

# Carmen J Marsit

## List of PR Articles by Year in descending order

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283

PR articles

17,663

PR citations

7572

67

PR h-index

8989

129

g-index

298

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21221

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7243

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27698

citing authors

#	ARTICLE	IF	PR CITATIONS
1	Epigenetic landscape of 5-hydroxymethylcytosine and associations with gene expression in placenta. <i>Epigenetics</i> , 2024, 19, .	3.1	2
2	Placental transcriptome variation associated with season, location, and urinary prenatal pyrethroid metabolites of Thai farm-working women. <i>Environmental Pollution</i> , 2024, 349, 123873.	7.8	5
3	Differential impact of prenatal PTSD symptoms and preconception trauma exposure on placental <i>NR3C1</i> and <i>FKBP5</i> methylation. <i>Stress</i> , 2024, 27, .	2.3	2
4	Childhood adversity, accelerated GrimAge, and associated health consequences. <i>Journal of Behavioral Medicine</i> , 2024, 47, 913-926.	2.5	8
5	Associations between placental hydroxymethylation and birthweight. , 2024, 2, 1-7.		0
6	Variation in placental microRNA expression associates with maternal family history of cardiovascular disease. <i>Journal of Developmental Origins of Health and Disease</i> , 2023, 14, 132-139.	1.4	1
7	Associations between prenatal organophosphate pesticide exposure and placental gene networks. <i>Environmental Research</i> , 2023, 224, 115490.	7.9	23
8	Pregnancy-related hemodynamic biomarkers in relation to trimester-specific maternal per- and polyfluoroalkyl substances exposures and adverse birth outcomes. <i>Environmental Pollution</i> , 2023, 323, 121331.	7.8	24
9	Placental transcriptomic signatures of prenatal exposure to Hydroxy-Polycyclic aromatic hydrocarbons. <i>Environment International</i> , 2023, 172, 107763.	10.3	30
10	Newborn metabolomic signatures of maternal per- and polyfluoroalkyl substance exposure and reduced length of gestation. <i>Nature Communications</i> , 2023, 14, .	13.9	85
11	Prioritization of potential causative genes for schizophrenia in placenta. <i>Nature Communications</i> , 2023, 14, .	13.9	27
12	Metabolic Perturbations Associated with an Exposure Mixture of Per- and Polyfluoroalkyl Substances in the Atlanta African American Maternal-Child Cohort. <i>Environmental Science &amp; Technology</i> , 2023, 57, 16206-16218.	11.1	31
13	Extracellular vesicle microRNA in early versus late pregnancy with birth outcomes in the MADRES study. <i>Epigenetics</i> , 2022, 17, 269-285.	3.1	24
14	Epigenome-wide scan identifies differentially methylated regions for lung cancer using pre-diagnostic peripheral blood. <i>Epigenetics</i> , 2022, 17, 460-472.	3.1	22
15	Association between placental toxic metal exposure and NICU Network Neurobehavioral Scales (NNNS) profiles in the Rhode Island Child Health Study (RICHS). <i>Environmental Research</i> , 2022, 204, 111939.	7.9	16
16	Urinary metals and maternal circulating extracellular vesicle microRNA in the MADRES pregnancy cohort. <i>Epigenetics</i> , 2022, 17, 1128-1142.	3.1	21
17	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> , 2022, 158, 106964.	10.3	134
18	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.	7.8	42

