

# Zhihong Zhu

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Polygenic risk score analysis for amyotrophic lateral sclerosis leveraging cognitive performance, educational attainment and schizophrenia. <i>European Journal of Human Genetics</i> , 2022, 30, 532-539.	2.8	16
2	Developmental exposure to vitamin D deficiency and subsequent risk of schizophrenia. <i>Schizophrenia Research</i> , 2022, 247, 26-32.	2.0	9
3	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	21.4	215
4	Genome-wide analyses of behavioural traits are subject to bias by misreports and longitudinal changes. <i>Nature Communications</i> , 2021, 12, 20211.	12.8	40
5	Finding hidden treasures in summary statistics from genome-wide association studies. <i>Nature Genetics</i> , 2021, 53, 431-432.	21.4	3
6	Association of Antihypertensive Drug Target Genes With Psychiatric Disorders. <i>JAMA Psychiatry</i> , 2021, 78, 623.	11.0	56
7	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	7.9	48
8	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. <i>Nature Communications</i> , 2021, 12, 5641.	12.8	46
9	Improved analyses of GWAS summary statistics by reducing data heterogeneity and errors. <i>Nature Communications</i> , 2021, 12, 7117.	12.8	31
10	Genome-wide association study identifies 143 loci associated with 25 hydroxyvitamin D concentration. <i>Nature Communications</i> , 2020, 11, 1647.	12.8	211
11	OSCA: a tool for omic-data-based complex trait analysis. <i>Genome Biology</i> , 2019, 20, 107.	8.8	105
12	Genetic regulation of methylation in human endometrium and blood and gene targets for reproductive diseases. <i>Clinical Epigenetics</i> , 2019, 11, 49.	4.1	26
13	Mendelian randomisation analyses find pulmonary factors mediate the effect of height on coronary artery disease. <i>Communications Biology</i> , 2019, 2, 119.	4.4	35
14	Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018, 9, 989.	12.8	136
15	Reply to Kardos et al.: Estimation of inbreeding depression from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E2494-E2495.	7.1	6
16	Integrative analysis of omics summary data reveals putative mechanisms underlying complex traits. <i>Nature Communications</i> , 2018, 9, 918.	12.8	250
17	Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018, 9, 224.	12.8	629
18	Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.	12.8	70

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19	Genetic regulation of disease risk and endometrial gene expression highlights potential target genes for endometriosis and polycystic ovarian syndrome. <i>Scientific Reports</i> , 2018, 8, 11424.	3.3	49
20	Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <i>Nature Communications</i> , 2018, 9, 2941.	12.8	570
21	Identifying gene targets for brain-related traits using transcriptomic and methylomic data from blood. <i>Nature Communications</i> , 2018, 9, 2282.	12.8	294
22	Detection and quantification of inbreeding depression for complex traits from SNP data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8602-8607.	7.1	48
23	Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.	21.4	119
24	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016, 8, 84.	8.2	91
25	Fast set-based association analysis using summary data from GWAS identifies novel gene loci for human complex traits. <i>Scientific Reports</i> , 2016, 6, 32894.	3.3	138
26	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
27	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
28	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016, 73, 497.	11.0	51
29	Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.	21.4	1,757
30	The association between lower educational attainment and depression owing to shared genetic effects? Results in ~25%000 subjects. <i>Molecular Psychiatry</i> , 2015, 20, 735-743.	7.9	59
31	Dominance Genetic Variation Contributes Little to the Missing Heritability for Human Complex Traits. <i>American Journal of Human Genetics</i> , 2015, 96, 377-385.	6.2	191
32	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. <i>American Journal of Human Genetics</i> , 2015, 97, 75-85.	6.2	116
33	Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. <i>Human Molecular Genetics</i> , 2015, 24, 7445-7449.	2.9	67
34	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015, 47, 1114-1120.	21.4	709
35	Development of GMDR-GPU for Gene-Gene Interaction Analysis and Its Application to WTCCC GWAS Data for Type 2 Diabetes. <i>PLoS ONE</i> , 2013, 8, e61943.	2.5	60
36	Genome-Wide Interaction-Based Association Analysis Identified Multiple New Susceptibility Loci for Common Diseases. <i>PLoS Genetics</i> , 2011, 7, e1001338.	3.5	75