Yu-Li Liu

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A Deep Learning Approach for Predicting Antidepressant Response in Major Depression Using Clinical and Genetic Biomarkers. Frontiers in Psychiatry, 2018, 9, 290.	2.6	122
2	CYP2B6 Polymorphisms Influence the Plasma Concentration and Clearance of the Methadone S-Enantiomer. Journal of Clinical Psychopharmacology, 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. Pharmacogenomics, 2011, 12, 1397-1406.	1.3	57
4	Genetic polymorphisms in the opioid receptor mu1 gene are associated with changes in libido and insomnia in methadone maintenance patients. European Neuropsychopharmacology, 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. PLoS Genetics, 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. Scientific Reports, 2016, 6, 36830.	3.3	44
7	<i>CYP1A2</i> genetic polymorphisms are associated with treatment response to the antidepressant paroxetine. Pharmacogenomics, 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. OMICS A Journal of Integrative Biology, 2013, 17, 519-526.	2.0	35
9	Transforming growth factor-Î ² signaling pathway-associated genes SMAD2 and TGFBR2 are implicated in metabolic syndrome in a Taiwanese population. Scientific Reports, 2017, 7, 13589.	3.3	33
10	<i>UGT2B7</i> genetic polymorphisms are associated with the withdrawal symptoms in methadone maintenance patients. Pharmacogenomics, 2012, 13, 879-888.	1.3	31
11	The Association of Genetic Polymorphisms in the κ-Opioid Receptor 1 Gene With Body Weight, Alcohol Use, and Withdrawal Symptoms in Patients With Methadone Maintenance. Journal of Clinical Psychopharmacology, 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. Journal of Human Genetics, 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. Scientific Reports, 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. Biomedical Chromatography, 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. Frontiers in Neurology, 2019, 10, 1065.	2.4	22
16	Assessment of CYP450 genetic variability effect on methadone dose and tolerance. Pharmacogenomics, 2014, 15, 977-986.	1.3	20
17	Prediction of Antidepressant Treatment Response and Remission Using an Ensemble Machine Learning Framework. Pharmaceuticals, 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. Oncotarget, 2017, 8, 24088-24098.	1.8	20

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19	Pharmacogenomics study in a Taiwanese methadone maintenance cohort. Journal of Food and Drug Analysis, 2013, 21, S62-S68.	1.9	17
20	GRK5 Is Associated with the Regulation of Methadone Dosage in Heroin Dependence. International Journal of Neuropsychopharmacology, 2018, 21, 910-917.	2.1	17
21	Hepatitis C Virus Infection Influences the S-Methadone Metabolite Plasma Concentration. PLoS ONE, 2013, 8, e69310.	2.5	17
22	Polygenic approaches to detect gene–environment interactions when external information is unavailable. Briefings in Bioinformatics, 2019, 20, 2236-2252.	6.5	14
23	Inflammatory chemokine eotaxin-1 is correlated with age in heroin dependent patients under methadone maintenance therapy. Drug and Alcohol Dependence, 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. Journal of Clinical Medicine, 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. Sleep Medicine, 2020, 73, 70-75.	1.6	13
26	Serum Level and Activity of Butylcholinesterase: A Biomarker for Post-Stroke Dementia. Journal of Clinical Medicine, 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. Frontiers in Neurology, 2019, 10, 402.	2.4	10
28	Association between polygenic liability for schizophrenia and substance involvement: A nationwide populationâ€based study in Taiwan. Genes, Brain and Behavior, 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. Journal of Human Genetics, 2020, 65, 381-386.	2.3	8
30	Genetic variants in NECTIN4 encoding an adhesion molecule are associated with continued opioid use. PLoS ONE, 2020, 15, e0234549.	2.5	7
31	APBB2 is associated with amphetamine use and plasma beta-amyloids in patients receiving methadone maintenance treatment. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2018, 83, 92-98.	4.8	6
32	CUX2, BRAP and ALDH2 are associated with metabolic traits in people with excessive alcohol consumption. Scientific Reports, 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. Journal of Personalized Medicine, 2021, 11, 597.	2.5	6
34	Increase in plasma CCL11 (Eotaxin-1) in patients with alcohol dependence and changes during detoxification. Brain, Behavior, and Immunity, 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. International Journal of Cardiology, 2015, 194, 36-38.	1.7	3
36	Increased Nectin-4 levels in chronic ketamine abusers and the relationship with lower urinary tract symptoms. Environmental Toxicology and Pharmacology, 2021, 87, 103714.	4.0	3

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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, , .		Ο
42	[P4–355]: NEURODEGENERATION BIOMARKER EOTAXINâ€1 ELEVATED AT EARLY AGE IN HEROINâ€DEPENDEI PATIENTS. Alzheimer's and Dementia, 2017, 13, P1426.	NT _{0.8}	0