Resource Summary Report

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HuGE Navigator - Human Genome Epidemiology Navigator

RRID:SCR_003172
Type: Tool

Proper Citation

HuGE Navigator - Human Genome Epidemiology Navigator (RRID:SCR_003172)

Resource Information

URL: http://hugenavigator.net/

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Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 5, 2023. Knowledge base of genetic associations and human genome epidemiology including information on population prevalence of genetic variants, gene-disease associations, gene-gene and gene- environment interactions, and evaluation of genetic tests. This tool explores HuGENet, the Human Genome Epidemiology Network, which is a global collaboration of individuals and organizations committed to the assessment of the impact of human genome variation on population health and how genetic information can be used to improve health and prevent disease. What does HuGE Navigator offer? *HuGEpedia - an encyclopedia of human genetic variation in health and disease, includes, Phenopedia and Genopedia. Phenopedia allows you to look up gene-disease association summaries by disease, and Genopedia allows you to look up gene-disease association summaries by gene. In general, HuGEpedia is a searchable database that summarizes published articles about human disease and genetic variation, including primary studies, reviews, and meta-analyses. It provides links to Pubmed abstracts, researcher contact info, trends, and more. *HuGEtools - searching and mining the literature in human genome epidemiology, includes, HuGE Literature Finder, HuGE Investigator Browser, Gene Prospector, HuGE Watch, Variant Name Mapper, and HuGE Risk Translator. *HuGE Literature Finder finds published articles in human genome epidemiology since 2001. The search query can include genes, disease, outcome, environmental factors, author, etc. Results can be filtered by these categories. It is also possible to see all articles in the database for a particular topic, such as genotype prevalence, pharmacogenomics, or clinical trial. *HuGE Investigator Browser finds investigators in a particular field of human genome epidemiology. This info is obtained using

a behind-the-scenes tool that automatically parses PubMed affiliation data. *Gene Prospector is a gateway for evaluating genes in relation to disease and risk factors. This tool allows you to enter a disease or risk factor and then supplies you with a table of genes associated w/your query that are ranked based on strength of evidence from the literature. This evidence is culled from the HuGE Literature Finder and NCBI Entrez Gene - And you're given the scoring formula. The Gene Prospector results table provides access to the Genopedia entry for each gene in the list, general info including links to other resources, SNP info, and associated literature from HuGE, PubMed, GWAS, and more. It is a great place to locate a lot of info about your disease/gene of interest very quickly. *HuGE Watch tracks the evolution of published literature, HuGE investigators, genes studied, or diseases studied in human genome epidemiology. For example, if you search Trend/Pattern for Diseases Studied you'll initially get a graph and chart of the number of diseases studied per year since 1997. You can refine these results by limiting the temporal trend to a category or study type such as Gene-gene Interaction or HuGE Review. *Variant Name Mapper maps common names and rs numbers of genetic variants using information from SNP500Cancer, SNPedia, pharmGKB, ALFRED, AlzGene, PDGene, SZgene, HuGE Navigator, LSDBs, and user submissions. *HuGE Risk Translator calculates the predictive value of genetic markers for disease risk. To do so, users must enter the frequency of risk variant, the population disease risk, and the odds ratio between the gene and disease. This information is necessary in order to yield a useful predictive result. *HuGEmix - a series of HuGE related informatics utilities and projects, includes, GAPscreener, HuGE Track, Open Source. GAPscreener is a screening tool for published literature on human genetic associations; HuGE Track is a custom track built for HuGE data in the UCSC Genome Browser; and Open Source is infrastructure for managing knowledge and information from PubMed.

Abbreviations: HuGE Navigator

Resource Type: data or information resource, data computation service, bibliography, database

Keywords: environment, epidemiology, gene, genetic, genetic associations, genetic markers, genome, disease, human, human disease, predictive value, prevalence, publications, risk factors, test evaluations, variance, FASEB list

Funding:

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HuGE Navigator - Human Genome Epidemiology Navigator

Resource ID: SCR_003172

Alternate IDs: nif-0000-00573

Alternate URLs: http://hugenavigator.net/HuGENavigator/home.do

Record Creation Time: 20220129T080217+0000

Record Last Update: 20250426T055612+0000

Ratings and Alerts

No rating or validation information has been found for HuGE Navigator - Human Genome Epidemiology Navigator.

