Resource Summary Report

Generated by NIF on Apr 26, 2025

KORA-gen

RRID:SCR_004510
Type: Tool

Proper Citation

KORA-gen (RRID:SCR_004510)

Resource Information

URL: http://epi.helmholtz-muenchen.de/kora-gen/index_e.php

Proper Citation: KORA-gen (RRID:SCR_004510)

Description: KORA-gen is infrastructure to provide phenotypes, genotypes and biosamples for collaborative genetic epidemiological research. From all four surveys that have been conducted so far, the following biological material is on hand: genomic DNA, blood serum, blood plasma and EBV immortalized cell lines (form KORA S4 only). These have been extracted from blood samples and are stored in nitrogen tanks and -80 degrees C refrigerators. Genomic DNA from more than 18.000 adult subjects from Augsburg and the surrounding counties is available at present. So far, EBV immortalized cell lines from 1.600 participants are cultivated. To meet the manifold demands of researchers with genetic and molecular questions KORA-gen fulfills the following prerequisites for successful genetic-epidemiological research: * representative samples from the general population, * well characterized disease phenotypes and intermediate phenotypes, * information on environmental factors, * availability of genomic DNA, serum, plasma and urine, as well as EBV immortalized cell lines. In total, four population based health surveys have been conducted between 1984 and 2000 with 18000 participants in the age range of 25 to 74 years, and a biological specimen bank was established in order to enable scientists to perform epidemiologic research with respect to molecular and genetic questions. The KORA study center conducts regular follow-up investigations and has collected a wealth of information on sociodemography, general medical history, environmental factors, smoking, nutrition, alcohol consumption, and various laboratory parameters. This unique resource will be increased further by follow-up studies of the cohort. The assessment of statistical questions covers the definition of the study design and the calculation of statistical power. Furthermore, we offer assistance in data analysis. Kora-gen can be used by external partners. Interested parties can inform themselves interactively via internet about the available data and rules of access. The genotypic data base is a common resource to all partners.

Abbreviations: KORA-gen

Synonyms: Cooperative Health Research in the Region of Augsburg-gen

Resource Type: biomaterial supply resource, material resource

Keywords: gene, genetic, epidemiology, dna, serum, plasma, urine, cell line, epstein-barr virus immortalized cell line, blood, frozen, nitrogen, disease phenotype, adult human, survey, population study, genotype, phenotype

Related Condition: General population, Well characterized disease phenotype, Well characterized disease intermediate phenotype

Funding:

Availability: Collaborators: Kora-gen can be used by external partners. Interested parties can inform themselves interactively via internet about the available data and rules of access. The genotypic data base is a common resource to all partners.

Resource Name: KORA-gen

Resource ID: SCR_004510

Alternate IDs: nlx_49266

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250426T055728+0000

Ratings and Alerts

No rating or validation information has been found for KORA-gen.

No alerts have been found for KORA-gen.

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 NIF.

Vakili D, et al. (2021) Panomics: New Databases for Advancing Cardiology. Frontiers in cardiovascular medicine, 8, 587768.

Troll M, et al. (2020) Investigation of Adiposity Measures and Operational Taxonomic unit (OTU) Data Transformation Procedures in Stool Samples from a German Cohort Study Using Machine Learning Algorithms. Microorganisms, 8(4).

Suhre K, et al. (2017) Connecting genetic risk to disease end points through the human blood plasma proteome. Nature communications, 8, 14357.

Benedetti E, et al. (2017) Network inference from glycoproteomics data reveals new reactions in the IgG glycosylation pathway. Nature communications, 8(1), 1483.

Treutlein J, et al. (2017) Genetic Contribution to Alcohol Dependence: Investigation of a Heterogeneous German Sample of Individuals with Alcohol Dependence, Chronic Alcoholic Pancreatitis, and Alcohol-Related Cirrhosis. Genes, 8(7).

Müller SH, et al. (2016) Genome-wide association study in essential tremor identifies three new loci. Brain : a journal of neurology, 139(Pt 12), 3163.

Thron C, et al. (2015) FTO Is Associated with Aortic Valve Stenosis in a Gender Specific Manner of Heterozygote Advantage: A Population-Based Case-Control Study. PloS one,

10(10), e0139419.

Enciso-Mora V, et al. (2013) Low penetrance susceptibility to glioma is caused by the TP53 variant rs78378222. British journal of cancer, 108(10), 2178.