

# Christian Magnus Page

## List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	2.9	211
2	Epigenome-Wide Meta-Analysis of Methylation in Children Related to Prenatal NO <sub>2</sub> Air Pollution Exposure. <i>Environmental Health Perspectives</i> , 2017, 125, 104-110.	6.0	176
3	Epigenome-wide meta-analysis of DNA methylation and childhood asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2019, 143, 2062-2074.	2.9	147
4	Meta-analysis of epigenome-wide association studies in neonates reveals widespread differential DNA methylation associated with birthweight. <i>Nature Communications</i> , 2019, 10, 1893.	12.8	140
5	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
6	Integrated analysis of environmental and genetic influences on cord blood DNA methylation in new-borns. <i>Nature Communications</i> , 2019, 10, 2548.	12.8	94
7	Genome-Wide DNA Methylation Profiles Indicate CD8+ T Cell Hypermethylation in Multiple Sclerosis. <i>PLoS ONE</i> , 2015, 10, e0117403.	2.5	88
8	The Evans™ Index revisited: New cut-off levels for use in radiological assessment of ventricular enlargement in the elderly. <i>European Journal of Radiology</i> , 2017, 95, 28-32.	2.6	84
9	Epigenome-wide meta-analysis of blood DNA methylation in newborns and children identifies numerous loci related to gestational age. <i>Genome Medicine</i> , 2020, 12, 25.	8.2	81
10	Hypertensive Disorders of Pregnancy and DNA Methylation in Newborns. <i>Hypertension</i> , 2019, 74, 375-383.	2.7	73
11	Cell type specific DNA methylation in cord blood: A 450K-reference data set and cell count-based validation of estimated cell type composition. <i>Epigenetics</i> , 2016, 11, 690-698.	2.7	69
12	Maternal alcohol consumption and offspring DNA methylation: findings from six general population-based birth cohorts. <i>Epigenomics</i> , 2018, 10, 27-42.	2.1	58
13	Environmental exposures and the risk of multiple sclerosis investigated in a Norwegian case-control study. <i>BMC Neurology</i> , 2014, 14, 196.	1.8	45
14	Misclassified exposure in epigenetic mediation analyses. Does DNA methylation mediate effects of smoking on birthweight?. <i>Epigenomics</i> , 2017, 9, 253-265.	2.1	42
15	DNA methylation and body mass index from birth to adolescence: meta-analyses of epigenome-wide association studies. <i>Genome Medicine</i> , 2020, 12, 105.	8.2	41
16	The multiple sclerosis susceptibility genes TAGAP and IL2RA are regulated by vitamin D in CD4+ T cells. <i>Genes and Immunity</i> , 2016, 17, 118-127.	4.1	35
17	Vitamin A and D intake in pregnancy, infant supplementation, and asthma development: the Norwegian Mother and Child Cohort. <i>American Journal of Clinical Nutrition</i> , 2018, 107, 789-798.	4.7	32
18	Vitamin D and risk of pregnancy related hypertensive disorders: mendelian randomisation study. <i>BMJ: British Medical Journal</i> , 2018, 361, k2167.	2.3	31

