

Philip L De Jager

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.

445
papers

47,762
citations

100
h-index

214
g-index

517
ext. papers

61,092
ext. citations

11.9
avg, IF

6.64
L-index

#	Paper	IF	Citations
445	Brain microRNAs are associated with variation in cognitive trajectory in advanced age.. <i>Translational Psychiatry</i> , 2022 , 12, 47	8.6	0
444	Hypogonadism in men with multiple sclerosis: Prevalence and clinical associations.. <i>Multiple Sclerosis and Related Disorders</i> , 2022 , 59, 103508	4	
443	Exploring cortical proteins underlying the relation of neuroticism to cognitive resilience. <i>Aging Brain</i> , 2022 , 100031		
442	Large-scale deep multi-layer analysis of Alzheimer's disease brain reveals strong proteomic disease-related changes not observed at the RNA level.. <i>Nature Neuroscience</i> , 2022 ,	25.5	18
441	Worsening physical functioning in patients with neuroinflammatory disease during the COVID-19 pandemic.. <i>Multiple Sclerosis and Related Disorders</i> , 2022 , 58, 103482	4	0
440	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults.. <i>Neurology</i> , 2022 ,	6.5	2
439	Manifestations of Alzheimer's disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90.. <i>Scientific Reports</i> , 2022 , 12, 6117	4.9	1
438	A multi-step genomic approach prioritized TBKBP1 gene as relevant for multiple sclerosis susceptibility.. <i>Journal of Neurology</i> , 2022 , 1	5.5	0
437	Mitochondrial respiratory chain protein co-regulation in the human brain. <i>Heliyon</i> , 2022 , 8, e09353	3.6	0
436	Single Cell/Nucleus Transcriptomics Comparison in Zebrafish and Humans Reveals Common and Distinct Molecular Responses to Alzheimer's Disease. <i>Cells</i> , 2022 , 11, 1807	7.9	0
435	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. <i>Nature Communications</i> , 2021 , 12, 7078	17.4	3
434	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
433	Characterization of mitochondrial DNA quantity and quality in the human aged and Alzheimer's disease brain. <i>Molecular Neurodegeneration</i> , 2021 , 16, 75	19	2
432	Cascading epigenomic analysis for identifying disease genes from the regulatory landscape of GWAS variants. <i>PLoS Genetics</i> , 2021 , 17, e1009918	6	0
431	Vaccination Against SARS-CoV-2 in Neuroinflammatory Disease: Early Safety/Tolerability Data.. <i>Multiple Sclerosis and Related Disorders</i> , 2021 , 57, 103433	4	7
430	Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021 , 12, 7035	17.4	0
429	Genome-wide epistasis analysis for Alzheimer's disease and implications for genetic risk prediction. <i>Alzheimer's Research and Therapy</i> , 2021 , 13, 55	9	3

