Raymond K Walters

List of Publications by Year
in descending order

27	19,731	293460 24	536525 29
papers	citations	h-index	g-index

41	41	41	33472
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Investigation of convergent and divergent genetic influences underlying schizophrenia and alcohol use disorder. Psychological Medicine, 2023, 53, 1196-1204.	2.7	7
2	The addiction risk factor: A unitary genetic vulnerability characterizes substance use disorders and their associations with common correlates. Neuropsychopharmacology, 2022, 47, 1739-1745.	2.8	50
3	The female protective effect against autism spectrum disorder. Cell Genomics, 2022, 2, 100134.	3.0	30
4	Shared genetic risk between eating disorderâ€•and substanceâ€•useâ€•related phenotypes: Evidence from genomeâ€•wide association studies. Addiction Biology, 2021, 26, e12880.	1.4	28
5	Risk variants and polygenic architecture of disruptive behavior disorders in the context of attention-deficit/hyperactivity disorder. Nature Communications, 2021, 12, 576.	5.8	28
6	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
7	Examining Sex-Differentiated Genetic Effects Across Neuropsychiatric and Behavioral Traits. Biological Psychiatry, 2021, 89, 1127-1137.	0.7	48
8	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2021, 597, E3-E4.	13.7	45
9	A large-scale genome-wide association study meta-analysis of cannabis use disorder. Lancet Psychiatry,the, 2020, 7, 1032-1045.	3.7	200
10	The mutational constraint spectrum quantified from variation in 141,456 humans. Nature, 2020, 581, 434-443.	13.7	6,140
11	Leveraging genome-wide data to investigate differences between opioid use vs. opioid dependence in 41,176 individuals from the Psychiatric Genomics Consortium. Molecular Psychiatry, 2020, 25, 1673-1687.	4.1	82
12	Large-Scale Exome Sequencing Study Implicates Both Developmental and Functional Changes in the Neurobiology of Autism. Cell, 2020, 180, 568-584.e23.	13.5	1,422
13	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	13.5	428
14	Genetic Markers of ADHD-Related Variations in Intracranial Volume. American Journal of Psychiatry, 2019, 176, 228-238.	4.0	68
15	Identification of common genetic risk variants for autism spectrum disorder. Nature Genetics, 2019, 51, 431-444.	9.4	1,538
16	Autism spectrum disorder and attention deficit hyperactivity disorder have a similar burden of rare protein-truncating variants. Nature Neuroscience, 2019, 22, 1961-1965.	7.1	148
17	Genomic Relationships, Novel Loci, and Pleiotropic Mechanisms across Eight Psychiatric Disorders. Cell, 2019, 179, 1469-1482.e11.	13.5	935
18	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	9.4	1,594

#	Article	IF	Citations
19	Multi-trait analysis of genome-wide association summary statistics using MTAG. Nature Genetics, 2018, 50, 229-237.	9.4	700
20	A Genetic Investigation of Sex Bias in the Prevalence of Attention-Deficit/Hyperactivity Disorder. Biological Psychiatry, 2018, 83, 1044-1053.	0.7	146
21	Transancestral GWAS of alcohol dependence reveals common genetic underpinnings with psychiatric disorders. Nature Neuroscience, 2018, 21, 1656-1669.	7.1	490
22	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. Nature Genetics, 2018, 50, 1112-1121.	9.4	1,835
23	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	6.0	1,085
24	Genomeâ€wide association metaâ€analysis of age at first cannabis use. Addiction, 2018, 113, 2073-2086.	1.7	24
25	Polygenic transmission disequilibrium confirms that common and rare variation act additively to create risk for autism spectrum disorders. Nature Genetics, 2017, 49, 978-985.	9.4	401
26	Human Demographic History Impacts Genetic Risk Prediction across Diverse Populations. American Journal of Human Genetics, 2017, 100, 635-649.	2.6	1,120
27	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	13.7	772