Ming Li

List of Publications by Year
in descending order

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120	15,929	136885	19169
papers	citations	32 h-index	118 g-index

125	125	125	38760
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. Nucleic Acids Research, 2010, 38, e164-e164.	6.5	10,960
2	Cortical abnormalities in adults and adolescents with major depression based on brain scans from 20 cohorts worldwide in the ENIGMA Major Depressive Disorder Working Group. Molecular Psychiatry, 2017, 22, 900-909.	4.1	852
3	Maltreatment in childhood substantially increases the risk of adult depression and anxiety in prospective cohort studies: systematic review, meta-analysis, and proportional attributable fractions. Psychological Medicine, 2016, 46, 717-730.	2.7	444
4	Crystal Structure and Functional Analysis of the HERG Potassium Channel N Terminus. Cell, 1998, 95, 649-655.	13.5	432
5	A genome-wide association study in Han Chinese identifies multiple susceptibility loci for IgA nephropathy. Nature Genetics, 2012, 44, 178-182.	9.4	256
6	Identification of a Tibetan-Specific Mutation in the Hypoxic Gene EGLN1 and Its Contribution to High-Altitude Adaptation. Molecular Biology and Evolution, 2013, 30, 1889-1898.	3.5	151
7	A human-specific AS3MT isoform and BORCS7 are molecular risk factors in the 10q24.32 schizophrenia-associated locus. Nature Medicine, 2016, 22, 649-656.	15.2	142
8	Five novel loci associated with antipsychotic treatment response in patients with schizophrenia: a genome-wide association study. Lancet Psychiatry,the, 2018, 5, 327-338.	3.7	110
9	Comprehensive integrative analyses identify GLT8D1 and CSNK2B as schizophrenia risk genes. Nature Communications, 2018, 9, 838.	5.8	80
10	Common variants on 2p16.1, 6p22.1 and 10q24.32 are associated with schizophrenia in Han Chinese population. Molecular Psychiatry, 2017, 22, 954-960.	4.1	74
11	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.	2.9	69
12	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.	4.0	68
13	Allelic differences between Europeans and Chinese for CREB1 SNPs and their implications in gene expression regulation, hippocampal structure and function, and bipolar disorder susceptibility. Molecular Psychiatry, 2014, 19, 452-461.	4.1	61
14	The protocadherin 17 gene affects cognition, personality, amygdala structure and function, synapse development and risk of major mood disorders. Molecular Psychiatry, 2018, 23, 400-412.	4.1	60
15	The schizophrenia risk gene ZNF804A: clinical associations, biological mechanisms and neuronal functions. Molecular Psychiatry, 2017, 22, 944-953.	4.1	59
16	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.	4.1	59
17	Genetic insights and neurobiological implications from NRXN1 in neuropsychiatric disorders. Molecular Psychiatry, 2019, 24, 1400-1414.	4.1	58
18	Convergent lines of evidence support CAMKK2 as a schizophrenia susceptibility gene. Molecular Psychiatry, 2014, 19, 774-783.	4.1	56

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19	Complement C7is a novel risk gene for Alzheimer's disease in Han Chinese. National Science Review, 2019, 6, 257-274.	4.6	55
20	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	4.6	52
21	Meta-analysis and brain imaging data support the involvement of VRK2 (rs2312147) in schizophrenia susceptibility. Schizophrenia Research, 2012, 142, 200-205.	1.1	48
22	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.	2.3	48
23	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. Molecular Biology and Evolution, 2016, 33, 1177-1187.	3.5	43
24	Molecular mechanisms underlying noncoding risk variations in psychiatric genetic studies. Molecular Psychiatry, 2017, 22, 497-511.	4.1	43
25	Replicated associations of TNFAIP3, TNIP1 and ETS1 with systemic lupus erythematosus in a southwestern Chinese population. Arthritis Research and Therapy, 2011, 13, R186.	1.6	42
26	Interactome analysis reveals ZNF804A, a schizophrenia risk gene, as a novel component of protein translational machinery critical for embryonic neurodevelopment. Molecular Psychiatry, 2018, 23, 952-962.	4.1	40
27	Genetic association and identification of a functional SNP at GSK3Î² for schizophrenia susceptibility. Schizophrenia Research, 2011, 133, 165-171.	1.1	39
28	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.	2.3	39
29	The cAMP responsive element-binding (CREB)-1 gene increases risk of major psychiatric disorders. Molecular Psychiatry, 2018, 23, 1957-1967.	4.1	38
30	Regulatory mechanisms of major depressive disorder risk variants. Molecular Psychiatry, 2020, 25, 1926-1945.	4.1	37
31	MAOA Variants and Genetic Susceptibility to Major Psychiatric Disorders. Molecular Neurobiology, 2016, 53, 4319-4327.	1.9	36
32	Common variants on 6q16.2, 12q24.31 and 16p13.3 are associated with major depressive disorder. Neuropsychopharmacology, 2018, 43, 2146-2153.	2.8	36
33	Genome sequence and global sequence variation map with 5.5 million SNPs in Chinese rhesus macaque. Genome Biology, 2011, 12, R63.	3.8	35
34	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant atSLC39A8in Europeans. Schizophrenia Bulletin, 2016, 42, sbv070.	2.3	35
35	The Gene Encoding Protocadherin 9 (PCDH9), a Novel Risk Factor for Major Depressive Disorder. Neuropsychopharmacology, 2018, 43, 1128-1137.	2.8	35
36	Novel Risk Loci Associated With Genetic Risk for Bipolar Disorder Among Han Chinese Individuals. JAMA Psychiatry, 2021, 78, 320.	6.0	35

