

# Nicholas Eriksson

## List of Publications by Year in descending order

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

Version: 2024-02-01

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	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
2	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. <i>Nature Genetics</i> , 2014, 46, 989-993.	21.4	1,685
3	Discovery of the first genome-wide significant risk loci for attention deficit/hyperactivity disorder. <i>Nature Genetics</i> , 2019, 51, 63-75.	21.4	1,594
4	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
5	Meta-analysis of 375,000 individuals identifies 38 susceptibility loci for migraine. <i>Nature Genetics</i> , 2016, 48, 856-866.	21.4	520
6	Comprehensive Research Synopsis and Systematic Meta-Analyses in Parkinson's Disease Genetics: The PDGene Database. <i>PLoS Genetics</i> , 2012, 8, e1002548.	3.5	495
7	Web-Based Genome-Wide Association Study Identifies Two Novel Loci and a Substantial Genetic Component for Parkinson's Disease. <i>PLoS Genetics</i> , 2011, 7, e1002141.	3.5	461
8	Web-Based, Participant-Driven Studies Yield Novel Genetic Associations for Common Traits. <i>PLoS Genetics</i> , 2010, 6, e1000993.	3.5	399
9	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
10	Genome-Wide Analysis Points to Roles for Extracellular Matrix Remodeling, the Visual Cycle, and Neuronal Development in Myopia. <i>PLoS Genetics</i> , 2013, 9, e1003299.	3.5	263
11	GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. <i>Nature Communications</i> , 2016, 7, 10448.	12.8	263
12	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	21.4	239
13	ShoRAH: estimating the genetic diversity of a mixed sample from next-generation sequencing data. <i>BMC Bioinformatics</i> , 2011, 12, 119.	2.6	235
14	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. <i>Nature Genetics</i> , 2013, 45, 907-911.	21.4	232
15	Viral Population Estimation Using Pyrosequencing. <i>PLoS Computational Biology</i> , 2008, 4, e1000074.	3.2	197
16	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. <i>Journal of Allergy and Clinical Immunology</i> , 2014, 133, 1564-1571.	2.9	195
17	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. <i>PLoS ONE</i> , 2012, 7, e34442.	2.5	128
18	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. <i>PLoS ONE</i> , 2011, 6, e23473.	2.5	117

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19	Serum Iron Levels and the Risk of Parkinson Disease: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2013, 10, e1001462.	8.4	116
20	Comparison of Family History and SNPs for Predicting Risk of Complex Disease. <i>PLoS Genetics</i> , 2012, 8, e1002973.	3.5	102
21	NeuroX, a fast and efficient genotyping platform for investigation of neurodegenerative diseases. <i>Neurobiology of Aging</i> , 2015, 36, 1605.e7-1605.e12.	3.1	96
22	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. <i>PLoS Genetics</i> , 2012, 8, e1002746.	3.5	92
23	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. <i>Psychological Science</i> , 2014, 25, 1975-1986.	3.3	92
24	Androgenetic Alopecia: Identification of Four Genetic Risk Loci and Evidence for the Contribution of WNT Signaling to Its Etiology. <i>Journal of Investigative Dermatology</i> , 2013, 133, 1489-1496.	0.7	83
25	A genetic variant near olfactory receptor genes influences cilantro preference. <i>Flavour</i> , 2012, 1, .	2.3	72
26	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. <i>Human Molecular Genetics</i> , 2015, 24, 2700-2708.	2.9	70
27	Genetic variants associated with breast size also influence breast cancer risk. <i>BMC Medical Genetics</i> , 2012, 13, 53.	2.1	65
28	A genome-wide cross-phenotype meta-analysis of the association of blood pressure with migraine. <i>Nature Communications</i> , 2020, 11, 3368.	12.8	49
29	Reducing Pervasive False-Positive Identical-by-Descent Segments Detected by Large-Scale Pedigree Analysis. <i>Molecular Biology and Evolution</i> , 2014, 31, 2212-2222.	8.9	44
30	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020, 49, 1022-1031.	1.9	34
31	Virtual research visits and direct-to-consumer genetic testing in Parkinson's disease. <i>Digital Health</i> , 2015, 1, 205520761559299.	1.8	22
32	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 2370-2380.	3.7	18
33	Self-report data as a tool for subtype identification in genetically-defined Parkinson's Disease. <i>Scientific Reports</i> , 2018, 8, 12992.	3.3	12
34	Elucidating the relationship between migraine risk and brain structure using genetic data. <i>Brain</i> , 2022, 145, 3214-3224.	7.6	7