

Yu-Li Liu

List of Publications by Year in descending order

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papers

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430843

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1117
citing authors

#	ARTICLE	IF	CITATIONS
1	A Deep Learning Approach for Predicting Antidepressant Response in Major Depression Using Clinical and Genetic Biomarkers. <i>Frontiers in Psychiatry</i> , 2018, 9, 290.	2.6	122
2	CYP2B6 Polymorphisms Influence the Plasma Concentration and Clearance of the Methadone S-Enantiomer. <i>Journal of Clinical Psychopharmacology</i> , 2011, 31, 463-469.	1.4	68
3	Genetic polymorphisms in <i>CYP3A4</i> are associated with withdrawal symptoms and adverse reactions in methadone maintenance patients. <i>Pharmacogenomics</i> , 2011, 12, 1397-1406.	1.3	57
4	Genetic polymorphisms in the opioid receptor $\mu 1$ gene are associated with changes in libido and insomnia in methadone maintenance patients. <i>European Neuropsychopharmacology</i> , 2012, 22, 695-703.	0.7	52
5	Genome-Wide Pharmacogenomic Study on Methadone Maintenance Treatment Identifies SNP rs17180299 and Multiple Haplotypes on CYP2B6, SPON1, and GSG1L Associated with Plasma Concentrations of Methadone R- and S-enantiomers in Heroin-Dependent Patients. <i>PLoS Genetics</i> , 2016, 12, e1005910.	3.5	50
6	Association and interaction of APOA5, BUD13, CETP, LIPA and health-related behavior with metabolic syndrome in a Taiwanese population. <i>Scientific Reports</i> , 2016, 6, 36830.	3.3	44
7	<i>CYP1A2</i> genetic polymorphisms are associated with treatment response to the antidepressant paroxetine. <i>Pharmacogenomics</i> , 2010, 11, 1535-1543.	1.3	37
8	Functional Genetic Polymorphisms in <i>CYP2C19</i> Gene in Relation to Cardiac Side Effects and Treatment Dose in a Methadone Maintenance Cohort. <i>OMICS A Journal of Integrative Biology</i> , 2013, 17, 519-526.	2.0	35
9	Transforming growth factor- $\beta 2$ signaling pathway-associated genes SMAD2 and TGFB2 are implicated in metabolic syndrome in a Taiwanese population. <i>Scientific Reports</i> , 2017, 7, 13589.	3.3	33
10	<i>UGT2B7</i> genetic polymorphisms are associated with the withdrawal symptoms in methadone maintenance patients. <i>Pharmacogenomics</i> , 2012, 13, 879-888.	1.3	31
11	The Association of Genetic Polymorphisms in the μ -Opioid Receptor 1 Gene With Body Weight, Alcohol Use, and Withdrawal Symptoms in Patients With Methadone Maintenance. <i>Journal of Clinical Psychopharmacology</i> , 2014, 34, 205-211.	1.4	29
12	OPRM1 genetic polymorphisms are associated with the plasma nicotine metabolite cotinine concentration in methadone maintenance patients: a cross sectional study. <i>Journal of Human Genetics</i> , 2013, 58, 84-90.	2.3	27
13	Gene-based analysis of genes related to neurotrophic pathway suggests association of BDNF and VEGFA with antidepressant treatment-response in depressed patients. <i>Scientific Reports</i> , 2018, 8, 6983.	3.3	26
14	Development of a method to measure methadone enantiomers and its metabolites without enantiomer standard compounds for the plasma of methadone maintenance patients. <i>Biomedical Chromatography</i> , 2010, 24, 782-788.	1.7	24
15	Association and Interaction Effects of Interleukin-12 Related Genes and Physical Activity on Cognitive Aging in Old Adults in the Taiwanese Population. <i>Frontiers in Neurology</i> , 2019, 10, 1065.	2.4	22
16	Assessment of CYP450 genetic variability effect on methadone dose and tolerance. <i>Pharmacogenomics</i> , 2014, 15, 977-986.	1.3	20
17	Prediction of Antidepressant Treatment Response and Remission Using an Ensemble Machine Learning Framework. <i>Pharmaceuticals</i> , 2020, 13, 305.	3.8	20
18	Effects of circadian clock genes and environmental factors on cognitive aging in old adults in a Taiwanese population. <i>Oncotarget</i> , 2017, 8, 24088-24098.	1.8	20

