Joseph Louie McClay

List of Publications by Year
in descending order

67 papers	16,789 citations	159585 30 h-index	110387 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. NeuroToxicology, 2022, 90, 172-183.	3.0	4
2	Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. Pharmacogenetics and Genomics, 2021, 31, 207-214.	1.5	5
3	Epigenetic regulation of drug metabolism in aging. Aging, 2021, 13, 16898-16899.	3.1	1
4	Epigenetic histone acetylation and Bdnf dysregulation in the hippocampus of rats exposed to repeated, low-dose diisopropylfluorophosphate. Life Sciences, 2021, 281, 119765.	4.3	12
5	Review and Consensus on Pharmacogenomic Testing in Psychiatry. Pharmacopsychiatry, 2021, 54, 5-17.	3.3	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. GeroScience, 2020, 42, 819-832.	4.6	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. NeuroToxicology, 2020, 80, 52-59.	3.0	16
8	The ANKS1B gene and its associated phenotypes: focus on CNS drug response. Pharmacogenomics, 2019, 20, 669-684.	1.3	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. Neuroscience Letters, 2019, 712, 134475.	2.1	16
11	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. Human Molecular Genetics, 2018, 27, 3246-3256.	2.9	33
12	Initial characterization of behavior and ketamine response in a mouse knockout of the post-synaptic effector gene Anks1b. Neuroscience Letters, 2017, 641, 26-32.	2.1	11
13	The role of epigenomics in personalized medicine. Expert Review of Precision Medicine and Drug Development, 2017, 2, 33-45.	0.7	61
14	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2017, 41, 711-718.	2.4	13
15	Effects of HIV-1 Tat and Methamphetamine on Blood-Brain Barrier Integrity and FunctionIn Vitro. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	24
16	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. Nicotine and Tobacco Research, 2016, 18, 626-631.	2.6	10
17	Combined Whole Methylome and Genomewide Association Study ImplicatesCNTN4in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	2.4	15
18	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. Genome Biology, 2015, 16, 291.	8.8	112

#	Article	IF	Citations
19	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	3.8	25
20	Neurochemical Metabolomics Reveals Disruption to Sphingolipid Metabolism Following Chronic Haloperidol Administration. Journal of NeuroImmune Pharmacology, 2015, 10, 425-434.	4.1	22
21	Methylome-Wide Association Study of Schizophrenia. JAMA Psychiatry, 2014, 71, 255.	11.0	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. Human Molecular Genetics, 2014, 23, 1175-1185.	2.9	147
23	Genome-Wide and Gene-Based Association Studies of Anxiety Disorders in European and African American Samples. PLoS ONE, 2014, 9, e112559.	2.5	22
24	Estimation of CpG coverage in whole methylome next-generation sequencing studies. BMC Bioinformatics, 2013, 14, 50.	2.6	24
25	Large-scale neurochemical metabolomics analysis identifies multiple compounds associated with methamphetamine exposure. Metabolomics, 2013, 9, 392-402.	3.0	38
26	Genes, Environments, and Developmental Research: Methods for a Multi-Site Study of Early Substance Abuse. Twin Research and Human Genetics, 2013, 16, 505-515.	0.6	12
27	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. JAMA Psychiatry, 2013, 70, 573.	11.0	138
28	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. Epigenomics, 2013, 5, 367-377.	2.1	81
29	Behavioral metabolomics analysis identifies novel neurochemical signatures in methamphetamine sensitization. Genes, Brain and Behavior, 2013, 12, 780-791.	2.2	22
30	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. Pharmacogenetics and Genomics, 2013, 23, 69-77.	1.5	43
31	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. PLoS ONE, 2013, 8, e55239.	2.5	6
32	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. Translational Psychiatry, 2012, 2, e129-e129.	4.8	41
33	Genome-wide association study of antipsychotic-induced QTc interval prolongation. Pharmacogenomics Journal, 2012, 12, 165-172.	2.0	78
34	The influence of five monoamine genes on trajectories of depressive symptoms across adolescence and young adulthood. Development and Psychopathology, 2012, 24, 267-285.	2.3	25
35	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. Psychological Medicine, 2012, 42, 1151-1162.	4.5	60
36	Institutional Profile: The Center for Biomarker Research and Personalized Medicine at Virginia Commonwealth University: advancing psychiatric drug treatment. Personalized Medicine, 2012, 9, 479-483.	1.5	1

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37	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 caseâ€“control samples. Epigenomics, 2012, 4, 605-621.	2.1	86
38	SNP-based analysis of neuroactive ligandâ€“receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: Data from the CATIE study. Schizophrenia Research, 2012, 135, 200-201.	2.0	47
39	The glial cell modulators, ibudilast and its amino analog, AV1013, attenuate methamphetamine locomotor activity and its sensitization in mice. European Journal of Pharmacology, 2012, 679, 75-80.	3.5	42
40	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. Molecular Psychiatry, 2011, 16, 76-85.	7.9	141
41	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. Molecular Psychiatry, 2011, 16, 321-332.	7.9	141
42	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. Neuropsychopharmacology, 2011, 36, 616-626.	5.4	103
43	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. Biological Psychiatry, 2010, 67, 279-282.	1.3	122
44	A Genomewide Association Study of Citalopram Response in Major Depressive Disorderâ€”A Psychometric Approach. Biological Psychiatry, 2010, 68, e25-e27.	1.3	18
45	MicroRNA expression profiling in the prefrontal cortex of individuals affected with schizophrenia and bipolar disorders. Schizophrenia Research, 2010, 124, 183-191.	2.0	258
46	1H Nuclear Magnetic Resonance Metabolomics Analysis Identifies Novel Urinary Biomarkers for Lung Function. Journal of Proteome Research, 2010, 9, 3083-3090.	3.7	60
47	In Silico Whole Genome Association Scan for Murine Prepulse Inhibition. PLoS ONE, 2009, 4, e5246.	2.5	9
48	Estimating the posterior probability that genome-wide association findings are true or false. Bioinformatics, 2009, 25, 1807-1813.	4.1	12
49	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. Schizophrenia Research, 2009, 107, 13-21.	2.0	34
50	AKT1 Is Associated with Schizophrenia Across Multiple Symptom Dimensions in the Irish Study of High Density Schizophrenia Families. Biological Psychiatry, 2008, 63, 449-457.	1.3	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 35â€‰kb containing the trace amine associate receptor 6 (TAAR6) gene is associated with schizophrenia in the Irish study of high-density schizophrenia families. Molecular Psychiatry, 2007, 12, 842-853.	7.9	26
53	Genetics and diagnostic refinement. Behavior Genetics, 2007, 37, 535-545.	2.1	5
54	Variance component analysis of polymorphic metabolic systems. Journal of Theoretical Biology, 2006, 240, 149-159.	1.7	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.	1.7	27
56	Microbial genetics: Split genes uncovered through science fusion. Heredity, 2005, 95, 1-2.	2.6	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.	1.3	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.	12.6	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.	7.9	55
62	Role of Genotype in the Cycle of Violence in Maltreated Children. Science, 2002, 297, 851-854.	12.6	4,118
63	High-Throughput Single-Nucleotide Polymorphism Genotyping by Fluorescent Competitive Allele-Specific Polymerase Chain Reaction (SNiPTag). Analytical Biochemistry, 2002, 301, 200-206.	2.4	18
64	Chasing behaviour genes into the next millennium. Trends in Biotechnology, 2000, 18, 22-26.	9.3	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.	2.9	22
66	The DNA sequence of human chromosome 22. Nature, 1999, 402, 489-495.	27.8	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.	1.8	251