Resource Summary Report

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Estonian Genome Center

RRID:SCR_004467
Type: Tool

Proper Citation

Estonian Genome Center (RRID:SCR_004467)

Resource Information

URL: http://www.geenivaramu.ee/en/

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Description: The Estonian Biobank is the population-based biobank of the EGCUT. The project is conducted in accordance with the Estonian Genes Research Act and all participants have signed a broad informed consent form (www.biobank.ee and Metspalu 2004, Drug Dev. Res.). As of December 2011, the biobank contains 51,515 participants (gene donors). The database of genotypic, phenotypic, health and genealogical information represents about 5% of Estonia"s adult population, and is the largest cohort ever gathered in Estonia. The age, sex and geographical distribution of this cohort reflect the structure of the adult population in Estonia. The database enables to conduct research in order to find links between genes, environmental factors, lifestyles and complex diseases or other traits. Active use of the biobank has started and although the first users are researchers all over the world with hundreds of different projects currently underway, industry is also interested. At the international level, the EGCUT will join the BBMRI follow-up program (ERIC) and through this channel provide service (biobanking, genotyping, sequencing and data analysis) for the centers in Europe who need it. Currently, the first follow-up study is underway and the molecular information of the cohort will be increased. For example, we have over 12 000 DNA samples analyzed by high density genotyping arrays and over 10 000 plasma samples analyzed by NMR scans, over 1000 individuals with RNA expression arrays, 2000 individuals with clinical laboratory analysis (over 40 tests) and over 60 full genomes are under deep sequencing. The infrastructure of the EGCUT includes a laboratory for DNA genotyping and next generation sequencing all based on Illumina platforms (HiScanSQ, HiSeq2000 and robotics), an IT unit (databases) with required computing power and storage space (1.2PB), data analysis team (bioinformatics and statistical genetics) and last but not least, a patient recruitment unit (health records, lifestyle and environmental information and biological samples ????? ???????????? DNA, plasma and WBC from all 51515 gene donors). This is all located on 1000m2 in a brand new laboratory building, Riia str 23, Tartu, Estonia.

Abbreviations: EGCUT, EGC

Synonyms: Estonian Genome Center University of Tartu, Estonian Biobank

Resource Type: biomaterial supply resource, material resource

Defining Citation: PMID:24518929, PMID:27256120

Keywords: biomedicine, population-based studies, population-based study, biobanking, genotyping, sequencing, data analysis, wbc, gene, environmental factor, disease, genomics, epidemiology, clinical data, dna, white blood cell, plasma, blood, lifestyle, demographic, genetic

Related Condition: General population

Availability: Public: The anonymous data (and biological materials) of the gene donors are available for research projects. Before an application can be accepted for review, The research project has to obtain an approval from the Ethics Review Committee on Human Research of the University of Tartu. The applicant will be asked to submit the results of the research project that were obtained using the data of the gene donors, To the EGCUT by the time specified in the contract. These results will complement the EGCUT database.

Resource Name: Estonian Genome Center

Resource ID: SCR_004467

Alternate IDs: nlx_45748

Alternate URLs: http://www.geenivaramu.ee/

Old URLs: http://www.geenivaramu.ee/index.php?lang=eng

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260812T044056+0000

Ratings and Alerts

No rating or validation information has been found for Estonian Genome Center.

No alerts have been found for Estonian Genome Center.

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 .

Kasak L, et al. (2017) Copy number variation profile in the placental and parental genomes of recurrent pregnancy loss families. Scientific reports, 7, 45327.

Lassen B, et al. (2016) Serological Evidence of Exposure to Globally Relevant Zoonotic Parasites in the Estonian Population. PloS one, 11(10), e0164142.

Mõttus R, et al. (2015) Within-trait heterogeneity in age group differences in personality domains and facets: implications for the development and coherence of personality traits. PloS one, 10(3), e0119667.

Vora T, et al. (2015) Impacts of a biobank: Bridging the gap in translational cancer medicine. Indian journal of medical and paediatric oncology : official journal of Indian Society of Medical & Paediatric Oncology, 36(1), 17.

Kasak L, et al. (2015) Extensive load of somatic CNVs in the human placenta. Scientific reports, 5, 8342.

Putku M, et al. (2015) CDH13 promoter SNPs with pleiotropic effect on cardiometabolic parameters represent methylation QTLs. Human genetics, 134(3), 291.

González JR, et al. (2014) A common 16p11.2 inversion underlies the joint susceptibility to asthma and obesity. American journal of human genetics, 94(3), 361.

Patrinos GP, et al. (2011) Recommendations for genetic variation data capture in developing countries to ensure a comprehensive worldwide data collection. Human mutation, 32(1), 2.