NilÃ¼fer Ertekin-Taner

List of Publications by Year
in descending order

127 papers	11,371 citations	44069 48 h-index	36028 97 g-index
166 all docs	166 docs citations	166 times ranked	14356 citing authors

#	Article	IF	Citations
1	Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. Nature Genetics, 2011, 43, 436-441.	21.4	1,676
2	Alzheimer's disease: early alterations in brain DNA methylation at ANK1, BIN1, RHBDF2 and other loci. Nature Neuroscience, 2014, 17, 1156-1163.	14.8	800
3	Rare coding variants in PLCG2, ABI3, and TREM2 implicate microglial-mediated innate immunity in Alzheimer's disease. Nature Genetics, 2017, 49, 1373-1384.	21.4	783
4	Large-scale proteomic analysis of Alzheimerâ€™s disease brain and cerebrospinal fluid reveals early changes in energy metabolism associated with microglia and astrocyte activation. Nature Medicine, 2020, 26, 769-780.	30.7	547
5	Human whole genome genotype and transcriptome data for Alzheimerâ€™s and other neurodegenerative diseases. Scientific Data, 2016, 3, 160089.	5.3	361
6	Variants in the ATP-Binding Cassette Transporter (ABCA7), Apolipoprotein E Ïµ4, and the Risk of Late-Onset Alzheimer Disease in African Americans. JAMA - Journal of the American Medical Association, 2013, 309, 1483.	7.4	360
7	TREM2 in neurodegeneration: evidence for association of the p.R47H variant with frontotemporal dementia and Parkinsonâ€™s disease. Molecular Neurodegeneration, 2013, 8, 19.	10.8	323
8	Genetic variation in PCDH11X is associated with susceptibility to late-onset Alzheimer's disease. Nature Genetics, 2009, 41, 192-198.	21.4	279
9	A novel Alzheimer disease locus located near the gene encoding tau protein. Molecular Psychiatry, 2016, 21, 108-117.	7.9	260
10	Brain Expression Genome-Wide Association Study (eGWAS) Identifies Human Disease-Associated Variants. PLoS Genetics, 2012, 8, e1002707.	3.5	225
11	Genetics of Alzheimer's Disease: A Centennial Review. Neurologic Clinics, 2007, 25, 611-667.	1.8	206
12	Meta-Analysis of the Alzheimerâ€™s Disease Human Brain Transcriptome and Functional Dissection in Mouse Models. Cell Reports, 2020, 32, 107908.	6.4	199
13	Assessment of the genetic variance of late-onset Alzheimer's disease. Neurobiology of Aging, 2016, 41, 200.e13-200.e20.	3.1	174
14	APOE4 exacerbates synapse loss and neurodegeneration in Alzheimerâ€™s disease patient iPSC-derived cerebral organoids. Nature Communications, 2020, 11, 5540.	12.8	172
15	Genome-wide association study of corticobasal degeneration identifies risk variants shared with progressive supranuclear palsy. Nature Communications, 2015, 6, 7247.	12.8	170
16	Effects of Multiple Genetic Loci on Age at Onset in Late-Onset Alzheimer Disease. JAMA Neurology, 2014, 71, 1394.	9.0	166
17	Transethnic genomeâ€wide scan identifies novel Alzheimer's disease loci. Alzheimer's and Dementia, 2017, 13, 727-738.	0.8	166
18	Alzheimerâ€™s Risk Factors Age, APOE Genotype, and Sex Drive Distinct Molecular Pathways. Neuron, 2020, 106, 727-742.e6.	8.1	152

