

Philip L De Jager

List of Publications by Year in descending order

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Version: 2024-02-01

432
papers

69,735
citations

1301

109
h-index

962

238
g-index

517
all docs

517
docs citations

517
times ranked

71606
citing authors

#	ARTICLE	IF	CITATIONS
1	Brain DNA Methylation Patterns in CLDN5 Associated With Cognitive Decline. <i>Biological Psychiatry</i> , 2022, 91, 389-398.	1.3	25
2	Associations of social network structure with cognition and amygdala volume in multiple sclerosis: An exploratory investigation. <i>Multiple Sclerosis Journal</i> , 2022, 28, 228-236.	3.0	4
3	Epigenomic features related to microglia are associated with attenuated effect of <i>APOE</i> ϵ 4 on Alzheimer's disease risk in humans. <i>Alzheimer's and Dementia</i> , 2022, 18, 688-699.	0.8	9
4	Vaccination Against SARS-CoV-2 in Neuroinflammatory Disease: Early Safety/Tolerability Data. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 57, 103433.	2.0	26
5	Worsening physical functioning in patients with neuroinflammatory disease during the COVID-19 pandemic. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 58, 103482.	2.0	11
6	Brain microRNAs are associated with variation in cognitive trajectory in advanced age. <i>Translational Psychiatry</i> , 2022, 12, 47.	4.8	7
7	Hypogonadism in men with multiple sclerosis: Prevalence and clinical associations. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 59, 103508.	2.0	2
8	Exploring cortical proteins underlying the relation of neuroticism to cognitive resilience. <i>Aging Brain</i> , 2022, 2, 100031.	1.3	0
9	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, 213-225.	14.8	202
10	Cortical Proteins and Individual Differences in Cognitive Resilience in Older Adults. <i>Neurology</i> , 2022, 98, .	1.1	22
11	Integration of GWAS and brain transcriptomic analyses in a multiethnic sample of 35,245 older adults identifies <i>DCDC2</i> gene as predictor of episodic memory maintenance. <i>Alzheimer's and Dementia</i> , 2022, 18, 1797-1811.	0.8	5
12	Neuropathologic Correlates of Human Cortical Proteins in Alzheimer Disease and Related Dementias. <i>Neurology</i> , 2022, 98, .	1.1	9
13	Whole genome sequencing-based copy number variations reveal novel pathways and targets in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2022, 18, 1846-1867.	0.8	13
14	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.	3.3	12
15	A multi-step genomic approach prioritized <i>TBKBP1</i> gene as relevant for multiple sclerosis susceptibility. <i>Journal of Neurology</i> , 2022, 269, 4510-4522.	3.6	2
16	Mitochondrial respiratory chain protein co-regulation in the human brain. <i>Heliyon</i> , 2022, 8, e09353.	3.2	4
17	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.	4.1	19
18	FMNL2 regulates gliovascular interactions and is associated with vascular risk factors and cerebrovascular pathology in Alzheimer's disease. <i>Acta Neuropathologica</i> , 2022, 144, 59-79.	7.7	19

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19	Neuroimmune contributions to Alzheimer's disease: a focus on human data. <i>Molecular Psychiatry</i> , 2022, 27, 3164-3181.	7.9	20
20	The impact of socioeconomic status on subsequent neurological outcomes in multiple sclerosis. <i>Multiple Sclerosis and Related Disorders</i> , 2022, 65, 103994.	2.0	12
21	RNASE6 is a novel modifier of APOE- ϵ 4 effects on cognition. <i>Neurobiology of Aging</i> , 2022, 118, 66-76.	3.1	5
22	Classifying multiple sclerosis patients on the basis of SDMT performance using machine learning. <i>Multiple Sclerosis Journal</i> , 2021, 27, 107-116.	3.0	19
23	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. <i>JAMA Neurology</i> , 2021, 78, 102.	9.0	144
24	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.	7.9	71
25	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.	3.6	11
26	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. <i>PLoS Genetics</i> , 2021, 17, e1009224.	3.5	43
27	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	12.8	75
28	Genome-wide epistasis analysis for Alzheimer's disease and implications for genetic risk prediction. <i>Alzheimer's Research and Therapy</i> , 2021, 13, 55.	6.2	24
29	Genetic control of the human brain proteome. <i>American Journal of Human Genetics</i> , 2021, 108, 400-410.	6.2	52
30	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.	7.7	6
31	Gut Microbiome in Progressive Multiple Sclerosis. <i>Annals of Neurology</i> , 2021, 89, 1195-1211.	5.3	115
32	Enhancing Top-Down Proteomics of Brain Tissue with FAIMS. <i>Journal of Proteome Research</i> , 2021, 20, 2780-2795.	3.7	36
33	Novel Variance-Component TWAS method for studying complex human diseases with applications to Alzheimer's dementia. <i>PLoS Genetics</i> , 2021, 17, e1009482.	3.5	36
34	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021, 24, 810-817.	14.8	85
35	Cortical proteins may provide motor resilience in older adults. <i>Scientific Reports</i> , 2021, 11, 11311.	3.3	14
36	Plasma amyloid β levels are driven by genetic variants near <i>APOE</i> , <i>BACE1</i> , <i>APP</i> , <i>PSEN2</i> : A genome-wide association study in over 12,000 non-demented participants. <i>Alzheimer's and Dementia</i> , 2021, 17, 1663-1674.	0.8	20

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37	A Genetic Study of Cerebral Atherosclerosis Reveals Novel Associations with NTNG1 and CNOT3. <i>Genes</i> , 2021, 12, 815.	2.4	3
38	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.	12.8	72
39	Neurological Immunotoxicity from Cancer Treatment. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6716.	4.1	9
40	Deconstructing the epigenomic architecture of human neurodegeneration. <i>Neurobiology of Disease</i> , 2021, 153, 105331.	4.4	1
41	A machine learning approach to brain epigenetic analysis reveals kinases associated with Alzheimer's disease. <i>Nature Communications</i> , 2021, 12, 4472.	12.8	28
42	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.	9.0	35
43	The association of epigenetic clocks in brain tissue with brain pathologies and common aging phenotypes. <i>Neurobiology of Disease</i> , 2021, 157, 105428.	4.4	36
44	Unified AI framework to uncover deep interrelationships between gene expression and Alzheimer's disease neuropathologies. <i>Nature Communications</i> , 2021, 12, 5369.	12.8	8
45	Serum metabolomic biomarkers of perceptual speed in cognitively normal and mildly impaired subjects with fasting state stratification. <i>Scientific Reports</i> , 2021, 11, 18964.	3.3	15
46	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.	8.1	75
47	Evaluation of ocrelizumab in older progressive multiple sclerosis patients. <i>Multiple Sclerosis and Related Disorders</i> , 2021, 55, 103171.	2.0	5
48	Myelin oligodendrocyte glycoprotein (MOG) antibody-mediated disease: The difficulty of predicting relapses. <i>Multiple Sclerosis and Related Disorders</i> , 2021, 56, 103229.	2.0	16
49	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.	21.4	158
50	RCT of a Telehealth Group-Based Intervention to Increase Physical Activity in Multiple Sclerosis. <i>Neurology: Clinical Practice</i> , 2021, 11, 291-297.	1.6	5
51	A cortical immune network map identifies distinct microglial transcriptional programs associated with β^2 -amyloid and Tau pathologies. <i>Translational Psychiatry</i> , 2021, 11, 50.	4.8	19
52	Manifestations and impact of the COVID-19 pandemic in neuroinflammatory diseases. <i>Annals of Clinical and Translational Neurology</i> , 2021, 8, 918-928.	3.7	21
53	Genetic factors implicated in the response to fingolimod treatment in multiple sclerosis patients: results from a pharmacogenetic meta-analysis. <i>Journal of the Neurological Sciences</i> , 2021, 429, 117750.	0.6	0
54	Characterization of mitochondrial DNA quantity and quality in the human aged and Alzheimer's disease brain. <i>Molecular Neurodegeneration</i> , 2021, 16, 75.	10.8	44

