# Jin Yu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3827639/publications.pdf

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|---|---|---|---|
| 26 papers | 31,371 citations | 430442 18 h-index | 610482 24 g-index |
| 31 all docs | 31 docs citations | 31 times ranked | 54923 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4. | 3.8 | 21 |
| 2 | Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801. | 2.8 | 12 |
| 3 | Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways. American Journal of Human Genetics, 2019, 105, 334-350. | 2.6 | 86 |
| 4 | Schizophrenia Polygenic Risk Score as a Predictor of Antipsychotic Efficacy in First-Episode Psychosis. American Journal of Psychiatry, 2019, 176, 21-28. | 4.0 | 127 |
| 5 | High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. Human Genetics, 2018, 137, 343-355. | 1.8 | 24 |
| 6 | Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098. | 5.8 | 484 |
| 7 | Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919. | 9.4 | 893 |
| 8 | Multi-Trait Analysis of GWAS and Biological Insights Into Cognition: A Response to Hill (2018). Twin Research and Human Genetics, 2018, 21, 394-397. | 0.3 | 3 |
| 9 | Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. Cell Reports, 2017, 21, 2597-2613. | 2.9 | 103 |
| 10 | Expanded genetic screening panel for the Ashkenazi Jewish population. Genetics in Medicine, 2016, 18, 522-528. | 1.1 | 33 |
| 11 | A global reference for human genetic variation. Nature, 2015, 526, 68-74. | 13.7 | 13,998 |
| 12 | Association of a Schizophrenia Risk Variant at theDRD2Locus With Antipsychotic Treatment Response in First-Episode Psychosis. Schizophrenia Bulletin, 2015, 41, 1248-1255. | 2.3 | 64 |
| 13 | Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644. | 1.1 | 13 |
| 14 | Cloud processing of 1000 genomes sequencing data using Amazon Web Service. , 2013, , . | | 2 |
| 15 | An integrative variant analysis pipeline for accurate genotype/haplotype inference in population NGS data. Genome Research, 2013, 23, 833-842. | 2.4 | 93 |
| 16 | Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901. | 9.4 | 132 |
| 17 | Nextâ€generation sequencing study finds an excess of rare, coding singleâ€nucleotide variants of ADAMTS13 in patients with deep vein thrombosis. Journal of Thrombosis and Haemostasis, 2013, 11, 1228-1239. | 1.9 | 52 |
| 18 | The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462. | 9.0 | 308 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | An integrative variant analysis suite for whole exome next-generation sequencing data. BMC Bioinformatics, 2012, 13, 8. | 1.2 | 252 |
| 20 | An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65. | 13.7 | 7,199 |
| 21 | Atlas2 Cloud: a framework for personal genome analysis in the cloud. BMC Genomics, 2012, 13, S19. | 1.2 | 42 |
| 22 | Identification of genetic risk variants for deep vein thrombosis by multiplexed next-generation sequencing of 186 hemostatic/pro-inflammatory genes. BMC Medical Genomics, 2012, 5, 7. | 0.7 | 32 |
| 23 | Rare Coding Single Nucleotide Variants of ADAMTS13 Are Associated with Deep Vein Thrombosis in a Next-Generation Sequencing Association Study. Blood, 2012, 120, 107-107. | 0.6 | 0 |
| 24 | The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84. | 13.9 | 173 |
| 25 | Identification of DEEP Vein Thrombosis GENETIC RISK Variants by NEXT GENERATION Sequencing of Hemostatic Genes. Blood, 2011, 118, 710-710. | 0.6 | 0 |
| 26 | A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073. | 13.7 | 7,209 |