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19	Novel late-onset Alzheimer disease loci variants associate with brain gene expression. Neurology, 2012, 79, 221-228.	1.1	144
20	Novel Alzheimer Disease Risk Loci and Pathways in African American Individuals Using the African Genome Resources Panel. JAMA Neurology, 2021, 78, 102.	9.0	144
21	TREM2 is associated with increased risk for Alzheimerâ€™s disease in African Americans. Molecular Neurodegeneration, 2015, 10, 19.	10.8	130
22	APOE Îµ4 is associated with severity of Lewy body pathology independent of Alzheimer pathology. Neurology, 2018, 91, e1182-e1195.	1.1	122
23	Systematic analysis of dark and camouflaged genes reveals disease-relevant genes hiding in plain sight. Genome Biology, 2019, 20, 97.	8.8	122
24	Conserved brain myelination networks are altered in Alzheimer's and other neurodegenerative diseases. Alzheimer's and Dementia, 2018, 14, 352-366.	0.8	116
25	Association of MAPT haplotypes with Alzheimerâ€™s disease risk and MAPT brain gene expression levels. Alzheimer's Research and Therapy, 2014, 6, 39.	6.2	106
26	Potential genetic modifiers of disease risk and age at onset in patients with frontotemporal lobar degeneration and GRN mutations: a genome-wide association study. Lancet Neurology, The, 2018, 17, 548-558.	10.2	97
27	Two rare AKAP9 variants are associated with Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2014, 10, 609.	0.8	94
28	Genetic risk factors for the posterior cortical atrophy variant of Alzheimer's disease. Alzheimer's and Dementia, 2016, 12, 862-871.	0.8	93
29	Genetic variants in a haplotype block spanningIDE are significantly associated with plasma A?42 levels and risk for Alzheimer disease. Human Mutation, 2004, 23, 334-342.	2.5	91
30	Late-onset Alzheimerâ€™s risk variants in memory decline, incident mild cognitive impairment, and Alzheimerâ€™s disease. Neurobiology of Aging, 2015, 36, 60-67.	3.1	90
31	Genome-wide analyses as part of the international FTLD-TDP whole-genome sequencing consortium reveals novel disease risk factors and increases support for immune dysfunction in FTLD. Acta Neuropathologica, 2019, 137, 879-899.	7.7	90
32	Two novel loci, COBL and SLC10A2, for Alzheimer's disease in African Americans. Alzheimer's and Dementia, 2017, 13, 119-129.	0.8	87
33	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.	7.7	87
34	Genetics of Alzheimer disease in the pre- and post-GWAS era. Alzheimer's Research and Therapy, 2010, 2, 3.	6.2	85
35	Imaging correlations of tau, amyloid, metabolism, and atrophy in typical and atypical Alzheimer's disease. Alzheimer's and Dementia, 2018, 14, 1005-1014.	0.8	80
36	Glutathione S-transferase omega genes in Alzheimer and Parkinson disease risk, age-at-diagnosis and brain gene expression: an association study with mechanistic implications. Molecular Neurodegeneration, 2012, 7, 13.	10.8	75

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37	ABI3 and PLCG2 missense variants as risk factors for neurodegenerative diseases in Caucasians and African Americans. Molecular Neurodegeneration, 2018, 13, 53.	10.8	75
38	Large eQTL meta-analysis reveals differing patterns between cerebral cortical and cerebellar brain regions. Scientific Data, 2020, 7, 340.	5.3	75
39	Fine mapping of the Â-T catenin gene to a quantitative trait locus on chromosome 10 in late-onset Alzheimer's disease pedigrees. Human Molecular Genetics, 2003, 12, 3133-3143.	2.9	72
40	TYROBP genetic variants in early-onset Alzheimer's disease. Neurobiology of Aging, 2016, 48, 222.e9-222.e15.	3.1	69
41	Sex and age interact to determine clinicopathologic differences in Alzheimerâ€™s disease. Acta Neuropathologica, 2018, 136, 873-885.	7.7	69
42	Linkage, whole genome sequence, and biological data implicate variants in RAB10 in Alzheimerâ€™s disease resilience. Genome Medicine, 2017, 9, 100.	8.2	67
43	[¹⁸F]AVâ€1451 clustering of entorhinal and cortical uptake in Alzheimer's disease. Annals of Neurology, 2018, 83, 248-257.	5.3	67
44	Elevated amyloid Î² protein (AÎ²42) and late onset Alzheimer's disease are associated with single nucleotide polymorphisms in the urokinase-type plasminogen activator gene. Human Molecular Genetics, 2005, 14, 447-460.	2.9	64
45	Late-onset Alzheimer disease risk variants mark brain regulatory loci. Neurology: Genetics, 2015, 1, e15.	1.9	64
46	Genome-wide association interaction analysis for Alzheimer's disease. Neurobiology of Aging, 2014, 35, 2436-2443.	3.1	61
47	Expression and processing analyses of wild type and p.R47H TREM2 variant in Alzheimerâ€™s disease brains. Molecular Neurodegeneration, 2016, 11, 72.	10.8	55
48	Late-onset Alzheimer disease genetic variants in posterior cortical atrophy and posterior AD. Neurology, 2014, 82, 1455-1462.	1.1	51
49	TLR5 decoy receptor as a novel anti-amyloid therapeutic for Alzheimerâ€™s disease. Journal of Experimental Medicine, 2018, 215, 2247-2264.	8.5	50
50	Selective Vulnerability of the Nucleus Basalis of Meynert Among Neuropathologic Subtypes of Alzheimer Disease. JAMA Neurology, 2020, 77, 225.	9.0	50
51	Gene expression, methylation and neuropathology correlations at progressive supranuclear palsy risk loci. Acta Neuropathologica, 2016, 132, 197-211.	7.7	49
52	Heritability of plasma amyloid ? in typical late-onset Alzheimer?s disease pedigrees. Genetic Epidemiology, 2001, 21, 19-30.	1.3	48
53	Concordant Association of Insulin Degrading Enzyme Gene (IDE) Variants with IDE mRNA, AÃŸ, and Alzheimer's Disease. PLoS ONE, 2010, 5, e8764.	2.5	48
54	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.	0.8	48

