Andrea A Baccarelli

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4040862/publications.pdf Version: 2024-02-01

		14655	12946
339	22,413	66	131
papers	citations	h-index	g-index
0.51	0.5.1	0.5.1	00500
351	351	351	22592
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	An epigenetic biomarker of aging for lifespan and healthspan. Aging, 2018, 10, 573-591.	3.1	1,552
2	DNA methylation GrimAge strongly predicts lifespan and healthspan. Aging, 2019, 11, 303-327.	3.1	1,128
3	DNA methylation age of blood predicts all-cause mortality in later life. Genome Biology, 2015, 16, 25.	8.8	928
4	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
5	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	6.2	717
6	Expert position paper on air pollution and cardiovascular disease. European Heart Journal, 2015, 36, 83-93.	2.2	646
7	Rapid DNA Methylation Changes after Exposure to Traffic Particles. American Journal of Respiratory and Critical Care Medicine, 2009, 179, 572-578.	5.6	608
8	DNA methylation aging clocks: challenges and recommendations. Genome Biology, 2019, 20, 249.	8.8	552
9	Epigenetic clock analysis of diet, exercise, education, and lifestyle factors. Aging, 2017, 9, 419-446.	3.1	521
10	Epigenetic clock for skin and blood cells applied to Hutchinson Gilford Progeria Syndrome and ex vivo studies. Aging, 2018, 10, 1758-1775.	3.1	406
11	Outdoor air pollution and cancer: An overview of the current evidence and public health recommendations. Ca-A Cancer Journal for Clinicians, 2020, 70, 460-479.	329.8	348
12	Effects of Particulate Matter on Genomic DNA Methylation Content and <i>iNOS</i> Promoter Methylation. Environmental Health Perspectives, 2009, 117, 217-222.	6.0	310
13	Cohort Profile: Project Viva. International Journal of Epidemiology, 2015, 44, 37-48.	1.9	275
14	Quantification of the pace of biological aging in humans through a blood test, the DunedinPoAm DNA methylation algorithm. ELife, 2020, 9, .	6.0	268
15	Maternal Prepregnancy Body Mass Index and Gestational Weight Gain on Pregnancy Outcomes. PLoS ONE, 2013, 8, e82310.	2.5	266
16	Air Pollution and Markers of Coagulation, Inflammation, and Endothelial Function. Epidemiology, 2012, 23, 332-340.	2.7	259
17	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. Genome Biology, 2016, 17, 255.	8.8	251
18	Extracellular vesicles: roles in gamete maturation, fertilization and embryo implantation. Human Reproduction Update, 2016, 22, dmv055.	10.8	248

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19	DunedinPACE, a DNA methylation biomarker of the pace of aging. ELife, 2022, 11, .	6.0	214
20	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. Human Molecular Genetics, 2017, 26, 4067-4085.	2.9	211
21	DNA methylation-based estimator of telomere length. Aging, 2019, 11, 5895-5923.	3.1	198
22	An epigenetic clock for gestational age at birth based on blood methylation data. Genome Biology, 2016, 17, 206.	8.8	193
23	Cardiovascular Epigenetics. Circulation: Cardiovascular Genetics, 2010, 3, 567-573.	5.1	186
24	Exposure to Particulate Air Pollution and Risk of Deep Vein Thrombosis. Archives of Internal Medicine, 2008, 168, 920.	3.8	184
25	Hallmarks of environmental insults. Cell, 2021, 184, 1455-1468.	28.9	177
26	The Role of DNA Methylation in Cardiovascular Risk and Disease. Circulation Research, 2016, 118, 119-131.	4.5	167
27	Using High-Resolution Satellite Aerosol Optical Depth To Estimate Daily PM _{2.5} Geographical Distribution in Mexico City. Environmental Science & Technology, 2015, 49, 8576-8584.	10.0	165
28	Blood Epigenetic Age may Predict Cancer Incidence and Mortality. EBioMedicine, 2016, 5, 68-73.	6.1	162
29	Air pollution and gene-specific methylation in the Normative Aging Study. Epigenetics, 2014, 9, 448-458.	2.7	159
30	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
31	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. Nature Communications, 2018, 9, 387.	12.8	151
32	Blood Leukocyte DNA Methylation Predicts Risk of Future Myocardial Infarction and Coronary Heart Disease. Circulation, 2019, 140, 645-657.	1.6	151
