

# Shaun M Purcell

## List of Publications by Year in descending order

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Version: 2024-02-01

78  
papers

73,307  
citations

50276  
46  
h-index

71685  
76  
g-index

95  
all docs

95  
docs citations

95  
times ranked

92421  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sleep and circadian informatics data harmonization: a workshop report from the Sleep Research Society and Sleep Research Network. <i>Sleep</i> , 2022, 45, .	1.1	8
2	Impact of chronic sleep restriction on sleep continuity, sleep structure, and neurobehavioral performance. <i>Sleep</i> , 2022, 45, .	1.1	4
3	Non-rapid eye movement sleep and wake neurophysiology in schizophrenia. <i>ELife</i> , 2022, 11, .	6.0	9
4	0194 Sources of variation in the spectral slope of the sleep EEG. <i>Sleep</i> , 2022, 45, A89-A89.	1.1	0
5	0285 Excessive daytime sleepiness with long sleep duration increases myocardial infarction risk. <i>Sleep</i> , 2022, 45, A129-A129.	1.1	0
6	Spectral sleep electroencephalographic correlates of sleep efficiency, and discrepancies between actigraphy and self-reported measures, in older men. <i>Journal of Sleep Research</i> , 2021, 30, e13033.	3.2	3
7	Macro and micro sleep architecture and cognitive performance in older adults. <i>Nature Human Behaviour</i> , 2021, 5, 123-145.	12.0	75
8	Sleep and Big Data: harnessing data, technology, and analytics for monitoring sleep and improving diagnostics, prediction, and interventions—an era for Sleep-Omics?. <i>Sleep</i> , 2021, 44, .	1.1	10
9	250 AI-Supported Sleep Staging from Activity and Heart Rate. <i>Sleep</i> , 2021, 44, A101-A101.	1.1	0
10	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. <i>Genome Medicine</i> , 2021, 13, 136.	8.2	16
11	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	7.9	15
12	Linking Sleep and Racial Health Disparities: Characterizing Sleep in the National Sleep Research Resource. <i>Innovation in Aging</i> , 2021, 5, 627-627.	0.1	0
13	Characterization of Single Gene Copy Number Variants in Schizophrenia. <i>Biological Psychiatry</i> , 2020, 87, 736-744.	1.3	10
14	Sex differences in obstructive sleep apnea phenotypes, the multi-ethnic study of atherosclerosis. <i>Sleep</i> , 2020, 43, .	1.1	87
15	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. <i>Nature Communications</i> , 2020, 11, 2929.	12.8	10
16	Statistical Power and the Classical Twin Design. <i>Twin Research and Human Genetics</i> , 2020, 23, 87-89.	0.6	8
17	Effects of a patient-derived de novo coding alteration of CACNA1I in mice connect a schizophrenia risk gene with sleep spindle deficits. <i>Translational Psychiatry</i> , 2020, 10, 29.	4.8	25
18	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. <i>American Journal of Human Genetics</i> , 2019, 105, 1057-1068.	6.2	10

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19	Epigenome-wide association analysis of daytime sleepiness in the Multi-Ethnic Study of Atherosclerosis reveals African-American-specific associations. <i>Sleep</i> , 2019, 42, .	1.1	27
20	Associations of variants in the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. <i>PLoS Genetics</i> , 2019, 15, e1007739.	3.5	28
21	Genome-wide association study identifies 30 loci associated with bipolar disorder. <i>Nature Genetics</i> , 2019, 51, 793-803.	21.4	1,191
22	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. <i>Nature Communications</i> , 2019, 10, 1100.	12.8	369
23	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. <i>Nature Genetics</i> , 2019, 51, 659-674.	21.4	154
24	Population-based identity-by-descent mapping combined with exome sequencing to detect rare risk variants for schizophrenia. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 223-231.	1.7	2
25	Biological and clinical insights from genetics of insomnia symptoms. <i>Nature Genetics</i> , 2019, 51, 387-393.	21.4	250
26	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. <i>Human Molecular Genetics</i> , 2019, 28, 675-687.	2.9	41
27	Contribution of Rare Copy Number Variants to Bipolar Disorder Risk Is Limited to Schizoaffective Cases. <i>Biological Psychiatry</i> , 2019, 86, 110-119.	1.3	45
28	Evaluation of an automated pipeline for large-scale EEG spectral analysis: the National Sleep Research Resource. <i>Sleep Medicine</i> , 2018, 47, 126-136.	1.6	7
29	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
30	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. <i>American Journal of Human Genetics</i> , 2018, 102, 1169-1184.	6.2	128
31	Statistics for X-chromosome associations. <i>Genetic Epidemiology</i> , 2018, 42, 539-550.	1.3	16
32	The Genetics of Endophenotypes of Neurofunction to Understand Schizophrenia (GENUS) consortium: A collaborative cognitive and neuroimaging genetics project. <i>Schizophrenia Research</i> , 2018, 195, 306-317.	2.0	17
33	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
34	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	1.3	84
35	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. <i>Nature Genetics</i> , 2017, 49, 274-281.	21.4	280
36	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. <i>Cell Reports</i> , 2017, 21, 679-691.	6.4	79

