

Protein Secondary Structure Prediction

Give a protein sequence:

AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLMGQEVVPVKVLEVDRQGRIRLSIKEATEQSQPAA

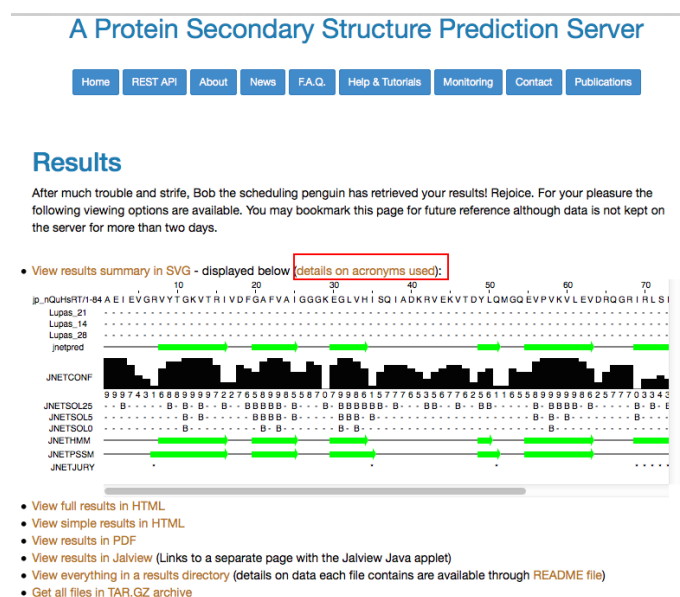
Advanced secondary structure prediction

Jpred server (<http://www.compbio.dundee.ac.uk/www-jpred/>) is often used to annotate secondary structure elements. A new release (4.0) came out on December 22, 2014; select the link to the submission form. Jpred improves on the previous methods in three ways:

1. It combines the predictions of several different prediction methods to obtain a consensus prediction.
2. It searches protein databases for sequences similar to the query (mystery protein in our case) and builds a multiple-sequence alignment of these protein sequences and the query. The predictor annotates the highly conserved regions in the alignment with regular secondary structure (alpha-helices and beta- strands), and regions containing insertions and deletions with random coil elements.
3. It searches protein databank (PDB) for sequences of proteins with experimentally determined structures and transfers the secondary structure elements to the query sequence.

Paste the given protein sequence in the submission box, click on “Advanced options”, and check the box next to “Skip searching PDB before prediction”. This will skip improvement 3 described above. Submit your request to the server.

Click on “details on acronyms used” to get information that can help you understand the result.



Question 1: Which regions of regulatory secondary structure might you be reasonably sure are correct? Show the screen shot of your output.

Now repeat the exercise, but this time, make sure to uncheck the box next to “Skip searching PDB before prediction”.

Question 2: List the top three matched proteins. Which protein structure match your prediction?