



# The Swedish Twin registry

Service directory and pricelist

The Swedish Twin Registry is a KI core facility that provides opportunities to perform various types of twin studies.



**Karolinska  
Institutet**

## **Our mission**

The mission of the Swedish Twin Registry (STR) is to provide a longitudinal research resource for epidemiological and molecular studies of twins. STR is open to applications from Swedish and international researchers. For foreign researchers we require collaboration with a Swedish university. A part of the operating costs for STR is levied through fees for access to the resource according to the practice of KI core facilities.

## **Background**

STR is domiciled at the Karolinska Institutet since 1959. It was originally established to study the importance of the environment for the development of cardiovascular disease and cancer. Since then, interest has expanded to almost all common diseases and health problems. We have contacted all living twins and we are now the world's largest twin registry. A substantial number of scientific articles have been published on data from STR and currently approximately 50 new articles come out each year.

## **Data**

Nationwide questionnaires and telephone interviews have been conducted for different birth cohorts since the 1960s. These are mainly containing information about self-reported health and different exposures. Additional information about health and disease is obtained through linkages to the Swedish health registries. DNA from 50 000 twins and serum of 12 000 twins are stored at KI Biobank and is subject to use to new investigations and analyses. Genome-wide genotyping (GWAS) of almost 50 000 participants have been completed and genotypes can be used for co-analysis to different outcomes and characteristics. For more detailed information on what data are available for the various cohorts, see [www.ki.se/forskning/for-forskare-str](http://www.ki.se/forskning/for-forskare-str).

## **Study Design**

Study designs that are requested and used today include both classical epidemiological studies for the evaluation of risk factors for morbidity and mortality as well as genetic association studies, heritability studies (classic twin design and molecular-based), epigenetics, proteomics and other so-called "omics" –hypotheses.

## **How to access to STR data and resources?**

A steering committee meets four times per year to take decisions for the projects to be implemented. Approval requires a project description that indicates on sound scientific methodology and that twins are not contacted unnecessarily. Access to data and resources further requires an ethical approval from the local ethics review board and that the charges to STR is paid according to the current tariff (see table on the last page).

## Different types of projects

### Heritability

By examining how many pairs are concordant / discordant for the disease among identical and fraternal twins the relative importance of genes (heritability) and environmental aspects of various diseases and conditions can be estimated. This can also be done for quantitative measures such as levels of biomarkers in serum. The corresponding estimate of the importance of genetics can also be molecularly accessed using genome-wide genotyping tests.

### Reasons for comorbidity

Bi- and multivariate twin analysis can provide information on why certain diseases are related (comorbidity). The question can also be investigated using available genome-wide genotyping tests.

### Association within twin pairs

By comparing a relationship observed in the population, whether it also exist within twin pairs, it is possible to examine the extent to which the association is due to genetics, for example, so-called co-twin control designs.

### Discordant monozygotic twins

Since identical twins share all of their inherited gene pool, hereditary genetic variation cannot explain the differences between monozygotic twins (for example, if one is sick while the other is healthy). Discordant monozygotic twins are therefore informative for effects / mechanisms related to environmental factors such as de novo mutations, epigenetics, levels of metabolites or proteins.



## How can STR assist?

### **Advice - Study arrangement and design**

We can share our experience from previous studies.

### **Are there twins and data that are of interest to my research question?**

We can investigate the number of pairs with a certain phenotype or exposure.

- Concordance / discordance tables (by zygosity and gender)
- Availability of data / genotypes / sample for these pairs

### **Analysis expertise in twin models**

- We can assist with quantitative genetic methodologies such as structural equation models (e.g. OpenMX, SAS, STATA, R)

### **Genotypes**

- Genome-wide genotyping (GWAS) is available for almost 50,000 twins. Three different Illumina platforms are used, HumanCoreExome (550K), OmniExpress (700K) and Global Screening Array (650K).

### **Biological surveys, biomarkers**

- For about 12,000 older twins, we measured blood pressure, height, weight, BMI, waist and hips circumferences and key blood markers: total cholesterol, HDL, LDL, triglycerides, CRP, glucose, HbA1C, ApoA1, ApoB and hemoglobin.

### **New contacts - collection of new data**

- Samples
- Name and address

## Price list, 2022

Effective as of 2022-02-08

<b>Service</b>	<b>Per</b>	<b>Price</b>
Searching concordance/discordance over sex and zygosity, availability of data	hour	750 SEK
Application	à	5000 SEK
Administrative cost for data extraction – new application	à	20 000 SEK
Administrative cost for data extraction - amendment or update of earlier approved application	à	7 500 SEK
Extensive data extractions	hour	750 SEK
DNA sample*	µg	125 SEK
Serum sample*	µl	12,50 SEK
GWAS TwinGene (Omni Express N=10 000)	phenotype	50 000 SEK
GWAS/exome chip (HumanCoreExome N=18 000)	phenotype	50 000 SEK
GWAS/GSA chip (Illumina N=18 000)	phenotype	100 000 SEK
Statistical or scientific consultation	hour	1000 SEK
Addresses and names for new contacts**	address	10 SEK

\* Depending on availability. Minimum cost per extraction 25 000 SEK, after that the listed unit price. For large extractions discounts may be discussed. For extractions regarding measures in full material which thereby can enrich STR as infrastructure the cost is decided from case to case.

\*\*Minimum cost per project is 10 000 SEK. For contacts regarding measures in full year cohorts which thereby can enrich STR as infrastructure the cost is decided from case to case.