

Carmen J Marsit

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

297 papers	16,964 citations	69 h-index	120 g-index
327 ext. papers	19,898 ext. citations	5.8 avg, IF	6.71 L-index

#	Paper	IF	Citations
297	Investigation of Prenatal Pesticide Exposure and Neurodevelopmental Deficits in Northern Thailand: Protocol for a Longitudinal Birth Cohort Study.. <i>JMIR Research Protocols</i> , 2022 , 11, e31696	2	0
296	Prenatal exposure to metal mixtures and newborn neurobehavior in the Rhode Island Child Health Study.. <i>Environmental Epidemiology</i> , 2022 , 6, e194	0.2	0
295	Placental genomics mediates genetic associations with complex health traits and disease.. <i>Nature Communications</i> , 2022 , 13, 706	17.4	0
294	High-resolution metabolomics of exposure to tobacco smoke during pregnancy and adverse birth outcomes in the Atlanta African American maternal-child cohort. <i>Environmental Pollution</i> , 2022 , 292, 118361	9.3	3
293	Association between placental toxic metal exposure and NICU Network Neurobehavioral Scales (NNS) profiles in the Rhode Island Child Health Study (RICHS). <i>Environmental Research</i> , 2022 , 204, 111939	7.9	3
292	PM exposure during pregnancy is associated with altered placental expression of lipid metabolic genes in a US birth cohort.. <i>Environmental Research</i> , 2022 , 113066	7.9	0
291	Influence of Environmental Factors on the Epigenome 2022 , 277-322		
290	Exposure to Contemporary and Emerging Chemicals in Commerce among Pregnant Women in the United States: The Environmental influences on Child Health Outcome (ECHO) Program.. <i>Environmental Science & Technology</i> , 2022 , 56, 6560-6573	10.3	1
289	Placental multi-omics integration identifies candidate functional genes for birthweight.. <i>Nature Communications</i> , 2022 , 13, 2384	17.4	1
288	Prenatal exposure to particulate matter and placental gene expression. <i>Environment International</i> , 2022 , 165, 107310	12.9	0
287	Selenium-associated differentially expressed microRNAs and their targeted mRNAs across the placental genome in two U.S. birth cohorts. <i>Epigenetics</i> , 2021 , 1-12	5.7	0
286	NEOage clocks - epigenetic clocks to estimate post-menstrual and postnatal age in preterm infants. <i>Aging</i> , 2021 , 13, 23527-23544	5.6	0
285	Urinary metals and maternal circulating extracellular vesicle microRNA in the MADRES pregnancy cohort. <i>Epigenetics</i> , 2021 , 1-15	5.7	3
284	Per- and polyfluoroalkyl substance (PFAS) exposure, maternal metabolomic perturbation, and fetal growth in African American women: A meet-in-the-middle approach. <i>Environment International</i> , 2021 , 158, 106964	12.9	8
283	Longitudinal changes in epigenetic age in youth with perinatally acquired HIV and youth who are perinatally HIV-exposed uninfected. <i>Aids</i> , 2021 , 35, 811-819	3.5	3
282	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021 , 16, 770-782	5.7	4
281	Epigenome-wide analysis identifies genes and pathways linked to acoustic cry variation in preterm infants. <i>Pediatric Research</i> , 2021 , 89, 1848-1854	3.2	1

280	In-utero exposure to zidovudine-containing antiretroviral therapy and clonal hematopoiesis in HIV-exposed uninfected newborns. <i>Aids</i> , 2021 , 35, 1525-1535	3.5	1
279	Extracellular vesicle microRNA in early versus late pregnancy with birth outcomes in the MADRES study. <i>Epigenetics</i> , 2021 , 1-17	5.7	4
278	Light Environment Influences Developmental Programming of the Metabolic and Visual Systems in Mice 2021 , 62, 22		2
277	Extracellular vesicle-enriched miRNA profiles across pregnancy in the MADRES cohort. <i>PLoS ONE</i> , 2021 , 16, e0251259	3.7	3
276	Epigenome-wide scan identifies differentially methylated regions for lung cancer using pre-diagnostic peripheral blood. <i>Epigenetics</i> , 2021 , 1-13	5.7	3
275	DNA methylation in children with prenatal methamphetamine exposure and environmental adversity. <i>Pediatric Research</i> , 2021 , 89, 1152-1156	3.2	3
274	Genome-wide DNA methylation differences and polychlorinated biphenyl (PCB) exposure in a US population. <i>Epigenetics</i> , 2021 , 16, 338-352	5.7	4
273	Methylome-wide Analysis Reveals Epigenetic Marks Associated With Resistance to Tuberculosis in Human Immunodeficiency Virus-Infected Individuals From East Africa. <i>Journal of Infectious Diseases</i> , 2021 , 224, 695-704	7	
272	Pre-diagnosis neutrophil-to-lymphocyte ratio and mortality in individuals who develop lung cancer. <i>Cancer Causes and Control</i> , 2021 , 32, 1227-1236	2.8	3
271	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. <i>Nature Communications</i> , 2021 , 12, 5095	17.4	5
270	Placental gene networks at the interface between maternal PM exposure early in gestation and reduced infant birthweight. <i>Environmental Research</i> , 2021 , 199, 111342	7.9	4
269	Developmental chronodisruption alters placental signaling in mice. <i>PLoS ONE</i> , 2021 , 16, e0255296	3.7	0
268	A scalable workflow to characterize the human exposome. <i>Nature Communications</i> , 2021 , 12, 5575	17.4	6
267	A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape. <i>Environmental Health Perspectives</i> , 2021 , 129, 97003	8.4	2
266	Prenatal risk factors and neonatal DNA methylation in very preterm infants. <i>Clinical Epigenetics</i> , 2021 , 13, 171	7.7	1
265	Evidence for the placenta-brain axis: multi-omic kernel aggregation predicts intellectual and social impairment in children born extremely preterm. <i>Molecular Autism</i> , 2020 , 11, 97	6.5	6
264	DNA Methylation-Derived Immune Cell Profiles, CpG Markers of Inflammation, and Pancreatic Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 1577-1585	4	7
263	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. <i>Environmental Epigenetics</i> , 2020 , 6, dvaa003	2.4	9

