

Jie Huang

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

4,328
citations

430874

18
h-index

526287

27
g-index

31
all docs

31
docs citations

31
times ranked

10586
citing authors

#	ARTICLE	IF	CITATIONS
1	Attention-deficit/hyperactivity disorder and ischemic stroke: A Mendelian randomization study. <i>International Journal of Stroke</i> , 2023, 18, 346-353.	5.9	3
2	Two pandemics in China, One Health in Chinese. <i>BMJ Global Health</i> , 2022, 7, e008550.	4.7	0
3	PAGEANT: personal access to genome and analysis of natural traits. <i>Nucleic Acids Research</i> , 2022, 50, e39-e39.	14.5	1
4	A Next Generation Sequencing-Based Protocol for Screening of Variants of Concern in Autism Spectrum Disorder. <i>Cells</i> , 2022, 11, 10.	4.1	16
5	Integration of rare expression outlier-associated variants improves polygenic risk prediction. <i>American Journal of Human Genetics</i> , 2022, 109, 1055-1064.	6.2	8
6	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. <i>Nature Genetics</i> , 2022, 54, 761-771.	21.4	68
7	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. <i>PLoS Genetics</i> , 2022, 18, e1010193.	3.5	12
8	Correlates of Successful Rheumatoid Arthritis Flare Management: Clinician-driven Treatment, Home-based Strategies, and Medication Change. <i>Journal of Rheumatology</i> , 2020, 47, 333-340.	2.0	5
9	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. <i>Nature Genetics</i> , 2020, 52, 680-691.	21.4	445
10	Genotyping Array Design and Data Quality Control in the Million Veteran Program. <i>American Journal of Human Genetics</i> , 2020, 106, 535-548.	6.2	118
11	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	30.7	177
12	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1255-1262.	4.4	69
13	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. <i>Nature Genetics</i> , 2019, 51, 1574-1579.	21.4	152
14	Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. <i>American Journal of Human Genetics</i> , 2019, 105, 763-772.	6.2	169
15	Effects of Genetic Variants Associated with Familial Hypercholesterolemia on Low-Density Lipoprotein-Cholesterol Levels and Cardiovascular Outcomes in the Million Veteran Program. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, .	3.6	15
16	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , 2018, 50, 1514-1523.	21.4	497
17	Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. <i>American Journal of Human Genetics</i> , 2018, 103, 691-706.	6.2	326
18	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	8.4	341

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19	A SNP panel and online tool for checking genotype concordance through comparing QR codes. PLoS ONE, 2017, 12, e0182438.	2.5	8
20	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
21	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	27.8	1,014
22	Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111.	12.8	300
23	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial <i>STXBP5</i> and <i>STX2</i> . Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
24	WikiGWA: an open platform for collecting and using genome-wide association results. European Journal of Human Genetics, 2013, 21, 471-473.	2.8	3
25	Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881.	1.4	90
26	1000 Genomes-based imputation identifies novel and refined associations for the Wellcome Trust Case Control Consortium phase 1 Data. European Journal of Human Genetics, 2012, 20, 801-805.	2.8	123
27	PRIME: a method for characterization and evaluation of pleiotropic regions from multiple genome-wide association studies. Bioinformatics, 2011, 27, 1201-1206.	4.1	63
28	Cross-Disorder Genomewide Analysis of Schizophrenia, Bipolar Disorder, and Depression. American Journal of Psychiatry, 2010, 167, 1254-1263.	7.2	190