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.
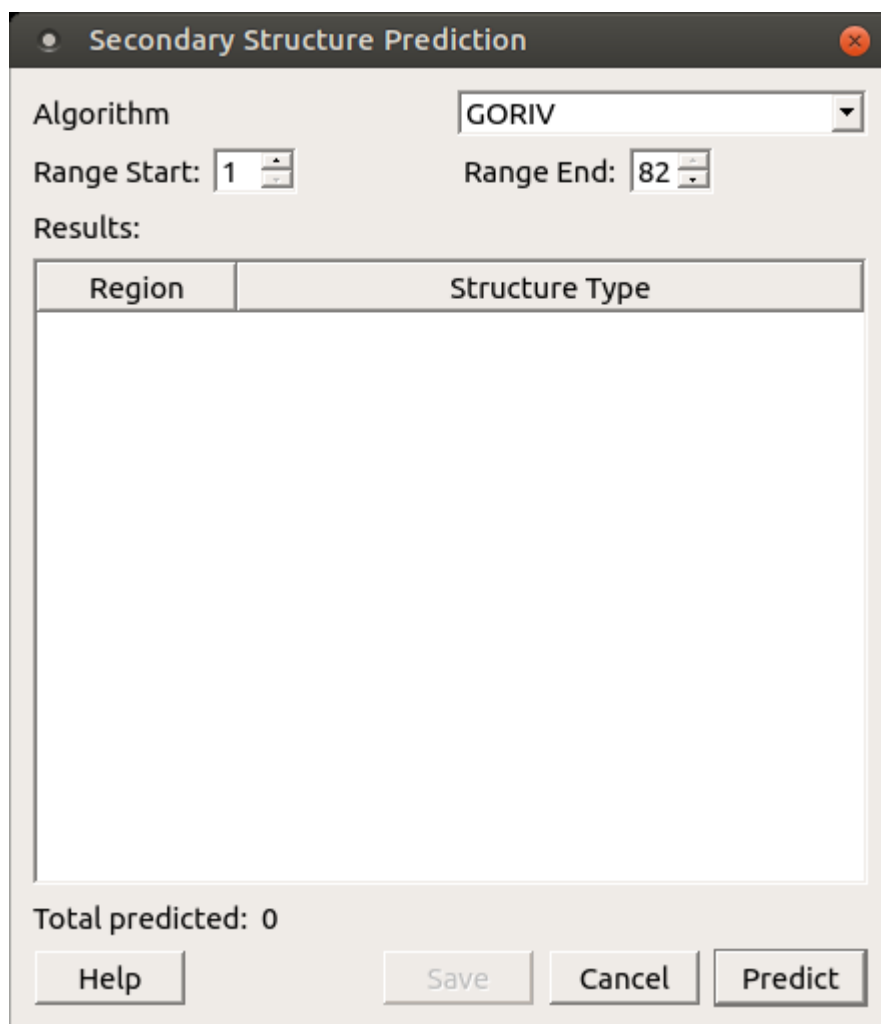
Currently, available algorithms are:

- **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.

Range start / *Range end* — select the sequence range for prediction.

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

Secondary Structure Prediction

Algorithm   GORIV

Range Start: 1   Range End: 82

Results:

	Region	Structure Type
1	[5..7]	beta_strand
2	[9..15]	beta_strand
3	[24..32]	alpha_helix
4	[39..75]	alpha_helix
5	[75..81]	beta_strand

Total predicted: 5

| Help | | Save | Cancel | Predict |

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