	DNA methylation changes in the placenta are associated with fetal manganese exposure. <i>Reproductive Toxicology</i> , 2015, 57, 43-49.	2.9	43
44	Fetal exposures and perinatal influences on the stool microbiota of premature infants. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2016, 29, 99-105.	1.5	42
45	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. <i>Modern Pathology</i> , 2014, 27, 145-155.	5.5	40
46	Variation in DNA methylation of human blood over a 1-year period using the Illumina MethylationEPIC array. <i>Epigenetics</i> , 2018, 13, 1056-1071.	2.7	39
47	Association of secondhand smoke exposures with DNA methylation in bladder carcinomas. <i>Cancer Causes and Control</i> , 2011, 22, 1205-1213.	1.8	38
48	Neonatal intensive care unit: predictive models for length of stay. <i>Journal of Perinatology</i> , 2013, 33, 147-153.	2.0	38
49	Licofelone Enhances the Efficacy of Paclitaxel in Ovarian Cancer by Reversing Drug Resistance and Tumor Stem-like Properties. <i>Cancer Research</i> , 2018, 78, 4370-4385.	0.9	38
50	Sex modulates hepatic mitochondrial adaptations to high-fat diet and physical activity. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2019, 317, E298-E311.	3.5	37
51	Placenta-Imprinted Gene Expression Association of Infant Neurobehavior. <i>Journal of Pediatrics</i> , 2012, 160, 854-860.e2.	1.8	36
52	Leukocyte-adjusted epigenome-wide association studies of blood from solid tumor patients. <i>Epigenetics</i> , 2014, 9, 884-895.	2.7	35
53	Prenatal Programming of Infant Neurobehaviour in a Healthy Population. <i>Paediatric and Perinatal Epidemiology</i> , 2016, 30, 367-375.	1.7	34
54	O-GlcNAc homeostasis contributes to cell fate decisions during hematopoiesis. <i>Journal of Biological Chemistry</i> , 2019, 294, 1363-1379.	3.4	33

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55	Integrative genomic analysis identifies epigenetic marks that mediate genetic risk for epithelial ovarian cancer. <i>BMC Medical Genomics</i> , 2014, 7, 8.	1.5	32
56	Integrative clustering methods for high-dimensional molecular data. <i>Translational Cancer Research</i> , 2014, 3, 202-216.	1.0	32
57	Epigenetic biomarkers of T-cells in human glioma. <i>Epigenetics</i> , 2012, 7, 1391-1402.	2.7	31
58	DNA methylation profiles delineate etiologic heterogeneity and clinically important subgroups of bladder cancer. <i>Carcinogenesis</i> , 2010, 31, 1972-1976.	2.8	29
59	Mitochondrial Haplotype Alters Mammary Cancer Tumorigenicity and Metastasis in an Oncogenic Driver-Dependent Manner. <i>Cancer Research</i> , 2017, 77, 6941-6949.	0.9	28
60	Maternal serum PFOA concentration and DNA methylation in cord blood: A pilot study. <i>Environmental Research</i> , 2017, 158, 174-178.	7.5	28
61	Methylation-derived Neutrophil-to-Lymphocyte Ratio and Lung Cancer Risk in Heavy Smokers. <i>Cancer Prevention Research</i> , 2018, 11, 727-734.	1.5	28
62	Polycomb group genes are targets of aberrant DNA methylation in renal cell carcinoma. <i>Epigenetics</i> , 2011, 6, 703-709.	2.7	27
63	Tracing human stem cell lineage during development using DNA methylation. <i>Genome Research</i> , 2018, 28, 1285-1295.	5.5	27
64	Ewing sarcoma family of tumors-derived small extracellular vesicle proteomics identify potential clinical biomarkers. <i>Oncotarget</i> , 2020, 11, 2995-3012.	1.8	25
65	Reduced mitochondrial reactive oxygen species production in peripheral nerves of mice fed a ketogenic diet. <i>Experimental Physiology</i> , 2018, 103, 1206-1212.	2.0	23
66	Coexpression of FOXP3 and a Helios isoform enhances the effectiveness of human engineered regulatory T cells. <i>Blood Advances</i> , 2020, 4, 1325-1339.	5.2	23
67	Effect of Bazedoxifene and Conjugated Estrogen (Duavee) on Breast Cancer Risk Biomarkers in High-Risk Women: A Pilot Study. <i>Cancer Prevention Research</i> , 2019, 12, 711-720.	1.5	22