428	Genetic control of the human brain proteome. <i>American Journal of Human Genetics</i> , 2021 , 108, 400-410	11	4
427	Proteomic identification of select protein variants of the SNARE interactome associated with cognitive reserve in a large community sample. <i>Acta Neuropathologica</i> , 2021 , 141, 755-770	14.3	3
426	Gut Microbiome in Progressive Multiple Sclerosis. <i>Annals of Neurology</i> , 2021 , 89, 1195-1211	9.4	27
425	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021 , 20, 2780-2795	5.6	8
424	Novel Variance-Component TWAS method for studying complex human diseases with applications to Alzheimer's dementia. <i>PLoS Genetics</i> , 2021 , 17, e1009482	6	2
423	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021 , 24, 810-817	25.5	13
422	Cortical proteins may provide motor resilience in older adults. <i>Scientific Reports</i> , 2021 , 11, 11311	4.9	2
421	Plasma amyloid β levels are driven by genetic variants near APOE, BACE1, APP, PSEN2: A genome-wide association study in over 12,000 non-demented participants. <i>Alzheimer's and Dementia</i> , 2021 , 17, 1663-1674	1.2	5
420	Associations of social network structure with cognition and amygdala volume in multiple sclerosis: An exploratory investigation. <i>Multiple Sclerosis Journal</i> , 2021 , 13524585211018349	5	1
419	A Genetic Study of Cerebral Atherosclerosis Reveals Novel Associations with and CNOT3. <i>Genes</i> , 2021 , 12,	4.2	1
418	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex. <i>Nature Communications</i> , 2021 , 12, 3517	17.4	8
417	Neurological Immunotoxicity from Cancer Treatment. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	4
416	Deconstructing the epigenomic architecture of human neurodegeneration. <i>Neurobiology of Disease</i> , 2021 , 153, 105331	7.5	
415	A machine learning approach to brain epigenetic analysis reveals kinases associated with Alzheimer's disease. <i>Nature Communications</i> , 2021 , 12, 4472	17.4	9
414	Classifying multiple sclerosis patients on the basis of SDMT performance using machine learning. <i>Multiple Sclerosis Journal</i> , 2021 , 27, 107-116	5	4
413	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel: A Meta-analysis. <i>JAMA Neurology</i> , 2021 , 78, 102-113	17.2	32
412	Brain expression of the vascular endothelial growth factor gene family in cognitive aging and alzheimer's disease. <i>Molecular Psychiatry</i> , 2021 , 26, 888-896	15.1	26
411	Social support is linked to mental health, quality of life, and motor function in multiple sclerosis. <i>Journal of Neurology</i> , 2021 , 268, 1827-1836	5.5	7

410	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. <i>PLoS Genetics</i> , 2021 , 17, e1009224	6	10
409	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021 , 12, 654	17.4	10
408	Brain DNA Methylation Patterns in CLDN5 Associated With Cognitive Decline. <i>Biological Psychiatry</i> , 2021 ,	7.9	5
407	Sex-Specific Association of the X Chromosome With Cognitive Change and Tau Pathology in Aging and Alzheimer Disease. <i>JAMA Neurology</i> , 2021 , 78, 1249-1254	17.2	4
406	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. <i>Neurobiology of Disease</i> , 2021 , 157, 105428	7.5	5
405	Unified AI framework to uncover deep interrelationships between gene expression and Alzheimer's disease neuropathologies. <i>Nature Communications</i> , 2021 , 12, 5369	17.4	2
404	Epigenomic features related to microglia are associated with attenuated effect of APOE ϵ 4 on Alzheimer's disease risk in humans. <i>Alzheimer's and Dementia</i> , 2021 ,	1.2	1
403	Serum metabolomic biomarkers of perceptual speed in cognitively normal and mildly impaired subjects with fasting state stratification. <i>Scientific Reports</i> , 2021 , 11, 18964	4.9	2
402	Stem cell-derived neurons reflect features of protein networks, neuropathology, and cognitive outcome of their aged human donors. <i>Neuron</i> , 2021 , 109, 3402-3420.e9	13.9	9
401	Evaluation of ocrelizumab in older progressive multiple sclerosis patients. <i>Multiple Sclerosis and Related Disorders</i> , 2021 , 55, 103171	4	0
400	Myelin oligodendrocyte glycoprotein (MOG) antibody-mediated disease: The difficulty of predicting relapses. <i>Multiple Sclerosis and Related Disorders</i> , 2021 , 56, 103229	4	3
399	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis. <i>Nature Genetics</i> , 2021 , 53, 143-146	36.3	36
398	RCT of a Telehealth Group-Based Intervention to Increase Physical Activity in Multiple Sclerosis: eFIT. <i>Neurology: Clinical Practice</i> , 2021 , 11, 291-297	1.7	1
397	A cortical immune network map identifies distinct microglial transcriptional programs associated with Amyloid and Tau pathologies. <i>Translational Psychiatry</i> , 2021 , 11, 50	8.6	7
396	Manifestations and impact of the COVID-19 pandemic in neuroinflammatory diseases. <i>Annals of Clinical and Translational Neurology</i> , 2021 , 8, 918-928	5.3	7
395	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies DCDC2 gene as predictor of episodic memory maintenance. <i>Alzheimer's and Dementia</i> , 2021 ,	1.2	1
394	Neuropathologic Correlates of Human Cortical Proteins in Alzheimer Disease and Related Dementias.. <i>Neurology</i> , 2021 ,	6.5	0
393	Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in the impact of APOE ϵ 4.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e057240	1.2	

392	A genome-wide investigation of clinicopathologic endophenotypes uncovers a new susceptibility locus for tau pathology at Neurotrimin (NTM).. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e051682	1.2	
391	Depression contributes to Alzheimer's disease through shared genetic risk.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e053251	1.2	
390	Cell type-specific Alzheimer's disease polygenic risk scores are associated with distinct disease processes in preclinical Alzheimer's disease.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e055304	1.2	
389	Transcriptomic modifiers of the cognitive consequences of apolipoprotein E.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e055817	1.2	
388	Testing a polygenic score for microglial activation against Alzheimer's disease pathology and cognition.. <i>Alzheimer's and Dementia</i> , 2021 , 17 Suppl 3, e057810	1.2	
387	Single cell RNA sequencing of human microglia uncovers a subset that is associated with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020 , 16, e038589	1.2	3
386	Genetic associations with brain amyloidosis. <i>Alzheimer's and Dementia</i> , 2020 , 16, e042191	1.2	
385	Identifying gene expression signatures in individuals with minimal cognitive impairment in the presence of advanced Alzheimer's disease pathology. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043424	1.2	
384	Identifying novel causal genes and proteins in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043523	1.2	
383	Genome-wide association analysis of neurofibrillary tangle burden identifies novel risk loci in the adult changes of thought (ACT) and the religious orders study and memory and aging project (ROSMAP) autopsy cohorts. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043573	1.2	
382	Integrating human brain proteomes and genome-wide association results implicates new genes in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043865	1.2	1
381	Alzheimer's disease GWAS weighted by multi-omics and endophenotypes identifies novel risk loci. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043977	1.2	2
380	Single nucleus and bulk homogenate RNA-sequencing comparison of vascular endothelial growth factor family associations with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020 , 16, e046170	1.2	
379	Leveraging predicted gene expression data for recapitulation of gene coexpression network analysis associations with AD pathology and cognitive decline. <i>Alzheimer's and Dementia</i> , 2020 , 16, e046394	1.2	
378	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020 , 11, 6285	17.4	22
377	EPIGENOMIC FEATURES RELATED TO MICROGLIA ARE ASSOCIATED WITH ATTENUATED EFFECT OF APOE ϵ ON ALZHEIMER'S DISEASE RISK IN HUMANS. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043533	1.2	0
376	The genetics of circulating BDNF: towards understanding the role of BDNF in brain structure and function in middle and old ages. <i>Brain Communications</i> , 2020 , 2, fcaa176	4.5	1
375	The educational impact of childhood-onset multiple sclerosis: Why assessing academic achievement is imperative. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 1633-1637	5	1

374	Association Between Common Variants in RBFox1, an RNA-Binding Protein, and Brain Amyloidosis in Early and Preclinical Alzheimer Disease. <i>JAMA Neurology</i> , 2020 , 77, 1288-1298	17.2	17
373	Synonymous variants associated with Alzheimer disease in multiplex families. <i>Neurology: Genetics</i> , 2020 , 6, e450	3.8	2
372	Switching from natalizumab to ocrelizumab in patients with multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 1964-1965	5	9
371	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. <i>Neuron</i> , 2020 , 107, 496-508.e6	13.9	12
370	Shared Causal Paths underlying Alzheimer's dementia and Type 2 Diabetes. <i>Scientific Reports</i> , 2020 , 10, 4107	4.9	13
369	Cortical Proteins Associated With Cognitive Resilience in Community-Dwelling Older Persons. <i>JAMA Psychiatry</i> , 2020 , 77, 1172-1180	14.5	21
368	Immunogenetics of neurological disease 2020 , 71-80		
367	Human Herpesvirus 6 Detection in Alzheimer's Disease Cases and Controls across Multiple Cohorts. <i>Neuron</i> , 2020 , 105, 1027-1035.e2	13.9	47
366	Genetic and gene expression signatures in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 576-583		7
365	Exceptionally low likelihood of Alzheimer's dementia in APOE2 homozygotes from a 5,000-person neuropathological study. <i>Nature Communications</i> , 2020 , 11, 667	17.4	113
364	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. <i>Nature Medicine</i> , 2020 , 26, 769-780	50.5	226
363	Genome-wide interaction analysis of pathological hallmarks in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2020 , 93, 61-68	5.6	16
362	Brain microRNAs associated with late-life depressive symptoms are also associated with cognitive trajectory and dementia. <i>Npj Genomic Medicine</i> , 2020 , 5, 6	6.2	25
361	eSupport: Feasibility trial of telehealth support group participation to reduce loneliness in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 1797-1800	5	11
360	APOE ϵ -specific associations of VEGF gene family expression with cognitive aging and Alzheimer's disease. <i>Neurobiology of Aging</i> , 2020 , 87, 18-25	5.6	7
359	Integrated analysis of the aging brain transcriptome and proteome in tauopathy. <i>Molecular Neurodegeneration</i> , 2020 , 15, 56	19	6
358	Bayesian Genome-wide TWAS Method to Leverage both cis- and trans-eQTL Information through Summary Statistics. <i>American Journal of Human Genetics</i> , 2020 , 107, 714-726	11	7
357	Cross-Species Analyses Identify Dlgap2 as a Regulator of Age-Related Cognitive Decline and Alzheimer's Dementia. <i>Cell Reports</i> , 2020 , 32, 108091	10.6	10

356	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020 , 7, 340	8.2	26
355	Considerations for integrative multi-omic approaches to explore Alzheimer's disease mechanisms. <i>Brain Pathology</i> , 2020 , 30, 984-991	6	4
354	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020 , 32, 107908	10.6	68
353	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. <i>Nature Communications</i> , 2020 , 11, 6129	17.4	102
352	Molecular estimation of neurodegeneration pseudotime in older brains. <i>Nature Communications</i> , 2020 , 11, 5781	17.4	6
351	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 are implicated in tau pathology. <i>Molecular Neurodegeneration</i> , 2020 , 15, 44	19	9
350	Association between DNA methylation levels in brain tissue and late-life depression in community-based participants. <i>Translational Psychiatry</i> , 2020 , 10, 262	8.6	13
349	A second X chromosome contributes to resilience in a mouse model of Alzheimer's disease. <i>Science Translational Medicine</i> , 2020 , 12,	17.5	40
348	Fatal COVID-19 in an MS patient on natalizumab: A case report. <i>Multiple Sclerosis Journal - Experimental, Translational and Clinical</i> , 2020 , 6, 2055217320942931	2	6
347	Deconvolving the contributions of cell-type heterogeneity on cortical gene expression. <i>PLoS Computational Biology</i> , 2020 , 16, e1008120	5	17
346	Peripheral serum metabolomic profiles inform central cognitive impairment. <i>Scientific Reports</i> , 2020 , 10, 14059	4.9	8
345	Phenome-wide examination of comorbidity burden and multiple sclerosis disease severity. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2020 , 7,	9.1	9
344	Association of social network structure and physical function in patients with multiple sclerosis. <i>Neurology</i> , 2020 , 95, e1565-e1574	6.5	6
343	Genetic data and cognitively defined late-onset Alzheimer's disease subgroups. <i>Molecular Psychiatry</i> , 2020 , 25, 2942-2951	15.1	27
342	A pharmacogenetic study implicates in the response to Interferon- β in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 1074-1082	5	1
341	A novel Tmem119-tdTomato reporter mouse model for studying microglia in the central nervous system. <i>Brain, Behavior, and Immunity</i> , 2020 , 83, 180-191	16.6	33
340	The genetic diversity of multiple sclerosis risk among Hispanic and African American populations living in the United States. <i>Multiple Sclerosis Journal</i> , 2020 , 26, 1329-1339	5	7
339	Bayesian integrative analysis of epigenomic and transcriptomic data identifies Alzheimer's disease candidate genes and networks. <i>PLoS Computational Biology</i> , 2020 , 16, e1007771	5	7

