Yunzhang Wang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7738777/publications.pdf

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26	1,116	623734	552781
papers	citations	14 h-index	26 g-index

31	31	31	1657
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Protein Nutritional Status and Frailty: A Mendelian Randomization Study. Journal of Nutrition, 2022, 152, 269-275.	2.9	4
2	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature Genetics, 2022, 54, 581-592.	21.4	142
3	A computational solution for bolstering reliability of epigenetic clocks: implications for clinical trials and longitudinal tracking. Nature Aging, 2022, 2, 644-661.	11.6	95
4	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
5	Frailty and comorbidity in predicting community <scp>COVID</scp>â€19 mortality in the <scp>U.K.</scp> Biobank: The effect of sampling. Journal of the American Geriatrics Society, 2021, 69, 1128-1139.	2.6	32
6	Epigenome-wide association study of level and change in cognitive abilities from midlife through late life. Clinical Epigenetics, 2021, 13, 85.	4.1	0
7	Clinical biomarkers and associations with healthspan and lifespan: Evidence from observational and genetic data. EBioMedicine, 2021, 66, 103318.	6.1	12
8	Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome Biology, 2021, 22, 194.	8.8	90
9	Frailty trajectories in three longitudinal studies of aging: Is the level or the rate of change more predictive of mortality?. Age and Ageing, 2021, 50, 2174-2182.	1.6	16
10	The epigenetic etiology of cardiovascular disease in a longitudinal Swedish twin study. Clinical Epigenetics, 2021, 13, 129.	4.1	6
11	A genomeâ€wide association study of the frailty index highlights brain pathways in ageing. Aging Cell, 2021, 20, e13459.	6.7	74
12	Deciphering the genetic and epidemiological landscape of mitochondrial DNA abundance. Human Genetics, 2021, 140, 849-861.	3.8	47
13	Fatty Acids and Frailty: A Mendelian Randomization Study. Nutrients, 2021, 13, 3539.	4.1	8
14	Frailty and the risk of dementia: is the association explained by shared environmental and genetic factors?. BMC Medicine, 2021, 19, 248.	5.5	11
15	Replicating associations between DNA methylation and body mass index in a longitudinal sample of older twins. International Journal of Obesity, 2020, 44, 1397-1405.	3.4	6
16	Age, Frailty, and Comorbidity as Prognostic Factors for Short-Term Outcomes in Patients With Coronavirus Disease 2019 in Geriatric Care. Journal of the American Medical Directors Association, 2020, 21, 1555-1559.e2.	2.5	141
17	DNA methylation outlier burden, health, and ageing in Generation Scotland and the Lothian Birth Cohorts of 1921 and 1936. Clinical Epigenetics, 2020, 12, 49.	4.1	17
18	Profiles of histidine-rich glycoprotein associate with age and risk of all-cause mortality. Life Science Alliance, 2020, 3, e202000817.	2.8	9

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19	Longitudinal trajectories, correlations and mortality associations of nine biological ages across 20-years follow-up. ELife, 2020, 9, .	6.0	177
20	Genetically-predicted life-long lowering of low-density lipoprotein cholesterol is associated with decreased frailty: A Mendelian randomization study in UK biobank. EBioMedicine, 2019, 45, 487-494.	6.1	19
21	Human aging DNA methylation signatures are conserved but accelerated in cultured fibroblasts. Epigenetics, 2019, 14, 961-976.	2.7	36
22	Comprehensive longitudinal study of epigenetic mutations in aging. Clinical Epigenetics, 2019, 11, 187.	4.1	21
23	Apolipoprotein E DNA methylation and late-life disease. International Journal of Epidemiology, 2018, 47, 899-907.	1.9	22
24	DNA Methylation and All-Cause Mortality in Middle-Aged and Elderly Danish Twins. Genes, 2018, 9, 78.	2.4	27
25	Epigenetic influences on aging: a longitudinal genome-wide methylation study in old Swedish twins. Epigenetics, 2018, 13, 975-987.	2.7	65
26	Implementing a method for studying longitudinal DNA methylation variability in association with age. Epigenetics, 2018, 13, 866-874.	2.7	13