Qingqin S Li

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9183747/publications.pdf

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45 8,470 23 papers citations h-index

h-index g-index

52 11958
times ranked citing authors

47

52 all docs 52 docs citations

#	Article	IF	CITATIONS
1	Suicide and Psychosis: Results From a Population-Based Cohort of Suicide Death ($\langle i \rangle N \langle j \rangle = 4380$). Schizophrenia Bulletin, 2022, 48, 457-462.	4.3	4
2	Daily steps and depressive symptoms: A longitudinal evaluation of patients with major depressive disorder in the precision medicine in mental health care study. Journal of Affective Disorders, 2022, 300, 334-340.	4.1	4
3	Extended familial risk of suicide death is associated with younger age at death and elevated polygenic risk of suicide. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2022, 189, 60-73.	1.7	4
4	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
5	Integrated miRNA-Seq and mRNA-Seq Study to Identify miRNAs Associated With Alzheimer's Disease Using Post-mortem Brain Tissue Samples. Frontiers in Neuroscience, 2021, 15, 620899.	2.8	22
6	Rare proteinâ€coding variants implicate genes involved in risk of suicide death. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 508-520.	1.7	14
7	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. Nature Genetics, 2021, 53, 817-829.	21.4	629
8	Genome-wide analyses of smoking behaviors in schizophrenia: Findings from the Psychiatric Genomics Consortium. Journal of Psychiatric Research, 2021, 137, 215-224.	3.1	10
9	Differentially expressed genes in Alzheimer's disease highlighting the roles of microglia genes including OLR1 and astrocyte gene CDK2AP1. Brain, Behavior, & Immunity - Health, 2021, 13, 100227.	2.5	28
10	Assessment of suicide attempt and death in bipolar affective disorder: a combined clinical and genetic approach. Translational Psychiatry, 2021, 11, 379.	4.8	8
11	Neurexin 1 variants as risk factors for suicide death. Molecular Psychiatry, 2021, , .	7.9	5
12	Association of peripheral blood DNA methylation level with Alzheimer's disease progression. Clinical Epigenetics, 2021, 13, 191.	4.1	29
13	Exploring the genetic overlap of suicideâ€related behaviors and substance use disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 445-455.	1.7	18
14	Genome-wide significant regions in 43 Utah high-risk families implicate multiple genes involved in risk for completed suicide. Molecular Psychiatry, 2020, 25, 3077-3090.	7.9	40
15	Epigenome-wide association study of Alzheimer's disease replicates 22 differentially methylated positions and 30 differentially methylated regions. Clinical Epigenetics, 2020, 12, 149.	4.1	43
16	Genome-Wide Association Study of Suicide Death and Polygenic Prediction of Clinical Antecedents. American Journal of Psychiatry, 2020, 177, 917-927.	7.2	66
17	Genome-wide association study and polygenic risk score analysis of esketamine treatment response. Scientific Reports, 2020, 10, 12649.	3.3	24
18	Genome-wide association studies of antidepressant class response and treatment-resistant depression. Translational Psychiatry, 2020, 10, 360.	4.8	33

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19	Harnessing peripheral DNA methylation differences in the Alzheimer's Disease Neuroimaging Initiative (ADNI) to reveal novel biomarkers of disease. Clinical Epigenetics, 2020, 12, 84.	4.1	57
20	The relationship between plasma serotonin and kynurenine pathway metabolite levels and the treatment response to escitalopram and desvenlafaxine. Brain, Behavior, and Immunity, 2020, 87, 404-412.	4.1	43
21	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. PLoS ONE, 2020, 15, e0241552.	2.5	7
22	Integrated genome-wide methylation and expression analyses reveal functional predictors of response to antidepressants. Translational Psychiatry, 2019, 9, 254.	4.8	33
23	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participants' perspective. Psychiatry Research, 2019, 278, 173-179.	3.3	6
24	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	21.4	1,191
25	Association of Whole-Genome and NETRIN1 Signaling Pathway–Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2019, 4, 91-100.	1.5	16
26	Bifactor Modeling of the Positive and Negative Syndrome Scale: Generalized Psychosis Spans Schizoaffective, Bipolar, and Schizophrenia Diagnoses. Schizophrenia Bulletin, 2018, 44, 1204-1216.	4.3	12
27	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
28	Common and Rare Genetic Risk Factors Converge in Protein Interaction Networks Underlying Schizophrenia. Frontiers in Genetics, 2018, 9, 434.	2.3	26
29	Predictive modeling of treatment resistant depression using data from STAR*D and an independent clinical study. PLoS ONE, 2018, 13, e0197268.	2.5	42
30	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	1.3	84
31	Measuring pathology using the PANSS across diagnoses: Inconsistency of the positive symptom domain across schizophrenia, schizoaffective, and bipolar disorder. Psychiatry Research, 2017, 258, 207-216.	3.3	14
32	A genome wide association study suggests the association of muskelin with early onset bipolar disorder: Implications for a GABAergic epileptogenic neurogenesis model. Journal of Affective Disorders, 2017, 208, 120-129.	4.1	17
33	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
34	Translating genome-wide association findings into new therapeutics for psychiatry. Nature Neuroscience, 2016, 19, 1392-1396.	14.8	115
35	SCN9A Variants May be Implicated in Neuropathic Pain Associated With Diabetic Peripheral Neuropathy and Pain Severity. Clinical Journal of Pain, 2015, 31, 976-982.	1.9	44
36	GPR139, an Orphan Receptor Highly Enriched in the Habenula and Septum, Is Activated by the Essential Amino Acids I-Tryptophan and I-Phenylalanine. Molecular Pharmacology, 2015, 88, 911-925.	2.3	55

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37	Sparse factors for the positive and negative syndrome scale: Which symptoms and stage of illness?. Psychiatry Research, 2015, 225, 283-290.	3.3	20
38	Variations in the FRA10AC1 Fragile Site and 15q21 Are Associated with Cerebrospinal Fluid A \hat{l}^2 1-42 Level. PLoS ONE, 2015, 10, e0134000.	2.5	39
39	SULT4A1haplotype: conflicting results on its role as a biomarker of antipsychotic response. Pharmacogenomics, 2014, 15, 1557-1564.	1.3	6
40	Genetic analysis of quantitative phenotypes in AD and MCI: imaging, cognition and biomarkers. Brain Imaging and Behavior, 2014, 8, 183-207.	2.1	161
41	Interferon alfa regulated gene expression in patients initiating interferon treatment for chronic hepatitis C. Hepatology, 2003, 37, 610-621.	7.3	105
42	Temporal Gene Expression Analysis of Monolayer Cultured Rat Hepatocytes. Chemical Research in Toxicology, 2001, 14, 1218-1231.	3.3	145
43	Bovine and Human Insulin Activate CD8+-Autoreactive CTL Expressing Both Type 1 and Type 2 Cytokines in C57BL/6 Mice. Journal of Immunology, 2000, 164, 86-92.	0.8	17
44	Conditional Ablation of $\hat{l}^2 1$ Integrin in Skin. Journal of Cell Biology, 2000, 150, 1149-1160.	5.2	363
45	Membrane Compartmentation Is Required for Efficient T Cell Activation. Immunity, 1998, 8, 723-732.	14.3	865