# 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:
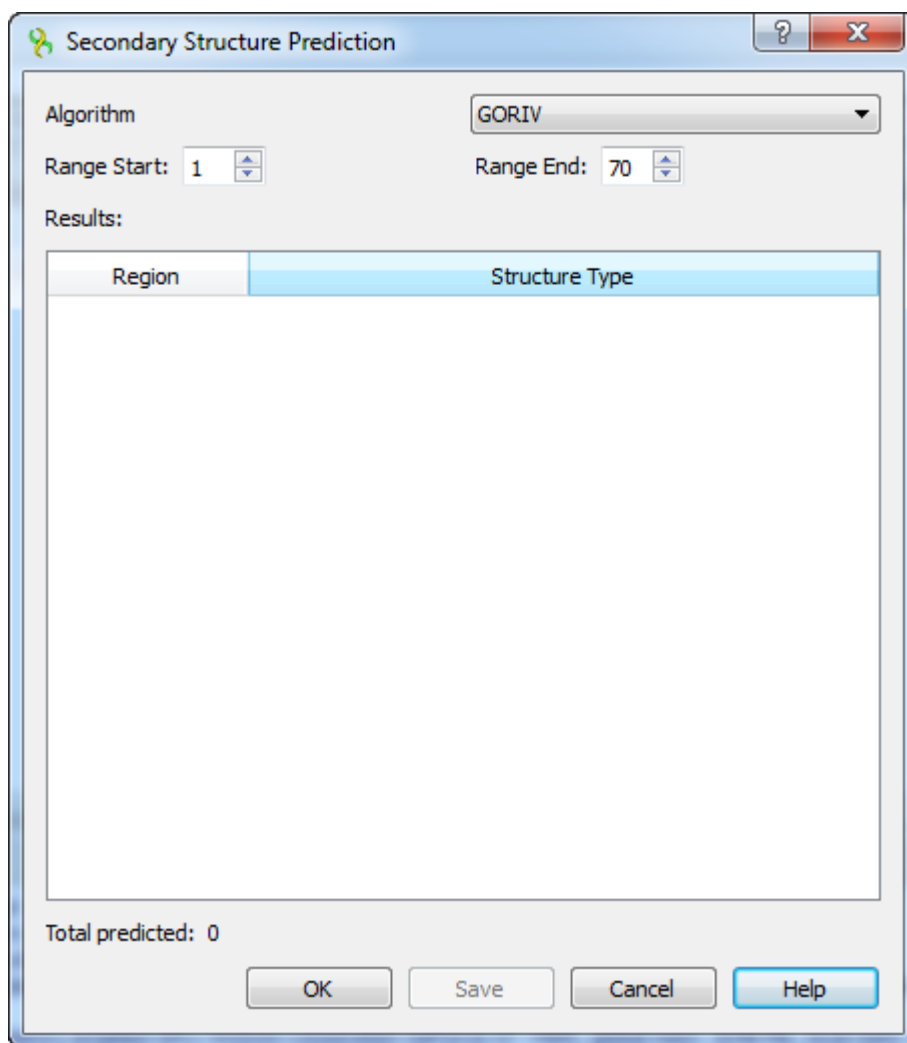
It supports the following options:

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:

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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.