33	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. Diabetes Care, 2020, 43, 98-105.	8.6	145
34	Effect of prenatal arsenic exposure on DNA methylation and leukocyte subpopulations in cord blood. Epigenetics, 2014, 9, 774-782.	2.7	140
35	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	12.8	140
36	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	3.1	137

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37	Platelet mitochondrial DNA methylation: a potential new marker of cardiovascular disease. Clinical Epigenetics, 2015, 7, 44.	4.1	132
38	Short-term exposure to high ambient air pollution increases airway inflammation and respiratory symptoms in chronic obstructive pulmonary disease patients in Beijing, China. Environment International, 2016, 94, 76-82.	10.0	131
39	The nasal methylome as a biomarker of asthma and airway inflammation in children. Nature Communications, 2019, 10, 3095.	12.8	129
40	Long-term exposure to air pollution is associated with biological aging. Oncotarget, 2016, 7, 74510-74525.	1.8	126
41	B vitamins attenuate the epigenetic effects of ambient fine particles in a pilot human intervention trial. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 3503-3508.	7.1	121
42	Epigenetic Pathways in Human Disease: The Impact of DNA Methylation on Stress-Related Pathogenesis and Current Challenges in Biomarker Development. EBioMedicine, 2017, 18, 327-350.	6.1	113
43	Cardiac Autonomic Dysfunction. Circulation, 2008, 117, 1802-1809.	1.6	112
44	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. Environmental Health Perspectives, 2019, 127, 57012.	6.0	111
45	Repetitive element DNA methylation and circulating endothelial and inflammation markers in the VA normative aging study. Epigenetics, 2010, 5, 222-228.	2.7	106
46	Neonatal Thyroid Function in Seveso 25 Years after Maternal Exposure to Dioxin. PLoS Medicine, 2008, 5, e161.	8.4	106
47	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	1.9	105
48	Ambient particulate matter and microRNAs in extracellular vesicles: a pilot study of older individuals. Particle and Fibre Toxicology, 2015, 13, 13.	6.2	96
49	Association of air particulate pollution with bone loss over time and bone fracture risk: analysis of data from two independent studies. Lancet Planetary Health, The, 2017, 1, e337-e347.	11.4	96
50	Persistent DNA methylation changes associated with prenatal mercury exposure and cognitive performance during childhood. Scientific Reports, 2017, 7, 288.	3.3	95
51	miRNA Profiles in Extracellular Vesicles From Serum Early in Pregnancies Complicated by Gestational Diabetes Mellitus. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 5157-5169.	3.6	95
52	Environmental exposures, epigenetics and cardiovascular disease. Current Opinion in Clinical Nutrition and Metabolic Care, 2012, 15, 323-329.	2.5	90
53	Urinary concentrations of biomarkers of phthalates and phthalate alternatives and IVF outcomes. Environment International, 2018, 111, 23-31.	10.0	85
54	Detection of long non-coding RNAs in human breastmilk extracellular vesicles: Implications for early child development. Epigenetics, 2016, 11, 721-729.	2.7	83

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55	Maternal gut and fetal brain connection: Increased anxiety and reduced social interactions in Wistar rat offspring following peri-conceptional antibiotic exposure. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2016, 71, 76-82.	4.8	82
56	Environmental Health and Long Non-coding RNAs. Current Environmental Health Reports, 2016, 3, 178-187.	6.7	82
57	Endocrine Disruptors: A Potential Risk Factor for Gestational Diabetes Mellitus. American Journal of Perinatology, 2016, 33, 1313-1318.	1.4	81
58	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. Genome Medicine, 2020, 12, 25.	8.2	81
59	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
60	Traffic-Related Air Pollution, Blood Pressure, and Adaptive Response of Mitochondrial Abundance. Circulation, 2016, 133, 378-387.	1.6	77
