Resource Summary Report

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Genetic Association Information Network (GAIN)

RRID:SCR_013703
Type: Tool

Proper Citation

Genetic Association Information Network (GAIN) (RRID:SCR_013703)

Resource Information

URL: http://fnih.org/work/past-programs/genetic-association-information-network-gain

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Description: The Genetic Association Information Network (GAIN) supports a series of Genome-Wide Association Studies (GWAS) designed to identify specific points of DNA variation associated with the occurrence of a particular common disease. Initially focusing on six major common diseases, GAIN focused on combining the results with clinical data to create a significant new resource for genetic researchers.

Abbreviations: GAIN

Resource Type: portal, organization portal, consortium, data or information resource

Keywords: tool development, biomarker research, data-sharing enabler, genome, genome wide association studies, FNIH,

Funding: Pfizer Inc ;
Affymetrix Inc

Resource Name: Genetic Association Information Network (GAIN)

Resource ID: SCR_013703

Record Creation Time: 20220129T080317+0000

Record Last Update: 20250522T060845+0000

Ratings and Alerts

No rating or validation information has been found for Genetic Association Information Network (GAIN).

No alerts have been found for Genetic Association Information Network (GAIN).

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Jo T, et al. (2025) LD-informed deep learning for Alzheimer's gene loci detection using WGS data. Alzheimer's & dementia (New York, N. Y.), 11(1), e70041.

Casanova NG, et al. (2023) Examination of eQTL Polymorphisms Associated with Increased Risk of Progressive Complicated Sarcoidosis in European and African Descent Subjects. European journal of respiratory medicine, 5(1), 359.

Peng P, et al. (2021) Investigating Causal Relationships Between Psychiatric Traits and Intracranial Aneurysms: A Bi-directional Two-Sample Mendelian Randomization Study. Frontiers in genetics, 12, 741429.

Lopes FL, et al. (2020) Polygenic risk for anxiety influences anxiety comorbidity and suicidal behavior in bipolar disorder. Translational psychiatry, 10(1), 298.

Jons WA, et al. (2019) Statistical methods for testing X chromosome variant associations: application to sex-specific characteristics of bipolar disorder. Biology of sex differences, 10(1), 57.

Kuo PH, et al. (2014) Identification of novel loci for bipolar I disorder in a multi-stage genome-wide association study. Progress in neuro-psychopharmacology & biological psychiatry, 51, 58.

Agim ZS, et al. (2013) Discovery, validation and characterization of Erbb4 and Nrg1 haplotypes using data from three genome-wide association studies of schizophrenia. PloS one, 8(1), e53042.

Akula N, et al. (2011) A network-based approach to prioritize results from genome-wide association studies. PloS one, 6(9), e24220.