Philip L De Jager

List of Publications by Citations

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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	Integrative analysis of 111 reference human epigenomes. *Nature*, **2015**, 518, 317-30	50.4	3849
444	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8	36.3	2714
443	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. *Nature*, **2011**, 476, 214-9	50.4	1948
442	Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature*, **2014**, 506, 376-81	50.4	1426
441	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. *Nature Genetics*, **2011**, 43, 436-41	36.3	1367
440	Risk alleles for multiple sclerosis identified by a genomewide study. *New England Journal of Medicine*, **2007**, 357, 851-62	59.2	1327
439	Genetic and epigenetic fine mapping of causal autoimmune disease variants. *Nature*, **2015**, 518, 337-43	50.4	1199
438	Genome-wide association study meta-analysis identifies seven new rheumatoid arthritis risk loci. *Nature Genetics*, **2010**, 42, 508-14	36.3	969
437	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. *Nature Genetics*, **2013**, 45, 1353-60	36.3	934
436	Charting a dynamic DNA methylation landscape of the human genome. *Nature*, **2013**, 500, 477-81	50.4	932
435	Genetic meta-analysis of diagnosed Alzheimer's disease identifies new risk loci and implicates A▯ tau, immunity and lipid processing. *Nature Genetics*, **2019**, 51, 414-430	36.3	917
434	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
433	Analysis of shared heritability in common disorders of the brain. *Science*, **2018**, 360,	33.3	666
432	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. *American Journal of Human Genetics*, **2015**, 97, 576-92	11	649
431	Alterations of the human gut microbiome in multiple sclerosis. *Nature Communications*, **2016**, 7, 12015	17.4	632
430	Gene expression elucidates functional impact of polygenic risk for schizophrenia. *Nature Neuroscience*, **2016**, 19, 1442-1453	25.5	622
429	Meta-analysis of genome scans and replication identify CD6, IRF8 and TNFRSF1A as new multiple sclerosis susceptibility loci. *Nature Genetics*, **2009**, 41, 776-82	36.3	621

428	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
427	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. *Nature Neuroscience*, **2014**, 17, 1156-63	25.5	579
426	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
425	Parkinson's disease: genetics and pathogenesis. *Annual Review of Pathology: Mechanisms of Disease*, **2011**, 6, 193-222	34	519
424	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. *Nature Genetics*, **2017**, 49, 1373-1384	36.3	508
423	Neurodegeneration in Lurcher mice caused by mutation in delta2 glutamate receptor gene. *Nature*, **1997**, 388, 769-73	50.4	479
422	Pervasive sharing of genetic effects in autoimmune disease. *PLoS Genetics*, **2011**, 7, e1002254	6	413
421	Genome-wide chromatin state transitions associated with developmental and environmental cues. *Cell*, **2013**, 152, 642-54	56.2	400
420	Defining the role of the MHC in autoimmunity: a review and pooled analysis. *PLoS Genetics*, **2008**, 4, e1000024	6	400
419	A high-density admixture map for disease gene discovery in african americans. *American Journal of Human Genetics*, **2004**, 74, 1001-13	11	379
418	Polarization of the effects of autoimmune and neurodegenerative risk alleles in leukocytes. *Science* , **2014**, 344, 519-23	33.3	372
417	CD33 Alzheimer's disease locus: altered monocyte function and amyloid biology. *Nature Neuroscience*, **2013**, 16, 848-50	25.5	370
416	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. *Nature Neuroscience*, **2014**, 17, 1164-70	25.5	356
415	The transcriptional landscape of age in human peripheral blood. *Nature Communications*, **2015**, 6, 8570	17.4	335
