Shuquan Rao

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genetic evidence suggests posttraumatic stress disorder as a subtype of major depressive disorder. Journal of Clinical Investigation, 2022, 132, .	3.9	68
2	Shared genetic liability between major depressive disorder and osteoarthritis. Bone and Joint Research, 2022, 11, 12-22.	1.3	20
3	Involvement of the long intergenic non-coding RNA LINC00461 in schizophrenia. BMC Psychiatry, 2022, 22, 59.	1.1	9
4	Convergent lines of evidence supporting involvement of NFKB1 in schizophrenia. Psychiatry Research, 2022, 312, 114588.	1.7	8
5	Genetic Relationships between Attention-Deficit/Hyperactivity Disorder, Autism Spectrum Disorder, and Intelligence. Neuropsychobiology, 2022, 81, 484-496.	0.9	26
6	Genome and epigenome editing identify CCR9 and SLC6A20 as target genes at the 3p21.31 locus associated with severe COVID-19. Signal Transduction and Targeted Therapy, 2021, 6, 85.	7.1	36
7	Editing GWAS: experimental approaches to dissect and exploit disease-associated genetic variation. Genome Medicine, 2021, 13, 41.	3.6	32
8	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
9	Dissecting ELANE neutropenia pathogenicity by human HSC gene editing. Cell Stem Cell, 2021, 28, 833-845.e5.	5.2	23
10	Inactivation of Wnt-LRP5 signaling suppresses the proliferation and migration of ovarian cancer cells. Translational Cancer Research, 2021, 10, 2277-2285.	0.4	2
11	Effect of the SIRT1 gene on regional cortical grey matter density in the Han Chinese population. British Journal of Psychiatry, 2020, 216, 254-258.	1.7	6
12	No Evidence for Widespread Positive Selection Signatures in Common Risk Alleles Associated with Schizophrenia. Schizophrenia Bulletin, 2020, 46, 603-611.	2.3	9
13	Identifying common genome-wide risk genes for major psychiatric traits. Human Genetics, 2020, 139, 185-198.	1.8	40
14	Functional annotation of genetic associations by transcriptome-wide association analysis provides insights into neutrophil development regulation. Communications Biology, 2020, 3, 790.	2.0	1
15	Multi-trait analysis for genome-wide association study of five psychiatric disorders. Translational Psychiatry, 2020, 10, 209.	2.4	132
16	Allelic frequency differences of DAOA variants between Caucasians and Asians and their association with major mood disorders. Signal Transduction and Targeted Therapy, 2019, 4, 39.	7.1	1
17	Brain function, structure and genomic data are linked but show different sensitivity to duration of illness and disease stage in schizophrenia. NeuroImage: Clinical, 2019, 23, 101887.	1.4	14
18	Gene Editing ELANE in Human Hematopoietic Stem and Progenitor Cells Reveals Disease Mechanisms and Therapeutic Strategies for Severe Congenital Neutropenia. Blood, 2019, 134, 3-3.	0.6	8

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19	An APOE -independent cis -eSNP on chromosome 19q13.32 influences tau levels and late-onset Alzheimer's disease risk. Neurobiology of Aging, 2018, 66, 178.e1-178.e8.	1.5	12
20	Changes in the level of Long Non-Coding RNA Gomafu gene expression in schizophrenia patients before and after antipsychotic medication. Schizophrenia Research, 2018, 195, 318-319.	1.1	14
21	Exploring different impaired speed of genetic-related brain function and structures in schizophrenic progress using multimodal analysis*. , 2018, 2018, 4126-4129.		4
22	Genetic association of rs1344706 in ZNF804A with bipolar disorder and schizophrenia susceptibility in Chinese populations. Scientific Reports, 2017, 7, 41140.	1.6	11
23	Peripheral blood nerve growth factor levels in major psychiatric disorders. Journal of Psychiatric Research, 2017, 86, 39-45.	1.5	25
24	Intergenic variants may predispose to major depression disorder through regulation of long non-coding RNA expression. Gene, 2017, 601, 21-26.	1.0	30
25	An Integrative Computational Approach to Evaluate Genetic Markers for Bipolar Disorder. Scientific Reports, 2017, 7, 6745.	1.6	7
26	Common variants in <i>CACNA1C</i> and MDD susceptibility: A comprehensive metaâ€analysis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 896-903.	1.1	33
27	Genetic association between NFKB1 â^'94 ins/del ATTG Promoter Polymorphism and cancer risk: a meta-analysis of 42 case-control studies. Scientific Reports, 2016, 6, 30220.	1.6	9
28	Accelerated leukocyte telomere erosion in schizophrenia: Evidence from the present study and a meta-analysis. Journal of Psychiatric Research, 2016, 79, 50-56.	1.5	38
29	A cis -eQTL in AHI1 confers risk to schizophrenia in European populations. Neuroscience Letters, 2016, 632, 130-135.	1.0	4
30	Common variants in FKBP5 gene and major depressive disorder (MDD) susceptibility: a comprehensive meta-analysis. Scientific Reports, 2016, 6, 32687.	1.6	48
31	Variants in <i>TERT</i> influencing telomere length are associated with paranoid schizophrenia risk. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2016, 171, 317-324.	1.1	23
32	Meta-analysis indicates that SNP rs9939609 within FTO is not associated with major depressive disorder (MDD) in Asian population. Journal of Affective Disorders, 2016, 193, 27-30.	2.0	18
33	Exome Sequencing Identifies a Novel Gene, WNK1, for Susceptibility to Pelvic Organ Prolapse (POP). PLoS ONE, 2015, 10, e0119482.	1.1	6
34	An association study of the m6A genes with major depressive disorder in Chinese Han population. Journal of Affective Disorders, 2015, 183, 279-286.	2.0	93