

# Xiong-Jian Luo

## List of Publications by Year in descending order

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64  
papers

1,636  
citations

257429

24  
h-index

345203

36  
g-index

66  
all docs

66  
docs citations

66  
times ranked

2775  
citing authors

#	ARTICLE	IF	CITATIONS
1	Regulatory variants at 2q33.1 confer schizophrenia risk by modulating distal gene <i>TYW5</i> expression. <i>Brain</i> , 2022, 145, 770-786.	7.6	8
2	Regulatory Variant rs2535629 in <i>ITIH3</i> Intron Confers Schizophrenia Risk By Regulating CTCF Binding and <i>SFMBT1</i> Expression. <i>Advanced Science</i> , 2022, 9, e2104786.	11.2	8
3	In vivo study sheds new light on the dendritic spine pathology hypothesis of schizophrenia. <i>Molecular Psychiatry</i> , 2022, 27, 1866-1868.	7.9	6
4	Functional variant rs2270363 on 16p13.3 confers schizophrenia risk by regulating <i>NMRAL1</i> . <i>Brain</i> , 2022, 145, 2569-2585.	7.6	4
5	Functional genomics elucidates regulatory mechanisms of Parkinson's disease-associated variants. <i>BMC Medicine</i> , 2022, 20, 68.	5.5	2
6	Comprehensive and integrative analyses identify <i>TYW5</i> as a schizophrenia risk gene. <i>BMC Medicine</i> , 2022, 20, 169.	5.5	5
7	Functional genomic analysis delineates regulatory mechanisms of GWAS-identified bipolar disorder risk variants. <i>Genome Medicine</i> , 2022, 14, 53.	8.2	6
8	dbBIP: a comprehensive bipolar disorder database for genetic research. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	3
9	Convergent lines of evidence support <i>NOTCH4</i> as a schizophrenia risk gene. <i>Journal of Medical Genetics</i> , 2021, 58, 666-678.	3.2	9
10	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. <i>Biological Psychiatry</i> , 2021, 89, 246-255.	1.3	20
11	Novel Risk Loci Associated With Genetic Risk for Bipolar Disorder Among Han Chinese Individuals. <i>JAMA Psychiatry</i> , 2021, 78, 320.	11.0	35
12	Functional variants fine-mapping and gene function characterization provide insights into the role of <i>ZNF323</i> in schizophrenia pathogenesis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2021, 186, 28-39.	1.7	8
13	Integrative Analyses Followed by Functional Characterization Reveal <i>TMEM180</i> as a Schizophrenia Risk Gene. <i>Schizophrenia Bulletin</i> , 2021, 47, 1364-1374.	4.3	7
14	A missense variant in <i>NDUFA6</i> confers schizophrenia risk by affecting <i>YY1</i> binding and <i>NAGA</i> expression. <i>Molecular Psychiatry</i> , 2021, 26, 6896-6911.	7.9	19
15	Genome wide association study identifies four loci for early onset schizophrenia. <i>Translational Psychiatry</i> , 2021, 11, 248.	4.8	15
16	Transcriptome-wide association study identifies new susceptibility genes and pathways for depression. <i>Translational Psychiatry</i> , 2021, 11, 306.	4.8	32
17	Proteome-wide Association Study Provides Insights Into the Genetic Component of Protein Abundance in Psychiatric Disorders. <i>Biological Psychiatry</i> , 2021, 90, 781-789.	1.3	34
18	Genome-wide association study followed by trans-ancestry meta-analysis identify 17 new risk loci for schizophrenia. <i>BMC Medicine</i> , 2021, 19, 177.	5.5	12

