TMHMM
Plugin

USER MANUAL

User manual for
TMHMM 1.7

Windows, macOS and Linux

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This software is for research purposes only.

QIAGEN Aarhus
Silkeborgvej 2
Prismet
DK-8000 Aarhus C
Denmark

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Chapter 1

Introduction

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 THMHH 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.

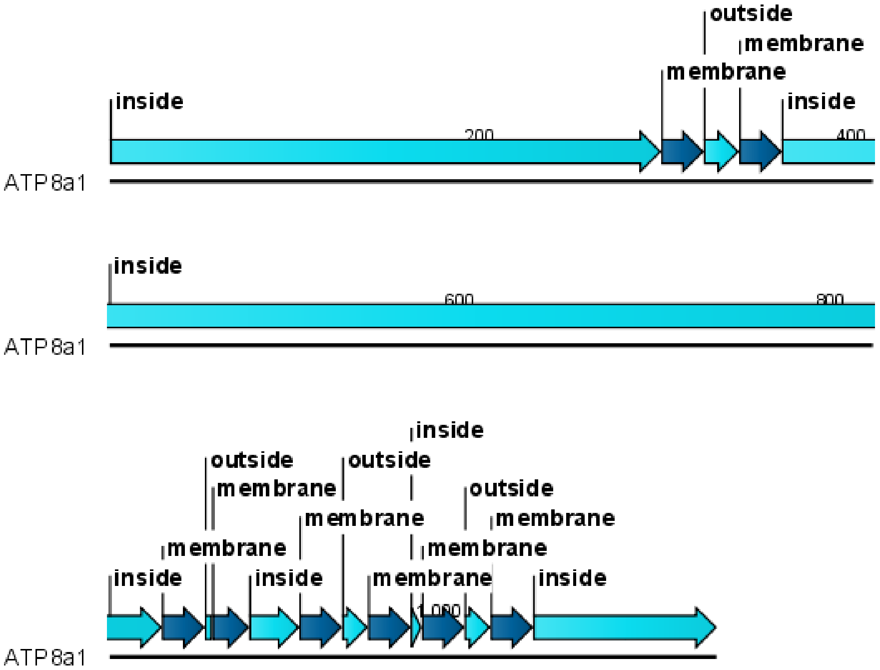


Figure 1.1: *Transmembrane segments shown as annotation on the sequence and the topology.*

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

Install and uninstall plugins

TMHMM is installed as a plugin.

Note: In order to install plugins and modules, the Workbench must be run in administrator mode. On Linux and Mac, it means you must be logged in as an administrator. On Windows, you can do this by right-clicking the program shortcut and choosing "Run as Administrator".

Plugins are installed and uninstalled using the plugin manager.

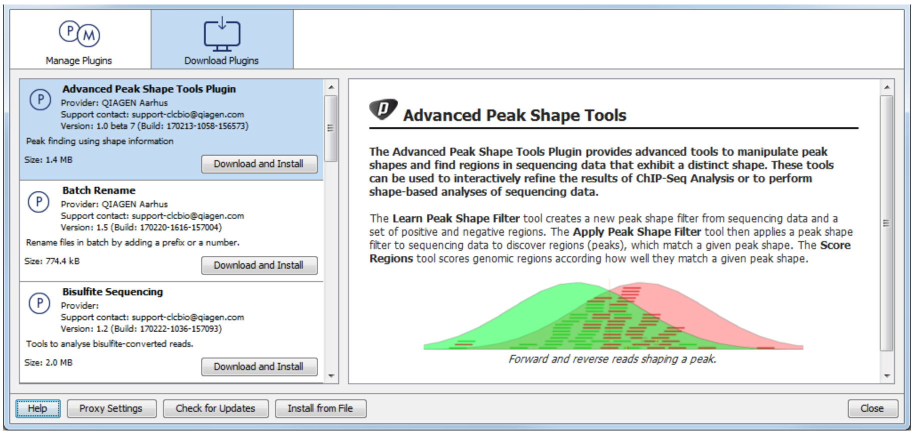
Help in the Menu Bar | **Plugins... (** ✣ **)** or **Plugins (** ✣ **) in the Toolbar**

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 QIAGEN Aarhus server.

2.1 Install

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).



Advanced Peak Shape Tools Plugin
Provider: QIAGEN Aarhus
Support contact: support-clcbio@qiagen.com
Version: 1.0 beta 7 (Build: 170213-1058-156573)
Peak finding using shape information
Size: 1.4 MB

Batch Rename
Provider: QIAGEN Aarhus
Support contact: support-clcbio@qiagen.com
Version: 1.5 (Build: 170220-1616-157004)
Rename files in batch by adding a prefix or a number.
Size: 774.4 kB

Bisulfite Sequencing
Provider:
Support contact: support-clcbio@qiagen.com
Version: 1.2 (Build: 170222-1036-157093)
Tools to analyse bisulfite-converted reads.
Size: 2.0 MB

Advanced Peak Shape Tools

The Advanced Peak Shape Tools Plugin provides advanced tools to manipulate peak shapes and find regions in sequencing data that exhibit a distinct shape. These tools can be used to interactively refine the results of ChIP-Seq Analysis or to perform shape-based analyses of sequencing data.

The **Learn Peak Shape Filter** tool creates a new peak shape filter from sequencing data and a set of positive and negative regions. The **Apply Peak Shape Filter** tool then applies a peak shape filter to sequencing data to discover regions (peaks), which match a given peak shape. The **Score Regions** tool scores genomic regions according how well they match a given peak shape.

