

# 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:

The dialog box is titled "Secondary Structure Prediction". It features a blue header bar with a question mark icon and a close button. The main content area includes an "Algorithm" dropdown menu currently set to "GORIV". Below this is a "Region" dropdown menu set to "Selected region", followed by two input fields containing the numbers "21" and "52" separated by a hyphen. A "Results:" label precedes a large empty rectangular area intended for displaying prediction results. At the bottom left, it states "Total predicted: 0". The bottom right corner contains four buttons: "Predict" (highlighted with a blue border), "Save", "Cancel", and "Help".

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 *Custom region*.

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

**Secondary Structure Prediction**

Algorithm: GORIV

Region: Whole sequence 1 - 70

Results:

	Region	Structure Type
1	[28..45]	alpha_helix
2	[45..50]	beta_strand
3	[62..69]	beta_strand

Total predicted: 3

Predict Save Cancel Help

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

**Create Annotation**

Group name: <auto>

Description:

Save annotation(s) to:

☒ Existing document: MyDocument.gb [Annotations]

☐ New document:

Create Cancel Help

Visual representation of the predicted annotation on the sequence:

