Minerva M Carrasquillo

List of Publications by Year in Descending Order

82 papers	15,104 citations	41 h-index	98 g-index
98 ext. papers	18,480 ext. citations	10.9 avg, IF	4.6 L-index

#	Paper	IF	Citations
82	Transcript levels in plasma contribute substantial predictive value as potential Alzheimer's disease biomarkers in African Americans.. *EBioMedicine*, **2022**, 103929	8.8	0
81	Alzheimer's disease and progressive supranuclear palsy share similar transcriptomic changes in distinct brain regions. *Journal of Clinical Investigation*, **2021**,	15.9	1
80	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. *PLoS ONE*, **2021**, 16, e0249305	3.7	0
79	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimer's disease. *Nature Communications*, **2021**, 12, 2311	17.4	10
78	Modulating innate immune activation states impacts the efficacy of specific A□mmunotherapy. *Molecular Neurodegeneration*, **2021**, 16, 32	19	1
77	Genome-wide analysis identifies a novel LINC-PINT splice variant associated with vascular amyloid pathology in Alzheimer's disease. *Acta Neuropathologica Communications*, **2021**, 9, 93	7.3	2
76	Plasma Biomarkers of Alzheimer's Disease in African Americans. *Journal of Alzheimer's Disease*, **2021**, 79, 323-334	4.3	3
75	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. *PLoS Genetics*, **2021**, 17, e1009224	6	10
74	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. *Acta Neuropathologica*, **2021**, 141, 667-680	14.3	2
73	Comparative evaluation for the globin gene depletion methods for mRNA sequencing using the whole blood-derived total RNAs. *BMC Genomics*, **2020**, 21, 890	4.5	1
72	MAPT haplotype-stratified GWAS reveals differential association for AD risk variants. *Alzheimer's and Dementia*, **2020**, 16, 983-1002	1.2	11
71	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. *Scientific Data*, **2020**, 7, 340	8.2	26
70	Deciphering cellular transcriptional alterations in Alzheimer's disease brains. *Molecular Neurodegeneration*, **2020**, 15, 38	19	13
69	Association of ABI3 and PLCG2 missense variants with disease risk and neuropathology in Lewy body disease and progressive supranuclear palsy. *Acta Neuropathologica Communications*, **2020**, 8, 172	7.3	3
68	Tau and apolipoprotein E modulate cerebrovascular tight junction integrity independent of cerebral amyloid angiopathy in Alzheimer's disease. *Alzheimer's and Dementia*, **2020**, 16, 1372-1383	1.2	12
67	A nonsynonymous mutation in PLCG2 reduces the risk of Alzheimer's disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. *Acta Neuropathologica*, **2019**, 138, 237-250	14.3	50
66	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. *Genome Biology*, **2019**, 20, 97	18.3	68

65	Ethnoracial differences in Alzheimer's disease from the FLorida Autopsied Multi-Ethnic (FLAME) cohort. *Alzheimer's and Dementia*, **2019**, 15, 635-643	1.2	17
64	Evaluation of Associations of Alzheimer's Disease Risk Variants that Are Highly Expressed in Microglia with Neuropathological Outcome Measures. *Journal of Alzheimer's Disease*, **2019**, 70, 659-666	4.3	5
63	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
62	TMEM106B haplotypes have distinct gene expression patterns in aged brain. *Molecular Neurodegeneration*, **2018**, 13, 35	19	15
61	Identification of missing variants by combining multiple analytic pipelines. *BMC Bioinformatics*, **2018**, 19, 139	3.6	9
60	Male-specific epistasis between WWC1 and TLN2 genes is associated with Alzheimer's disease. *Neurobiology of Aging*, **2018**, 72, 188.e3-188.e12	5.6	13
59	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. *Acta Neuropathologica*, **2018**, 136, 709-727	14.3	28
58	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. *Alzheimer's and Dementia*, **2018**, 14, 352-366	1.2	72
57	ABI3 and PLCG2 missense variants as risk factors for neurodegenerative diseases in Caucasians and African Americans. *Molecular Neurodegeneration*, **2018**, 13, 53	19	41
56	loss-of-function variants, expression, and neurologic disease risk. *Neurology: Genetics*, **2017**, 3, e126	3.8	22
55	Comprehensive Screening for Disease Risk Variants in Early-Onset Alzheimer's Disease Genes in African Americans Identifies Novel PSEN Variants. *Journal of Alzheimer's Disease*, **2017**, 56, 1215-1222	4.3	2
54	Transethnic genome-wide scan identifies novel Alzheimer's disease loci. *Alzheimer's and Dementia*, **2017**, 13, 727-738	1.2	106
53	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. *Neurology: Genetics*, **2017**, 3, e141	3.8	15
52	A candidate regulatory variant at the TREM gene cluster associates with decreased Alzheimer's disease risk and increased TREML1 and TREM2 brain gene expression. *Alzheimer's and Dementia*, **2017**, 13, 663-673	1.2	35
51	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
50	A novel Alzheimer disease locus located near the gene encoding tau protein. *Molecular Psychiatry*, **2016**, 21, 108-17	15.1	175
49	Evaluating pathogenic dementia variants in posterior cortical atrophy. *Neurobiology of Aging*, **2016**, 37, 38-44	5.6	19
48	Human whole genome genotype and transcriptome data for Alzheimer's and other neurodegenerative diseases. *Scientific Data*, **2016**, 3, 160089	8.2	179