61	Effects of particulate air pollution on blood pressure in a highly exposed population in Beijing, China: a repeated-measure study. Environmental Health, 2011, 10, 108.	4.0	76
62	Air pollution exposure and lung function in highly exposed subjects in Beijing, China: a repeated-measure study. Particle and Fibre Toxicology, 2014, 11, 51.	6.2	76
63	Extracellular microRNAs in follicular fluid and their potential association with oocyte fertilization and embryo quality: an exploratory study. Journal of Assisted Reproduction and Genetics, 2017, 34, 525-533.	2.5	76
64	Exposure to Low Levels of Lead <i>in Utero</i> and Umbilical Cord Blood DNA Methylation in Project Viva: An Epigenome-Wide Association Study. Environmental Health Perspectives, 2017, 125, 087019.	6.0	73
65	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. Hypertension, 2019, 74, 375-383.	2.7	73
66	Second trimester extracellular microRNAs in maternal blood and fetal growth: An exploratory study. Epigenetics, 2017, 12, 804-810.	2.7	70
67	Prenatal particulate matter exposure and mitochondrial dysfunction at the maternal-fetal interface: Effect modification by maternal lifetime trauma and child sex. Environment International, 2018, 112, 49-58.	10.0	70
68	Ambient particulate air pollution and circulating C-reactive protein level: A systematic review and meta-analysis. International Journal of Hygiene and Environmental Health, 2019, 222, 756-764.	4.3	70
69	Long-term ambient particle exposures and blood DNA methylation age: findings from the VA normative aging study. Environmental Epigenetics, 2016, 2, dvw006.	1.8	68
70	Effects of particulate matter exposure on multiple sclerosis hospital admission in Lombardy region, Italy. Environmental Research, 2016, 145, 68-73.	7.5	68
71	Meta-analysis of epigenome-wide association studies of cognitive abilities. Molecular Psychiatry, 2018, 23, 2133-2144.	7.9	68
72	Nasal cell DNA methylation, inflammation, lung function and wheezing in children with asthma. Epigenomics, 2012, 4, 91-100.	2.1	66

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73	Offspring DNA methylation of the aryl-hydrocarbon receptor repressor gene is associated with maternal BMI, gestational age, and birth weight. Epigenetics, 2015, 10, 913-921.	2.7	65
74	Maternal Lifetime Stress and Prenatal Psychological Functioning and Decreased Placental Mitochondrial DNA Copy Number in the PRISM Study. American Journal of Epidemiology, 2017, 186, 1227-1236.	3.4	65
75	Air Pollution, Smoking, and Plasma Homocysteine. Environmental Health Perspectives, 2007, 115, 176-181.	6.0	64
76	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. Epigenomics, 2019, 11, 1487-1500.	2.1	64
77	Effects of particulate matter exposure on blood 5-hydroxymethylation: results from the Beijing truck driver air pollution study. Epigenetics, 2015, 10, 633-642.	2.7	63
78	Blood Telomere Length Attrition and Cancer Development in the Normative Aging Study Cohort. EBioMedicine, 2015, 2, 591-596.	6.1	62
79	A longitudinal study of DNA methylation as a potential mediator of age-related diabetes risk. GeroScience, 2017, 39, 475-489.	4.6	62
80	An integrative cross-omics analysis of DNA methylation sites of glucose and insulin homeostasis. Nature Communications, 2019, 10, 2581.	12.8	62
81	Prenatal Metal Concentrations and Childhood Cardiometabolic Risk Using Bayesian Kernel Machine Regression to Assess Mixture and Interaction Effects. Epidemiology, 2019, 30, 263-273.	2.7	62
82	Birth weight-for-gestational age is associated with DNA methylation at birth and in childhood. Clinical Epigenetics, 2016, 8, 118.	4.1	61
83	Testing for the indirect effect under the null for genomeâ€wide mediation analyses. Genetic Epidemiology, 2017, 41, 824-833.	1.3	60
84	Effects of shortâ€ŧerm exposure to inhalable particulate matter on DNA methylation of tandem repeats. Environmental and Molecular Mutagenesis, 2014, 55, 322-335.	2.2	59
85	Maternal alcohol consumption and offspring DNA methylation: findings from six general population-based birth cohorts. Epigenomics, 2018, 10, 27-42.	2.1	58
