

# SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population

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## Creator/Principal investigator(s)

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## Description

The SweGen contains whole-genome variant frequencies for 1000 Swedish individuals generated within the SweGen project. The data is intended to be used as a resource for the research community and clinical genetics laboratories.

DNA from blood samples were whole genome sequenced using Illumina X technology at SciLifeLab Uppsala and SciLifeLab Stockholm. The sequencing data was analyzed with the GATK best practices pipeline to obtain a joint called variant frequency dataset. For more information, see:  
<https://www.nature.com/articles/ejhg2017130>

## Data contains personal data

No

## Language

[English](#)

## Population

1000 individuals representing a cross section of the Swedish population

## Study design

Observational study

## Number of individuals/objects

1000

## Data format / data structure

[Numeric](#)

[Text](#)

[Interactive resource](#)

## Data collection 1

- Mode of collection: Registry extract and/or access to biobank sample
- Source of the data: Biological samples

**Responsible department/unit**

Department of Immunology, Genetics and Pathology

**Research area**

[Medical and health sciences](#) (Standard för svensk indelning av forskningsämnen 2011)

**Keywords**

[Genetics, population](#)

**Publications**

Ameur A, Dahlberg J, Olason P, Vezzi F, Karlsson R, Martin M, Viklund J, Kähäri AK, Lundin P, Che H, Thutkawkorapin J, Eisfeldt J, Lampa S, Dahlberg M, Hagberg J, Jareborg N, Liljedahl U, Jonasson I, Johansson Å, Feuk L, Lundeberg J, Syvänen AC, Lundin S, Nilsson D, Nystedt B, Magnusson PK, Gyllensten U. SweGen: a whole-genome data resource of genetic variability in a cross-section of the Swedish population. *Eur J Hum Genet.* 2017 Nov;25(11):1253-1260, doi:10.1038/ejhg.2017.130  
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**Accessibility level**

Access to data through an external actor

Access to data is restricted

**Homepage**

[SweFreq — The Swedish Frequency resource for genomics](#)

**Download metadata**

[DataCite](#)

[DDI 2.5](#)

[DDI 3.3](#)

[DCAT-AP-SE 2.0](#)

[JSON-LD](#)

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