

## Structural Bioinformatics (C003526)

**Course size** *(nominal values; actual values may depend on programme)*

**Credits 3.0**                      **Study time 80 h**

**Course offerings and teaching methods in academic year 2025-2026**

A (semester 1)	English	Gent	lecture seminar
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**Lecturers in academic year 2025-2026**

Savvides, Savvas	WE10	lecturer-in-charge
Mehdipour, Ahmadreza	TW17	co-lecturer

**Offered in the following programmes in 2025-2026**

	<b>crdts</b>	<b>offering</b>
<a href="#">Master of Science in Teaching in Science and Technology(main subject Biochemistry and Biotechnology)</a>	3	A
<a href="#">Master of Science in Bioinformatics(main subject Systems Biology)</a>	3	A
<a href="#">Master of Science in Biochemistry and Biotechnology</a>	3	A
<a href="#">Exchange programme in Biochemistry and Biotechnology (master's level)</a>	3	A

**Teaching languages**

English

**Keywords**

Secondary structure determination, structure prediction, hybrid methods in structural biology, structure quality validation, molecular visualization, structural databases, molecular docking, force fields, molecular dynamics, structural bioinformatics.

**Position of the course**

This course will give an overview of the field of structural bioinformatics. This field studies the structure and function of proteins.

This course contributes to the following program competences: Ma.WE.BB.1.2, Ma.WE.BB.1.3, Ma.WE.BB.2.5, Ma.WE.BB.2.6

**Contents**

- Protein sequence alignments, homology, classification, protein families.
- Structure superposition and comparison.
- Prediction of three-dimensional protein structure
  - Homology modeling
  - Fold recognition
  - Ab initio
- Quality of protein structures
  - Quality indicators of experimentally determined macromolecular structures via X-ray crystallography, electron-microscopy, NMR etc.)
  - Quality control of structures and Errors in protein structures
- Secondary structure prediction
  - Secondary structure preferences of amino acids
  - First, second and third generation algorithms
  - Transmembrane helix prediction
- Integrative methods in structural biology
- Structural databases
- Introduction to molecular docking and dynamics

**Initial competences**

Basic knowledge of molecular biology  
Basic knowledge of bioinformatics  
Basic knowledge of structural biology is a plus

### **Final competences**

- 1 Have a perspective of the largest research domains in structural bioinformatics and the problems that pose themselves.
- 2 Have insight in the concepts used by the different algorithms in structural bioinformatics.
- 3 To be able to identify and apply appropriate online tools, software, and approaches to analyze protein structures and sequences towards research in biochemistry, biotechnology, and structural biology.

### **Conditions for credit contract**

Access to this course unit via a credit contract is determined after successful competences assessment

### **Conditions for exam contract**

This course unit cannot be taken via an exam contract

### **Teaching methods**

Seminar, Lecture

### **Study material**

Type: Slides

Name: Lecture materials'

Indicative price: Free or paid by faculty

Optional: no

Additional information: Lecture materials via UFORA Online resources and software Lecture recordings

### **References**

### **Course content-related study coaching**

Weekly office-hour

### **Assessment moments**

continuous assessment

### **Examination methods in case of periodic assessment during the first examination period**

### **Examination methods in case of periodic assessment during the second examination period**

### **Examination methods in case of permanent assessment**

Assignment

### **Possibilities of retake in case of permanent assessment**

examination during the second examination period is possible

### **Extra information on the examination methods**

The exam will assume a 'take-home' format.

The exam will be completed independently by each student against a specified deadline and will be submitted online according to specified instructions and format.

### **Calculation of the examination mark**

Evaluation methods: Assignment 100%