Jubao Duan

List of Publications by Year
in descending order

69 papers	19,595 citations	61984 43 h-index	98798 67 g-index
81 all docs	81 docs citations	81 times ranked	27864 citing authors

#	Article	IF	Citations
1	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
2	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
3	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	27.8	1,789
4	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	21.4	1,395
5	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
6	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
7	Common variants on chromosome 6p22.1 are associated with schizophrenia. Nature, 2009, 460, 753-757.	27.8	1,063
8	Identification of loci associated with schizophrenia by genome-wide association and follow-up. Nature Genetics, 2008, 40, 1053-1055.	21.4	977
9	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
10	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
11	Synonymous mutations in the human dopamine receptor D2 (DRD2) affect mRNA stability and synthesis of the receptor. Human Molecular Genetics, 2003, 12, 205-216.	2.9	800
12	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
13	Narcolepsy is strongly associated with the T-cell receptor alpha locus. Nature Genetics, 2009, 41, 708-711.	21.4	445
14	Copy Number Variants in Schizophrenia: Confirmation of Five Previous Findings and New Evidence for 3q29 Microdeletions and VIPR2 Duplications. American Journal of Psychiatry, 2011, 168, 302-316.	7.2	398
15	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
16	No Significant Association of 14 Candidate Genes With Schizophrenia in a Large European Ancestry Sample: Implications for Psychiatric Genetics. American Journal of Psychiatry, 2008, 165, 497-506.	7.2	323
17	Joint Analysis of Psychiatric Disorders Increases Accuracy of Risk Prediction for Schizophrenia, Bipolar Disorder, and Major Depressive Disorder. American Journal of Human Genetics, 2015, 96, 283-294.	6.2	225
18	Somatic Genomics and Clinical Features of Lung Adenocarcinoma: A Retrospective Study. PLoS Medicine, 2016, 13, e1002162.	8.4	148

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19	Genomewide Linkage Scan of 409 European-Ancestry and African American Families with Schizophrenia: Suggestive Evidence of Linkage at 8p23.3-p21.2 and 11p13.1-q14.1 in the Combined Sample. American Journal of Human Genetics, 2006, 78, 315-333.	6.2	141
20	Characterizing the genetic basis of methylome diversity in histologically normal human lung tissue. Nature Communications, 2014, 5, 3365.	12.8	123
21	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. American Journal of Human Genetics, 2018, 102, 1185-1194.	6.2	119
22	Mammalian Mutation Pressure, Synonymous Codon Choice, and mRNA Degradation. Journal of Molecular Evolution, 2003, 57, 694-701.	1.8	113
23	Genome-Wide Association Study of Clinical Dimensions of Schizophrenia: Polygenic Effect on Disorganized Symptoms. American Journal of Psychiatry, 2012, 169, 1309-1317.	7.2	112
24	Open Chromatin Profiling in hiPSC-Derived Neurons Prioritizes Functional Noncoding Psychiatric Risk Variants and Highlights Neurodevelopmental Loci. Cell Stem Cell, 2017, 21, 305-318.e8.	11.1	106
25	A Comparison of Ten Polygenic Score Methods for Psychiatric Disorders Applied Across Multiple Cohorts. Biological Psychiatry, 2021, 90, 611-620.	1.3	103
26	Polymorphisms in the Trace Amine Receptor 4 (TRAR4) Gene on Chromosome 6q23.2 Are Associated with Susceptibility to Schizophrenia. American Journal of Human Genetics, 2004, 75, 624-638.	6.2	101
27	Winner's Curse Correction and Variable Thresholding Improve Performance of Polygenic Risk Modeling Based on Genome-Wide Association Study Summary-Level Data. PLoS Genetics, 2016, 12, e1006493.	3.5	98
28	Epigenome-wide analysis of DNA methylation in lung tissue shows concordance with blood studies and identifies tobacco smoke-inducible enhancers. Human Molecular Genetics, 2017, 26, 3014-3027.	2.9	97
29	A Rare Functional Noncoding Variant at the GWAS-Implicated MIR137/MIR2682 Locus Might Confer Risk to Schizophrenia and Bipolar Disorder. American Journal of Human Genetics, 2014, 95, 744-753.	6.2	91
30	Allele-specific open chromatin in human iPSC neurons elucidates functional disease variants. Science, 2020, 369, 561-565.	12.6	77
31	Transcriptome study of differential expression in schizophrenia. Human Molecular Genetics, 2013, 22, 5001-5014.	2.9	73
32	Smoking and Genetic Risk Variation Across Populations of <scp>E</scp>uropean, <scp>A</scp>sian, and <scp>A</scp>frican <scp>A</scp>merican Ancestryâ€”A Metaâ€Analysis of Chromosome 15q25. Genetic Epidemiology, 2012, 36, 340-351.	1.3	69
33	Genome-wide survey of interindividual differences of RNA stability in human lymphoblastoid cell lines. Scientific Reports, 2013, 3, 1318.	3.3	66
34	Reciprocal Duplication of the Williams-Beuren Syndrome Deletion on Chromosome 7q11.23 Is Associated with Schizophrenia. Biological Psychiatry, 2014, 75, 371-377.	1.3	66
35	Genome-Wide Association Study of Multiplex Schizophrenia Pedigrees. American Journal of Psychiatry, 2012, 169, 963-973.	7.2	61
36	Reversal of dendritic phenotypes in 16p11.2 microduplication mouse model neurons by pharmacological targeting of a network hub. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8520-8525.	7.1	61

