

# Julien Bryois

## List of Publications by Year in descending order

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Version: 2024-02-01

34  
papers

12,436  
citations

186209

28  
h-index

377752

34  
g-index

47  
all docs

47  
docs citations

47  
times ranked

17148  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. <i>Nature</i> , 2022, 604, 502-508.	13.7	929
2	Shared genetic risk between eating disorder and substance use related phenotypes: Evidence from genome-wide association studies. <i>Addiction Biology</i> , 2021, 26, e12880.	1.4	28
3	Genome-wide association study of more than 40,000 bipolar disorder cases provides new insights into the underlying biology. <i>Nature Genetics</i> , 2021, 53, 817-829.	9.4	629
4	Conditional GWAS analysis to identify disorder-specific SNPs for psychiatric disorders. <i>Molecular Psychiatry</i> , 2021, 26, 2070-2081.	4.1	48
5	Examination of the shared genetic basis of anorexia nervosa and obsessive compulsive disorder. <i>Molecular Psychiatry</i> , 2020, 25, 2036-2046.	4.1	83
6	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
7	Reproducible Genetic Risk Loci for Anxiety: Results From 1/4200,000 Participants in the Million Veteran Program. <i>American Journal of Psychiatry</i> , 2020, 177, 223-232.	4.0	185
8	Genetic identification of cell types underlying brain complex traits yields insights into the etiology of Parkinson's disease. <i>Nature Genetics</i> , 2020, 52, 482-493.	9.4	216
9	Increased burden of ultra-rare structural variants localizing to boundaries of topologically associated domains in schizophrenia. <i>Nature Communications</i> , 2020, 11, 1842.	5.8	56
10	Genome-wide association study identifies eight risk loci and implicates metabo-psychiatric origins for anorexia nervosa. <i>Nature Genetics</i> , 2019, 51, 1207-1214.	9.4	641
11	Single cell analysis of autism patient with bi-allelic NRXN1-alpha deletion reveals skewed fate choice in neural progenitors and impaired neuronal functionality. <i>Experimental Cell Research</i> , 2019, 383, 111469.	1.2	39
12	Genome-wide association study of post-traumatic stress disorder reexperiencing symptoms in >165,000 US veterans. <i>Nature Neuroscience</i> , 2019, 22, 1394-1401.	7.1	145
13	Obesity remodels activity and transcriptional state of a lateral hypothalamic brake on feeding. <i>Science</i> , 2019, 364, 1271-1274.	6.0	113
14	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. <i>Nature Genetics</i> , 2019, 51, 394-403.	9.4	593
15	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019, 51, 1670-1678.	9.4	440
16	Genome-wide analysis identifies molecular systems and 149 genetic loci associated with income. <i>Nature Communications</i> , 2019, 10, 5741.	5.8	110
17	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. <i>Nature Genetics</i> , 2019, 51, 404-413.	9.4	1,625
18	Biological annotation of genetic loci associated with intelligence in a meta-analysis of 87,740 individuals. <i>Molecular Psychiatry</i> , 2019, 24, 182-197.	4.1	47

#	ARTICLE	IF	CITATIONS
19	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
20	Comprehensive functional genomic resource and integrative model for the human brain. <i>Science</i> , 2018, 362, .	6.0	618
21	Genetic identification of brain cell types underlying schizophrenia. <i>Nature Genetics</i> , 2018, 50, 825-833.	9.4	497
22	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. <i>Nature Genetics</i> , 2018, 50, 920-927.	9.4	564
23	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. <i>Nature Genetics</i> , 2018, 50, 912-919.	9.4	893
24	Evaluation of chromatin accessibility in prefrontal cortex of individuals with schizophrenia. <i>Nature Communications</i> , 2018, 9, 3121.	5.8	141
25	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.	1.4	33
26	Time-dependent genetic effects on gene expression implicate aging processes. <i>Genome Research</i> , 2017, 27, 545-552.	2.4	31
27	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	3.6	86
28	Tissue-Specific Effects of Genetic and Epigenetic Variation on Gene Regulation and Splicing. <i>PLoS Genetics</i> , 2015, 11, e1004958.	1.5	185
29	Cis and Trans Effects of Human Genomic Variants on Gene Expression. <i>PLoS Genetics</i> , 2014, 10, e1004461.	1.5	117
30	Whole Exome Sequencing of a Dominant Retinitis Pigmentosa Family Identifies a Novel Deletion in <i>PRPF31</i> . , 2014, 55, 2121.		26
31	Coordinated Effects of Sequence Variation on DNA Binding, Chromatin Structure, and Transcription. <i>Science</i> , 2013, 342, 744-747.	6.0	364
32	Passive and active DNA methylation and the interplay with genetic variation in gene regulation. <i>ELife</i> , 2013, 2, e00523.	2.8	374
33	Automated protein-DNA interaction screening of <i>Drosophila</i> regulatory elements. <i>Nature Methods</i> , 2011, 8, 1065-1070.	9.0	76
34	Correction: Passive and active DNA methylation and the interplay with genetic variation in gene regulation. <i>ELife</i> , 0, 2, .	2.8	15