

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	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	27.8	5,653
2	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. <i>Nature Genetics</i> , 2013, 45, 1452-1458.	21.4	3,741
3	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. <i>Nature</i> , 2011, 476, 214-219.	27.8	2,400
4	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	27.8	1,974
5	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.	21.4	1,962
6	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. <i>Nature Genetics</i> , 2011, 43, 436-441.	21.4	1,676
7	Genetic and epigenetic fine mapping of causal autoimmune disease variants. <i>Nature</i> , 2015, 518, 337-343.	27.8	1,669
8	Risk Alleles for Multiple Sclerosis Identified by a Genomewide Study. <i>New England Journal of Medicine</i> , 2007, 357, 851-862.	27.0	1,529
9	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. <i>Nature Genetics</i> , 2013, 45, 1353-1360.	21.4	1,213
10	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
11	Charting a dynamic DNA methylation landscape of the human genome. <i>Nature</i> , 2013, 500, 477-481.	27.8	1,168
12	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. <i>Nature Genetics</i> , 2010, 42, 508-514.	21.4	1,132
13	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.	6.2	1,098
14	Analysis of shared heritability in common disorders of the brain. <i>Science</i> , 2018, 360, .	12.6	1,085
15	Alterations of the human gut microbiome in multiple sclerosis. <i>Nature Communications</i> , 2016, 7, 12015.	12.8	957
16	Gene expression elucidates functional impact of polygenic risk for schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1442-1453.	14.8	952
17	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.	21.4	870
18	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. <i>Nature Neuroscience</i> , 2014, 17, 1156-1163.	14.8	800

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19	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. <i>Nature Genetics</i> , 2017, 49, 1373-1384.	21.4	783
20	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. <i>Science</i> , 2013, 340, 1467-1471.	12.6	750
21	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. <i>Nature Genetics</i> , 2009, 41, 776-782.	21.4	729
22	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. <i>Science</i> , 2019, 365, .	12.6	710
23	Parkinson's Disease: Genetics and Pathogenesis. <i>Annual Review of Pathology: Mechanisms of Disease</i> , 2011, 6, 193-222.	22.4	654
24	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
25	Pervasive Sharing of Genetic Effects in Autoimmune Disease. <i>PLoS Genetics</i> , 2011, 7, e1002254.	3.5	540
26	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. <i>Cell Reports</i> , 2017, 21, 366-380.	6.4	538
27	The transcriptional landscape of age in human peripheral blood. <i>Nature Communications</i> , 2015, 6, 8570.	12.8	533
28	Neurodegeneration in Lurcher mice caused by mutation in Grm2 glutamate receptor gene. <i>Nature</i> , 1997, 388, 769-773.	27.8	522
29	Defining the Role of the MHC in Autoimmunity: A Review and Pooled Analysis. <i>PLoS Genetics</i> , 2008, 4, e1000024.	3.5	488
30	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. <i>Nature Neuroscience</i> , 2014, 17, 1164-1170.	14.8	488
31	CD33 Alzheimer's disease locus: altered monocyte function and amyloid biology. <i>Nature Neuroscience</i> , 2013, 16, 848-850.	14.8	485
32	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. <i>Nature Communications</i> , 2018, 9, 2098.	12.8	484
33	Polarization of the Effects of Autoimmune and Neurodegenerative Risk Alleles in Leukocytes. <i>Science</i> , 2014, 344, 519-523.	12.6	480
34	Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. <i>Cell</i> , 2013, 152, 642-654.	28.9	473
35	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. <i>Nature Neuroscience</i> , 2018, 21, 811-819.	14.8	422
36	A High-Density Admixture Map for Disease Gene Discovery in African Americans. <i>American Journal of Human Genetics</i> , 2004, 74, 1001-1013.	6.2	416

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37	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
