

Resource Summary Report

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Genetic Association Database

RRID:SCR_013264

Type: Tool

Proper Citation

Genetic Association Database (RRID:SCR_013264)

Resource Information

URL: <http://geneticassociationdb.nih.gov/>

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Description: The Genetic Association Database is an archive of human genetic association studies of complex diseases and disorders. The goal of this database is to allow the user to rapidly identify medically relevant polymorphism from the large volume of polymorphism and mutational data, in the context of standardized nomenclature. The data is from published scientific papers. Study data is recorded in the context of official human gene nomenclature with additional molecular reference numbers and links. It is gene centered. That is, each record is a record of a gene or marker. If a study investigated 6 genes for a particular disorder, there will be 6 records. Anyone may view this database and anyone may submit records. You do not have to be an author on the original study to submit a record. All submitted records will be reviewed before inclusion in the archive. Both genetic and environmental factors contribute to human diseases. Most common diseases are influenced by a large number of genetic and environmental factors, most of which individually have only a modest effect on the disease. Though genetic contributions are relatively well characterized for some monogenetic diseases, there has been no effort at curating the extensive list of environmental etiological factors. From a comprehensive search of the MeSH annotation of MEDLINE articles, they identified 3,342 environmental etiological factors associated with 3,159 diseases. They also identified 1,100 genes associated with 1,034 complex diseases from the NIH Genetic Association Database (GAD), a database of genetic association studies. 863 diseases have both genetic and environmental etiological factors available. Integrating genetic and environmental factors results in the etiome, which they define as the comprehensive compendium of disease etiology.

Synonyms: GAD

Resource Type: data or information resource, database

Keywords: environmental, etiological, etiology, factor, gene, general human genetics databases, genetic, association, complex, disease, disorder, human, medically, molecular, monogenetic, mutational, nomenclature, polymorphism, scientific, FASEB list

Related Condition: Aging

Resource Name: Genetic Association Database

Resource ID: SCR_013264

Alternate IDs: nif-0000-21163

Record Creation Time: 20220129T080315+0000

Record Last Update: 20260821T194006+0000

Ratings and Alerts

No rating or validation information has been found for Genetic Association Database.

No alerts have been found for Genetic Association Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 170 mentions in open access literature.

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

Liu Z, et al. (2026) Qingfei Tongluo Jiedu Formula Regulates M2 Macrophage Polarization via the Butyric Acid-GPR109A-MAPK Pathway for the Treatment of Mycoplasma pneumoniae Pneumonia. Pharmaceuticals (Basel, Switzerland), 19(2).

Song J, et al. (2026) Network analysis of Mycoplasma pneumoniae pneumonia and Epstein-Barr virus co-infection. BMC infectious diseases, 26(1).

Xie Y, et al. (2025) FoxO1 as a Hub in Immunosenescence Induced by Hepatocellular Carcinoma and the Effect of Yangyin Fuzheng Jiedu Prescription. Drug design, development and therapy, 19, 1543.

Wei X, et al. (2024) Interpreting the Mechanism of Active Ingredients in Polygonati Rhizoma in Treating Depression by Combining Systemic Pharmacology and In Vitro Experiments. Nutrients, 16(8).

Qu L, et al. (2024) FBXL16: a new regulator of neuroinflammation and cognition in Alzheimer's disease through the ubiquitination-dependent degradation of amyloid precursor protein. Biomarker research, 12(1), 144.

Manoochchhri H, et al. (2024) Key target genes related to anti-breast cancer activity of ATRA: A network pharmacology, molecular docking and experimental investigation. *Heliyon*, 10(14), e34300.

Yan Z, et al. (2024) Multi-omics integration reveals potential stage-specific druggable targets in T-cell acute lymphoblastic leukemia. *Genes & diseases*, 11(5), 100949.

Zhu P, et al. (2024) Exploring the effects of calycosin on anthracycline-induced cardiotoxicity: a network pharmacology, molecular docking, and experimental study. *Frontiers in cardiovascular medicine*, 11, 1286620.

Hu E, et al. (2023) A novel microbial and hepatic biotransformation-integrated network pharmacology strategy explores the therapeutic mechanisms of bioactive herbal products in neurological diseases: the effects of Astragaloside IV on intracerebral hemorrhage as an example. *Chinese medicine*, 18(1), 40.

Gao S, et al. (2023) Oridonin suppresses gastric cancer SGC-7901 cell proliferation by targeting the TNF-alpha/androgen receptor/TGF-beta signalling pathway axis. *Journal of cellular and molecular medicine*, 27(18), 2661.

Yoon W, et al. (2023) Biomedical relation extraction with knowledge base-refined weak supervision. *Database : the journal of biological databases and curation*, 2023.

Gutierrez Guarnizo SA, et al. (2023) Pathogenic signal peptide variants in the human genome. *NAR genomics and bioinformatics*, 5(4), lqad093.

Xie Y, et al. (2023) Mechanisms and network pharmacological analysis of Yangyin Fuzheng Jiedu prescription in the treatment of hepatocellular carcinoma. *Cancer medicine*, 12(3), 3237.

Chen L, et al. (2023) Design, synthesis and anticancer activity studies of 3-(coumarin-3-yl)-acrolein derivatives: Evidenced by integrating network pharmacology and vitro assay. *Frontiers in pharmacology*, 14, 1141121.

Ai LY, et al. (2022) Integrated Analysis of lncRNA and mRNA Expression Profiles Indicates Age-Related Changes in Meniscus. *Frontiers in cell and developmental biology*, 10, 844555.

Gul A, et al. (2022) Study on the Mechanism of ??stikuddus Sherbiti in Ischemic Cerebrovascular Diseases: Based on Network Pharmacology. *Evidence-based complementary and alternative medicine : eCAM*, 2022, 5581864.

Liu J, et al. (2022) Investigating the Mechanisms of Jieduquyuziyin Prescription Improves Lupus Nephritis and Fibrosis via FXR in MRL/lpr Mice. *Oxidative medicine and cellular longevity*, 2022, 4301033.

Aguiar T, et al. (2022) Unraveling the Genetic Architecture of Hepatoblastoma Risk: Birth Defects and Increased Burden of Germline Damaging Variants in Gastrointestinal/Renal Cancer Predisposition and DNA Repair Genes. *Frontiers in genetics*, 13, 858396.

Song C, et al. (2022) Network Pharmacology-Based Prediction and Verification of Ginsenoside Rh2-Induced Apoptosis of A549 Cells via the PI3K/Akt Pathway. *Frontiers in*

pharmacology, 13, 878937.

Gu Y, et al. (2022) Exploring the mechanism of Buyang Huanwu decoction in the treatment of lumbar disc herniation based on network pharmacology and molecular docking. *Medicine*, 101(32), e29534.