Zhihong Zhu

List of Publications by Year
in descending order

36 papers	7,688 citations	186265 28 h-index	345221 36 g-index
47 all docs	47 docs citations	47 times ranked	14059 citing authors

#	Article	IF	Citations
1	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. Nature Genetics, 2016, 48, 481-487.	21.4	1,757
2	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
3	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	21.4	709
4	Causal associations between risk factors and common diseases inferred from GWAS summary data. Nature Communications, 2018, 9, 224.	12.8	629
5	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature Communications, 2018, 9, 2941.	12.8	570
6	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. Nature Communications, 2018, 9, 2282.	12.8	294
7	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. Nature Communications, 2018, 9, 918.	12.8	250
8	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
9	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. Nature Communications, 2020, 11, 1647.	12.8	211
10	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. American Journal of Human Genetics, 2015, 96, 377-385.	6.2	191
11	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. Scientific Reports, 2016, 6, 32894.	3.3	138
12	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. Nature Communications, 2018, 9, 989.	12.8	136
13	Genotypeâ€“covariate interaction effects and the heritability of adult body mass index. Nature Genetics, 2017, 49, 1174-1181.	21.4	119
14	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116
15	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
16	OSCA: a tool for omic-data-based complex trait analysis. Genome Biology, 2019, 20, 107.	8.8	105
17	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.	8.2	91
18	Genome-Wide Interaction-Based Association Analysis Identified Multiple New Susceptibility Loci for Common Diseases. PLoS Genetics, 2011, 7, e1001338.	3.5	75

#	Article	IF	Citations
19	Global genetic differentiation of complex traits shaped by natural selection in humans. Nature Communications, 2018, 9, 1865.	12.8	70
20	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. Human Molecular Genetics, 2015, 24, 7445-7449.	2.9	67
21	Development of GMDR-GPU for Gene-Gene Interaction Analysis and Its Application to WTCCC GWAS Data for Type 2 Diabetes. PLoS ONE, 2013, 8, e61943.	2.5	60
22	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25â€‰000 subjects. Molecular Psychiatry, 2015, 20, 735-743.	7.9	59
23	Association of Antihypertensive Drug Target Genes With Psychiatric Disorders. JAMA Psychiatry, 2021, 78, 623.	11.0	56
24	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.	11.0	51
25	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. Scientific Reports, 2018, 8, 11424.	3.3	49
26	Detection and quantification of inbreeding depression for complex traits from SNP data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8602-8607.	7.1	48
27	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. Molecular Psychiatry, 2021, 26, 2070-2081.	7.9	48
28	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. Nature Communications, 2021, 12, 5641.	12.8	46
29	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. Nature Communications, 2021, 12, 20211.	12.8	40
30	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. Communications Biology, 2019, 2, 119.	4.4	35
31	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. Nature Communications, 2021, 12, 7117.	12.8	31
32	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. Clinical Epigenetics, 2019, 11, 49.	4.1	26
33	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. European Journal of Human Genetics, 2022, 30, 532-539.	2.8	16
34	Developmental exposure to vitamin D deficiency and subsequent risk of schizophrenia. Schizophrenia Research, 2022, 247, 26-32.	2.0	9
35	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E2494-E2495.	7.1	6
36	Finding hidden treasures in summary statistics from genome-wide association studies. Nature Genetics, 2021, 53, 431-432.	21.4	3