Nicholas Eriksson

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/12181395/publications.pdf

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34 papers	11,683 citations	172457 29 h-index	377865 34 g-index
35 all docs	35 docs citations	35 times ranked	20566 citing authors

#	Article	IF	Citations
1	Elucidating the relationship between migraine risk and brain structure using genetic data. Brain, 2022, 145, 3214-3224.	7.6	7
2	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	3.7	18
3	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. Nature Communications, 2020, 11, 3368.	12.8	49
4	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	1.9	34
5	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. Nature Genetics, 2019, 51, 63-75.	21.4	1,594
6	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	21.4	2,224
7	Self-report data as a tool for subtype identification in genetically-defined Parkinsonâ€™s Disease. Scientific Reports, 2018, 8, 12992.	3.3	12
8	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
9	Analysis of shared heritability in common disorders of the brain. Science, 2018, 360, .	12.6	1,085
10	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
11	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. Nature Genetics, 2016, 48, 856-866.	21.4	520
12	GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. Nature Communications, 2016, 7, 10448.	12.8	263
13	Virtual research visits and direct-to-consumer genetic testing in Parkinsonâ€™s disease. Digital Health, 2015, 1, 205520761559299.	1.8	22
14	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. Human Molecular Genetics, 2015, 24, 2700-2708.	2.9	70
15	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. Neurobiology of Aging, 2015, 36, 1605.e7-1605.e12.	3.1	96
16	Reducing Pervasive False-Positive Identical-by-Descent Segments Detected by Large-Scale Pedigree Analysis. Molecular Biology and Evolution, 2014, 31, 2212-2222.	8.9	44
17	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. Journal of Allergy and Clinical Immunology, 2014, 133, 1564-1571.	2.9	195
18	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	21.4	1,685

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19	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	3.3	92
20	Androgenetic Alopecia: Identification of Four Genetic Risk Loci and Evidence for the Contribution of WNT Signaling to Its Etiology. Journal of Investigative Dermatology, 2013, 133, 1489-1496.	0.7	83
21	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. Nature Genetics, 2013, 45, 907-911.	21.4	232
22	Genome-Wide Analysis Points to Roles for Extracellular Matrix Remodeling, the Visual Cycle, and Neuronal Development in Myopia. PLoS Genetics, 2013, 9, e1003299.	3.5	263
23	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. PLoS Medicine, 2013, 10, e1001462.	8.4	116
24	Comparison of Family History and SNPs for Predicting Risk of Complex Disease. PLoS Genetics, 2012, 8, e1002973.	3.5	102
25	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. PLoS Genetics, 2012, 8, e1002548.	3.5	495
26	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	3.5	92
27	Genetic variants associated with breast size also influence breast cancer risk. BMC Medical Genetics, 2012, 13, 53.	2.1	65
28	A genetic variant near olfactory receptor genes influences cilantro preference. Flavour, 2012, 1, .	2.3	72
29	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. PLoS ONE, 2012, 7, e34442.	2.5	128
30	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. PLoS ONE, 2011, 6, e23473.	2.5	117
31	ShoRAH: estimating the genetic diversity of a mixed sample from next-generation sequencing data. BMC Bioinformatics, 2011, 12, 119.	2.6	235
32	Web-Based Genome-Wide Association Study Identifies Two Novel Loci and a Substantial Genetic Component for Parkinson's Disease. PLoS Genetics, 2011, 7, e1002141.	3.5	461
33	Web-Based, Participant-Driven Studies Yield Novel Genetic Associations for Common Traits. PLoS Genetics, 2010, 6, e1000993.	3.5	399
34	Viral Population Estimation Using Pyrosequencing. PLoS Computational Biology, 2008, 4, e1000074.	3.2	197