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19	Selenium-associated differentially expressed microRNAs and their targeted mRNAs across the placental genome in two U.S. birth cohorts. <i>Epigenetics</i> , 2022, 17, 1234-1245.	3.1	7
20	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.	1.3	12
21	Prenatal exposure to metal mixtures and newborn neurobehavior in the Rhode Island Child Health Study. <i>Environmental Epidemiology</i> , 2022, 6, e194.	3.4	22
22	Placental genomics mediates genetic associations with complex health traits and disease. <i>Nature Communications</i> , 2022, 13, .	13.9	47
23	PM2.5 exposure during pregnancy is associated with altered placental expression of lipid metabolic genes in a US birth cohort. <i>Environmental Research</i> , 2022, 211, 113066.	7.9	29
24	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 &amp; Technology</i> , 2022, 56, 6560-6573.	11.1	88
25	Placental multi-omics integration identifies candidate functional genes for birthweight. <i>Nature Communications</i> , 2022, 13, .	13.9	26
26	Placental Gene Transcript Proportions are Altered in the Presence of In Utero Arsenic and Cadmium Exposures, Genetic Variants, and Birth Weight Differences. <i>Frontiers in Genetics</i> , 2022, 13, .	2.4	3
27	Prenatal exposure to particulate matter and placental gene expression. <i>Environment International</i> , 2022, 165, 107310.	10.3	33
28	Maternal Pre-pregnancy BMI Associates With Sex-Specific Placental microRNA Patterns. <i>Current Developments in Nutrition</i> , 2022, 6, 671.	0.2	0
29	CpG methylation patterns in placenta and neonatal blood are differentially associated with neonatal inflammation. <i>Pediatric Research</i> , 2022, 93, 1072-1084.	2.4	6
30	Prenatal lead (Pb) exposure is associated with differential placental DNA methylation and hydroxymethylation in a human population. <i>Epigenetics</i> , 2022, 17, 2404-2420.	3.1	12
31	A meta-analysis of pre-pregnancy maternal body mass index and placental DNA methylation identifies 27 CpG sites with implications for mother-child health. <i>Communications Biology</i> , 2022, 5, .	4.4	14
32	Select Early-Life Environmental Exposures and DNA Methylation in the Placenta. <i>Current Environmental Health Reports</i> , 2022, 10, 22-34.	8.3	30
33	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. <i>Epigenetics</i> , 2021, 16, 770-782.	3.1	16
34	Genome-wide DNA methylation differences and polychlorinated biphenyl (PCB) exposure in a US population. <i>Epigenetics</i> , 2021, 16, 338-352.	3.1	21
35	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.	3.8	2
36	In-utero exposure to zidovudine-containing antiretroviral therapy and clonal hematopoiesis in HIV-exposed uninfected newborns. <i>Aids</i> , 2021, 35, 1525-1535.	2.5	2

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37	Light Environment Influences Developmental Programming of the Metabolic and Visual Systems in Mice. , 2021, 62, 22.		8
38	DNA methylation in former extremely low birth weight newborns: association with cardiovascular and endocrine function. Pediatric Research, 2021, 91, 1469-1477.	2.4	6
39	Extracellular vesicle-enriched miRNA profiles across pregnancy in the MADRES cohort. PLoS ONE, 2021, 16, e0251259.	2.4	20
40	Pre-diagnosis neutrophil-to-lymphocyte ratio and mortality in individuals who develop lung cancer. Cancer Causes and Control, 2021, 32, 1227-1236.	1.8	12
41	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. Nature Communications, 2021, 12, .	13.9	71
42	Placental gene networks at the interface between maternal PM2.5 exposure early in gestation and reduced infant birthweight. Environmental Research, 2021, 199, 111342.	7.9	36
43	Developmental chronodisruption alters placental signaling in mice. PLoS ONE, 2021, 16, e0255296.	2.4	6
44	A scalable workflow to characterize the human exposome. Nature Communications, 2021, 12, .	13.9	64
45	A Comprehensive Assessment of Associations between Prenatal Phthalate Exposure and the Placental Transcriptomic Landscape. Environmental Health Perspectives, 2021, 129, .	8.8	43
46	Prenatal risk factors and neonatal DNA methylation in very preterm infants. Clinical Epigenetics, 2021, 13, .	4.0	16
47	Longitudinal changes in epigenetic age in youth with perinatally acquired HIV and youth who are perinatally HIV-exposed uninfected. Aids, 2021, 35, 811-819.	2.5	14
48	NEOage clocks - epigenetic clocks to estimate post-menstrual and postnatal age in preterm infants. Aging, 2021, 13, 23527-23544.	2.5	15
49	In-depth characterization of the placental imprintome reveals novel differentially methylated regions across birth weight categories. Epigenetics, 2020, 15, 47-60.	3.1	17
50	Copper associates with differential methylation in placentae from two US birth cohorts. Epigenetics, 2020, 15, 215-230.	3.1	26
51	Genome-wide characterization of cytosine-specific 5-hydroxymethylation in normal breast tissue. Epigenetics, 2020, 15, 398-418.	3.1	15
52	Epigenome-Wide Association Study Using Prediagnostic Bloods Identifies New Genomic Regions Associated With Pancreatic Cancer Risk. JNCI Cancer Spectrum, 2020, 4, .	3.0	11
53	Serious neonatal morbidities are associated with differences in DNA methylation among very preterm infants. Clinical Epigenetics, 2020, 12, .	4.0	39
54	Associations of maternal diet and placenta leptin methylation. Molecular and Cellular Endocrinology, 2020, 505, 110739.	3.5	21

