# CLC **Sequence Viewer**

USER MANUAL

Manual for

# *CLC Sequence Viewer 8.0.0*

Windows, macOS and Linux

June 1, 2018

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

QIAGEN Aarhus
Silkeborgvej 2
Prismet
DK-8000 Aarhus C
Denmark

# Contents

# Part I

# Introduction

# Chapter 1

# Introduction to *CLC Sequence Viewer*

## Contents

Welcome to *CLC Sequence Viewer 8.0.0* — a software package supporting your daily bioinformatics work.

We strongly encourage you to read this user manual in order to get the best possible basis for working with the software package.

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

## 1.1 Contact information

The *CLC Sequence Viewer* is developed by:

QIAGEN Aarhus
Silkeborgvej 2
Prismet
8000 Aarhus C
Denmark

http://www.qiagenbioinformatics.com

Email: ts-bioinformatics@qiagen.com

The QIAGEN Aarhus team is continuously improving the *CLC Sequence Viewer* with our users' interests in mind. We welcome all requests and feedback from users, as well as suggestions for new features or more general improvements to the program.

Users of the freely available CLC Sequence Viewer can make use of any of our online documentation sources, including the manuals (http://www.qiagenbioinformatics.com/support/manuals/), tutorials (http://www.qiagenbioinformatics.com/support/tutorials/) and other entries in our FAQ area (http://helpdesk.clcbio.com/index.php?pg=kb).

## 1.2 Download and installation

The *CLC Sequence Viewer* is developed for Windows, macOS and Linux. The software for either platform can be downloaded from http://www.qiagenbioinformatics.com/product-downloads/.

### 1.2.1 Program download

Before you download the program you are asked to fill in the **Download** dialog.

In the dialog you must choose:

- Which operating system you use
- Whether you would like to receive information about future releases

When the download of the installer (an application which facilitates the installation of the program) is complete, follow the platform specific instructions below to complete the installation procedure.

### 1.2.2 Installation on Microsoft Windows

When you have downloaded an installer, locate the downloaded installer and double-click the icon. The default location for downloaded files is your desktop.

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.

- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
- Choose a name for the Start Menu folder used to launch *CLC Sequence Viewer* and click **Next**.
- Choose if *CLC Sequence Viewer* should be used to open CLC files and click **Next**.
- Choose where you would like to create shortcuts for launching *CLC Sequence Viewer* and click **Next**.
- Choose if you would like to associate .clc files to *CLC Sequence Viewer*. If you check this option, double-clicking a file with a "clc" extension will open the *CLC Sequence Viewer*.
- Wait for the installation process to complete, choose whether you would like to launch *CLC Sequence Viewer* right away, and click **Finish**.

When the installation is complete the program can be launched from the Start Menu or from one of the shortcuts you chose to create.

### 1.2.3 Installation on macOS

Starting the installation process is done in the following way: When you have downloaded an installer, locate the downloaded installer and double-click the icon. The default location for downloaded files is your desktop.

Launch the installer by double-clicking on the "*CLC Sequence Viewer*" icon.

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.
- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
- Choose if *CLC Sequence Viewer* should be used to open CLC files and click **Next**.
- Choose whether you would like to create desktop icon for launching *CLC Sequence Viewer* and click **Next**.
- Choose if you would like to associate .clc files to *CLC Sequence Viewer*. If you check this option, double-clicking a file with a "clc" extension will open the *CLC Sequence Viewer*.
- Wait for the installation process to complete, choose whether you would like to launch *CLC Sequence Viewer* right away, and click **Finish**.

When the installation is complete the program can be launched from your Applications folder, or from the desktop shortcut you chose to create. If you like, you can drag the application icon to the dock for easy access.

### 1.2.4 Installation on Linux with an installer

Navigate to the directory containing the installer and execute it. This can be done by running a command similar to:

```
# sh CLCSequenceViewer_7_8_64.sh
```

Installing the program is done in the following steps:

- On the welcome screen, click **Next**.
- Read and accept the License agreement and click **Next**.
- Choose where you would like to install the application and click **Next**.
  *For a system-wide installation you can choose for example /opt or /usr/local. If you do not have root privileges you can choose to install in your home directory.*
- Choose where you would like to create symbolic links to the program
  **DO NOT create symbolic links in the same location as the application.**
  Symbolic links should be installed in a location which is included in your environment PATH. For a system-wide installation you can choose for example /usr/local/bin. If you do not have root privileges you can create a 'bin' directory in your home directory and install symbolic links there. You can also choose not to create symbolic links.
- Wait for the installation process to complete and click **Finish**.

