Joseph Louie McClay

List of Publications by Year
in descending order

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	Influence of Life Stress on Depression: Moderation by a Polymorphism in the 5-HTT Gene. Science, 2003, 301, 386-389.	6.0	7,147
2	Role of Genotype in the Cycle of Violence in Maltreated Children. Science, 2002, 297, 851-854.	6.0	4,118
3	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
4	The DNA sequence of human chromosome 22. Nature, 1999, 402, 489-495.	13.7	1,086
5	MicroRNA expression profiling in the prefrontal cortex of individuals affected with schizophrenia and bipolar disorders. Schizophrenia Research, 2010, 124, 183-191.	1.1	258
6	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
7	Methylome-Wide Association Study of Schizophrenia. JAMA Psychiatry, 2014, 71, 255.	6.0	210
8	AKT1 Is Associated with Schizophrenia Across Multiple Symptom Dimensions in the Irish Study of High Density Schizophrenia Families. Biological Psychiatry, 2008, 63, 449-457.	0.7	148
9	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.	1.4	147
10	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. Molecular Psychiatry, 2011, 16, 76-85.	4.1	141
11	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. Molecular Psychiatry, 2011, 16, 321-332.	4.1	141
12	A Comprehensive Family-Based Replication Study of Schizophrenia Genes. JAMA Psychiatry, 2013, 70, 573.	6.0	138
13	Genomewide Association Study of Movement-Related Adverse Antipsychotic Effects. Biological Psychiatry, 2010, 67, 279-282.	0.7	122
14	High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. Genome Biology, 2015, 16, 291.	3.8	112
15	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
16	Genome-Wide Pharmacogenomic Study of Neurocognition As an Indicator of Antipsychotic Treatment Response in Schizophrenia. Neuropsychopharmacology, 2011, 36, 616-626.	2.8	103
17	Review and Consensus on Pharmacogenomic Testing in Psychiatry. Pharmacopsychiatry, 2021, 54, 5-17.	1.7	96
18	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case–control samples. Epigenomics, 2012, 4, 605-621.	1.0	86

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19	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. Epigenomics, 2013, 5, 367-377.	1.0	81
20	Genome-wide association study of antipsychotic-induced QTc interval prolongation. Pharmacogenomics Journal, 2012, 12, 165-172.	0.9	78
21	The role of epigenomics in personalized medicine. Expert Review of Precision Medicine and Drug Development, 2017, 2, 33-45.	0.4	61
22	1H Nuclear Magnetic Resonance Metabolomics Analysis Identifies Novel Urinary Biomarkers for Lung Function. Journal of Proteome Research, 2010, 9, 3083-3090.	1.8	60
23	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. Psychological Medicine, 2012, 42, 1151-1162.	2.7	60
24	The dopamine D4 receptor and the hyperactivity phenotype: a developmental-epidemiological study. Molecular Psychiatry, 2002, 7, 383-391.	4.1	55
25	SNP-based analysis of neuroactive ligand–receptor interaction pathways implicates PGE2 as a novel mediator of antipsychotic treatment response: Data from the CATIE study. Schizophrenia Research, 2012, 135, 200-201.	1.1	47
26	Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. Pharmacogenetics and Genomics, 2013, 23, 69-77.	0.7	43
27	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.	1.7	42
28	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. Translational Psychiatry, 2012, 2, e129-e129.	2.4	41
29	Large-scale neurochemical metabolomics analysis identifies multiple compounds associated with methamphetamine exposure. Metabolomics, 2013, 9, 392-402.	1.4	38
30	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. Schizophrenia Research, 2009, 107, 13-21.	1.1	34
31	Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. Human Molecular Genetics, 2018, 27, 3246-3256.	1.4	33
32	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
33	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. Molecular Psychiatry, 2007, 12, 842-853.	4.1	26
34	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.	2.1	26
35	The influence of five monoamine genes on trajectories of depressive symptoms across adolescence and young adulthood. Development and Psychopathology, 2012, 24, 267-285.	1.4	25
36	Refinement of schizophrenia GWAS loci using methylome-wide association data. Human Genetics, 2015, 134, 77-87.	1.8	25

