

# Joseph Louie McClay

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

64  
papers

14,136  
citations

29  
h-index

70  
g-index

70  
ext. papers

15,737  
ext. citations

7  
avg, IF

5.43  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 64 | Influence of life stress on depression: moderation by a polymorphism in the 5-HTT gene. <i>Science</i> , <b>2003</b> , 301, 386-9   | 33.3 | 6113      |
| 63 | Role of genotype in the cycle of violence in maltreated children. <i>Science</i> , <b>2002</b> , 297, 851-4   | 33.3 | 3452      |
| 62 | 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. <i>Biological Psychiatry</i> , <b>2005</b> , 57, 1117-27 | 7.9  | 1020      |
| 61 | The DNA sequence of human chromosome 22. <i>Nature</i> , <b>1999</b> , 402, 489-95  | 50.4 | 917       |
| 60 | MicroRNA expression profiling in the prefrontal cortex of individuals affected with schizophrenia and bipolar disorders. <i>Schizophrenia Research</i> , <b>2010</b> , 124, 183-91  | 3.6  | 225       |
| 59 | A 12-cistron Escherichia coli operon (hyf) encoding a putative proton-translocating formate hydrogenlyase system. <i>Microbiology (United Kingdom)</i> , <b>1997</b> , 143 ( Pt 11), 3633-3647  | 2.9  | 223       |
| 58 | Methylome-wide association study of schizophrenia: identifying blood biomarker signatures of environmental insults. <i>JAMA Psychiatry</i> , <b>2014</b> , 71, 255-64   | 14.5 | 172       |
| 57 | AKT1 is associated with schizophrenia across multiple symptom dimensions in the Irish study of high density schizophrenia families. <i>Biological Psychiatry</i> , <b>2008</b> , 63, 449-57   | 7.9  | 131       |
| 56 | Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. <i>Molecular Psychiatry</i> , <b>2011</b> , 16, 76-85  | 15.1 | 124       |
| 55 | Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. <i>Molecular Psychiatry</i> , <b>2011</b> , 16, 321-32   | 15.1 | 123       |
| 54 | 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> , <b>2014</b> , 23, 1175-85  | 5.6  | 122       |
| 53 | A comprehensive family-based replication study of schizophrenia genes. <i>JAMA Psychiatry</i> , <b>2013</b> , 70, 573-81.5  | 11.5 | 115       |
| 52 | Genomewide association study of movement-related adverse antipsychotic effects. <i>Biological Psychiatry</i> , <b>2010</b> , 67, 279-82   | 7.9  | 107       |
| 51 | Association analysis of MAOA and COMT with neuroticism assessed by peers. <i>American Journal of Medical Genetics Part A</i> , <b>2003</b> , 120B, 90-6   |      | 96        |
| 50 | Genome-wide pharmacogenomic study of neurocognition as an indicator of antipsychotic treatment response in schizophrenia. <i>Neuropsychopharmacology</i> , <b>2011</b> , 36, 616-26   | 8.7  | 87        |
| 49 | High density methylation QTL analysis in human blood via next-generation sequencing of the methylated genomic DNA fraction. <i>Genome Biology</i> , <b>2015</b> , 16, 291   | 18.3 | 86        |
| 48 | MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case-control samples. <i>Epigenomics</i> , <b>2012</b> , 4, 605-21   | 4.4  | 79        |

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| 47 | Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. <i>Epigenomics</i> , <b>2013</b> , 5, 367-77  | 4.4  | 63 |
| 46 | Genome-wide association study of antipsychotic-induced QTc interval prolongation. <i>Pharmacogenomics Journal</i> , <b>2012</b> , 12, 165-72  | 3.5  | 61 |
| 45 | (1)H nuclear magnetic resonance metabolomics analysis identifies novel urinary biomarkers for lung function. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 3083-90   | 5.6  | 55 |
| 44 | Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. <i>Psychological Medicine</i> , <b>2012</b> , 42, 1151-62   | 6.9  | 51 |
| 43 | The dopamine D4 receptor and the hyperactivity phenotype: a developmental-epidemiological study. <i>Molecular Psychiatry</i> , <b>2002</b> , 7, 383-91  | 15.1 | 47 |
| 42 | The role of epigenomics in personalized medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , <b>2017</b> , 2, 33-45  | 1.6  | 42 |
| 41 | Review and Consensus on Pharmacogenomic Testing in Psychiatry. <i>Pharmacopsychiatry</i> , <b>2021</b> , 54, 5-17   | 2    | 40 |
| 40 | 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> , <b>2012</b> , 679, 75-80                   | 5.3  | 36 |
| 39 | Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. <i>Translational Psychiatry</i> , <b>2012</b> , 2, e129   | 8.6  | 34 |
| 38 | A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. <i>Schizophrenia Research</i> , <b>2009</b> , 107, 13-21   | 3.6  | 34 |
| 37 | Large-scale neurochemical metabolomics analysis identifies multiple compounds associated with methamphetamine exposure. <i>Metabolomics</i> , <b>2013</b> , 9, 392-402  | 4.7  | 33 |
| 36 | Genome-wide association study of patient-rated and clinician-rated global impression of severity during antipsychotic treatment. <i>Pharmacogenetics and Genomics</i> , <b>2013</b> , 23, 69-77                                     | 1.9  | 33 |
| 35 | 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> , <b>2012</b> , 135, 200-1 | 3.6  | 28 |
| 34 | The influence of five monoamine genes on trajectories of depressive symptoms across adolescence and young adulthood. <i>Development and Psychopathology</i> , <b>2012</b> , 24, 267-85  | 4.3  | 25 |
| 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. <i>Molecular Psychiatry</i> , <b>2007</b> , 12, 842-53   | 15.1 | 25 |
| 32 | Catechol-O-methyltransferase and the clinical features of psychosis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , <b>2006</b> , 141B, 935-8  | 3.5  | 25 |
| 31 | Building a schizophrenia genetic network: transcription factor 4 regulates genes involved in neuronal development and schizophrenia risk. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 3246-3256                             | 5.6  | 20 |
| 30 | Estimation of CpG coverage in whole methylome next-generation sequencing studies. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 50  | 3.6  | 19 |