38	Common Genetic Variants Modulate Pathogen-Sensing Responses in Human Dendritic Cells. <i>Science</i> , 2014, 343, 1246980.	12.6	391
39	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. <i>Nature Neuroscience</i> , 2017, 20, 1418-1426.	14.8	377
40	A transcriptomic atlas of aged human microglia. <i>Nature Communications</i> , 2018, 9, 539.	12.8	375
41	De novo copy number variants identify new genes and loci in isolated sporadic tetralogy of Fallot. <i>Nature Genetics</i> , 2009, 41, 931-935.	21.4	373
42	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
43	Variants in the ATP-Binding Cassette Transporter (ABCA7), Apolipoprotein E ϵ 4, and the Risk of Late-Onset Alzheimer Disease in African Americans. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1483.	7.4	360
44	A multi-omic atlas of the human frontal cortex for aging and Alzheimer's disease research. <i>Scientific Data</i> , 2018, 5, 180142.	5.3	357
45	Automated high-dimensional flow cytometric data analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 8519-8524.	7.1	355
46	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
47	GWAS of Cerebrospinal Fluid Tau Levels Identifies Risk Variants for Alzheimer's Disease. <i>Neuron</i> , 2013, 78, 256-268.	8.1	344
48	Self-antigen tetramers discriminate between myelin autoantibodies to native or denatured protein. <i>Nature Medicine</i> , 2007, 13, 211-217.	30.7	342
49	Blood Kidney Injury Molecule-1 Is a Biomarker of Acute and Chronic Kidney Injury and Predicts Progression to ESRD in Type I Diabetes. <i>Journal of the American Society of Nephrology: JASN</i> , 2014, 25, 2177-2186.	6.1	341
50	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
51	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. <i>Annals of Neurology</i> , 2011, 70, 897-912.	5.3	314
52	Class II HLA interactions modulate genetic risk for multiple sclerosis. <i>Nature Genetics</i> , 2015, 47, 1107-1113.	21.4	312
53	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. <i>Nature Genetics</i> , 2018, 50, 1584-1592.	21.4	307
54	Genome-Wide Association Meta-analysis of Neuropathologic Features of Alzheimer's Disease and Related Dementias. <i>PLoS Genetics</i> , 2014, 10, e1004606.	3.5	305

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55	Infection-Triggered Familial or Recurrent Cases of Acute Necrotizing Encephalopathy Caused by Mutations in a Component of the Nuclear Pore, RANBP2. <i>American Journal of Human Genetics</i> , 2009, 84, 44-51.	6.2	291
56	A High-Density Screen for Linkage in Multiple Sclerosis. <i>American Journal of Human Genetics</i> , 2005, 77, 454-467.	6.2	268
57	A novel Alzheimer disease locus located near the gene encoding tau protein. <i>Molecular Psychiatry</i> , 2016, 21, 108-117.	7.9	260
58	Fine-Mapping the Genetic Association of the Major Histocompatibility Complex in Multiple Sclerosis: HLA and Non-HLA Effects. <i>PLoS Genetics</i> , 2013, 9, e1003926.	3.5	250
59	CWAS of Longevity in CHARGE Consortium Confirms APOE and FOXO3 Candidacy. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2015, 70, 110-118.	3.6	250
60	Parsing the Interferon Transcriptional Network and Its Disease Associations. <i>Cell</i> , 2016, 164, 564-578.	28.9	250
61	Novel genetic loci associated with hippocampal volume. <i>Nature Communications</i> , 2017, 8, 13624.	12.8	250
62	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
63	A whole-genome admixture scan finds a candidate locus for multiple sclerosis susceptibility. <i>Nature Genetics</i> , 2005, 37, 1113-1118.	21.4	243
64	Life Extension Factor Klotho Enhances Cognition. <i>Cell Reports</i> , 2014, 7, 1065-1076.	6.4	243
65	Association of Brain DNA Methylation in <i>SORL1</i> , <i>ABCA7</i> , <i>HLA-DRB5</i> , <i>SLC24A4</i> , and <i>BIN1</i> With Pathological Diagnosis of Alzheimer Disease. <i>JAMA Neurology</i> , 2015, 72, 15.	9.0	239
66	Integration of genetic risk factors into a clinical algorithm for multiple sclerosis susceptibility: a weighted genetic risk score. <i>Lancet Neurology</i> , The, 2009, 8, 1111-1119.	10.2	233