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37	Analysis of common genetic variants identifiesRELNas a risk gene for schizophrenia in Chinese population. World Journal of Biological Psychiatry, 2013, 14, 91-99.	1.3	33
38	Integrative omics of schizophrenia: from genetic determinants to clinical classification and risk prediction. Molecular Psychiatry, 2022, 27, 113-126.	4.1	33
39	The Interleukin 3 Gene (IL3) Contributes to Human Brain Volume Variation by Regulating Proliferation and Survival of Neural Progenitors. PLoS ONE, 2012, 7, e50375.	1.1	33
40	Functional divergence of the brain-size regulating gene MCPH1during primate evolution and the origin of humans. BMC Biology, 2013, 11, 62.	1.7	32
41	Transcriptome-wide association study identifies new susceptibility genes and pathways for depression. Translational Psychiatry, 2021, 11, 306.	2.4	32
42	ZNF804A and schizophrenia susceptibility in Asian populations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 794-802.	1.1	30
43	Translational genomics and beyond in bipolar disorder. Molecular Psychiatry, 2021, 26, 186-202.	4.1	30
44	Rare and common variants at 16p11.2 are associated with schizophrenia. Schizophrenia Research, 2017, 184, 105-108.	1.1	28
45	<i>VRK2</i>, a Candidate Gene for Psychiatric and Neurological Disorders. Molecular Neuropsychiatry, 2018, 4, 119-133.	3.0	28
46	Population genomics of wild Chinese rhesus macaques reveals a dynamic demographic history and local adaptation, with implications for biomedical research. GigaScience, 2018, 7, .	3.3	27
47	Integrative analyses of major histocompatibility complex loci in the genome-wide association studies of major depressive disorder. Neuropsychopharmacology, 2019, 44, 1552-1561.	2.8	27
48	Further confirmation of netrin 1 receptor (DCC) as a depression risk gene via integrations of multi-omics data. Translational Psychiatry, 2020, 10, 98.	2.4	26
49	Meta-Analysis Indicates That the European GWAS-Identified Risk SNP rs1344706 within ZNF804A Is Not Associated with Schizophrenia in Han Chinese Population. PLoS ONE, 2013, 8, e65780.	1.1	26
50	The depression GWAS risk allele predicts smaller cerebellar gray matter volume and reduced SIRT1 mRNA expression in Chinese population. Translational Psychiatry, 2019, 9, 333.	2.4	25
51	Identification of the primate-specific gene BTN3A2 as an additional schizophrenia risk gene in the MHC loci. EBioMedicine, 2019, 44, 530-541.	2.7	24
52	DEGS2 polymorphism associated with cognition in schizophrenia is associated with gene expression in brain. Translational Psychiatry, 2015, 5, e550-e550.	2.4	23
53	Genome-wide Association Study of Creativity Reveals Genetic Overlap With Psychiatric Disorders, Risk Tolerance, and Risky Behaviors. Schizophrenia Bulletin, 2020, 46, 1317-1326.	2.3	23
54	Replicated associations of FADS1, MAD1L1, and a rare variant at 10q26.13 with bipolar disorder in Chinese population. Translational Psychiatry, 2018, 8, 270.	2.4	21

