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List of Publications by Year in Descending Order

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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	Review and Consensus on Pharmacogenomic Testing in Psychiatry. <i>Pharmacopsychiatry</i> , 2021 , 54, 5-17	2	40
63	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	1.9	0
62	Epigenetic regulation of drug metabolism in aging. <i>Aging</i> , 2021 , 13, 16898-16899	5.6	
61	Epigenetic histone acetylation and Bdnf dysregulation in the hippocampus of rats exposed to repeated, low-dose diisopropylfluorophosphate. <i>Life Sciences</i> , 2021 , 281, 119765	6.8	2
60	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	8.9	13
59	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	4.4	9
58	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	3.3	6
57	The gene and its associated phenotypes: focus on CNS drug response. <i>Pharmacogenomics</i> , 2019 , 20, 669-684	6.8	3
56	Epigenetic biomarkers in personalized medicine 2019 , 375-395		1
55	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	5.6	20
54	Initial characterization of behavior and ketamine response in a mouse knockout of the post-synaptic effector gene Anks1b. <i>Neuroscience Letters</i> , 2017 , 641, 26-32	3.3	9
53	The role of epigenomics in personalized medicine. <i>Expert Review of Precision Medicine and Drug Development</i> , 2017 , 2, 33-45	1.6	42
52	Deep Sequencing of 71 Candidate Genes to Characterize Variation Associated with Alcohol Dependence. <i>Alcoholism: Clinical and Experimental Research</i> , 2017 , 41, 711-718	3.7	8
51	Effects of HIV-1 Tat and Methamphetamine on Blood-Brain Barrier Integrity and Function. <i>Antimicrobial Agents and Chemotherapy</i> , 2017 , 61,	5.9	18
50	Deep Sequencing of Three Loci Implicated in Large-Scale Genome-Wide Association Study Smoking Meta-Analyses. <i>Nicotine and Tobacco Research</i> , 2016 , 18, 626-31	4.9	9
49	Neurochemical Metabolomics Reveals Disruption to Sphingolipid Metabolism Following Chronic Haloperidol Administration. <i>Journal of NeuroImmune Pharmacology</i> , 2015 , 10, 425-34	6.9	17
48	Combined Whole Methylome and Genomewide Association Study Implicates CNTN4 in Alcohol Use. <i>Alcoholism: Clinical and Experimental Research</i> , 2015 , 39, 1396-405	3.7	13

47	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	18.3	86
46	Refinement of schizophrenia GWAS loci using methylome-wide association data. <i>Human Genetics</i> , 2015 , 134, 77-87	6.3	16
45	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, 1175-85	5.6	122
44	Methylome-wide association study of schizophrenia: identifying blood biomarker signatures of environmental insults. <i>JAMA Psychiatry</i> , 2014 , 71, 255-64	14.5	172
43	Genome-wide and gene-based association studies of anxiety disorders in European and African American samples. <i>PLoS ONE</i> , 2014 , 9, e112559	3.7	18
42	Estimation of CpG coverage in whole methylome next-generation sequencing studies. <i>BMC Bioinformatics</i> , 2013 , 14, 50	3.6	19
41	Large-scale neurochemical metabolomics analysis identifies multiple compounds associated with methamphetamine exposure. <i>Metabolomics</i> , 2013 , 9, 392-402	4.7	33
40	Genes, environments, and developmental research: methods for a multi-site study of early substance abuse. <i>Twin Research and Human Genetics</i> , 2013 , 16, 505-15	2.2	10
39	A comprehensive family-based replication study of schizophrenia genes. <i>JAMA Psychiatry</i> , 2013 , 70, 573-81	11.5	115
38	Testing two models describing how methylome-wide studies in blood are informative for psychiatric conditions. <i>Epigenomics</i> , 2013 , 5, 367-77	4.4	63
37	Behavioral metabolomics analysis identifies novel neurochemical signatures in methamphetamine sensitization. <i>Genes, Brain and Behavior</i> , 2013 , 12, 780-91	3.6	16
36	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	1.9	33
35	Genotype-based ancestral background consistently predicts efficacy and side effects across treatments in CATIE and STAR*D. <i>PLoS ONE</i> , 2013 , 8, e55239	3.7	6
34	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	5.3	36
33	MBD-seq as a cost-effective approach for methylome-wide association studies: demonstration in 1500 case-control samples. <i>Epigenomics</i> , 2012 , 4, 605-21	4.4	79
32	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, 200-1	3.6	28
31	Genome-wide pharmacogenomic study of citalopram-induced side effects in STAR*D. <i>Translational Psychiatry</i> , 2012 , 2, e129	8.6	34
30	Genome-wide association study of antipsychotic-induced QTc interval prolongation. <i>Pharmacogenomics Journal</i> , 2012 , 12, 165-72	3.5	61

