

# Alexandra M Binder

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,716  
citations

331670  
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477307  
29  
g-index

31  
all docs

31  
docs citations

31  
times ranked

3572  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenetic Clocks. , 2022, , 261-276.		2
2	Associations Between Prenatal Urinary Biomarkers of Phthalate Exposure and Preterm Birth. JAMA Pediatrics, 2022, 176, 895.	6.2	31
3	Abstract PS7-28: Association between epigenetic age acceleration and postmenopausal breast cancer risk in the Women's Health Initiative. , 2021, , .		0
4	Epigenetic age associates with psychosocial stress and resilience in children of Latinx immigrants. Epigenomics, 2021, 13, 1677-1699.	2.1	7
5	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
6	Differential gene expression and limited epigenetic dysregulation at the materno-fetal interface in preeclampsia. Human Molecular Genetics, 2020, 29, 335-350.	2.9	5
7	In utero exposure to endocrine-disrupting chemicals and telomere length at birth. Environmental Research, 2020, 182, 109053.	7.5	15
8	Association between indicators of systemic inflammation biomarkers during puberty with breast density and onset of menarche. Breast Cancer Research, 2020, 22, 104.	5.0	8
9	Methylation of immune-regulatory cytokine genes and pancreatic cancer outcomes. Epigenomics, 2020, 12, 1273-1285.	2.1	8
10	Epigenetic mutation load is weakly correlated with epigenetic age acceleration. Aging, 2020, 12, 17863-17894.	3.1	12
11	Accurate ethnicity prediction from placental DNA methylation data. Epigenetics and Chromatin, 2019, 12, 51.	3.9	40
12	Placental epigenetic clocks: estimating gestational age using placental DNA methylation levels. Aging, 2019, 11, 4238-4253.	3.1	79
13	Differences in DNA Methylation and Functional Expression in Lactase Persistent and Non-persistent Individuals. Scientific Reports, 2018, 8, 5649.	3.3	31
14	Childhood and adolescent phenol and phthalate exposure and the age of menarche in Latina girls. Environmental Health, 2018, 17, 32.	4.0	56
15	Considerations for Design and Analysis of DNA Methylation Studies. Methods in Molecular Biology, 2018, 1708, 31-46.	0.9	19
16	Faster ticking rate of the epigenetic clock is associated with faster pubertal development in girls. Epigenetics, 2018, 13, 85-94.	2.7	86
17	Inverse association between estrogen receptor- $\alpha$ DNA methylation and breast composition in adolescent Chilean girls. Clinical Epigenetics, 2018, 10, 122.	4.1	3
18	Prepubertal and Pubertal Endocrine-Disrupting Chemical Exposure and Breast Density among Chilean Adolescents. Cancer Epidemiology Biomarkers and Prevention, 2018, 27, 1491-1499.	2.5	29

#	ARTICLE	IF	CITATIONS
19	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.	12.1	188
20	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.	3.8	26
21	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.	2.7	26
22	Impact of folic acid intake during pregnancy on genomic imprinting of <i>IGF2/H19</i> and $\alpha$ -carbon metabolism. <i>FASEB Journal</i> , 2017, 31, 5149-5158.	0.5	53
23	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.	2.5	33
24	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.	6.0	82
25	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.	4.1	70
26	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.	5.1	39
27	The impact of first trimester phthalate and phenol exposure on <i>IGF2/H19</i> genomic imprinting and birth outcomes. <i>Environmental Research</i> , 2014, 133, 396-406.	7.5	127
28	Genome-wide DNA methylation in neonates exposed to maternal depression, anxiety, or SSRI medication during pregnancy. <i>Epigenetics</i> , 2014, 9, 964-972.	2.7	158
29	Pyrosequencing Evaluation of Widely Available Bisulfite Conversion Methods: Considerations for Application. <i>Medical Epigenetics</i> , 2014, 2, 28-36.	262.3	26
30	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.	2.6	22
31	Recommendations for the design and analysis of epigenome-wide association studies. <i>Nature Methods</i> , 2013, 10, 949-955.	19.0	345