

Xueqiu Jian

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

8,346
citations

361413

20
h-index

434195

31
g-index

32
all docs

32
docs citations

32
times ranked

17304
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. <i>Brain</i> , 2022, 145, 1992-2007.	7.6	6
2	New insights into the genetic etiology of Alzheimer's disease and related dementias. <i>Nature Genetics</i> , 2022, 54, 412-436.	21.4	700
3	Multimomics integrative analysis identifies APOE allele-specific blood biomarkers associated to Alzheimer's disease etiopathogenesis. <i>Aging</i> , 2021, 13, 9277-9329.	3.1	15
4	Common variants in Alzheimer's disease and risk stratification by polygenic risk scores. <i>Nature Communications</i> , 2021, 12, 3417.	12.8	140
5	Association of low-frequency and rare coding variants with information processing speed. <i>Translational Psychiatry</i> , 2021, 11, 613.	4.8	2
6	Whole exome sequencing study identifies novel rare and common Alzheimer's-Associated variants involved in immune response and transcriptional regulation. <i>Molecular Psychiatry</i> , 2020, 25, 1859-1875.	7.9	191
7	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	12.8	61
8	Genome-wide association study of cognitive function in diverse Hispanics/Latinos: results from the Hispanic Community Health Study/Study of Latinos. <i>Translational Psychiatry</i> , 2020, 10, 245.	4.8	9
9	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
10	Association of variants in <i>HTRA1</i> and <i>NOTCH3</i> with MRI-defined extremes of cerebral small vessel disease in older subjects. <i>Brain</i> , 2019, 142, 1009-1023.	7.6	37
11	A prospective study of serum metabolites and risk of ischemic stroke. <i>Neurology</i> , 2019, 92, e1890-e1898.	1.1	48
12	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates $A\beta$, tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	21.4	1,962
13	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
14	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019, 92, .	1.1	30
15	Apolipoprotein E genotypes among diverse middle-aged and older Latinos: Study of Latinos-Investigation of Neurocognitive Aging results (HCHS/SOL). <i>Scientific Reports</i> , 2018, 8, 17578.	3.3	26
16	Genome-wide association study of 23,500 individuals identifies 7 loci associated with brain ventricular volume. <i>Nature Communications</i> , 2018, 9, 3945.	12.8	31
17	Imaging Endophenotypes of Stroke as a Target for Genetic Studies. <i>Stroke</i> , 2018, 49, 1557-1562.	2.0	10
18	Exome Chip Analysis Identifies Low-Frequency and Rare Variants in <i>MRPL38</i> for White Matter Hyperintensities on Brain Magnetic Resonance Imaging. <i>Stroke</i> , 2018, 49, 1812-1819.	2.0	17

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19	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
20	Rare coding variants in <i>PLCG2</i> , <i>ABI3</i> , and <i>TREM2</i> implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	21.4	783
21	In Silico Prediction of Deleteriousness for Nonsynonymous and Splice-Altering Single Nucleotide Variants in the Human Genome. <i>Methods in Molecular Biology</i> , 2017, 1498, 191-197.	0.9	17
22	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	10.2	130
23	Comparison and integration of deleteriousness prediction methods for nonsynonymous SNVs in whole exome sequencing studies. <i>Human Molecular Genetics</i> , 2015, 24, 2125-2137.	2.9	892
24	In silico prediction of splice-altering single nucleotide variants in the human genome. <i>Nucleic Acids Research</i> , 2014, 42, 13534-13544.	14.5	396
25	In silico tools for splicing defect prediction: a survey from the viewpoint of end users. <i>Genetics in Medicine</i> , 2014, 16, 497-503.	2.4	124
26	dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. <i>Human Mutation</i> , 2013, 34, E2393-E2402.	2.5	546
27	Polymorphisms in <i>ABLIM1</i> are Associated with Personality Traits and Alcohol Dependence. <i>Journal of Molecular Neuroscience</i> , 2012, 46, 265-271.	2.3	15
28	Family-based association analysis of alcohol dependence in the COGA sample and replication in the Australian twin-family study. <i>Journal of Neural Transmission</i> , 2011, 118, 1293-1299.	2.8	18
29	dbNSFP: A lightweight database of human nonsynonymous SNPs and their functional predictions. <i>Human Mutation</i> , 2011, 32, 894-899.	2.5	706