

TMpred

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TMpred output for unknown

[EMBNET-Server] Date: Fri Oct 20 10:38:19 2017

Sequence: PIS...KVL, length: 560

Prediction parameters: TM-helix length between 17 and 33

1.) Possible transmembrane helices

The sequence positions in brackets denominate the core region.
Only scores above 500 are considered significant.

Inside to outside helices : 0 found

Outside to inside helices : 0 found

2.) Table of correspondences

Here is shown, which of the inside->outside helices correspond to which of the outside->inside helices.

Helices shown in brackets are considered insignificant.
A "+"-symbol indicates a preference of this orientation.
A "++"-symbol indicates a strong preference of this orientation.

inside->outside | outside->inside

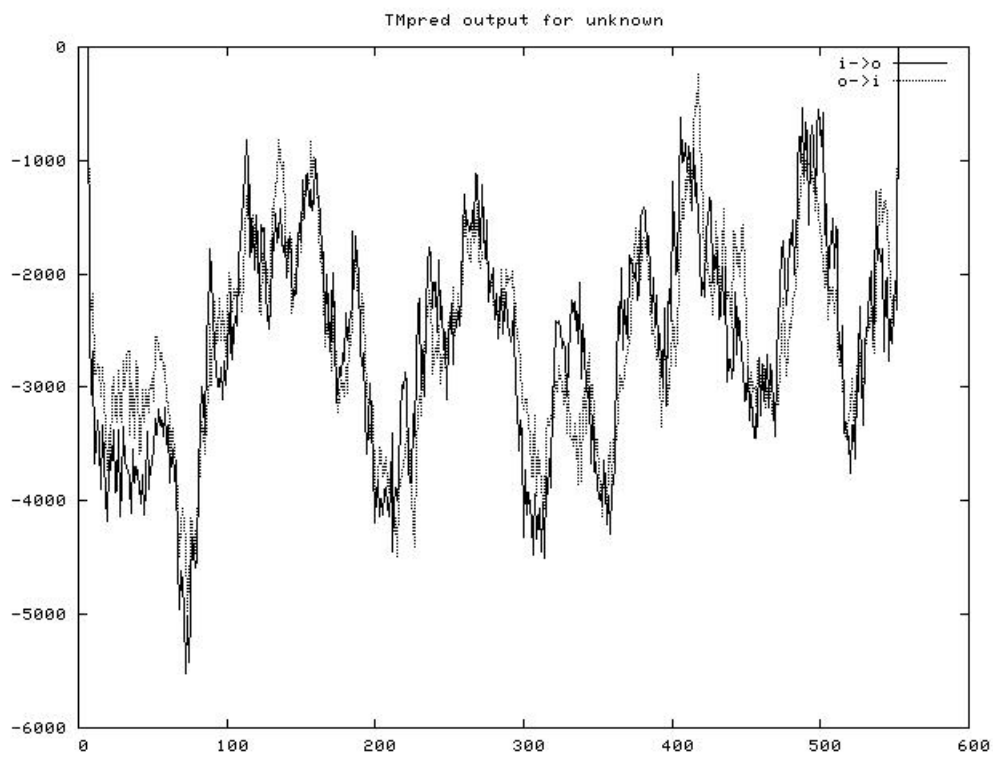
3.) Suggested models for transmembrane topology

These suggestions are purely speculative and should be used with **extreme caution** since they are based on the assumption that all transmembrane helices have been found.

In most cases, the Correspondence Table shown above or the prediction plot that is also created should be used for the topology assignment of unknown proteins.

2 possible models considered, only significant TM-segments used

!!! probably no transmembrane protein - no possible model found !!!



You can get the prediction graphics shown above in one of the following formats:

- [GIF-format](#)
- [Postscript-format](#)
- [numerical format](#)

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