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19	The schizophrenia susceptibility gene NACA regulates dendritic spine density: further evidence for the dendritic spine pathology of schizophrenia. <i>Molecular Psychiatry</i> , 2021, 26, 7102-7104.	7.9	7
20	Genome-Wide Meta-Analysis Identifies Two Novel Risk Loci for Epilepsy. <i>Frontiers in Neuroscience</i> , 2021, 15, 722592.	2.8	11
21	Transcriptome-Wide Association Study Provides Insights Into the Genetic Component of Gene Expression in Anxiety. <i>Frontiers in Genetics</i> , 2021, 12, 740134.	2.3	14
22	Identification of a Risk Locus at 7p22.3 for Schizophrenia and Bipolar Disorder in East Asian Populations. <i>Frontiers in Genetics</i> , 2021, 12, 789512.	2.3	0
23	Identification of a functional SNP rs7304782 at schizophrenia risk locus 12q24.31 and validation of its association with schizophrenia in Chinese populations. <i>Psychiatry Research</i> , 2020, 294, 113491.	3.3	1
24	SZDB2.0: an updated comprehensive resource for schizophrenia research. <i>Human Genetics</i> , 2020, 139, 1285-1297.	3.8	35
25	A functional missense variant in ITIH3 affects protein expression and neurodevelopment and confers schizophrenia risk in the Han Chinese population. <i>Journal of Genetics and Genomics</i> , 2020, 47, 233-248.	3.9	10
26	Regulatory mechanisms of major depressive disorder risk variants. <i>Molecular Psychiatry</i> , 2020, 25, 1926-1945.	7.9	37
27	TNIP1 Polymorphisms with the Risk of Hepatocellular Carcinoma Based on Chronic Hepatitis B Infection in Chinese Han Population. <i>Biochemical Genetics</i> , 2019, 57, 117-128.	1.7	3
28	Identification of the primate-specific gene BTN3A2 as an additional schizophrenia risk gene in the MHC loci. <i>EBioMedicine</i> , 2019, 44, 530-541.	6.1	24
29	Functional genomics reveal gene regulatory mechanisms underlying schizophrenia risk. <i>Nature Communications</i> , 2019, 10, 670.	12.8	94
30	Integration of GWAS and brain eQTL identifies FLOT1 as a risk gene for major depressive disorder. <i>Neuropsychopharmacology</i> , 2019, 44, 1542-1551.	5.4	37
31	Integrative analyses of major histocompatibility complex loci in the genome-wide association studies of major depressive disorder. <i>Neuropsychopharmacology</i> , 2019, 44, 1552-1561.	5.4	27
32	The depression GWAS risk allele predicts smaller cerebellar gray matter volume and reduced SIRT1 mRNA expression in Chinese population. <i>Translational Psychiatry</i> , 2019, 9, 333.	4.8	25
33	<i>Complement C7</i> is a novel risk gene for Alzheimer's disease in Han Chinese. <i>National Science Review</i> , 2019, 6, 257-274.	9.5	55
34	Comprehensive integrative analyses identify GLT8D1 and CSNK2B as schizophrenia risk genes. <i>Nature Communications</i> , 2018, 9, 838.	12.8	80
35	The integrated landscape of causal genes and pathways in schizophrenia. <i>Translational Psychiatry</i> , 2018, 8, 67.	4.8	75
36	The Gene Encoding Protocadherin 9 (PCDH9), a Novel Risk Factor for Major Depressive Disorder. <i>Neuropsychopharmacology</i> , 2018, 43, 1128-1137.	5.4	35