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|----|---|-----|----|
| 29 | 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. <i>Human Molecular Genetics</i> , <b>2000</b> , 9, 2993-9 | 5.6 | 19 |
| 28 | Effects of HIV-1 Tat and Methamphetamine on Blood-Brain Barrier Integrity and Function. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2017</b> , 61,  | 5.9 | 18 |
| 27 | Genome-wide and gene-based association studies of anxiety disorders in European and African American samples. <i>PLoS ONE</i> , <b>2014</b> , 9, e112559  | 3.7 | 18 |
| 26 | Neurochemical Metabolomics Reveals Disruption to Sphingolipid Metabolism Following Chronic Haloperidol Administration. <i>Journal of NeuroImmune Pharmacology</i> , <b>2015</b> , 10, 425-34  | 6.9 | 17 |
| 25 | A genomewide association study of citalopram response in major depressive disorder-a psychometric approach. <i>Biological Psychiatry</i> , <b>2010</b> , 68, e25-7  | 7.9 | 17 |
| 24 | Refinement of schizophrenia GWAS loci using methylome-wide association data. <i>Human Genetics</i> , <b>2015</b> , 134, 77-87   | 6.3 | 16 |
| 23 | Behavioral metabolomics analysis identifies novel neurochemical signatures in methamphetamine sensitization. <i>Genes, Brain and Behavior</i> , <b>2013</b> , 12, 780-91  | 3.6 | 16 |
| 22 | High-throughput single-nucleotide polymorphism genotyping by fluorescent competitive allele-specific polymerase chain reaction (SNIPTag). <i>Analytical Biochemistry</i> , <b>2002</b> , 301, 200-6   | 3.1 | 16 |
| 21 | 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> , <b>2020</b> , 42, 819-832   | 8.9 | 13 |
| 20 | Combined Whole Methylome and Genomewide Association Study Implicates CNTN4 in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2015</b> , 39, 1396-405   | 3.7 | 13 |
| 19 | Estimating the posterior probability that genome-wide association findings are true or false. <i>Bioinformatics</i> , <b>2009</b> , 25, 1807-13   | 7.2 | 11 |
| 18 | Genes, environments, and developmental research: methods for a multi-site study of early substance abuse. <i>Twin Research and Human Genetics</i> , <b>2013</b> , 16, 505-15  | 2.2 | 10 |
| 17 | Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. <i>Nicotine and Tobacco Research</i> , <b>2016</b> , 18, 626-31  | 4.9 | 9  |
| 16 | Initial characterization of behavior and ketamine response in a mouse knockout of the post-synaptic effector gene Anks1b. <i>Neuroscience Letters</i> , <b>2017</b> , 641, 26-32  | 3.3 | 9  |
| 15 | 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> , <b>2020</b> , 80, 52-59   | 4.4 | 9  |
| 14 | In silico whole genome association scan for murine prepulse inhibition. <i>PLoS ONE</i> , <b>2009</b> , 4, e5246  | 3.7 | 9  |
| 13 | Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , <b>2017</b> , 41, 711-718   | 3.7 | 8  |
| 12 | The role of molecular genetics in the postgenomic era. <b>2003</b> , 19-40  |     | 7  |

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|----|---|------|---|
| 11 | 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> , <b>2019</b> , 712, 134475 | 3.3  | 6 |
| 10 | Genotype-based ancestral background consistently predicts efficacy and side effects across treatments in CATIE and STAR*D. <i>PLoS ONE</i> , <b>2013</b> , 8, e55239  | 3.7  | 6 |
| 9  | Variance component analysis of polymorphic metabolic systems. <i>Journal of Theoretical Biology</i> , <b>2006</b> , 240, 149-59   | 2.3  | 5 |
| 8  | Chasing behaviour genes into the next millennium. <i>Trends in Biotechnology</i> , <b>2000</b> , 18, 22-6   | 15.1 | 5 |
| 7  | Genetics and diagnostic refinement. <i>Behavior Genetics</i> , <b>2007</b> , 37, 535-45   | 3.2  | 4 |
| 6  | The gene and its associated phenotypes: focus on CNS drug response. <i>Pharmacogenomics</i> , <b>2019</b> , 20, 669-684   | 3.2  | 3 |
| 5  | Epigenetic histone acetylation and Bdnf dysregulation in the hippocampus of rats exposed to repeated, low-dose diisopropylfluorophosphate. <i>Life Sciences</i> , <b>2021</b> , 281, 119765   | 6.8  | 2 |
| 4  | Epigenetic biomarkers in personalized medicine <b>2019</b> , 375-395  |      | 1 |
| 3  | Institutional Profile: The Center for Biomarker Research and Personalized Medicine at Virginia Commonwealth University: advancing psychiatric drug treatment. <i>Personalized Medicine</i> , <b>2012</b> , 9, 479-483                             | 2.2  | 1 |
| 2  | Histone acetylation at the sulfotransferase 1a1 gene is associated with its hepatic expression in normal aging. <i>Pharmacogenetics and Genomics</i> , <b>2021</b> , 31, 207-214  | 1.9  | 0 |
| 1  | Epigenetic regulation of drug metabolism in aging. <i>Aging</i> , <b>2021</b> , 13, 16898-16899   | 5.6  |   |