## Christiaan A De Leeuw

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/7696715/publications.pdf

Version: 2024-02-01

40 papers 15,302 citations

201575 27 h-index 254106 43 g-index

51 all docs

51 docs citations

51 times ranked

21063 citing authors

#	Article	IF	CITATIONS
1	MAGMA: Generalized Gene-Set Analysis of GWAS Data. PLoS Computational Biology, 2015, 11, e1004219.	1.5	2,344
2	Meta-analysis of the heritability of human traits based on fifty years of twin studies. Nature Genetics, 2015, 47, 702-709.	9.4	1,750
3	Genome-wide meta-analysis identifies new loci and functional pathways influencing Alzheimer's disease risk. Nature Genetics, 2019, 51, 404-413.	9.4	1,625
4	Genome-wide association analysis identifies 13 new risk loci for schizophrenia. Nature Genetics, 2013, 45, 1150-1159.	9.4	1,395
5	Genome-wide association study identifies 30 loci associated with bipolar disorder. Nature Genetics, 2019, 51, 793-803.	9.4	1,191
6	Genome-wide association meta-analysis in 269,867 individuals identifies new genetic and functional links to intelligence. Nature Genetics, 2018, 50, 912-919.	9.4	893
7	A global overview of pleiotropy and genetic architecture in complex traits. Nature Genetics, 2019, 51, 1339-1348.	9.4	774
8	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	6.0	750
9	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. Cell, 2018, 173, 1705-1715.e16.	13.5	623
10	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403.	9.4	593
11	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.	9.4	564
12	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
13	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	9.4	248
14	Common genetic variants associated with cognitive performance identified using the proxy-phenotype method. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13790-13794.	3.3	244
15	The statistical properties of gene-set analysis. Nature Reviews Genetics, 2016, 17, 353-364.	7.7	230
16	Genetic mapping of cell type specificity for complex traits. Nature Communications, 2019, 10, 3222.	5.8	212
17	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. JAMA Psychiatry, 2017, 74, 1242.	6.0	174
18	No Evidence That Schizophrenia Candidate Genes Are More Associated With Schizophrenia Than Noncandidate Genes. Biological Psychiatry, 2017, 82, 702-708.	0.7	170

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19	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. Biological Psychiatry, 2020, 88, 169-184.	0.7	137
20	An integrated framework for local genetic correlation analysis. Nature Genetics, 2022, 54, 274-282.	9.4	115
21	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
22	Specific Glial Functions Contribute to Schizophrenia Susceptibility. Schizophrenia Bulletin, 2014, 40, 925-935.	2.3	105
23	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
24	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and AlcoholÂUse. Biological Psychiatry, 2019, 85, 946-955.	0.7	69
25	Conditional and interaction gene-set analysis reveals novel functional pathways for blood pressure. Nature Communications, 2018, 9, 3768.	5.8	50
26	Genome-wide meta-analysis of brain volume identifies genomic loci and genes shared with intelligence. Nature Communications, 2020, 11, 5606.	5.8	50
27	The genetic architecture of human cortical folding. Science Advances, 2021, 7, eabj9446.	4.7	50
28	Understanding the assumptions underlying Mendelian randomization. European Journal of Human Genetics, 2022, 30, 653-660.	1.4	40
29	Myelination-related genes are associated with decreased white matter integrity in schizophrenia. European Journal of Human Genetics, 2016, 24, 381-386.	1.4	27
30	Synaptic and brain-expressed gene sets relate to the shared genetic risk across five psychiatric disorders. Psychological Medicine, 2020, 50, 1695-1705.	2.7	26
31	Involvement of astrocyte metabolic coupling in Tourette syndrome pathogenesis. European Journal of Human Genetics, 2015, 23, 1519-1522.	1.4	22
32	Genome-wide gene-environment interactions in neuroticism: an exploratory study across 25 environments. Translational Psychiatry, 2021, 11, 180.	2.4	19
33	Involvement of astrocyte and oligodendrocyte gene sets in migraine. Cephalalgia, 2016, 36, 640-647.	1.8	15
34	JAG: A Computational Tool to Evaluate the Role of Gene-Sets in Complex Traits. Genes, 2015, 6, 238-251.	1.0	13
35	Functional Gene-Set Analysis Does Not Support a Major Role for Synaptic Function in Attention Deficit/Hyperactivity Disorder (ADHD). Genes, 2014, 5, 604-614.	1.0	10
36	Systematic assessment of variability in the proteome of iPSC derivatives. Stem Cell Research, 2021, 56, 102512.	0.3	8

#	Article	IF	CITATIONS
37	Sensitive period-regulating genetic pathways and exposure to adversity shape risk for depression. Neuropsychopharmacology, 2022, 47, 497-506.	2.8	8
38	Augmenting Data With Published Results in Bayesian Linear Regression. Multivariate Behavioral Research, 2012, 47, 369-391.	1.8	3
39	Functional Gene Group Analysis Indicates No Role for Heterotrimeric G Proteins in Cognitive Ability. PLoS ONE, 2014, 9, e91690.	1.1	3
40	Genome-wide association study of cerebellar volume provides insights into heritable mechanisms underlying brain development and mental health. Communications Biology, 2022, 5, .	2.0	3