68	AHRR methylation in heavy smokers: associations with smoking, lung cancer risk, and lung cancer mortality. <i>BMC Cancer</i> , 2020, 20, 905.	2.6	22
69	Methylation of leukocyte DNA and ovarian cancer: relationships with disease status and outcome. <i>BMC Medical Genomics</i> , 2014, 7, 21.	1.5	21
70	Difference in Housing Temperature-Induced Energy Expenditure Elicits Sex-Specific Diet-Induced Metabolic Adaptations in Mice. <i>Obesity</i> , 2020, 28, 1922-1931.	3.0	21
71	CpG island methylation profile in non-invasive oral rinse samples is predictive of oral and pharyngeal carcinoma. <i>Clinical Epigenetics</i> , 2015, 7, 125.	4.1	19
72	Integrative epigenetic and genetic pan-cancer somatic alteration portraits. <i>Epigenetics</i> , 2017, 12, 561-574.	2.7	18

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73	Mediation analysis of alcohol consumption, DNA methylation, and epithelial ovarian cancer. <i>Journal of Human Genetics</i> , 2018, 63, 339-348.	2.3	18
74	DNA methylation derived systemic inflammation indices are associated with head and neck cancer development and survival. <i>Oral Oncology</i> , 2018, 85, 87-94.	1.5	17
75	Comparisons of oral, intestinal, and pancreatic bacterial microbiomes in patients with pancreatic cancer and other gastrointestinal diseases. <i>Journal of Oral Microbiology</i> , 2021, 13, 1887680.	2.7	17
76	The aquaglyceroporin AQP9 contributes to the sex-specific effects of in utero arsenic exposure on placental gene expression. <i>Environmental Health</i> , 2017, 16, 59.	4.0	16
77	VaDiR: an integrated approach to Variant Detection in RNA. <i>GigaScience</i> , 2018, 7, .	6.4	16
78	Randomized Phase IIB Trial of the Lignan Secoisolariciresinol Diglucoside in Premenopausal Women at Increased Risk for Development of Breast Cancer. <i>Cancer Prevention Research</i> , 2020, 13, 623-634.	1.5	16
79	GLI3 Links Environmental Arsenic Exposure and Human Fetal Growth. <i>EBioMedicine</i> , 2015, 2, 536-543.	6.1	15
80	Mitochondrial Haplotype of the Host Stromal Microenvironment Alters Metastasis in a Non-cell Autonomous Manner. <i>Cancer Research</i> , 2020, 80, 1118-1129.	0.9	15
81	A ketogenic diet differentially affects neuron and astrocyte transcription. <i>Journal of Neurochemistry</i> , 2021, 157, 1930-1945.	3.9	15
82	Epigenetic and genetic burden measures are associated with tumor characteristics in invasive breast carcinoma. <i>Epigenetics</i> , 2016, 11, 344-353.	2.7	14
83	Enlarged leukocyte referent libraries can explain additional variance in blood-based epigenome-wide association studies. <i>Epigenomics</i> , 2016, 8, 1185-1192.	2.1	14
84	DNA methylation ageing clocks and pancreatic cancer risk: pooled analysis of three prospective nested case-control studies. <i>Epigenetics</i> , 2021, 16, 1306-1316.	2.7	14
85	Developing a genetic signature to predict drug response in ovarian cancer. <i>Oncotarget</i> , 2018, 9, 14828-14848.	1.8	14
86	Recursively partitioned mixture model clustering of DNA methylation data using biologically informed correlation structures. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 225-40.	0.6	13
87	Immune profiles and DNA methylation alterations related with non-muscle-invasive bladder cancer outcomes. <i>Clinical Epigenetics</i> , 2022, 14, 14.	4.1	13
88	Ensemble-based methods for forecasting census in hospital units. <i>BMC Medical Research Methodology</i> , 2013, 13, 67.	3.1	12
89	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Clinical Cancer Informatics</i> , 2017, 1, 1-15.	2.1	12
90	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021, 16, 770-782.	2.7	12

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91	Sex and BNIP3 genotype, rather than acute lipid injection, modulate hepatic mitochondrial function and steatosis risk in mice. <i>Journal of Applied Physiology</i> , 2020, 128, 1251-1261.	2.5	12