262	Sex-specific DNA methylation differences in people exposed to polybrominated biphenyl. <i>Epigenomics</i> , 2020 , 12, 757-770	4.4	5
261	Identification of Let-7f-5p as a novel biomarker of recurrence in non-muscle invasive bladder cancer. <i>Cancer Biomarkers</i> , 2020 , 29, 101-110	3.8	5
260	Molecular markers of neuroendocrine function and mitochondrial biogenesis associated with early life stress. <i>Psychoneuroendocrinology</i> , 2020 , 116, 104632	5	6
259	Combined neurodevelopmental exposure to deltamethrin and corticosterone is associated with Nr3c1 hypermethylation in the midbrain of male mice. <i>Neurotoxicology and Teratology</i> , 2020 , 80, 106887	3.9	6
258	Epidemiological concepts in environmental epigenetics 2020 , 89-105		0
257	Selenium-associated DNA methylation modifications in placenta and neurobehavioral development of newborns: An epigenome-wide study of two U.S. birth cohorts. <i>Environment International</i> , 2020 , 137, 105508	12.9	8
256	Genome-wide characterization of cytosine-specific 5-hydroxymethylation in normal breast tissue. <i>Epigenetics</i> , 2020 , 15, 398-418	5.7	3
255	Epigenome-Wide Association Study Using Prediagnostic Bloods Identifies New Genomic Regions Associated With Pancreatic Cancer Risk. <i>JNCI Cancer Spectrum</i> , 2020 , 4, pkaa041	4.6	3
254	Serious neonatal morbidities are associated with differences in DNA methylation among very preterm infants. <i>Clinical Epigenetics</i> , 2020 , 12, 151	7.7	7
253	Associations of maternal diet and placenta leptin methylation. <i>Molecular and Cellular Endocrinology</i> , 2020 , 505, 110739	4.4	5
252	Seasonally variant gene expression in full-term human placenta. <i>FASEB Journal</i> , 2020 , 34, 10431-10442	0.9	4
251	AHRR methylation in heavy smokers: associations with smoking, lung cancer risk, and lung cancer mortality. <i>BMC Cancer</i> , 2020 , 20, 905	4.8	7
250	In-depth characterization of the placental imprintome reveals novel differentially methylated regions across birth weight categories. <i>Epigenetics</i> , 2020 , 15, 47-60	5.7	5
249	Chrysotile fibers in tissue adjacent to laryngeal squamous cell carcinoma in cases with a history of occupational asbestos exposure. <i>Modern Pathology</i> , 2020 , 33, 228-234	9.8	2
248	Copper associates with differential methylation in placentae from two US birth cohorts. <i>Epigenetics</i> , 2020 , 15, 215-230	5.7	2
247	Mitochondrial and glycolysis-regulatory gene expression profiles are associated with intrauterine growth restriction. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2020 , 33, 1336-1345	2	5
246	Exposure to polybrominated biphenyl (PBB) associates with genome-wide DNA methylation differences in peripheral blood. <i>Epigenetics</i> , 2019 , 14, 52-66	5.7	25
245	MicroRNA Dysregulation and Non-Muscle-Invasive Bladder Cancer Prognosis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 782-788	4	12

244	Epigenetically regulated imprinted gene expression associated with IVF and infertility: possible influence of prenatal stress and depression. <i>Journal of Assisted Reproduction and Genetics</i> , 2019 , 36, 1299-1313	3.4	13
243	DNA methylation of NR3c1 in infancy: Associations between maternal caregiving and infant sex. <i>Infant Mental Health Journal</i> , 2019 , 40, 513-522	2.3	9
242	Exposure to polybrominated biphenyl and stochastic epigenetic mutations: application of a novel epigenetic approach to environmental exposure in the Michigan polybrominated biphenyl registry. <i>Epigenetics</i> , 2019 , 14, 1003-1018	5.7	10
241	A Neurodevelopmental Model of Combined Pyrethroid and Chronic Stress Exposure. <i>Toxics</i> , 2019 , 7,	4.7	3
240	Placental Expression of Imprinted Genes, Overall and in Sex-Specific Patterns, Associated with Placental Cadmium Concentrations and Birth Size. <i>Environmental Health Perspectives</i> , 2019 , 127, 57005	8.4	13
239	Epigenome-wide Analysis Identifies Genes and Pathways Linked to Neurobehavioral Variation in Preterm Infants. <i>Scientific Reports</i> , 2019 , 9, 6322	4.9	22
238	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019 , 51, 804-814	36.3	181
237	Microorganisms in the Placenta: Links to Early-Life Inflammation and Neurodevelopment in Children. <i>Clinical Microbiology Reviews</i> , 2019 , 32,	34	13
236	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019 , 10, 1893	17.4	79
235	Maternal circadian disruption is associated with variation in placental DNA methylation. <i>PLoS ONE</i> , 2019 , 14, e0215745	3.7	9
234	Prenatal arsenic exposure alters the placental expression of multiple epigenetic regulators in a sex-dependent manner. <i>Environmental Health</i> , 2019 , 18, 18	6	18
233	Placental imprinted gene expression mediates the effects of maternal psychosocial stress during pregnancy on fetal growth. <i>Journal of Developmental Origins of Health and Disease</i> , 2019 , 10, 196-205	2.4	4
232	Social Stress-Related Epigenetic Changes Associated With Increased Heart Rate Variability in Infants. <i>Frontiers in Behavioral Neuroscience</i> , 2019 , 13, 294	3.5	3
231	Associations Between the Features of Gross Placental Morphology and Birthweight. <i>Pediatric and Developmental Pathology</i> , 2019 , 22, 194-204	2.2	8
230	Accurate ethnicity prediction from placental DNA methylation data. <i>Epigenetics and Chromatin</i> , 2019 , 12, 51	5.8	20
229	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019 , 11, 4238-4253	5.6	29
228	Environmental exposure to polybrominated biphenyl (PBB) associates with an increased rate of biological aging. <i>Aging</i> , 2019 , 11, 5498-5517	5.6	7
227	Associations Between Features of Placental Morphology and Birth Weight in Dichorionic Twins. <i>American Journal of Epidemiology</i> , 2019 , 188, 518-526	3.8	5

