

Peter Heutink

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	A multimodal 3D neuro-microphysiological system with neurite-trapping microelectrodes.. <i>Biofabrication</i> , 2021 ,	10.5	2
55	Novel regulators of PrPC biosynthesis revealed by genome-wide RNA interference. <i>PLoS Pathogens</i> , 2021 , 17, e1010013	7.6	0
54	Investigation of Autosomal Genetic Sex Differences in Parkinson's Disease. <i>Annals of Neurology</i> , 2021 , 90, 35-42	9.4	6
53	Genome-wide survival study identifies a novel synaptic locus and polygenic score for cognitive progression in Parkinson's disease. <i>Nature Genetics</i> , 2021 , 53, 787-793	36.3	15
52	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021 , 12, 3297	17.4	3
51	A Multi-omics Data Resource for Frontotemporal Dementia Research. <i>Advances in Experimental Medicine and Biology</i> , 2021 , 1281, 269-282	3.6	
50	Concomitant gain and loss of function pathomechanisms in C9ORF72 amyotrophic lateral sclerosis. <i>Life Science Alliance</i> , 2021 , 4,	5.8	1
49	iPS Cell-Based Model for Haplotype as a Risk Factor for Human Tauopathies Identifies No Major Differences in TAU Expression. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 726866	5.7	1
48	Finding genetically-supported drug targets for Parkinson's disease using Mendelian randomization of the druggable genome.. <i>Nature Communications</i> , 2021 , 12, 7342	17.4	2
47	InVitro Differentiated Human Stem Cell-Derived Neurons Reproduce Synaptic Synchronicity Arising during Neurodevelopment. <i>Stem Cell Reports</i> , 2020 , 15, 22-37	8	6
46	Penetrance of Parkinson's Disease in LRRK2 p.G2019S Carriers Is Modified by a Polygenic Risk Score. <i>Movement Disorders</i> , 2020 , 35, 774-780	7	27
45	Automated Production of Human Induced Pluripotent Stem Cell-Derived Cortical and Dopaminergic Neurons with Integrated Live-Cell Monitoring. <i>Journal of Visualized Experiments</i> , 2020 ,	1.6	6
44	Genetic modifiers of risk and age at onset in GBA associated Parkinson's disease and Lewy body dementia. <i>Brain</i> , 2020 , 143, 234-248	11.2	69
43	Deep learning-based cell composition analysis from tissue expression profiles. <i>Science Advances</i> , 2020 , 6, eaba2619	14.3	25
42	Functional annotation of human long noncoding RNAs via molecular phenotyping. <i>Genome Research</i> , 2020 , 30, 1060-1072	9.7	41
41	Genetic risk of Parkinson disease and progression:: An analysis of 13 longitudinal cohorts. <i>Neurology: Genetics</i> , 2019 , 5, e348	3.8	57
40	Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and Synuclein mechanisms. <i>Movement Disorders</i> , 2019 , 34, 866-875	7	136

39	Genomewide association study of Parkinson's disease clinical biomarkers in 12 longitudinal patients' cohorts. <i>Movement Disorders</i> , 2019 , 34, 1839-1850	7	69
38	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2019 , 18, 1091-1102	24.1	562
37	Antisense Transcription in Loci Associated to Hereditary Neurodegenerative Diseases. <i>Molecular Neurobiology</i> , 2019 , 56, 5392-5415	6.2	15
36	Potential genetic modifiers of disease risk and age at onset in patients with frontotemporal lobar degeneration and GRN mutations: a genome-wide association study. <i>Lancet Neurology</i> , 2018 , 17, 548-558	24.1	60
35	No supportive evidence for TIA1 gene mutations in a European cohort of ALS-FTD spectrum patients. <i>Neurobiology of Aging</i> , 2018 , 69, 293.e9-293.e11	5.6	11
34	Shared activity patterns arising at genetic susceptibility loci reveal underlying genomic and cellular architecture of human disease. <i>PLoS Computational Biology</i> , 2018 , 14, e1005934	5	8
33	Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. <i>Nature Neuroscience</i> , 2018 , 21, 1482-1492	25.5	48
32	Prediction of cognition in Parkinson's disease with a clinical-genetic score: a longitudinal analysis of nine cohorts. <i>Lancet Neurology</i> , 2017 , 16, 620-629	24.1	98
31	NeuroChip, an updated version of the NeuroX genotyping platform to rapidly screen for variants associated with neurological diseases. <i>Neurobiology of Aging</i> , 2017 , 57, 247.e9-247.e13	5.6	54
30	Genome-wide Pleiotropy Between Parkinson Disease and Autoimmune Diseases. <i>JAMA Neurology</i> , 2017 , 74, 780-792	17.2	150
29	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017 , 35, 872-878	44.5	282
28	FANTOM5 CAGE profiles of human and mouse samples. <i>Scientific Data</i> , 2017 , 4, 170112	8.2	88
27	α-Adrenoreceptor is a regulator of the Synuclein gene driving risk of Parkinson's disease. <i>Science</i> , 2017 , 357, 891-898	33.3	238
26	Establishing the role of rare coding variants in known Parkinson's disease risk loci. <i>Neurobiology of Aging</i> , 2017 , 59, 220.e11-220.e18	5.6	11
25	Transcription start site profiling of 15 anatomical regions of the Macaca mulatta central nervous system. <i>Scientific Data</i> , 2017 , 4, 170163	8.2	2
24	Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. <i>Annals of Neurology</i> , 2016 , 80, 674-685	9.4	154
23	Is the MC1R variant p.R160W associated with Parkinson's?. <i>Annals of Neurology</i> , 2016 , 79, 159-61	9.4	14
22	Pilot whole-exome sequencing of a German early-onset Alzheimer's disease cohort reveals a substantial frequency of PSEN2 variants. <i>Neurobiology of Aging</i> , 2016 , 37, 208.e11-208.e17	5.6	24