414	De novo copy number variants identify new genes and loci in isolated sporadic tetralogy of Fallot. *Nature Genetics*, **2009**, 41, 931-5	36.3	325
413	Temporal Tracking of Microglia Activation in Neurodegeneration at Single-Cell Resolution. *Cell Reports*, **2017**, 21, 366-380	10.6	313
412	Multiple sclerosis genomic map implicates peripheral immune cells and microglia in susceptibility. *Science*, **2019**, 365,	33.3	309
411	Common genetic variants modulate pathogen-sensing responses in human dendritic cells. *Science*, **2014**, 343, 1246980	33.3	309

410	Automated high-dimensional flow cytometric data analysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 8519-24	11.5	303
409	Variants in the ATP-binding cassette transporter (ABCA7), apolipoprotein E ?4,and the risk of late-onset Alzheimer disease in African Americans. *JAMA - Journal of the American Medical Association*, **2013**, 309, 1483-92	27.4	275
408	Self-antigen tetramers discriminate between myelin autoantibodies to native or denatured protein. *Nature Medicine*, **2007**, 13, 211-7	50.5	266
407	Genome-wide meta-analysis identifies novel multiple sclerosis susceptibility loci. *Annals of Neurology*, **2011**, 70, 897-912	9.4	263
406	GWAS of cerebrospinal fluid tau levels identifies risk variants for Alzheimer's disease. *Neuron*, **2013**, 78, 256-68	13.9	255
405	Study of 300,486 individuals identifies 148 independent genetic loci influencing general cognitive function. *Nature Communications*, **2018**, 9, 2098	17.4	254
404	Blood kidney injury molecule-1 is a biomarker of acute and chronic kidney injury and predicts progression to ESRD in type I diabetes. *Journal of the American Society of Nephrology: JASN*, **2014**, 25, 2177-86	12.7	250
403	A high-density screen for linkage in multiple sclerosis. *American Journal of Human Genetics*, **2005**, 77, 454-67	11	235
402	Large-scale proteomic analysis of Alzheimer's disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. *Nature Medicine*, **2020**, 26, 769-780	50.5	226
401	A transcriptomic atlas of aged human microglia. *Nature Communications*, **2018**, 9, 539	17.4	223
400	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
399	A whole-genome admixture scan finds a candidate locus for multiple sclerosis susceptibility. *Nature Genetics*, **2005**, 37, 1113-8	36.3	220
398	A molecular network of the aging human brain provides insights into the pathology and cognitive decline of Alzheimer's disease. *Nature Neuroscience*, **2018**, 21, 811-819	25.5	220
397	Genome-wide association meta-analysis of neuropathologic features of Alzheimer's disease and related dementias. *PLoS Genetics*, **2014**, 10, e1004606	6	219
396	Class II HLA interactions modulate genetic risk for multiple sclerosis. *Nature Genetics*, **2015**, 47, 1107-1113	36.3	215
395	Altered bile acid profile associates with cognitive impairment in Alzheimer's disease-An emerging role for gut microbiome. *Alzheimers and Dementia*, **2019**, 15, 76-92	1.2	208
394	Mapping of multiple susceptibility variants within the MHC region for 7 immune-mediated diseases. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 18680-5	11.5	204
393	An xQTL map integrates the genetic architecture of the human brain's transcriptome and epigenome. *Nature Neuroscience*, **2017**, 20, 1418-1426	25.5	201

392	Association of CR1, CLU and PICALM with Alzheimer's disease in a cohort of clinically characterized and neuropathologically verified individuals. *Human Molecular Genetics*, **2010**, 19, 3295-301	5.6	199
391	Infection-triggered familial or recurrent cases of acute necrotizing encephalopathy caused by mutations in a component of the nuclear pore, RANBP2. *American Journal of Human Genetics*, **2009**, 84, 44-51	11	196
390	Integration of genetic risk factors into a clinical algorithm for multiple sclerosis susceptibility: a weighted genetic risk score. *Lancet Neurology, The*, **2009**, 8, 1111-9	24.1	192