92	Epigenome-wide scan identifies differentially methylated regions for lung cancer using pre-diagnostic peripheral blood. <i>Epigenetics</i> , 2022, 17, 460-472.	2.7	12
93	A Curated Cancer Clinical Outcomes Database (C3OD) for accelerating patient recruitment in cancer clinical trials. <i>JAMIA Open</i> , 2018, 1, 166-171.	2.0	11
94	Serum dioxin and DNA methylation in the sperm of operation ranch hand veterans exposed to Agent Orange. <i>Environmental Health</i> , 2019, 18, 91.	4.0	11
95	MicroRNA Profiling as a Methodology to Diagnose MÃ©niÃ©re's Disease: Potential Application of Machine Learning. <i>Otolaryngology - Head and Neck Surgery</i> , 2021, 164, 399-406.	1.9	11
96	Interactions of Age and Blood Immune Factors and Noninvasive Prediction of Glioma Survival. <i>Journal of the National Cancer Institute</i> , 2022, 114, 446-457.	6.3	11
97	Pre-diagnosis neutrophil-to-lymphocyte ratio and mortality in individuals who develop lung cancer. <i>Cancer Causes and Control</i> , 2021, 32, 1227-1236.	1.8	10
98	Relevant Word Order Vectorization for Improved Natural Language Processing in Electronic Health Records. <i>Scientific Reports</i> , 2019, 9, 9253.	3.3	9
99	DNA Methylationâ€Derived Immune Cell Profiles, CpG Markers of Inflammation, and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020, 29, 1577-1585.	2.5	9
100	Subject level clustering using a negative binomial model for small transcriptomic studies. <i>BMC Bioinformatics</i> , 2018, 19, 474.	2.6	8
101	Epigenome-Wide Association Study Using Prediagnostic Bloods Identifies New Genomic Regions Associated With Pancreatic Cancer Risk. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa041.	2.9	8
102	Methylation-derived inflammatory measures and lung cancer risk and survival. <i>Clinical Epigenetics</i> , 2021, 13, 222.	4.1	8
103	Developmental genes targeted for epigenetic variation between twin-twin transfusion syndrome children. <i>Clinical Epigenetics</i> , 2013, 5, 18.	4.1	6
104	Absence of an embryonic stem cell DNA methylation signature in human cancer. <i>BMC Cancer</i> , 2019, 19, 711.	2.6	6
105	Improving survival prediction using a novel feature selection and feature reduction framework based on the integration of clinical and molecular data. , 2019, , .		6
106	A Novel Framework for the Identification of Reference DNA Methylation Libraries for Reference-Based Deconvolution of Cellular Mixtures. <i>Frontiers in Bioinformatics</i> , 2022, 2, .	2.1	6
107	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).. <i>Journal of Clinical Oncology</i> , 2019, 37, TPS56-TPS56.	1.6	5
108	Rates of bone reabsorption and union in mandibular reconstruction using the osteocutaneous radial forearm free flap. <i>Head and Neck</i> , 2022, 44, 420-430.	2.0	5

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109	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
110	A recursively partitioned mixture model for clustering time-course gene expression data. Translational Cancer Research, 2014, 3, 217-232.	1.0	4
111	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
112	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
113	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
114	Improving the efficiency of clinical trials by standardizing processes for Investigator Initiated Trials. Contemporary Clinical Trials Communications, 2020, 18, 100579.	1.1	3
115	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
116	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
117	The era of integrative genomics: more data or better methods?. Epigenomics, 2014, 6, 463-467.	2.1	2
118	Preoperative Risk Factors Predicting Postoperative Complications in Radical Cystectomy for Bladder Cancer. Bladder Cancer, 2020, 6, 151-159.	0.4	2
