

Joseph Louie McClay

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

16,789
citations

159358

30
h-index

110170

64
g-index

71
all docs

71
docs citations

71
times ranked

15201
citing authors

#	ARTICLE	IF	CITATIONS
1	Repeated exposure to chlorpyrifos is associated with a dose-dependent chronic neurobehavioral deficit in adult rats. <i>NeuroToxicology</i> , 2022, 90, 172-183.	1.4	4
2	Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. <i>Pharmacogenetics and Genomics</i> , 2021, 31, 207-214.	0.7	5
3	Epigenetic regulation of drug metabolism in aging. <i>Aging</i> , 2021, 13, 16898-16899.	1.4	1
4	Epigenetic histone acetylation and Bdnf dysregulation in the hippocampus of rats exposed to repeated, low-dose diisopropylfluorophosphate. <i>Life Sciences</i> , 2021, 281, 119765.	2.0	12
5	Review and Consensus on Pharmacogenomic Testing in Psychiatry. <i>Pharmacopsychiatry</i> , 2021, 54, 5-17.	1.7	96
6	DNA methylation and histone acetylation changes to cytochrome P450 2E1 regulation in normal aging and impact on rates of drug metabolism in the liver. <i>GeroScience</i> , 2020, 42, 819-832.	2.1	26
7	Molecular mechanisms for the antidepressant-like effects of a low-dose ketamine treatment in a DFP-based rat model for Gulf War Illness. <i>NeuroToxicology</i> , 2020, 80, 52-59.	1.4	16
8	The <i>ANKK1B</i> gene and its associated phenotypes: focus on CNS drug response. <i>Pharmacogenomics</i> , 2019, 20, 669-684.	0.6	13
9	Epigenetic biomarkers in personalized medicine. , 2019, , 375-395.		3
10	Cell-type specific differences in antiretroviral penetration and the effects of HIV-1 Tat and morphine among primary human brain endothelial cells, astrocytes, pericytes, and microglia. <i>Neuroscience Letters</i> , 2019, 712, 134475.	1.0	16
11	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. <i>Human Molecular Genetics</i> , 2018, 27, 3246-3256.	1.4	33
12	Initial characterization of behavior and ketamine response in a mouse knockout of the post-synaptic effector gene <i>Anks1b</i> . <i>Neuroscience Letters</i> , 2017, 641, 26-32.	1.0	11
13	The role of epigenomics in personalized medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , 2017, 2, 33-45.	0.4	61
14	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2017, 41, 711-718.	1.4	13
15	Effects of HIV-1 Tat and Methamphetamine on Blood-Brain Barrier Integrity and Function <i>In Vitro</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2017, 61, .	1.4	24
16	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. <i>Nicotine and Tobacco Research</i> , 2016, 18, 626-631.	1.4	10
17	Combined Whole Methylome and Genomewide Association Study Implicates <i>CNTN4</i> in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2015, 39, 1396-1405.	1.4	15
18	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , 2015, 16, 291.	3.8	112

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19	Refinement of schizophrenia GWAS loci using methylome-wide association data. <i>Human Genetics</i> , 2015, 134, 77-87.	1.8	25
20	Neurochemical Metabolomics Reveals Disruption to Sphingolipid Metabolism Following Chronic Haloperidol Administration. <i>Journal of NeuroImmune Pharmacology</i> , 2015, 10, 425-434.	2.1	22
21	Methylome-Wide Association Study of Schizophrenia. <i>JAMA Psychiatry</i> , 2014, 71, 255.	6.0	210
22	A methylome-wide study of aging using massively parallel sequencing of the methyl-CpG-enriched genomic fraction from blood in over 700 subjects. <i>Human Molecular Genetics</i> , 2014, 23, 1175-1185.	1.4	147
23	Genome-Wide and Gene-Based Association Studies of Anxiety Disorders in European and African American Samples. <i>PLoS ONE</i> , 2014, 9, e112559.	1.1	22
24	Estimation of CpG coverage in whole methylome next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2013, 14, 50.	1.2	24
25	Large-scale neurochemical metabolomics analysis identifies multiple compounds associated with methamphetamine exposure. <i>Metabolomics</i> , 2013, 9, 392-402.	1.4	38
26	Genes, Environments, and Developmental Research: Methods for a Multi-Site Study of Early Substance Abuse. <i>Twin Research and Human Genetics</i> , 2013, 16, 505-515.	0.3	12
27	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. <i>JAMA Psychiatry</i> , 2013, 70, 573.	6.0	138
28	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. <i>Epigenomics</i> , 2013, 5, 367-377.	1.0	81
29	Behavioral metabolomics analysis identifies novel neurochemical signatures in methamphetamine sensitization. <i>Genes, Brain and Behavior</i> , 2013, 12, 780-791.	1.1	22
30	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. <i>Pharmacogenetics and Genomics</i> , 2013, 23, 69-77.	0.7	43
31	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. <i>PLoS ONE</i> , 2013, 8, e55239.	1.1	6
32	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. <i>Translational Psychiatry</i> , 2012, 2, e129-e129.	2.4	41
33	Genome-wide association study of antipsychotic-induced QTc interval prolongation. <i>Pharmacogenomics Journal</i> , 2012, 12, 165-172.	0.9	78
34	The influence of five monoamine genes on trajectories of depressive symptoms across adolescence and young adulthood. <i>Development and Psychopathology</i> , 2012, 24, 267-285.	1.4	25
35	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. <i>Psychological Medicine</i> , 2012, 42, 1151-1162.	2.7	60
36	Institutional Profile: The Center for Biomarker Research and Personalized Medicine at Virginia Commonwealth University: advancing psychiatric drug treatment. <i>Personalized Medicine</i> , 2012, 9, 479-483.	0.8	1

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37	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case-control samples. <i>Epigenomics</i> , 2012, 4, 605-621.	1.0	86
38	SNP-based analysis of neuroactive ligand-receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: Data from the CATIE study. <i>Schizophrenia Research</i> , 2012, 135, 200-201.	1.1	47
39	The glial cell modulators, ibudilast and its amino analog, AV1013, attenuate methamphetamine locomotor activity and its sensitization in mice. <i>European Journal of Pharmacology</i> , 2012, 679, 75-80.	1.7	42
40	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. <i>Molecular Psychiatry</i> , 2011, 16, 76-85.	4.1	141
41	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. <i>Molecular Psychiatry</i> , 2011, 16, 321-332.	4.1	141
42	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. <i>Neuropsychopharmacology</i> , 2011, 36, 616-626.	2.8	103
43	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. <i>Biological Psychiatry</i> , 2010, 67, 279-282.	0.7	122
44	A Genomewide Association Study of Citalopram Response in Major Depressive Disorder—A Psychometric Approach. <i>Biological Psychiatry</i> , 2010, 68, e25-e27.	0.7	18
45	MicroRNA expression profiling in the prefrontal cortex of individuals affected with schizophrenia and bipolar disorders. <i>Schizophrenia Research</i> , 2010, 124, 183-191.	1.1	258
46	1H Nuclear Magnetic Resonance Metabolomics Analysis Identifies Novel Urinary Biomarkers for Lung Function. <i>Journal of Proteome Research</i> , 2010, 9, 3083-3090.	1.8	60
47	In Silico Whole Genome Association Scan for Murine Prepulse Inhibition. <i>PLoS ONE</i> , 2009, 4, e5246.	1.1	9
48	Estimating the posterior probability that genome-wide association findings are true or false. <i>Bioinformatics</i> , 2009, 25, 1807-1813.	1.8	12
49	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. <i>Schizophrenia Research</i> , 2009, 107, 13-21.	1.1	34
50	AKT1 Is Associated with Schizophrenia Across Multiple Symptom Dimensions in the Irish Study of High Density Schizophrenia Families. <i>Biological Psychiatry</i> , 2008, 63, 449-457.	0.7	148
51	A Theoretical Systems Biology Analysis Suggests Gene-Environment Interaction Effects are Common at the Most Basic Levels of Biological Organization. , 2008, , .		0
52	A region of 35 kb containing the trace amine associate receptor 6 (TAAR6) gene is associated with schizophrenia in the Irish study of high-density schizophrenia families. <i>Molecular Psychiatry</i> , 2007, 12, 842-853.	4.1	26
53	Genetics and diagnostic refinement. <i>Behavior Genetics</i> , 2007, 37, 535-545.	1.4	5
54	Variance component analysis of polymorphic metabolic systems. <i>Journal of Theoretical Biology</i> , 2006, 240, 149-159.	0.8	6

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55	Catechol-O-methyltransferase and the clinical features of psychosis. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2006, 141B, 935-938.	1.1	27
56	Microbial genetics: Split genes uncovered through science fusion. Heredity, 2005, 95, 1-2.	1.2	4
57	Moderation of the Effect of Adolescent-Onset Cannabis Use on Adult Psychosis by a Functional Polymorphism in the Catechol-O-Methyltransferase Gene: Longitudinal Evidence of a Gene X Environment Interaction. Biological Psychiatry, 2005, 57, 1117-1127.	0.7	1,210
58	Association analysis of MAOA and COMT with neuroticism assessed by peers. American Journal of Medical Genetics Part A, 2003, 120B, 90-96.	2.4	109
59	Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene. Science, 2003, 301, 386-389.	6.0	7,147
60	The role of molecular genetics in the postgenomic era.. , 2003, , 19-40.		9
61	The dopamine D4 receptor and the hyperactivity phenotype: a developmental-epidemiological study. Molecular Psychiatry, 2002, 7, 383-391.	4.1	55
62	Role of Genotype in the Cycle of Violence in Maltreated Children. Science, 2002, 297, 851-854.	6.0	4,118
63	High-Throughput Single-Nucleotide Polymorphism Genotyping by Fluorescent Competitive Allele-Specific Polymerase Chain Reaction (SNiPTag). Analytical Biochemistry, 2002, 301, 200-206.	1.1	18
64	Chasing behaviour genes into the next millennium. Trends in Biotechnology, 2000, 18, 22-26.	4.9	8
65	Allele association studies with SSR and SNP markers at known physical distances within a 1 Mb region embracing the ALDH2 locus in the Japanese, demonstrates linkage disequilibrium extending up to 400 kb. Human Molecular Genetics, 2000, 9, 2993-2999.	1.4	22
66	The DNA sequence of human chromosome 22. Nature, 1999, 402, 489-495.	13.7	1,086
67	A 12-cistron Escherichia coli operon (hyf) encoding a putative proton-translocating formate hydrogenlyase system. Microbiology (United Kingdom), 1997, 143, 3633-3647.	0.7	251