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	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
4	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
5	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. Nature Communications, 2018, 9, 2098.	5.8	484
6	The 1000 Genomes Project: data management and community access. Nature Methods, 2012, 9, 459-462.	9.0	308
7	An integrative variant analysis suite for whole exome next-generation sequencing data. BMC Bioinformatics, 2012, 13, 8.	1.2	252
8	The functional spectrum of low-frequency coding variation. Genome Biology, 2011, 12, R84.	13.9	173
9	Whole-genome sequenceâ€“based analysis of high-density lipoprotein cholesterol. Nature Genetics, 2013, 45, 899-901.	9.4	132
10	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
11	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
12	An integrative variant analysis pipeline for accurate genotype/haplotype inference in population NGS data. Genome Research, 2013, 23, 833-842.	2.4	93
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.	2.6	86
14	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
15	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
16	Atlas2 Cloud: a framework for personal genome analysis in the cloud. BMC Genomics, 2012, 13, S19.	1.2	42
17	Expanded genetic screening panel for the Ashkenazi Jewish population. Genetics in Medicine, 2016, 18, 522-528.	1.1	33
18	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

#	Article	IF	Citations
19	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
20	Novel ultra-rare exonic variants identified in a founder population implicate cadherins in schizophrenia. Neuron, 2021, 109, 1465-1478.e4.	3.8	21
21	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
22	Identifying nootropic drug targets via large-scale cognitive GWAS and transcriptomics. Neuropsychopharmacology, 2021, 46, 1788-1801.	2.8	12
23	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
24	Cloud processing of 1000 genomes sequencing data using Amazon Web Service. , 2013, , .		2
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	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