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55	Seasonally variant gene expression in full-term human placenta. <i>FASEB Journal</i> , 2020, 34, 10431-10442.	0.7	13
56	Epigenome-wide analysis identifies genes and pathways linked to acoustic cry variation in preterm infants. <i>Pediatric Research</i> , 2020, 89, 1848-1854.	2.4	5
57	AHRR methylation in heavy smokers: associations with smoking, lung cancer risk, and lung cancer mortality. <i>BMC Cancer</i> , 2020, 20, .	3.1	32
58	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, .	4.5	47
59	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.	1.2	13
60	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. <i>Environmental Epigenetics</i> , 2020, 6, .	1.7	23
61	Sex-specific DNA methylation differences in people exposed to polybrominated biphenyl. <i>Epigenomics</i> , 2020, 12, 757-770.	2.3	20
62	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.	1.6	13
63	Molecular markers of neuroendocrine function and mitochondrial biogenesis associated with early life stress. <i>Psychoneuroendocrinology</i> , 2020, 116, 104632.	2.8	30
64	Social Stress-Related Epigenetic Changes Associated With Increased Heart Rate Variability in Infants. <i>Frontiers in Behavioral Neuroscience</i> , 2020, 13, .	2.4	7
65	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.	1.6	21
66	DNA methylation in children with prenatal methamphetamine exposure and environmental adversity. <i>Pediatric Research</i> , 2020, 89, 1152-1156.	2.4	14
67	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.	10.3	31
68	Associations Between the Features of Gross Placental Morphology and Birthweight. <i>Pediatric and Developmental Pathology</i> , 2019, 22, 194-204.	1.3	23
69	Accurate ethnicity prediction from placental DNA methylation data. <i>Epigenetics and Chromatin</i> , 2019, 12, .	3.3	62
70	Exposure to polybrominated biphenyl (PBB) associates with genome-wide DNA methylation differences in peripheral blood. <i>Epigenetics</i> , 2019, 14, 52-66.	3.1	48
71	MicroRNA Dysregulation and Non-Muscle-Invasive Bladder Cancer Prognosis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 782-788.	1.2	21
72	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.	2.5	18

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73	DNA methylation of <i>NR3c1</i> in infancy: Associations between maternal caregiving and infant sex. <i>Infant Mental Health Journal</i> , 2019, 40, 513-522.	2.2	26
74	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.	3.1	19
75	A Neurodevelopmental Model of Combined Pyrethroid and Chronic Stress Exposure. <i>Toxics</i> , 2019, 7, 24.	4.1	20
76	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, .	8.8	27
77	Epigenome-wide Analysis Identifies Genes and Pathways Linked to Neurobehavioral Variation in Preterm Infants. <i>Scientific Reports</i> , 2019, 9, .	3.5	53
78	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	26.1	554
79	Microorganisms in the Placenta: Links to Early-Life Inflammation and Neurodevelopment in Children. <i>Clinical Microbiology Reviews</i> , 2019, 32, .	17.4	33
80	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, .	13.9	174
81	Maternal circadian disruption is associated with variation in placental DNA methylation. <i>PLoS ONE</i> , 2019, 14, e0215745.	2.4	32
82	Prenatal arsenic exposure alters the placental expression of multiple epigenetic regulators in a sex-dependent manner. <i>Environmental Health</i> , 2019, 18, .	5.5	39
83	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, .	5.5	33
84	Association between zidovudine-containing antiretroviral therapy exposure in utero and leukocyte telomere length at birth. <i>Aids</i> , 2019, 33, 2091-2096.	2.5	3
85	Smoking during pregnancy increases chemerin expression in neonatal tissue. <i>Experimental Physiology</i> , 2019, 104, 93-99.	2.6	6
86	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.	10.3	12
87	Chrysotile fibers in tissue adjacent to laryngeal squamous cell carcinoma in cases with a history of occupational asbestos exposure. <i>Modern Pathology</i> , 2019, 33, 228-234.	4.9	10
88	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	2.5	133
89	Environmental exposure to polybrominated biphenyl (PBB) associates with an increased rate of biological aging. <i>Aging</i> , 2019, 11, 5498-5517.	2.5	20
90	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.	2.5	11