47	Genetic risk factors for the posterior cortical atrophy variant of Alzheimer's disease. *Alzheimer's and Dementia*, **2016**, 12, 862-71	1.2	64
46	ABCA7 Deficiency Accelerates Amyloid-β Generation and Alzheimer's Neuronal Pathology. *Journal of Neuroscience*, **2016**, 36, 3848-59	6.6	80
45	Assessment of the genetic variance of late-onset Alzheimer's disease. *Neurobiology of Aging*, **2016**, 41, 200.e13-200.e20	5.6	119
44	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. *Acta Neuropathologica*, **2016**, 132, 197-211	14.3	35
43	Shared genetic contribution to Ischaemic Stroke and Alzheimer's Disease. *Annals of Neurology*, **2016**, 79, 739-747	9.4	42
42	TREM2 is associated with increased risk for Alzheimer's disease in African Americans. *Molecular Neurodegeneration*, **2015**, 10, 19	19	108
41	Late-onset Alzheimer disease risk variants mark brain regulatory loci. *Neurology: Genetics*, **2015**, 1, e15	3.8	51
40	Convergent genetic and expression data implicate immunity in Alzheimer's disease. *Alzheimer's and Dementia*, **2015**, 11, 658-71	1.2	146
39	Late-onset Alzheimer's risk variants in memory decline, incident mild cognitive impairment, and Alzheimer's disease. *Neurobiology of Aging*, **2015**, 36, 60-7	5.6	69
38	Genetically-controlled Vesicle-Associated Membrane Protein 1 expression may contribute to Alzheimer's pathophysiology and susceptibility. *Molecular Neurodegeneration*, **2015**, 10, 18	19	11
37	Blood type gene locus has no influence on ACE association with Alzheimer's disease. *Neurobiology of Aging*, **2015**, 36, 1767.e1-1767.e2	5.6	2
36	Exonic Re-Sequencing of the Chromosome 2q24.3 Parkinson's Disease Locus. *PLoS ONE*, **2015**, 10, e0128586	3.7	
35	Late-onset Alzheimer disease genetic variants in posterior cortical atrophy and posterior AD. *Neurology*, **2014**, 82, 1455-62	6.5	42
34	Differential clinicopathologic and genetic features of late-onset amnestic dementias. *Acta Neuropathologica*, **2014**, 128, 411-21	14.3	90
33	Genome-wide association interaction analysis for Alzheimer's disease. *Neurobiology of Aging*, **2014**, 35, 2436-2443	5.6	49
32	Evaluation of memory endophenotypes for association with CLU, CR1, and PICALM variants in black and white subjects. *Alzheimer's and Dementia*, **2014**, 10, 205-13	1.2	35
31	Association of MAPT haplotypes with Alzheimer's disease risk and MAPT brain gene expression levels. *Alzheimer's Research and Therapy*, **2014**, 6, 39	9	78
30	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