389	GWAS of longevity in CHARGE consortium confirms APOE and FOXO3 candidacy. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2015**, 70, 110-8	6.4	188
388	Genome-wide association study in a high-risk isolate for multiple sclerosis reveals associated variants in STAT3 gene. *American Journal of Human Genetics*, **2010**, 86, 285-91	11	188
387	Fine-mapping the genetic association of the major histocompatibility complex in multiple sclerosis: HLA and non-HLA effects. *PLoS Genetics*, **2013**, 9, e1003926	6	186
386	IL2RA genetic heterogeneity in multiple sclerosis and type 1 diabetes susceptibility and soluble interleukin-2 receptor production. *PLoS Genetics*, **2009**, 5, e1000322	6	183
385	Genetic analysis of human traits in vitro: drug response and gene expression in lymphoblastoid cell lines. *PLoS Genetics*, **2008**, 4, e1000287	6	182
384	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
383	Intersection of population variation and autoimmunity genetics in human T cell activation. *Science*, **2014**, 345, 1254665	33.3	175
382	Common variants at 12q14 and 12q24 are associated with hippocampal volume. *Nature Genetics*, **2012**, 44, 545-51	36.3	175
381	Novel genetic loci associated with hippocampal volume. *Nature Communications*, **2017**, 8, 13624	17.4	173
380	Association of Brain DNA methylation in SORL1, ABCA7, HLA-DRB5, SLC24A4, and BIN1 with pathological diagnosis of Alzheimer disease. *JAMA Neurology*, **2015**, 72, 15-24	17.2	168
379	Life extension factor klotho enhances cognition. *Cell Reports*, **2014**, 7, 1065-76	10.6	166
378	Integrative transcriptome analyses of the aging brain implicate altered splicing in Alzheimer's disease susceptibility. *Nature Genetics*, **2018**, 50, 1584-1592	36.3	162
377	The role of the CD58 locus in multiple sclerosis. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 5264-9	11.5	160
376	A multi-omic atlas of the human frontal cortex for aging and Alzheimer's disease research. *Scientific Data*, **2018**, 5, 180142	8.2	155
375	Normalization of plasma 25-hydroxy vitamin D is associated with reduced risk of surgery in Crohn's disease. *Inflammatory Bowel Diseases*, **2013**, 19, 1921-7	4.5	152

374	Parsing the Interferon Transcriptional Network and Its Disease Associations. *Cell*, **2016**, 164, 564-78	56.2	151
373	Novel genetic loci underlying human intracranial volume identified through genome-wide association. *Nature Neuroscience*, **2016**, 19, 1569-1582	25.5	147
372	Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimers and Dementia*, **2015**, 11, 658-71	1.2	146
371	Evidence for polygenic susceptibility to multiple sclerosis--the shape of things to come. *American Journal of Human Genetics*, **2010**, 86, 621-5	11	146
370	Admixture mapping of an allele affecting interleukin 6 soluble receptor and interleukin 6 levels. *American Journal of Human Genetics*, **2007**, 80, 716-26	11	145
369	Sex-Specific Association of Apolipoprotein E With Cerebrospinal Fluid Levels of Tau. *JAMA Neurology*, **2018**, 75, 989-998	17.2	142
368	A genome-wide association study of depressive symptoms. *Biological Psychiatry*, **2013**, 73, 667-78	7.9	135
367	Effects of multiple genetic loci on age at onset in late-onset Alzheimer disease: a genome-wide association study. *JAMA Neurology*, **2014**, 71, 1394-404	17.2	129
366	Functionally defective germline variants of sialic acid acetylesterase in autoimmunity. *Nature*, **2010**, 466, 243-7	50.4	129
365	CR1 is associated with amyloid plaque burden and age-related cognitive decline. *Annals of Neurology*, **2011**, 69, 560-9	9.4	128
364	Genome-wide association study and gene expression analysis identifies CD84 as a predictor of response to etanercept therapy in rheumatoid arthritis. *PLoS Genetics*, **2013**, 9, e1003394	6	127
