Minerva M Carrasquillo

List of Publications by Year
in descending order

81	20,937	57631	58464
papers	citations	44 h-index	82 g-index

98	98	98	20485
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Alzheimerâ€™s disease and progressive supranuclear palsy share similar transcriptomic changes in distinct brain regions. Journal of Clinical Investigation, 2022, 132, .	3.9	13
2	Transcript levels in plasma contribute substantial predictive value as potential Alzheimer's disease biomarkers in African Americans. EBioMedicine, 2022, , 103929.	2.7	2
3	Investigating Heterogeneity and Neuroanatomic Correlates of Longitudinal Clinical Decline in Atypical Alzheimer Disease. Neurology, 2022, 98, .	1.5	12
4	Plasma Biomarkers of Alzheimerâ€™s Disease in African Americans. Journal of Alzheimer's Disease, 2021, 79, 323-334.	1.2	11
5	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224.	1.5	43
6	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. Acta Neuropathologica, 2021, 141, 667-680.	3.9	5
7	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. PLoS ONE, 2021, 16, e0249305.	1.1	5
8	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimerâ€™s disease. Nature Communications, 2021, 12, 2311.	5.8	44
9	Modulating innate immune activation states impacts the efficacy of specific AÎ² immunotherapy. Molecular Neurodegeneration, 2021, 16, 32.	4.4	4
10	Genome-wide analysis identifies a novel LINC-PINT splice variant associated with vascular amyloid pathology in Alzheimerâ€™s disease. Acta Neuropathologica Communications, 2021, 9, 93.	2.4	9
11	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	2.4	75
12	Deciphering cellular transcriptional alterations in Alzheimerâ€™s disease brains. Molecular Neurodegeneration, 2020, 15, 38.	4.4	42
13	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.	2.4	8
14	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.	0.4	34
15	Comparative evaluation for the globin gene depletion methods for mRNA sequencing using the whole blood-derived total RNAs. BMC Genomics, 2020, 21, 890.	1.2	12
16	MAPT haplotypeâ€“stratified GWAS reveals differential association for AD risk variants. Alzheimer's and Dementia, 2020, 16, 983-1002.	0.4	21
17	Evaluation of Associations of Alzheimerâ€™s Disease Risk Variants that Are Highly Expressed in Microglia with Neuropathological Outcome Measures. Journal of Alzheimer's Disease, 2019, 70, 659-666.	1.2	6
18	A nonsynonymous mutation in PLCG2 reduces the risk of Alzheimerâ€™s disease, dementia with Lewy bodies and frontotemporal dementia, and increases the likelihood of longevity. Acta Neuropathologica, 2019, 138, 237-250.	3.9	87

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19	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. Genome Biology, 2019, 20, 97.	3.8	122
20	Ethnoracial differences in Alzheimer's disease from the FLorida Autopsied Multiâ€Ethnic (FLAME) cohort. Alzheimer's and Dementia, 2019, 15, 635-643.	0.4	29
21	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates AÎ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
22	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. Alzheimer's and Dementia, 2018, 14, 352-366.	0.4	116
23	ABI3 and PLCG2 missense variants as risk factors for neurodegenerative diseases in Caucasians and African Americans. Molecular Neurodegeneration, 2018, 13, 53.	4.4	75
24	TMEM106B haplotypes have distinct gene expression patterns in aged brain. Molecular Neurodegeneration, 2018, 13, 35.	4.4	30
25	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	1.2	10
26	Male-specific epistasis between WWC1 and TLN2 genes is associated with Alzheimer's disease. Neurobiology of Aging, 2018, 72, 188.e3-188.e12.	1.5	24
27	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. Acta Neuropathologica, 2018, 136, 709-727.	3.9	47
28	ABCA7 loss-of-function variants, expression, and neurologic disease risk. Neurology: Genetics, 2017, 3, e126.	0.9	26
29	Comprehensive Screening for Disease Risk Variants in Early-Onset Alzheimerâ€™s Disease Genes in African Americans Identifies Novel PSEN Variants. Journal of Alzheimer's Disease, 2017, 56, 1215-1222.	1.2	4
30	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.4	166
31	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. Neurology: Genetics, 2017, 3, e141.	0.9	25
32	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.	0.4	48
33	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	9.4	783
34	Human whole genome genotype and transcriptome data for Alzheimerâ€™s and other neurodegenerative diseases. Scientific Data, 2016, 3, 160089.	2.4	361
35	Genetic risk factors for the posterior cortical atrophy variant of Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 862-871.	0.4	93
36	ABCA7 Deficiency Accelerates Amyloid-Î² Generation and Alzheimer's Neuronal Pathology. Journal of Neuroscience, 2016, 36, 3848-3859.	1.7	109

