



# **TMHMM** Plugin

USER MANUAL

# User manual for TMHMM 1.4

Windows, Mac OS X and Linux

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**This software is for research purposes only.**

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# Chapter 1

## Introduction to the TMHMM

### 1.1 Transmembrane helix prediction

Many proteins are integral membrane proteins. Most membrane proteins have hydrophobic regions which span the hydrophobic core of the membrane bi-layer and hydrophilic regions located on the outside or the inside of the membrane. Many receptor proteins have several transmembrane helices spanning the cellular membrane.

For prediction of transmembrane helices, CLC Workbench uses TMHMM version 2.0 [Krogh et al., 2001] located at <http://www.cbs.dtu.dk/services/TMHMM/>, thus an active internet connection is required to run the transmembrane helix prediction. Additional information on TMHMM and Center for Biological Sequence analysis (CBS) can be found at <http://www.cbs.dtu.dk> and in the original research paper [Krogh et al., 2001].

When the plugin is downloaded and installed, you can use it to predict transmembrane helices:

**Toolbox | Protein Analysis**  **| Transmembrane Helix Prediction** 

If a sequence was selected before choosing the Toolbox action, this sequence is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences or sequence lists from the selected elements.

The predictions obtained can either be shown as annotations on the sequence, in a table or as the detailed and text output from the TMHMM method.

- Add annotations to sequence
- Create table
- Text

Click **Next** if you wish to adjust how to handle the results, then click **Finish**.

You can perform the analysis on several protein sequences at a time. This will add annotations to all the sequences and open a view for each sequence if a transmembrane helix is found. If a transmembrane helix is not found a dialog box will be presented.

After running the prediction as described above, the protein sequence will show predicted transmembrane helices as annotations on the original sequence (see figure 1.1). Moreover,

annotations showing the topology will be shown, i.e., which part the proteins is located on the inside or on the outside.

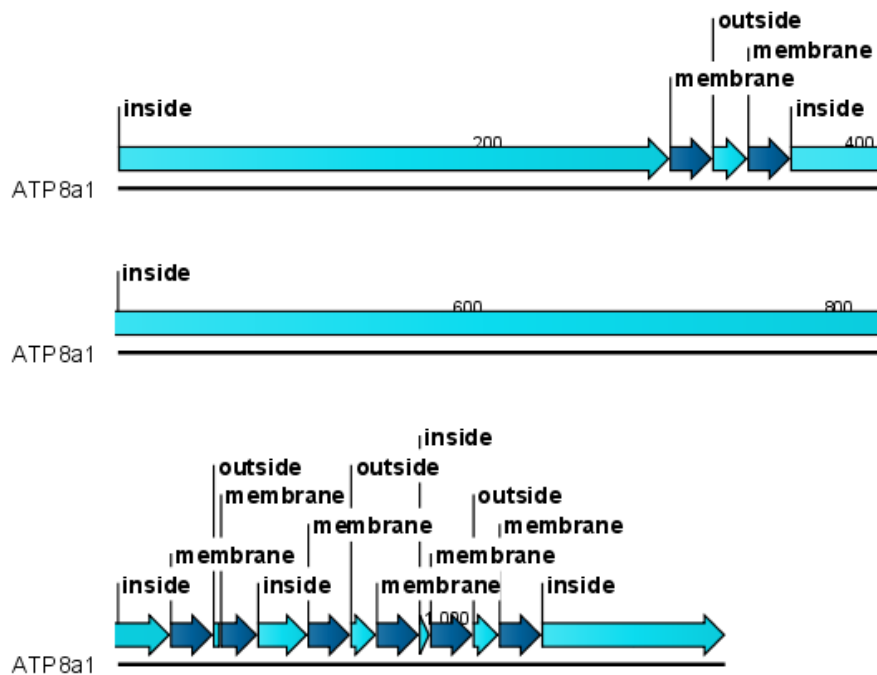


Figure 1.1: Transmembrane segments shown as annotation on the sequence and the topology.