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37	Estimation of CpG coverage in whole methylome next-generation sequencing studies. BMC Bioinformatics, 2013, 14, 50.	1.2	24
38	Effects of HIV-1 Tat and Methamphetamine on Blood-Brain Barrier Integrity and Function*In Vitro*. Antimicrobial Agents and Chemotherapy, 2017, 61, .	1.4	24
39	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
40	Behavioral metabolomics analysis identifies novel neurochemical signatures in methamphetamine sensitization. Genes, Brain and Behavior, 2013, 12, 780-791.	1.1	22
41	Neurochemical Metabolomics Reveals Disruption to Sphingolipid Metabolism Following Chronic Haloperidol Administration. Journal of NeuroImmune Pharmacology, 2015, 10, 425-434.	2.1	22
42	Genome-Wide and Gene-Based Association Studies of Anxiety Disorders in European and African American Samples. PLoS ONE, 2014, 9, e112559.	1.1	22
43	High-Throughput Single-Nucleotide Polymorphism Genotyping by Fluorescent Competitive Allele-Specific Polymerase Chain Reaction (SNiPTag). Analytical Biochemistry, 2002, 301, 200-206.	1.1	18
44	A Genomewide Association Study of Citalopram Response in Major Depressive Disorder—A Psychometric Approach. Biological Psychiatry, 2010, 68, e25-e27.	0.7	18
45	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.	1.0	16
46	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.	1.4	16
47	Combined Whole Methylome and Genomewide Association Study Implicates*CNTN4*in Alcohol Use. Alcoholism: Clinical and Experimental Research, 2015, 39, 1396-1405.	1.4	15
48	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2017, 41, 711-718.	1.4	13
49	The *ANKS1B* gene and its associated phenotypes: focus on CNS drug response. Pharmacogenomics, 2019, 20, 669-684.	0.6	13
50	Estimating the posterior probability that genome-wide association findings are true or false. Bioinformatics, 2009, 25, 1807-1813.	1.8	12
51	Genes, Environments, and Developmental Research: Methods for a Multi-Site Study of Early Substance Abuse. Twin Research and Human Genetics, 2013, 16, 505-515.	0.3	12
52	Epigenetic histone acetylation and Bdnf dysregulation in the hippocampus of rats exposed to repeated, low-dose diisopropylfluorophosphate. Life Sciences, 2021, 281, 119765.	2.0	12
53	Initial characterization of behavior and ketamine response in a mouse knockout of the post-synaptic effector gene Anks1b. Neuroscience Letters, 2017, 641, 26-32.	1.0	11
54	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. Nicotine and Tobacco Research, 2016, 18, 626-631.	1.4	10

#	ARTICLE	IF	CITATIONS
55	In Silico Whole Genome Association Scan for Murine Prepulse Inhibition. PLoS ONE, 2009, 4, e5246.	1.1	9
56	The role of molecular genetics in the postgenomic era.. , 2003, , 19-40.		9
57	Chasing behaviour genes into the next millennium. Trends in Biotechnology, 2000, 18, 22-26.	4.9	8
58	Variance component analysis of polymorphic metabolic systems. Journal of Theoretical Biology, 2006, 240, 149-159.	0.8	6
59	Genotype-Based Ancestral Background Consistently Predicts Efficacy and Side Effects across Treatments in CATIE and STAR*D. PLoS ONE, 2013, 8, e55239.	1.1	6
60	Genetics and diagnostic refinement. Behavior Genetics, 2007, 37, 535-545.	1.4	5
61	Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. Pharmacogenetics and Genomics, 2021, 31, 207-214.	0.7	5
62	Microbial genetics: Split genes uncovered through science fusion. Heredity, 2005, 95, 1-2.	1.2	4
63	Repeated exposure to chlorpyrifos is associated with a dose-dependent chronic neurobehavioral deficit in adult rats. NeuroToxicology, 2022, 90, 172-183.	1.4	4
64	Epigenetic biomarkers in personalized medicine. , 2019, , 375-395.		3
65	Institutional Profile: The Center for Biomarker Research and Personalized Medicine at Virginia Commonwealth University: advancing psychiatric drug treatment. Personalized Medicine, 2012, 9, 479-483.	0.8	1
66	Epigenetic regulation of drug metabolism in aging. Aging, 2021, 13, 16898-16899.	1.4	1
67	A Theoretical Systems Biology Analysis Suggests Gene-Environment Interaction Effects are Common at the Most Basic Levels of Biological Organization. , 2008, , .		0