Forward and reverse reads shaping a peak.

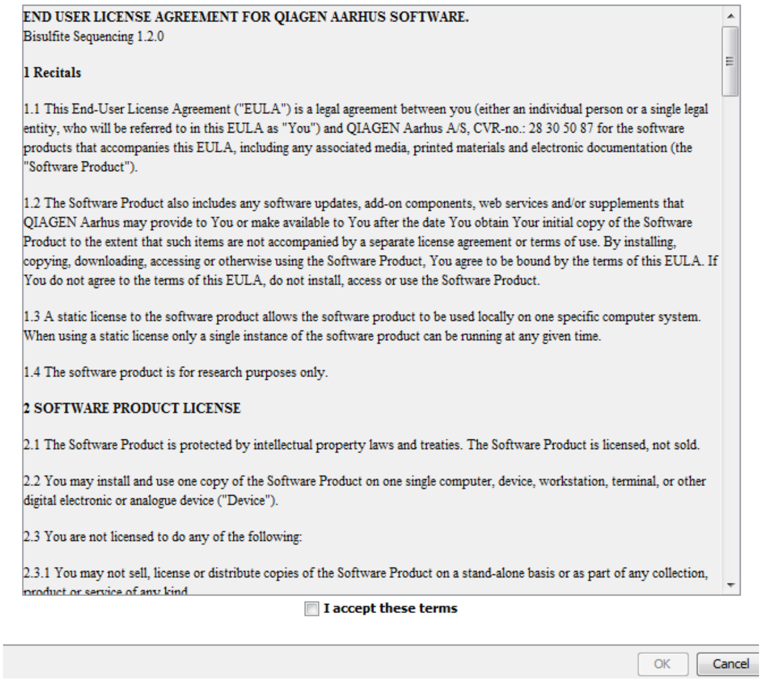
Figure 2.1: *The plugins that are available for download.*

Select TMHMM to display additional information about the plugin on the right side of the dialog.

Click **Download and Install** to add the plugin functionalities to your workbench.

Accepting the license agreement

The end user license agreement (EULA) must be read and accepted as part of the installation process. figure 2.2.



END USER LICENSE AGREEMENT FOR QIAGEN AARHUS SOFTWARE.
Bisulfite Sequencing 1.2.0

1 Recitals

1.1 This End-User License Agreement ("EULA") is a legal agreement between you (either an individual person or a single legal entity, who will be referred to in this EULA as "You") and QIAGEN Aarhus A/S, CVR-no.: 28 30 50 87 for the software products that accompanies this EULA, including any associated media, printed materials and electronic documentation (the "Software Product").

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1.4 The software product is for research purposes only.

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2.3 You are not licensed to do any of the following:

2.3.1 You may not sell, license or distribute copies of the Software Product on a stand-alone basis or as part of any collection, product or service of any kind

Figure 2.2: *The End User Licenense Agreement is presented during the installation process.*

Please read the EULA text carefully, and if you agree to it, check the box next to the text **I accept these terms**. If further information is requested from you, please fill this in before clicking on the **Finish** button.

If TMHMM is not shown on the server but you have the installer file on your computer (for example if you have downloaded it from our website), you can install the plugin by clicking the **Install from File** button at the bottom of the dialog and specifying the plugin *.cpa file saved on your computer.

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

2.2 Uninstall

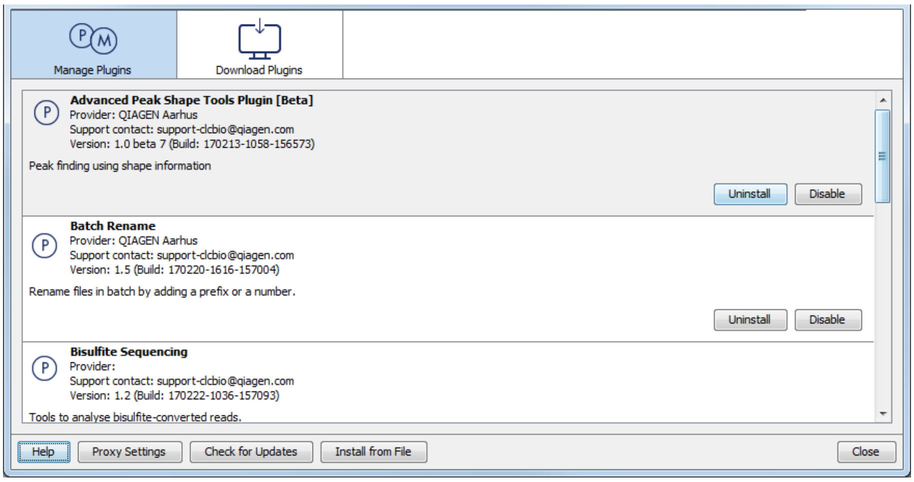
Plugins are uninstalled using the plugin manager:

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

This will open the dialog shown in figure 2.3.

The installed plugins are shown in the **Manage plugins** tab of the plugin manager. To uninstall, select TMHMM and click **Uninstall**.

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



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Provider:
Support contact: support-clcbio@qiagen.com
Version: 1.2 (Build: 170222-1036-157093)

Tools to analyse bisulfite-converted reads.

Figure 2.3: *The plugin manager with plugins installed.*

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.