338	Characteristics of Epigenetic Clocks Across Blood and Brain Tissue in Older Women and Men. <i>Frontiers in Neuroscience</i> , 2020 , 14, 555307	5.1	6
337	The Caribbean-Hispanic Alzheimer's brain transcriptome reveals ancestry-specific disease mechanisms. <i>Alzheimer's and Dementia</i> , 2020 , 16, e043068	1.2	2
336	Using Transcriptomic Hidden Variables to Infer Context-Specific Genotype Effects in the Brain. <i>American Journal of Human Genetics</i> , 2019 , 105, 562-572	11	3
335	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019 , 365,	33.3	309
334	Genetic risk for Alzheimer's dementia predicts motor deficits through multi-omic systems in older adults. <i>Translational Psychiatry</i> , 2019 , 9, 241	8.6	2
333	Cognition may link cortical IGFBP5 levels with motor function in older adults. <i>PLoS ONE</i> , 2019 , 14, e0220968	3.7	6
332	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019 , 10, 409	17.4	59
331	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by APOE Genotype. <i>JAMA Neurology</i> , 2019 , 76, 1099-1108	17.2	18
330	CpG-related SNPs in the MS4A region have a dose-dependent effect on risk of late-onset Alzheimer disease. <i>Aging Cell</i> , 2019 , 18, e12964	9.9	6
329	Genome-wide association studies of alcohol dependence, DSM-IV criterion count and individual criteria. <i>Genes, Brain and Behavior</i> , 2019 , 18, e12579	3.6	22
328	Association of Cortical β Amyloid Protein in the Absence of Insoluble Deposits With Alzheimer Disease. <i>JAMA Neurology</i> , 2019 , 76, 818-826	17.2	17
327	The Impact of MRI T1 Hypointense Brain Lesions on Cerebral Deep Gray Matter Volume Measures in Multiple Sclerosis. <i>Journal of Neuroimaging</i> , 2019 , 29, 458-462	2.8	1
326	An UNC5C Allele Predicts Cognitive Decline and Hippocampal Atrophy in Clinically Normal Older Adults. <i>Journal of Alzheimer's Disease</i> , 2019 , 68, 1161-1170	4.3	1
325	Gene expression and DNA methylation are extensively coordinated with MRI-based brain microstructural characteristics. <i>Brain Imaging and Behavior</i> , 2019 , 13, 963-972	4.1	10
324	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. <i>Communications Biology</i> , 2019 , 2, 285	6.7	14
323	cindr, the Drosophila Homolog of the CD2AP Alzheimer's Disease Risk Gene, Is Required for Synaptic Transmission and Proteostasis. <i>Cell Reports</i> , 2019 , 28, 1799-1813.e5	10.6	16
322	The landscape of myeloid and astrocyte phenotypes in acute multiple sclerosis lesions. <i>Acta Neuropathologica Communications</i> , 2019 , 7, 130	7.3	27
321	Microstructural changes in the brain mediate the association of AK4, IGFBP5, HSPB2, and ITPK1 with cognitive decline. <i>Neurobiology of Aging</i> , 2019 , 84, 17-25	5.6	4

