Resource Summary Report

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KI Biobank - TwinGene

RRID:SCR_006006
Type: Tool

Proper Citation

KI Biobank - TwinGene (RRID:SCR_006006)

Resource Information

URL: http://ki.se/en/meb/twingene-and-genomeeutwin

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Description: In collaboration with GenomeEUtwin, the TwinGene project investigates the importance of quantitative trait loci and environmental factors for cardiovascular disease. It is well known that genetic factors are of considerable importance for some familial lipid syndromes and that Type A Behavior pattern and increased lipid levels infer increased risk for cardiovascular disease. It is furthermore known that genetic factors are of importance levels of blood lipid biomarkers. The interplay of genetic and environmental effects for these risk factors in a normal population is less well understood and virtually unknown for the elderly. In the TwinGene project twins born before 1958 are contacted to participate. Health and medication data are collected from self-reported questionnaires, and blood sampling material is mailed to the subject who then contacts a local health care center for blood sampling and a health check-up. In the simple health check-up, height, weight, circumference of waist and hip, and blood pressure are measured. Blood is sampled for DNA extraction, serum collection and clinical chemistry tests of C-reactive protein, total cholesterol, triglycerides, HDL and LDL cholesterol, apolipo??protein A1 and B, glucose and HbA1C. The TwinGene cohort contains more than 10000 of the expected final number of 16000 individuals. Molecular genetic techniques are being used to identify Quantitative Trait Loci (QTLs) for cardiovascular disease and biomarkers in the TwinGene participants. Genome-wide linkage and association studies are ongoing. DZ twins have been genome-scanned with 1000 STS markers and a subset of 300 MZ twins have been genome-scanned with Illumina 317K SNP platform. Association of positional candidate SNPs arising from these genomscans are planned. The TwinGene project is associated with the large European collaboration denoted GenomEUtwin (www.genomeutwin.org, see below) which since 2002 has aimed at gathering genetic data on twins in Europe and setting up the infrastructure needed to enable pooling of data and joint analyses. It has been the funding source for obtaining the genome scan data. Types of samples: * EDTA whole blood * DNA * Serum Number of sample donors: 12 044 (sample collection completed)

Abbreviations: TwinGene

Resource Type: biomaterial supply resource, material resource

Keywords: quantitative trait loci, environmental factor, cardiovascular disease, environment, genetic, gene, lipid syndrome, lipid, health, medication, questionnaire, c-reactive protein, total cholesterol, triglyceride, hdl, ldl, cholesterol, apolipo-protein a1, apolipo-protein b, glucose, hba1c, genome-wide linkage study, genome-wide association study, genome

Related Condition: Twin

Funding: NIH ;
European Union ;
VR ;
SSF

Resource Name: KI Biobank - TwinGene

Resource ID: SCR_006006

Alternate IDs: nlx_151387

Old URLs: http://ki.se/ki/jsp/polopoly.jsp?d=29354&a=31600&l=en

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260725T191236+0000

Ratings and Alerts

No rating or validation information has been found for KI Biobank - TwinGene.

No alerts have been found for KI Biobank - TwinGene.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at nidm-terms .

Chen Y, et al. (2025) Genetic and metabolomic pathways linking frailty, chronic kidney disease, and kidney failure: a Mendelian randomization and multi-omics analysis. Renal failure, 47(1), 2584751.

Tirkkonen A, et al. (2025) Predicting cardiovascular morbidity and mortality with SCORE2 (OP) and Framingham risk estimates in combination with indicators of biological ageing.

Age and ageing, 54(4).

Karlsson IK, et al. (2023) Leukocyte DNA methylation in Alzheimer´s disease associated genes: replication of findings from neuronal cells. Epigenetics, 18(1), 2158285.

Karlsson IK, et al. (2022) Adiposity and the risk of dementia: mediating effects from inflammation and lipid levels. European journal of epidemiology, 37(12), 1261.

Lind L, et al. (2020) A Multi-Cohort Metabolomics Analysis Discloses Sphingomyelin (32:1) Levels to be Inversely Related to Incident Ischemic Stroke. Journal of stroke and cerebrovascular diseases : the official journal of National Stroke Association, 29(2), 104476.

Konki M, et al. (2019) Peripheral blood DNA methylation differences in twin pairs discordant for Alzheimer's disease. Clinical epigenetics, 11(1), 130.

Lee MK, et al. (2017) Genome-wide association study of facial morphology reveals novel associations with FREM1 and PARK2. PloS one, 12(4), e0176566.

Liu W, et al. (2017) Cancer risk susceptibility loci in a Swedish population. Oncotarget, 8(66), 110300.

Ameur A, et al. (2017) SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population. European journal of human genetics : EJHG, 25(11), 1253.

Maddock J, et al. (2017) Vitamin D and cognitive function: A Mendelian randomisation study. Scientific reports, 7(1), 13230.

Nowak C, et al. (2016) Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. PLoS genetics, 12(10), e1006379.

Trzaskowski M, et al. (2016) Application of linear mixed models to study genetic stability of height and body mass index across countries and time. International journal of epidemiology, 45(2), 417.

Sariaslan A, et al. (2016) Schizophrenia and subsequent neighborhood deprivation: revisiting the social drift hypothesis using population, twin and molecular genetic data. Translational psychiatry, 6(5), e796.

Arpegård J, et al. (2015) Comparison of heritability of Cystatin C- and creatinine-based estimates of kidney function and their relation to heritability of cardiovascular disease. Journal of the American Heart Association, 4(1), e001467.

Wood AR, et al. (2014) Defining the role of common variation in the genomic and biological architecture of adult human height. Nature genetics, 46(11), 1173.

Chen D, et al. (2014) A cis-eQTL of HLA-DRB1 and a frameshift mutation of MICA contribute to the pattern of association of HLA alleles with cervical cancer. Cancer medicine, 3(2), 445.

Fuks KB, et al. (2014) Arterial blood pressure and long-term exposure to traffic-related air pollution: an analysis in the European Study of Cohorts for Air Pollution Effects (ESCAPE). Environmental health perspectives, 122(9), 896.

Ganna A, et al. (2014) Large-scale metabolomic profiling identifies novel biomarkers for incident coronary heart disease. PLoS genetics, 10(12), e1004801.

Ganna A, et al. (2013) Utilizing twins as controls for non-twin case-materials in genome wide association studies. PloS one, 8(12), e83101.