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37	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.	21.4	838
38	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
39	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. <i>Genome Medicine</i> , 2017, 9, 114.	8.2	86
40	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
41	GENOME-WIDE ASSOCIATION STUDY (GWAS) AND GENOME-WIDE BY ENVIRONMENT INTERACTION STUDY (GWEIS) OF DEPRESSIVE SYMPTOMS IN AFRICAN AMERICAN AND HISPANIC/LATINA WOMEN. <i>Depression and Anxiety</i> , 2016, 33, 265-280.	4.1	99
42	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	11.0	97
43	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	14.8	952
44	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1433-1441.	14.8	427
45	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	14.8	90
46	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	27.8	9,051
47	Patterns of genic intolerance of rare copy number variation in 59,898 human exomes. <i>Nature Genetics</i> , 2016, 48, 1107-1111.	21.4	167
48	Quantifying prior disease penetrance using large population control cohorts. <i>Science Translational Medicine</i> , 2016, 8, 322ra9.	12.4	289
49	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. <i>Lancet Psychiatry</i> , 2016, 3, 350-357.	7.4	107
50	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. <i>Nature Neuroscience</i> , 2016, 19, 571-577.	14.8	388
51	Reduced Sleep Spindles in Schizophrenia: A Treatable Endophenotype That Links Risk Genes to Impaired Cognition?. <i>Biological Psychiatry</i> , 2016, 80, 599-608.	1.3	171
52	Second-generation PLINK: rising to the challenge of larger and richer datasets. <i>GigaScience</i> , 2015, 4, 7.	6.4	8,062
53	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. <i>European Journal of Human Genetics</i> , 2015, 23, 555-557.	2.8	21
54	Effect of predicted protein-truncating genetic variants on the human transcriptome. <i>Science</i> , 2015, 348, 666-669.	12.6	252

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55	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	6.2	1,098
56	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	21.4	2,045
57	The relationship between sleep quality and neurocognition in bipolar disorder. Journal of Affective Disorders, 2015, 187, 156-162.	4.1	33
58	Genetic Association Analysis of 300 Genes Identifies a Risk Haplotype in SLC18A2 for Post-traumatic Stress Disorder in Two Independent Samples. Neuropsychopharmacology, 2014, 39, 1872-1879.	5.4	49
59	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	6.4	225
60	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	27.0	2,669
61	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	2.9	70
62	Genetic modifiers and subtypes in schizophrenia: Investigations of age at onset, severity, sex and family history. Schizophrenia Research, 2014, 154, 48-53.	2.0	68
63	Statistical power and significance testing in large-scale genetic studies. Nature Reviews Genetics, 2014, 15, 335-346.	16.3	484
64	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	27.8	1,510
65	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	27.8	1,305
66	Partitioning Heritability of Regulatory and Cell-Type-Specific Variants across 11 Common Diseases. American Journal of Human Genetics, 2014, 95, 535-552.	6.2	569
67	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	27.8	2,254
68	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	21.4	943
69	Common Variants on Xq28 Conferring Risk of Schizophrenia in Han Chinese. Schizophrenia Bulletin, 2014, 40, 777-786.	4.3	49
70	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	21.4	2,067
71	Antidepressant Response and Polygenes. Biological Psychiatry, 2013, 73, 600-601.	1.3	1
72	zCall: a rare variant caller for array-based genotyping. Bioinformatics, 2012, 28, 2543-2545.	4.1	195

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73	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	21.4	2,634
74	Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms and rare CNVs. Nature Genetics, 2008, 40, 1253-1260.	21.4	712
75	PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. American Journal of Human Genetics, 2007, 81, 559-575.	6.2	26,761
76	Environmental Mediation and The Twin Design. Behavior Genetics, 2005, 35, 491-498.	2.1	52
77	Pleiotropy in complex traits: challenges and strategies. , 0, .		1
78	Targeted Genome Sequencing Identifies Multiple Rare Variants in Caveolin-1 Associated with Obstructive Sleep Apnea. American Journal of Respiratory and Critical Care Medicine, 0, , .	5.6	5