Shaun M Purcell

List of Publications by Year
in descending order

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78 papers	73,307 citations	57681 46 h-index	81351 76 g-index
95 all docs	95 docs citations	95 times ranked	100710 citing authors

#	Article	IF	Citations
1	Sleep and circadian informatics data harmonization: a workshop report from the Sleep Research Society and Sleep Research Network. Sleep, 2022, 45, .	0.6	8
2	Impact of chronic sleep restriction on sleep continuity, sleep structure, and neurobehavioral performance. Sleep, 2022, 45, .	0.6	4
3	Non-rapid eye movement sleep and wake neurophysiology in schizophrenia. ELife, 2022, 11, .	2.8	9
4	0194 Sources of variation in the spectral slope of the sleep EEG. Sleep, 2022, 45, A89-A89.	0.6	0
5	0285 Excessive daytime sleepiness with long sleep duration increases myocardial infarction risk. Sleep, 2022, 45, A129-A129.	0.6	0
6	Spectral sleep electroencephalographic correlates of sleep efficiency, and discrepancies between actigraphy and selfâ€reported measures, in older men. Journal of Sleep Research, 2021, 30, e13033.	1.7	3
7	Macro and micro sleep architecture and cognitive performance in older adults. Nature Human Behaviour, 2021, 5, 123-145.	6.2	75
8	Sleep and Big Data: harnessing data, technology, and analytics for monitoring sleep and improving diagnostics, prediction, and interventionsâ€"an era for Sleep-Omics?. Sleep, 2021, 44, .	0.6	10
9	250 AI-Supported Sleep Staging from Activity and Heart Rate. Sleep, 2021, 44, A101-A101.	0.6	0
10	Whole-genome association analyses of sleep-disordered breathing phenotypes in the NHLBI TOPMed program. Genome Medicine, 2021, 13, 136.	3.6	16
11	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. Molecular Psychiatry, 2021, 26, 5239-5250.	4.1	15
12	Linking Sleep and Racial Health Disparities: Characterizing Sleep in the National Sleep Research Resource. Innovation in Aging, 2021, 5, 627-627.	0.0	0
13	Characterization of Single Gene Copy Number Variants in Schizophrenia. Biological Psychiatry, 2020, 87, 736-744.	0.7	10
14	Sex differences in obstructive sleep apnea phenotypes, the multi-ethnic study of atherosclerosis. Sleep, 2020, 43, .	0.6	87
15	mTADA is a framework for identifying risk genes from de novo mutations in multiple traits. Nature Communications, 2020, 11, 2929.	5.8	10
16	Statistical Power and the Classical Twin Design. Twin Research and Human Genetics, 2020, 23, 87-89.	0.3	8
17	Effects of a patient-derived de novo coding alteration of CACNA1I in mice connect a schizophrenia risk gene with sleep spindle deficits. Translational Psychiatry, 2020, 10, 29.	2.4	25
18	Sequencing Analysis at 8p23 Identifies Multiple Rare Variants in DLC1 Associated with Sleep-Related Oxyhemoglobin Saturation Level. American Journal of Human Genetics, 2019, 105, 1057-1068.	2.6	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. Sleep, 2019, 42, .	0.6	27
20	Associations of variants In the hexokinase 1 and interleukin 18 receptor regions with oxyhemoglobin saturation during sleep. PLoS Genetics, 2019, 15, e1007739.	1.5	28
21	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
22	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. Nature Communications, 2019, 10, 1100.	5.8	369
23	Gene expression imputation across multiple brain regions provides insights into schizophrenia risk. Nature Genetics, 2019, 51, 659-674.	9.4	154
24	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.	1.1	2
25	Biological and clinical insights from genetics of insomnia symptoms. Nature Genetics, 2019, 51, 387-393.	9.4	250
26	Admixture mapping identifies novel loci for obstructive sleep apnea in Hispanic/Latino Americans. Human Molecular Genetics, 2019, 28, 675-687.	1.4	41
27	Contribution of Rare Copy Number Variants toÂBipolar Disorder Risk Is Limited to Schizoaffective Cases. Biological Psychiatry, 2019, 86, 110-119.	0.7	45
28	Evaluation of an automated pipeline for large-scale EEG spectral analysis: the National Sleep Research Resource. Sleep Medicine, 2018, 47, 126-136.	0.8	7
29	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
30	Landscape of Conditional eQTL in Dorsolateral Prefrontal Cortex and Co-localization with Schizophrenia GWAS. American Journal of Human Genetics, 2018, 102, 1169-1184.	2.6	128
31	Statistics for Xâ€chromosome associations. Genetic Epidemiology, 2018, 42, 539-550.	0.6	16
32	The Genetics of Endophenotypes of Neurofunction to Understand Schizophrenia (GENUS) consortium: A collaborative cognitive and neuroimaging genetics project. Schizophrenia Research, 2018, 195, 306-317.	1.1	17
33	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
34	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. Biological Psychiatry, 2017, 82, 322-329.	0.7	84
35	Genome-wide association analyses of sleep disturbance traits identify new loci and highlight shared genetics with neuropsychiatric and metabolic traits. Nature Genetics, 2017, 49, 274-281.	9.4	280
36	Arc Requires PSD95 for Assembly into Postsynaptic Complexes Involved with Neural Dysfunction and Intelligence. Cell Reports, 2017, 21, 679-691.	2.9	79