320	Early complement genes are associated with visual system degeneration in multiple sclerosis. <i>Brain</i> , 2019 , 142, 2722-2736	11.2	13
319	Sex differences in the genetic predictors of Alzheimer's pathology. <i>Brain</i> , 2019 , 142, 2581-2589	11.2	32
318	Integrating Gene and Protein Expression Reveals Perturbed Functional Networks in Alzheimer's Disease. <i>Cell Reports</i> , 2019 , 28, 1103-1116.e4	10.6	34
317	Somatic mosaicism of sex chromosomes in the blood and brain. <i>Brain Research</i> , 2019 , 1721, 146345	3.7	18
316	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019 , 10, 2907	17.4	62
315	TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. <i>American Journal of Human Genetics</i> , 2019 , 105, 258-266	11	31
314	Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA Splicing and Neurodegeneration in Alzheimer's Disease. <i>Cell Reports</i> , 2019 , 29, 301-316.e10	10.6	50
313	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
312	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A β tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019 , 51, 414-430	36.3	917
311	P4-496: MYELOID CELL-SPECIFIC ALZHEIMER'S DISEASE POLYGENIC RISK SCORE PREDICTS NEURODEGENERATION AND A β RELATED COGNITIVE DECLINE IN COGNITIVELY NORMAL OLDER ADULTS 2019 , 15, P1503-P1504	4.6	36
310	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019 , 51, 1624-1636	36	81
309	Sleep fragmentation, microglial aging, and cognitive impairment in adults with and without Alzheimer's dementia. <i>Science Advances</i> , 2019 , 5, eaax7331	14.3	22
308	DNA methylation variability in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019 , 76, 35-44	5.6	16
307	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer's human brains. <i>Nature Neuroscience</i> , 2019 , 22, 37-46	25.5	99
306	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019 ,	6.5	17
305	Candidate-based screening via gene modulation in human neurons and astrocytes implicates FERMT2 in A β and TAU proteostasis. <i>Human Molecular Genetics</i> , 2019 , 28, 718-735	5.6	17
304	Altered bile acid profile associates with cognitive impairment in Alzheimer's disease-An emerging role for gut microbiome. <i>Alzheimer's and Dementia</i> , 2019 , 15, 76-92	1.2	208
303	A Bayesian Framework for Generalized Linear Mixed Modeling Identifies New Candidate Loci for Late-Onset Alzheimer's Disease. <i>Genetics</i> , 2018 , 209, 51-64	4	5

302	What is the epigenome and is it involved in multiple sclerosis?. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 268-269		0
301	How do we measure the epigenome(s)?. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 446-448	5	
300	MS genetic risk promotes IFN γ CD4 T cells. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018 , 5, e414	9.1	4
299	Loneliness 5 years ante-mortem is associated with disease-related differential gene expression in postmortem dorsolateral prefrontal cortex. <i>Translational Psychiatry</i> , 2018 , 8, 2	8.6	15
298	A transcriptomic atlas of aged human microglia. <i>Nature Communications</i> , 2018 , 9, 539	17.4	223
297	The era of GWAS is over - No. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 258-260	5	2
296	Integrated biology approach reveals molecular and pathological interactions among Alzheimer's A β 2, Tau, TREM2, and TYROBP in Drosophila models. <i>Genome Medicine</i> , 2018 , 10, 26	14.4	11
295	Designing an epigenomic study. <i>Multiple Sclerosis Journal</i> , 2018 , 24, 604-609	5	
294	Elevated DNA methylation across a 48-kb region spanning the HOXA gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimer's and Dementia</i> , 2018 , 14, 1580-1588	1.2	73
293	Genetic influence of plasma homocysteine on Alzheimer's disease. <i>Neurobiology of Aging</i> , 2018 , 62, 243-247	5.76	243.714
292	Evaluation of TDP-43 proteinopathy and hippocampal sclerosis in relation to APOE ϵ 4 haplotype status: a community-based cohort study. <i>Lancet Neurology</i> , 2018 , 17, 773-781	24.1	64
291	Multi-omic Directed Networks Describe Features of Gene Regulation in Aged Brains and Expand the Set of Genes Driving Cognitive Decline. <i>Frontiers in Genetics</i> , 2018 , 9, 294	4.5	14
290	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018 , 360,	33.3	666
289	Polygenic analysis of inflammatory disease variants and effects on microglia in the aging brain. <i>Molecular Neurodegeneration</i> , 2018 , 13, 38	19	22
288	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018 , 50, 1140-1150	36.3	74
287	Common variation near IRF6 is associated with IFN γ -induced liver injury in multiple sclerosis. <i>Nature Genetics</i> , 2018 , 50, 1081-1085	36.3	28
286	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. <i>JAMA Neurology</i> , 2018 , 75, 989-998	17.2	142
285	ϵ 4 genotype, incident AD and MCI, cognitive decline, and AD pathology in older adults. <i>Neurology</i> , 2018 , 90, e2127-e2134	6.5	25