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55	Divergent brain gene expression patterns associate with distinct cell-specific tau neuropathology traits in progressive supranuclear palsy. Acta Neuropathologica, 2018, 136, 709-727.	7.7	47
56	Transcriptomic analysis to identify genes associated with selective hippocampal vulnerability in Alzheimerâ€™s disease. Nature Communications, 2021, 12, 2311.	12.8	44
57	Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS Genetics, 2021, 17, e1009224.	3.5	43
58	Global and local ancestry in Africanâ€Americans: Implications for Alzheimer's disease risk. Alzheimer's and Dementia, 2016, 12, 233-243.	0.8	42
59	Deciphering cellular transcriptional alterations in Alzheimerâ€™s disease brains. Molecular Neurodegeneration, 2020, 15, 38.	10.8	42
60	Evaluation of memory endophenotypes for association with CLU , CR1, and PICALM variants in black and white subjects. , 2014, 10, 205-213.		40
61	Systems biology approach to late-onset Alzheimer's disease genome-wide association study identifies novel candidate genes validated using brain expression data and Caenorhabditis elegans experiments. , 2017, 13, 1133-1142.		40
62	Association of Long Runs of Homozygosity With Alzheimer Disease Among African American Individuals. JAMA Neurology, 2015, 72, 1313.	9.0	39
63	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.	0.8	34
64	Mitophagy alterations in Alzheimer's disease are associated with granulovacuolar degeneration and early tau pathology. Alzheimer's and Dementia, 2021, 17, 417-430.	0.8	34
65	MAPT haplotype H1G is associated with increased risk of dementia with Lewy bodies. Alzheimer's and Dementia, 2016, 12, 1297-1304.	0.8	32
66	Gene expression endophenotypes: a novel approach for gene discovery in Alzheimer's disease. Molecular Neurodegeneration, 2011, 6, 31.	10.8	31
67	Role for the microtubule-associated protein tau variant p.A152T in risk of Î±-synucleinopathies. Neurology, 2015, 85, 1680-1686.	1.1	31
68	LRRK2 variation and dementia with Lewy bodies. Parkinsonism and Related Disorders, 2016, 31, 98-103.	2.2	30
69	TMEM106B haplotypes have distinct gene expression patterns in aged brain. Molecular Neurodegeneration, 2018, 13, 35.	10.8	30
70	Ethnoracial differences in Alzheimer's disease from the FLorida Autopsied Multiâ€Ethnic (FLAME) cohort. Alzheimer's and Dementia, 2019, 15, 635-643.	0.8	29
71	Genetics of Gene Expression in the Aging Human Brain Reveal TDP-43 Proteinopathy Pathophysiology. Neuron, 2020, 107, 496-508.e6.	8.1	29
72	Atlas of Transcription Factor Binding Sites from ENCODE DNase Hypersensitivity Data across 27 Tissue Types. Cell Reports, 2020, 32, 108029.	6.4	28