86	Effect of particulate matter-bound metals exposure on prothrombotic biomarkers: A systematic review. Environmental Research, 2019, 177, 108573.	7.5	58
87	Methylome-wide association study provides evidence of particulate matter air pollution-associated DNA methylation. Environment International, 2019, 132, 104723.	10.0	58
88	Prenatal Exposure to Mercury: Associations with Clobal DNA Methylation and Hydroxymethylation in Cord Blood and in Childhood. Environmental Health Perspectives, 2017, 125, 087022.	6.0	57
89	In <i>utero</i> arsenic exposure and epigenome-wide associations in placenta, umbilical artery, and human umbilical vein endothelial cells. Epigenetics, 2015, 10, 1054-1063.	2.7	56
90	Placental mitochondrial DNA and CYP1A1 gene methylation as molecular signatures for tobacco smoke exposure in pregnant women and the relevance for birth weight. Journal of Translational Medicine, 2017, 15, 5.	4.4	56

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91	Prenatal particulate air pollution exposure and body composition in urban preschool children: Examining sensitive windows and sex-specific associations. Environmental Research, 2017, 158, 798-805.	7.5	56
92	Identifying sensitive windows for prenatal particulate air pollution exposure and mitochondrial DNA content in cord blood. Environment International, 2017, 98, 198-203.	10.0	56
93	Exposure to childhood abuse is associated with human sperm DNA methylation. Translational Psychiatry, 2018, 8, 194.	4.8	56
94	Short-term airborne particulate matter exposure alters the epigenetic landscape of human genes associated with the mitogen-activated protein kinase network: a cross-sectional study. Environmental Health, 2014, 13, 94.	4.0	55
95	Altered miRNA expression in the cervix during pregnancy associated with lead and mercury exposure. Epigenomics, 2015, 7, 885-896.	2.1	53
96	An epigenome-wide association study of total serum IgE in Hispanic children. Journal of Allergy and Clinical Immunology, 2017, 140, 571-577.	2.9	53
97	Urinary concentrations of phthalate metabolites, bisphenols and personal care product chemical biomarkers in pregnant women in Israel. Environment International, 2018, 116, 319-325.	10.0	53
98	Prenatal exposure to mixtures of xenoestrogens and repetitive element DNA methylation changes in human placenta. Environment International, 2014, 71, 81-87.	10.0	52
99	Traffic-derived particulate matter exposure and histone H3 modification: A repeated measures study. Environmental Research, 2017, 153, 112-119.	7.5	52
100	Differential DNA methylation and PM _{2.5} species in a 450K epigenome-wide association study. Epigenetics, 2017, 12, 139-148.	2.7	52
101	Impacts of air pollution, temperature, and relative humidity on leukocyte distribution: An epigenetic perspective. Environment International, 2019, 126, 395-405.	10.0	52
102	Association between prenatal particulate air pollution exposure and telomere length in cord blood: Effect modification by fetal sex. Environmental Research, 2019, 172, 495-501.	7.5	51
103	Phthalates exposure and uterine fibroid burden among women undergoing surgical treatment for fibroids: a preliminary study. Fertility and Sterility, 2019, 111, 112-121.	1.0	51
104	GDM Women's Pre-Pregnancy Overweight/Obesity and Gestational Weight Gain on Offspring Overweight Status. PLoS ONE, 2015, 10, e0129536.	2.5	50
105	Fetal growth restriction and methylation of growth-related genes in the placenta. Epigenomics, 2016, 8, 33-42.	2.1	50
106	The association of lead exposure during pregnancy and childhood anthropometry in the Mexican PROGRESS cohort. Environmental Research, 2017, 152, 226-232.	7.5	50
107	Epigenetics: linking social and environmental exposures to preterm birth. Pediatric Research, 2016, 79, 136-140.	2.3	49
108	Chemical constituents and sources of ambient particulate air pollution and biomarkers of endothelial function in a panel of healthy adults in Beijing, China. Science of the Total Environment, 2016, 560-561, 141-149.	8.0	48

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109	Childhood abuse, promoter methylation of leukocyte <i>NR3C1</i> and the potential modifying effect of emotional support. Epigenomics, 2016, 8, 1507-1517.	2.1	48