363	Limited statistical evidence for shared genetic effects of eQTLs and autoimmune-disease-associated loci in three major immune-cell types. *Nature Genetics*, **2017**, 49, 600-605	36.3	124
362	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. *Neurology*, **2012**, 79, 221-8	6.5	124
361	Multiethnic genome-wide association study of cerebral white matter hyperintensities on MRI. *Circulation: Cardiovascular Genetics*, **2015**, 8, 398-409		119
360	Higher brain BDNF gene expression is associated with slower cognitive decline in older adults. *Neurology*, **2016**, 86, 735-41	6.5	119
359	Tau Activates Transposable Elements in Alzheimer's Disease. *Cell Reports*, **2018**, 23, 2874-2880	10.6	116
358	Genome-wide meta-analysis identifies multiple novel associations and ethnic heterogeneity of psoriasis susceptibility. *Nature Communications*, **2015**, 6, 6916	17.4	115
357	A genome-wide scan for common variants affecting the rate of age-related cognitive decline. *Neurobiology of Aging*, **2012**, 33, 1017.e1-15	5.6	115

356	Exceptionally low likelihood of Alzheimer’s dementia in APOE2 homozygotes from a 5,000-person neuropathological study. *Nature Communications*, **2020**, 11, 667	17.4	113
355	Functional screening in Drosophila identifies Alzheimer’s disease susceptibility genes and implicates Tau-mediated mechanisms. *Human Molecular Genetics*, **2014**, 23, 870-7	5.6	113
354	Genetic susceptibility for Alzheimer disease neuritic plaque pathology. *JAMA Neurology*, **2013**, 70, 1150-7	17.2	113
353	Soluble IL-2RA levels in multiple sclerosis subjects and the effect of soluble IL-2RA on immune responses. *Journal of Immunology*, **2009**, 182, 1541-7	5.3	113
352	Genome-wide association study identifies four novel loci associated with Alzheimer’s endophenotypes and disease modifiers. *Acta Neuropathologica*, **2017**, 133, 839-856	14.3	107
351	CD33 modulates TREM2: convergence of Alzheimer loci. *Nature Neuroscience*, **2015**, 18, 1556-8	25.5	107
350	Replication analysis identifies TYK2 as a multiple sclerosis susceptibility factor. *European Journal of Human Genetics*, **2009**, 17, 1309-13	5.3	107
349	Transethnic genome-wide scan identifies novel Alzheimer’s disease loci. *Alzheimer's and Dementia*, **2017**, 13, 727-738	1.2	106
348	Multicolored stain-free histopathology with coherent Raman imaging. *Laboratory Investigation*, **2012**, 92, 1492-502	5.9	105
347	Single cell RNA sequencing of human microglia uncovers a subset associated with Alzheimer’s disease. *Nature Communications*, **2020**, 11, 6129	17.4	102
346	Identification of additional risk loci for stroke and small vessel disease: a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2016**, 15, 695-707	24.1	100
345	Epigenome-wide study uncovers large-scale changes in histone acetylation driven by tau pathology in aging and Alzheimer’s human brains. *Nature Neuroscience*, **2019**, 22, 37-46	25.5	99
344	Genome-wide association study of the rate of cognitive decline in Alzheimer’s disease. *Alzheimer's and Dementia*, **2014**, 10, 45-52	1.2	98
343	CD33: increased inclusion of exon 2 implicates the Ig V-set domain in Alzheimer’s disease susceptibility. *Human Molecular Genetics*, **2014**, 23, 2729-36	5.6	93
342	Comprehensive follow-up of the first genome-wide association study of multiple sclerosis identifies KIF21B and TMEM39A as susceptibility loci. *Human Molecular Genetics*, **2010**, 19, 953-62	5.6	91
341	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
340	Gene-wide analysis detects two new susceptibility genes for Alzheimer’s disease. *PLoS ONE*, **2014**, 9, e94661	3.7	90
339	GWAS of longitudinal amyloid accumulation on 18F-florbetapir PET in Alzheimer’s disease implicates microglial activation gene IL1RAP. *Brain*, **2015**, 138, 3076-88	11.2	88

338	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
337	Common risk alleles for inflammatory diseases are targets of recent positive selection. *American Journal of Human Genetics*, **2013**, 92, 517-29	11	88
