



### **Prerequisite Terminologies:**

In order to have a better understanding of the main topic, you should have the basic concept of the following terms:

- Protein Secondary structures
- JalView
- Coiled coil domains

### **Introduction:**

Jpred4 is the latest version of the JPred Protein Secondary Structure Prediction Server, which provides secondary structure predictions of proteins by the JNet algorithm, one of the most accurate methods for secondary structure prediction. In addition to protein secondary structure, JPred also makes predictions of solvent accessibility and coiled-coil regions.

### **Steps:**

- Click on the link provided as follows, to visit the webserver of JPred tool:  
<https://www.compbio.dundee.ac.uk/jpred/>
- Prepare your query protein sequence in simple text format and paste in the query box available there.

- To upload a file, click on “Advanced Options” button and then click on the “Choose file” button to and then select the query file from your system to upload it on the server.
- Then select the input type, i.e, either you are using a single sequence or multiple aligned sequences.
- Then check the box, if you don’t want to search PDB before making any prediction.
- You can also provide your email address and your query\_name, to get the results link via email.
- Then click on the “Make Prediction” button to get the results.

### ➤ **Results Analysis:**

- On the top of the results page, it provides the summary of the results generated against your query protein.
- Then it provides the hyperlink ‘View results summary in SVG’, which provides the graphical view of the results summary and the secondary structures predicted in the query protein.
  - On the top, it provides the query protein sequence and its length.
  - The arrows in the graphical summary results represent the beta-sheets that have been predicted by the JPred server.
    - The direction of the arrow head represents the direction of the beta-sheet, i.e., left hand side or right hand side beta-sheet.
  - The long red colored rod like structures in the graphical summary results represent the loops within the query protein predicted by the JPred server.
  - The JNETCONF score represents the probability of the predicted structures in the query protein.
 

**Note:** Higher the value of JNETCONF score, higher the probability of the structures.
  - The predicted structures plotted against the ‘JNETJURY’ provides the consensus structures of the query protein.
    - The consensus structures are represented by asterisk (\*) signs.

- At the bottom of the results page, it provides various hyperlinks to download the entire results in HTML, PDF and other formats as well.
- It also provides the hyperlink to view the results in Jalview.

## **Summary:**

In this video tutorial of Protein Secondary Structure prediction, we learned about the JPred server to predict the secondary structures available in our query protein. We also got to analyze the results to comprehend the information in a better manner.