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73	Genome-wide pleiotropy analysis of neuropathological traits related to Alzheimerâ€™s disease. Alzheimer's Research and Therapy, 2018, 10, 22.	6.2	27
74	ABCA7 loss-of-function variants, expression, and neurologic disease risk. Neurology: Genetics, 2017, 3, e126.	1.9	26
75	Molecular estimation of neurodegeneration pseudotime in older brains. Nature Communications, 2020, 11, 5781.	12.8	26
76	African American exome sequencing identifies potential risk variants at Alzheimer disease loci. Neurology: Genetics, 2017, 3, e141.	1.9	25
77	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. Alzheimer's and Dementia, 2021, 17, 984-1004.	0.8	25
78	Apolipoprotein E regulates lipid metabolism and Î±-synuclein pathology in human iPSC-derived cerebral organoids. Acta Neuropathologica, 2021, 142, 807-825.	7.7	25
79	Male-specific epistasis between WWC1 and TLN2 genes is associated with Alzheimer's disease. Neurobiology of Aging, 2018, 72, 188.e3-188.e12.	3.1	24
80	Evaluating pathogenic dementia variants in posterior cortical atrophy. Neurobiology of Aging, 2016, 37, 38-44.	3.1	23
81	Genomeâ€wide transcriptome analysis identifies novel dysregulated genes implicated in Alzheimer's pathology. Alzheimer's and Dementia, 2020, 16, 1213-1223.	0.8	23
82	Transcriptional landscape of human microglia implicates age, sex, and APOEâ€related immunometabolic pathway perturbations. Aging Cell, 2022, 21, e13606.	6.7	23
83	Risk factors for severe COVID-19 differ by age for hospitalized adults. Scientific Reports, 2022, 12, 6568.	3.3	23
84	Genetic architecture of resilience of executive functioning. Brain Imaging and Behavior, 2012, 6, 621-633.	2.1	22
85	RAB39B gene mutations are not a common cause of Parkinson's disease or dementia with Lewy bodies. Neurobiology of Aging, 2016, 45, 107-108.	3.1	21
86	MAPT haplotypeâ€“stratified GWAS reveals differential association for AD risk variants. Alzheimer's and Dementia, 2020, 16, 983-1002.	0.8	21
87	Atlas of RNA editing events affecting protein expression in aged and Alzheimerâ€™s disease human brain tissue. Nature Communications, 2021, 12, 7035.	12.8	19
88	Association and heterogeneity at the GAPDH locus in Alzheimer's disease. Neurobiology of Aging, 2012, 33, 203.e25-203.e33.	3.1	17
89	MRI and flortaucipir relationships in Alzheimer's phenotypes are heterogeneous. Annals of Clinical and Translational Neurology, 2020, 7, 707-721.	3.7	17
90	Microglia show differential transcriptomic response to AÎ² peptide aggregates ex vivo and in vivo. Life Science Alliance, 2021, 4, e202101108.	2.8	17

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91	TREM2 p.R47H substitution is not associated with dementia with Lewy bodies. Neurology: Genetics, 2016, 2, e85.	1.9	16
92	Utility of Plasma Neurofilament Light in the 1Florida Alzheimerâ€™s Disease Research Center (ADRC). Journal of Alzheimer's Disease, 2021, 79, 59-70.	2.6	16
93	Prominent amyloid plaque pathology and cerebral amyloid angiopathy in APP V717I (London) carrier â€“ phenotypic variability in autosomal dominant Alzheimerâ€™s disease. Acta Neuropathologica Communications, 2020, 8, 31.	5.2	14
94	Alternative Approaches in Gene Discovery and Characterization in Alzheimerâ€™s Disease. Current Genetic Medicine Reports, 2013, 1, 39-51.	1.9	13
95	Alzheimerâ€™s disease and progressive supranuclear palsy share similar transcriptomic changes in distinct brain regions. Journal of Clinical Investigation, 2022, 132, .	8.2	13
96	Whole genome sequencingâ€“based copy number variations reveal novel pathways and targets in Alzheimer's disease. Alzheimer's and Dementia, 2022, 18, 1846-1867.	0.8	13
97	LRRTM3 Interacts with APP and BACE1 and Has Variants Associating with Late-Onset Alzheimerâ€™s Disease (LOAD). PLoS ONE, 2013, 8, e64164.	2.5	12
98	An alternative transcript of the Alzheimer's disease risk gene SORL1 encodes a truncated receptor. Neurobiology of Aging, 2018, 71, 266.e11-266.e24.	3.1	12
99	Comparative evaluation for the globin gene depletion methods for mRNA sequencing using the whole blood-derived total RNAs. BMC Genomics, 2020, 21, 890.	2.8	12
100	Manifestations of Alzheimerâ€™s disease genetic risk in the blood are evident in a multiomic analysis in healthy adults aged 18 to 90. Scientific Reports, 2022, 12, 6117.	3.3	12
101	Investigating Heterogeneity and Neuroanatomic Correlates of Longitudinal Clinical Decline in Atypical Alzheimer Disease. Neurology, 2022, 98, .	1.1	12
102	Plasma Biomarkers of Alzheimerâ€™s Disease in African Americans. Journal of Alzheimer's Disease, 2021, 79, 323-334.	2.6	11
103	Relationship of APOE, age at onset, amyloid and clinical phenotype in Alzheimer disease. Neurobiology of Aging, 2021, 108, 90-98.	3.1	11
104	Identification of missing variants by combining multiple analytic pipelines. BMC Bioinformatics, 2018, 19, 139.	2.6	10
105	The influence of Î²-amyloid on [¹⁸ F]AV-1451 in semantic variant of primary progressive aphasia. Neurology, 2019, 92, e710-e722.	1.1	10
106	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.	5.2	9
107	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimer's disease risk in humans. Alzheimer's and Dementia, 2022, 18, 688-699.	0.8	9
108	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.	5.2	8

