

Resource Summary Report

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AlzGene: Field Synopsis of Genetic Association Studies in AD

RRID:SCR_006749

Type: Tool

Proper Citation

AlzGene: Field Synopsis of Genetic Association Studies in AD (RRID:SCR_006749)

Resource Information

URL: <http://www.alzgene.org/>

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Description: The AlzGene database provides a comprehensive, unbiased and regularly updated field synopsis of genetic association studies performed in Alzheimer's disease. In addition, hundreds of up-to-date meta-analyses are available for all eligible polymorphisms with sufficient data. In addition to identifying the epsilon4 allele of APOE and related effects, we pinpointed over a dozen potential Alzheimer disease susceptibility genes (ACE, CHRNA2, CST3, ESR1, GAPDH, IDE, MTHFR, NCSTN, PRNP, PSEN1, TF, TFAM and TNF) with statistically significant allelic summary odds ratios (ranging from 1.11-1.38 for risk alleles and 0.92-0.67 for protective alleles). Our database provides a powerful tool for deciphering the genetics of Alzheimer disease, and it serves as a potential model for tracking the most viable gene candidates in other genetically complex diseases.

Synonyms: Alzgene, AlzGene database

Resource Type: data or information resource, database

Defining Citation: [PMID:17192785](#)

Keywords: FASEB list

Funding: An anonymous donor ;
Cure Alzheimers Fund

Resource Name: AlzGene: Field Synopsis of Genetic Association Studies in AD

Resource ID: SCR_006749

Alternate IDs: nlx_33861

Record Creation Time: 20220129T080237+0000

Record Last Update: 20260729T044139+0000

Ratings and Alerts

No rating or validation information has been found for AlzGene: Field Synopsis of Genetic Association Studies in AD.

No alerts have been found for AlzGene: Field Synopsis of Genetic Association Studies in AD.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 172 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#).

Yi D, et al. (2025) Tau pathway-based gene analysis on PET identifies CLU and FYN in a Korean cohort. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 21(2), e14416.

Zhao X, et al. (2025) Unveiling genetic architecture of white matter microstructure through unsupervised deep representation learning of fractional anisotropy maps. *Research square*.

Vandal M, et al. (2025) CD2AP at the junction of nephropathy and Alzheimer's disease. *Molecular neurodegeneration*, 20(1), 63.

Lee S, et al. (2024) On the effect heterogeneity of established disease susceptibility loci for Alzheimer's disease across different genetic ancestries. *Alzheimer's & dementia : the journal of the Alzheimer's Association*, 20(5), 3397.

Seo H, et al. (2024) Learning semi-supervised enrichment of longitudinal imaging-genetic data for improved prediction of cognitive decline. *BMC medical informatics and decision making*, 24(Suppl 1), 61.

Shukla R, et al. (2024) AlzGenPred - CatBoost-based gene classifier for predicting Alzheimer's disease using high-throughput sequencing data. *Scientific reports*, 14(1), 30294.

Thierry M, et al. (2024) The influence of APOE ϵ 4 on the pTau interactome in sporadic Alzheimer's disease. *Acta neuropathologica*, 147(1), 91.

Zhao X, et al. (2023) Prioritizing genes associated with brain disorders by leveraging enhancer-promoter interactions in diverse neural cells and tissues. *Genome medicine*, 15(1), 56.

Li C, et al. (2023) Inference for a Large Directed Acyclic Graph with Unspecified Interventions. *Journal of machine learning research : JMLR*, 24.

van Bree EJ, et al. (2022) A hidden layer of structural variation in transposable elements reveals potential genetic modifiers in human disease-risk loci. *Genome research*, 32(4), 656.

Sheng J, et al. (2022) Predictive classification of Alzheimer's disease using brain imaging and genetic data. *Scientific reports*, 12(1), 2405.

Jia Y, et al. (2022) Genetic dissection of glutathione S-transferase omega-1: identification of novel downstream targets and Alzheimer's disease pathways. *Neural regeneration research*, 17(11), 2452.

Park JH, et al. (2021) Novel Alzheimer's disease risk variants identified based on whole-genome sequencing of APOE ϵ 4 carriers. *Translational psychiatry*, 11(1), 296.

Ke F, et al. (2021) Identifying Imaging Genetics Biomarkers of Alzheimer's Disease by Multi-Task Sparse Canonical Correlation Analysis and Regression. *Frontiers in genetics*, 12, 706986.

Fabrizio C, et al. (2021) Artificial Intelligence for Alzheimer's Disease: Promise or Challenge? *Diagnostics (Basel, Switzerland)*, 11(8).

Gaweda-Walerych K, et al. (2021) Two Rare Variants in PLA2G7 and BACE1 Genes-Do They Contribute to Semantic Dementia Clinical Phenotype? *Genes*, 12(11).

Sindi S, et al. (2021) Telomere Length Change in a Multidomain Lifestyle Intervention to Prevent Cognitive Decline: A Randomized Clinical Trial. *The journals of gerontology. Series A, Biological sciences and medical sciences*, 76(3), 491.

Calabrò M, et al. (2021) The biological pathways of Alzheimer disease: a review. *AIMS neuroscience*, 8(1), 86.

Li X, et al. (2021) Applications and Challenges of Machine Learning Methods in Alzheimer's Disease Multi-Source Data Analysis. *Current genomics*, 22(8), 564.

Ryu S, et al. (2021) Genetic signature of human longevity in PKC and NF- κ B signaling. *Aging cell*, 20(7), e13362.