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37	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	1.5	174
38	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	3.9	49
39	Shared genetic contribution to ischemic stroke and Alzheimer's disease. Annals of Neurology, 2016, 79, 739-747.	2.8	56
40	Evaluating pathogenic dementia variants in posterior cortical atrophy. Neurobiology of Aging, 2016, 37, 38-44.	1.5	23
41	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	4.1	260
42	Genetically-controlled Vesicle-Associated Membrane Protein 1 expression may contribute to Alzheimerâ€™s pathophysiology and susceptibility. Molecular Neurodegeneration, 2015, 10, 18.	4.4	13
43	Blood type gene locus has no influence on ACE association with Alzheimer's disease. Neurobiology of Aging, 2015, 36, 1767.e1-1767.e2.	1.5	2
44	TREM2 is associated with increased risk for Alzheimerâ€™s disease in African Americans. Molecular Neurodegeneration, 2015, 10, 19.	4.4	130
45	Late-onset Alzheimer disease risk variants mark brain regulatory loci. Neurology: Genetics, 2015, 1, e15.	0.9	64
46	Convergent genetic and expression data implicate immunity in Alzheimer's disease. Alzheimer's and Dementia, 2015, 11, 658-671.	0.4	173
47	Late-onset Alzheimerâ€™s risk variants in memory decline, incident mild cognitive impairment, and Alzheimerâ€™s disease. Neurobiology of Aging, 2015, 36, 60-67.	1.5	90
48	Exonic Re-Sequencing of the Chromosome 2q24.3 Parkinsonâ€™s Disease Locus. PLoS ONE, 2015, 10, e0128586.	1.1	0
49	Association of MAPT haplotypes with Alzheimerâ€™s disease risk and MAPT brain gene expression levels. Alzheimer's Research and Therapy, 2014, 6, 39.	3.0	106
50	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	4.5	166
51	Late-onset Alzheimer disease genetic variants in posterior cortical atrophy and posterior AD. Neurology, 2014, 82, 1455-1462.	1.5	51
52	Differential clinicopathologic and genetic features of late-onset amnestic dementias. Acta Neuropathologica, 2014, 128, 411-421.	3.9	119
53	Genome-wide association interaction analysis for Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2436-2443.	1.5	61
54	Evaluation of memory endophenotypes for association with CLU , CR1, and PICALM variants in black and white subjects. , 2014, 10, 205-213.		40

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55	Gene-Wide Analysis Detects Two New Susceptibility Genes for Alzheimer's Disease. PLoS ONE, 2014, 9, e94661.	1.1	155
56	Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. Nature Genetics, 2013, 45, 1452-1458.	9.4	3,741
57	TREM2 Variants in Alzheimer's Disease. New England Journal of Medicine, 2013, 368, 117-127.	13.9	2,385
58	LRRTM3 Interacts with APP and BACE1 and Has Variants Associating with Late-Onset Alzheimerâ€™s Disease (LOAD). PLoS ONE, 2013, 8, e64164.	1.1	12
59	Linking Protective GAB2 Variants, Increased Cortical GAB2 Expression and Decreased Alzheimerâ€™s Disease Pathology. PLoS ONE, 2013, 8, e64802.	1.1	13
60	Brain Expression Genome-Wide Association Study (eGWAS) Identifies Human Disease-Associated Variants. PLoS Genetics, 2012, 8, e1002707.	1.5	225
61	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.	1.1	6
62	The Role of Variation at AÎ²PP, PSEN1, PSEN2, and MAPT in Late Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2012, 28, 377-387.	1.2	53
63	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.5	144
64	Ataxin-2 repeat-length variation and neurodegeneration. Human Molecular Genetics, 2011, 20, 3207-3212.	1.4	147
65	Investigating Statistical Epistasis in Complex Disorders. Journal of Alzheimer's Disease, 2011, 25, 635-644.	1.2	8
66	A Multi-Center Study of ACE and the Risk of Late-Onset Alzheimer's Disease. Journal of Alzheimer's Disease, 2011, 24, 587-597.	1.2	33
67	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	9.4	1,676
68	Common variants at ABCA7, MS4A6A/MS4A4E, EPHA1, CD33 and CD2AP are associated with Alzheimer's disease. Nature Genetics, 2011, 43, 429-435.	9.4	1,708
69	Investigation of 15 of the top candidate genes for late-onset Alzheimerâ€™s disease. Human Genetics, 2011, 129, 273-282.	1.8	57
70	Replication of EPHA1 and CD33 associations with late-onset Alzheimer's disease: a multi-centre case-control study. Molecular Neurodegeneration, 2011, 6, 54.	4.4	67
71	Replication of BIN1 Association with Alzheimer's Disease and Evaluation of Genetic Interactions. Journal of Alzheimer's Disease, 2011, 24, 751-758.	1.2	61
72	Genome-wide Screen Identifies rs646776 near Sortilin as a Regulator of Progranulin Levels in Human Plasma. American Journal of Human Genetics, 2010, 87, 890-897.	2.6	130

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73	Genetic Evidence Implicates the Immune System and Cholesterol Metabolism in the Aetiology of Alzheimer's Disease. PLoS ONE, 2010, 5, e13950.	1.1	347
74	Concordant Association of Insulin Degrading Enzyme Gene (IDE) Variants with IDE mRNA, AÃŸ, and Alzheimer's Disease. PLoS ONE, 2010, 5, e8764.	1.1	48
75	Replication of CLU, CR1, and PICALM Associations With Alzheimer Disease. Archives of Neurology, 2010, 67, 961-4.	4.9	188
76	Genetic variation in PCDH11X is associated with susceptibility to late-onset Alzheimer's disease. Nature Genetics, 2009, 41, 192-198.	9.4	279
77	Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. Nature Genetics, 2009, 41, 1088-1093.	9.4	2,697
78	Genome-wide association study and mouse model identify interaction between RET and EDNRB pathways in Hirschsprung disease. Nature Genetics, 2002, 32, 237-244.	9.4	255
79	High-Throughput Variation Detection and Genotyping Using Microarrays. Genome Research, 2001, 11, 1913-1925.	2.4	258
80	Allele Frequency Distributions in Pooled DNA Samples: Applications to Mapping Complex Diseaseâ€‰Genes. Genome Research, 1998, 8, 111-123.	2.4	120
81	SSLPs to map genetic differences between the 129 inbred strains and closed-colony, random-bred CD-I mice. Mammalian Genome, 1997, 8, 441-442.	1.0	18