Todd M Everson

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8489293/publications.pdf

Version: 2024-02-01

35 papers 1,196 citations

18 h-index 395343 33 g-index

40 all docs 40 docs citations

40 times ranked

2302 citing authors

#	Article	IF	CITATIONS
1	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
2	The emergence of developmental behavioral epigenomics. Epigenomics, 2022, 14, 499-502.	1.0	2
3	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
4	Placental microRNA expression associates with birthweight through control of adipokines: results from two independent cohorts. Epigenetics, 2021, 16, 770-782.	1.3	12
5	Epigenome-wide analysis identifies genes and pathways linked to acoustic cry variation in preterm infants. Pediatric Research, 2021, 89, 1848-1854.	1.1	4
6	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
7	Placental DNA methylation signatures of maternal smoking during pregnancy and potential impacts on fetal growth. Nature Communications, 2021, 12, 5095.	5.8	41
8	Prenatal risk factors and neonatal DNA methylation in very preterm infants. Clinical Epigenetics, 2021, 13, 171.	1.8	13
9	NEOage clocks - epigenetic clocks to estimate post-menstrual and postnatal age in preterm infants. Aging, 2021, 13, 23527-23544.	1.4	7
10	Copper associates with differential methylation in placentae from two US birth cohorts. Epigenetics, 2020, 15, 215-230.	1.3	11
11	Serious neonatal morbidities are associated with differences in DNA methylation among very preterm infants. Clinical Epigenetics, 2020, 12, 151.	1.8	22
12	Seasonally variant gene expression in fullâ€ŧerm human placenta. FASEB Journal, 2020, 34, 10431-10442.	0.2	9
13	Placental IncRNA expression associated with placental cadmium concentrations and birth weight. Environmental Epigenetics, 2020, 6, dvaa003.	0.9	17
14	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
15	Epigenome-wide association study of asthma and wheeze characterizes loci within HK1. Allergy, Asthma and Clinical Immunology, 2019, 15, 43.	0.9	10
16	Cardenas et al. Reply to "DNA Methylation and Prenatal Exposures― American Journal of Epidemiology, 2019, 188, 1890-1891.	1.6	0
17	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
18	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

#	Article	IF	Citations
19	Epigenome-wide Analysis Identifies Genes and Pathways Linked to Neurobehavioral Variation in Preterm Infants. Scientific Reports, 2019, 9, 6322.	1.6	43
20	Maternal circadian disruption is associated with variation in placental DNA methylation. PLoS ONE, 2019, 14, e0215745.	1,1	22
21	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
22	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
23	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
24	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
25	Placental imprinting variation associated with assisted reproductive technologies and subfertility. Epigenetics, 2017, 12, 653-661.	1.3	42
26	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
27	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
28	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
29	Maternal cadmium, placental PCDHAC1, and fetal development. Reproductive Toxicology, 2016, 65, 263-271.	1.3	29
30	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
31	Trihalomethane exposure and biomonitoring for the liver injury indicator, alanine aminotransferase, in the United States population (NHANES 1999–2006). Science of the Total Environment, 2015, 521-522, 226-234.	3.9	23
32	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
33	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
34	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
35	Epigenetic mechanisms and models in the origins of asthma. Current Opinion in Allergy and Clinical Immunology, 2013, 13, 63-69.	1.1	38