

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 L.J, Marsden R.L, Ward J.J, Sodhi J.S. & Jones D.T. (2005) Protein structure prediction servers at University College London. *Nucl. Acids Res.* 33(Web Server issue): W36-38.

Jones D.T. (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:

Secondary Structure Prediction

Algorithm: GORIV

Range Start: 1 Range End: 82

Results:

| Region | Structure Type |
|--------|----------------|
|--------|----------------|

Total predicted: 0

Buttons: Help, Save, Cancel, Predict

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

Buttons: Help, Save, Cancel, Predict

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