

Sonja Kunze

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7030062/publications.pdf>

Version: 2024-02-01

30
papers

2,888
citations

471061

17
h-index

454577

30
g-index

30
all docs

30
docs citations

30
times ranked

5727
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA methylation-based measures of biological age: meta-analysis predicting time to death. <i>Aging</i> , 2016, 8, 1844-1865.	1.4	786
2	Epigenome-wide association study of body mass index, and the adverse outcomes of adiposity. <i>Nature</i> , 2017, 541, 81-86.	13.7	743
3	Prenatal and early life influences on epigenetic age in children: a study of mother-offspring pairs from two cohort studies. <i>Human Molecular Genetics</i> , 2016, 25, 191-201.	1.4	205
4	Epigenetic upregulation of FKBP5 by aging and stress contributes to NF- κ B-driven inflammation and cardiovascular risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 11370-11379.	3.3	193
5	Characterization of whole-genome autosomal differences of DNA methylation between men and women. <i>Epigenetics and Chromatin</i> , 2015, 8, 43.	1.8	176
6	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. <i>Aging</i> , 2019, 11, 2045-2070.	1.4	137
7	The dynamics of smoking-related disturbed methylation: a two time-point study of methylation change in smokers, non-smokers and former smokers. <i>BMC Genomics</i> , 2017, 18, 805.	1.2	85
8	Association between DNA Methylation in Whole Blood and Measures of Glucose Metabolism: KORA F4 Study. <i>PLoS ONE</i> , 2016, 11, e0152314.	1.1	81
9	DNA Methylation Signatures of Depressive Symptoms in Middle-aged and Elderly Persons. <i>JAMA Psychiatry</i> , 2018, 75, 949.	6.0	78
10	Anxiety Associated Increased CpG Methylation in the Promoter of <i>Asb1</i> : A Translational Approach Evidenced by Epidemiological and Clinical Studies and a Murine Model. <i>Neuropsychopharmacology</i> , 2018, 43, 342-353.	2.8	43
11	Association of maternal prenatal smoking <i>GFI1</i> -locus and cardio-metabolic phenotypes in 18,212 adults. <i>EBioMedicine</i> , 2018, 38, 206-216.	2.7	43
12	Association of Methylation Signals With Incident Coronary Heart Disease in an Epigenome-Wide Assessment of Circulating Tumor Necrosis Factor \pm . <i>JAMA Cardiology</i> , 2018, 3, 463.	3.0	33
13	IgG glycosylation and DNA methylation are interconnected with smoking. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 637-648.	1.1	33
14	Validated inference of smoking habits from blood with a finite DNA methylation marker set. <i>European Journal of Epidemiology</i> , 2019, 34, 1055-1074.	2.5	31
15	Smoking-related changes in DNA methylation and gene expression are associated with cardio-metabolic traits. <i>Clinical Epigenetics</i> , 2020, 12, 157.	1.8	31
16	A metabolome-wide association study in the general population reveals decreased levels of serum laurycarnitine in people with depression. <i>Molecular Psychiatry</i> , 2021, 26, 7372-7383.	4.1	23
17	RL-SKAT: An Exact and Efficient Score Test for Heritability and Set Tests. <i>Genetics</i> , 2017, 207, 1275-1283.	1.2	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. <i>Epigenetics</i> , 2018, 13, 1039-1055.	1.3	19

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19	Are Epigenetic Factors Implicated in Chronic Widespread Pain?. PLoS ONE, 2016, 11, e0165548.	1.1	19
20	Quantitative Region-Specific DNA Methylation Analysis by the EpiTYPER [®] Technology. Methods in Molecular Biology, 2018, 1708, 515-535.	0.4	16
21	Novel DNA Methylation Sites Influence GPR15 Expression in Relation to Smoking. Biomolecules, 2018, 8, 74.	1.8	13
22	DNAm-based signatures of accelerated aging and mortality in blood are associated with low renal function. Clinical Epigenetics, 2021, 13, 121.	1.8	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.	1.4	13
24	IRF4 SNPs influence the risk for childhood allergic asthma: A critical role for proinflammatory immune regulation. Pediatric Allergy and Immunology, 2018, 29, 34-41.	1.1	11
25	Genetically defined elevated homocysteine levels do not result in widespread changes of DNA methylation in leukocytes. PLoS ONE, 2017, 12, e0182472.	1.1	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.	1.1	8
27	Integrative analysis of clinical and epigenetic biomarkers of mortality. Aging Cell, 2022, 21, e13608.	3.0	8
28	Validating biomarkers and models for epigenetic inference of alcohol consumption from blood. Clinical Epigenetics, 2021, 13, 198.	1.8	7
29	Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests. Nature Communications, 2018, 9, 4919.	5.8	6
30	17q12-21 risk variants influence cord blood immune regulation and multitrigger wheeze. Pediatric Allergy and Immunology, 2022, 33, .	1.1	5