67	Mapping of multiple susceptibility variants within the MHC region for 7 immune-mediated diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18680-18685.	7.1	231
68	Association of CR1, CLU and PICALM with Alzheimer's disease in a cohort of clinically characterized and neuropathologically verified individuals. <i>Human Molecular Genetics</i> , 2010, 19, 3295-3301.	2.9	223
69	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. <i>JAMA Neurology</i> , 2018, 75, 989.	9.0	223
70	Intersection of population variation and autoimmunity genetics in human T cell activation. <i>Science</i> , 2014, 345, 1254665.	12.6	218
71	Tau Activates Transposable Elements in Alzheimer's Disease. <i>Cell Reports</i> , 2018, 23, 2874-2880.	6.4	216
72	Novel genetic loci underlying human intracranial volume identified through genome-wide association. <i>Nature Neuroscience</i> , 2016, 19, 1569-1582.	14.8	213

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73	Common variants at 12q14 and 12q24 are associated with hippocampal volume. <i>Nature Genetics</i> , 2012, 44, 545-551.	21.4	212
74	IL2RA Genetic Heterogeneity in Multiple Sclerosis and Type 1 Diabetes Susceptibility and Soluble Interleukin-2 Receptor Production. <i>PLoS Genetics</i> , 2009, 5, e1000322.	3.5	210
75	Genome-wide Association Study in a High-Risk Isolate for Multiple Sclerosis Reveals Associated Variants in STAT3 Gene. <i>American Journal of Human Genetics</i> , 2010, 86, 285-291.	6.2	210
76	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.	21.4	205
77	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
78	Genetic Analysis of Human Traits In Vitro: Drug Response and Gene Expression in Lymphoblastoid Cell Lines. <i>PLoS Genetics</i> , 2008, 4, e1000287.	3.5	200
79	Genome-wide association study identifies four novel loci associated with Alzheimer's endophenotypes and disease modifiers. <i>Acta Neuropathologica</i> , 2017, 133, 839-856.	7.7	199
80	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
81	Genetic architecture of subcortical brain structures in 38,851 individuals. <i>Nature Genetics</i> , 2019, 51, 1624-1636.	21.4	192
82	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
83	The role of the <i>CD58</i> locus in multiple sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5264-5269.	7.1	185
84	Convergent genetic and expression data implicate immunity in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2015, 11, 658-671.	0.8	173
85	Higher brain <i>BDNF</i> gene expression is associated with slower cognitive decline in older adults. <i>Neurology</i> , 2016, 86, 735-741.	1.1	170
86	Normalization of Plasma 25-Hydroxy Vitamin D Is Associated with Reduced Risk of Surgery in Crohn's Disease. <i>Inflammatory Bowel Diseases</i> , 2013, 19, 1.	1.9	168
87	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. <i>JAMA Neurology</i> , 2014, 71, 1394.	9.0	166
88	Transethnic genome-wide scan identifies novel Alzheimer's disease loci. <i>Alzheimer's and Dementia</i> , 2017, 13, 727-738.	0.8	166
89	Evidence for Polygenic Susceptibility to Multiple Sclerosis "The Shape of Things to Come. <i>American Journal of Human Genetics</i> , 2010, 86, 621-625.	6.2	162
90	Multiethnic Genome-Wide Association Study of Cerebral White Matter Hyperintensities on MRI. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 398-409.	5.1	162

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91	Admixture Mapping of an Allele Affecting Interleukin 6 Soluble Receptor and Interleukin 6 Levels. <i>American Journal of Human Genetics</i> , 2007, 80, 716-726.	6.2	160
92	A genome-wide scan for common variants affecting the rate of age-related cognitive decline. <i>Neurobiology of Aging</i> , 2012, 33, 1017.e1-1017.e15.	3.1	160
93	Polygenic risk of Alzheimer disease is associated with early- and late-life processes. <i>Neurology</i> , 2016, 87, 481-488.	1.1	159
94	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
95	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. <i>PLoS ONE</i> , 2014, 9, e94661.	2.5	155
96	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. <i>Nature Communications</i> , 2015, 6, 6916.	12.8	154
