Resource Summary Report

Generated by kravitz2 on Sep 5, 2026

Resource for Genetic Epidemiology Research on Adult Health and Aging

RRID:SCR_010472
Type: Tool

Proper Citation

Resource for Genetic Epidemiology Research on Adult Health and Aging (RRID:SCR_010472)

Resource Information

URL: http://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs000674.v1.p1

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Description: Human genetics data from an immense (78,000) and ethnically diverse population available for secondary analysis to qualified researchers through the database of Genotypes and Phenotypes (dbGaP). It offers the opportunity to identify potential genetic risks and influences on a broad range of health conditions, particularly those related to aging. The GERA cohort is part of the Research Program on Genes, Environment, and Health (RPGEH), which includes more than 430,000 adult members of the Kaiser Permanente Northern California system. Data from this larger cohort include electronic medical records, behavioral and demographic information from surveys, and saliva samples from 200,000 participants obtained with informed consent for genomic and other analyses. The RPGEH database was made possible largely through early support from the Robert Wood Johnson Foundation to accelerate such health research. The genetic information in the GERA cohort translates into more than 55 billion bits of genetic data. Using newly developed techniques, the researchers conducted genome-wide scans to rapidly identify single nucleotide polymorphisms (SNPs) in the genomes of the people in the GERA cohort. These data will form the basis of genome-wide association studies (GWAS) that can look at hundreds of thousands to millions of SNPs at the same time. The RPGEH then combined the genetic data with information derived from Kaiser Permanente''s comprehensive longitudinal electronic medical records, as well as extensive survey data on participants'' health habits and backgrounds, providing researchers with an unparalleled research resource. As information is added to the Kaiser-UCSF database, the dbGaP database will also be updated.

Abbreviations: GERA

Synonyms: Genetic Epidemiology Research on Aging

Resource Type: data or information resource, database

Keywords: genotype, phenotype, genome-wide association study, saliva, dna, male, female, health condition, electronic medical record, single nucleotide polymorphism, adult human, late adult human, gene, genome

Related Condition: Aging, Cardiovascular disease, Osteoarthritis, Depressive Disorder, Insomnia, Eye disease, Cancer, Diabetes

Funding: NIMH ;
NIH Office of the Director ;
NIA AG036607

Availability: Application required, Non-commercial, Data Use Certification Agreement

Resource Name: Resource for Genetic Epidemiology Research on Adult Health and Aging

Resource ID: SCR_010472

Alternate IDs: nlx_157735

Record Creation Time: 20220129T080259+0000

Record Last Update: 20260904T000323+0000

Ratings and Alerts

No rating or validation information has been found for Resource for Genetic Epidemiology Research on Adult Health and Aging.

No alerts have been found for Resource for Genetic Epidemiology Research on Adult Health and Aging.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Huerta-Chagoya A, et al. (2024) Rare variant analyses in 51,256 type 2 diabetes cases and 370,487 controls reveal the pathogenicity spectrum of monogenic diabetes genes. Nature genetics, 56(11), 2370.

Huang X, et al. (2024) Evaluation of multiple breast cancer polygenic risk score panels in women of Latin American heritage. Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology.

Frank P, et al. (2020) Genetic susceptibility, inflammation and specific types of depressive symptoms: evidence from the English Longitudinal Study of Ageing. Translational psychiatry, 10(1), 140.

Murk W, et al. (2016) Exhaustive Genome-Wide Search for SNP-SNP Interactions Across 10 Human Diseases. G3 (Bethesda, Md.), 6(7), 2043.

Loh PR, et al. (2016) Reference-based phasing using the Haplotype Reference Consortium panel. Nature genetics, 48(11), 1443.

Zhang H, et al. (2016) A Powerful Procedure for Pathway-Based Meta-analysis Using Summary Statistics Identifies 43 Pathways Associated with Type II Diabetes in European Populations. PLoS genetics, 12(6), e1006122.

Galinsky KJ, et al. (2016) Fast Principal-Component Analysis Reveals Convergent Evolution of ADH1B in Europe and East Asia. American journal of human genetics, 98(3), 456.

Loh PR, et al. (2016) Fast and accurate long-range phasing in a UK Biobank cohort. Nature genetics, 48(7), 811.

Loh PR, et al. (2015) Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance-components analysis. Nature genetics, 47(12), 1385.