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55	Cascading epigenomic analysis for identifying disease genes from the regulatory landscape of GWAS variants. <i>PLoS Genetics</i> , 2021, 17, e1009918.	3.5	2
56	Atlas of RNA editing events affecting protein expression in aged and Alzheimer's disease human brain tissue. <i>Nature Communications</i> , 2021, 12, 7035.	12.8	19
57	Proximal and distal effects of genetic susceptibility to multiple sclerosis on the T cell epigenome. <i>Nature Communications</i> , 2021, 12, 7078.	12.8	15
58	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
59	Multi-region brain transcriptomes uncover two subtypes of aging individuals with differences in the impact of <i>APOEε4</i> . <i>Alzheimer's and Dementia</i> , 2021, 17, e057240.	0.8	1
60	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.	0.8	0
61	Depression contributes to Alzheimer's disease through shared genetic risk.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e053251.	0.8	0
62	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.	0.8	0
63	Transcriptomic modifiers of the cognitive consequences of apolipoprotein E.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e055817.	0.8	0
64	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.	0.8	0
65	Genetic data and cognitively defined late-onset Alzheimer's disease subgroups. <i>Molecular Psychiatry</i> , 2020, 25, 2942-2951.	7.9	57
66	A pharmacogenetic study implicates NIN2 in the response to Interferon- γ in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1074-1082.	3.0	5
67	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.	4.1	56
68	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.	3.0	23
69	eSupport: Feasibility trial of telehealth support group participation to reduce loneliness in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1797-1800.	3.0	16
70	APOE ϵ 4-specific associations of VEGF gene family expression with cognitive aging and Alzheimer's disease. <i>Neurobiology of Aging</i> , 2020, 87, 18-25.	3.1	24
71	Integrated analysis of the aging brain transcriptome and proteome in tauopathy. <i>Molecular Neurodegeneration</i> , 2020, 15, 56.	10.8	22
72	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.	6.2	53

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73	Cross-Species Analyses Identify Dlgap2 as a Regulator of Age-Related Cognitive Decline and Alzheimer's Disease. <i>Cell Reports</i> , 2020, 32, 108091.	6.4	27
74	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
75	Considerations for integrative multi-omic approaches to explore Alzheimer's disease mechanisms. <i>Brain Pathology</i> , 2020, 30, 984-991.	4.1	11
76	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. <i>Cell Reports</i> , 2020, 32, 107908.	6.4	199
77	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 6129.	12.8	371
78	Molecular estimation of neurodegeneration pseudotime in older brains. <i>Nature Communications</i> , 2020, 11, 5781.	12.8	26
79	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.	10.8	32
80	Association between DNA methylation levels in brain tissue and late-life depression in community-based participants. <i>Translational Psychiatry</i> , 2020, 10, 262.	4.8	24
81	A second X chromosome contributes to resilience in a mouse model of Alzheimer's disease. <i>Science Translational Medicine</i> , 2020, 12, .	12.4	107
82	Fatal COVID-19 in an MS patient on natalizumab: A case report. <i>Multiple Sclerosis Journal - Experimental, Translational and Clinical</i> , 2020, 6, 205521732094293.	1.0	8
83	Deconvolving the contributions of cell-type heterogeneity on cortical gene expression. <i>PLoS Computational Biology</i> , 2020, 16, e1008120.	3.2	66
84	Peripheral serum metabolomic profiles inform central cognitive impairment. <i>Scientific Reports</i> , 2020, 10, 14059.	3.3	25
85	Phenome-wide examination of comorbidity burden and multiple sclerosis disease severity. <i>Neurology: Neuroimmunology and Neuroinflammation</i> , 2020, 7, .	6.0	17
86	Association of social network structure and physical function in patients with multiple sclerosis. <i>Neurology</i> , 2020, 95, e1565-e1574.	1.1	21
87	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.	0.8	18
88	Genetic associations with brain amyloidosis. <i>Alzheimer's and Dementia</i> , 2020, 16, e042191.	0.8	0
89	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.	0.8	0
90	Identifying novel causal genes and proteins in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e043523.	0.8	1

