

# Bioinformatics

Programme course

3 credits

Bioinformatik

TFTB45

Valid from: 2017 Spring semester

**Determined by**

Board of Studies for Chemistry, Biology  
and Biotechnology

**Date determined**

2017-01-25

**Offered for the last time**

Autumn semester 2025

**Replaced by**

TFTB55

## Main field of study

Biotechnology, Chemical Biology, Chemistry

## Course level

First cycle

## Advancement level

G2F

## Course offered for

- Protein Science, Master's Programme
- Chemical Biology, M Sc in Engineering
- Chemical Biology

## Entry requirements

Note: Admission requirements for non-programme students usually also include admission requirements for the programme and threshold requirements for progression within the programme, or corresponding.

## Prerequisites

Biochemistry, Cell Biology, Microbiology, Gene Technology and Molecular Genetics

## Intended learning outcomes

The course aims to provide basic knowledge in bioinformatics, namely the theories and practical applications of computer-based methods for the analysis of DNA and protein sequences as well as for studies of protein structures. This involves both theoretical understanding and practical skills in handling methods. The course will also show how the subject is developed through examples from research frontline.

After the course you should be able to:

- use the most important open databases for literature, sequence data and structural information,
- perform comparisons of sequences and give good interpretations of the results,
- extract important structural information about genes, proteins, and genomes
- discuss the possibilities and limitations of bioinformatics tools,
- plan for new bioinformatics problems and to solve them by combining the tools you learn in this course.

## Course content

Computer-based methods for analyzing DNA and protein sequences and for studying the structure of proteins. Databases and methods for database searches, including SRS (a user-friendly database interface). Sequence comparisons (both DNA and protein level). Multiple sequence comparisons and multiple sequence fitting (alignment). Sequence patterns and how to characterize them. Protein domains. Use of bioinformatics for functional characterization of genes and proteins. Secondary structure and post-translational modifications. Parts of the course highlights both the underlying theoretical models and biological and biotechnological applications of the methods and computer programs are presented

## Teaching and working methods

Lectures and practical exercises. Lectures presents underlying theory and applications. The practical laboratory work aims to illustrate and deepen knowledge on realistic problems and issues

## Examination

LAB1	Laboratory work	1 credits	U, G
TEN1	Written examination	2 credits	U, 3, 4, 5

## Grades

Four-grade scale, LiU, U, 3, 4, 5

## Department

Institutionen för fysik, kemi och biologi

## Director of Studies or equivalent

Magdalena Svensson

## Examiner

Björn Wallner

## Education components

Preliminary scheduled hours: 25 h

Recommended self-study hours: 55 h

## Course literature

Kompendium / Compendium Vetenskapliga artiklar / Scientific articles

## Common rules

Regulations (apply to LiU in its entirety)

The university is a government agency whose operations are regulated by legislation and ordinances, which include the Higher Education Act and the Higher Education Ordinance. In addition to legislation and ordinances, operations are subject to several policy documents. The Linköping University rule book collects currently valid decisions of a regulatory nature taken by the university board, the vice-chancellor and faculty/department boards.

LiU's rule book for education at first-cycle and second-cycle levels is available at [http://stydokument.liu.se/Regelsamling/Innehall/Utbildning\\_pa\\_grund-\\_och\\_avancerad\\_niva](http://stydokument.liu.se/Regelsamling/Innehall/Utbildning_pa_grund-_och_avancerad_niva).