Resource Summary Report

Generated by kravitz2 on Jul 31, 2026

Human Genome Epidemiology Network

RRID:SCR_013117
Type: Tool

Proper Citation

Human Genome Epidemiology Network (RRID:SCR_013117)

Resource Information

URL: http://www.cdc.gov/genomics/hugenet/default.htm

Proper Citation: Human Genome Epidemiology Network (RRID:SCR_013117)

Description: Human Genome Epidemiology Network, or HuGENet, 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. Its goals include: establishing an information exchange that promotes global collaboration in developing peer-reviewed information on the relationship between human genomic variation and health and on the quality of genetic tests for screening and prevention; providing training and technical assistance to researchers and practitioners interested in assessing the role of human genomic variation on population health and how such information can be used in practice; developing an updated and accessible knowledge base on the World Wide Web; and promoting the use of this knowledge base by health care providers, researchers, industry, government, and the public for making decisions involving the use of genetic information for disease prevention and health promotion. HuGENet collaborators come from multiple disciplines such as epidemiology, genetics, clinical medicine, policy, public health, education, and biomedical sciences. Currently, there are 4 HuGENet Coordinating Centers for the implementation of HuGENet activities: CDC"s Office of Public Health Genomics, Atlanta, Georgia; HuGENet UK Coordinating Center, Cambridge, UK; University of Ioannina, Greece; University of Ottawa , Ottawa, Canada. HuGENet includes: HuGE e-Journal Club: The HuGE e-Journal Club is an electronic discussion forum where new human genome epidemiologic (HuGE) findings, published in the scientific literature in the CDC"s Office of Public Health Genomics Weekly Update, will be abstracted, summarized, presented, and discussed via a newly created HuGENet listserv. HuGE Reviews: A HuGE Review identifies human genetic variations at one or more loci, and describes what is known about the frequency of these variants in different populations, identifies diseases that these variants are associated with and summarizes the magnitude of risks and associated risk factors, and evaluates associated genetic tests. Reviews point to gaps in existing epidemiologic and clinical knowledge, thus stimulating further research in these areas. HuGE Fact Sheets: HuGE Fact Sheets summarize information about a particular gene, its

variants, and associated diseases. HuGE Case Studies: An on-line presentation designed to sharpen your epidemiological skills and enhance your knowledge on genomic variation and human diseases. Its purpose is to train health professionals in the practical application of human genome epidemiology (HuGE), which translates gene discoveries to disease prevention by integrating population-based data on gene-disease relationships and interventions. Students will acquire conceptual and practical tools for critically evaluating the growing scientific literature in specific disease areas. HUGENet Publications: Articles related to the HuGENet movement written by our HuGENet collaborators. HuGE Navigator: An integrated, searchable 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. HuGE Workshops: HuGENet has sponsored meetings and workshops with national and international partners since 2001. Available are detailed summaries, agendas or the ability to download speaker slides. HuGE Book: Human Genome Epidemiology: A Scientific Foundation for Using Genetic Information to Improve Health and Prevent Disease. (The findings and conclusions in this book are those of the author(s) and do not necessarily represent the views of the funding agency.) HuGENet Collaborators: HuGENet is interested in establishing collaborations with individuals and organizations working on population based research involving genetic information. HuGE Funding: Funding opportunities for specific population-based genetic epidemiology research projects are available. Research initiatives whose aims include assessing the prevalence of human genetic variation, the association between genetic variants and human diseases, the measurement of gene-gene or gene-environment interaction, and the evaluation of genetic tests for screening and prevention are compiled to create a posted listing. Additional information and application details can be found by clicking on the respective links.

Synonyms: HuGENet

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

Keywords: epidemiology, gene, genetic, genetic variants, genome, articles, collaboration, disease, disease prevention, genomics, health promotion, human, human diseases

Resource Name: Human Genome Epidemiology Network

Resource ID: SCR_013117

Alternate IDs: nif-0000-00574

Record Creation Time: 20220129T080314+0000

Record Last Update: 20260801T042712+0000

Ratings and Alerts

No rating or validation information has been found for Human Genome Epidemiology Network.

No alerts have been found for Human Genome Epidemiology Network.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 25 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Huang J, et al. (2024) Discovering the link between IL12RB1 gene polymorphisms and tuberculosis susceptibility: a comprehensive meta-analysis. Frontiers in public health, 12, 1249880.

Teo K, et al. (2021) rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of hepatology, 74(1), 20.

Chawar C, et al. (2021) A systematic review of GWAS identified SNPs associated with outcomes of medications for opioid use disorder. Addiction science & clinical practice, 16(1), 70.

Singh P, et al. (2021) Transcriptomic and epigenomic analyses uncovered Lrrc15 as a contributing factor to cartilage damage in osteoarthritis. Scientific reports, 11(1), 21107.

Hillmer A, et al. (2021) Genetic basis of cannabis use: a systematic review. BMC medical genomics, 14(1), 203.

Duan F, et al. (2021) Identification and epidemiological evaluation of gastric cancer risk factors: based on a field synopsis and meta-analysis in Chinese population. Aging, 13(17), 21451.

Hillmer A, et al. (2020) Genetic determinants of cannabis use: a systematic review protocol. Systematic reviews, 9(1), 190.

Altaf-Ul-Amin M, et al. (2020) Discovery of inflammatory bowel disease-associated miRNAs using a novel bipartite clustering approach. BMC medical genomics, 13(Suppl 3), 10.

Pope DH, et al. (2020) Genetics of Degenerative Cervical Myelopathy: A Systematic Review and Meta-Analysis of Candidate Gene Studies. Journal of clinical medicine, 9(1).

Blakeway H, et al. (2020) What is the evidence for interactions between filaggrin null mutations and environmental exposures in the aetiology of atopic dermatitis? A systematic review. The British journal of dermatology, 183(3), 443.

Ali Z, et al. (2019) The Effect of CYP2C19 and Nongenetic Factors on Clopidogrel Responsiveness in the MENA Region: A Systematic Review. Clinical and applied thrombosis/hemostasis : official journal of the International Academy of Clinical and Applied Thrombosis/Hemostasis, 25, 1076029619875520.

Donald N, et al. (2018) The association of low penetrance genetic risk modifiers with colorectal cancer in lynch syndrome patients: a systematic review and meta-analysis. Familial cancer, 17(1), 43.

Eguchi R, et al. (2018) An integrative network-based approach to identify novel disease genes and pathways: a case study in the context of inflammatory bowel disease. BMC bioinformatics, 19(1), 264.

Aggarwal N, et al. (2017) The Association of Low-Penetrance Variants in DNA Repair Genes with Colorectal Cancer: A Systematic Review and Meta-Analysis. Clinical and translational gastroenterology, 8(7), e109.

Zwingerman N, et al. (2017) Sex-specific effect of CPB2 Ala147Thr but not Thr325Ile variants on the risk of venous thrombosis: A comprehensive meta-analysis. PloS one, 12(5), e0177768.

Li SX, et al. (2017) Interaction between genes and macronutrient intake on the risk of developing type 2 diabetes: systematic review and findings from European Prospective Investigation into Cancer (EPIC)-InterAct. The American journal of clinical nutrition, 106(1), 263.

Li X, et al. (2016) Systematic meta-analyses and field synopsis of genetic and epigenetic studies in paediatric inflammatory bowel disease. Scientific reports, 6, 34076.

Chen Y, et al. (2016) Association between the APEX1 Asp148Glu polymorphism and prostate cancer, especially among Asians: a new evidence-based analysis. Oncotarget, 7(32), 52530.

Wu R, et al. (2016) Impact of HLA-B*58:01 allele and allopurinol-induced cutaneous adverse drug reactions: evidence from 21 pharmacogenetic studies. Oncotarget, 7(49), 81870.

Sookoian S, et al. (2016) Meta-analysis of the influence of TM6SF2 E167K variant on Plasma Concentration of Aminotransferases across different Populations and Diverse Liver Phenotypes. Scientific reports, 6, 27718.