If you choose to create symbolic links in a location which is included in your PATH, the program can be executed by running the command:

```
# clcseqview7
```

Otherwise you start the application by navigating to the location where you choose to install it and running the command:

```
# ./clcseqview7
```

## 1.3 System requirements

The system requirements of *CLC Sequence Viewer* are these:

- Windows 7, Windows 8, Windows 10, Windows Server 2012, and Windows Server 2016
- OS X 10.10, 10.11 and macOS 10.12, 10.13
- Linux: RHEL 6.7 and later, SUSE Linux Enterprise Server 11 and later. The software is expected to run without problem on other recent Linux systems, but we do not guarantee this.
- 1 GB RAM required

- 2 GB RAM recommended
- 1024 x 768 display required
- 1600 x 1200 display recommended

### 1.3.1 CLC Sequence Viewer vs. Workbenches

*CLC Sequence Viewer* is a free, user friendly application offering access to basic bioinformatics analyses. It can also be used to view some of the analysis outputs of CLC commercial workbenches, with the exceptions of some more advanced data types, such as track-based data, and data stored on a *CLC Genomics Server*.

The analysis and viewing functionalities of the *CLC Sequence Viewer* are also available by running the *CLC Genomics Workbench*, version 11.0 and higher, in Viewing Mode. Using the Viewing Mode of *CLC Genomics Workbench*, you can also view all data types supported by the *CLC Genomics Workbench*, such as tracks, heat maps and PCA plots. If you have access to a *CLC Genomics Server*, you can also connect to it and view data held on the server. Viewing Mode does not require a license and can be used for free. See section **??** for further details.

Workflows and tools on commercial Workbenches can only be viewed using a commercial Workbench with a valid license installed.

CLC Workbenches, including *CLC Sequence Viewer*, are available for Windows, Mac and Linux platforms.

## 1.4 When the program is installed: Getting started

*CLC Sequence Viewer* includes an extensive **Help** function, which can be found in the **Help** menu of the program's **Menu bar** (or by pressing F1). The help topics are sorted in a table of contents and the topics can be searched.

Tutorials describing hands-on examples of how to use the individual tools and features of the *CLC Sequence Viewer* can be found at http://www.qiagenbioinformatics.com/support/tutorials/. We also recommend our **Online presentations** where a product specialist demonstrates our software. This is a very easy way to get started using the program. Read more about video tutorials and other online presentations here: http://tv.qiagenbioinformatics.com/.

### 1.4.1 Quick start

When the program opens for the first time, the background of the workspace is visible.

In the background you can see quick start shortcuts, which will help you getting started.

These can be seen in figure 1.1.

The function of the quick start shortcuts is explained here:

- **Import data.** Opens the **Import** dialog, which you let you browse for, and import data from your file system.

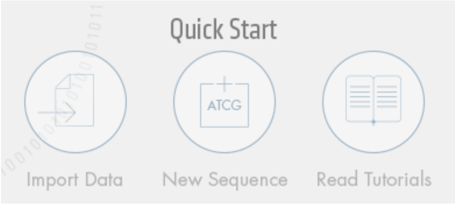


Figure 1.1: *Quick start short cuts, available in the background of the workspace.*

- **New sequence.** Opens a dialog which allows you to enter your own sequence.
- **Read tutorials.** Opens the tutorials menu with a number of tutorials. These are also available from the **Help** menu in the **Menu bar**.

It might be easier to understand the logic of the program by trying to do simple operations on existing data. Therefore *CLC Sequence Viewer* includes includes an example data set available in the **Help** menu of the program.

## 1.5 Plugins

When you install *CLC Sequence Viewer*, it has a standard set of features. However, you can upgrade and customize the program using a variety of plugins.

As the range of plugins is continuously updated and expanded, they will not be listed here. Instead we refer to http://www.qiagenbioinformatics.com/plugins/ for a full list of plugins with descriptions of their functionalities.