226	Transcriptome-wide analysis of changes in the fetal placenta associated with prenatal arsenic exposure in the New Hampshire Birth Cohort Study. <i>Environmental Health</i> , 2019 , 18, 100	6	8
225	Association between zidovudine-containing antiretroviral therapy exposure in utero and leukocyte telomere length at birth. <i>Aids</i> , 2019 , 33, 2091-2096	3.5	2
224	Smoking during pregnancy increases chemerin expression in neonatal tissue. <i>Experimental Physiology</i> , 2019 , 104, 93-99	2.4	2
223	Maternal swimming pool exposure during pregnancy in relation to birth outcomes and cord blood DNA methylation among private well users. <i>Environment International</i> , 2019 , 123, 459-466	12.9	5
222	Birthweight in infants conceived through in vitro fertilization following blastocyst or cleavage-stage embryo transfer: a national registry study. <i>Journal of Assisted Reproduction and Genetics</i> , 2018 , 35, 1027-1037	3.4	6
221	Epigenetic mechanisms in the placenta related to infant neurodevelopment. <i>Epigenomics</i> , 2018 , 10, 321-333	4.3	26
220	Effect of frozen/thawed embryo transfer on birthweight, macrosomia, and low birthweight rates in US singleton infants. <i>American Journal of Obstetrics and Gynecology</i> , 2018 , 218, 433.e1-433.e10	6.4	34
219	Methylation-to-Expression Feature Models of Breast Cancer Accurately Predict Overall Survival, Distant-Recurrence Free Survival, and Pathologic Complete Response in Multiple Cohorts. <i>Scientific Reports</i> , 2018 , 8, 5190	4.9	5
218	Prenatal exposure to maternal depression and anxiety on imprinted gene expression in placenta and infant neurodevelopment and growth. <i>Pediatric Research</i> , 2018 , 83, 1075-1083	3.2	7
217	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 22-23u	7.8	62
216	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018 , 142, 874-882	7.5	46
215	Comparison of diameter-based and image-based measures of surface area from gross placental pathology for use in epidemiologic studies. <i>Placenta</i> , 2018 , 69, 82-85	3.4	0
214	Integrating -Omics Approaches into Human Population-Based Studies of Prenatal and Early-Life Exposures. <i>Current Environmental Health Reports</i> , 2018 , 5, 328-337	6.5	16
213	Arsenic exposure and risk of nonalcoholic fatty liver disease (NAFLD) among U.S. adolescents and adults: an association modified by race/ethnicity, NHANES 2005-2014. <i>Environmental Health</i> , 2018 , 17, 6	6	32
212	Expression of Genes Involved in Stress, Toxicity, Inflammation, and Autoimmunity in Relation to Cadmium, Mercury, and Lead in Human Blood: A Pilot Study. <i>Toxics</i> , 2018 , 6,	4.7	8
211	Pan-Cancer Analysis Reveals Differential Susceptibility of Bidirectional Gene Promoters to DNA Methylation, Somatic Mutations, and Copy Number Alterations. <i>International Journal of Molecular Sciences</i> , 2018 , 19,	6.3	6
210	Intrauterine multi-metal exposure is associated with reduced fetal growth through modulation of the placental gene network. <i>Environment International</i> , 2018 , 120, 373-381	12.9	28
209	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018 , 14, e1007799	6	13

208	Epigenetic Programming by Maternal Behavior in the Human Infant. <i>Pediatrics</i> , 2018 , 142,	7.4	38
207	Methylation-derived Neutrophil-to-Lymphocyte Ratio and Lung Cancer Risk in Heavy Smokers. <i>Cancer Prevention Research</i> , 2018 , 11, 727-734	3.2	17
206	Variation in DNA methylation of human blood over a 1-year period using the Illumina MethylationEPIC array. <i>Epigenetics</i> , 2018 , 13, 1056-1071	5.7	20
205	Environmentally Induced Epigenetic Plasticity in Development: Epigenetic Toxicity and Epigenetic Adaptation. <i>Current Epidemiology Reports</i> , 2018 , 5, 450-460	2.9	4
204	Cadmium-Associated Differential Methylation throughout the Placental Genome: Epigenome-Wide Association Study of Two U.S. Birth Cohorts. <i>Environmental Health Perspectives</i> , 2018 , 126, 017010	8.4	50
203	Transdisciplinary approaches enhance the production of translational knowledge. <i>Translational Research</i> , 2017 , 182, 123-134	11	31
202	Using neonatal skin to study the developmental programming of aging. <i>Experimental Gerontology</i> , 2017 , 94, 93-98	4.5	3
201	Sexual epigenetic dimorphism in the human placenta: implications for susceptibility during the prenatal period. <i>Epigenomics</i> , 2017 , 9, 267-278	4.4	57
200	Placental imprinting variation associated with assisted reproductive technologies and subfertility. <i>Epigenetics</i> , 2017 , 12, 653-661	5.7	27
199	Pulmonary microRNA profiling: implications in upper lobe predominant lung disease. <i>Clinical Epigenetics</i> , 2017 , 9, 56	7.7	24
198	Prenatal exposure to neurotoxic metals is associated with increased placental glucocorticoid receptor DNA methylation. <i>Epigenetics</i> , 2017 , 12, 607-615	5.7	41
197	Temporal variability of urinary cadmium in spot urine samples and first morning voids. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2017 , 27, 306-312	6.7	11
196	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	4	40
195	Maternal ambient air pollution, preterm birth and markers of fetal growth in Rhode Island: results of a hospital-based linkage study. <i>Journal of Epidemiology and Community Health</i> , 2017 , 71, 1131-1136	5.1	22
194	Small-Magnitude Effect Sizes in Epigenetic End Points are Important in Children's Environmental Health Studies: The Children's Environmental Health and Disease Prevention Research Center's Epigenetics Working Group. <i>Environmental Health Perspectives</i> , 2017 , 125, 511-526	8.4	158
193	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017 , 26, 4067-4085	5.6	151
192	Maternal residential air pollution and placental imprinted gene expression. <i>Environment International</i> , 2017 , 108, 204-211	12.9	20
191	Change in FK506 binding protein 5 (FKBP5) methylation over time among preschoolers with adversity. <i>Development and Psychopathology</i> , 2017 , 29, 1627-1634	4.3	58