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37	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
38	Deconvolution of transcriptional networks identifies TCF4 as a master regulator in schizophrenia. Science Advances, 2019, 5, eaau4139.	10.3	59
39	MicroRNA-9 and MicroRNA-326 Regulate Human Dopamine D2 Receptor Expression, and the MicroRNA-mediated Expression Regulation Is Altered by a Genetic Variant. Journal of Biological Chemistry, 2014, 289, 13434-13444.	3.4	53
40	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. International Journal of Epidemiology, 2015, 44, 1706-1721.	1.9	53
41	Parental Origin of Interstitial Duplications at 15q11.2-q13.3 in Schizophrenia and Neurodevelopmental Disorders. PLoS Genetics, 2016, 12, e1005993.	3.5	51
42	The Internet-Based MGS2 Control Sample: Self Report of Mental Illness. American Journal of Psychiatry, 2010, 167, 854-865.	7.2	48
43	DNA variation and psychopharmacology of the human serotonin receptor 1B(HTR1B) gene. Pharmacogenomics, 2002, 3, 745-762.	1.3	47
44	Genome-wide approaches to schizophrenia. Brain Research Bulletin, 2010, 83, 93-102.	3.0	47
45	Neuregulin 1 (NRG1) and schizophrenia: analysis of a US family sample and the evidence in the balance. Psychological Medicine, 2005, 35, 1599-1610.	4.5	46
46	Genome-Wide Association Study of Male Sexual Orientation. Scientific Reports, 2017, 7, 16950.	3.3	44
47	<i>DTNBP1 (Dystrobrevin Binding Protein 1)</i> and Schizophrenia: Association Evidence in the 3â€² End of the Gene. Human Heredity, 2007, 64, 97-106.	0.8	35
48	A sequence variant in human KALRN impairs protein function and coincides with reduced cortical thickness. Nature Communications, 2014, 5, 4858.	12.8	31
49	ASCL1- and DLX2-induced GABAergic neurons from hiPSC-derived NPCs. Journal of Neuroscience Methods, 2020, 334, 108548.	2.5	30
50	BIN1 is a key regulator of proinflammatory and neurodegeneration-related activation in microglia. Molecular Neurodegeneration, 2022, 17, 33.	10.8	26
51	Open chromatin dynamics reveals stage-specific transcriptional networks in hiPSC-based neurodevelopmental model. Stem Cell Research, 2018, 29, 88-98.	0.7	18
52	Publicly Available hiPSC Lines with Extreme Polygenic Risk Scores for Modeling Schizophrenia. Complex Psychiatry, 2020, 6, 68-82.	0.9	18
53	Transcriptomic signatures of schizophrenia revealed by dopamine perturbation in an ex vivo model. Translational Psychiatry, 2018, 8, 158.	4.8	15
54	Cell type-specific and cross-population polygenic risk score analyses of MIR137 gene pathway in schizophrenia. IScience, 2021, 24, 102785.	4.1	15

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55	Path from schizophrenia genomics to biology: gene regulation and perturbation in neurons derived from induced pluripotent stem cells and genome editing. Neuroscience Bulletin, 2015, 31, 113-127.	2.9	12
56	Single-Step Method of Total RNA Isolation by Sodium Dodecyl Sulfate/Phenol Extraction from Cultured Cells. Analytical Biochemistry, 1997, 251, 291-292.	2.4	11
57	Transcriptome outlier analysis implicates schizophrenia susceptibility genes and enriches putatively functional rare genetic variants. Human Molecular Genetics, 2015, 24, 4674-4685.	2.9	9
58	The Genetic Relevance of Human Induced Pluripotent Stem Cell-Derived Microglia to Alzheimerâ€™s Disease and Major Neuropsychiatric Disorders. Molecular Neuropsychiatry, 2019, 5, 85-96.	2.9	9
59	Dopamine perturbation of gene co-expression networks reveals differential response in schizophrenia for translational machinery. Translational Psychiatry, 2018, 8, 278.	4.8	8
60	Annotating functional effects of non-coding variants in neuropsychiatric cell types by deep transfer learning. PLoS Computational Biology, 2022, 18, e1010011.	3.2	7
61	Modeling common and rare genetic risk factors of neuropsychiatric disorders in human induced pluripotent stem cells. Schizophrenia Research, 2022, , .	2.0	6
62	Cell-Type-Specific Proteogenomic Signal Diffusion for Integrating Multi-Omics Data Predicts Novel Schizophrenia Risk Genes. Patterns, 2020, 1, 100091.	5.9	5
63	A computational method for direct imputation of cell type-specific expression profiles and cellular compositions from bulk-tissue RNA-Seq in brain disorders. NAR Genomics and Bioinformatics, 2021, 3, lqab056.	3.2	5
64	CCmed: cross-condition mediation analysis for identifying replicable trans-associations mediated by cis-gene expression. Bioinformatics, 2021, 37, 2513-2520.	4.1	4
65	Sex-specific nicotine sensitization and imprinting of self-administration in rats inform GWAS findings on human addiction phenotypes. Neuropsychopharmacology, 2021, 46, 1746-1756.	5.4	4
66	LANDSCAPE OF ALLELE-SPECIFIC OPEN CHROMATIN IN HUMAN IPSC-DIFFERENTIATED NEURONS AND IT IMPLICATION FOR MENTAL DISORDERS. European Neuropsychopharmacology, 2019, 29, S799-S800.	0.7	3
67	From Schizophrenia Genetics to Disease Biology: Harnessing New Concepts and Technologies. Journal of Psychiatry and Brain Science, 2019, 4, .	0.5	3
68	Open Chromatin Profiling Identifies Functional Noncoding Risk Variants In Human Ipsc Model of Psychiatric Disorders. European Neuropsychopharmacology, 2019, 29, S765.	0.7	0
69	RNAseq TRANSCRIPTOME STUDY OF SCHIZOPHRENIA IN THE MGS AFRICAN AMERICAN SAMPLE. European Neuropsychopharmacology, 2019, 29, S874-S875.	0.7	0