**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.

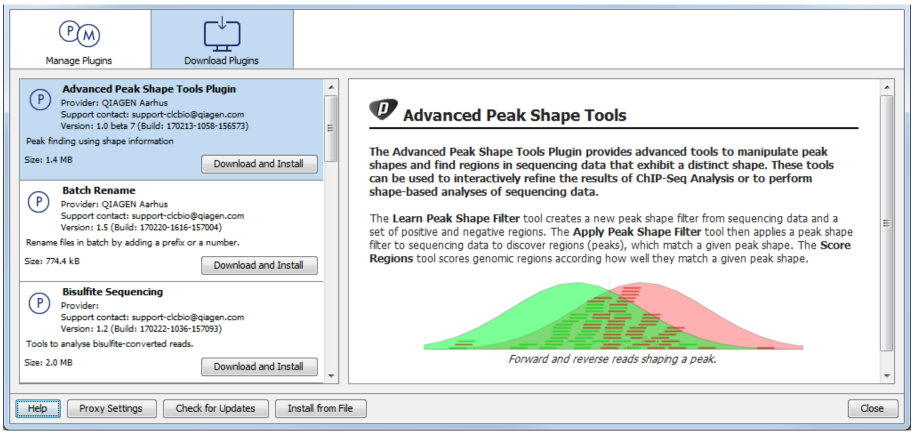
### 1.5.1 Install

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 1.2).

Select the plugin of interest 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**

Part of the installation involves checking and accepting the end user license agreement (EULA) as seen in figure 1.3.



**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

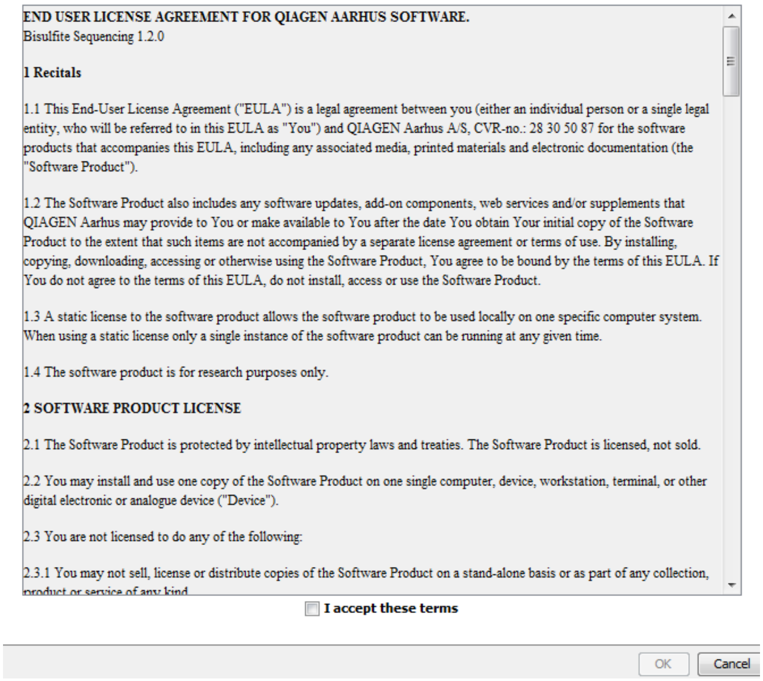
**Advanced Peak Shape Tools**

**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 1.2: *The plugins that are available for download.*



**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").

1.2 The Software Product also includes any software updates, add-on components, web services and/or supplements that QIAGEN Aarhus may provide to You or make available to You after the date You obtain Your initial copy of the Software Product to the extent that such items are not accompanied by a separate license agreement or terms of use. By installing, copying, downloading, accessing or otherwise using the Software Product, You agree to be bound by the terms of this EULA. If You do not agree to the terms of this EULA, do not install, access or use the Software Product.

1.3 A static license to the software product allows the software product to be used locally on one specific computer system. When using a static license only a single instance of the software product can be running at any given time.

1.4 The software product is for research purposes only.

**2 SOFTWARE PRODUCT LICENSE**

2.1 The Software Product is protected by intellectual property laws and treaties. The Software Product is licensed, not sold.