336	Polygenic risk of Alzheimer disease is associated with early- and late-life processes. *Neurology*, **2016** , 87, 481-8	6.5	86
335	Neurodegeneration in Lurcher mice occurs via multiple cell death pathways. *Journal of Neuroscience*, **2000**, 20, 3687-94	6.6	85
334	Genetic architecture of subcortical brain structures in 38,851 individuals. *Nature Genetics*, **2019**, 51, 1624-1636	36.3	81
333	Interindividual variation in human T regulatory cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E1111-20	11.5	80
332	Epigenomics of Alzheimer's disease. *Translational Research*, **2015**, 165, 200-20	11	79
331	A coding variant in CR1 interacts with APOE-ε4 to influence cognitive decline. *Human Molecular Genetics*, **2012**, 21, 2377-88	5.6	78
330	Genetic determinants of co-accessible chromatin regions in activated T cells across humans. *Nature Genetics*, **2018**, 50, 1140-1150	36.3	74
329	NMNAT2:HSP90 Complex Mediates Proteostasis in Proteinopathies. *PLoS Biology*, **2016**, 14, e1002472	9.7	74
328	Elevated DNA methylation across a 48-kb region spanning the HOXA gene cluster is associated with Alzheimer's disease neuropathology. *Alzheimer's and Dementia*, **2018**, 14, 1580-1588	1.2	73
327	Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. *Cell*, **2018**, 175, 1679-1687.e7	58.2	72
326	Genetic variants in Alzheimer disease - molecular and brain network approaches. *Nature Reviews Neurology*, **2016**, 12, 413-27	15	71
325	Modification of Multiple Sclerosis Phenotypes by African Ancestry at HLA. *Archives of Neurology*, **2009**, 66, 226-33		71
324	An Analysis of Two Genome-wide Association Meta-analyses Identifies a New Locus for Broad Depression Phenotype. *Biological Psychiatry*, **2017**, 82, 322-329	7.9	68
323	Functional screening of Alzheimer pathology genome-wide association signals in Drosophila. *American Journal of Human Genetics*, **2011**, 88, 232-8	11	68
322	Meta-Analysis of the Alzheimer's Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. *Cell Reports*, **2020**, 32, 107908	10.6	68
321	24-hour rhythms of DNA methylation and their relation with rhythms of RNA expression in the human dorsolateral prefrontal cortex. *PLoS Genetics*, **2014**, 10, e1004792	6	67

320	The CD6 multiple sclerosis susceptibility allele is associated with alterations in CD4+ T cell proliferation. *Journal of Immunology*, **2011**, 187, 3286-91	5.3	67
319	Association of APOE with tau-tangle pathology with and without β-amyloid. *Neurobiology of Aging*, **2016**, 37, 19-25	5.6	66
318	A method for high-throughput, sensitive analysis of IgG Fc and Fab glycosylation by capillary electrophoresis. *Journal of Immunological Methods*, **2015**, 417, 34-44	2.5	64
317	Single-Cell Detection of Secreted Aβ and sAPPα from Human IPSC-Derived Neurons and Astrocytes. *Journal of Neuroscience*, **2016**, 36, 1730-46	6.6	64
316	Evaluation of TDP-43 proteinopathy and hippocampal sclerosis in relation to APOE ε4 haplotype status: a community-based cohort study. *Lancet Neurology, The*, **2018**, 17, 773-781	24.1	64
315	Genome-wide comparison of African-ancestry populations from CARe and other cohorts reveals signals of natural selection. *American Journal of Human Genetics*, **2011**, 89, 368-81	11	63
314	Nuclei multiplexing with barcoded antibodies for single-nucleus genomics. *Nature Communications*, **2019**, 10, 2907	17.4	62
313	A genome-wide profiling of brain DNA hydroxymethylation in Alzheimer's disease. *Alzheimer's and Dementia*, **2017**, 13, 674-688	1.2	61
312	Cytometric profiling in multiple sclerosis uncovers patient population structure and a reduction of CD8low cells. *Brain*, **2008**, 131, 1701-11	11.2	61
311	Enhancing linkage analysis of complex disorders: an evaluation of high-density genotyping. *Human Molecular Genetics*, **2004**, 13, 1943-9	5.6	61