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55	Convergent Lines of Evidence Support LRP8 as a Susceptibility Gene for Psychosis. Molecular Neurobiology, 2016, 53, 6608-6619.	1.9	20
56	Systems-level analysis of risk genes reveals the modular nature of schizophrenia. Schizophrenia Research, 2018, 201, 261-269.	1.1	20
57	Functional Genomics Identify a Regulatory Risk Variation rs4420550 in the 16p11.2 Schizophrenia-Associated Locus. Biological Psychiatry, 2021, 89, 246-255.	0.7	20
58	Independent replications and integrative analyses confirm TRANK1 as a susceptibility gene for bipolar disorder. Neuropsychopharmacology, 2021, 46, 1103-1112.	2.8	20
59	MCPH1/BRIT1 represses transcription of the human telomerase reverse transcriptase gene. Gene, 2012, 495, 1-9.	1.0	19
60	Evaluation of European Schizophrenia GWAS Loci in Asian Populations via Comprehensive Meta-Analyses. Molecular Neurobiology, 2017, 54, 4071-4080.	1.9	19
61	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.	2.3	19
62	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.	4.1	19
63	A missense variant in NDUFA6 confers schizophrenia risk by affecting YY1 binding and NAGA expression. Molecular Psychiatry, 2021, 26, 6896-6911.	4.1	19
64	A comprehensive metaâ€analysis of ZNF804A SNPs in the risk of schizophrenia among Asian populations. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 437-446.	1.1	18
65	Promoter variant rs2301228 on the neural cell adhesion molecule 1 gene confers risk of schizophrenia in Han Chinese. Schizophrenia Research, 2014, 160, 88-96.	1.1	17
66	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.	2.8	17
67	Phenotypes, mechanisms and therapeutics: insights from bipolar disorder GWAS findings. Molecular Psychiatry, 2022, 27, 2927-2939.	4.1	17
68	A common variant of the cardiomyopathy associated 5 gene (CMYA5) is associated with schizophrenia in Chinese population. Schizophrenia Research, 2011, 129, 217-219.	1.1	16
69	TheCHRM3gene is implicated in abnormal thalamo-orbital frontal cortex functional connectivity in first-episode treatment-naive patients with schizophrenia. Psychological Medicine, 2016, 46, 1523-1534.	2.7	16
70	Further evidence ofVRK2rs2312147 associated with schizophrenia. World Journal of Biological Psychiatry, 2016, 17, 457-466.	1.3	15
71	Genome wide association study identifies four loci for early onset schizophrenia. Translational Psychiatry, 2021, 11, 248.	2.4	15
72	Evidence of AS3MTd2d3-Associated Variants within 10q24.32-33 in the Genetic Risk of Major Affective Disorders. Molecular Neuropsychiatry, 2016, 2, 213-218.	3.0	14

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73	Regional selection of the brain size regulating gene CASC5 provides new insight into human brain evolution. Human Genetics, 2017, 136, 193-204.	1.8	14
74	Revisiting tandem repeats in psychiatric disorders from perspectives of genetics, physiology, and brain evolution. Molecular Psychiatry, 2022, 27, 466-475.	4.1	14
75	Genetic analysis of common variants in the CMYA5 (cardiomyopathy-associated 5) gene with schizophrenia. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2013, 46, 64-69.	2.5	13
76	The schizophrenia susceptibility gene ZNF804A confers risk of major mood disorders. World Journal of Biological Psychiatry, 2017, 18, 557-562.	1.3	13
77	A Functional MiR-124 Binding-Site Polymorphism in IQGAP1 Affects Human Cognitive Performance. PLoS ONE, 2014, 9, e107065.	1.1	13
78	SLC6A15 rs1545843 and Depression: Implications From Brain Imaging Data. American Journal of Psychiatry, 2013, 170, 805-805.	4.0	12
79	Interactome Analyses implicated CAMK2A in the genetic predisposition and pharmacological mechanism of Bipolar Disorder. Journal of Psychiatric Research, 2019, 115, 165-175.	1.5	12
80	Genome-wide association study followed by trans-ancestry meta-analysis identify 17 new risk loci for schizophrenia. BMC Medicine, 2021, 19, 177.	2.3	12
81	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.	1.7	11
82	The schizophrenia risk isoform ZNF804AE3E4 affects dendritic spine. Schizophrenia Research, 2020, 218, 324-325.	1.1	11
83	Impact of the genome-wide schizophrenia risk single nucleotide polymorphism (rs1625579) in miR-137 on brain structures in healthy individuals. Psychiatric Genetics, 2013, 23, 267.	0.6	10
84	Common variants of IRF3 conferring risk of schizophrenia. Journal of Psychiatric Research, 2015, 64, 67-73.	1.5	10
85	The impact of CACNA1C allelic variation on regional gray matter volume in Chinese population. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 396-401.	1.1	10
86	Adaptive evolution of interleukin-3 (IL3), a gene associated with brain volume variation in general human populations. Human Genetics, 2016, 135, 377-392.	1.8	10
87	Further Evidence of an Association between NCAN rs1064395 and Bipolar Disorder. Molecular Neuropsychiatry, 2018, 4, 30-34.	3.0	10
88	Further evidence for the association between LRP8 and schizophrenia. Schizophrenia Research, 2020, 215, 499-505.	1.1	10
89	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.	1.7	10
90	Proteinâ€“protein interaction analysis reveals common molecular processes/pathways that contribute to risk of schizophrenia. Schizophrenia Research, 2013, 143, 390-392.	1.1	9