110	High pesticide exposure events and <scp>DNA</scp> methylation among pesticide applicators in the agricultural health study. Environmental and Molecular Mutagenesis, 2017, 58, 19-29.	2.2	48
111	Molecular and cellular mechanisms linking air pollution and bone damage. Environmental Research, 2020, 185, 109465.	7.5	47
112	Changes in DNA Methylation in Mouse Lungs after a Single Intra-Tracheal Administration of Nanomaterials. PLoS ONE, 2017, 12, e0169886.	2.5	47
113	Prenatal maternal antidepressants, anxiety, and depression and offspring DNA methylation: epigenome-wide associations at birth and persistence into early childhood. Clinical Epigenetics, 2019, 11, 56.	4.1	46
114	Psychological factors and DNA methylation of genes related to immune/inflammatory system markers: the VA Normative Aging Study. BMJ Open, 2016, 6, e009790.	1.9	45
115	Effect of School Integrated Pest Management or Classroom Air Filter Purifiers on Asthma Symptoms in Students With Active Asthma. JAMA - Journal of the American Medical Association, 2021, 326, 839.	7.4	45
116	Epigenetic effects of low perinatal doses of flame retardant BDE-47 on mitochondrial and nuclear genes in rat offspring. Toxicology, 2015, 328, 152-159.	4.2	44
117	Prenatal lead exposure and fetal growth: Smaller infants have heightened susceptibility. Environment International, 2017, 99, 228-233.	10.0	44
118	Whole blood microRNA markers are associated with acute respiratory distress syndrome. Intensive Care Medicine Experimental, 2017, 5, 38.	1.9	44
119	Extracellular vesicle-enriched microRNAs interact in the association between long-term particulate matter and blood pressure in elderly men. Environmental Research, 2018, 167, 640-649.	7.5	43
120	Epigenome-wide association study reveals methylation pathways associated with childhood allergic sensitization. Epigenetics, 2019, 14, 445-466.	2.7	43
121	Epigenetic age acceleration is associated with allergy and asthma in children in Project Viva. Journal of Allergy and Clinical Immunology, 2019, 143, 2263-2270.e14.	2.9	43
122	Methylparaben in meconium and risk of maternal thyroid dysfunction, adverse birth outcomes, and Attention-Deficit Hyperactivity Disorder (ADHD). Environment International, 2020, 139, 105716.	10.0	42
123	DNA methylation-based biomarkers of age acceleration and all-cause death, myocardial infarction, stroke, and cancer in two cohorts: The NAS, and KORA F4. EBioMedicine, 2021, 63, 103151.	6.1	42
124	Pesticide Use and Relative Leukocyte Telomere Length in the Agricultural Health Study. PLoS ONE, 2015, 10, e0133382.	2.5	42
125	The role of outdoor and indoor air quality in the spread of SARS-CoV-2: Overview and recommendations by the research group on COVID-19 and particulate matter (RESCOP commission). Environmental Research, 2022, 211, 113038.	7.5	42
126	Prospective changes in global DNA methylation and cancer incidence and mortality. British Journal of Cancer, 2016, 115, 465-472.	6.4	41

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127	Increased methylation of repetitive elements and DNA repair genes is associated with higher DNA oxidation in children in an urbanized, industrial environment. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2017, 813, 27-36.	1.7	41
128	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	8.2	41
129	Cardiac Autonomic Dysfunction: Particulate Air Pollution Effects Are Modulated by Epigenetic Immunoregulation of <i>Tollâ€like Receptor 2</i> and Dietary Flavonoid Intake. Journal of the American Heart Association, 2015, 4, e001423.	3.7	40
130	Effects of environmental noise exposure on DNA methylation in the brain and metabolic health. Environmental Research, 2017, 153, 73-82.	7.5	39
131	Prenatal particulate air pollution and newborn telomere length: Effect modification by maternal antioxidant intakes and infant sex. Environmental Research, 2020, 187, 109707.	7.5	39
