Xiong-Jian Luo

List of Publications by Year
in descending order

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	Functional genomics reveal gene regulatory mechanisms underlying schizophrenia risk. Nature Communications, 2019, 10, 670.	12.8	94
2	SZDB: A Database for Schizophrenia Genetic Research. Schizophrenia Bulletin, 2017, 43, sbw102.	4.3	91
3	Comprehensive integrative analyses identify GLT8D1 and CSNK2B as schizophrenia risk genes. Nature Communications, 2018, 9, 838.	12.8	80
4	The integrated landscape of causal genes and pathways in schizophrenia. Translational Psychiatry, 2018, 8, 67.	4.8	75
5	GATA3 controls the specification of prosensory domain and neuronal survival in the mouse cochlea. Human Molecular Genetics, 2013, 22, 3609-3623.	2.9	70
6	Allelic Differences Between Han Chinese and Europeans for Functional Variants in ZNF804A and Their Association With Schizophrenia. American Journal of Psychiatry, 2011, 168, 1318-1325.	7.2	68
7	Down-Regulation ofSIRT1Gene Expression in Major Depressive Disorder. American Journal of Psychiatry, 2016, 173, 1046-1046.	7.2	55
8	Complement C7is a novel risk gene for Alzheimer's disease in Han Chinese. National Science Review, 2019, 6, 257-274.	9.5	55
9	Systematic Integration of Brain eQTL and GWAS IdentifiesZNF323as a Novel Schizophrenia Risk Gene and Suggests Recent Positive Selection Based on Compensatory Advantage on Pulmonary Function. Schizophrenia Bulletin, 2015, 41, 1294-1308.	4.3	48
10	Systematic Prioritization and Integrative Analysis of Copy Number Variations in Schizophrenia Reveal Key Schizophrenia Susceptibility Genes. Schizophrenia Bulletin, 2014, 40, 1285-1299.	4.3	41
11	Genetic association and identification of a functional SNP at GSK3Î² for schizophrenia susceptibility. Schizophrenia Research, 2011, 133, 165-171.	2.0	39
12	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. Schizophrenia Bulletin, 2014, 40, 39-49.	4.3	39
13	Integration of GWAS and brain eQTL identifies FLOT1 as a risk gene for major depressive disorder. Neuropsychopharmacology, 2019, 44, 1542-1551.	5.4	37
14	Regulatory mechanisms of major depressive disorder risk variants. Molecular Psychiatry, 2020, 25, 1926-1945.	7.9	37
15	MAOA Variants and Genetic Susceptibility to Major Psychiatric Disorders. Molecular Neurobiology, 2016, 53, 4319-4327.	4.0	36
16	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. Neuropsychopharmacology, 2018, 43, 2146-2153.	5.4	36
17	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant atSLC39A8in Europeans. Schizophrenia Bulletin, 2016, 42, sbv070.	4.3	35
18	The Gene Encoding Protocadherin 9 (PCDH9), a Novel Risk Factor for Major Depressive Disorder. Neuropsychopharmacology, 2018, 43, 1128-1137.	5.4	35

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19	SZDB2.0: an updated comprehensive resource for schizophrenia research. Human Genetics, 2020, 139, 1285-1297.	3.8	35
20	Novel Risk Loci Associated With Genetic Risk for Bipolar Disorder Among Han Chinese Individuals. JAMA Psychiatry, 2021, 78, 320.	11.0	35
21	Proteome-wide Association Study Provides Insights Into the Genetic Component of Protein Abundance in Psychiatric Disorders. Biological Psychiatry, 2021, 90, 781-789.	1.3	34
22	Analysis of common genetic variants identifiesRELNas a risk gene for schizophrenia in Chinese population. World Journal of Biological Psychiatry, 2013, 14, 91-99.	2.6	33
23	The Interleukin 3 Gene (IL3) Contributes to Human Brain Volume Variation by Regulating Proliferation and Survival of Neural Progenitors. PLoS ONE, 2012, 7, e50375.	2.5	33
24	Transcriptome-wide association study identifies new susceptibility genes and pathways for depression. Translational Psychiatry, 2021, 11, 306.	4.8	32
25	ZNF804A and schizophrenia susceptibility in Asian populations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 794-802.	1.7	30
26	Integrative analyses of major histocompatibility complex loci in the genome-wide association studies of major depressive disorder. Neuropsychopharmacology, 2019, 44, 1552-1561.	5.4	27
27	The depression GWAS risk allele predicts smaller cerebellar gray matter volume and reduced SIRT1 mRNA expression in Chinese population. Translational Psychiatry, 2019, 9, 333.	4.8	25
28	Identification of SLC25A37 as a major depressive disorder risk gene. Journal of Psychiatric Research, 2016, 83, 168-175.	3.1	24
29	Identification of the primate-specific gene BTN3A2 as an additional schizophrenia risk gene in the MHC loci. EBioMedicine, 2019, 44, 530-541.	6.1	24
30	LMO4 Functions As a Negative Regulator of Sensory Organ Formation in the Mammalian Cochlea. Journal of Neuroscience, 2014, 34, 10072-10077.	3.6	21
31	Systems-level analysis of risk genes reveals the modular nature of schizophrenia. Schizophrenia Research, 2018, 201, 261-269.	2.0	20
32	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. Biological Psychiatry, 2021, 89, 246-255.	1.3	20
33	Evaluation of European Schizophrenia GWAS Loci in Asian Populations via Comprehensive Meta-Analyses. Molecular Neurobiology, 2017, 54, 4071-4080.	4.0	19
34	A missense variant in NDUFA6 confers schizophrenia risk by affecting YY1 binding and NAGA expression. Molecular Psychiatry, 2021, 26, 6896-6911.	7.9	19
35	A common variant of the cardiomyopathy associated 5 gene (CMYA5) is associated with schizophrenia in Chinese population. Schizophrenia Research, 2011, 129, 217-219.	2.0	16
36	Common Variants in the MKL1 Gene Confer Risk of Schizophrenia. Schizophrenia Bulletin, 2015, 41, 715-727.	4.3	15