29	Gene-wide analysis detects two new susceptibility genes for Alzheimer's disease. *PLoS ONE*, **2014**, 9, e94661	3.7	90
28	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*, **2013**, 45, 1452-8	36.3	2714
27	TREM2 variants in Alzheimer's disease. *New England Journal of Medicine*, **2013**, 368, 117-27	59.2	1805
26	LRRTM3 interacts with APP and BACE1 and has variants associating with late-onset Alzheimer's disease (LOAD). *PLoS ONE*, **2013**, 8, e64164	3.7	10
25	Linking protective GAB2 variants, increased cortical GAB2 expression and decreased Alzheimer's disease pathology. *PLoS ONE*, **2013**, 8, e64802	3.7	12
24	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. *Neurology*, **2012**, 79, 221-8	6.5	124
23	Brain expression genome-wide association study (eGWAS) identifies human disease-associated variants. *PLoS Genetics*, **2012**, 8, e1002707	6	174
22	Commentary on 'Functional analysis of APOE locus genetic variation implicates regional enhancers in the regulation of both TOMM40 and APOE'. *Journal of Human Genetics*, **2012**, 57, 3-4	4.3	5
21	The role of variation at APP, PSEN1, PSEN2, and MAPT in late onset Alzheimer's disease. *Journal of Alzheimer's Disease*, **2012**, 28, 377-87	4.3	47
20	Ataxin-2 repeat-length variation and neurodegeneration. *Human Molecular Genetics*, **2011**, 20, 3207-12	5.6	128
19	Investigating statistical epistasis in complex disorders. *Journal of Alzheimer's Disease*, **2011**, 25, 635-44	4.3	5
18	A multi-center study of ACE and the risk of late-onset Alzheimer's disease. *Journal of Alzheimer's Disease*, **2011**, 24, 587-97	4.3	29
17	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
16	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. *Nature Genetics*, **2011**, 43, 429-35	36.3	1421
15	Investigation of 15 of the top candidate genes for late-onset Alzheimer's disease. *Human Genetics*, **2011**, 129, 273-82	6.3	53
14	Replication of EPHA1 and CD33 associations with late-onset Alzheimer's disease: a multi-centre case-control study. *Molecular Neurodegeneration*, **2011**, 6, 54	19	55
13	Replication of BIN1 association with Alzheimer's disease and evaluation of genetic interactions. *Journal of Alzheimer's Disease*, **2011**, 24, 751-8	4.3	55
12	Genetic evidence implicates the immune system and cholesterol metabolism in the aetiology of Alzheimer's disease. *PLoS ONE*, **2010**, 5, e13950	3.7	276

11	Concordant association of insulin degrading enzyme gene (IDE) variants with IDE mRNA, Abeta, and Alzheimer's disease. *PLoS ONE*, **2010**, 5, e8764	3.7	40
10	Replication of CLU, CR1, and PICALM associations with alzheimer disease. *Archives of Neurology*, **2010**, 67, 961-4		167
9	Genome-wide screen identifies rs646776 near sortilin as a regulator of progranulin levels in human plasma. *American Journal of Human Genetics*, **2010**, 87, 890-7	11	110
8	Genetic variation in PCDH11X is associated with susceptibility to late-onset Alzheimer's disease. *Nature Genetics*, **2009**, 41, 192-8	36.3	235
7	Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. *Nature Genetics*, **2009**, 41, 1088-93	36.3	2018
6	Genome-wide association study and mouse model identify interaction between RET and EDNRB pathways in Hirschsprung disease. *Nature Genetics*, **2002**, 32, 237-44	36.3	229
5	High-throughput variation detection and genotyping using microarrays. *Genome Research*, **2001**, 11, 1913-25	9.7	239
4	Allele frequency distributions in pooled DNA samples: applications to mapping complex disease genes. *Genome Research*, **1998**, 8, 111-23	9.7	104
3	SSLPs to map genetic differences between the 129 inbred strains and closed-colony, random-bred CD-1 mice. *Mammalian Genome*, **1997**, 8, 441-2	3.2	15
2	Leveraging selective hippocampal vulnerability among Alzheimer disease subtypes reveals a novel tau binding partner SERPINA5		2
1	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions		7