284	The human brainome: network analysis identifies HSPA2 as a novel Alzheimer's disease target. <i>Brain</i> , 2018 , 141, 2721-2739	11.2	19
283	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. <i>Annals of Neurology</i> , 2018 , 84, 78-88	9.4	56
282	Tau Activates Transposable Elements in Alzheimer's Disease. <i>Cell Reports</i> , 2018 , 23, 2874-2880	10.6	116
281	P2-137: COMPARISON OF GENE EXPRESSION PROFILE OF ALZHEIMER'S DISEASE USING MODULAR MAXIMIZATION ALGORITHM REVEALS OPPOSING ROLES FOR TGIF AND EGR3 2018 , 14, P720-P720		
280	F2-03-04: SYSTEMS BIOLOGY/ANALYSIS OF COMPLEX SYSTEMS 2018 , 14, P605-P606		
279	P3-136: MODULE QUANTITATIVE TRAIT LOCI ANALYSIS IMPLICATES TMEM106B AND RBFOX1 AS KEY BRAIN TRANSCRIPTOME REGULATORS IN OLDER ADULTS 2018 , 14, P1120-P1120		
278	O5-04-04: CANDIDATE EPIGENETIC MODIFIERS OF TAU PATHOLOGICAL BURDEN IN PRIMARY AGE-RELATED TAUOPATHY 2018 , 14, P1652-P1652		
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273	A scalable online tool for quantitative social network assessment reveals potentially modifiable social environmental risks. <i>Nature Communications</i> , 2018 , 9, 3930	17.4	19
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271	Deconstructing and targeting the genomic architecture of human neurodegeneration. <i>Nature Neuroscience</i> , 2018 , 21, 1310-1317	25.5	27
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260	Selection of first-line therapy in multiple sclerosis using risk-benefit decision analysis. <i>Neurology</i> , 2017 , 88, 677-684	6.5	15
259	Assessment of Early Evidence of Multiple Sclerosis in a Prospective Study of Asymptomatic High-Risk Family Members. <i>JAMA Neurology</i> , 2017 , 74, 293-300	17.2	23
258	Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. <i>Nature Genetics</i> , 2017 , 49, 600-605	26.3	124
257	Genome-wide association study identifies four novel loci associated with Alzheimer's endophenotypes and disease modifiers. <i>Acta Neuropathologica</i> , 2017 , 133, 839-856	14.3	107
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255	Circadian alterations during early stages of Alzheimer's disease are associated with aberrant cycles of DNA methylation in BMAL1. <i>Alzheimer's and Dementia</i> , 2017 , 13, 689-700	1.2	55
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239	A human microglia-like cellular model for assessing the effects of neurodegenerative disease gene variants. <i>Science Translational Medicine</i> , 2017 , 9,	17.5	59
238	[P4083]: A DOPAMINE RECEPTOR GENETIC VARIANT ENHANCES PERCEPTUAL SPEED IN COGNITIVELY HEALTHY SUBJECTS 2017 , 13, P1291-P1291		
237	[P1154]: APOE ε IS ASSOCIATED WITH HIGHER TDP-43 PROTEINOPATHY BURDEN IN ALZHEIMER'S DISEASE 2017 , 13, P301-P302		
236	[P2115]: A TMEM106B LOCUS IS IMPLICATED IN COGNITIVE DECLINE IN ALZHEIMER'S DISEASE 2017 , 13, P650-P651		
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205	P4-031: Integrative Network Analysis of Multiple Alzheimer's Disease Rnaseq Studies From the Accelerating Medicine Partnership-Alzheimer's Disease Consortium 2016 , 12, P1026-P1027		1
