Pashupati P Mishra

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/84822/publications.pdf

Version: 2024-02-01

36 papers	1,599 citations	623734 14 h-index	345221 36 g-index
41 all docs	41 docs citations	41 times ranked	3329 citing authors

#	Article	IF	Citations
1	Genome-wide meta-analysis of phytosterols reveals five novel loci and a detrimental effect on coronary atherosclerosis. Nature Communications, 2022, 13, 143.	12.8	17
2	Methylation pattern of polymorphically imprinted nc886 is not conserved across mammalia. PLoS ONE, 2022, 17, e0261481.	2.5	3
3	Multi-Omics Integration in a Twin Cohort and Predictive Modeling of Blood Pressure Values. OMICS A Journal of Integrative Biology, 2022, 26, 130-141.	2.0	6
4	Genome-wide Association Meta-analysis of Childhood and Adolescent Internalizing Symptoms. Journal of the American Academy of Child and Adolescent Psychiatry, 2022, 61, 934-945.	0.5	26
5	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
6	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
7	Examining the effect of mitochondrial DNA variants on blood pressure in two Finnish cohorts. Scientific Reports, 2021, 11, 611.	3.3	7
8	DNA methylation signatures of aggression and closely related constructs: A meta-analysis of epigenome-wide studies across the lifespan. Molecular Psychiatry, 2021, 26, 2148-2162.	7.9	21
9	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. Scientific Reports, 2021, 11, 3100.	3.3	15
10	Modular genome-wide gene expression architecture shared by early traits of osteoporosis and atherosclerosis in the Young Finns Study. Scientific Reports, 2021, 11, 7111.	3.3	7
11	Adulthood blood levels of hsa-miR-29b-3p associate with preterm birth and adult metabolic and cognitive health. Scientific Reports, 2021, 11, 9203.	3.3	10
12	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
13	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. European Journal of Epidemiology, 2021, 36, 1143-1155.	5.7	10
14	Methylation status of nc886 epiallele reflects periconceptional conditions and is associated with glucose metabolism through nc886 RNAs. Clinical Epigenetics, 2021, 13, 143.	4.1	13
15	Human Prostate Tissue MicroRNAs and Their Predicted Target Pathways Linked to Prostate Cancer Risk Factors. Cancers, 2021, 13, 3537.	3.7	2
16	C-reactive protein and temperament: An instrumental variable analysis. Brain, Behavior, & Immunity - Health, 2021, 14, 100241.	2.5	1
17	Uncovering the shared lipidomic markers of subclinical osteoporosis-atherosclerosis comorbidity: The Young Finns Study. Bone, 2021, 151, 116030.	2.9	13
18	Assessment of plasma ceramides as predictor for subclinical atherosclerosis. Atherosclerosis Plus, 2021, 45, 25-31.	0.7	3

#	ARTICLE	IF	CITATIONS
19	Mitochondrial genome-wide analysis of nuclear DNA methylation quantitative trait loci. Human Molecular Genetics, 2021, , .	2.9	1
20	Reproductive history and blood cell DNA methylation later in life: the Young Finns Study. Clinical Epigenetics, 2021, 13, 227.	4.1	2
21	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature Communications, 2021, 12, 7173.	12.8	8
22	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
23	Cardiorespiratory fitness and heart rate recovery predict sudden cardiac death independent of ejection fraction. Heart, 2020, 106, 434-440.	2.9	6
24	Lipidomic architecture shared by subclinical markers of osteoporosis and atherosclerosis: The Cardiovascular Risk in Young Finns Study. Bone, 2020, 131, 115160.	2.9	20
25	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
26	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. Diabetes Care, 2020, 43, 875-884.	8.6	43
27	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. Bioscience Reports, 2020, 40, .	2.4	8
28	Similarity of salivary microbiome in parents and adult children. PeerJ, 2020, 8, e8799.	2.0	11
29	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
30	Whole blood microRNA levels associate with glycemic status and correlate with target mRNAs in pathways important to type 2 diabetes. Scientific Reports, 2019, 9, 8887.	3.3	55
31	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
32	Extensive phenotype data and machine learning in prediction of mortality in acute coronary syndrome â€“ the MADDEC study. Annals of Medicine, 2019, 51, 156-163.	3.8	44
33	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	3.1	137
34	Increased tooth brushing frequency is associated with reduced gingival pocket bacterial diversity in patients with intracranial aneurysms. PeerJ, 2019, 7, e6316.	2.0	11
35	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
36	Robust multi-group gene set analysis with few replicates. BMC Bioinformatics, 2016, 17, 526.	2.6	4