21	Comprehensive promoter level expression quantitative trait loci analysis of the human frontal lobe. <i>Genome Medicine</i> , 2016 , 8, 65	14.4	14
20	Variation in PARK10 is not associated with risk and age at onset of Parkinson's disease in large clinical cohorts. <i>Neurobiology of Aging</i> , 2015 , 36, 2907.e13-7	5.6	5
19	Polygenic risk of Parkinson disease is correlated with disease age at onset. <i>Annals of Neurology</i> , 2015 , 77, 582-91	9.4	77
18	Diagnosis of Parkinson's disease on the basis of clinical and genetic classification: a population-based modelling study. <i>Lancet Neurology, The</i> , 2015 , 14, 1002-9	24.1	141
17	Evidence for Immune Response, Axonal Dysfunction and Reduced Endocytosis in the Substantia Nigra in Early Stage Parkinson's Disease. <i>PLoS ONE</i> , 2015 , 10, e0128651	3.7	72
16	CHCHD2 and Parkinson's disease. <i>Lancet Neurology, The</i> , 2015 , 14, 678-9	24.1	43
15	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014 , 507, 462-70	50.4	1301
14	An atlas of active enhancers across human cell types and tissues. <i>Nature</i> , 2014 , 507, 455-461	50.4	1595
13	Large-scale meta-analysis of genome-wide association data identifies six new risk loci for Parkinson's disease. <i>Nature Genetics</i> , 2014 , 46, 989-93	36.3	1261
12	Copy number variation in obsessive-compulsive disorder and tourette syndrome: a cross-disorder study. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2014 , 53, 910-9	7.2	86
11	Accurate prediction of a minimal region around a genetic association signal that contains the causal variant. <i>European Journal of Human Genetics</i> , 2014 , 22, 238-42	5.3	7
10	C9orf72; abnormal RNA expression is the key. <i>Experimental Neurology</i> , 2014 , 262 Pt B, 102-10	5.7	13
9	Brain-specific noncoding RNAs are likely to originate in repeats and may play a role in up-regulating genes in cis. <i>International Journal of Biochemistry and Cell Biology</i> , 2014 , 54, 331-7	5.6	15
8	The Val158Met COMT polymorphism is a modifier of the age at onset in Parkinson's disease with a sexual dimorphism. <i>Journal of Neurology, Neurosurgery and Psychiatry</i> , 2013 , 84, 666-73	5.5	40
7	Using genome-wide complex trait analysis to quantify 'missing heritability' in Parkinson's disease. <i>Human Molecular Genetics</i> , 2012 , 21, 4996-5009	5.6	145
6	Novel parkin mutations detected in patients with early-onset Parkinson's disease. <i>Movement Disorders</i> , 2005 , 20, 424-431	7	51
5	Lodewijk A. Sandkuijl, M.D. (July 31, 1953–December 4, 2002). <i>American Journal of Human Genetics</i> , 2003 , 72, 781-784	11	1
4	A genome-wide search for linkage-disequilibrium with type 1 diabetes in a recent genetically isolated population from the Netherlands. <i>Diabetes</i> , 2002 , 51, 856-9	0.9	34

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| 3 | Integrated multi-omics analysis reveals common and distinct dysregulated pathways for genetic subtypes of Frontotemporal Dementia | 2 |
| 2 | Deep-learning-based cell composition analysis from tissue expression profiles | 1 |
| 1 | 17q21.31 sub-haplotypes underlying H1-associated risk for Parkinson's disease are associated with LRR37A/2 expression in astrocytes | 1 |