

Hang Zhou

List of Publications by Year in descending order

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Version: 2024-02-01

39
papers

3,246
citations

279778

23
h-index

289230

40
g-index

60
all docs

60
docs citations

60
times ranked

3946
citing authors

#	ARTICLE	IF	CITATIONS
1	Investigation of convergent and divergent genetic influences underlying schizophrenia and alcohol use disorder. <i>Psychological Medicine</i> , 2023, 53, 1196-1204.	4.5	7
2	The addiction risk factor: A unitary genetic vulnerability characterizes substance use disorders and their associations with common correlates. <i>Neuropsychopharmacology</i> , 2022, 47, 1739-1745.	5.4	50
3	Identifying and Reducing Bias in Genome-Wide Association Studies of Alcohol-Related Traits. <i>American Journal of Psychiatry</i> , 2022, 179, 14-16.	7.2	4
4	Genome-wide meta-analysis of alcohol use disorder in East Asians. <i>Neuropsychopharmacology</i> , 2022, 47, 1791-1797.	5.4	10
5	Epigenome-wide association study of posttraumatic stress disorder identifies novel loci in U.S. military veterans. <i>Translational Psychiatry</i> , 2022, 12, 65.	4.8	10
6	Unique and joint associations of polygenic risk for major depression and opioid use disorder with endogenous opioid system function. <i>Neuropsychopharmacology</i> , 2022, 47, 1784-1790.	5.4	2
7	Associations between moderate alcohol consumption, brain iron, and cognition in UK Biobank participants: Observational and mendelian randomization analyses. <i>PLoS Medicine</i> , 2022, 19, e1004039.	8.4	28
8	Functional connectome-wide associations of schizophrenia polygenic risk. <i>Molecular Psychiatry</i> , 2021, 26, 2553-2561.	7.9	53
9	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	2.6	28
10	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	21.4	629
11	The impact of removing former drinkers from genome-wide association studies of AUDIT. <i>Addiction</i> , 2021, 116, 3044-3054.	3.3	11
12	Bi-ancestral depression GWAS in the Million Veteran Program and meta-analysis in >1.2 million individuals highlight new therapeutic directions. <i>Nature Neuroscience</i> , 2021, 24, 954-963.	14.8	207
13	Multivariate analysis of 1.5 million people identifies genetic associations with traits related to self-regulation and addiction. <i>Nature Neuroscience</i> , 2021, 24, 1367-1376.	14.8	137
14	Genome-wide scan identifies opioid overdose risk locus close to MCOLN1. <i>Addiction Biology</i> , 2020, 25, e12811.	2.6	10
15	Reproducible Genetic Risk Loci for Anxiety: Results From ~200,000 Participants in the Million Veteran Program. <i>American Journal of Psychiatry</i> , 2020, 177, 223-232.	7.2	185
16	Genome-wide association study of smoking trajectory and meta-analysis of smoking status in 842,000 individuals. <i>Nature Communications</i> , 2020, 11, 5302.	12.8	59
17	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020, 7, 1032-1045.	7.4	200
18	Association of <i>OPRM1</i> Functional Coding Variant With Opioid Use Disorder. <i>JAMA Psychiatry</i> , 2020, 77, 1072.	11.0	135

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19	Genome-wide meta-analysis of problematic alcohol use in 435,563 individuals yields insights into biology and relationships with other traits. <i>Nature Neuroscience</i> , 2020, 23, 809-818.	14.8	242
20	Genome-wide association study of alcohol dependence in male Han Chinese and cross-ethnic polygenic risk score comparison. <i>Translational Psychiatry</i> , 2019, 9, 249.	4.8	21
21	Genetic associations with suicide attempt severity and genetic overlap with major depression. <i>Translational Psychiatry</i> , 2019, 9, 22.	4.8	84
22	Genome-wide association study of alcohol consumption and use disorder in 274,424 individuals from multiple populations. <i>Nature Communications</i> , 2019, 10, 1499.	12.8	346
23	Genomewide Gene-by-Sex Interaction Scans Identify ADGRV1 for Sex Differences in Opioid Dependent African Americans. <i>Scientific Reports</i> , 2019, 9, 18070.	3.3	9
24	GWAS and network analysis of co-occurring nicotine and alcohol dependence identifies significantly associated alleles and network. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 3-11.	1.7	1
25	Genomewide Association Study of Alcohol Dependence and Related Traits in a Thai Population. <i>Alcoholism: Clinical and Experimental Research</i> , 2018, 42, 861-868.	2.4	32
26	Genome-wide Association Study Identifies a Regulatory Variant of RGMA Associated With Opioid Dependence in European Americans. <i>Biological Psychiatry</i> , 2018, 84, 762-770.	1.3	64
27	Genome-wide association study identifies glutamate ionotropic receptor GRIA4 as a risk gene for comorbid nicotine dependence and major depression. <i>Translational Psychiatry</i> , 2018, 8, 208.	4.8	14
28	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. <i>Journal of Genetics and Genomics</i> , 2018, 45, 419-432.	3.9	38
29	F131. Genome-Wide Association Study Identifies Glutamate Ionotropic Receptor GRIA4 as a Risk Gene for Comorbid Nicotine Dependence and Major Depression. <i>Biological Psychiatry</i> , 2018, 83, S288-S289.	1.3	0
30	Genome-wide association study of cognitive flexibility assessed by the Wisconsin Card Sorting Test. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2018, 177, 511-519.	1.7	4
31	Translational studies support a role for serotonin 2B receptor (HTR2B) gene in aggression-related cannabis response. <i>Molecular Psychiatry</i> , 2018, 23, 2277-2286.	7.9	20
32	Genetic Risk Variants Associated With Comorbid Alcohol Dependence and Major Depression. <i>JAMA Psychiatry</i> , 2017, 74, 1234.	11.0	74
33	Polygenic Scores for Major Depressive Disorder and Risk of Alcohol Dependence. <i>JAMA Psychiatry</i> , 2017, 74, 1153.	11.0	73
34	Inferring the Dynamics of Effective Population Size Using Autosomal Genomes. <i>Scientific Reports</i> , 2016, 6, 20079.	3.3	1
35	A Novel Candidate Region for Genetic Adaptation to High Altitude in Andean Populations. <i>PLoS ONE</i> , 2015, 10, e0125444.	2.5	46
36	Recent Coselection in Human Populations Revealed by Protein-Protein Interaction Network. <i>Genome Biology and Evolution</i> , 2015, 7, 136-153.	2.5	19

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37	Variation and signatures of selection on the human face. <i>Journal of Human Evolution</i> , 2014, 75, 143-152.	2.6	38
38	Detecting Genetic Association of Common Human Facial Morphological Variation Using High Density 3D Image Registration. <i>PLoS Computational Biology</i> , 2013, 9, e1003375.	3.2	50
39	Global patterns of genetic diversity and signals of natural selection for human ADME genes. <i>Human Molecular Genetics</i> , 2011, 20, 528-540.	2.9	84