Jin Yu

List of Publications by Citations

27 papers	22,677 citations	18 h-index	31 g-index
31 ext. papers	28,128 ext. citations	15.3 avg, IF	5.9 L-index

#	Paper	IF	Citations
27	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
26	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
25	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
24	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. *Nature Genetics*, **2018**, 50, 912-919	36.3	475
23	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
22	An integrative variant analysis suite for whole exome next-generation sequencing data. *BMC Bioinformatics*, **2012**, 13, 8	3.6	211
21	The 1000 Genomes Project: data management and community access. *Nature Methods*, **2012**, 9, 459-62	21.6	202
20	The functional spectrum of low-frequency coding variation. *Genome Biology*, **2011**, 12, R84	18.3	161
19	Whole-genome sequence-based analysis of high-density lipoprotein cholesterol. *Nature Genetics*, **2013**, 45, 899-901	36.3	117
18	Large-Scale Cognitive GWAS Meta-Analysis Reveals Tissue-Specific Neural Expression and Potential Nootropic Drug Targets. *Cell Reports*, **2017**, 21, 2597-2613	10.6	71
17	An integrative variant analysis pipeline for accurate genotype/haplotype inference in population NGS data. *Genome Research*, **2013**, 23, 833-42	9.7	69
16	Schizophrenia Polygenic Risk Score as a Predictor of Antipsychotic Efficacy in First-Episode Psychosis. *American Journal of Psychiatry*, **2019**, 176, 21-28	11.9	68
15	Association of a Schizophrenia Risk Variant at the DRD2 Locus With Antipsychotic Treatment Response in First-Episode Psychosis. *Schizophrenia Bulletin*, **2015**, 41, 1248-55	7.3	52
14	Next-generation sequencing study finds an excess of rare, coding single-nucleotide variants of ADAMTS13 in patients with deep vein thrombosis. *Journal of Thrombosis and Haemostasis*, **2013**, 11, 1228-39	15.4	41
13	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	11	37
12	Atlas2 Cloud: a framework for personal genome analysis in the cloud. *BMC Genomics*, **2012**, 13 Suppl 6, S19	4.5	34
11	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	3.7	26

List of Publications

10	Expanded genetic screening panel for the Ashkenazi Jewish population. *Genetics in Medicine*, **2016**, 18, 522-8	8.1	24
9	High-depth whole genome sequencing of an Ashkenazi Jewish reference panel: enhancing sensitivity, accuracy, and imputation. *Human Genetics*, **2018**, 137, 343-355	6.3	16
8	Population genomic analysis of 962 whole genome sequences of humans reveals natural selection in non-coding regions. *PLoS ONE*, **2015**, 10, e0121644	3.7	12
7	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. *Neuron*, **2021**, 109, 1465-1478.e4	13.9	8
6	Multi-Trait Analysis of GWAS and Biological Insights Into Cognition: A Response to Hill (2018). *Twin Research and Human Genetics*, **2018**, 21, 394-397	2.2	2
5	Pleiotropic Meta-Analysis of Cognition, Education, and Schizophrenia Differentiates Roles of Early Neurodevelopmental and Adult Synaptic Pathways		2
4	Novel Ultra-Rare Exonic Variants Identified in a Founder Population Implicate Cadherins in Schizophrenia		1
3	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. *Neuropsychopharmacology*, **2021**, 46, 1788-1801	8.7	1
2	Identification of DEEP Vein Thrombosis GENETIC RISK Variants by NEXT GENERATION Sequencing of Hemostatic Genes. *Blood*, **2011**, 118, 710-710	2.2	
1	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	2.2	