97	Functionally defective germline variants of sialic acid acetyltransferase in autoimmunity. <i>Nature</i> , 2010, 466, 243-247.	27.8	150
98	A Genome-Wide Association Study of Depressive Symptoms. <i>Biological Psychiatry</i> , 2013, 73, 667-678.	1.3	149
99	<i>CR1</i> is associated with amyloid plaque burden and age-related cognitive decline. <i>Annals of Neurology</i> , 2011, 69, 560-569.	5.3	148
100	Genome-wide association study of the rate of cognitive decline in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2014, 10, 45-52.	0.8	147
101	Functional screening in <i>Drosophila</i> identifies Alzheimer's disease susceptibility genes and implicates Tau-mediated mechanisms. <i>Human Molecular Genetics</i> , 2014, 23, 870-877.	2.9	147
102	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
103	Genome-Wide Association Study and Gene Expression Analysis Identifies CD84 as a Predictor of Response to Etanercept Therapy in Rheumatoid Arthritis. <i>PLoS Genetics</i> , 2013, 9, e1003394.	3.5	146
104	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. <i>Neurology</i> , 2012, 79, 221-228.	1.1	144
105	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
106	Genetic Susceptibility for Alzheimer Disease Neuritic Plaque Pathology. <i>JAMA Neurology</i> , 2013, 70, 1150.	9.0	143
107	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. <i>Nature Genetics</i> , 2018, 50, 1140-1150.	21.4	139
108	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

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109	Soluble IL-2RA Levels in Multiple Sclerosis Subjects and the Effect of Soluble IL-2RA on Immune Responses. <i>Journal of Immunology</i> , 2009, 182, 1541-1547.	0.8	136
110	CD33 modulates TREM2: convergence of Alzheimer loci. <i>Nature Neuroscience</i> , 2015, 18, 1556-1558.	14.8	134
111	Multicolored stain-free histopathology with coherent Raman imaging. <i>Laboratory Investigation</i> , 2012, 92, 1492-1502.	3.7	130
112	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , The, 2016, 15, 695-707.	10.2	130
113	CD33: increased inclusion of exon 2 implicates the Ig V-set domain in Alzheimer's disease susceptibility. <i>Human Molecular Genetics</i> , 2014, 23, 2729-2736.	2.9	128
114	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. <i>Nature Communications</i> , 2019, 10, 409.	12.8	121
115	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
116	GWAS of longitudinal amyloid accumulation on ¹⁸ F-florbetapir PET in Alzheimer's disease implicates microglial activation gene <i>IL1RAP</i> . <i>Brain</i> , 2015, 138, 3076-3088.	7.6	117
117	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. <i>Nature Communications</i> , 2019, 10, 2907.	12.8	117
118	Replication analysis identifies TYK2 as a multiple sclerosis susceptibility factor. <i>European Journal of Human Genetics</i> , 2009, 17, 1309-1313.	2.8	115
119	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. <i>Cell</i> , 2018, 175, 1679-1687.e7.	28.9	115
120	Gut Microbiome in Progressive Multiple Sclerosis. <i>Annals of Neurology</i> , 2021, 89, 1195-1211.	5.3	115
121	Interindividual variation in human T regulatory cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1111-20.	7.1	112
122	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	7.1	110
123	Comprehensive follow-up of the first genome-wide association study of multiple sclerosis identifies KIF21B and TMEM39A as susceptibility loci. <i>Human Molecular Genetics</i> , 2010, 19, 953-962.	2.9	108
124	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
125	A human microglia-like cellular model for assessing the effects of neurodegenerative disease gene variants. <i>Science Translational Medicine</i> , 2017, 9, .	12.4	106
126	NMNAT2:HSP90 Complex Mediates Proteostasis in Proteinopathies. <i>PLoS Biology</i> , 2016, 14, e1002472.	5.6	105

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127	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. <i>Annals of Neurology</i> , 2018, 84, 78-88.	5.3	102
128	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> , The, 2018, 17, 773-781.	10.2	101