Each annotation will carry a tooltip note saying that the corresponding annotation is predicted with TMHMM version 2.0. Additional notes can be added through the **Edit annotation** (🔍) right-click mouse menu. Undesired annotations can be removed through the **Delete Annotation** (🗑️) right-click mouse menu.

## Chapter 2

# Installation

The TMHMM is installed as a plugin. Plugins are installed using the plugin manager. In order to install plugins on Windows, the Workbench must be run in administrator mode: Right-click the program shortcut and choose "Run as Administrator". Then follow the procedure described below.

**Help in the Menu Bar | Plugins... (  )**

or **Plugins (  ) in the Toolbar**

The plugin manager has two tabs at the top:

- **Manage Plugins.** This is an overview of plugins that are installed.
- **Download Plugins.** This is an overview of available plugins on CLC bio's server.

To install a plugin, click the **Download Plugins** tab. This will display an overview of the plugins that are available for download and installation (see figure 2.1).

Clicking a plugin will display additional information at the right side of the dialog. This will also display a button: **Download and Install**.

Click the TMHMM and press **Download and Install**. A dialog displaying progress is now shown, and the plugin is downloaded and installed.

If the TMHMM is not shown on the server, and you have it on your computer (for example if you have downloaded it from our website), you can install it by clicking the **Install from File** button at the bottom of the dialog. This will open a dialog where you can browse for the plugin. The plugin file should be a file of the type ".cpa".

When you close the dialog, you will be asked whether you wish to restart the CLC Workbench. The plugin will not be ready for use until you have restarted.

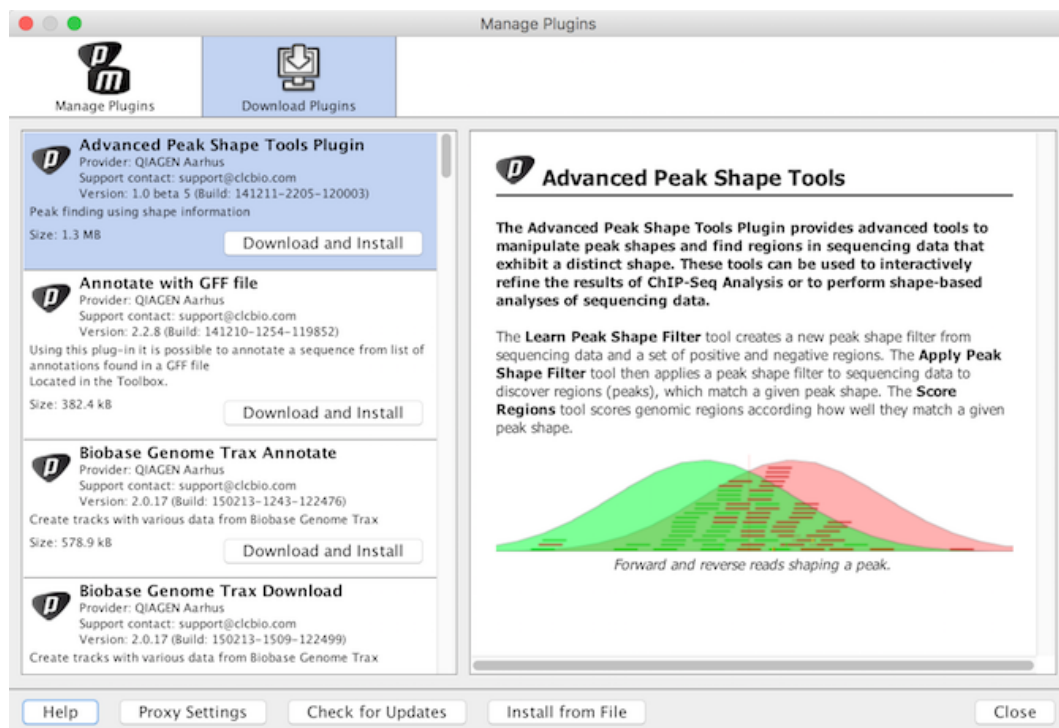


Figure 2.1: The plugins that are available for download.