119	Equivalent change enrichment analysis: assessing equivalent and inverse change in biological pathways between diverse experiments. BMC Genomics, 2020, 21, 180.	2.8	2
120	A core of differentially methylated CpG loci in gMDSCs isolated from neonatal and adult sources. Clinical Epigenetics, 2022, 14, 27.	4.1	2
121	Patients with type 2 diabetes and elevated fibrosis are under-referred to hepatology and have unrecognized hepatic decompensation. Journal of Gastroenterology and Hepatology (Australia), 0, , .	2.8	2
122	Individualizing Care for Ovarian Cancer Patients Using Big Data. Journal of the National Cancer Institute, 2014, 106, .	6.3	1
123	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
124	Leveraging cell-specific differentially methylated regions to identify leukocyte infiltration in adipose tissue. Genetic Epidemiology, 2019, 43, 1018-1029.	1.3	1
125	Adherent cell depletion promotes the expansion of renal cell carcinoma infiltrating T cells with optimal characteristics for adoptive transfer. , 2020, 8, e000706.		1
126	Model-Based Clustering of DNA Methylation Array Data. Translational Bioinformatics, 2015, , 91-123.	0.0	1

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127	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
128	Semisupervised Methods for Analyzing High-dimensional Genomic Data. , 2013, , 93-106.		0
129	digitâ€”a tool fordetection andidentification ofgenomicinterchromosomaltranslocations. Nucleic Acids Research, 2017, 45, gkx010.	14.5	0
130	IMMU-07. IMMUNE PROFILES IN THE SAN FRANCISCO ADULT GLIOMA STUDY (AGS) USING IMMUNOMETHYLOMICS. Neuro-Oncology, 2018, 20, vi122-vi122.	1.2	0
131	Optimizing Retrieval of Biospecimens Using the Curated Cancer Clinical Outcomes Database (C3OD). Cancer Informatics, 2019, 18, 117693511988683.	1.9	0
132	Ninetyâ€”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
133	Utilization of Technology to Improve Efficiency in Investigational Drug Management Processes. Journal of Pharmacy Technology, 2020, 36, 84-90.	1.0	0
134	Identification of a foetal epigenetic compartment in adult human kidney. Epigenetics, 2021, , 1-21.	2.7	0
135	Abstract 774: Methylation-derived biologic age, telomere length, and lung cancer mortality in heavy smokers from CARET. , 2021, , .		0
136	Abstract LB086: Methylation-derived neutrophil-to-lymphocyte ratio and lung cancer risk and survival. , 2021, , .		0
137	Abstract 3640: Age-related DNA methylation in normal breast tissues.. , 2013, , .		0
138	Abstract 3642: Profiles of DNA methylation in peripheral blood are associated with bladder cancer survival.. , 2013, , .		0
139	Preoperative risk factors predicting postoperative complications in radical cystectomy for bladder cancer.. Journal of Clinical Oncology, 2017, 35, 395-395.	1.6	0
140	Case Study: Electronic Data Capture System Validation at an Academic Institution. , 2019, 25, 16-22.		0
141	Perturbation of BRMS1 interactome reveals pathways that impact metastasis. PLoS ONE, 2021, 16, e0259128.	2.5	0
142	605. Factors Underlying Antifungal Price Trends in the United States. Open Forum Infectious Diseases, 2020, 7, S364-S364.	0.9	0
143	BIOM-13. DNA METHYLATION MARKS GLUCOCORTICOID PATHWAY RESPONSE IN DEXAMETHASONE-TREATED BRAIN TUMOR PATIENTS. Neuro-Oncology, 2020, 22, ii4-ii4.	1.2	0
144	EPCO-25. AN IMMUNOMETHYLOMIC PLATFORM INTEGRATING SYSTEMIC IMMUNE PROFILES AND EPIGENETIC AGE IN NEURO-ONCOLOGY. Neuro-Oncology, 2020, 22, ii74-ii74.	1.2	0

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145	Human cytomegalovirus alters immune cell profile with potential implications for patient survival in head and neck cancer. Carcinogenesis, 2022, , .	2.8	0
146	Maternal Pre-pregnancy BMI Associates With Sex-Specific Placental microRNA Patterns. Current Developments in Nutrition, 2022, 6, 671.	0.3	0
147	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