

Sven Stringer

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8672635/publications.pdf>

Version: 2024-02-01

25
papers

6,762
citations

394421

19
h-index

552781

26
g-index

36
all docs

36
docs citations

36
times ranked

11823
citing authors

#	ARTICLE	IF	CITATIONS
1	Combined cellomics and proteomics analysis reveals shared neuronal morphology and molecular pathway phenotypes for multiple schizophrenia risk genes. <i>Molecular Psychiatry</i> , 2021, 26, 784-799.	7.9	22
2	Attention-deficit/hyperactivity disorder and lifetime cannabis use: genetic overlap and causality. <i>Molecular Psychiatry</i> , 2020, 25, 2493-2503.	7.9	59
3	A global overview of pleiotropy and genetic architecture in complex traits. <i>Nature Genetics</i> , 2019, 51, 1339-1348.	21.4	774
4	65GENOME-WIDE ANALYSIS OF INSOMNIA AND SLEEP-RELATED TRAITS IN OVER 1 MILLION INDIVIDUALS IDENTIFIES NOVEL GENES AND PATHWAYS. <i>European Neuropsychopharmacology</i> , 2019, 29, S1104-S1105.	0.7	0
5	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.	21.4	593
6	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. <i>Nature Genetics</i> , 2019, 51, 404-413.	21.4	1,625
7	A tutorial on conducting genome-wide association studies: Quality control and statistical analysis. <i>International Journal of Methods in Psychiatric Research</i> , 2018, 27, e1608.	2.1	465
8	Item-level analyses reveal genetic heterogeneity in neuroticism. <i>Nature Communications</i> , 2018, 9, 905.	12.8	181
9	MIR137 schizophrenia-associated locus controls synaptic function by regulating synaptogenesis, synapse maturation and synaptic transmission. <i>Human Molecular Genetics</i> , 2018, 27, 1879-1891.	2.9	58
10	Conditional and interaction gene-set analysis reveals novel functional pathways for blood pressure. <i>Nature Communications</i> , 2018, 9, 3768.	12.8	50
11	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.	21.4	564
12	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.	21.4	893
13	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. <i>Nature Neuroscience</i> , 2018, 21, 1161-1170.	14.8	436
14	Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. <i>Nature Genetics</i> , 2017, 49, 1107-1112.	21.4	425
15	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. <i>Nature Genetics</i> , 2017, 49, 1584-1592.	21.4	248
16	The International Cannabis Consortium: What Did We Learn About The Genetics Of Cannabis Use. <i>European Neuropsychopharmacology</i> , 2017, 27, S494-S495.	0.7	0
17	Majority of human traits do not show evidence for sex-specific genetic and environmental effects. <i>Scientific Reports</i> , 2017, 7, 8688.	3.3	21
18	Genetically-Informed Patient Selection for iPSC Studies of Complex Diseases May Aid in Reducing Cellular Heterogeneity. <i>Frontiers in Cellular Neuroscience</i> , 2017, 11, 164.	3.7	37

#	ARTICLE	IF	CITATIONS
19	Happiness, health, and mortality. <i>Lancet</i> , The, 2016, 388, 26.	13.7	0
20	What Cure Models Can Teach us About Genome-Wide Survival Analysis. <i>Behavior Genetics</i> , 2016, 46, 269-280.	2.1	5
21	A guide on gene prioritization in studies of psychiatric disorders. <i>International Journal of Methods in Psychiatric Research</i> , 2015, 24, 245-256.	2.1	6
22	Genetic liability for schizophrenia predicts risk of immune disorders. <i>Schizophrenia Research</i> , 2014, 159, 347-352.	2.0	40
23	A systems medicine research approach for studying alcohol addiction. <i>Addiction Biology</i> , 2013, 18, 883-896.	2.6	76
24	Assumptions and Properties of Limiting Pathway Models for Analysis of Epistasis in Complex Traits. <i>PLoS ONE</i> , 2013, 8, e68913.	2.5	11
25	Underestimated Effect Sizes in GWAS: Fundamental Limitations of Single SNP Analysis for Dichotomous Phenotypes. <i>PLoS ONE</i> , 2011, 6, e27964.	2.5	48