Xiao Xiao

List of Publications by Year
in descending order

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51 papers	1,029 citations	471509 17 h-index	526287 27 g-index
51 all docs	51 docs citations	51 times ranked	1853 citing authors

#	Article	IF	Citations
1	Five novel loci associated with antipsychotic treatment response in patients with schizophrenia: a genome-wide association study. Lancet Psychiatry,the, 2018, 5, 327-338.	7.4	110
2	BDNF Val66Met polymorphism and bipolar disorder in European populations: A risk association in case-control, family-based and GWAS studies. Neuroscience and Biobehavioral Reviews, 2016, 68, 218-233.	6.1	69
3	The genome-wide risk alleles for psychiatric disorders at 3p21.1 show convergent effects on mRNA expression, cognitive function, and mushroom dendritic spine. Molecular Psychiatry, 2020, 25, 48-66.	7.9	59
4	Genetic insights and neurobiological implications from NRXN1 in neuropsychiatric disorders. Molecular Psychiatry, 2019, 24, 1400-1414.	7.9	58
5	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	9.5	52
6	Vesicular glutamate transporter 1 (VGLUT1)-mediated glutamate release and membrane GluA1 activation is involved in the rapid antidepressant-like effects of scopolamine in mice. Neuropharmacology, 2018, 131, 209-222.	4.1	35
7	The Gene Encoding Protocadherin 9 (PCDH9), a Novel Risk Factor for Major Depressive Disorder. Neuropsychopharmacology, 2018, 43, 1128-1137.	5.4	35
8	Novel Risk Loci Associated With Genetic Risk for Bipolar Disorder Among Han Chinese Individuals. JAMA Psychiatry, 2021, 78, 320.	11.0	35
9	Translational genomics and beyond in bipolar disorder. Molecular Psychiatry, 2021, 26, 186-202.	7.9	30
10	Rare and common variants at 16p11.2 are associated with schizophrenia. Schizophrenia Research, 2017, 184, 105-108.	2.0	28
11	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
12	Further confirmation of netrin 1 receptor (DCC) as a depression risk gene via integrations of multi-omics data. Translational Psychiatry, 2020, 10, 98.	4.8	26
13	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
14	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
15	Genome-wide Association Study of Creativity Reveals Genetic Overlap With Psychiatric Disorders, Risk Tolerance, and Risky Behaviors. Schizophrenia Bulletin, 2020, 46, 1317-1326.	4.3	23
16	Replicated associations of FADS1, MAD1L1, and a rare variant at 10q26.13 with bipolar disorder in Chinese population. Translational Psychiatry, 2018, 8, 270.	4.8	21
17	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. Biological Psychiatry, 2021, 89, 246-255.	1.3	20
18	Independent replications and integrative analyses confirm TRANK1 as a susceptibility gene for bipolar disorder. Neuropsychopharmacology, 2021, 46, 1103-1112.	5.4	20