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91	GWASâ€identified schizophrenia risk SNPs at TSPAN18 are highly diverged between Europeans and East Asians. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 1032-1040.	1.1	9
92	Common variants at 2q11.2, 8q21.3, and 11q13.2 are associated with major mood disorders. Translational Psychiatry, 2017, 7, 1273.	2.4	9
93	Identification of a Bipolar Disorder Vulnerable Gene CHDH at 3p21.1. Molecular Neurobiology, 2017, 54, 5166-5176.	1.9	9
94	Convergent lines of evidence support NOTCH4 as a schizophrenia risk gene. Journal of Medical Genetics, 2021, 58, 666-678.	1.5	9
95	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.	0.9	9
96	Transcriptomic analyses of humans and mice provide insights into depression. Zoological Research, 2020, 41, 632-643.	0.9	9
97	New Evidence of Gut Microbiota Involvement in the Neuropathogenesis of Bipolar Depression by TRANK1 Modulation: Joint Clinical and Animal Data. Frontiers in Immunology, 2021, 12, 789647.	2.2	9
98	Meta-analysis supports association of a non-synonymous SNP in ZNF804A with schizophrenia. Schizophrenia Research, 2013, 149, 188-189.	1.1	8
99	Whole genome analyses reveal significant convergence in obsessive-compulsive disorder between humans and dogs. Science Bulletin, 2021, 66, 187-196.	4.3	8
100	Regulatory variants at 2q33.1 confer schizophrenia risk by modulating distal gene TYW5 expression. Brain, 2022, 145, 770-786.	3.7	8
101	Regulatory Variant rs2535629 in ITIH3 Intron Confers Schizophrenia Risk By Regulating CTCF Binding and SFMBT1 Expression. Advanced Science, 2022, 9, e2104786.	5.6	8
102	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.	1.1	7
103	Genetic association and meta-analysis of a schizophrenia GWAS variant rs10489202 in East Asian populations. Translational Psychiatry, 2018, 8, 144.	2.4	7
104	Association of SYNE1 locus with bipolar disorder in Chinese population. Hereditas, 2019, 156, 19.	0.5	7
105	Integrative Analyses Followed by Functional Characterization Reveal TMEM180 as a Schizophrenia Risk Gene. Schizophrenia Bulletin, 2021, 47, 1364-1374.	2.3	7
106	Functional genomic analysis delineates regulatory mechanisms of GWAS-identified bipolar disorder risk variants. Genome Medicine, 2022, 14, 53.	3.6	6
107	Replication of Han Chinese GWAS loci for schizophrenia via meta-analysis of four independent samples. Schizophrenia Research, 2016, 172, 75-77.	1.1	5
108	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.	1.1	4

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109	Joint-Tissue Integrative Analysis Identified Hundreds of Schizophrenia Risk Genes. Molecular Neurobiology, 2021, , 1.	1.9	4
110	Functional variant rs2270363 on 16p13.3 confers schizophrenia risk by regulating NMRAL1. Brain, 2022, 145, 2569-2585.	3.7	4
111	Allelic variation at 5-HTTLPR is associated with brain morphology in a Chinese population. Psychiatry Research, 2015, 226, 399-402.	1.7	3
112	Regulation of TRANK1 by GSK-3 in the brain: unexpected interactions. Molecular Psychiatry, 2021, 26, 6109-6111.	4.1	3
113	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.	1.5	2
114	Epistatic interactions of NRG1 and ERBB4 on antipsychotic treatment response in first-episode schizophrenia patients. Schizophrenia Research, 2022, 241, 197-200.	1.1	2
115	Functional genomics elucidates regulatory mechanisms of Parkinsonâ€™s disease-associated variants. BMC Medicine, 2022, 20, 68.	2.3	2
116	An Evaluation of Association between a Novel Hippocampal Biology Related SNP (rs7294919) and Schizophrenia. PLoS ONE, 2013, 8, e80696.	1.1	1
117	Reply to: ZNF804A and schizophrenia: An open peer commentary. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2013, 162, 73-74.	1.1	0
118	Up-Regulation ofNOTCH4Gene Expression in Bipolar Disorder: Future Studies. American Journal of Psychiatry, 2013, 170, 560a-561.	4.0	0
119	Weak Association Between the Glutamate Decarboxylase 1 Gene (GAD1) and Schizophrenia in Han Chinese Population. Frontiers in Neuroscience, 2021, 15, 677153.	1.4	0
120	Identification of a Risk Locus at 7p22.3 for Schizophrenia and Bipolar Disorder in East Asian Populations. Frontiers in Genetics, 2021, 12, 789512.	1.1	0