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37	Genome wide association study identifies four loci for early onset schizophrenia. Translational Psychiatry, 2021, 11, 248.	4.8	15
38	Transcriptome-Wide Association Study Provides Insights Into the Genetic Component of Gene Expression in Anxiety. Frontiers in Genetics, 2021, 12, 740134.	2.3	14
39	Genome-wide association study followed by trans-ancestry meta-analysis identify 17 new risk loci for schizophrenia. BMC Medicine, 2021, 19, 177.	5.5	12
40	Impact of a cis-associated gene expression SNP on chromosome 20q11.22 on bipolar disorder susceptibility, hippocampal structure and cognitive performance. British Journal of Psychiatry, 2016, 208, 128-137.	2.8	11
41	Genome-Wide Meta-Analysis Identifies Two Novel Risk Loci for Epilepsy. Frontiers in Neuroscience, 2021, 15, 722592.	2.8	11
42	Adaptive evolution of interleukin-3 (IL3), a gene associated with brain volume variation in general human populations. Human Genetics, 2016, 135, 377-392.	3.8	10
43	A functional missense variant in ITIH3 affects protein expression and neurodevelopment and confers schizophrenia risk in the Han Chinese population. Journal of Genetics and Genomics, 2020, 47, 233-248.	3.9	10
44	Proteinâ€“protein interaction analysis reveals common molecular processes/pathways that contribute to risk of schizophrenia. Schizophrenia Research, 2013, 143, 390-392.	2.0	9
45	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	4.8	9
46	Convergent lines of evidence support NOTCH4 as a schizophrenia risk gene. Journal of Medical Genetics, 2021, 58, 666-678.	3.2	9
47	Do nuclear-encoded core subunits of mitochondrial complex I confer genetic susceptibility to schizophrenia in Han Chinese populations?. Scientific Reports, 2015, 5, 11076.	3.3	8
48	Functional variants fineâ€mapping and gene function characterization provide insights into the role of ZNF323 in schizophrenia pathogenesis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 28-39.	1.7	8
49	Regulatory variants at 2q33.1 confer schizophrenia risk by modulating distal gene TYW5 expression. Brain, 2022, 145, 770-786.	7.6	8
50	Regulatory Variant rs2535629 in ITIH3 Intron Confers Schizophrenia Risk By Regulating CTCF Binding and SFMBT1 Expression. Advanced Science, 2022, 9, e2104786.	11.2	8
51	Integrative Analyses Followed by Functional Characterization Reveal TMEM180 as a Schizophrenia Risk Gene. Schizophrenia Bulletin, 2021, 47, 1364-1374.	4.3	7
52	The schizophrenia susceptibility gene NAGA regulates dendritic spine density: further evidence for the dendritic spine pathology of schizophrenia. Molecular Psychiatry, 2021, 26, 7102-7104.	7.9	7
53	In vivo study sheds new light on the dendritic spine pathology hypothesis of schizophrenia. Molecular Psychiatry, 2022, 27, 1866-1868.	7.9	6
54	Functional genomic analysis delineates regulatory mechanisms of GWAS-identified bipolar disorder risk variants. Genome Medicine, 2022, 14, 53.	8.2	6

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55	Comprehensive and integrative analyses identify TYW5 as a schizophrenia risk gene. BMC Medicine, 2022, 20, 169.	5.5	5
56	No association between schizophrenia susceptibility variants and macroscopic structural brain volume variation in healthy subjects. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 160-168.	1.7	4
57	Functional variant rs2270363 on 16p13.3 confers schizophrenia risk by regulating NMRAL1. Brain, 2022, 145, 2569-2585.	7.6	4
58	Allelic variation at 5-HTTLPR is associated with brain morphology in a Chinese population. Psychiatry Research, 2015, 226, 399-402.	3.3	3
59	TNIP1 Polymorphisms with the Risk of Hepatocellular Carcinoma Based on Chronic Hepatitis B Infection in Chinese Han Population. Biochemical Genetics, 2019, 57, 117-128.	1.7	3
60	dbBIP: a comprehensive bipolar disorder database for genetic research. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	3
61	Failure of replicating the association between hippocampal volume and 3 single-nucleotide polymorphisms identified from the European genome-wide association study in Asian populations. Neurobiology of Aging, 2014, 35, 2883.e1-2883.e2.	3.1	2
62	Functional genomics elucidates regulatory mechanisms of Parkinsonâ€™s disease-associated variants. BMC Medicine, 2022, 20, 68.	5.5	2
63	Identification of a functional SNP rs7304782 at schizophrenia risk locus 12q24.31 and validation of its association with schiz ophrenia in Chinese populations. Psychiatry Research, 2020, 294, 113491.	3.3	1
64	Identification of a Risk Locus at 7p22.3 for Schizophrenia and Bipolar Disorder in East Asian Populations. Frontiers in Genetics, 2021, 12, 789512.	2.3	0