

Wei Zhao

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

13,926
citations

136885

32
h-index

214721

47
g-index

49
all docs

49
docs citations

49
times ranked

22372
citing authors

#	ARTICLE	IF	CITATIONS
1	The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. <i>Epigenetics</i> , 2022, 17, 589-611.	1.3	47
2	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. <i>Brain</i> , 2022, 145, 1992-2007.	3.7	6
3	Epigenetics of single-site and multi-site atherosclerosis in African Americans from the Genetic Epidemiology Network of Arteriopathy (GENOA). <i>Clinical Epigenetics</i> , 2022, 14, 10.	1.8	6
4	DNA Methylation Mediates the Association Between Individual and Neighborhood Social Disadvantage and Cardiovascular Risk Factors. <i>Frontiers in Cardiovascular Medicine</i> , 2022, 9, .	1.1	5
5	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. <i>Epigenetics</i> , 2021, 16, 862-875.	1.3	10
6	Epigenetic age acceleration is associated with cardiometabolic risk factors and clinical cardiovascular disease risk scores in African Americans. <i>Clinical Epigenetics</i> , 2021, 13, 55.	1.8	37
7	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021, 12, 3987.	5.8	18
8	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021, 11, 613.	2.4	2
9	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
10	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	5.8	8
11	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021, 12, 7174.	5.8	30
12	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. <i>Translational Psychiatry</i> , 2020, 10, 245.	2.4	9
13	Underlying features of epigenetic aging clocks in vivo and in vitro. <i>Aging Cell</i> , 2020, 19, e13229.	3.0	120
14	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	5.8	89
15	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2020, 26, 2111-2125.	4.1	17
16	Role of Rare and Low-Frequency Variants in Gene-Alcohol Interactions on Plasma Lipid Levels. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, e002772.	1.6	11
17	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	6.2	75
18	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84

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19	Education and Lifestyle Factors Are Associated with DNA Methylation Clocks in Older African Americans. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 3141.	1.2	88
20	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
21	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
22	Novel DNA methylation sites associated with cigarette smoking among African Americans. <i>Epigenetics</i> , 2019, 14, 383-391.	1.3	38
23	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	9.4	112
24	A Peripheral Blood DNA Methylation Signature of Hepatic Fat Reveals a Potential Causal Pathway for Nonalcoholic Fatty Liver Disease. <i>Diabetes</i> , 2019, 68, 1073-1083.	0.3	41
25	Longitudinal analysis of epigenome-wide DNA methylation reveals novel smoking-related loci in African Americans. <i>Epigenetics</i> , 2019, 14, 171-184.	1.3	7
26	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	9.4	356
27	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	2.6	123
28	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	5.8	484
29	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
30	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. <i>Nature</i> , 2017, 544, 235-239.	13.7	292
31	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017, 101, 888-902.	2.6	154
32	Neighborhood characteristics influence DNA methylation of genes involved in stress response and inflammation: The Multi-Ethnic Study of Atherosclerosis. <i>Epigenetics</i> , 2017, 12, 662-673.	1.3	118
33	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016, 17, 255.	3.8	251
34	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	9.4	870
35	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
36	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678

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37	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
38	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	9.4	223
39	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
40	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
41	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
42	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.	5.1	162
43	A comprehensive 1000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015, 47, 1121-1130.	9.4	2,054
44	Genome-wide Studies of Verbal Declarative Memory in Nondemented Older People: The Cohorts for Heart and Aging Research in Genomic Epidemiology Consortium. <i>Biological Psychiatry</i> , 2015, 77, 749-763.	0.7	67
45	IQGAP3 Promotes EGFR-ERK Signaling and the Growth and Metastasis of Lung Cancer Cells. <i>PLoS ONE</i> , 2014, 9, e97578.	1.1	63
46	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	6.0	750