## Sonja Kunze

List of Publications by Year in descending order

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SONIA KUNZE

#	Article	IF	CITATIONS
1	DNA methylation-based measures of biological age: meta-analysis predicting time to death. Aging, 2016, 8, 1844-1865.	3.1	786
2	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. Nature, 2017, 541, 81-86.	27.8	743
3	Prenatal and early life influences on epigenetic age in children: a study of mother–offspring pairs from two cohort studies. Human Molecular Genetics, 2016, 25, 191-201.	2.9	205
4	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF-ήB–driven inflammation and cardiovascular risk. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 11370-11379.	7.1	193
5	Characterization of whole-genome autosomal differences of DNA methylation between men and women. Epigenetics and Chromatin, 2015, 8, 43.	3.9	176
6	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	3.1	137
7	The dynamics of smoking-related disturbed methylation: a two time-point study of methylation change in smokers, non-smokers and former smokers. BMC Genomics, 2017, 18, 805.	2.8	85
8	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. PLoS ONE, 2016, 11, e0152314.	2.5	81
9	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. JAMA Psychiatry, 2018, 75, 949.	11.0	78
10	Anxiety Associated Increased CpG Methylation in the Promoter of Asb1: A Translational Approach Evidenced by Epidemiological and Clinical Studies and a Murine Model. Neuropsychopharmacology, 2018, 43, 342-353.	5.4	43
11	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
12	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor α. JAMA Cardiology, 2018, 3, 463.	6.1	33
13	lgG glycosylation and DNA methylation are interconnected with smoking. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 637-648.	2.4	33
14	Validated inference of smoking habits from blood with a finite DNA methylation marker set. European Journal of Epidemiology, 2019, 34, 1055-1074.	5.7	31
15	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. Clinical Epigenetics, 2020, 12, 157.	4.1	31
16	A metabolome-wide association study in the general population reveals decreased levels of serum laurylcarnitine in people with depression. Molecular Psychiatry, 2021, 26, 7372-7383.	7.9	23
17	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. Genetics, 2017, 207, 1275-1283.	2.9	19
18	Metastable DNA methylation sites associated with longitudinal lung function decline and aging in humans: an epigenome-wide study in the NAS and KORA cohorts. Epigenetics, 2018, 13, 1039-1055.	2.7	19

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19	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. PLoS ONE, 2016, 11, e0165548.	2.5	19
20	Quantitative Region-Specific DNA Methylation Analysis by the EpiTYPERâ,,¢ Technology. Methods in Molecular Biology, 2018, 1708, 515-535.	0.9	16
21	Novel DNA Methylation Sites Influence GPR15 Expression in Relation to Smoking. Biomolecules, 2018, 8, 74.	4.0	13
22	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	4.1	13
23	Accelerated epigenetic aging as a risk factor for chronic obstructive pulmonary disease and decreased lung function in two prospective cohort studies. Aging, 2020, 12, 16539-16554.	3.1	13
24	<i>IRFâ€I</i> SNPs influence the risk for childhood allergic asthma: A critical role for proâ€inflammatory immune regulation. Pediatric Allergy and Immunology, 2018, 29, 34-41.	2.6	11
25	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	2.5	10
26	A genome-wide analysis of DNA methylation identifies a novel association signal for Lp(a) concentrations in the LPA promoter. PLoS ONE, 2020, 15, e0232073.	2.5	8
27	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	6.7	8
28	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. Clinical Epigenetics, 2021, 13, 198.	4.1	7
29	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. Nature Communications, 2018, 9, 4919.	12.8	6
30	17q12â€21 riskâ€variants influence cord blood immune regulation and multitriggerâ€wheeze. Pediatric Allergy and Immunology, 2022, 33, .	2.6	5