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109	Longitudinal Amyloid-Î² PET in Atypical Alzheimerâ€™s Disease and Frontotemporal Lobar Degeneration. Journal of Alzheimer's Disease, 2020, 74, 377-389.	2.6	7
110	Cilostazol Versus Aspirin for Secondary Stroke Prevention: Systematic Review and Meta-Analysis. Journal of Stroke and Cerebrovascular Diseases, 2021, 30, 105581.	1.6	7
111	Expression of an alternatively spliced variant of SORL1 in neuronal dendrites is decreased in patients with Alzheimerâ€™s disease. Acta Neuropathologica Communications, 2021, 9, 43.	5.2	7
112	Analysis of intraoperative human brain tissue transcriptome reveals putative risk genes and altered molecular pathways in glioma-related seizures. Epilepsy Research, 2021, 173, 106618.	1.6	7
113	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.	2.6	6
114	Effects of sex and APOE on Parkinsonâ€™s Disease-related cognitive decline. Neurologia I Neurochirurgia Polska, 2021, 55, 559-566.	1.2	6
115	The quest for Alzheimer disease genesâ€"focus on CSF tau. Nature Reviews Neurology, 2013, 9, 368-370.	10.1	5
116	Latent trait modeling of tau neuropathology in progressive supranuclear palsy. Acta Neuropathologica, 2021, 141, 667-680.	7.7	5
117	Impact of variant-level batch effects on identification of genetic risk factors in large sequencing studies. PLoS ONE, 2021, 16, e0249305.	2.5	5
118	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.	2.6	4
119	Modulating innate immune activation states impacts the efficacy of specific Aî² immunotherapy. Molecular Neurodegeneration, 2021, 16, 32.	10.8	4
120	Clinical, Imaging, and Pathologic Characteristics of Patients With Right vs Left Hemisphereâ€"Predominant Logopenic Progressive Aphasia. Neurology, 2021, 97, e523-e534.	1.1	4
121	Clinical Deep Phenotyping of ABCA7 Mutation Carriers. Neurology: Genetics, 2022, 8, e655.	1.9	4
122	Epigenomic features related to microglia are associated with attenuated effect of APOE Îµ4 on Alzheimerâ€™s disease risk in humans. Alzheimer's and Dementia, 2020, 16, e043533.	0.8	2
123	Transcript levels in plasma contribute substantial predictive value as potential Alzheimer's disease biomarkers in African Americans. EBioMedicine, 2022, , 103929.	6.1	2
124	Target-enriched sequencing of chromosome 17q21.31 in sporadic tauopathies reveals no candidate variants. Neurobiology of Aging, 2018, 66, 177.e7-177.e10.	3.1	1
125	Other Genes Implicated in Alzheimerâ€™s Disease. , 2013, , 209-230.		0
126	O3-04-01: NEXT-GENERATION RNA SEQUENCING IN ALZHEIMER'S DISEASE AND PROGRESSIVE SUPRANUCLEAR PALSY. , 2014, 10, P214-P215.		0

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127	S4â€02â€04: Accelerating Medicines Partnership: Identifying Therapeutic Targets for Alzheimer's Disease with Comparative Transcriptomics. Alzheimer's and Dementia, 2016, 12, P322.	0.8	0