Wei Zhao

List of Publications by Year
in descending order

57 papers	13,762 citations	126858 33 h-index	138417 58 g-index
66 all docs	66 docs citations	66 times ranked	23160 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
2	A comprehensive 1000 Genomesâ€“based genome-wide association meta-analysis of coronary artery disease. Nature Genetics, 2015, 47, 1121-1130.	9.4	2,054
3	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
4	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. Nature Genetics, 2012, 44, 991-1005.	9.4	746
5	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
6	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
7	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. Lancet Diabetes and Endocrinology,the, 2015, 3, 507-513.	5.5	389
8	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	9.4	362
9	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
10	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. Nature, 2017, 544, 235-239.	13.7	292
11	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
12	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
13	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. Nature Genetics, 2017, 49, 1113-1119.	9.4	260
14	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. Nature Genetics, 2013, 45, 690-696.	9.4	232
15	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	9.4	223
16	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. Nature Genetics, 2017, 49, 1450-1457.	9.4	218
17	Meta-Analysis of Genome-Wide Association Studies in African Americans Provides Insights into the Genetic Architecture of Type 2 Diabetes. PLoS Genetics, 2014, 10, e1004517.	1.5	191
18	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	2.6	189

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19	Apolipoprotein(a) isoform size, lipoprotein(a) concentration, and coronary artery disease: a mendelian randomisation analysis. Lancet Diabetes and Endocrinology,the, 2017, 5, 524-533.	5.5	165
20	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	2.6	154
21	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. Nature Communications, 2016, 7, 10531.	5.8	149
22	Causal Assessment of Serum Urate Levels inÂCardiometabolic Diseases Through a Mendelian Randomization Study. Journal of the American College of Cardiology, 2016, 67, 407-416.	1.2	138
23	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
24	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. Nature Communications, 2017, 8, 910.	5.8	118
25	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. Cell Metabolism, 2016, 24, 234-245.	7.2	103
26	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	1.1	94
27	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
28	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. PLoS Genetics, 2017, 13, e1006728.	1.5	88
29	A Novel MMP12 Locus Is Associated with Large Artery Atherosclerotic Stroke Using a Genome-Wide Age-at-Onset Informed Approach. PLoS Genetics, 2014, 10, e1004469.	1.5	75
30	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. Stroke, 2016, 47, 307-316.	1.0	54
31	Loss of Cardioprotective Effects at the ADAMTS7 Locus as a Result of Gene-Smoking Interactions. Circulation, 2017, 135, 2336-2353.	1.6	51
32	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. Diabetes, 2017, 66, 543-550.	0.3	45
33	Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases. PLoS Genetics, 2020, 16, e1008538.	1.5	40
34	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. Journal of the American Society of Nephrology: JASN, 2017, 28, 981-994.	3.0	39
35	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
36	Genome-wide interrogation reveals hundreds of long intergenic noncoding RNAs that associate with cardiometabolic traits. Human Molecular Genetics, 2016, 25, ddw154.	1.4	30

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37	Elevated Plasma Ceramides Are Associated With Antiretroviral Therapy Use and Progression of Carotid Artery Atherosclerosis in HIV Infection. Circulation, 2019, 139, 2003-2011.	1.6	30
38	Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683.	4.3	29
39	Physical activity, smoking, and genetic predisposition to obesity in people from Pakistan: the PROMIS study. BMC Medical Genetics, 2015, 16, 114.	2.1	27
40	Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. Journal of Lipid Research, 2016, 57, 433-442.	2.0	24
41	Epidemiology and Public Health Policy of Tobacco Use and Cardiovascular Disorders in Low- and Middle-Income Countries. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1811-1819.	1.1	20
42	Common and Rare Genetic Variation in CCR2 , CCR5 , or CX3CR1 and Risk of Atherosclerotic Coronary Heart Disease and Glucometabolic Traits. Circulation: Cardiovascular Genetics, 2016, 9, 250-258.	5.1	20
43	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	4.1	17
44	A novel interaction between the FLJ33534 locus and smoking in obesity: a genome-wide study of 14â€‰131 Pakistani adults. International Journal of Obesity, 2016, 40, 186-190.	1.6	15
45	Support vector machines classifiers of physical activities in preschoolers. Physiological Reports, 2013, 1, e00006.	0.7	14
46	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
47	Anxiety and depression in spasmodic dysphonia patients. World Journal of Otorhinolaryngology - Head and Neck Surgery, 2018, 4, 110-116.	0.7	9
48	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. Translational Psychiatry, 2020, 10, 245.	2.4	9
49	A Simple and Sensitive HPLC Method For Quantification of the Metabolin of Meclofenoxate In Human Plasma. Journal of Chromatographic Science, 2010, 48, 353-357.	0.7	8
50	Gene-by-Psychosocial Factor Interactions Influence Diastolic Blood Pressure in European and African Ancestry Populations: Meta-Analysis of Four Cohort Studies. International Journal of Environmental Research and Public Health, 2017, 14, 1596.	1.2	5
51	Multiplexed Targeted Resequencing Identifies Coding and Regulatory Variation Underlying Phenotypic Extremes of High-Density Lipoprotein Cholesterol in Humans. Circulation Genomic and Precision Medicine, 2018, 11, e002070.	1.6	5
52	Combined linkage and association analysis identifies rare and low frequency variants for blood pressure at 1q31. European Journal of Human Genetics, 2019, 27, 269-277.	1.4	5
53	A replication study of 49 Type 2 diabetes risk variants in a Punjabi Pakistani population. Diabetic Medicine, 2016, 33, 1112-1117.	1.2	4
54	Using Mendelian Randomization Studies to Assess Causality and Identify New Therapeutic Targets in Cardiovascular Medicine. Current Genetic Medicine Reports, 2016, 4, 207-212.	1.9	4

#	Article	IF	Citations
55	Association of low-frequency and rare coding variants with information processing speed. Translational Psychiatry, 2021, 11, 613.	2.4	2
56	Otolaryngology Needs in a Free Clinic Providing Indigent Care. Laryngoscope, 2016, 126, 1321-1326.	1.1	1
57	Characterizing the Empirical Distribution of Prokaryotic Genome n-mers in the Presence of Nullomers. Journal of Computational Biology, 2014, 21, 732-740.	0.8	0