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19	Association of Maternal Psychosocial Stress With Increased Risk of Asthma Development in Offspring. <i>American Journal of Epidemiology</i> , 2018, 187, 1199-1209.	3.4	30
20	Epigenome-wide methylation differences in a group of lean and obese women – A HUNT Study. <i>Scientific Reports</i> , 2018, 8, 16330.	3.3	27
21	Body mass index and subfertility: multivariable regression and Mendelian randomization analyses in the Norwegian Mother, Father and Child Cohort Study. <i>Human Reproduction</i> , 2021, 36, 3141-3151.	0.9	27
22	25-Hydroxyvitamin D in pregnancy and genome wide cord blood DNA methylation in two pregnancy cohorts (MoBa and ALSPAC). <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2016, 159, 102-109.	2.5	26
23	Global test for high-dimensional mediation: Testing groups of potential mediators. <i>Statistics in Medicine</i> , 2019, 38, 3346-3360.	1.6	26
24	DNA methylation in newborns conceived by assisted reproductive technology. <i>Nature Communications</i> , 2022, 13, 1896.	12.8	26
25	The Association between Hair Cortisol and Self-Reported Symptoms of Depression in Pregnant Women. <i>PLoS ONE</i> , 2016, 11, e0161804.	2.5	25
26	Epigenetic DNA methylation changes associated with headache chronification: A retrospective case-control study. <i>Cephalgia</i> , 2018, 38, 312-322.	3.9	25
27	Prenatal iron exposure and childhood type 1 diabetes. <i>Scientific Reports</i> , 2018, 8, 9067.	3.3	25
28	Maternal anxiety during pregnancy and newborn epigenome-wide DNA methylation. <i>Molecular Psychiatry</i> , 2021, 26, 1832-1845.	7.9	24
29	An EPIC predictor of gestational age and its application to newborns conceived by assisted reproductive technologies. <i>Clinical Epigenetics</i> , 2021, 13, 82.	4.1	24
30	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. <i>Mutation Research - Reviews in Mutation Research</i> , 2022, 789, 108415.	5.5	24
31	Genome-wide DNA methylation in saliva and body size of adolescent girls. <i>Epigenomics</i> , 2016, 8, 1495-1505.	2.1	22
32	Prenatal maternal depressive symptoms and infant DNA methylation: a longitudinal epigenome-wide study. <i>Nordic Journal of Psychiatry</i> , 2019, 73, 257-263.	1.3	20
33	Cisplatin treatment of testicular cancer patients introduces long-term changes in the epigenome. <i>Clinical Epigenetics</i> , 2019, 11, 179.	4.1	18
34	Association of medically assisted reproduction with offspring cord blood DNA methylation across cohorts. <i>Human Reproduction</i> , 2021, 36, 2403-2413.	0.9	17
35	Paternal body mass index and offspring DNA methylation: findings from the PACE consortium. <i>International Journal of Epidemiology</i> , 2021, 50, 1297-1315.	1.9	16
36	Blood-based epigenetic estimators of chronological age in human adults using DNA methylation data from the Illumina MethylationEPIC array. <i>BMC Genomics</i> , 2020, 21, 747.	2.8	14

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37	Maternal history of miscarriages and measures of fertility in relation to childhood asthma. Thorax, 2019, 74, 106-113.	5.6	13
38	Smoking and infertility: multivariable regression and Mendelian randomization analyses in the Norwegian Mother, Father and Child Cohort Study. Fertility and Sterility, 2022, 118, 180-190.	1.0	11
39	A Bayesian mixed modeling approach for estimating heritability. BMC Proceedings, 2018, 12, 31.	1.6	9
40	Identification of response signatures for tankyrase inhibitor treatment in tumor cell lines. IScience, 2021, 24, 102807.	4.1	8
41	Associations between epigenetic age acceleration and infertility. Human Reproduction, 2022, 37, 2063-2074.	0.9	8
42	Assessing the Power of Exome Chips. PLoS ONE, 2015, 10, e0139642.	2.5	6
43	Melanoma staging: Varying precision and terminal digit clustering in Breslow thickness data is evident in a population-based study. Journal of the American Academy of Dermatology, 2018, 79, 118-125.e1.	1.2	6
44	Longitudinal associations of DNA methylation and sleep in children: a meta-analysis. Clinical Epigenetics, 2022, 14, .	4.1	6
45	Epigenetics, heritability and longitudinal analysis. BMC Genetics, 2018, 19, 77.	2.7	5
46	Assessing genome-wide significance for the detection of differentially methylated regions. Statistical Applications in Genetics and Molecular Biology, 2018, 17, .	0.6	4
47	Lifetime Ultraviolet Radiation Exposure and DNA Methylation in Blood Leukocytes: The Norwegian Women and Cancer Study. Scientific Reports, 2020, 10, 4521.	3.3	4
48	Quality control for Illumina 450K methylation data in the absence of iDat files using correlation structure in pedigrees and repeated measures. BMC Genetics, 2018, 19, 66.	2.7	3
49	Age and sex effects on DNA methylation sites linked to genes implicated in severe COVID-19 and SARS-CoV-2 host cell entry. PLoS ONE, 2022, 17, e0269105.	2.5	2