204	EC-02-04: Interactions Between TREM2 And CD33 and the Discovery of Novel Targets for AD Therapy 2016 , 12, P214-P214		
203	F2-01-02: Pathway Discovery, Validation and Compound Identification for Alzheimer's Disease 2016 , 12, P215-P215		
202	O2-10-04: A Regulatory Variant at the TREM Gene Cluster Associates with Decreased Alzheimer's Disease Risk and Increased TREM1 and TREM2 Brain Gene Expression 2016 , 12, P251-P252		
201	P4-293: APOE ϵ 4/TOMM40 ϵ 23 Haplotypes and the Risk of Alzheimer's Disease in Older Caucasian and African Americans 2016 , 12, P1146-P1146		
200	P4-295: TOMM40 ϵ 23 Variant and Cognitive Decline in Community Based Older Persons with APOE E3/3 GENOTYPE 2016 , 12, P1146-P1147		
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21	A Consensus Proteomic Analysis of Alzheimer's Disease Brain and Cerebrospinal Fluid Reveals Early Changes in Energy Metabolism Associated with Microglia and Astrocyte Activation		1
20	Integrative analyses of splicing in the aging brain: role in susceptibility to Alzheimer's Disease		8
19	A meta-analysis of epigenome-wide association studies in Alzheimer's disease highlights novel differentially methylated loci across cortex		8
18	The Caribbean-Hispanic Alzheimer's Brain Transcriptome Reveals Ancestry-Specific Disease Mechanisms		3
17	Single Cell-type Integrative Network Modeling Identified Novel Microglial-specific Targets for the Phagosome in Alzheimer's disease		1
16	Multi-cellular communities are perturbed in the aging human brain and with Alzheimer's disease		4
15	A Bayesian approach to mediation analysis predicts 206 causal target genes in Alzheimer's disease		7

14	A cortical immune network map identifies a subset of human microglia involved in Tau pathology	8
13	Epigenome-wide study uncovers tau pathology-driven changes of chromatin organization in the aging human brain	4
12	Altered Bile Acid Profile Associates with Cognitive Impairment in Alzheimer's Disease [An Emerging Role for Gut Microbiome	2
11	A single cell-based atlas of human microglial states reveals associations with neurological disorders and histopathological features of the aging brain	13
10	Genetic data and cognitively-defined late-onset Alzheimer's disease subgroups	5
9	TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits	4
8	BIN1 protein isoforms are differentially expressed in astrocytes, neurons, and microglia: neuronal and astrocyte BIN1 implicated in Tau pathology	1
7	Deconvolving the contributions of cell-type heterogeneity on cortical gene expression	4
6	Brain microRNAs associated with late-life depressive symptoms are also associated with cognitive trajectory and dementia	1
5	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions	7
4	A Novel Tmem119-tdTomato Reporter Mouse Model for Studying Microglia in the Central Nervous System	1
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