Peter Heutink

List of Publications by Citations

56 papers	7,194 citations	27 h-index	69 g-index
69 ext. papers	9,838 ext. citations	12.8 avg, IF	4.21 L-index

#	Paper	IF	Citations
56	An atlas of active enhancers across human cell types and tissues. *Nature*, **2014**, 507, 455-461	50.4	1595
55	A promoter-level mammalian expression atlas. *Nature*, **2014**, 507, 462-70	50.4	1301
54	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. *Nature Genetics*, **2014**, 46, 989-93	36.3	1261
53	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	24.1	562
52	An integrated expression atlas of miRNAs and their promoters in human and mouse. *Nature Biotechnology*, **2017**, 35, 872-878	44.5	282
51	-Adrenoreceptor is a regulator of the synuclein gene driving risk of Parkinson's disease. *Science* , **2017**, 357, 891-898	33.3	238
50	Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. *Annals of Neurology*, **2016**, 80, 674-685	9.4	154
49	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. *JAMA Neurology*, **2017**, 74, 780-792	17.2	150
48	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. *Human Molecular Genetics*, **2012**, 21, 4996-5009	5.6	145
47	Diagnosis of Parkinson's disease on the basis of clinical and genetic classification: a population-based modelling study. *Lancet Neurology, The*, **2015**, 14, 1002-9	24.1	141
46	Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and synuclein mechanisms. *Movement Disorders*, **2019**, 34, 866-875	7	136
45	Prediction of cognition in Parkinson's disease with a clinical-genetic score: a longitudinal analysis of nine cohorts. *Lancet Neurology, The*, **2017**, 16, 620-629	24.1	98
44	FANTOM5 CAGE profiles of human and mouse samples. *Scientific Data*, **2017**, 4, 170112	8.2	88
43	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, 910-9	7.2	86
42	Polygenic risk of Parkinson disease is correlated with disease age at onset. *Annals of Neurology*, **2015**, 77, 582-91	9.4	77
41	Evidence for Immune Response, Axonal Dysfunction and Reduced Endocytosis in the Substantia Nigra in Early Stage Parkinson's Disease. *PLoS ONE*, **2015**, 10, e0128651	3.7	72
40	Genomewide association study of Parkinson's disease clinical biomarkers in 12 longitudinal patients' cohorts. *Movement Disorders*, **2019**, 34, 1839-1850	7	69

39	Genetic modifiers of risk and age at onset in GBA associated Parkinson's disease and Lewy body dementia. *Brain*, **2020**, 143, 234-248	11.2	69
38	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	24.1	60
37	Genetic risk of Parkinson disease and progression:: An analysis of 13 longitudinal cohorts. *Neurology: Genetics*, **2019**, 5, e348	3.8	57
36	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	5.6	54
35	Novel parkin mutations detected in patients with early-onset Parkinson's disease. *Movement Disorders*, **2005**, 20, 424-431	7	51
34	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. *Nature Neuroscience*, **2018**, 21, 1482-1492	25.5	48
33	CHCHD2 and Parkinson's disease. *Lancet Neurology, The*, **2015**, 14, 678-9	24.1	43
32	Functional annotation of human long noncoding RNAs via molecular phenotyping. *Genome Research*, **2020**, 30, 1060-1072	9.7	41
31	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, 666-73	5.5	40
30	A genome-wide search for linkage-disequilibrium with type 1 diabetes in a recent genetically isolated population from the Netherlands. *Diabetes*, **2002**, 51, 856-9	0.9	34
29	Penetrance of Parkinson's Disease in LRRK2 p.G2019S Carriers Is Modified by a Polygenic Risk Score. *Movement Disorders*, **2020**, 35, 774-780	7	27
28	Deep learning-based cell composition analysis from tissue expression profiles. *Science Advances*, **2020**, 6, eaba2619	14.3	25
27	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	5.6	24
26	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, 331-7	5.6	15
25	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinson's disease. *Nature Genetics*, **2021**, 53, 787-793	36.3	15
24	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. *Molecular Neurobiology*, **2019**, 56, 5392-5415	6.2	15
23	Is the MC1R variant p.R160W associated with Parkinson's?. *Annals of Neurology*, **2016**, 79, 159-61	9.4	14
22	Comprehensive promoter level expression quantitative trait loci analysis of the human frontal lobe. *Genome Medicine*, **2016**, 8, 65	14.4	14

21	C9orf72; abnormal RNA expression is the key. *Experimental Neurology*, **2014**, 262 Pt B, 102-10	5.7	13
20	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	5.6	11
19	Establishing the role of rare coding variants in known Parkinson's disease risk loci. *Neurobiology of Aging*, **2017**, 59, 220.e11-220.e18	5.6	11
18	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. *PLoS Computational Biology*, **2018**, 14, e1005934	5	8
17	Accurate prediction of a minimal region around a genetic association signal that contains the causal variant. *European Journal of Human Genetics*, **2014**, 22, 238-42	5.3	7
16	In Vitro Differentiated Human Stem Cell-Derived Neurons Reproduce Synaptic Synchronicity Arising during Neurodevelopment. *Stem Cell Reports*, **2020**, 15, 22-37	8	6
15	Automated Production of Human Induced Pluripotent Stem Cell-Derived Cortical and Dopaminergic Neurons with Integrated Live-Cell Monitoring. *Journal of Visualized Experiments*, **2020**,	1.6	6
14	Investigation of Autosomal Genetic Sex Differences in Parkinson's Disease. *Annals of Neurology*, **2021**, 90, 35-42	9.4	6
13	Variation in PARK10 is not associated with risk and age at onset of Parkinson's disease in large clinical cohorts. *Neurobiology of Aging*, **2015**, 36, 2907.e13-7	5.6	5
12	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. *Nature Communications*, **2021**, 12, 3297	17.4	3
11	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. *Scientific Data*, **2017**, 4, 170163	8.2	2
10	A multimodal 3D neuro-microphysiological system with neurite-trapping microelectrodes.. *Biofabrication*, **2021**,	10.5	2
9	Integrated multi-omics analysis reveals common and distinct dysregulated pathways for genetic subtypes of Frontotemporal Dementia		2
8	Finding genetically-supported drug targets for Parkinson's disease using Mendelian randomization of the druggable genome.. *Nature Communications*, **2021**, 12, 7342	17.4	2
7	Lodewijk A. Sandkuijl, M.D. (July 31, 1953 December 4, 2002). *American Journal of Human Genetics*, **2003**, 72, 781-784	11	1
6	Deep-learning-based cell composition analysis from tissue expression profiles		1
5	17q21.31 sub-haplotypes underlying H1-associated risk for Parkinson disease are associated with LRRC37A/2 expression in astrocytes		1
4	Concomitant gain and loss of function pathomechanisms in C9ORF72 amyotrophic lateral sclerosis. *Life Science Alliance*, **2021**, 4,	5.8	1

3	iPS Cell-Based Model for Haplotype as a Risk Factor for Human Tauopathies Identifies No Major Differences in TAU Expression. *Frontiers in Cell and Developmental Biology*, **2021**, 9, 726866	5.7	1
2	Novel regulators of PrPC biosynthesis revealed by genome-wide RNA interference. *PLoS Pathogens*, **2021**, 17, e1010013	7.6	0
1	A Multi-omics Data Resource for Frontotemporal Dementia Research. *Advances in Experimental Medicine and Biology*, **2021**, 1281, 269-282	3.6	