190	Stress exposure and psychopathology alter methylation of the serotonin receptor 2A (HTR2A) gene in preschoolers. <i>Development and Psychopathology</i> , 2017 , 29, 1619-1626	4.3	20
189	Dynamic stress-related epigenetic regulation of the glucocorticoid receptor gene promoter during early development: The role of child maltreatment. <i>Development and Psychopathology</i> , 2017 , 29, 1635-1648	4.3	32
188	Expression quantitative trait loci (eQTLs) in human placentas suggest developmental origins of complex diseases. <i>Human Molecular Genetics</i> , 2017 , 26, 3432-3441	5.6	29
187	Expression of placental regulatory genes is associated with fetal growth. <i>Journal of Perinatal Medicine</i> , 2017 , 45, 887-893	2.7	10
186	An epigenome-wide DNA methylation study of PTSD and depression in World Trade Center responders. <i>Translational Psychiatry</i> , 2017 , 7, e1158	8.6	63
185	Maternal exposure to selenium and cadmium, fetal growth, and placental expression of steroidogenic and apoptotic genes. <i>Environmental Research</i> , 2017 , 158, 233-244	7.9	28
184	Genome-wide DNA methylation at birth in relation to in utero arsenic exposure and the associated health in later life. <i>Environmental Health</i> , 2017 , 16, 50	6	41
183	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	6	12
182	Medical morbidities and DNA methylation of NR3C1 in preterm infants. <i>Pediatric Research</i> , 2017 , 81, 68-74	3.2	13
181	A METHYLATION-TO-EXPRESSION FEATURE MODEL FOR GENERATING ACCURATE PROGNOSTIC RISK SCORES AND IDENTIFYING DISEASE TARGETS IN CLEAR CELL KIDNEY CANCER. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2017 , 22, 509-520	1.3	4
180	Whole-transcriptome analysis delineates the human placenta gene network and its associations with fetal growth. <i>BMC Genomics</i> , 2017 , 18, 520	4.5	34
179	Maternal cadmium, placental PCDHAC1, and fetal development. <i>Reproductive Toxicology</i> , 2016 , 65, 263-274	3.7	21
178	Methylation of the Glucocorticoid Receptor Gene Promoter in Preschoolers: Links With Internalizing Behavior Problems. <i>Child Development</i> , 2016 , 87, 86-97	4.9	45
177	Placental Epigenetics in Children's Environmental Health. <i>Seminars in Reproductive Medicine</i> , 2016 , 34, 36-41	1.4	20
176	Placental Metal Concentrations in Relation to Maternal and Infant Toenails in a U.S. Cohort. <i>Environmental Science & Technology</i> , 2016 , 50, 1587-94	10.3	37
175	Seroepidemiology of Human Polyomaviruses in a US Population. <i>American Journal of Epidemiology</i> , 2016 , 183, 61-9	3.8	83
174	Epigenome-Wide Assessment of DNA Methylation in the Placenta and Arsenic Exposure in the New Hampshire Birth Cohort Study (USA). <i>Environmental Health Perspectives</i> , 2016 , 124, 1253-60	8.4	75
173	Prenatal Stress, Fearfulness, and the Epigenome: Exploratory Analysis of Sex Differences in DNA Methylation of the Glucocorticoid Receptor Gene. <i>Frontiers in Behavioral Neuroscience</i> , 2016 , 10, 147	3.5	51

172	Methylation of the Glucocorticoid Receptor (NR3C1) in Placenta Is Associated with Infant Cry Acoustics. <i>Frontiers in Behavioral Neuroscience</i> , 2016 , 10, 100	3.5	12
171	Maternal smoking during pregnancy is associated with mitochondrial DNA methylation. <i>Environmental Epigenetics</i> , 2016 , 2,	2.4	16
170	Prenatal Programming of Infant Neurobehaviour in a Healthy Population. <i>Paediatric and Perinatal Epidemiology</i> , 2016 , 30, 367-75	2.7	23
169	Methylation of the leukocyte glucocorticoid receptor gene promoter in adults: associations with early adversity and depressive, anxiety and substance-use disorders. <i>Translational Psychiatry</i> , 2016 , 6, e848	8.6	79
168	Regions of variable DNA methylation in human placenta associated with newborn neurobehavior. <i>Epigenetics</i> , 2016 , 11, 603-13	5.7	64
167	Prenatal Major Depressive Disorder, Placenta Glucocorticoid and Serotonergic Signaling, and Infant Cortisol Response. <i>Psychosomatic Medicine</i> , 2016 , 78, 979-990	3.7	47
166	Reference-free deconvolution of DNA methylation data and mediation by cell composition effects. <i>BMC Bioinformatics</i> , 2016 , 17, 259	3.6	134
165	Maternal residential proximity to major roadways, birth weight, and placental DNA methylation. <i>Environment International</i> , 2016 , 92-93, 43-9	12.9	44
164	Hydroxymethylation is uniquely distributed within term placenta, and is associated with gene expression. <i>FASEB Journal</i> , 2016 , 30, 2874-84	0.9	28
163	Epigenetic Regulation of Placental NR3C1: Mechanism Underlying Prenatal Programming of Infant Neurobehavior by Maternal Smoking?. <i>Child Development</i> , 2016 , 87, 49-60	4.9	34
162	Introduction to the Special Section on Epigenetics. <i>Child Development</i> , 2016 , 87, 29-37	4.9	50
161	The Contributions of Maternal Sensitivity and Maternal Depressive Symptoms to Epigenetic Processes and Neuroendocrine Functioning. <i>Child Development</i> , 2016 , 87, 73-85	4.9	59
160	Influence of environmental exposure on human epigenetic regulation. <i>Journal of Experimental Biology</i> , 2015 , 218, 71-9	3	153
159	Placental expression profile of imprinted genes impacts birth weight. <i>Epigenetics</i> , 2015 , 10, 842-9	5.7	68
158	Expression of imprinted genes in placenta is associated with infant neurobehavioral development. <i>Epigenetics</i> , 2015 , 10, 834-41	5.7	41
157	The Role of Placental 11-Beta Hydroxysteroid Dehydrogenase Type 1 and Type 2 Methylation on Gene Expression and Infant Birth Weight. <i>Biology of Reproduction</i> , 2015 , 92, 149	3.9	29
156	Select Prenatal Environmental Exposures and Subsequent Alterations of Gene-Specific and Repetitive Element DNA Methylation in Fetal Tissues. <i>Current Environmental Health Reports</i> , 2015 , 2, 126-36	6.5	31
155	Cell-composition effects in the analysis of DNA methylation array data: a mathematical perspective. <i>BMC Bioinformatics</i> , 2015 , 16, 95	3.6	68

