Brien P Riley

List of Publications by Year
in descending order

39 papers	5,419 citations	361413 20 h-index	302126 39 g-index
47 all docs	47 docs citations	47 times ranked	9168 citing authors

#	Article	IF	Citations
1	Sex-Dependent Shared and Nonshared Genetic Architecture Across Mood and Psychotic Disorders. Biological Psychiatry, 2022, 91, 102-117.	1.3	61
2	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	27.8	929
3	A serotonergic biobehavioral signature differentiates cocaine use disorder participants administered mirtazapine. Translational Psychiatry, 2022, 12, 187.	4.8	1
4	Large-scale integration of DNA methylation and gene expression array platforms identifies both cis and trans relationships. Epigenetics, 2022, 17, 1753-1773.	2.7	2
5	Increasing the resolution and precision of psychiatric genomeâ€wide association studies by reâ€imputing summary statistics using a large, diverse reference panel. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2021, 186, 16-27.	1.7	4
6	DECO: a framework for jointly analyzing de novo and rare case/control variants, and biological pathways. Briefings in Bioinformatics, 2021, 22, .	6.5	6
7	Recruiting for diversity: a pilot test of recruitment strategies for a national alcohol survey with mail-in genetic data collection. Journal of Community Genetics, 2021, 12, 459-468.	1.2	4
8	Assessing the Role of Long Noncoding RNA in Nucleus Accumbens in Subjects With Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2020, 44, 2468-2480.	2.4	12
9	<scp>TWAS</scp> pathway method greatly enhances the number of leads for uncovering the molecular underpinnings of psychiatric disorders. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2020, 183, 454-463.	1.7	16
10	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. Nature Communications, 2020, 11, 2929.	12.8	10
11	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. Molecular Psychiatry, 2020, 25, 1673-1687.	7.9	82
12	Cross-species alcohol dependence-associated gene networks: Co-analysis of mouse brain gene expression and human genome-wide association data. PLoS ONE, 2019, 14, e0202063.	2.5	14
13	Populationâ€based identityâ€byâ€descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 223-231.	1.7	2
14	Polygenic Risk Score Prediction of Alcohol Dependence Symptoms Across Populationâ€Based and Clinically Ascertained Samples. Alcoholism: Clinical and Experimental Research, 2018, 42, 520-530.	2.4	25
15	Cross-species molecular dissection across alcohol behavioral domains. Alcohol, 2018, 72, 19-31.	1.7	12
16	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
17	Polygenic prediction of the phenome, across ancestry, in emerging adulthood. Psychological Medicine, 2018, 48, 1814-1823.	4.5	29
18	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	14.8	490

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19	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
20	Dimensionality and Genetic Correlates of Problem Behavior in Low-Income African American Adolescents. Journal of Clinical Child and Adolescent Psychology, 2017, 46, 824-839.	3.4	5
21	Genomewide Association Study of Alcohol Dependence Identifies Risk Loci Altering Ethanolâ€Response Behaviors in Model Organisms. Alcoholism: Clinical and Experimental Research, 2017, 41, 911-928.	2.4	43
22	The Genetic Architecture of Major Depressive Disorder in Han Chinese Women. JAMA Psychiatry, 2017, 74, 162.	11.0	82
23	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	21.4	838
24	Molecular Genetic Influences on Normative and Problematic Alcohol Use in a Population-Based Sample of College Students. Frontiers in Genetics, 2017, 8, 30.	2.3	24
25	JEPEGMIX: gene-level joint analysis of functional SNPs in cosmopolitan cohorts. Bioinformatics, 2016, 32, 295-297.	4.1	8
26	A simple yet accurate correction for winner's curse can predict signals discovered in much larger genome scans. Bioinformatics, 2016, 32, 2598-2603.	4.1	44
27	Meta-analysis of Positive and Negative Symptoms Reveals Schizophrenia Modifier Genes: Table 1.. Schizophrenia Bulletin, 2016, 42, 279-287.	4.3	40
28	DISTMIX: direct imputation of summary statistics for unmeasured SNPs from mixed ethnicity cohorts. Bioinformatics, 2015, 31, 3099-3104.	4.1	25
29	SWI/SNF chromatin remodeling regulates alcohol response behaviors in Caenorhabditis elegans and is associated with alcohol dependence in humans. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3032-3037.	7.1	28
30	Genome-wide gene pathway analysis of psychotic illness symptom dimensions based on a new schizophrenia-specific model of the OPCRIT. Schizophrenia Research, 2015, 164, 181-186.	2.0	19
31	JEPEG: a summary statistics based tool for gene-level joint testing of functional variants. Bioinformatics, 2015, 31, 1176-1182.	4.1	27
32	Integrating mRNA and miRNA Weighted Gene Co-Expression Networks with eQTLs in the Nucleus Accumbens of Subjects with Alcohol Dependence. PLoS ONE, 2015, 10, e0137671.	2.5	71
33	An inherited duplication at the gene p21 Protein-Activated Kinase 7 (PAK7) is a risk factor for psychosis. Human Molecular Genetics, 2014, 23, 3316-3326.	2.9	37
34	No evidence that runs of homozygosity are associated with schizophrenia in an Irish genome-wide association dataset. Schizophrenia Research, 2014, 154, 79-82.	2.0	18
35	Molecular Validation of the Schizophrenia Spectrum. Schizophrenia Bulletin, 2014, 40, 60-65.	4.3	41
36	Limited Associations of Dopamine System Genes With Alcohol Dependence and Related Traits in the Irish Affected Sib Pair Study of Alcohol Dependence (IASPSAD). Alcoholism: Clinical and Experimental Research, 2011, 35, 376-385.	2.4	38

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37	No association of dysbindin with symptom factors of schizophrenia in an Irish caseâ€“control sample. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 700-705.	1.7	5
38	Commentary on â€˜The case for geneâ€“environment interactions in psychiatryâ€™. Current Opinion in Psychiatry, 2008, 21, 324-325.	6.3	8
39	Identification of Susceptibility Loci for Alcohol-Related Traits in the Irish Affected Sib Pair Study of Alcohol Dependence. Alcoholism: Clinical and Experimental Research, 2006, 30, 1807-1816.	2.4	46