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91	Epigenetic Mechanisms in The Placenta Related to Infant Neurodevelopment. <i>Epigenomics</i> , 2018, 10, 321-333.	2.3	60
92	Effect of frozen/thawed embryo transfer on birthweight, macromacrosomia, and low birthweight rates in singleton infants. <i>American Journal of Obstetrics and Gynecology</i> , 2018, 218, 433.e1-433.e10.	2.4	76
93	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, .	3.5	10
94	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.	2.4	23
95	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	5.1	136
96	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018, 142, 874-882.	4.5	82
97	Genetic regulation of the placental transcriptome underlies birth weight and risk of childhood obesity. <i>PLoS Genetics</i> , 2018, 14, e1007799.	3.3	56
98	Epigenetic Programming by Maternal Behavior in the Human Infant. <i>Pediatrics</i> , 2018, 142, .	4.7	81
99	Mitochondrial and glycolysis-regulatory gene expression profiles are associated with intrauterine growth restriction. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2018, , 1-10.	1.8	10
100	Methylation-derived Neutrophil-to-Lymphocyte Ratio and Lung Cancer Risk in Heavy Smokers. <i>Cancer Prevention Research</i> , 2018, 11, 727-734.	1.5	31
101	Variation in DNA methylation of human blood over a 1-year period using the Illumina MethylationEPIC array. <i>Epigenetics</i> , 2018, 13, 1056-1071.	3.1	48
102	Environmentally Induced Epigenetic Plasticity in Development: Epigenetic Toxicity and Epigenetic Adaptation. <i>Current Epidemiology Reports</i> , 2018, 5, 450-460.	3.3	18
103	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, .	8.8	78
104	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.	1.2	1
105	Integrating -Omics Approaches into Human Population-Based Studies of Prenatal and Early-Life Exposures. <i>Current Environmental Health Reports</i> , 2018, 5, 328-337.	8.3	44
106	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, .	5.5	90
107	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, 35.	4.1	18
108	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, 2296.	4.5	18

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109	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.	10.3	63
110	Associations Between Features of Placental Morphology and Birth Weight in Dichorionic Twins. <i>American Journal of Epidemiology</i> , 2018, 188, 518-526.	3.4	11
111	Transdisciplinary approaches enhance the production of translational knowledge. <i>Translational Research</i> , 2017, 182, 123-134.	4.2	51
112	Using neonatal skin to study the developmental programming of aging. <i>Experimental Gerontology</i> , 2017, 94, 93-98.	3.8	4
113	SExual Epigenetic Dimorphism in The Human Placenta: Implications for Susceptibility During The Prenatal Period. <i>Epigenomics</i> , 2017, 9, 267-278.	2.3	122
114	Placental imprinting variation associated with assisted reproductive technologies and subfertility. <i>Epigenetics</i> , 2017, 12, 653-661.	3.1	52
115	Pulmonary microRNA profiling: implications in upper lobe predominant lung disease. <i>Clinical Epigenetics</i> , 2017, 9, .	4.0	39
116	Prenatal exposure to neurotoxic metals is associated with increased placental glucocorticoid receptor DNA methylation. <i>Epigenetics</i> , 2017, 12, 607-615.	3.1	72
117	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.	1.2	72
118	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.	3.0	248
119	Maternal residential air pollution and placental imprinted gene expression. <i>Environment International</i> , 2017, 108, 204-211.	10.3	33
120	Change in FK506 binding protein 5 ( <i>FKBP5</i> ) methylation over time among preschoolers with adversity. <i>Development and Psychopathology</i> , 2017, 29, 1627-1634.	3.4	74
121	Stress exposure and psychopathology alter methylation of the serotonin receptor 2A ( <i>HTR2A</i> ) gene in preschoolers. <i>Development and Psychopathology</i> , 2017, 29, 1619-1626.	3.4	47
122	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.	3.4	50
123	Expression quantitative trait loci (eQTLs) in human placentas suggest developmental origins of complex diseases. <i>Human Molecular Genetics</i> , 2017, 26, 3432-3441.	3.0	70
124	Expression of placental regulatory genes is associated with fetal growth. <i>Journal of Perinatal Medicine</i> , 2017, 45, 887-893.	1.3	16
125	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	45
126	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, .	5.5	62