154	DNA methylation changes in the placenta are associated with fetal manganese exposure. <i>Reproductive Toxicology</i> , 2015 , 57, 43-9	3.4	30
153	Methylation of exons 1D, 1F, and 1H of the glucocorticoid receptor gene promoter and exposure to adversity in preschool-aged children. <i>Development and Psychopathology</i> , 2015 , 27, 577-85	4.3	46
152	Placental arsenic concentrations in relation to both maternal and infant biomarkers of exposure in a US cohort. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2015 , 25, 599-603	6.7	34
151	Understanding the Role of the Immune System in the Development of Cancer: New Opportunities for Population-Based Research. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015 , 24, 1811-9	4	15
150	Infant peripheral blood repetitive element hypomethylation associated with antiretroviral therapy in utero. <i>Epigenetics</i> , 2015 , 10, 708-16	5.7	14
149	E2F4 Program Is Predictive of Progression and Intravesical Immunotherapy Efficacy in Bladder Cancer. <i>Molecular Cancer Research</i> , 2015 , 13, 1316-24	6.6	9
148	Differential DNA methylation in umbilical cord blood of infants exposed to mercury and arsenic in utero. <i>Epigenetics</i> , 2015 , 10, 508-15	5.7	91
147	Placental epigenetic patterning of glucocorticoid response genes is associated with infant neurodevelopment. <i>Epigenomics</i> , 2015 , 7, 767-79	4.4	46
146	Association between maternal urinary arsenic species and infant cord blood leptin levels in a New Hampshire Pregnancy Cohort. <i>Environmental Research</i> , 2015 , 136, 180-6	7.9	22
145	Examining the joint contribution of placental NR3C1 and HSD11B2 methylation for infant neurobehavior. <i>Psychoneuroendocrinology</i> , 2015 , 52, 32-42	5	45
144	Obesity and head and neck cancer risk and survival by human papillomavirus serology. <i>Cancer Causes and Control</i> , 2015 , 26, 111-9	2.8	10
143	Genetic polymorphisms modify bladder cancer recurrence and survival in a USA population-based prognostic study. <i>BJU International</i> , 2015 , 115, 238-47	5.6	22
142	Childhood maltreatment and methylation of FK506 binding protein 5 gene (FKBP5). <i>Development and Psychopathology</i> , 2015 , 27, 1637-45	4.3	65
141	Neurobehavior related to epigenetic differences in preterm infants. <i>Epigenomics</i> , 2015 , 7, 1123-36	4.4	59
140	Epigenome-wide and transcriptome-wide analyses reveal gestational diabetes is associated with alterations in the human leukocyte antigen complex. <i>Clinical Epigenetics</i> , 2015 , 7, 79	7.7	54
139	MicroRNA molecular profiling from matched tumor and bio-fluids in bladder cancer. <i>Molecular Cancer</i> , 2015 , 14, 194	42.1	119
138	Prenatal predictors of infant self-regulation: the contributions of placental DNA methylation of NR3C1 and neuroendocrine activity. <i>Frontiers in Behavioral Neuroscience</i> , 2015 , 9, 130	3.5	43
137	A coding variant in TMC8 (EVER2) is associated with high risk HPV infection and head and neck cancer risk. <i>PLoS ONE</i> , 2015 , 10, e0123716	3.7	6

136	Placental DNA Methylation Related to Both Infant Toenail Mercury and Adverse Neurobehavioral Outcomes. <i>Environmental Health Perspectives</i> , 2015 , 123, 723-9	8.4	62
135	Maternal psychiatric disease and epigenetic evidence suggest a common biology for poor fetal growth. <i>BMC Pregnancy and Childbirth</i> , 2015 , 15, 192	3.2	34
134	GLI3 Links Environmental Arsenic Exposure and Human Fetal Growth. <i>EBioMedicine</i> , 2015 , 2, 536-43	8.8	12
133	Expression of tumor suppressive microRNA-34a is associated with a reduced risk of bladder cancer recurrence. <i>International Journal of Cancer</i> , 2015 , 137, 1158-66	7.5	30
132	Sex-specific associations between placental leptin promoter DNA methylation and infant neurobehavior. <i>Psychoneuroendocrinology</i> , 2014 , 40, 1-9	5	46
131	Epigenetic Regulation of Infant Neurobehavioral Outcomes. <i>Medical Epigenetics</i> , 2014 , 2, 71-79		31
130	Global and gene-specific DNA methylation across multiple tissues in early infancy: implications for children's health research. <i>FASEB Journal</i> , 2014 , 28, 2088-97	0.9	62
129	Maternal obesity and gestational diabetes are associated with placental leptin DNA methylation. <i>American Journal of Obstetrics and Gynecology</i> , 2014 , 211, 654.e1-9	6.4	69
128	Maternal smoking during pregnancy and infant stress response: test of a prenatal programming hypothesis. <i>Psychoneuroendocrinology</i> , 2014 , 48, 29-40	5	78
127	Leukocyte-adjusted epigenome-wide association studies of blood from solid tumor patients. <i>Epigenetics</i> , 2014 , 9, 884-95	5.7	29
126	A novel approach to the discovery of survival biomarkers in glioblastoma using a joint analysis of DNA methylation and gene expression. <i>Epigenetics</i> , 2014 , 9, 873-83	5.7	22
125	Infant toenails as a biomarker of in utero arsenic exposure. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2014 , 24, 467-73	6.7	37
124	Body mass and smoking are modifiable risk factors for recurrent bladder cancer. <i>Cancer</i> , 2014 , 120, 408-14	6.4	56
123	The developmental basis of epigenetic regulation of HTR2A and psychiatric outcomes. <i>Journal of Cellular Biochemistry</i> , 2014 , 115, 2065-72	4.7	29
122	Reference-free cell mixture adjustments in analysis of DNA methylation data. <i>Bioinformatics</i> , 2014 , 30, 1431-9	7.2	316
121	Are epigenetic changes in the intrauterine environment related to newborn neurobehavior?. <i>Epigenomics</i> , 2014 , 6, 175-8	4.4	19
120	Distinct patterns of DNA methylation in conventional adenomas involving the right and left colon. <i>Modern Pathology</i> , 2014 , 27, 145-55	9.8	32
119	Placental FKBP5 genetic and epigenetic variation is associated with infant neurobehavioral outcomes in the RICHs cohort. <i>PLoS ONE</i> , 2014 , 9, e104913	3.7	81