129	Common Risk Alleles for Inflammatory Diseases Are Targets of Recent Positive Selection. <i>American Journal of Human Genetics</i> , 2013, 92, 517-529.	6.2	100
130	Epigenomics of Alzheimer's disease. <i>Translational Research</i> , 2015, 165, 200-220.	5.0	97
131	Genetic variants in Alzheimer disease " molecular and brain network approaches. <i>Nature Reviews Neurology</i> , 2016, 12, 413-427.	10.1	97
132	Association of APOE with tau-tangle pathology with and without β -amyloid. <i>Neurobiology of Aging</i> , 2016, 37, 19-25.	3.1	97
133	A method for high-throughput, sensitive analysis of IgG Fc and Fab glycosylation by capillary electrophoresis. <i>Journal of Immunological Methods</i> , 2015, 417, 34-44.	1.4	95
134	Modification of Multiple Sclerosis Phenotypes by African Ancestry at HLA. <i>Archives of Neurology</i> , 2009, 66, 226-33.	4.5	92
135	A coding variant in CR1 interacts with APOE- ϵ 4 to influence cognitive decline. <i>Human Molecular Genetics</i> , 2012, 21, 2377-2388.	2.9	90
136	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
137	Identification of genes associated with dissociation of cognitive performance and neuropathological burden: Multistep analysis of genetic, epigenetic, and transcriptional data. <i>PLoS Medicine</i> , 2017, 14, e1002287.	8.4	88
138	Sex-specific genetic predictors of Alzheimer's disease biomarkers. <i>Acta Neuropathologica</i> , 2018, 136, 857-872.	7.7	87
139	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
140	Neurodegeneration in <i>Lurcher</i> Mice Occurs via Multiple Cell Death Pathways. <i>Journal of Neuroscience</i> , 2000, 20, 3687-3694.	3.6	86
141	The <i>CD6</i> Multiple Sclerosis Susceptibility Allele Is Associated with Alterations in CD4+ T Cell Proliferation. <i>Journal of Immunology</i> , 2011, 187, 3286-3291.	0.8	85
142	Brain proteome-wide association study implicates novel proteins in depression pathogenesis. <i>Nature Neuroscience</i> , 2021, 24, 810-817.	14.8	85
143	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. <i>Biological Psychiatry</i> , 2017, 82, 322-329.	1.3	84
144	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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145	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
146	PhIP-Seq characterization of autoantibodies from patients with multiple sclerosis, type 1 diabetes and rheumatoid arthritis. <i>Journal of Autoimmunity</i> , 2013, 43, 1-9.	6.5	83
147	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2017, 13, 674-688.	0.8	83
148	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.	0.8	83
149	Functional Screening of Alzheimer Pathology Genome-wide Association Signals in <i>Drosophila</i> . <i>American Journal of Human Genetics</i> , 2011, 88, 232-238.	6.2	81
150	24-Hour Rhythms of DNA Methylation and Their Relation with Rhythms of RNA Expression in the Human Dorsolateral Prefrontal Cortex. <i>PLoS Genetics</i> , 2014, 10, e1004792.	3.5	80
151	Single-Cell Detection of Secreted A β ² and sAPP β from Human iPSC-Derived Neurons and Astrocytes. <i>Journal of Neuroscience</i> , 2016, 36, 1730-1746.	3.6	80
152	Genome-wide Comparison of African-Ancestry Populations from CARE and Other Cohorts Reveals Signals of Natural Selection. <i>American Journal of Human Genetics</i> , 2011, 89, 368-381.	6.2	79
153	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimer's Disease. <i>Journal of Alzheimer's Disease</i> , 2016, 53, 921-932.	2.6	77
154	APOE and cerebral amyloid angiopathy in community-dwelling older persons. <i>Neurobiology of Aging</i> , 2015, 36, 2946-2953.	3.1	76
155	Multiple sclerosis risk loci and disease severity in 7,125 individuals from 10 studies. <i>Neurology: Genetics</i> , 2016, 2, e87.	1.9	76
156	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. <i>Scientific Data</i> , 2020, 7, 340.	5.3	75
157	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
158	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
159	Cytometric profiling in multiple sclerosis uncovers patient population structure and a reduction of CD8 ^{low} cells. <i>Brain</i> , 2008, 131, 1701-1711.	7.6	73
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