## Chapter 3

# Uninstall

Plugins are uninstalled using the plugin manager:

**Help in the Menu Bar | Plugins... (  )**

or **Plugins (  ) in the Toolbar**

This will open the dialog shown in figure 3.1.

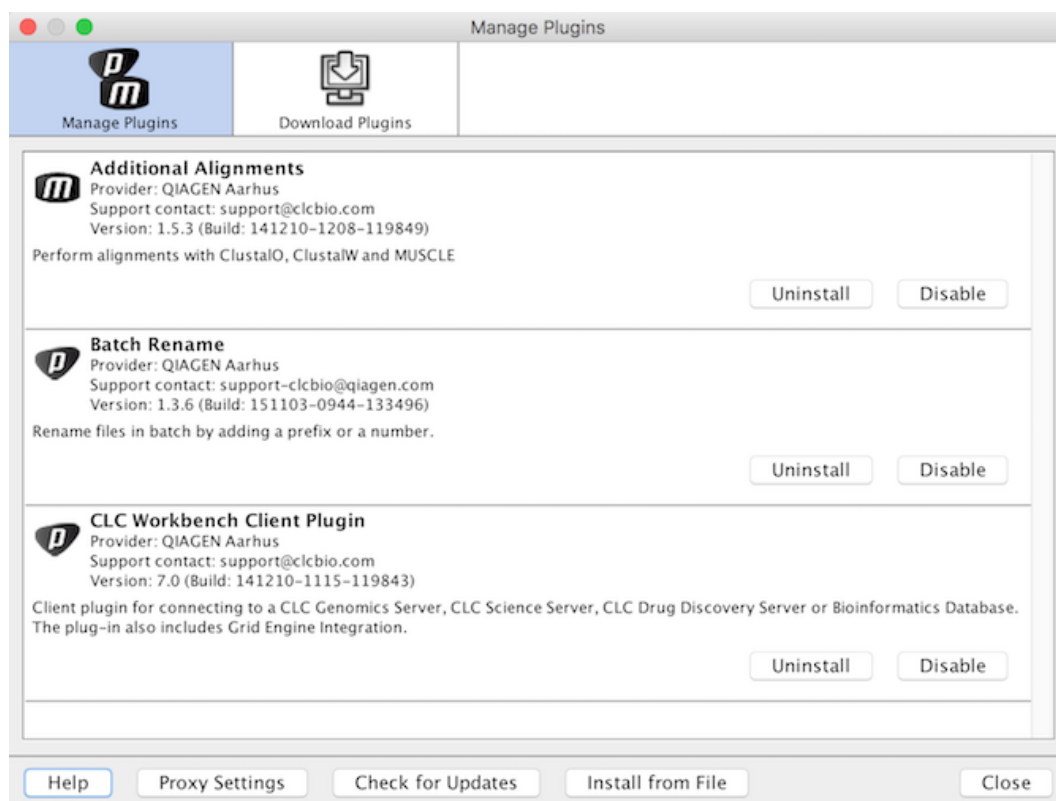


Figure 3.1: The plugin manager with plugins installed.

The installed plugins are shown in this dialog. To uninstall:

**Click the TMHMM | Uninstall**



If you do not wish to completely uninstall the plugin but you don't want it to be used next time you start the Workbench, click the **Disable** button.

When you close the dialog, you will be asked whether you wish to restart the workbench. The plugin will not be uninstalled until the workbench is restarted.

# Bibliography

[Krogh et al., 2001] Krogh, A., Larsson, B., von Heijne, G., and Sonnhammer, E. L. (2001). Predicting transmembrane protein topology with a hidden Markov model: application to complete genomes. *J Mol Biol*, 305(3):567–580.