118	A recursively partitioned mixture model for clustering time-course gene expression data. <i>Translational Cancer Research</i> , 2014 , 3, 217-232	0.3	3
117	Gastric reflux is an independent risk factor for laryngopharyngeal carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 1061-8	4	51
116	Placental DNA methylation alterations associated with maternal tobacco smoking at the RUNX3 gene are also associated with gestational age. <i>Epigenomics</i> , 2013 , 5, 619-30	4.4	83
115	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	6	55
114	Tissue-specific Leptin promoter DNA methylation is associated with maternal and infant perinatal factors. <i>Molecular and Cellular Endocrinology</i> , 2013 , 381, 160-7	4.4	77
113	Genetic and epigenetic variation of the glucocorticoid receptor (NR3C1) in placenta and infant neurobehavior. <i>Developmental Psychobiology</i> , 2013 , 55, 673-83	3	83
112	Blood-derived DNA methylation markers of cancer risk. <i>Advances in Experimental Medicine and Biology</i> , 2013 , 754, 233-52	3.6	24
111	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	1.2	11
110	Placental miRNA expression profiles are associated with measures of infant neurobehavioral outcomes. <i>Pediatric Research</i> , 2013 , 74, 272-8	3.2	31
109	Differential DNA methylation in umbilical cord blood of infants exposed to low levels of arsenic in utero. <i>Environmental Health Perspectives</i> , 2013 , 121, 971-7	8.4	147
108	Epigenetic basis for the development of depression in children. <i>Clinical Obstetrics and Gynecology</i> , 2013 , 56, 556-65	1.7	36
107	Placental HTR2A methylation is associated with infant neurobehavioral outcomes. <i>Epigenetics</i> , 2013 , 8, 796-801	5.7	49
106	Blood-based profiles of DNA methylation predict the underlying distribution of cell types: a validation analysis. <i>Epigenetics</i> , 2013 , 8, 816-26	5.7	174
105	The roles of DNA methylation of NR3C1 and 11βHSD2 and exposure to maternal mood disorder in utero on newborn neurobehavior. <i>Epigenetics</i> , 2013 , 8, 1321-9	5.7	212
104	Developmental genes targeted for epigenetic variation between twin-twin transfusion syndrome children. <i>Clinical Epigenetics</i> , 2013 , 5, 18	7.7	5
103	Patterning in placental 11-B hydroxysteroid dehydrogenase methylation according to prenatal socioeconomic adversity. <i>PLoS ONE</i> , 2013 , 8, e74691	3.7	109
102	Placenta-imprinted gene expression association of infant neurobehavior. <i>Journal of Pediatrics</i> , 2012 , 160, 854-860.e2	3.6	34
101	LINE-1 hypomethylation is associated with bladder cancer risk among nonsmoking Chinese. <i>International Journal of Cancer</i> , 2012 , 130, 1151-9	7.5	71

100	SLC39A2 and FSIP1 polymorphisms as potential modifiers of arsenic-related bladder cancer. <i>Human Genetics</i> , 2012 , 131, 453-61	6.3	32
99	A case-control study of polymorphisms in xenobiotic and arsenic metabolism genes and arsenic-related bladder cancer in New Hampshire. <i>Toxicology Letters</i> , 2012 , 210, 100-6	4.4	53
98	Identification of an epigenetic profile classifier that is associated with survival in head and neck cancer. <i>Cancer Research</i> , 2012 , 72, 2728-37	10.1	33
97	DNA methylation arrays as surrogate measures of cell mixture distribution. <i>BMC Bioinformatics</i> , 2012 , 13, 86	3.6	1815
96	Childhood adversity and epigenetic modulation of the leukocyte glucocorticoid receptor: preliminary findings in healthy adults. <i>PLoS ONE</i> , 2012 , 7, e30148	3.7	360
95	HSD3B and gene-gene interactions in a pathway-based analysis of genetic susceptibility to bladder cancer. <i>PLoS ONE</i> , 2012 , 7, e51301	3.7	14
94	Peripheral blood DNA methylation profiles are indicative of head and neck squamous cell carcinoma: an epigenome-wide association study. <i>Epigenetics</i> , 2012 , 7, 291-9	5.7	69
93	In utero exposures, infant growth, and DNA methylation of repetitive elements and developmentally related genes in human placenta. <i>Environmental Health Perspectives</i> , 2012 , 120, 296-302	8.4	150
92	Gene-environment interactions of novel variants associated with head and neck cancer. <i>Head and Neck</i> , 2012 , 34, 1111-8	4.2	18
91	Allergies and risk of head and neck cancer. <i>Cancer Causes and Control</i> , 2012 , 23, 1317-22	2.8	14
90	Key epigenetic changes associated with lung cancer development: results from dense methylation array profiling. <i>Epigenetics</i> , 2012 , 7, 559-66	5.7	37
89	Biomarkers of HPV in head and neck squamous cell carcinoma. <i>Cancer Research</i> , 2012 , 72, 5004-13	10.1	103
88	Peripheral blood immune cell methylation profiles are associated with nonhematopoietic cancers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012 , 21, 1293-302	4	94
87	Placental 11-beta hydroxysteroid dehydrogenase methylation is associated with newborn growth and a measure of neurobehavioral outcome. <i>PLoS ONE</i> , 2012 , 7, e33794	3.7	144
86	Acute hypersensitivity of pluripotent testicular cancer-derived embryonal carcinoma to low-dose 5-aza deoxycytidine is associated with global DNA Damage-associated p53 activation, anti-pluripotency and DNA demethylation. <i>PLoS ONE</i> , 2012 , 7, e53003	3.7	45
85	Influence of Environmental Factors on the Epigenome 2012 , 197-224		1
84	Endocrine disruptors, environmental oxygen, epigenetics and pregnancy. <i>Frontiers in Bioscience - Elite</i> , 2011 , 3, 690-700	1.6	57
83	Global methylation in exposure biology and translational medical science. <i>Environmental Health Perspectives</i> , 2011 , 119, 1528-33	8.4	84

