Paul D Yousefi

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8752893/publications.pdf

Version: 2024-02-01

27 papers 2,895 citations

430442 18 h-index 26 g-index

29 all docs 29 docs citations

times ranked

29

5192 citing authors

#	Article	IF	Citations
1	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. American Journal of Human Genetics, 2016, 98, 680-696.	2.6	717
2	Epigenetic Signatures of Cigarette Smoking. Circulation: Cardiovascular Genetics, 2016, 9, 436-447.	5.1	678
3	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
4	Sex differences in DNA methylation assessed by 450ÂK BeadChip in newborns. BMC Genomics, 2015, 16, 911.	1.2	155
5	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. Nature Communications, 2019, 10, 1893.	5.8	140
6	Genome-wide methylation data mirror ancestry information. Epigenetics and Chromatin, 2017, 10, 1.	1.8	120
7	Prenatal Particulate Air Pollution and DNA Methylation in Newborns: An Epigenome-Wide Meta-Analysis. Environmental Health Perspectives, 2019, 127, 57012.	2.8	111
8	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. International Journal of Epidemiology, 2018, 47, 22-23u.	0.9	105
9	The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 0, 7, 41.	0.9	95
10	Prenatal phthalate exposure and altered patterns of DNA methylation in cord blood. Environmental and Molecular Mutagenesis, 2017, 58, 398-410.	0.9	71
11	DNA methylation-based predictors of health: applications and statistical considerations. Nature Reviews Genetics, 2022, 23, 369-383.	7.7	67
12	Considerations for normalization of DNA methylation data by Illumina 450K BeadChip assay in population studies. Epigenetics, 2013, 8, 1141-1152.	1.3	60
13	Maternal phthalate exposure during pregnancy is associated with DNA methylation of LINE-1 and Alu repetitive elements in Mexican-American children. Environmental Research, 2016, 148, 55-62.	3.7	49
14	The EWAS Catalog: a database of epigenome-wide association studies. Wellcome Open Research, 2022, 7, 41.	0.9	45
15	Estimation of blood cellular heterogeneity in newborns and children for epigenomeâ€wide association studies. Environmental and Molecular Mutagenesis, 2015, 56, 751-758.	0.9	43
16	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. Genome Medicine, 2020, 12, 105.	3.6	41
17	PON1 as a model for integration of genetic, epigenetic, and expression data on candidate susceptibility genes. Environmental Epigenetics, 2015, 1, .	0.9	32
18	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. Molecular Psychiatry, 2021, 26, 1832-1845.	4.1	24

#	ARTICLE	IF	CITATIONS
19	Relationship between expression and methylation of obesity-related genes in children. Mutagenesis, 2015, 30, 411-420.	1.0	23
20	Do nuclear magnetic resonance (NMR)-based metabolomics improve the prediction of pregnancy-related disorders? Findings from a UK birth cohort with independent validation. BMC Medicine, 2020, 18, 366.	2.3	22
21	Human urinary mutagenicity after wood smoke exposure during traditional temazcal use. Mutagenesis, 2014, 29, 367-377.	1.0	15
22	CpG Methylation across the adipogenic PPAR $\hat{1}^3$ gene and its relationship with birthweight and child BMI at 9Âyears. BMC Medical Genetics, 2017, 18, 7.	2.1	13
23	Validation and characterisation of a DNA methylation alcohol biomarker across the life course. Clinical Epigenetics, 2019, 11, 163.	1.8	13
24	Do Mass Spectrometry-Derived Metabolomics Improve the Prediction of Pregnancy-Related Disorders? Findings from a UK Birth Cohort with Independent Validation. Metabolites, 2021, 11, 530.	1.3	12
25	DNA methylation changes associated with prenatal mercury exposure: A meta-analysis of prospective cohort studies from PACE consortium. Environmental Research, 2022, 204, 112093.	3.7	11
26	Epigenetic modelling of former, current and never smokers. Clinical Epigenetics, 2021, 13, 206.	1.8	11
27	Genetic modification of the effect of maternal household air pollution exposure on birth weight in Guatemalan newborns. Reproductive Toxicology, 2014, 50, 19-26.	1.3	8