310	Neuropathological correlates and genetic architecture of microglial activation in elderly human brain. *Nature Communications*, **2019**, 10, 409	17.4	59
309	A human microglia-like cellular model for assessing the effects of neurodegenerative disease gene variants. *Science Translational Medicine*, **2017**, 9,	17.5	59
308	Alzheimer disease susceptibility loci: evidence for a protein network under natural selection. *American Journal of Human Genetics*, **2012**, 90, 720-6	11	57
307	Early elevation of serum tumor necrosis factor-α is associated with poor outcome in subarachnoid hemorrhage. *Journal of Investigative Medicine*, **2012**, 60, 1054-8	2.9	57
306	Identification of genes associated with dissociation of cognitive performance and neuropathological burden: Multistep analysis of genetic, epigenetic, and transcriptional data. *PLoS Medicine*, **2017**, 14, e1002287	11.6	56
305	Targeted brain proteomics uncover multiple pathways to Alzheimer's dementia. *Annals of Neurology*, **2018**, 84, 78-88	9.4	56
304	Circadian alterations during early stages of Alzheimer's disease are associated with aberrant cycles of DNA methylation in BMAL1. *Alzheimer's and Dementia*, **2017**, 13, 689-700	1.2	55
303	The TMEM106B locus and TDP-43 pathology in older persons without FTLD. *Neurology*, **2015**, 84, 927-34	6.5	55

302	PhIP-Seq characterization of autoantibodies from patients with multiple sclerosis, type 1 diabetes and rheumatoid arthritis. *Journal of Autoimmunity*, **2013**, 43, 1-9	15.5	55
301	Similar risk of depression and anxiety following surgery or hospitalization for Crohn's disease and ulcerative colitis. *American Journal of Gastroenterology*, **2013**, 108, 594-601	0.7	54
300	A TREM1 variant alters the accumulation of Alzheimer-related amyloid pathology. *Annals of Neurology*, **2015**, 77, 469-77	9.4	54
299	Evaluation of a Genetic Risk Score to Improve Risk Prediction for Alzheimer's Disease. *Journal of Alzheimer's Disease*, **2016**, 53, 921-32	4.3	54
298	Genetic variation in the IL7RA/IL7 pathway increases multiple sclerosis susceptibility. *Human Genetics*, **2010**, 127, 525-35	6.3	53
297	Genetic variation in toll-like receptor 9 and susceptibility to systemic lupus erythematosus. *Arthritis and Rheumatism*, **2006**, 54, 1279-82		53
296	APOE and cerebral amyloid angiopathy in community-dwelling older persons. *Neurobiology of Aging* , **2015**, 36, 2946-2953	5.6	52
295	Multiple sclerosis risk loci and disease severity in 7,125 individuals from 10 studies. *Neurology: Genetics*, **2016**, 2, e87	3.8	52
294	High-dimensional immunomonitoring models of HIV-1-specific CD8 T-cell responses accurately identify subjects achieving spontaneous viral control. *Blood*, **2013**, 121, 801-11	2.2	51
293	An RNA profile identifies two subsets of multiple sclerosis patients differing in disease activity. *Science Translational Medicine*, **2012**, 4, 153ra131	17.5	51
292	Allelic variant in CTLA4 alters T cell phosphorylation patterns. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 18607-12	11.5	51
291	Tau-Mediated Disruption of the Spliceosome Triggers Cryptic RNA Splicing and Neurodegeneration in Alzheimer's Disease. *Cell Reports*, **2019**, 29, 301-316.e10	10.6	50
290	Sex-specific genetic predictors of Alzheimer's disease biomarkers. *Acta Neuropathologica*, **2018**, 136, 857-872	14.3	48
289	Human Herpesvirus 6 Detection in Alzheimer's Disease Cases and Controls across Multiple Cohorts. *Neuron*, **2020**, 105, 1027-1035.e2	13.9	47
288	Evaluation of an online platform for multiple sclerosis research: patient description, validation of severity scale, and exploration of BMI effects on disease course. *PLoS ONE*, **2013**, 8, e59707	3.7	47
287	Modeling disease severity in multiple sclerosis using electronic health records. *PLoS ONE*, **2013**, 8, e78927	3.7	47