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127	The aquaglyceroporin AQP9 contributes to the sex-specific effects of in utero arsenic exposure on placental gene expression. <i>Environmental Health</i> , 2017, 16, .	5.5	20
128	Whole-transcriptome analysis delineates the human placenta gene network and its associations with fetal growth. <i>BMC Genomics</i> , 2017, 18, .	3.3	69
129	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.	8.8	279
130	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, 1253-1260.	8.8	115
131	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, .	2.4	76
132	Methylation of the Glucocorticoid Receptor (NR3C1) in Placenta Is Associated with Infant Cry Acoustics. <i>Frontiers in Behavioral Neuroscience</i> , 2016, 10, .	2.4	16
133	Maternal smoking during pregnancy is associated with mitochondrial DNA methylation. <i>Environmental Epigenetics</i> , 2016, 2, dvw020.	1.7	31
134	Prenatal Programming of Infant Neurobehaviour in a Healthy Population. <i>Paediatric and Perinatal Epidemiology</i> , 2016, 30, 367-375.	2.2	36
135	Regions of variable DNA methylation in human placenta associated with newborn neurobehavior. <i>Epigenetics</i> , 2016, 11, 603-613.	3.1	103
136	Prenatal Major Depressive Disorder, Placenta Glucocorticoid and Serotonergic Signaling, and Infant Cortisol Response. <i>Psychosomatic Medicine</i> , 2016, 78, 979-990.	2.2	72
137	Reference-free deconvolution of DNA methylation data and mediation by cell composition effects. <i>BMC Bioinformatics</i> , 2016, 17, .	3.0	238
138	Maternal residential proximity to major roadways, birth weight, and placental DNA methylation. <i>Environment International</i> , 2016, 92-93, 43-49.	10.3	75
139	Hydroxymethylation is uniquely distributed within term placenta, and is associated with gene expression. <i>FASEB Journal</i> , 2016, 30, 2874-2884.	0.7	42
140	Epigenetic Regulation of Placental <i>NR3C1</i> : Mechanism Underlying Prenatal Programming of Infant Neurobehavior by Maternal Smoking?. <i>Child Development</i> , 2016, 87, 49-60.	3.6	48
141	Introduction to the Special Section on Epigenetics. <i>Child Development</i> , 2016, 87, 29-37.	3.6	66
142	The Contributions of Maternal Sensitivity and Maternal Depressive Symptoms to Epigenetic Processes and Neuroendocrine Functioning. <i>Child Development</i> , 2016, 87, 73-85.	3.6	86
143	Maternal cadmium, placental PCDHAC1, and fetal development. <i>Reproductive Toxicology</i> , 2016, 65, 263-271.	2.8	38
144	Methylation of the Glucocorticoid Receptor Gene Promoter in Preschoolers: Links With Internalizing Behavior Problems. <i>Child Development</i> , 2016, 87, 86-97.	3.6	84

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145	Placental Epigenetics in Children's Environmental Health. <i>Seminars in Reproductive Medicine</i> , 2016, 34, 036-041.	1.0	33
146	Placental Metal Concentrations in Relation to Maternal and Infant Toenails in a U.S. Cohort. <i>Environmental Science &amp; Technology</i> , 2016, 50, 1587-1594.	11.1	60
147	Seroepidemiology of Human Polyomaviruses in a US Population. <i>American Journal of Epidemiology</i> , 2016, 183, 61-69.	3.4	135
148	Temporal variability of urinary cadmium in spot urine samples and first morning voids. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2016, 27, 306-312.	4.1	14
149	Medical morbidities and DNA methylation of NR3C1 in preterm infants. <i>Pediatric Research</i> , 2016, 81, 68-74.	2.4	25
150	Childhood maltreatment and methylation of FK506 binding protein 5 gene ( <i>FKBP5</i> ). <i>Development and Psychopathology</i> , 2015, 27, 1637-1645.	3.4	116
151	Neurobehavior Related to Epigenetic Differences in Preterm Infants. <i>Epigenomics</i> , 2015, 7, 1123-1136.	2.3	84
152	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, .	4.0	78
153	MicroRNA molecular profiling from matched tumor and bio-fluids in bladder cancer. <i>Molecular Cancer</i> , 2015, 14, .	32.3	181
154	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, .	2.4	54
155	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.	2.4	11
156	Placental DNA Methylation Related to Both Infant Toenail Mercury and Adverse Neurobehavioral Outcomes. <i>Environmental Health Perspectives</i> , 2015, 123, 723-729.	8.8	87
157	Maternal psychiatric disease and epigenetic evidence suggest a common biology for poor fetal growth. <i>BMC Pregnancy and Childbirth</i> , 2015, 15, .	2.5	63
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