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91	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.	0.8	0
92	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.	0.8	1
93	Alzheimer's disease GWAS weighted by multi-omics and endophenotypes identifies novel risk loci. <i>Alzheimer's and Dementia</i> , 2020, 16, e043977.	0.8	4
94	Single nucleus and bulk homogenate RNA-seq comparison of vascular endothelial growth factor family associations with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2020, 16, e046170.	0.8	0
95	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.	0.8	0
96	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
97	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> , 2020, 16, e043533.	0.8	2
98	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.	3.3	14
99	The educational impact of childhood-onset multiple sclerosis: Why assessing academic achievement is imperative. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1633-1637.	3.0	1
100	Association Between Common Variants in <i>RBFOX1</i> , an RNA-Binding Protein, and Brain Amyloidosis in Early and Preclinical Alzheimer Disease. <i>JAMA Neurology</i> , 2020, 77, 1288.	9.0	41
101	Synonymous variants associated with Alzheimer disease in multiplex families. <i>Neurology: Genetics</i> , 2020, 6, e450.	1.9	9
102	Switching from natalizumab to ocrelizumab in patients with multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020, 26, 1964-1965.	3.0	13
103	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. <i>Neuron</i> , 2020, 107, 496-508.e6.	8.1	29
104	Shared Causal Paths underlying Alzheimer's dementia and Type 2 Diabetes. <i>Scientific Reports</i> , 2020, 10, 4107.	3.3	37
105	Cortical Proteins Associated With Cognitive Resilience in Community-Dwelling Older Persons. <i>JAMA Psychiatry</i> , 2020, 77, 1172.	11.0	70
106	Immunogenetics of neurological disease. , 2020, , 71-80.		0
107	Human Herpesvirus 6 Detection in Alzheimer's Disease Cases and Controls across Multiple Cohorts. <i>Neuron</i> , 2020, 105, 1027-1035.e2.	8.1	87
108	Genetic and gene expression signatures in multiple sclerosis. <i>Multiple Sclerosis Journal</i> , 2020, 26, 576-581.	3.0	17

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109	Exceptionally low likelihood of Alzheimer's dementia in APOE2 homozygotes from a 5,000-person neuropathological study. <i>Nature Communications</i> , 2020, 11, 667.	12.8	246
110	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.	30.7	547
111	Bayesian integrative analysis of epigenomic and transcriptomic data identifies Alzheimer's disease candidate genes and networks. <i>PLoS Computational Biology</i> , 2020, 16, e1007771.	3.2	10
112	Characteristics of Epigenetic Clocks Across Blood and Brain Tissue in Older Women and Men. <i>Frontiers in Neuroscience</i> , 2020, 14, 555307.	2.8	32
113	The Caribbean-Hispanic Alzheimer's brain transcriptome reveals ancestry-specific disease mechanisms. <i>Alzheimer's and Dementia</i> , 2020, 16, e043068.	0.8	3
114	Genome-wide interaction analysis of pathological hallmarks in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2020, 93, 61-68.	3.1	63
115	Brain microRNAs associated with late-life depressive symptoms are also associated with cognitive trajectory and dementia. <i>Npj Genomic Medicine</i> , 2020, 5, 6.	3.8	43
116	Gene expression and DNA methylation are extensively coordinated with MRI-based brain microstructural characteristics. <i>Brain Imaging and Behavior</i> , 2019, 13, 963-972.	2.1	24
117	A genome-wide association study identifies genetic loci associated with specific lobar brain volumes. <i>Communications Biology</i> , 2019, 2, 285.	4.4	27
118	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.	6.4	27
119	The landscape of myeloid and astrocyte phenotypes in acute multiple sclerosis lesions. <i>Acta Neuropathologica Communications</i> , 2019, 7, 130.	5.2	41
120	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.	3.1	11
121	Early complement genes are associated with visual system degeneration in multiple sclerosis. <i>Brain</i> , 2019, 142, 2722-2736.	7.6	30
122	Sex differences in the genetic predictors of Alzheimer's pathology. <i>Brain</i> , 2019, 142, 2581-2589.	7.6	65
123	Integrating Gene and Protein Expression Reveals Perturbed Functional Networks in Alzheimer's Disease. <i>Cell Reports</i> , 2019, 28, 1103-1116.e4.	6.4	67
124	Somatic mosaicism of sex chromosomes in the blood and brain. <i>Brain Research</i> , 2019, 1721, 146345.	2.2	30
125	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	12.8	117
126	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.	6.2	84

