## Sven Stringer

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. Nature Genetics, 2019, 51, 404-413.	21.4	1,625
2	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	21.4	893
3	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	21.4	774
4	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403.	21.4	593
5	Meta-analysis of genome-wide association studies for neuroticism in 449,484 individuals identifies novel genetic loci and pathways. Nature Genetics, 2018, 50, 920-927.	21.4	564
6	A tutorial on conducting genomeâ€wide association studies: Quality control and statistical analysis. International Journal of Methods in Psychiatric Research, 2018, 27, e1608.	2.1	465
7	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal effect of schizophrenia liability. Nature Neuroscience, 2018, 21, 1161-1170.	14.8	436
8	Genome-wide association meta-analysis of 78,308 individuals identifies new loci and genes influencing human intelligence. Nature Genetics, 2017, 49, 1107-1112.	21.4	425
9	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	21.4	248
10	Item-level analyses reveal genetic heterogeneity in neuroticism. Nature Communications, 2018, 9, 905.	12.8	181
11	A systems medicine research approach for studying alcohol addiction. Addiction Biology, 2013, 18, 883-896.	2.6	76
12	Attention-deficit/hyperactivity disorder and lifetime cannabis use: genetic overlap and causality. Molecular Psychiatry, 2020, 25, 2493-2503.	7.9	59
13	MIR137 schizophrenia-associated locus controls synaptic function by regulating synaptogenesis, synapse maturation and synaptic transmission. Human Molecular Genetics, 2018, 27, 1879-1891.	2.9	58
14	Conditional and interaction gene-set analysis reveals novel functional pathways for blood pressure. Nature Communications, 2018, 9, 3768.	12.8	50
15	Underestimated Effect Sizes in GWAS: Fundamental Limitations of Single SNP Analysis for Dichotomous Phenotypes. PLoS ONE, 2011, 6, e27964.	2.5	48
16	Genetic liability for schizophrenia predicts risk of immune disorders. Schizophrenia Research, 2014, 159, 347-352.	2.0	40
17	Genetically-Informed Patient Selection for iPSC Studies of Complex Diseases May Aid in Reducing Cellular Heterogeneity. Frontiers in Cellular Neuroscience, 2017, 11, 164.	3.7	37
18	Combined cellomics and proteomics analysis reveals shared neuronal morphology and molecular pathway phenotypes for multiple schizophrenia risk genes. Molecular Psychiatry, 2021, 26, 784-799.	7.9	22

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19	Majority of human traits do not show evidence for sex-specific genetic and environmental effects. Scientific Reports, 2017, 7, 8688.	3.3	21
20	Assumptions and Properties of Limiting Pathway Models for Analysis of Epistasis in Complex Traits. PLoS ONE, 2013, 8, e68913.	2.5	11
21	A guide on gene prioritization in studies of psychiatric disorders. International Journal of Methods in Psychiatric Research, 2015, 24, 245-256.	2.1	6
22	What Cure Models Can Teach us About Genome-Wide Survival Analysis. Behavior Genetics, 2016, 46, 269-280.	2.1	5
23	Happiness, health, and mortality. Lancet, The, 2016, 388, 26.	13.7	0
24	The International Cannabis Consortium: What Did We Learn About The Genetics Of Cannabis Use. European Neuropsychopharmacology, 2017, 27, S494-S495.	0.7	0
25	65GENOME-WIDE ANALYSIS OF INSOMNIA AND SLEEP-RELATED TRAITS IN OVER 1 MILLION INDIVIDUALS IDENTIFIES NOVEL GENES AND PATHWAYS. European Neuropsychopharmacology, 2019, 29, S1104-S1105.	0.7	0