286	A major histocompatibility Class I locus contributes to multiple sclerosis susceptibility independently from HLA-DRB1*15:01. *PLoS ONE*, **2010**, 5, e11296	3.7	46
285	Human genetics in rheumatoid arthritis guides a high-throughput drug screen of the CD40 signaling pathway. *PLoS Genetics*, **2013**, 9, e1003487	6	45

284	5’RNA-Seq identifies Fhl1 as a genetic modifier in cardiomyopathy. *Journal of Clinical Investigation*, **2014**, 124, 1364-70	15.9	44
283	New data and an old puzzle: the negative association between schizophrenia and rheumatoid arthritis. *International Journal of Epidemiology*, **2015**, 44, 1706-21	7.8	43
282	CIITA variation in the presence of HLA-DRB1*1501 increases risk for multiple sclerosis. *Human Molecular Genetics*, **2010**, 19, 2331-40	5.6	43
281	Alzheimer’s loci: epigenetic associations and interaction with genetic factors. *Annals of Clinical and Translational Neurology*, **2015**, 2, 636-47	5.3	42
280	Shared genetic contribution to Ischaemic Stroke and Alzheimer’s Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
279	Exploration of changes in disability after menopause in a longitudinal multiple sclerosis cohort. *Multiple Sclerosis Journal*, **2016**, 22, 935-43	5	41
278	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
277	New therapeutic approaches for multiple sclerosis. *Annual Review of Medicine*, **2007**, 58, 417-32	17.4	40
276	A second X chromosome contributes to resilience in a mouse model of Alzheimer’s disease. *Science Translational Medicine*, **2020**, 12,	17.5	40
275	Diurnal and seasonal molecular rhythms in human neocortex and their relation to Alzheimer’s disease. *Nature Communications*, **2017**, 8, 14931	17.4	39
274	ImmVar project: Insights and design considerations for future studies of "healthy" immune variation. *Seminars in Immunology*, **2015**, 27, 51-7	10.7	39
273	Relation of genomic variants for Alzheimer disease dementia to common neuropathologies. *Neurology*, **2016**, 87, 489-96	6.5	39
272	Interrogating the complex role of chromosome 16p13.13 in multiple sclerosis susceptibility: independent genetic signals in the CIITA-CLEC16A-SOCS1 gene complex. *Human Molecular Genetics*, **2011**, 20, 3517-24	5.6	39
271	A common polymorphism near PER1 and the timing of human behavioral rhythms. *Annals of Neurology*, **2012**, 72, 324-34	9.4	38
270	Common variants in DRD2 are associated with sleep duration: the CARe consortium. *Human Molecular Genetics*, **2016**, 25, 167-79	5.6	37
269	Dissecting the role of non-coding RNAs in the accumulation of amyloid and tau neuropathologies in Alzheimer’s disease. *Molecular Neurodegeneration*, **2017**, 12, 51	19	37
268	Regulation of gene expression in autoimmune disease loci and the genetic basis of proliferation in CD4+ effector memory T cells. *PLoS Genetics*, **2014**, 10, e1004404	6	37
267	A random change point model for cognitive decline in Alzheimer’s disease and mild cognitive impairment. *Neuroepidemiology*, **2012**, 39, 73-83	5.4	37

266	Sex difference in daily rhythms of clock gene expression in the aged human cerebral cortex. *Journal of Biological Rhythms*, **2013**, 28, 117-29	3.2	36
265	Population structure and HLA DRB1 1501 in the response of subjects with multiple sclerosis to first-line treatments. *Journal of Neuroimmunology*, **2011**, 233, 168-74	3.5	36
264	Integrating human brain proteomes with genome-wide association data implicates new proteins in Alzheimer's disease pathogenesis. *Nature Genetics*, **2021**, 53, 143-146	36.3	36
263	A candidate regulatory variant at the TREM gene cluster associates with decreased Alzheimer's disease risk and increased TREML1 and TREM2 brain gene expression. *Alzheimers and Dementia*, **2017**, 13, 663-673	1.2	35
262	Intermediate phenotypes identify divergent pathways to Alzheimer's disease. *PLoS ONE*, **2010**, 5, e11244	3.7	35
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