Tian Ge

List of Publications by Year
in descending order

39 papers	4,616 citations	257429 24 h-index	345203 36 g-index
57 all docs	57 docs citations	57 times ranked	6788 citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
2	Polygenic prediction via Bayesian regression and continuous shrinkage priors. Nature Communications, 2019, 10, 1776.	12.8	832
3	Global signal regression strengthens association between resting-state functional connectivity and behavior. NeuroImage, 2019, 196, 126-141.	4.2	292
4	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
5	Improving polygenic prediction in ancestrally diverse populations. Nature Genetics, 2022, 54, 573-580.	21.4	209
6	Resting brain dynamics at different timescales capture distinct aspects of human behavior. Nature Communications, 2019, 10, 2317.	12.8	208
7	Transcriptional profiles of supragranular-enriched genes associate with corticocortical network architecture in the human brain. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E469-78.	7.1	190
8	Penetrance and Pleiotropy of Polygenic Risk Scores for Schizophrenia in 106,160 Patients Across Four Health Care Systems. American Journal of Psychiatry, 2019, 176, 846-855.	7.2	168
9	Heritability analysis with repeat measurements and its application to resting-state functional connectivity. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5521-5526.	7.1	122
10	An Exposure-Wide and Mendelian Randomization Approach to Identifying Modifiable Factors for the Prevention of Depression. American Journal of Psychiatry, 2020, 177, 944-954.	7.2	119
11	The default network of the human brain is associated with perceived social isolation. Nature Communications, 2020, 11, 6393.	12.8	108
12	Individual-Specific Areal-Level Parcellations Improve Functional Connectivity Prediction of Behavior. Cerebral Cortex, 2021, 31, 4477-4500.	2.9	104
13	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
14	Dissociable influences of <i>APOE</i> ε4 and polygenic risk of AD dementia on amyloid and cognition. Neurology, 2018, 90, e1605-e1612.	1.1	71
15	Massively expedited genome-wide heritability analysis (MEGHA). Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2479-2484.	7.1	69
16	Loneliness and meaning in life are reflected in the intrinsic network architecture of the brain. Social Cognitive and Affective Neuroscience, 2019, 14, 423-433.	3.0	61
17	Transcriptional and imaging-genetic association of cortical interneurons, brain function, and schizophrenia risk. Nature Communications, 2020, 11, 2889.	12.8	59
18	Heritability of individualized cortical network topography. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	59

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19	Morphometricity as a measure of the neuroanatomical signature of a trait. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E5749-56.	7.1	53
20	Clinical laboratory test-wide association scan of polygenic scores identifies biomarkers of complex disease. Genome Medicine, 2021, 13, 6.	8.2	49
21	Development and validation of a trans-ancestry polygenic risk score for type 2 diabetes in diverse populations. Genome Medicine, 2022, 14, .	8.2	48
22	Cross-ethnicity/race generalization failure of behavioral prediction from resting-state functional connectivity. Science Advances, 2022, 8, eabj1812.	10.3	45
23	The schizophrenia risk locus in SLC39A8 alters brain metal transport and plasma glycosylation. Scientific Reports, 2020, 10, 13162.	3.3	43
24	A Polygenic Score for Higher Educational Attainment is Associated with Larger Brains. Cerebral Cortex, 2019, 29, 3496-3504.	2.9	36
25	The causal role of circulating vitamin D concentrations in human complex traits and diseases: a large-scale Mendelian randomization study. Scientific Reports, 2021, 11, 184.	3.3	34
26	Use of the PsycheMERGE Network to Investigate the Association Between Depression Polygenic Scores and White Blood Cell Count. JAMA Psychiatry, 2021, 78, 1365.	11.0	31
27	Age differences in the functional architecture of the human brain. Cerebral Cortex, 2022, 33, 114-134.	2.9	31
28	Effects of copy number variations on brain structure and risk for psychiatric illness: Large‐scale studies from the<scp>ENIGMA</scp>working groups on<scp>CNVs</scp>. Human Brain Mapping, 2022, 43, 300-328.	3.6	30
29	Functional density and edge maps: Characterizing functional architecture in individuals and improving cross-subject registration. NeuroImage, 2017, 158, 346-355.	4.2	28
30	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
31	The Shared Genetic Basis of Educational Attainment and Cerebral Cortical Morphology. Cerebral Cortex, 2019, 29, 3471-3481.	2.9	23
32	Accelerated estimation and permutation inference for ACE modeling. Human Brain Mapping, 2019, 40, 3488-3507.	3.6	19
33	Population heterogeneity in clinical cohorts affects the predictive accuracy of brain imaging. PLoS Biology, 2022, 20, e3001627.	5.6	17
34	A Set-Based Mixed Effect Model for Gene-Environment Interaction and Its Application to Neuroimaging Phenotypes. Frontiers in Neuroscience, 2017, 11, 191.	2.8	13
35	Polygenic risk for major depression is associated with lifetime suicide attempt in <scp>US</scp> soldiers independent of personal and parental history of major depression. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 469-475.	1.7	5
36	Reply to Risk and Zhu: Mixed-effects modeling as a principled approach to heritability analysis with repeat measurements. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E123-E123.	7.1	0

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37	P4â€496: MYELOID CELLâ€SPECIFIC ALZHEIMER'S DISEASE POLYGENIC RISK SCORE PREDICTS NEURODEGENERATION AND AÎ²â€RELATED COGNITIVE DECLINE IN COGNITIVELY NORMAL OLDER ADULTS. Alzheimer's and Dementia, 2019, 15, P1503.	0.8	0
38	Cell type-specific Alzheimer's disease polygenic risk scores are associated with distinct disease processes in preclinical Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e055304.	0.8	0
39	Improving the computation efficiency of polygenic risk score modeling: faster in Julia. Life Science Alliance, 2022, 5, e202201382.	2.8	0