29	The influence of five monoamine genes on trajectories of depressive symptoms across adolescence and young adulthood. <i>Development and Psychopathology</i> , 2012 , 24, 267-85	4.3	25
28	Pharmacogenomic study of side-effects for antidepressant treatment options in STAR*D. <i>Psychological Medicine</i> , 2012 , 42, 1151-62	6.9	51
27	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 ²	3.2	1
26	Genome-wide pharmacogenomic analysis of response to treatment with antipsychotics. <i>Molecular Psychiatry</i> , 2011 , 16, 76-85	15.1	124
25	Genomewide pharmacogenomic study of metabolic side effects to antipsychotic drugs. <i>Molecular Psychiatry</i> , 2011 , 16, 321-32	15.1	123
24	Genome-wide pharmacogenomic study of neurocognition as an indicator of antipsychotic treatment response in schizophrenia. <i>Neuropsychopharmacology</i> , 2011 , 36, 616-26	8.7	87
23	Genomewide association study of movement-related adverse antipsychotic effects. <i>Biological Psychiatry</i> , 2010 , 67, 279-82	7.9	107
22	A genomewide association study of citalopram response in major depressive disorder-a psychometric approach. <i>Biological Psychiatry</i> , 2010 , 68, e25-7	7.9	17
21	MicroRNA expression profiling in the prefrontal cortex of individuals affected with schizophrenia and bipolar disorders. <i>Schizophrenia Research</i> , 2010 , 124, 183-91	3.6	225
20	(1)H nuclear magnetic resonance metabolomics analysis identifies novel urinary biomarkers for lung function. <i>Journal of Proteome Research</i> , 2010 , 9, 3083-90	5.6	55
19	In silico whole genome association scan for murine prepulse inhibition. <i>PLoS ONE</i> , 2009 , 4, e5246	3.7	9
18	Estimating the posterior probability that genome-wide association findings are true or false. <i>Bioinformatics</i> , 2009 , 25, 1807-13	7.2	11
17	A systematic method for estimating individual responses to treatment with antipsychotics in CATIE. <i>Schizophrenia Research</i> , 2009 , 107, 13-21	3.6	34
16	AKT1 is associated with schizophrenia across multiple symptom dimensions in the Irish study of high density schizophrenia families. <i>Biological Psychiatry</i> , 2008 , 63, 449-57	7.9	131
15	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, 842-53	15.1	25
14	Genetics and diagnostic refinement. <i>Behavior Genetics</i> , 2007 , 37, 535-45	3.2	4
13	Variance component analysis of polymorphic metabolic systems. <i>Journal of Theoretical Biology</i> , 2006 , 240, 149-59	2.3	5
12	Catechol-O-methyltransferase and the clinical features of psychosis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2006 , 141B, 935-8	3.5	25

11	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> , 2005 , 57, 1117-27	7.9	1020
10	Association analysis of MAOA and COMT with neuroticism assessed by peers. <i>American Journal of Medical Genetics Part A</i> , 2003 , 120B, 90-6		96
9	Influence of life stress on depression: moderation by a polymorphism in the 5-HTT gene. <i>Science</i> , 2003 , 301, 386-9	33.3	6113
8	The role of molecular genetics in the postgenomic era. 2003 , 19-40		7
7	High-throughput single-nucleotide polymorphism genotyping by fluorescent competitive allele-specific polymerase chain reaction (SNiPTag). <i>Analytical Biochemistry</i> , 2002 , 301, 200-6	3.1	16
6	The dopamine D4 receptor and the hyperactivity phenotype: a developmental-epidemiological study. <i>Molecular Psychiatry</i> , 2002 , 7, 383-91	15.1	47
5	Role of genotype in the cycle of violence in maltreated children. <i>Science</i> , 2002 , 297, 851-4	33.3	3452
4	Chasing behaviour genes into the next millennium. <i>Trends in Biotechnology</i> , 2000 , 18, 22-6	15.1	5
3	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> , 2000 , 9, 2993-9	5.6	19
2	The DNA sequence of human chromosome 22. <i>Nature</i> , 1999 , 402, 489-95	50.4	917
1	A 12-cistron Escherichia coli operon (hyf) encoding a putative proton-translocating formate hydrogenlyase system. <i>Microbiology (United Kingdom)</i> , 1997 , 143 (Pt 11), 3633-3647	2.9	223