

Secondary Structure Prediction

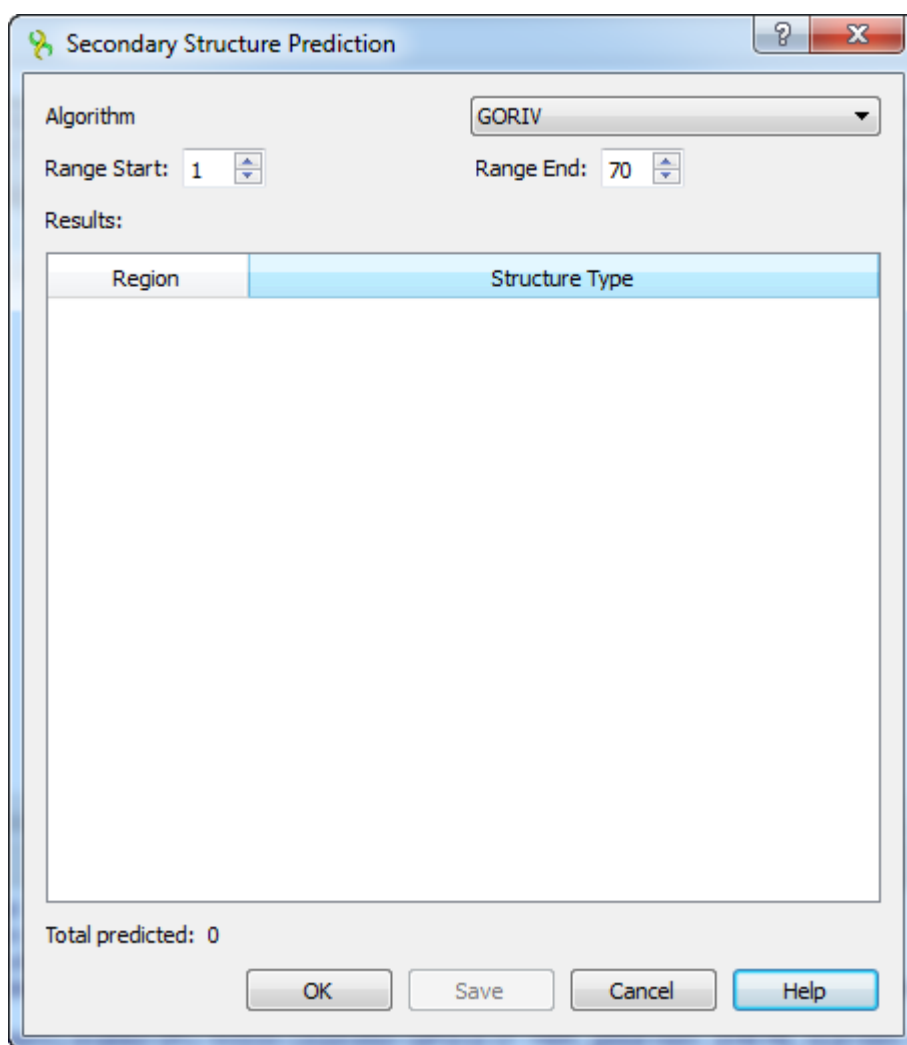
The *Secondary Structure Prediction* plugin provides a set of algorithms for the protein secondary structure (alpha-helix, beta-sheet) prediction from a raw sequence.

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).
- 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 — visual representation of the prediction results, for example:

Secondary Structure Prediction

Algorithm: GORIV

Range Start: 1 Range End: 70

Results:

	Region	Structure Type
1	[27..44]	gorIV_results
2	[44..49]	gorIV_results
3	[61..68]	gorIV_results

Total predicted: 3

OK Save Cancel Help

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