

**Practical 8**  
**14 March 2022**

**Questions**

1. Obtain the hydrophobicity profile for the sequences (Q1.fasta) and identify the  $\alpha$ -helices and  $\beta$ -strands.

Hydrophobicity values:

A: 13.85 D: 11.61 C: 15.37 E: 11.38 F: 13.93 G: 13.34 H: 13.82 I: 15.28 K: 11.58 L: 14.13

M: 13.86 N: 13.02 P: 12.35 Q: 12.61 R: 13.10 S: 13.39 T: 12.70 V: 14.56 W: 15.48 Y: 13.88

2. Calculate the amphipathic index for the helices and strands found in Q1. Use stretch lengths of 8 and 6 for  $\alpha$ -helices and  $\beta$ -strands, respectively.

3. Plot the hydrophobicity profile for the sequence (Q2.fasta) with window lengths 9 and 19 and list the transmembrane segments.

4. Use ScanProsite tool (<https://prosite.expasy.org/scanprosite/> - select option 2), to search for the patterns a) [SV]-T-[VT]-[DERK](2)-{IL} and b) [FILV]Qxxx{RK}Gxxx[RK]xx[FILVWY] in UniProtKB (Include Swiss-Prot, isoforms). List the number of matches for each pattern.

5. Write a program to identify the patterns (refer Q4) in the sequence database (Q4.fasta). List the matches along with the sequence header and location of the matches in the sequence.

6. Identify the beta barrel membrane proteins with the following pattern:

[K,R,H,Q,F,E]-x-G-[I,V,L,F,A,C]-x-[I,V,L,F,M,Y,W]-x-[I,V,L,F,W]

Use: [http://www.bioinformatics.org/sms2/protein\\_pattern.html](http://www.bioinformatics.org/sms2/protein_pattern.html)

and

<http://prosite.expasy.org/scanprosite/>

Hint: Modify the patterns according to the input format of the server.

**Deadline: 20<sup>th</sup> March 2022**