Neerja Karnani

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4933870/publications.pdf

Version: 2024-02-01

37 papers	1,526 citations	17 h-index	395343 33 g-index
40	40	40	2929
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Maternal Prenatal Anxiety and the Fetal Origins of Epigenetic Aging. Biological Psychiatry, 2022, 91, 303-312.	0.7	29
2	Dichotomy in the Impact of Elevated Maternal Glucose Levels on Neonatal Epigenome. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e1277-e1292.	1.8	4
3	Variability in newborn telomere length is explained by inheritance and intrauterine environment. BMC Medicine, 2022, 20, 20.	2.3	20
4	Maternal Glycemic Dysregulation During Pregnancy and Neonatal Blood DNA Methylation: Meta-analyses of Epigenome-Wide Association Studies. Diabetes Care, 2022, 45, 614-623.	4.3	19
5	Population-centric risk prediction modeling for gestational diabetes mellitus: A machine learning approach. Diabetes Research and Clinical Practice, 2022, 185, 109237.	1.1	7
6	Reply to: Crossing the "Birth Border―for Epigenetic Effects. Biological Psychiatry, 2022, 92, e25-e26.	0.7	1
7	Associations Between Eczema and Attention Deficit Hyperactivity Disorder Symptoms in Children. Frontiers in Pediatrics, 2022, 10, 837741.	0.9	9
8	The socioeconomic landscape of the exposome during pregnancy. Environment International, 2022, 163, 107205.	4.8	6
9	Determinants of cord blood adipokines and association with neonatal abdominal adipose tissue distribution. International Journal of Obesity, 2022, 46, 637-645.	1.6	6
10	<u>I</u> ntegrative <u>M</u> ulti- <u>Om</u> ics database (iMOMdb) of Asian Pregnant Women. Human Molecular Genetics, 2022, , .	1.4	2
11	Machine Learning–Derived Prenatal Predictive Risk Model to Guide Intervention and Prevent the Progression of Gestational Diabetes Mellitus to Type 2 Diabetes: Prediction Model Development Study. JMIR Diabetes, 2022, 7, e32366.	0.9	15
12	Cohort profile: Singapore Preconception Study of Long-Term Maternal and Child Outcomes (S-PRESTO). European Journal of Epidemiology, 2021, 36, 129-142.	2.5	38
13	The placental lipidome of maternal antenatal depression predicts socio-emotional problems in the offspring. Translational Psychiatry, 2021, 11, 107.	2.4	11
14	Altered H19/miRâ€675 expression in skeletal muscle is associated with low muscle mass in communityâ€dwelling older adults. JCSM Rapid Communications, 2021, 4, 207-221.	0.6	0
15	Brown Adipose Tissue, Adiposity, and Metabolic Profile in Preschool Children. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 2901-2914.	1.8	8
16	Analyses of child cardiometabolic phenotype following assisted reproductive technologies using a pragmatic trial emulation approach. Nature Communications, 2021, 12, 5613.	5.8	19
17	Genetic Link Determining the Maternal-Fetal Circulation of Vitamin D. Frontiers in Genetics, 2021, 12, 721488.	1.1	9
18	Determinants of intramyocellular lipid accumulation in early childhood. International Journal of Obesity, 2020, 44, 1141-1151.	1.6	10

#	Article	IF	CITATIONS
19	The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23329-23335.	3.3	140
20	Mismatch between poor fetal growth and rapid postnatal weight gain in the first 2 years of life is associated with higher blood pressure and insulin resistance without increased adiposity in childhood: the GUSTO cohort study. International Journal of Epidemiology, 2020, 49, 1591-1603.	0.9	23
21	Ethnic diversity in infant gut microbiota is apparent before the introduction of complementary diets. Gut Microbes, 2020, 11, 1362-1373.	4.3	34
22	Complex genetic dependencies among growth and neurological phenotypes in healthy children: Towards deciphering developmental mechanisms. PLoS ONE, 2020, 15, e0242684.	1.1	9
23	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	13.5	126
24	HOXA9 is a novel myopia risk gene. BMC Ophthalmology, 2019, 19, 28.	0.6	8
25	Analysis of two birth tissues provides new insights into the epigenetic landscape of neonates born preterm. Clinical Epigenetics, 2019, 11, 26.	1.8	23
26	Mitochondrial oxidative capacity and NAD+ biosynthesis are reduced in human sarcopenia across ethnicities. Nature Communications, 2019, 10, 5808.	5.8	159
27	Improving mass-univariate analysis of neuroimaging data by modelling important unknown covariates: Application to Epigenome-Wide Association Studies. NeuroImage, 2018, 173, 57-71.	2.1	8
28	Cell type-specific DNA methylation in neonatal cord tissue and cord blood: a 850K-reference panel and comparison of cell types. Epigenetics, 2018, 13, 941-958.	1.3	30
29	TIP60 represses activation of endogenous retroviral elements. Nucleic Acids Research, 2018, 46, 9456-9470.	6.5	33
30	Effects of Antenatal Maternal Depressive Symptoms and Socio-Economic Status on Neonatal Brain Development are Modulated by Genetic Risk. Cerebral Cortex, 2017, 27, 3080-3092.	1.6	90
31	Developmental pathways to adiposity begin before birth and are influenced by genotype, prenatal environment and epigenome. BMC Medicine, 2017, 15, 50.	2.3	97
32	Choice of surrogate tissue influences neonatal EWAS findings. BMC Medicine, 2017, 15, 211.	2.3	28
33	Gene, Environment and Methylation (GEM): a tool suite to efficiently navigate large scale epigenome wide association studies and integrate genotype and interaction between genotype and environment. BMC Bioinformatics, 2016, 17, 299.	1.2	53
34	TIP60 inhibits metastasis by ablating DNMT1â^'SNAIL2-driven epithelial-mesenchymal transition program. Journal of Molecular Cell Biology, 2016, 8, 1-16.	1.5	17
35	Comparison of Methyl-capture Sequencing vs. Infinium 450K methylation array for methylome analysis in clinical samples. Epigenetics, $2016, 11, 36-48$.	1.3	47
36	<i>HIF3A</i> association with adiposity: the story begins before birth. Epigenomics, 2015, 7, 937-950.	1.0	68

#	Article	IF	CITATIONS
37	The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes. Genome Research, 2014, 24, 1064-1074.	2.4	317