132	Acute particulate matter affects cardiovascular autonomic modulation and IFN-Î ³ methylation in healthy volunteers. Environmental Research, 2018, 161, 97-103.	7.5	38
133	Characterization of genome-wide H3K27ac profiles reveals a distinct PM2.5-associated histone modification signature. Environmental Health, 2015, 14, 65.	4.0	37
134	Endotoxin and β-1,3- <scp>d</scp> -Glucan in Concentrated Ambient Particles Induce Rapid Increase in Blood Pressure in Controlled Human Exposures. Hypertension, 2015, 66, 509-516.	2.7	37
135	Cumulative lifetime maternal stress and epigenome-wide placental DNA methylation in the PRISM cohort. Epigenetics, 2018, 13, 665-681.	2.7	37
136	Prenatal exposure to PM 2.5 and birth weight: A pooled analysis from three North American longitudinal pregnancy cohort studies. Environment International, 2017, 107, 173-180.	10.0	36
137	The effect of morphine upon DNA methylation in ten regions of the rat brain. Epigenetics, 2017, 12, 1038-1047.	2.7	36
138	Telomere Length, Long-Term Black Carbon Exposure, and Cognitive Function in a Cohort of Older Men: The VA Normative Aging Study. Environmental Health Perspectives, 2017, 125, 76-81.	6.0	36
139	Epigenome-wide association study of total serum immunoglobulin E in children: a life course approach. Clinical Epigenetics, 2018, 10, 55.	4.1	36
140	Prenatal arsenic exposure, child marriage, and pregnancy weight gain: Associations with preterm birth in Bangladesh. Environment International, 2018, 112, 23-32.	10.0	36
141	Identifying critical windows of prenatal particulate matter (PM2.5) exposure and early childhood blood pressure. Environmental Research, 2020, 182, 109073.	7.5	36
142	Large-Scale Hypothesis Testing for Causal Mediation Effects with Applications in Genome-wide Epigenetic Studies. Journal of the American Statistical Association, 2022, 117, 67-81.	3.1	35
143	CYP2E1 epigenetic regulation in chronic, low-level toluene exposure: Relationship with oxidative stress and smoking habit. Toxicology and Applied Pharmacology, 2015, 286, 207-215.	2.8	34
144	Investigating causal relation between prenatal arsenic exposure and birthweight: Are smaller infants more susceptible?. Environment International, 2017, 108, 32-40.	10.0	34

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145	Human milk extracellular vesicle miRNA expression and associations with maternal characteristics in a population-based cohort from the Faroe Islands. Scientific Reports, 2021, 11, 5840.	3.3	34
146	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α. JAMA Cardiology, 2018, 3, 463.	6.1	33
147	Trends and Patterns of Phthalates and Phthalate Alternatives Exposure in Pregnant Women from Mexico City during 2007–2010. Environmental Science & Technology, 2020, 54, 1740-1749.	10.0	33
148	Short-term air pollution, cognitive performance and nonsteroidal anti-inflammatory drug use in the Veterans Affairs Normative Aging Study. Nature Aging, 2021, 1, 430-437.	11.6	33
149	Prenatal fine particulate exposure associated with reduced childhood lung function and nasal epithelia GSTP1 hypermethylation: Sex-specific effects. Respiratory Research, 2018, 19, 76.	3.6	32
150	Phthalate Exposures and MicroRNA Expression in Uterine Fibroids: The FORGE Study. Epigenetics Insights, 2020, 13, 251686572090405.	2.0	32
151	B-vitamin Supplementation Mitigates Effects of Fine Particles on Cardiac Autonomic Dysfunction and Inflammation: A Pilot Human Intervention Trial. Scientific Reports, 2017, 7, 45322.	3.3	31
152	Placental IncRNA Expression Is Associated With Prenatal Phthalate Exposure. Toxicological Sciences, 2018, 163, 116-122.	3.1	31
153	Association of Prenatal Acetaminophen Exposure Measured in Meconium With Risk of Attention-Deficit/Hyperactivity Disorder Mediated by Frontoparietal Network Brain Connectivity. JAMA Pediatrics, 2020, 174, 1073.	6.2	31
154	Association between preconception maternal beverage intake and inÂvitro fertilization outcomes. Fertility and Sterility, 2017, 108, 1026-1033.	1.0	30
155	Aberrant promoter methylation in genes related to hematopoietic malignancy in workers exposed to a VOC mixture. Toxicology and Applied Pharmacology, 2018, 339, 65-72.	2.8	30