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19	Pharmacogenomics study in a Taiwanese methadone maintenance cohort. <i>Journal of Food and Drug Analysis</i> , 2013, 21, S62-S68.	1.9	17
20	GRK5 Is Associated with the Regulation of Methadone Dosage in Heroin Dependence. <i>International Journal of Neuropsychopharmacology</i> , 2018, 21, 910-917.	2.1	17
21	Hepatitis C Virus Infection Influences the S-Methadone Metabolite Plasma Concentration. <i>PLoS ONE</i> , 2013, 8, e69310.	2.5	17
22	Polygenic approaches to detect gene-environment interactions when external information is unavailable. <i>Briefings in Bioinformatics</i> , 2019, 20, 2236-2252.	6.5	14
23	Inflammatory chemokine eotaxin-1 is correlated with age in heroin dependent patients under methadone maintenance therapy. <i>Drug and Alcohol Dependence</i> , 2018, 183, 19-24.	3.2	13
24	LRRTM4 and PCSK5 Genetic Polymorphisms as Markers for Cognitive Impairment in A Hypotensive Aging Population: A Genome-Wide Association Study in Taiwan. <i>Journal of Clinical Medicine</i> , 2019, 8, 1124.	2.4	13
25	An association study in the Taiwan Biobank reveals RORA as a novel locus for sleep duration in the Taiwanese Population. <i>Sleep Medicine</i> , 2020, 73, 70-75.	1.6	13
26	Serum Level and Activity of Butylcholinesterase: A Biomarker for Post-Stroke Dementia. <i>Journal of Clinical Medicine</i> , 2019, 8, 1778.	2.4	11
27	A Post-hoc Study of D-Amino Acid Oxidase in Blood as an Indicator of Post-stroke Dementia. <i>Frontiers in Neurology</i> , 2019, 10, 402.	2.4	10
28	Association between polygenic liability for schizophrenia and substance involvement: A nationwide population-based study in Taiwan. <i>Genes, Brain and Behavior</i> , 2020, 19, e12639.	2.2	9
29	Genetic polymorphisms in the opioid receptor delta 1 (OPRD1) gene are associated with methadone dose in methadone maintenance treatment for heroin dependence. <i>Journal of Human Genetics</i> , 2020, 65, 381-386.	2.3	8
30	Genetic variants in NECTIN4 encoding an adhesion molecule are associated with continued opioid use. <i>PLoS ONE</i> , 2020, 15, e0234549.	2.5	7
31	APBB2 is associated with amphetamine use and plasma beta-amyloids in patients receiving methadone maintenance treatment. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2018, 83, 92-98.	4.8	6
32	CUX2, BRAP and ALDH2 are associated with metabolic traits in people with excessive alcohol consumption. <i>Scientific Reports</i> , 2020, 10, 18118.	3.3	6
33	Prediction of Probable Major Depressive Disorder in the Taiwan Biobank: An Integrated Machine Learning and Genome-Wide Analysis Approach. <i>Journal of Personalized Medicine</i> , 2021, 11, 597.	2.5	6
34	Increase in plasma CCL11 (Eotaxin-1) in patients with alcohol dependence and changes during detoxification. <i>Brain, Behavior, and Immunity</i> , 2022, 99, 83-90.	4.1	5
35	Chemokine IP-10 is correlated with cardiac responses and status of infection with HIV and HCV in methadone maintenance patients. <i>International Journal of Cardiology</i> , 2015, 194, 36-38.	1.7	3
36	Increased Nectin-4 levels in chronic ketamine abusers and the relationship with lower urinary tract symptoms. <i>Environmental Toxicology and Pharmacology</i> , 2021, 87, 103714.	4.0	3

#	ARTICLE	IF	CITATIONS
37	Pharmacogenomics study on cadherin 2 network with regard to HIV infection and methadone treatment outcome. PLoS ONE, 2017, 12, e0174647.	2.5	3
38	Adhesion Molecules as Potential Novel Biomarkers for Opioid Dependence. Current Pharmaceutical Design, 2020, 26, 253-259.	1.9	3
39	Missense mutation at CLDN8 associated with a high plasma interferon gamma-inducible protein 10 level in methadone-maintained patients with urine test positive for morphine. PLoS ONE, 2017, 12, e0187639.	2.5	2
40	Association of the D-amino acid oxidase gene with methadone dose in heroin dependent patients under methadone maintenance treatment. Journal of Human Genetics, 2022, 67, 273-278.	2.3	1
41	Comparing multiple testing correction methods between two softwares for single nucleotide polymorphisms association analyses: Using OPRD1 and diastolic blood pressure in methadone maintenance patients as an example. , 2013, , .		0
42	[P4â€“355]: NEURODEGENERATION BIOMARKER EOTAXINâ€“1 ELEVATED AT EARLY AGE IN HEROINâ€“DEPENDENT PATIENTS. Alzheimer's and Dementia, 2017, 13, P1426.	0.8	0