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37	Systems-level analysis of risk genes reveals the modular nature of schizophrenia. <i>Schizophrenia Research</i> , 2018, 201, 261-269.	2.0	20
38	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. <i>Neuropsychopharmacology</i> , 2018, 43, 2146-2153.	5.4	36
39	SZDB: A Database for Schizophrenia Genetic Research. <i>Schizophrenia Bulletin</i> , 2017, 43, sbw102.	4.3	91
40	Evaluation of European Schizophrenia GWAS Loci in Asian Populations via Comprehensive Meta-Analyses. <i>Molecular Neurobiology</i> , 2017, 54, 4071-4080.	4.0	19
41	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. <i>Translational Psychiatry</i> , 2017, 7, 1273.	4.8	9
42	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant at <i>SLC39A8</i> in Europeans. <i>Schizophrenia Bulletin</i> , 2016, 42, sbv070.	4.3	35
43	No association between schizophrenia susceptibility variants and macroscopic structural brain volume variation in healthy subjects. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2016, 171, 160-168.	1.7	4
44	Identification of <i>SLC25A37</i> as a major depressive disorder risk gene. <i>Journal of Psychiatric Research</i> , 2016, 83, 168-175.	3.1	24
45	Down-Regulation of <i>SIRT1</i> Gene Expression in Major Depressive Disorder. <i>American Journal of Psychiatry</i> , 2016, 173, 1046-1046.	7.2	55
46	Adaptive evolution of interleukin-3 ( <i>IL3</i> ), a gene associated with brain volume variation in general human populations. <i>Human Genetics</i> , 2016, 135, 377-392.	3.8	10
47	Impact of a <i>cis</i> -associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. <i>British Journal of Psychiatry</i> , 2016, 208, 128-137.	2.8	11
48	MAOA Variants and Genetic Susceptibility to Major Psychiatric Disorders. <i>Molecular Neurobiology</i> , 2016, 53, 4319-4327.	4.0	36
49	Do nuclear-encoded core subunits of mitochondrial complex I confer genetic susceptibility to schizophrenia in Han Chinese populations?. <i>Scientific Reports</i> , 2015, 5, 11076.	3.3	8
50	Allelic variation at 5-HTTLPR is associated with brain morphology in a Chinese population. <i>Psychiatry Research</i> , 2015, 226, 399-402.	3.3	3
51	Systematic Integration of Brain eQTL and GWAS Identifies <i>ZNF323</i> as a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. <i>Schizophrenia Bulletin</i> , 2015, 41, 1294-1308.	4.3	48
52	Common Variants in the <i>MKL1</i> Gene Confer Risk of Schizophrenia. <i>Schizophrenia Bulletin</i> , 2015, 41, 715-727.	4.3	15
53	Protein-Protein Interaction and Pathway Analyses of Top Schizophrenia Genes Reveal Schizophrenia Susceptibility Genes Converge on Common Molecular Networks and Enrichment of Nucleosome (Chromatin) Assembly Genes in Schizophrenia Susceptibility Loci. <i>Schizophrenia Bulletin</i> , 2014, 40, 39-49.	4.3	39
54	<i>LMO4</i> Functions As a Negative Regulator of Sensory Organ Formation in the Mammalian Cochlea. <i>Journal of Neuroscience</i> , 2014, 34, 10072-10077.	3.6	21

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55	Failure of replicating the association between hippocampal volume and 3 single-nucleotide polymorphisms identified from the European genome-wide association study in Asian populations. <i>Neurobiology of Aging</i> , 2014, 35, 2883.e1-2883.e2.	3.1	2
56	Systematic Prioritization and Integrative Analysis of Copy Number Variations in Schizophrenia Reveal Key Schizophrenia Susceptibility Genes. <i>Schizophrenia Bulletin</i> , 2014, 40, 1285-1299.	4.3	41
57	Protein-protein interaction analysis reveals common molecular processes/pathways that contribute to risk of schizophrenia. <i>Schizophrenia Research</i> , 2013, 143, 390-392.	2.0	9
58	Analysis of common genetic variants identifies <i>RELN</i> as a risk gene for schizophrenia in Chinese population. <i>World Journal of Biological Psychiatry</i> , 2013, 14, 91-99.	2.6	33
59	GATA3 controls the specification of prosensory domain and neuronal survival in the mouse cochlea. <i>Human Molecular Genetics</i> , 2013, 22, 3609-3623.	2.9	70
60	<i>ZNF804A</i> and schizophrenia susceptibility in Asian populations. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2012, 159B, 794-802.	1.7	30
61	The Interleukin 3 Gene (IL3) Contributes to Human Brain Volume Variation by Regulating Proliferation and Survival of Neural Progenitors. <i>PLoS ONE</i> , 2012, 7, e50375.	2.5	33
62	A common variant of the cardiomyopathy associated 5 gene (CMYA5) is associated with schizophrenia in Chinese population. <i>Schizophrenia Research</i> , 2011, 129, 217-219.	2.0	16
63	Genetic association and identification of a functional SNP at GSK3 $\beta$ for schizophrenia susceptibility. <i>Schizophrenia Research</i> , 2011, 133, 165-171.	2.0	39
64	Allelic Differences Between Han Chinese and Europeans for Functional Variants in ZNF804A and Their Association With Schizophrenia. <i>American Journal of Psychiatry</i> , 2011, 168, 1318-1325.	7.2	68