

Practical 8
1 April 2024

Questions

- ✓ 1. Obtain the hydrophobicity profile for the sequences (Q1.fasta) and identify the α -helices and β -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 α -helices and β -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. **max a 100000**
- ✓ 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
and
<http://prosite.expasy.org/scanprosite/>
Hint: Modify the patterns according to the input format of the server.

Deadline: 7th April 2024