156	Prenatal lead exposure modifies the effect of shorter gestation on increased blood pressure in children. Environment International, 2018, 120, 464-471.	10.0	30
157	Effects of Physical Exercise on Endothelial Function and DNA Methylation. International Journal of Environmental Research and Public Health, 2019, 16, 2530.	2.6	30
158	A Novel Genetic Score Approach Using Instruments to Investigate Interactions between Pathways and Environment: Application to Air Pollution. PLoS ONE, 2014, 9, e96000.	2.5	30
159	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
160	Association between length of gestation and cervical DNA methylation of <i>PTGER2</i> and LINE 1-HS. Epigenetics, 2014, 9, 1083-1091.	2.7	29
161	Blood methylomics in response to arsenic exposure in a low-exposed US population. Journal of Exposure Science and Environmental Epidemiology, 2014, 24, 145-149.	3.9	28
162	Regulation of birthweight by placenta-derived miRNAs: evidence from an arsenic-exposed birth cohort in Bangladesh. Epigenetics, 2018, 13, 573-590.	2.7	28

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163	Prenatal manganese and cord blood mitochondrial DNA copy number: Effect modification by maternal anemic status. Environment International, 2019, 126, 484-493.	10.0	28
164	Maternal Phthalate and Personal Care Products Exposure Alters Extracellular Placental miRNA Profile in Twin Pregnancies. Reproductive Sciences, 2019, 26, 289-294.	2.5	28
165	Prospective Associations of Early Pregnancy Metal Mixtures with Mitochondria DNA Copy Number and Telomere Length in Maternal and Cord Blood. Environmental Health Perspectives, 2021, 129, 117007.	6.0	28
166	CpGFilter: model-based CpG probe filtering with replicates for epigenome-wide association studies. Bioinformatics, 2016, 32, 469-471.	4.1	27
167	Epigenetics—a potential mediator between air pollution and preterm birth. Environmental Epigenetics, 2016, 2, dvv008.	1.8	27
168	Altered cord blood mitochondrial DNA content and pregnancy lead exposure in the PROGRESS cohort. Environment International, 2019, 125, 437-444.	10.0	27
169	Pessimistic orientation in relation to telomere length in older men: The VA Normative Aging Study. Psychoneuroendocrinology, 2014, 42, 68-76.	2.7	26
170	Longitudinal Study of DNA Methylation of Inflammatory Genes and Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1531-1538.	2.5	26
171	Empirical comparison of reduced representation bisulfite sequencing and Infinium BeadChip reproducibility and coverage of DNA methylation in humans. Npj Genomic Medicine, 2017, 2, 13.	3.8	26
172	Battle of epigenetic proportions: comparing Illumina's EPIC methylation microarrays and TruSeq targeted bisulfite sequencing. Epigenetics, 2020, 15, 174-182.	2.7	26
173	Mitochondria and aging in older individuals: an analysis of DNA methylation age metrics, leukocyte telomere length, and mitochondrial DNA copy number in the VA normative aging study. Aging, 2020, 12, 2070-2083.	3.1	26
174	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
175	Comparative validation of an epigenetic mortality risk score with three aging biomarkers for predicting mortality risks among older adult males. International Journal of Epidemiology, 2019, 48, 1958-1971.	1.9	25
176	Prenatal gestational diabetes mellitus exposure and accelerated offspring DNA methylation age in early childhood. Epigenetics, 2021, 16, 186-195.	2.7	25
177	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. Molecular Psychiatry, 2021, 26, 1832-1845.	7.9	24
178	Blood DNA Methylation and Incident Coronary Heart Disease. JAMA Cardiology, 2021, 6, 1237.	6.1	24
179	Gestational Perfluoroalkyl Substance Exposure and DNA Methylation at Birth and 12 Years of Age: A Longitudinal Epigenome-Wide Association Study. Environmental Health Perspectives, 2022, 130, 37005.	6.0	24
180	Epigenome-wide cross-tissue predictive modeling and comparison of cord blood and placental methylation in a birth cohort. Epigenomics, 2017, 9, 231-240.	2.1	23

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