No alerts have been found for HuGE Navigator - Human Genome Epidemiology Navigator.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 117 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Amor M, et al. (2024) Identification of regulatory networks and crosstalk factors in brown adipose tissue and liver of a cold-exposed cardiometabolic mouse model. Cardiovascular diabetology, 23(1), 298.

Xiang S, et al. (2024) Modeling Path Importance for Effective Alzheimer's Disease Drug Repurposing. Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing, 29, 306.

Wang RS, et al. (2023) Uncovering common pathobiological processes between COVID-19 and pulmonary arterial hypertension by integrating Omics data. Pulmonary circulation, 13(1), e12191.

Xiang S, et al. (2023) Modeling Path Importance for Effective Alzheimer's Disease Drug Repurposing. ArXiv.

Mercer HM, et al. (2023) Alterations in RNA editing in skeletal muscle following exercise training in individuals with Parkinson's disease. PloS one, 18(12), e0287078.

Daily JW, et al. (2023) Association of Plant-Based and High-Protein Diets with a Lower Obesity Risk Defined by Fat Mass in Middle-Aged and Elderly Persons with a High Genetic Risk of Obesity. Nutrients, 15(4).

Allen-Brady K, et al. (2022) Systematic review and meta-analysis of genetic association studies of pelvic organ prolapse. International urogynecology journal, 33(1), 67.

Park S, et al. (2021) Interactions between Polygenic Risk Scores, Dietary Pattern, and Menarche Age with the Obesity Risk in a Large Hospital-Based Cohort. Nutrients, 13(11).

Tremblay J, et al. (2021) Polygenic risk scores predict diabetes complications and their response to intensive blood pressure and glucose control. Diabetologia, 64(9), 2012.

Rikos D, et al. (2021) Replication of chromosomal loci involved in Parkinson's disease: A quantitative synthesis of GWAS. Toxicology reports, 8, 1762.

Li X, et al. (2021) Association of genetic variants in enamel-formation genes with dental caries: A meta- and gene-cluster analysis. Saudi journal of biological sciences, 28(3), 1645.

Li X, et al. (2020) The association between genetic variants in lactotransferrin and dental caries: a meta- and gene-based analysis. BMC medical genetics, 21(1), 114.

Soltész B, et al. (2020) The genetic risk for hypertension is lower among the Hungarian Roma population compared to the general population. PloS one, 15(6), e0234547.

Sigurdson MK, et al. (2020) Redundant meta-analyses are common in genetic epidemiology. Journal of clinical epidemiology, 127, 40.

Jallow MW, et al. (2020) Differences in the frequency of genetic variants associated with iron imbalance among global populations. PloS one, 15(7), e0235141.

Ou Y, et al. (2020) Relationship between the IL-10 (-1082 A/G) polymorphism and the risk of immune/idiopathic thrombocytopenic purpura: A meta-analysis. Cytokine, 125, 154820.

Du L, et al. (2019) Gene Polymorphisms and Susceptibility to Functional Dyspepsia: A Systematic Review and Meta-Analysis. Gastroenterology research and practice, 2019, 3420548.

Di P, et al. (2019) Prediction of the allergic mechanism of haptens via a reaction-substructure-compound-target-pathway network system. Toxicology letters, 317, 68.

Imani MM, et al. (2019) Polymorphic Variants of V-Maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog B (rs13041247 and rs11696257) and Risk of Non-Syndromic Cleft Lip/Palate: Systematic Review and Meta-Analysis. International journal of environmental research and public health, 16(15).

Peng Y, et al. (2019) Insights into mechanisms and severity of drug-induced liver injury via computational systems toxicology approach. Toxicology letters, 312, 22.