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19	Evaluation of European Schizophrenia GWAS Loci in Asian Populations via Comprehensive Meta-Analyses. Molecular Neurobiology, 2017, 54, 4071-4080.	4.0	19
20	A Human-Specific Schizophrenia Risk Tandem Repeat Affects Alternative Splicing of a Human-Unique Isoform AS3MTd2d3 and Mushroom Dendritic Spine Density. Schizophrenia Bulletin, 2021, 47, 219-227.	4.3	19
21	An alternative splicing hypothesis for neuropathology of schizophrenia: evidence from studies on historical candidate genes and multi-omics data. Molecular Psychiatry, 2022, 27, 95-112.	7.9	19
22	Identification of a functional human-unique 351-bp Alu insertion polymorphism associated with major depressive disorder in the 1p31.1 GWAS risk loci. Neuropsychopharmacology, 2020, 45, 1196-1206.	5.4	17
23	Phenotypes, mechanisms and therapeutics: insights from bipolar disorder GWAS findings. Molecular Psychiatry, 2022, 27, 2927-2939.	7.9	17
24	Further evidence ofVRK2rs2312147 associated with schizophrenia. World Journal of Biological Psychiatry, 2016, 17, 457-466.	2.6	15
25	Genome wide association study identifies four loci for early onset schizophrenia. Translational Psychiatry, 2021, 11, 248.	4.8	15
26	Evidence of AS3MTd2d3-Associated Variants within 10q24.32-33 in the Genetic Risk of Major Affective Disorders. Molecular Neuropsychiatry, 2016, 2, 213-218.	2.9	14
27	Revisiting tandem repeats in psychiatric disorders from perspectives of genetics, physiology, and brain evolution. Molecular Psychiatry, 2022, 27, 466-475.	7.9	14
28	The schizophrenia susceptibility gene ZNF804A confers risk of major mood disorders. World Journal of Biological Psychiatry, 2017, 18, 557-562.	2.6	13
29	Interactome Analyses implicated CAMK2A in the genetic predisposition and pharmacological mechanism of Bipolar Disorder. Journal of Psychiatric Research, 2019, 115, 165-175.	3.1	12
30	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
31	The schizophrenia risk isoform ZNF804AE3E4 affects dendritic spine. Schizophrenia Research, 2020, 218, 324-325.	2.0	11
32	Further Evidence of an Association between NCAN rs1064395 and Bipolar Disorder. Molecular Neuropsychiatry, 2018, 4, 30-34.	2.9	10
33	Further evidence for the association between LRP8 and schizophrenia. Schizophrenia Research, 2020, 215, 499-505.	2.0	10
34	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
35	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	4.8	9
36	Identification of a Bipolar Disorder Vulnerable Gene CHDH at 3p21.1. Molecular Neurobiology, 2017, 54, 5166-5176.	4.0	9

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37	Convergent lines of evidence support NOTCH4 as a schizophrenia risk gene. Journal of Medical Genetics, 2021, 58, 666-678.	3.2	9
38	Identification of a functional 339 bp <italic>Alu</italic> insertion polymorphism in the schizophrenia-associated locus at 10q24.32. Zoological Research, 2020, 41, 84-89.	2.1	9
39	Transcriptomic analyses of humans and mice provide insights into depression. Zoological Research, 2020, 41, 632-643.	2.1	9
40	Regulatory variants at 2q33.1 confer schizophrenia risk by modulating distal gene TYW5 expression. Brain, 2022, 145, 770-786.	7.6	8
41	Regulatory Variant rs2535629 in ITIH3 Intron Confers Schizophrenia Risk By Regulating CTCF Binding and SFMBT1 Expression. Advanced Science, 2022, 9, e2104786.	11.2	8
42	ATAD3B and SKIL polymorphisms associated with antipsychotic-induced QTc interval change in patients with schizophrenia: a genome-wide association study. Translational Psychiatry, 2022, 12, 56.	4.8	8
43	Replication analyses of four chromosomal deletions with schizophrenia via independent largeâ€scale metaâ€analyses. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 1161-1169.	1.7	7
44	Genetic association and meta-analysis of a schizophrenia GWAS variant rs10489202 in East Asian populations. Translational Psychiatry, 2018, 8, 144.	4.8	7
45	Integrative Analyses Followed by Functional Characterization Reveal TMEM180 as a Schizophrenia Risk Gene. Schizophrenia Bulletin, 2021, 47, 1364-1374.	4.3	7
46	Joint-Tissue Integrative Analysis Identified Hundreds of Schizophrenia Risk Genes. Molecular Neurobiology, 2021, , 1.	4.0	4
47	Functional variant rs2270363 on 16p13.3 confers schizophrenia risk by regulating NMRAL1. Brain, 2022, 145, 2569-2585.	7.6	4
48	Regulation of TRANK1 by GSK-3 in the brain: unexpected interactions. Molecular Psychiatry, 2021, 26, 6109-6111.	7.9	3
49	Epistatic interactions of NRG1 and ERBB4 on antipsychotic treatment response in first-episode schizophrenia patients. Schizophrenia Research, 2022, 241, 197-200.	2.0	2
50	Functional genomics elucidates regulatory mechanisms of Parkinsonâ€™s disease-associated variants. BMC Medicine, 2022, 20, 68.	5.5	2
51	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