Todd M Everson

List of Publications by Year
in descending order

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35 papers	1,196 citations	430442 18 h-index	395343 33 g-index
40 all docs	40 docs citations	40 times ranked	2302 citing authors

#	Article	IF	Citations
1	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.	1.4	211
2	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
3	Prognostic impact of definitive local therapy of the primary tumor in men with metastatic prostate cancer at diagnosis: A population-based, propensity score analysis. Cancer Epidemiology, 2014, 38, 435-441.	0.8	77
4	Cadmium-Associated Differential Methylation throughout the Placental Genome: Epigenome-Wide Association Study of Two U.S. Birth Cohorts. Environmental Health Perspectives, 2018, 126, 017010.	2.8	69
5	DNA methylation loci associated with atopy and high serum IgE: a genome-wide application of recursive Random Forest feature selection. Genome Medicine, 2015, 7, 89.	3.6	58
6	Genome-wide DNA methylation at birth in relation to in utero arsenic exposure and the associated health in later life. Environmental Health, 2017, 16, 50.	1.7	54
7	Mediation by Placental DNA Methylation of the Association of Prenatal Maternal Smoking and Birth Weight. American Journal of Epidemiology, 2019, 188, 1878-1886.	1.6	48
8	The interplay of DNA methylation over time with Th2 pathway genetic variants on asthma risk and temporal asthma transition. Clinical Epigenetics, 2014, 6, 8.	1.8	47
9	Epigenome-wide Analysis Identifies Genes and Pathways Linked to Neurobehavioral Variation in Preterm Infants. Scientific Reports, 2019, 9, 6322.	1.6	43
10	Placental imprinting variation associated with assisted reproductive technologies and subfertility. Epigenetics, 2017, 12, 653-661.	1.3	42
11	Maternal exposure to selenium and cadmium, fetal growth, and placental expression of steroidogenic and apoptotic genes. Environmental Research, 2017, 158, 233-244.	3.7	41
12	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. Nature Communications, 2021, 12, 5095.	5.8	41
13	Epigenetic mechanisms and models in the origins of asthma. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 63-69.	1.1	38
14	Integrating -Omics Approaches into Human Population-Based Studies of Prenatal and Early-Life Exposures. Current Environmental Health Reports, 2018, 5, 328-337.	3.2	32
15	Maternal cadmium, placental PCDHAC1 , and fetal development. Reproductive Toxicology, 2016, 65, 263-271.	1.3	29
16	Placental Expression of Imprinted Genes, Overall and in Sex-Specific Patterns, Associated with Placental Cadmium Concentrations and Birth Size. Environmental Health Perspectives, 2019, 127, 57005.	2.8	24
17	Trihalomethane exposure and biomonitoring for the liver injury indicator, alanine aminotransferase, in the United States population (NHANES 1999â€“2006). Science of the Total Environment, 2015, 521-522, 226-234.	3.9	23
18	Maternal circadian disruption is associated with variation in placental DNA methylation. PLoS ONE, 2019, 14, e0215745.	1.1	22

#	Article	IF	Citations
19	Serious neonatal morbidities are associated with differences in DNA methylation among very preterm infants. Clinical Epigenetics, 2020, 12, 151.	1.8	22
20	Selenium-associated DNA methylation modifications in placenta and neurobehavioral development of newborns: An epigenome-wide study of two U.S. birth cohorts. Environment International, 2020, 137, 105508.	4.8	19
21	Placental lncRNA expression associated with placental cadmium concentrations and birth weight. Environmental Epigenetics, 2020, 6, dvaa003.	0.9	17
22	Forensic Epidemiologic and Biomechanical Analysis of a Pelvic Cavity Blowout Injury Associated with Ejection from a Personal Watercraft (Jetâ€Ski). Journal of Forensic Sciences, 2013, 58, 237-244.	0.9	16
23	Metal biomarker mixtures and blood pressure in the United States: cross-sectional findings from the 1999-2006 National Health and Nutrition Examination Survey (NHANES). Environmental Health, 2021, 20, 15.	1.7	16
24	Prenatal exposure to maternal depression and anxiety on imprinted gene expression in placenta and infant neurodevelopment and growth. Pediatric Research, 2018, 83, 1075-1083.	1.1	15
25	Prenatal risk factors and neonatal DNA methylation in very preterm infants. Clinical Epigenetics, 2021, 13, 171.	1.8	13
26	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. Epigenetics, 2021, 16, 770-782.	1.3	12
27	Copper associates with differential methylation in placentae from two US birth cohorts. Epigenetics, 2020, 15, 215-230.	1.3	11
28	Epigenome-wide association study of asthma and wheeze characterizes loci within HK1. Allergy, Asthma and Clinical Immunology, 2019, 15, 43.	0.9	10
29	Seasonally variant gene expression in fullâ€term human placenta. FASEB Journal, 2020, 34, 10431-10442.	0.2	9
30	NEOage clocks - epigenetic clocks to estimate post-menstrual and postnatal age in preterm infants. Aging, 2021, 13, 23527-23544.	1.4	7
31	Methylation risk scores for childhood aeroallergen sensitization: Results from the LISA birth cohort. Allergy: European Journal of Allergy and Clinical Immunology, 2022, 77, 2803-2817.	2.7	5
32	Epigenome-wide analysis identifies genes and pathways linked to acoustic cry variation in preterm infants. Pediatric Research, 2021, 89, 1848-1854.	1.1	4
33	Selenium-associated differentially expressed microRNAs and their targeted mRNAs across the placental genome in two U.S. birth cohorts. Epigenetics, 2022, 17, 1234-1245.	1.3	3
34	The emergence of developmental behavioral epigenomics. Epigenomics, 2022, 14, 499-502.	1.0	2
35	Cardenas et al. Reply to â€œDNA Methylation and Prenatal Exposuresâ€• American Journal of Epidemiology, 2019, 188, 1890-1891.	1.6	0