Peter Heutink

List of Publications by Year
in descending order

54 papers	11,365 citations	147566 31 h-index	161609 54 g-index
69 all docs	69 docs citations	69 times ranked	20741 citing authors

#	Article	IF	Citations
1	An atlas of active enhancers across human cell types and tissues. Nature, 2014, 507, 455-461.	13.7	2,269
2	A promoter-level mammalian expression atlas. Nature, 2014, 507, 462-470.	13.7	1,838
3	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. Nature Genetics, 2014, 46, 989-993.	9.4	1,685
4	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. Lancet Neurology, The, 2019, 18, 1091-1102.	4.9	1,414
5	An integrated expression atlas of miRNAs and their promoters in human and mouse. Nature Biotechnology, 2017, 35, 872-878.	9.4	456
6	Î²2-Adrenoreceptor is a regulator of the Î±-synuclein gene driving risk of Parkinsonâ€™s disease. Science, 2017, 357, 891-898.	6.0	341
7	Parkinson's disease age at onset genomeâ€wide association study: Defining heritability, genetic loci, and Î±â€synuclein mechanisms. Movement Disorders, 2019, 34, 866-875.	2.2	258
8	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. JAMA Neurology, 2017, 74, 780.	4.5	245
9	Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. Annals of Neurology, 2016, 80, 674-685.	2.8	226
10	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	2.4	195
11	Diagnosis of Parkinson's disease on the basis of clinical and genetic classification: a population-based modelling study. Lancet Neurology, The, 2015, 14, 1002-1009.	4.9	179
12	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. Human Molecular Genetics, 2012, 21, 4996-5009.	1.4	176
13	Genetic modifiers of risk and age at onset in GBA associated Parkinsonâ€™s disease and Lewy body dementia. Brain, 2020, 143, 234-248.	3.7	149
14	Prediction of cognition in Parkinson's disease with a clinicalâ€“genetic score: a longitudinal analysis of nine cohorts. Lancet Neurology, The, 2017, 16, 620-629.	4.9	131
15	Genomewide association study of Parkinson's disease clinical biomarkers in 12 longitudinal patients' cohorts. Movement Disorders, 2019, 34, 1839-1850.	2.2	122
16	Polygenic risk of <scp>P</scp>arkinson disease is correlated with disease age at onset. Annals of Neurology, 2015, 77, 582-591.	2.8	115
17	Evidence for Immune Response, Axonal Dysfunction and Reduced Endocytosis in the Substantia Nigra in Early Stage Parkinsonâ€™s Disease. PLoS ONE, 2015, 10, e0128651.	1.1	114
18	Deep learningâ€“based cell composition analysis from tissue expression profiles. Science Advances, 2020, 6, eaba2619.	4.7	113

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19	Copy Number Variation in Obsessive-Compulsive Disorder and Tourette Syndrome: A Cross-Disorder Study. Journal of the American Academy of Child and Adolescent Psychiatry, 2014, 53, 910-919.	0.3	111
20	Genetic risk of Parkinson disease and progression:. Neurology: Genetics, 2019, 5, e348.	0.9	109
21	Functional annotation of human long noncoding RNAs via molecular phenotyping. Genome Research, 2020, 30, 1060-1072.	2.4	109
22	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. Neurobiology of Aging, 2017, 57, 247.e9-247.e13.	1.5	108
23	Potential genetic modifiers of disease risk and age at onset in patients with frontotemporal lobar degeneration and GRN mutations: a genome-wide association study. Lancet Neurology, The, 2018, 17, 548-558.	4.9	97
24	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinsonâ€™s disease. Nature Genetics, 2021, 53, 787-793.	9.4	82
25	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. Nature Neuroscience, 2018, 21, 1482-1492.	7.1	79
26	Novel parkin mutations detected in patients with early-onset Parkinson's disease. Movement Disorders, 2005, 20, 424-431.	2.2	60
27	Penetrance of Parkinson's Disease in LRRK2 p.G2019S Carriers Is Modified by a Polygenic Risk Score. Movement Disorders, 2020, 35, 774-780.	2.2	57
28	CHCHD2 and Parkinson's disease. Lancet Neurology, The, 2015, 14, 678-679.	4.9	50
29	Finding genetically-supported drug targets for Parkinsonâ€™s disease using Mendelian randomization of the druggable genome. Nature Communications, 2021, 12, 7342.	5.8	44
30	The Val158Met COMT polymorphism is a modifier of the age at onset in Parkinson's disease with a sexual dimorphism. Journal of Neurology, Neurosurgery and Psychiatry, 2013, 84, 666-673.	0.9	43
31	Pilot whole-exome sequencing of a German early-onset Alzheimer's disease cohort reveals a substantial frequency of PSEN2 variants. Neurobiology of Aging, 2016, 37, 208.e11-208.e17.	1.5	38
32	A Genome-Wide Search for Linkage-Disequilibrium With Type 1 Diabetes in a Recent Genetically Isolated Population From the Netherlands. Diabetes, 2002, 51, 856-859.	0.3	37
33	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. Molecular Neurobiology, 2019, 56, 5392-5415.	1.9	29
34	Investigation of Autosomal Genetic Sex Differences in Parkinson's Disease. Annals of Neurology, 2021, 90, 35-42.	2.8	29
35	Brain-specific noncoding RNAs are likely to originate in repeats and may play a role in up-regulating genes in cis. International Journal of Biochemistry and Cell Biology, 2014, 54, 331-337.	1.2	20
36	Comprehensive promoter level expression quantitative trait loci analysis of the human frontal lobe. Genome Medicine, 2016, 8, 65.	3.6	20