82	Epigenomics in environmental health. <i>Frontiers in Genetics</i> , 2011 , 2, 84	4.5	90
81	A genome-wide association study of upper aerodigestive tract cancers conducted within the INHANCE consortium. <i>PLoS Genetics</i> , 2011 , 7, e1001333	6	136
80	Behavioral epigenetics. <i>Annals of the New York Academy of Sciences</i> , 2011 , 1226, 14-33	6.5	101
79	Association of secondhand smoke exposures with DNA methylation in bladder carcinomas. <i>Cancer Causes and Control</i> , 2011 , 22, 1205-13	2.8	30
78	A novel survival multifactor dimensionality reduction method for detecting gene-gene interactions with application to bladder cancer prognosis. <i>Human Genetics</i> , 2011 , 129, 101-10	6.3	46
77	Exposure and fetal growth-associated miRNA alterations in the human placenta. <i>Clinical Epigenetics</i> , 2011 , 2, 401-4	7.7	19
76	History of Parvovirus B19 infection is associated with a DNA methylation signature in childhood acute lymphoblastic leukemia. <i>Epigenetics</i> , 2011 , 6, 1436-43	5.7	16
75	DNA hypermethylation profiles associated with glioma subtypes and EZH2 and IGFBP2 mRNA expression. <i>Neuro-Oncology</i> , 2011 , 13, 280-9	1	54
74	The relationship between tumor MSLN methylation and serum mesothelin (SMRP) in mesothelioma. <i>Epigenetics</i> , 2011 , 6, 1029-34	5.7	21
73	Cardiovascular disease risk factors and DNA methylation at the LINE-1 repeat region in peripheral blood from Samoan Islanders. <i>Epigenetics</i> , 2011 , 6, 1257-64	5.7	78
72	DNA methylation, isocitrate dehydrogenase mutation, and survival in glioma. <i>Journal of the National Cancer Institute</i> , 2011 , 103, 143-53	9.7	194
71	DNA methylation array analysis identifies profiles of blood-derived DNA methylation associated with bladder cancer. <i>Journal of Clinical Oncology</i> , 2011 , 29, 1133-9	2.2	105
70	Infant growth restriction is associated with distinct patterns of DNA methylation in human placentas. <i>Epigenetics</i> , 2011 , 6, 920-7	5.7	119
69	Global hypomethylation identifies Loci targeted for hypermethylation in head and neck cancer. <i>Clinical Cancer Research</i> , 2011 , 17, 3579-89	12.9	68
68	Polycomb group genes are targets of aberrant DNA methylation in renal cell carcinoma. <i>Epigenetics</i> , 2011 , 6, 703-9	5.7	23
67	The influence of aging, environmental exposures and local sequence features on the variation of DNA methylation in blood. <i>Epigenetics</i> , 2011 , 6, 908-19	5.7	51
66	Birthweight is associated with DNA promoter methylation of the glucocorticoid receptor in human placenta. <i>Epigenetics</i> , 2011 , 6, 566-72	5.7	135
65	Integrative DNA methylation and gene expression analyses identify DNA packaging and epigenetic regulatory genes associated with low motility sperm. <i>PLoS ONE</i> , 2011 , 6, e20280	3.7	96

64	miR-16 and miR-21 expression in the placenta is associated with fetal growth. <i>PLoS ONE</i> , 2011 , 6, e21210	3.7	104
63	Mature microRNA sequence polymorphism in MIR196A2 is associated with risk and prognosis of head and neck cancer. <i>Clinical Cancer Research</i> , 2010 , 16, 3713-20	12.9	109
62	Implications of LINE1 methylation for bladder cancer risk in women. <i>Clinical Cancer Research</i> , 2010 , 16, 1682-9	12.9	138
61	Semi-supervised recursively partitioned mixture models for identifying cancer subtypes. <i>Bioinformatics</i> , 2010 , 26, 2578-85	7.2	77
60	Maternal cigarette smoking during pregnancy is associated with downregulation of miR-16, miR-21, and miR-146a in the placenta. <i>Epigenetics</i> , 2010 , 5, 583-9	5.7	164
59	Integrated profiling reveals a global correlation between epigenetic and genetic alterations in mesothelioma. <i>Cancer Research</i> , 2010 , 70, 5686-94	10.1	49
58	Breast cancer DNA methylation profiles are associated with tumor size and alcohol and folate intake. <i>PLoS Genetics</i> , 2010 , 6, e1001043	6	128
57	Arsenic exposure predicts bladder cancer survival in a US population. <i>World Journal of Urology</i> , 2010 , 28, 487-92	4	13
56	Bisphenol A exposure leads to specific microRNA alterations in placental cells. <i>Reproductive Toxicology</i> , 2010 , 29, 401-6	3.4	214
55	Downregulated microRNAs in the differential diagnosis of malignant pleural mesothelioma. <i>International Journal of Cancer</i> , 2010 , 127, 2859-69	7.5	82
54	Genetic and epigenetic somatic alterations in head and neck squamous cell carcinomas are globally coordinated but not locally targeted. <i>PLoS ONE</i> , 2010 , 5, e9651	3.7	31
53	Identification of methylated genes associated with aggressive bladder cancer. <i>PLoS ONE</i> , 2010 , 5, e12334	3.7	71
52	A let-7 microRNA-binding site polymorphism in the KRAS 3'SUTR is associated with reduced survival in oral cancers. <i>Carcinogenesis</i> , 2009 , 30, 1003-7	4.6	171
51	Differentiation of lung adenocarcinoma, pleural mesothelioma, and nonmalignant pulmonary tissues using DNA methylation profiles. <i>Cancer Research</i> , 2009 , 69, 6315-21	10.1	62
50	Genetic variation in the vitamin C transporter, SLC23A2, modifies the risk of HPV16-associated head and neck cancer. <i>Carcinogenesis</i> , 2009 , 30, 977-81	4.6	49
49	MicroRNA expression ratio is predictive of head and neck squamous cell carcinoma. <i>Clinical Cancer Research</i> , 2009 , 15, 2850-5	12.9	215
48	Epigenetic profiles distinguish pleural mesothelioma from normal pleura and predict lung asbestos burden and clinical outcome. <i>Cancer Research</i> , 2009 , 69, 227-34	10.1	128
47	Copy number variation has little impact on bead-array-based measures of DNA methylation. <i>Bioinformatics</i> , 2009 , 25, 1999-2005	7.2	32

