

Alexandra M Binder

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11861661/publications.pdf>

Version: 2024-02-01

31
papers

1,716
citations

331538

21
h-index

477173

29
g-index

31
all docs

31
docs citations

31
times ranked

3572
citing authors

#	ARTICLE	IF	CITATIONS
1	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.	9.0	345
2	Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , 2018, 67, 1995-2005.	6.1	188
3	Genome-wide DNA methylation in neonates exposed to maternal depression, anxiety, or SSRI medication during pregnancy. <i>Epigenetics</i> , 2014, 9, 964-972.	1.3	158
4	The impact of first trimester phthalate and phenol exposure on IGF2/H19 genomic imprinting and birth outcomes. <i>Environmental Research</i> , 2014, 133, 396-406.	3.7	127
5	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. <i>Genome Biology</i> , 2021, 22, 194.	3.8	90
6	Faster ticking rate of the epigenetic clock is associated with faster pubertal development in girls. <i>Epigenetics</i> , 2018, 13, 85-94.	1.3	86
7	First-Trimester Urine Concentrations of Phthalate Metabolites and Phenols and Placenta miRNA Expression in a Cohort of U.S. Women. <i>Environmental Health Perspectives</i> , 2016, 124, 380-387.	2.8	82
8	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. <i>Aging</i> , 2019, 11, 4238-4253.	1.4	79
9	Epigenome-wide and transcriptome-wide analyses reveal gestational diabetes is associated with alterations in the human leukocyte antigen complex. <i>Clinical Epigenetics</i> , 2015, 7, 79.	1.8	70
10	Childhood and adolescent phenol and phthalate exposure and the age of menarche in Latina girls. <i>Environmental Health</i> , 2018, 17, 32.	1.7	56
11	Impact of folic acid intake during pregnancy on genomic imprinting of <i>IGF2/H19</i> and ^{14}C carbon metabolism. <i>FASEB Journal</i> , 2017, 31, 5149-5158.	0.2	53
12	Accurate ethnicity prediction from placental DNA methylation data. <i>Epigenetics and Chromatin</i> , 2019, 12, 51.	1.8	40
13	Aberrant methylation of imprinted genes is associated with negative hormone receptor status in invasive breast cancer. <i>International Journal of Cancer</i> , 2015, 137, 537-547.	2.3	39
14	DNA methylation of candidate genes in peripheral blood from patients with type 2 diabetes or the metabolic syndrome. <i>PLoS ONE</i> , 2017, 12, e0180955.	1.1	33
15	Differences in DNA Methylation and Functional Expression in Lactase Persistent and Non-persistent Individuals. <i>Scientific Reports</i> , 2018, 8, 5649.	1.6	31
16	Associations Between Prenatal Urinary Biomarkers of Phthalate Exposure and Preterm Birth. <i>JAMA Pediatrics</i> , 2022, 176, 895.	3.3	31
17	Prepubertal and Pubertal Endocrine-Disrupting Chemical Exposure and Breast Density among Chilean Adolescents. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2018, 27, 1491-1499.	1.1	29
18	Pyrosequencing Evaluation of Widely Available Bisulfite Conversion Methods: Considerations for Application. <i>Medical Epigenetics</i> , 2014, 2, 28-36.	262.3	26

#	ARTICLE	IF	CITATIONS
19	Empirical comparison of reduced representation bisulfite sequencing and Infinium BeadChip reproducibility and coverage of DNA methylation in humans. <i>Npj Genomic Medicine</i> , 2017, 2, 13.	1.7	26
20	Locus-specific DNA methylation in the placenta is associated with levels of pro-inflammatory proteins in cord blood and they are both independently affected by maternal smoking during pregnancy. <i>Epigenetics</i> , 2017, 12, 875-885.	1.3	26
21	The causal effect of red blood cell folate on genome-wide methylation in cord blood: a Mendelian randomization approach. <i>BMC Bioinformatics</i> , 2013, 14, 353.	1.2	22
22	Considerations for Design and Analysis of DNA Methylation Studies. <i>Methods in Molecular Biology</i> , 2018, 1708, 31-46.	0.4	19
23	In utero exposure to endocrine-disrupting chemicals and telomere length at birth. <i>Environmental Research</i> , 2020, 182, 109053.	3.7	15
24	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. <i>Aging</i> , 2020, 12, 17863-17894.	1.4	12
25	Association between indicators of systemic inflammation biomarkers during puberty with breast density and onset of menarche. <i>Breast Cancer Research</i> , 2020, 22, 104.	2.2	8
26	Methylation of immune-regulatory cytokine genes and pancreatic cancer outcomes. <i>Epigenomics</i> , 2020, 12, 1273-1285.	1.0	8
27	Epigenetic age associates with psychosocial stress and resilience in children of Latinx immigrants. <i>Epigenomics</i> , 2021, 13, 1677-1699.	1.0	7
28	Differential gene expression and limited epigenetic dysregulation at the materno-fetal interface in preeclampsia. <i>Human Molecular Genetics</i> , 2020, 29, 335-350.	1.4	5
29	Inverse association between estrogen receptor- α DNA methylation and breast composition in adolescent Chilean girls. <i>Clinical Epigenetics</i> , 2018, 10, 122.	1.8	3
30	Epigenetic Clocks. , 2022, , 261-276.		2
31	Abstract PS7-28: Association between epigenetic age acceleration and postmenopausal breast cancer risk in the Women's Health Initiative. , 2021, , .		0