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37	Automated Production of Human Induced Pluripotent Stem Cell-Derived Cortical and Dopaminergic Neurons with Integrated Live-Cell Monitoring. Journal of Visualized Experiments, 2020, , .	0.2	19
38	Is the MC1R variant p.R160W associated with Parkinson's?. Annals of Neurology, 2016, 79, 159-161.	2.8	18
39	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. PLoS Computational Biology, 2018, 14, e1005934.	1.5	17
40	C9orf72; abnormal RNA expression is the key. Experimental Neurology, 2014, 262, 102-110.	2.0	15
41	Establishing the role of rare coding variants in known Parkinson's disease risk loci. Neurobiology of Aging, 2017, 59, 220.e11-220.e18.	1.5	15
42	No supportive evidence for TIA1 gene mutations in a European cohort of ALS-FTD spectrum patients. Neurobiology of Aging, 2018, 69, 293.e9-293.e11.	1.5	15
43	InÂVitro Differentiated Human Stem Cell-Derived Neurons Reproduce Synaptic Synchronicity Arising during Neurodevelopment. Stem Cell Reports, 2020, 15, 22-37.	2.3	15
44	Concomitant gain and loss of function pathomechanisms in C9ORF72 amyotrophic lateral sclerosis. Life Science Alliance, 2021, 4, e202000764.	1.3	11
45	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. Nature Communications, 2021, 12, 3297.	5.8	11
46	A multimodal 3D neuro-microphysiological system with neurite-trapping microelectrodes. Biofabrication, 2022, 14, 025004.	3.7	11
47	Distinct cell type-specific protein signatures in GRN and MAPT genetic subtypes of frontotemporal dementia. Acta Neuropathologica Communications, 2022, 10, .	2.4	11
48	Accurate prediction of a minimal region around a genetic association signal that contains the causal variant. European Journal of Human Genetics, 2014, 22, 238-242.	1.4	7
49	Variation in PARK10 is not associated with risk and age at onset ofÂParkinson's disease in large clinical cohorts. Neurobiology of Aging, 2015, 36, 2907.e13-2907.e17.	1.5	5
50	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. Scientific Data, 2017, 4, 170163.	2.4	4
51	iPS Cell-Based Model for MAPT Haplotype as a Risk Factor for Human Tauopathies Identifies No Major Differences in TAU Expression. Frontiers in Cell and Developmental Biology, 2021, 9, 726866.	1.8	4
52	Novel regulators of PrPC biosynthesis revealed by genome-wide RNA interference. PLoS Pathogens, 2021, 17, e1010013.	2.1	4
53	Lodewijk A. Sandkuijl, M.D. (July 31, 1953â€“December 4, 2002). American Journal of Human Genetics, 2003, 72, 781-784.	2.6	1
54	A Multi-omics Data Resource for Frontotemporal Dementia Research. Advances in Experimental Medicine and Biology, 2021, 1281, 269-282.	0.8	0