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127	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.	6.4	118
128	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
129	Using Transcriptomic Hidden Variables to Infer Context-Specific Genotype Effects in the Brain. <i>American Journal of Human Genetics</i> , 2019, 105, 562-572.	6.2	7
130	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	12.6	710
131	Genetic risk for Alzheimer's dementia predicts motor deficits through multi-omic systems in older adults. <i>Translational Psychiatry</i> , 2019, 9, 241.	4.8	11
132	Cognition may link cortical IGFBP5 levels with motor function in older adults. <i>PLoS ONE</i> , 2019, 14, e0220968.	2.5	8
133	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019, 10, 409.	12.8	121
134	Analysis of Whole-Exome Sequencing Data for Alzheimer Disease Stratified by <i>APOE</i> Genotype. <i>JAMA Neurology</i> , 2019, 76, 1099.	9.0	32
135	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.	6.7	8
136	Genome-wide association studies of alcohol dependence, DSM-IV criterion count and individual criteria. <i>Genes, Brain and Behavior</i> , 2019, 18, e12579.	2.2	56
137	Association of Cortical β -Amyloid Protein in the Absence of Insoluble Deposits With Alzheimer Disease. <i>JAMA Neurology</i> , 2019, 76, 818.	9.0	25
138	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.	2.0	2
139	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.	2.6	5
140	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates β , tau, immunity and lipid processing. <i>Nature Genetics</i> , 2019, 51, 414-430.	21.4	1,962
141	P4496: MYELOID CELL-SPECIFIC ALZHEIMER'S DISEASE POLYGENIC RISK SCORE PREDICTS NEURODEGENERATION AND β -RELATED COGNITIVE DECLINE IN COGNITIVELY NORMAL OLDER ADULTS. <i>Alzheimer's and Dementia</i> , 2019, 15, P1503.	0.8	0
142	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
143	Sleep fragmentation, microglial aging, and cognitive impairment in adults with and without Alzheimer's dementia. <i>Science Advances</i> , 2019, 5, eaax7331.	10.3	55
144	DNA methylation variability in Alzheimer's disease. <i>Neurobiology of Aging</i> , 2019, 76, 35-44.	3.1	25

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145	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.	14.8	188
146	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019, 92, .	1.1	30
147	Candidate-based screening via gene modulation in human neurons and astrocytes implicates <i>FERMT2</i> and <i>TAU</i> proteostasis. <i>Human Molecular Genetics</i> , 2019, 28, 718-735.	2.9	33
148	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.	0.8	396
149	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.	2.9	12
150	What is the epigenome and is it involved in multiple sclerosis?. <i>Multiple Sclerosis Journal</i> , 2018, 24, 268-269.	3.0	1
151	How do we measure the epigenome(s)?. <i>Multiple Sclerosis Journal</i> , 2018, 24, 446-448.	3.0	0
152	MS <i>AHI1</i> genetic risk promotes $IFN\gamma$ CD4 T cells. <i>Neurology: Neuroimmunology and NeuroInflammation</i> , 2018, 5, e414.	6.0	6
153	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.	4.8	25
154	A transcriptomic atlas of aged human microglia. <i>Nature Communications</i> , 2018, 9, 539.	12.8	375
155	The era of GWAS is over — No. <i>Multiple Sclerosis Journal</i> , 2018, 24, 258-260.	3.0	2
156	Integrated biology approach reveals molecular and pathological interactions among Alzheimer's $A\beta_{42}$, Tau, TREM2, and TYROBP in <i>Drosophila</i> models. <i>Genome Medicine</i> , 2018, 10, 26.	8.2	23
157	Designing an epigenomic study. <i>Multiple Sclerosis Journal</i> , 2018, 24, 604-609.	3.0	0
158	Elevated DNA methylation across a 48 kb region spanning the <i>HOXA</i> gene cluster is associated with Alzheimer's disease neuropathology. <i>Alzheimer's and Dementia</i> , 2018, 14, 1580-1588.	0.8	138
159	Genetic influence of plasma homocysteine on Alzheimer's disease. <i>Neurobiology of Aging</i> , 2018, 62, 243.e7-243.e14.	3.1	18
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162	P3136: MODULE QUANTITATIVE TRAIT LOCI ANALYSIS IMPLICATES <i>TMEM106B</i> AND <i>RBFOX1</i> AS KEY BRAIN TRANSCRIPTOME REGULATORS IN OLDER ADULTS. <i>Alzheimer's and Dementia</i> , 2018, 14, P1120.	0.8	0

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