46	EGFR pathway polymorphisms and bladder cancer susceptibility and prognosis. <i>Carcinogenesis</i> , 2009 , 30, 1155-60	4.6	36
45	Epigenetic profiling reveals etiologically distinct patterns of DNA methylation in head and neck squamous cell carcinoma. <i>Carcinogenesis</i> , 2009 , 30, 416-22	4.6	93
44	Aging and environmental exposures alter tissue-specific DNA methylation dependent upon CpG island context. <i>PLoS Genetics</i> , 2009 , 5, e1000602	6	773
43	A case-control study of smoking and bladder cancer risk: emergent patterns over time. <i>Journal of the National Cancer Institute</i> , 2009 , 101, 1553-61	9.7	128
42	Smoking modifies the relationship between XRCC1 haplotypes and HPV16-negative head and neck squamous cell carcinoma. <i>International Journal of Cancer</i> , 2009 , 124, 2690-6	7.5	28
41	Bladder cancer SNP panel predicts susceptibility and survival. <i>Human Genetics</i> , 2009 , 125, 527-39	6.3	72
40	Epigenetics in the placenta. <i>American Journal of Reproductive Immunology</i> , 2009 , 62, 78-89	3.8	157
39	A population-based case-control study of marijuana use and head and neck squamous cell carcinoma. <i>Cancer Prevention Research</i> , 2009 , 2, 759-68	3.2	52
38	DNA repair genotype interacts with arsenic exposure to increase bladder cancer risk. <i>Toxicology Letters</i> , 2009 , 187, 10-4	4.4	33
37	MicroRNA expression in head and neck cancer associates with alcohol consumption and survival. <i>Carcinogenesis</i> , 2009 , 30, 2059-63	4.6	123
36	Model-based clustering of DNA methylation array data: a recursive-partitioning algorithm for high-dimensional data arising as a mixture of beta distributions. <i>BMC Bioinformatics</i> , 2008 , 9, 365	3.6	152
35	Genetic and epigenetic tumor suppressor gene silencing are distinct molecular phenotypes driven by growth promoting mutations in nonsmall cell lung cancer. <i>Journal of Cancer Epidemiology</i> , 2008 , 2008, 215809	2.8	3
34	A genotype-phenotype examination of cyclin D1 on risk and outcome of squamous cell carcinoma of the head and neck. <i>Clinical Cancer Research</i> , 2008 , 14, 2371-7	12.9	23
33	Asbestos exposure predicts cell cycle control gene promoter methylation in pleural mesothelioma. <i>Carcinogenesis</i> , 2008 , 29, 1555-9	4.6	74
32	Human papillomavirus-16 modifies the association between fruit consumption and head and neck squamous cell carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008 , 17, 3419-26	4	16
31	Chromosome 12p deletions in TEL-AML1 childhood acute lymphoblastic leukemia are associated with retrotransposon elements and occur postnatally. <i>Cancer Research</i> , 2008 , 68, 9935-44	10.1	20
30	Histological classification and stage of newly diagnosed bladder cancer in a population-based study from the Northeastern United States. <i>Scandinavian Journal of Urology and Nephrology</i> , 2008 , 42, 237-42		33
29	Line region hypomethylation is associated with lifestyle and differs by human papillomavirus status in head and neck squamous cell carcinomas. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008 , 17, 966-71	4	45

28	Asbestos burden predicts survival in pleural mesothelioma. <i>Environmental Health Perspectives</i> , 2008 , 116, 723-6	8.4	22
27	Hypermethylation of E-cadherin is an independent predictor of improved survival in head and neck squamous cell carcinoma. <i>Cancer</i> , 2008 , 113, 1566-71	6.4	49
26	Dairy products, leanness, and head and neck squamous cell carcinoma. <i>Head and Neck</i> , 2008 , 30, 1193-205	4.2	20
25	Global DNA methylation level in whole blood as a biomarker in head and neck squamous cell carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007 , 16, 108-14	4	256
24	Penalized item response theory models: application to epigenetic alterations in bladder cancer. <i>Biometrics</i> , 2007 , 63, 1269-77	1.8	9
23	Fundamental differences in cell cycle deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers. <i>Cancer Research</i> , 2007 , 67, 4605-19	10.1	351
22	Promoter hypermethylation is associated with current smoking, age, gender and survival in bladder cancer. <i>Carcinogenesis</i> , 2007 , 28, 1745-51	4.6	68
21	Survival following the diagnosis of noninvasive bladder cancer: WHO/International Society of Urological Pathology versus WHO classification systems. <i>Journal of Urology</i> , 2007 , 178, 1196-200; discussion 1200	2.5	31
20	Epigenetic inactivation of the SFRP genes is associated with drinking, smoking and HPV in head and neck squamous cell carcinoma. <i>International Journal of Cancer</i> , 2006 , 119, 1761-6	7.5	101
19	Glutathione S-transferase polymorphisms and the synergy of alcohol and tobacco in oral, pharyngeal, and laryngeal carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 2196-202	4	64
18	Examination of a CpG island methylator phenotype and implications of methylation profiles in solid tumors. <i>Cancer Research</i> , 2006 , 66, 10621-9	10.1	85
17	MicroRNA responses to cellular stress. <i>Cancer Research</i> , 2006 , 66, 10843-8	10.1	343
16	Carcinogen exposure and epigenetic silencing in bladder cancer. <i>Annals of the New York Academy of Sciences</i> , 2006 , 1076, 810-21	6.5	44
15	Carcinogen exposure and gene promoter hypermethylation in bladder cancer. <i>Carcinogenesis</i> , 2006 , 27, 112-6	4.6	139
14	PTEN expression in non-small-cell lung cancer: evaluating its relation to tumor characteristics, allelic loss, and epigenetic alteration. <i>Human Pathology</i> , 2005 , 36, 768-76	3.7	209
13	Alterations of 9p in squamous cell carcinoma and adenocarcinoma of the lung: association with smoking, TP53, and survival. <i>Cancer Genetics and Cytogenetics</i> , 2005 , 162, 115-21		12
12	Hypermethylation of RASSF1A and BLU tumor suppressor genes in non-small cell lung cancer: implications for tobacco smoking during adolescence. <i>International Journal of Cancer</i> , 2005 , 114, 219-23	7.5	54
11	Loss of heterozygosity on chromosome 9q and p53 alterations in human bladder cancer. <i>Cancer</i> , 2005 , 104, 1918-23	6.4	26

10	Epigenetic silencing of the PRSS3 putative tumor suppressor gene in non-small cell lung cancer. <i>Molecular Carcinogenesis</i> , 2005 , 44, 146-50	5	24
9	The race associated allele of Semaphorin 3B (SEMA3B) T415I and its role in lung cancer in African-Americans and Latino-Americans. <i>Carcinogenesis</i> , 2005 , 26, 1446-9	4.6	15
8	TP53 mutation, allelism and survival in non-small cell lung cancer. <i>Carcinogenesis</i> , 2005 , 26, 1770-3	4.6	53
7	Epigenetic inactivation of SFRP genes and TP53 alteration act jointly as markers of invasive bladder cancer. <i>Cancer Research</i> , 2005 , 65, 7081-5	10.1	120
6	Loss of heterozygosity of chromosome 3p21 is associated with mutant TP53 and better patient survival in non-small-cell lung cancer. <i>Cancer Research</i> , 2004 , 64, 8702-7	10.1	42
5	Inactivation of the Fanconi anemia/BRCA pathway in lung and oral cancers: implications for treatment and survival. <i>Oncogene</i> , 2004 , 23, 1000-4	9.2	196
4	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: Findings from the Pregnancy and Childhood Epigenetics (PACE) consortium		1
3	Cadmium-associated differential methylation throughout the placental genome: epigenome-wide association study of two US birth cohorts		1
2	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth		3
1	Reference-free deconvolution of DNA methylation data and mediation by cell composition effects		1