

Wei Zhao

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44
papers

8,886
citations

28
h-index

49
g-index

49
ext. papers

12,008
ext. citations

18.4
avg, IF

3.82
L-index

#	Paper	IF	Citations
44	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	7.7	0
43	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
42	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021 , 11, 613	8.6	0
41	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
40	Epigenome-wide association study identifies DNA methylation sites associated with target organ damage in older African Americans. <i>Epigenetics</i> , 2021 , 16, 862-875	5.7	6
39	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	7.7	8
38	A multi-ethnic epigenome-wide association study of leukocyte DNA methylation and blood lipids. <i>Nature Communications</i> , 2021 , 12, 3987	17.4	3
37	The Socioeconomic Gradient in Epigenetic Ageing Clocks: Evidence from the Multi-Ethnic Study of Atherosclerosis and the Health and Retirement Study. <i>Epigenetics</i> , 2021 , 1-23	5.7	8
36	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021 , 12, 7173	17.4	1
35	Meta-analyses identify DNA methylation associated with kidney function and damage. <i>Nature Communications</i> , 2021 , 12, 7174	17.4	0
34	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020 , 11, 6285	17.4	22
33	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	5.2	8
32	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	8.6	1
31	Underlying features of epigenetic aging clocks in vivo and in vitro. <i>Aging Cell</i> , 2020 , 19, e13229	9.9	37
30	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,	4.6	49
29	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
28	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41

27	Novel DNA methylation sites associated with cigarette smoking among African Americans. <i>Epigenetics</i> , 2019 , 14, 383-391	5.7	21
26	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	36.3	59
25	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	0.9	25
24	Longitudinal analysis of epigenome-wide DNA methylation reveals novel smoking-related loci in African Americans. <i>Epigenetics</i> , 2019 , 14, 171-184	5.7	4
23	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019 , 3, 950-961	12.8	32
22	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
21	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018 , 50, 559-571	36.3	221
20	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	11	59
19	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	3.7	31
18	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018 , 9, 2098	17.4	254
17	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. <i>Nature</i> , 2017 , 544, 235-239	50.4	208
16	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. <i>American Journal of Human Genetics</i> , 2017 , 101, 888-902	11	83
15	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	5.7	73
14	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
13	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
12	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016 , 48, 1162-70	36.3	152
11	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	36.3	251
10	DNA methylation signatures of chronic low-grade inflammation are associated with complex diseases. <i>Genome Biology</i> , 2016 , 17, 255	18.3	171

9	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
8	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
7	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-462	50.4	119
6	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015 , 8, 398-409		119
5	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. <i>Nature Genetics</i> , 2015 , 47, 1121-1130	36.3	1290
4	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, 749-63	7.9	48
3	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
2	IQGAP3 promotes EGFR-ERK signaling and the growth and metastasis of lung cancer cells. <i>PLoS ONE</i> , 2014 , 9, e97578	3.7	51
1	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. <i>Science</i> , 2013 , 340, 1467-71	33.3	563