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List of Publications by Year in descending order

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

#	Article	IF	CITATIONS
1	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
2	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
3	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. Aging, 2019, 11, 2045-2070.	3.1	137
4	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
5	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
6	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
7	Extensive phenotype data and machine learning in prediction of mortality in acute coronary syndrome $\hat{a}\in$ the MADDEC study. Annals of Medicine, 2019, 51, 156-163.	3.8	44
8	Association of maternal prenatal smoking GFI1-locus and cardio-metabolic phenotypes in 18,212 adults. EBioMedicine, 2018, 38, 206-216.	6.1	43
9	Epigenetic Link Between Statin Therapy and Type 2 Diabetes. Diabetes Care, 2020, 43, 875-884.	8.6	43
10	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
11	Meta-analyses identify DNA methylation associated with kidney function and damage. Nature Communications, 2021, 12, 7174.	12.8	30
12	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
13	DNA methylation signature of chronic low-grade inflammation and its role in cardio-respiratory diseases. Nature Communications, 2022, 13, 2408.	12.8	26
14	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
15	Lipidomic architecture shared by subclinical markers of osteoporosis and atherosclerosis: The Cardiovascular Risk in Young Finns Study. Bone, 2020, 131, 115160.	2.9	20
16	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
17	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
18	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

#	Article	IF	Citations
19	Uncovering the shared lipidomic markers of subclinical osteoporosis-atherosclerosis comorbidity: The Young Finns Study. Bone, 2021, 151, 116030.	2.9	13
20	Increased tooth brushing frequency is associated with reduced gingival pocket bacterial diversity in patients with intracranial aneurysms. Peerl, 2019, 7, e6316.	2.0	11
21	Similarity of salivary microbiome in parents and adult children. PeerJ, 2020, 8, e8799.	2.0	11
22	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
23	Meta-analysis of epigenome-wide association studies of carotid intima-media thickness. European Journal of Epidemiology, 2021, 36, 1143-1155.	5.7	10
24	Epigenome-450K-wide methylation signatures of active cigarette smoking: The Young Finns Study. Bioscience Reports, 2020, 40, .	2.4	8
25	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
26	Examining the effect of mitochondrial DNA variants on blood pressure in two Finnish cohorts. Scientific Reports, 2021, 11, 611.	3.3	7
27	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
28	Cardiorespiratory fitness and heart rate recovery predict sudden cardiac death independent of ejection fraction. Heart, 2020, 106, 434-440.	2.9	6
29	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
30	Robust multi-group gene set analysis with few replicates. BMC Bioinformatics, 2016, 17, 526.	2.6	4
31	Assessment of plasma ceramides as predictor for subclinical atherosclerosis. Atherosclerosis Plus, 2021, 45, 25-31.	0.7	3
32	Methylation pattern of polymorphically imprinted nc886 is not conserved across mammalia. PLoS ONE, 2022, 17, e0261481.	2.5	3
33	Human Prostate Tissue MicroRNAs and Their Predicted Target Pathways Linked to Prostate Cancer Risk Factors. Cancers, 2021, 13, 3537.	3.7	2
34	Reproductive history and blood cell DNA methylation later in life: the Young Finns Study. Clinical Epigenetics, 2021, 13, 227.	4.1	2
35	C-reactive protein and temperament: An instrumental variable analysis. Brain, Behavior, & Immunity - Health, 2021, 14, 100241.	2.5	1
36	Mitochondrial genome-wide analysis of nuclear DNA methylation quantitative trait loci. Human Molecular Genetics, 2021 , , .	2.9	1