# Jie Huang

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6913080/publications.pdf

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| 28 | 4,328 | 430874 | 526287 |
|---|---|---|---|
| papers | citations | 18 | 27 |
| | | h-index | g-index |

| 31 | 31 | 31 | 10586 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90. | 27.8 | 1,014 |
| 2 | Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523. | 21.4 | 497 |
| 3 | 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. Nature Genetics, 2020, 52, 680-691. | 21.4 | 445 |
| 4 | 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. PLoS Medicine, 2017, 14, e1002383. | 8.4 | 341 |
| 5 | Genome Analyses of >200,000 Individuals Identify 58 Loci for Chronic Inflammation and Highlight Pathways that Link Inflammation and Complex Disorders. American Journal of Human Genetics, 2018, 103, 691-706. | 6.2 | 326 |
| 6 | Improved imputation of low-frequency and rare variants using the UK10K haplotype reference panel. Nature Communications, 2015, 6, 8111. | 12.8 | 300 |
| 7 | Cross-Disorder Genomewide Analysis of Schizophrenia, Bipolar Disorder, and Depression. American Journal of Psychiatry, 2010, 167, 1254-1263. | 7.2 | 190 |
| 8 | Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279. | 30.7 | 177 |
| 9 | Harmonizing Genetic Ancestry and Self-identified Race/Ethnicity in Genome-wide Association Studies. American Journal of Human Genetics, 2019, 105, 763-772. | 6.2 | 169 |
| 10 | Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579. | 21.4 | 152 |
| 11 | 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 |
| 12 | Genotyping Array Design and Data Quality Control in the Million Veteran Program. American Journal of Human Genetics, 2020, 106, 535-548. | 6.2 | 118 |
| 13 | Genome-wide association study for circulating levels of PAI-1 provides novel insights into its regulation. Blood, 2012, 120, 4873-4881. | 1.4 | 90 |
| 14 | High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1255-1262. | 4.4 | 69 |
| 15 | A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771. | 21.4 | 68 |
| 16 | Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312. | 21.4 | 66 |
| 17 | PRIMe: a method for characterization and evaluation of pleiotropic regions from multiple genome-wide association studies. Bioinformatics, 2011, 27, 1201-1206. | 4.1 | 63 |
| 18 | Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial STXBP5 and STX2. Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101. | 2.4 | 43 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | A Next Generation Sequencing-Based Protocol for Screening of Variants of Concern in Autism Spectrum Disorder. Cells, 2022, 11, 10. | 4.1 | 16 |
| 20 | Effects of Genetic Variants Associated with Familial Hypercholesterolemia on Low-Density Lipoprotein-Cholesterol Levels and Cardiovascular Outcomes in the Million Veteran Program. Circulation Genomic and Precision Medicine, 2018, 11, . | 3.6 | 15 |
| 21 | A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193. | 3.5 | 12 |
| 22 | A SNP panel and online tool for checking genotype concordance through comparing QR codes. PLoS ONE, 2017, 12, e0182438. | 2.5 | 8 |
| 23 | Integration of rare expression outlier-associated variants improves polygenic risk prediction. American Journal of Human Genetics, 2022, 109, 1055-1064. | 6.2 | 8 |
| 24 | Correlates of Successful Rheumatoid Arthritis Flare Management: Clinician-driven Treatment, Home-based Strategies, and Medication Change. Journal of Rheumatology, 2020, 47, 333-340. | 2.0 | 5 |
| 25 | WikiGWA: an open platform for collecting and using genome-wide association results. European Journal of Human Genetics, 2013, 21, 471-473. | 2.8 | 3 |
| 26 | Attention-deficit/hyperactivity disorder and ischemic stroke: A Mendelian randomization study. International Journal of Stroke, 2023, 18, 346-353. | 5.9 | 3 |
| 27 | PAGEANT: personal access to genome and analysis of natural traits. Nucleic Acids Research, 2022, 50, e39-e39. | 14.5 | 1 |
| 28 | Two pandemics in China, One Health in Chinese. BMJ Global Health, 2022, 7, e008550. | 4.7 | 0 |