

# Softwarewerkzeuge der Bioinformatik

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## Project 1 – Sequence Analysis

**Deadline: 28.11.2019 18:00**

Submit the report as a PDF via email to [markus-hollander@web.de](mailto:markus-hollander@web.de) (address also for questions).

Please follow all points mentioned in the project report guidelines that you can find on the lecture website. The following points will be assessed:

- Is is the correct approach?
- Were all parameters, tools etc. mentioned?
- Are the results complete and correct?
- Were the results sufficiently and correctly discussed if the task demanded it?
- Does the documentation of the tasks fulfil the guidelines?

On the lecture website you will find an amino acid sequence with your group number that you should use to solve the following tasks.

### Task 1.1: (10 points)

Identify your (known) protein. Gather at least the following information about the given protein: gene, organism, cellular compartment, protein family and function.

### Task 1.2: (15 points)

Compare the PRINTS- and PROSITE-motifs as well as the conserved regions of your protein.

### Task 1.3: (15 points)

In addition, identify transmembrane regions and analyse their conservation. Use TOPCONS (<http://topcons.cbr.su.se/>) to find the transmembrane regions. Is the conservation more pronounced in transmembrane helices (THMs) or in loops?

**Remark:** *This task was not practised during the tutorial.*

### Task 1.4: (20 points)

Discuss how your protein is related to other proteins with **similar sequence** in the same and in other organisms.

### Task 1.5: (20 points)

Compare your protein to various human proteins with **similar function** regarding motifs, sequence similarity, transmembrane regions and protein family.

### Task 1.6: (20 points)

Examine and compare proteins of the TCDB-subfamily to which your protein belongs regarding their sequence length, sequence similarity, transmembrane regions, motifs and function.

Viel Spaß!