## **Secondary Structure Prediction**

The Secondary Structure Prediction plugin provides a set of algorithms for the protein secondary structure (alpha-helix, beta-sheet) prediction from a raw sequence.

Currently, available algorithms are:

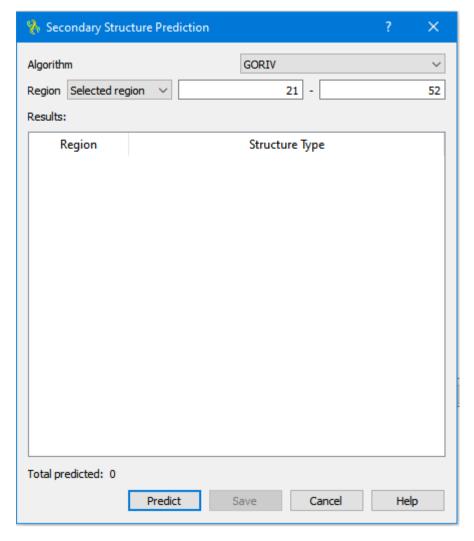
• GORIV Jean Garnier, Jean-Francois Gibrat, and Barry Robson,"GOR Method for Predicting Protein Secondary Structure from Amino Acid Sequence", in Methods in Enzymology, vol.266, pp. 540 - 553, (1996).

The improved version of the GOR method in J. Garnier, D. Osguthorpe, and B. Robson, J. Mol. Biol., vol. 120, p. 97 (1978).

• PsiPred Bryson K, McGuffin LJ, Marsden RL, Ward JJ, Sodhi JS. & Jones DT. (2005) Protein structure prediction servers at University College London. Nucl. Acids Res. 33(Web Server issue): W36-38.

Jones DT. (1999) Protein secondary structure prediction based on position-specific scoring matrices. J. Mol. Biol. 292: 195-202.

You can access these analysis capabilities for a protein sequence using the Analyze Predict secondary structure... context menu item. The dialog will appear:

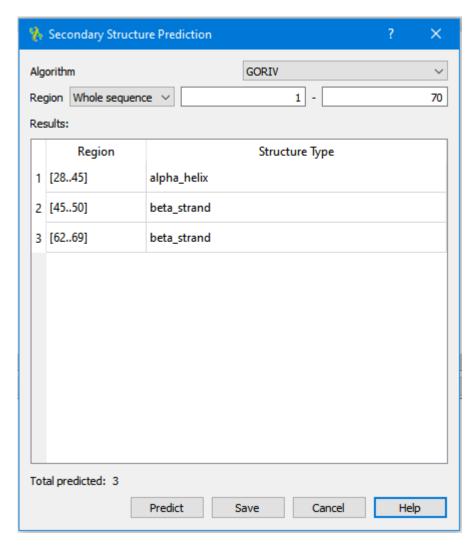


It supports the following options:

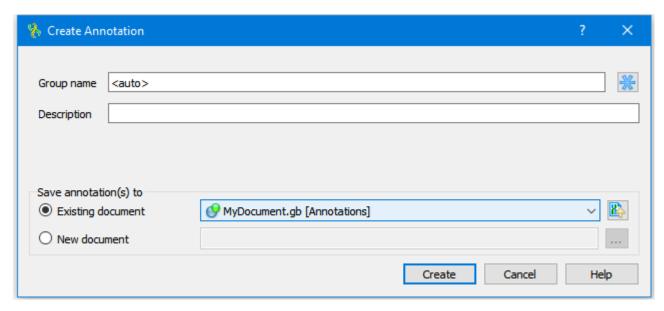
Algorithm — you can choose the preferred algorithm. Currently, "GORIV" and "PsiPred" algorithms are available.

Region — select the sequence range for prediction. Region can be either a Selected region if select range before selection, Whole sequence or Cus tom region.

Results — the visual representation of the prediction results, for example:



Save — select this button to save the results as annotations of the current protein sequence.



Visual representation of the predicted annotation on the sequence:

