

Qingqin S Li

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

8,470
citations

279798

23
h-index

214800

47
g-index

52
all docs

52
docs citations

52
times ranked

11958
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
3	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	27.8	929
4	Membrane Compartmentation Is Required for Efficient T Cell Activation. <i>Immunity</i> , 1998, 8, 723-732.	14.8	865
5	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
6	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
7	Conditional Ablation of $\beta 1$ Integrin in Skin. <i>Journal of Cell Biology</i> , 2000, 150, 1149-1160.	5.2	363
8	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. <i>Brain Imaging and Behavior</i> , 2014, 8, 183-207.	2.1	161
9	Temporal Gene Expression Analysis of Monolayer Cultured Rat Hepatocytes. <i>Chemical Research in Toxicology</i> , 2001, 14, 1218-1231.	3.3	145
10	Translating genome-wide association findings into new therapeutics for psychiatry. <i>Nature Neuroscience</i> , 2016, 19, 1392-1396.	14.8	115
11	Interferon alfa regulated gene expression in patients initiating interferon treatment for chronic hepatitis C. <i>Hepatology</i> , 2003, 37, 610-621.	7.3	105
12	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	1.3	84
13	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. <i>American Journal of Psychiatry</i> , 2020, 177, 917-927.	7.2	66
14	Harnessing peripheral DNA methylation differences in the Alzheimer's Disease Neuroimaging Initiative (ADNI) to reveal novel biomarkers of disease. <i>Clinical Epigenetics</i> , 2020, 12, 84.	4.1	57
15	GPR139, an Orphan Receptor Highly Enriched in the Habenula and Septum, Is Activated by the Essential Amino Acids L-Tryptophan and L-Phenylalanine. <i>Molecular Pharmacology</i> , 2015, 88, 911-925.	2.3	55
16	SCN9A Variants May be Implicated in Neuropathic Pain Associated With Diabetic Peripheral Neuropathy and Pain Severity. <i>Clinical Journal of Pain</i> , 2015, 31, 976-982.	1.9	44
17	Epigenome-wide association study of Alzheimer's disease replicates 22 differentially methylated positions and 30 differentially methylated regions. <i>Clinical Epigenetics</i> , 2020, 12, 149.	4.1	43
18	The relationship between plasma serotonin and kynurenine pathway metabolite levels and the treatment response to escitalopram and desvenlafaxine. <i>Brain, Behavior, and Immunity</i> , 2020, 87, 404-412.	4.1	43

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19	Predictive modeling of treatment resistant depression using data from STAR*D and an independent clinical study. <i>PLoS ONE</i> , 2018, 13, e0197268.	2.5	42
20	Genome-wide significant regions in 43 Utah high-risk families implicate multiple genes involved in risk for completed suicide. <i>Molecular Psychiatry</i> , 2020, 25, 3077-3090.	7.9	40
21	Variations in the FRA10AC1 Fragile Site and 15q21 Are Associated with Cerebrospinal Fluid A β ²¹⁻⁴² Level. <i>PLoS ONE</i> , 2015, 10, e0134000.	2.5	39
22	Integrated genome-wide methylation and expression analyses reveal functional predictors of response to antidepressants. <i>Translational Psychiatry</i> , 2019, 9, 254.	4.8	33
23	Genome-wide association studies of antidepressant class response and treatment-resistant depression. <i>Translational Psychiatry</i> , 2020, 10, 360.	4.8	33
24	Association of peripheral blood DNA methylation level with Alzheimer's disease progression. <i>Clinical Epigenetics</i> , 2021, 13, 191.	4.1	29
25	Differentially expressed genes in Alzheimer's disease highlighting the roles of microglia genes including OLR1 and astrocyte gene CDK2AP1. <i>Brain, Behavior, & Immunity - Health</i> , 2021, 13, 100227.	2.5	28
26	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. <i>Frontiers in Genetics</i> , 2018, 9, 434.	2.3	26
27	Genome-wide association study and polygenic risk score analysis of esketamine treatment response. <i>Scientific Reports</i> , 2020, 10, 12649.	3.3	24
28	Integrated miRNA-Seq and mRNA-Seq Study to Identify miRNAs Associated With Alzheimer's Disease Using Post-mortem Brain Tissue Samples. <i>Frontiers in Neuroscience</i> , 2021, 15, 620899.	2.8	22
29	Sparse factors for the positive and negative syndrome scale: Which symptoms and stage of illness?. <i>Psychiatry Research</i> , 2015, 225, 283-290.	3.3	20
30	Exploring the genetic overlap of suicide-related behaviors and substance use disorders. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 445-455.	1.7	18
31	Bovine and Human Insulin Activate CD8 ⁺ -Autoreactive CTL Expressing Both Type 1 and Type 2 Cytokines in C57BL/6 Mice. <i>Journal of Immunology</i> , 2000, 164, 86-92.	0.8	17
32	A genome wide association study suggests the association of muskelin with early onset bipolar disorder: Implications for a GABAergic epileptogenic neurogenesis model. <i>Journal of Affective Disorders</i> , 2017, 208, 120-129.	4.1	17
33	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.5	16
34	Measuring pathology using the PANSS across diagnoses: Inconsistency of the positive symptom domain across schizophrenia, schizoaffective, and bipolar disorder. <i>Psychiatry Research</i> , 2017, 258, 207-216.	3.3	14
35	Rare protein-coding variants implicate genes involved in risk of suicide death. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 508-520.	1.7	14
36	Bifactor Modeling of the Positive and Negative Syndrome Scale: Generalized Psychosis Spans Schizoaffective, Bipolar, and Schizophrenia Diagnoses. <i>Schizophrenia Bulletin</i> , 2018, 44, 1204-1216.	4.3	12

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37	Genome-wide analyses of smoking behaviors in schizophrenia: Findings from the Psychiatric Genomics Consortium. <i>Journal of Psychiatric Research</i> , 2021, 137, 215-224.	3.1	10
38	Assessment of suicide attempt and death in bipolar affective disorder: a combined clinical and genetic approach. <i>Translational Psychiatry</i> , 2021, 11, 379.	4.8	8
39	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. <i>PLoS ONE</i> , 2020, 15, e0241552.	2.5	7
40	SULT4A1 haplotype: conflicting results on its role as a biomarker of antipsychotic response. <i>Pharmacogenomics</i> , 2014, 15, 1557-1564.	1.3	6
41	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participantsâ€™ perspective. <i>Psychiatry Research</i> , 2019, 278, 173-179.	3.3	6
42	Neurexin 1 variants as risk factors for suicide death. <i>Molecular Psychiatry</i> , 2021, , .	7.9	5
43	Suicide and Psychosis: Results From a Population-Based Cohort of Suicide Death (<i>n</i> = 4380). <i>Schizophrenia Bulletin</i> , 2022, 48, 457-462.	4.3	4
44	Daily steps and depressive symptoms: A longitudinal evaluation of patients with major depressive disorder in the precision medicine in mental health care study. <i>Journal of Affective Disorders</i> , 2022, 300, 334-340.	4.1	4
45	Extended familial risk of suicide death is associated with younger age at death and elevated polygenic risk of suicide. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2022, 189, 60-73.	1.7	4