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37	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. Nature Genetics, 2017, 49, 27-35.	9.4	838
38	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
39	Integrated Bayesian analysis of rare exonic variants to identify risk genes for schizophrenia and neurodevelopmental disorders. Genome Medicine, 2017, 9, 114.	3.6	86
40	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	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. Depression and Anxiety, 2016, 33, 265-280.	2.0	99
42	Exome Sequencing of Familial Bipolar Disorder. JAMA Psychiatry, 2016, 73, 590.	6.0	97
43	Gene expression elucidates functional impact of polygenic risk for schizophrenia. Nature Neuroscience, 2016, 19, 1442-1453.	7.1	952
44	Increased burden of ultra-rare protein-altering variants among 4,877 individuals with schizophrenia. Nature Neuroscience, 2016, 19, 1433-1441.	7.1	427
45	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. Nature Neuroscience, 2016, 19, 1563-1565.	7.1	90
46	Analysis of protein-coding genetic variation in 60,706 humans. Nature, 2016, 536, 285-291.	13.7	9,051
47	Patterns of genic intolerance of rare copy number variation in 59,898 human exomes. Nature Genetics, 2016, 48, 1107-1111.	9.4	167
48	Quantifying prion disease penetrance using large population control cohorts. Science Translational Medicine, 2016, 8, 322ra9.	5.8	289
49	Polygenic overlap between schizophrenia risk and antipsychotic response: a genomic medicine approach. Lancet Psychiatry,the, 2016, 3, 350-357.	3.7	107
50	Rare loss-of-function variants in SETD1A are associated with schizophrenia and developmental disorders. Nature Neuroscience, 2016, 19, 571-577.	7.1	388
51	Reduced Sleep Spindles in Schizophrenia: A Treatable Endophenotype That Links Risk Genes to Impaired Cognition?. Biological Psychiatry, 2016, 80, 599-608.	0.7	171
52	Second-generation PLINK: rising to the challenge of larger and richer datasets. GigaScience, 2015, 4, 7.	3.3	8,062
53	No evidence for rare recessive and compound heterozygous disruptive variants in schizophrenia. European Journal of Human Genetics, 2015, 23, 555-557.	1.4	21
54	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252

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55	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. American Journal of Human Genetics, 2015, 97, 576-592.	2.6	1,098
56	Partitioning heritability by functional annotation using genome-wide association summary statistics. Nature Genetics, 2015, 47, 1228-1235.	9.4	2,045
57	The relationship between sleep quality and neurocognition in bipolar disorder. Journal of Affective Disorders, 2015, 187, 156-162.	2.0	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.	2.8	49
59	A Role for Noncoding Variation in Schizophrenia. Cell Reports, 2014, 9, 1417-1429.	2.9	225
60	Clonal Hematopoiesis and Blood-Cancer Risk Inferred from Blood DNA Sequence. New England Journal of Medicine, 2014, 371, 2477-2487.	13.9	2,669
61	De novo CNVs in bipolar affective disorder and schizophrenia. Human Molecular Genetics, 2014, 23, 6677-6683.	1.4	70
62	Genetic modifiers and subtypes in schizophrenia: Investigations of age at onset, severity, sex and family history. Schizophrenia Research, 2014, 154, 48-53.	1.1	68
63	Statistical power and significance testing in large-scale genetic studies. Nature Reviews Genetics, 2014, 15, 335-346.	7.7	484
64	De novo mutations in schizophrenia implicate synaptic networks. Nature, 2014, 506, 179-184.	13.7	1,510
65	A polygenic burden of rare disruptive mutations in schizophrenia. Nature, 2014, 506, 185-190.	13.7	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.	2.6	569
67	Synaptic, transcriptional and chromatin genes disrupted in autism. Nature, 2014, 515, 209-215.	13.7	2,254
68	A framework for the interpretation of de novo mutation in human disease. Nature Genetics, 2014, 46, 944-950.	9.4	943
69	Common Variants on Xq28 Conferring Risk of Schizophrenia in Han Chinese. Schizophrenia Bulletin, 2014, 40, 777-786.	2.3	49
70	Genetic relationship between five psychiatric disorders estimated from genome-wide SNPs. Nature Genetics, 2013, 45, 984-994.	9.4	2,067
71	Antidepressant Response and Polygenes. Biological Psychiatry, 2013, 73, 600-601.	0.7	1
72	zCall: a rare variant caller for array-based genotyping. Bioinformatics, 2012, 28, 2543-2545.	1.8	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.	9.4	2,634
74	Integrated genotype calling and association analysis of SNPs, common copy number polymorphisms and rare CNVs. Nature Genetics, 2008, 40, 1253-1260.	9.4	712
75	PLINK: A Tool Set for Whole-Genome Association and Population-Based Linkage Analyses. American Journal of Human Genetics, 2007, 81, 559-575.	2.6	26,761
76	Environmental Mediation and The Twin Design. Behavior Genetics, 2005, 35, 491-498.	1.4	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, , .	2.5	5