Wei Zhao

List of Publications by Citations

60 papers	9,511 citations	31 h-index	66 g-index
66 ext. papers	12,251 ext. citations	16.4 avg, IF	3.77 L-index

#	Paper	IF	Citations
60	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
59	A comprehensive 1,000 Genomes-based genome-wide association meta-analysis of coronary artery disease. *Nature Genetics*, **2015**, 47, 1121-1130	36.3	1290
58	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
57	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. *Nature Genetics*, **2012**, 44, 991-1005	36.3	621
56	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
55	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
54	Association of HDL cholesterol efflux capacity with incident coronary heart disease events: a prospective case-control study. *Lancet Diabetes and Endocrinology,the*, **2015**, 3, 507-13	18.1	300
53	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
52	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221
51	Human knockouts and phenotypic analysis in a cohort with a high rate of consanguinity. *Nature*, **2017**, 544, 235-239	50.4	208
50	A meta-analysis identifies new loci associated with body mass index in individuals of African ancestry. *Nature Genetics*, **2013**, 45, 690-6	36.3	192
49	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
48	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. *Nature Genetics*, **2017**, 49, 1113-1119	36.3	184
47	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
46	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. *Nature Genetics*, **2016**, 48, 1162-70	36.3	152
45	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	6	151
44	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, 545-54	11	145

43	Identification of new susceptibility loci for type 2 diabetes and shared etiological pathways with coronary heart disease. *Nature Genetics*, **2017**, 49, 1450-1457	36.3	136
42	Apolipoprotein(a) isoform size, lipoprotein(a) concentration, and coronary artery disease: a mendelian randomisation analysis. *Lancet Diabetes and Endocrinology,the*, **2017**, 5, 524-533	18.1	111
41	Causal Assessment of Serum Urate Levels in Cardiometabolic Diseases Through a Mendelian Randomization Study. *Journal of the American College of Cardiology*, **2016**, 67, 407-416	15.1	101
40	Genome-wide association studies in the Japanese population identify seven novel loci for type 2 diabetes. *Nature Communications*, **2016**, 7, 10531	17.4	99
39	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. *American Journal of Human Genetics*, **2017**, 101, 888-902	11	83
38	Genome-wide meta-analysis associates HLA-DQA1/DRB1 and LPA and lifestyle factors with human longevity. *Nature Communications*, **2017**, 8, 910	17.4	78
37	Loss of Function of GALNT2 Lowers High-Density Lipoproteins in Humans, Nonhuman Primates, and Rodents. *Cell Metabolism*, **2016**, 24, 234-45	24.6	78
36	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	6	63
35	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	11	59
34	Single-trait and multi-trait genome-wide association analyses identify novel loci for blood pressure in African-ancestry populations. *PLoS Genetics*, **2017**, 13, e1006728	6	58
33	Genome-wide analysis yields new loci associating with aortic valve stenosis. *Nature Communications* , **2018**, 9, 987	17.4	56
32	Genome-Wide Association Analysis of Young-Onset Stroke Identifies a Locus on Chromosome 10q25 Near HABP2. *Stroke*, **2016**, 47, 307-16	6.7	39
31	Loss of Cardioprotective Effects at the Locus as a Result of Gene-Smoking Interactions. *Circulation*, **2017**, 135, 2336-2353	16.7	36
30	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. *PLoS ONE*, **2018**, 13, e0198166	3.7	31
29	and 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	12.7	30
28	Genome-wide interrogation reveals hundreds of long intergenic noncoding RNAs that associate with cardiometabolic traits. *Human Molecular Genetics*, **2016**, 25, 3125-3141	5.6	25
27	Systolic Blood Pressure and Risk of Type 2 Diabetes: A Mendelian Randomization Study. *Diabetes*, **2017**, 66, 543-550	0.9	22
26	Elevated Plasma Ceramides Are Associated With Antiretroviral Therapy Use and Progression of Carotid Artery Atherosclerosis in HIV Infection. *Circulation*, **2019**, 139, 2003-2011	16.7	21

25	Physical activity, smoking, and genetic predisposition to obesity in people from Pakistan: the PROMIS study. *BMC Medical Genetics*, **2015**, 16, 114	2.1	21
24	Genomic profiling of human vascular cells identifies TWIST1 as a causal gene for common vascular diseases. *PLoS Genetics*, **2020**, 16, e1008538	6	20
23	Epidemiology and public health policy of tobacco use and cardiovascular disorders in low- and middle-income countries. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 1811-9	9.4	15
22	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. *Human Molecular Genetics*, **2019**, 28, 2615-2633	5.6	14
21	Genetic association of long-chain acyl-CoA synthetase 1 variants with fasting glucose, diabetes, and subclinical atherosclerosis. *Journal of Lipid Research*, **2016**, 57, 433-42	6.3	14
20	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, 250-8		14
19	A novel interaction between the FLJ33534 locus and smoking in obesity: a genome-wide study of 14 131 Pakistani adults. *International Journal of Obesity*, **2016**, 40, 186-90	5.5	13
18	Support vector machines classifiers of physical activities in preschoolers. *Physiological Reports*, **2013**, 1, e00006	2.6	12
17	Human knockouts in a cohort with a high rate of consanguinity		8
16	Scalable generalized linear mixed model for region-based association tests in large biobanks and cohorts		7
15	A simple and sensitive HPLC method for quantification of the metabolin of meclofenoxate in human plasma. *Journal of Chromatographic Science*, **2010**, 48, 353-7	1.4	6
14	Discovery and systematic characterization of risk variants and genes for coronary artery disease in over a million participants		5
13	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	5.2	5
12	Using Mendelian Randomization studies to Assess Causality and Identify New Therapeutic Targets in Cardiovascular Medicine. *Current Genetic Medicine Reports*, **2016**, 4, 207-212	2.2	4
11	Anxiety and depression in spasmodic dysphonia patients. *World Journal of Otorhinolaryngology - Head and Neck Surgery*, **2018**, 4, 110-116	2.6	4
10	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation		4
9	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. *Molecular Psychiatry*, **2021**, 26, 2111-2125	15.1	3
8	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,	4.6	3

7	A replication study of 49 Type 2 diabetes risk variants in a Punjabi Pakistani population. *Diabetic Medicine*, **2016**, 33, 1112-7	3.5	3
6	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	5.3	3
5	Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes		2
4	Otolaryngology Needs in a Free Clinic Providing Indigent Care. *Laryngoscope*, **2016**, 126, 1321-6	3.6	1
3	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	8.6	1
2	Association of low-frequency and rare coding variants with information processing speed. *Translational Psychiatry*, **2021**, 11, 613	8.6	0
1	Characterizing the empirical distribution of prokaryotic genome n-mers in the presence of nullomers. *Journal of Computational Biology*, **2014**, 21, 732-40	1.7	