2.2 You may install and use one copy of the Software Product on one single computer, device, workstation, terminal, or other digital electronic or analogue device ("Device").

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

☐ **I accept these terms**

Figure 1.3: *Read the license agreement carefully.*

Please read the EULA text carefully before clicking in the box next to the text **I accept these terms** to accept. If requested, fill in your personal information before clicking **Finish**.

If the plugin 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.

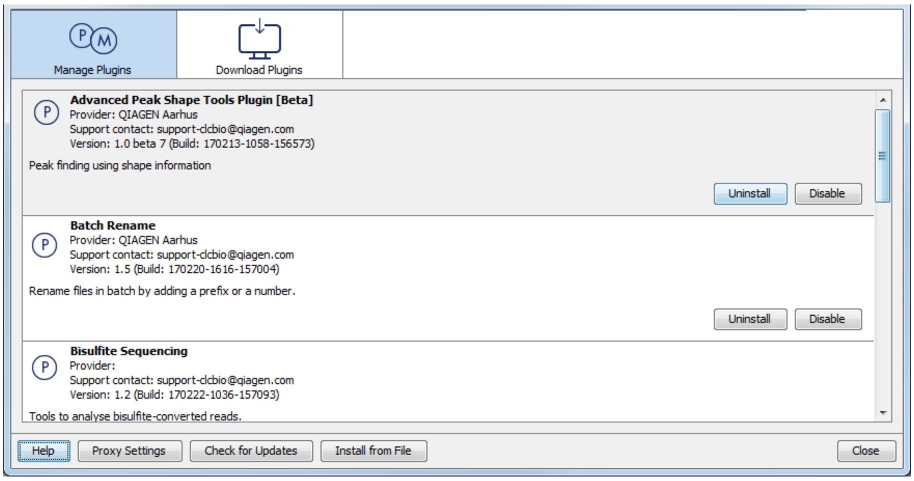
When you close the dialog, you will be asked whether you wish to restart the workbench. The plugin will not be ready for use until you have restarted.

### 1.5.2 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 1.4.



**Advanced Peak Shape Tools Plugin [Beta]**
Provider: QIAGEN Aarhus
Support contact: support-clcbio@qiagen.com
Version: 1.0 beta 7 (Build: 170213-1058-156573)

Peak finding using shape information

**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.

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

Tools to analyse bisulfite-converted reads.

Figure 1.4: *The plugin manager with plugins installed.*

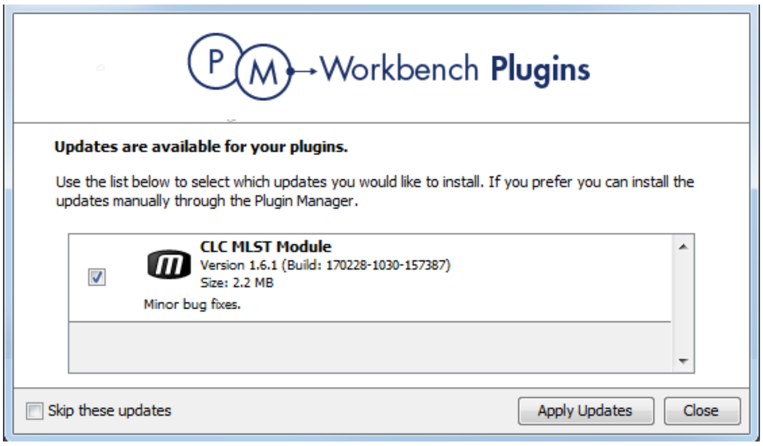
The installed plugins are shown in the **Manage plugins** tab of the plugin manager. To uninstall, select the plugin in the list and click **Uninstall**.

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.

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.

### 1.5.3 Updating plugins

If a new version of a plugin is available, you will get a notification during start-up as shown in figure 1.5.



**Updates are available for your plugins.**

Use the list below to select which updates you would like to install. If you prefer you can install the updates manually through the Plugin Manager.

☑ **CLC MLST Module**
Version 1.6.1 (Build: 170228-1030-157387)
Size: 2.2 MB

Minor bug fixes.

Figure 1.5: *Plugin updates.*

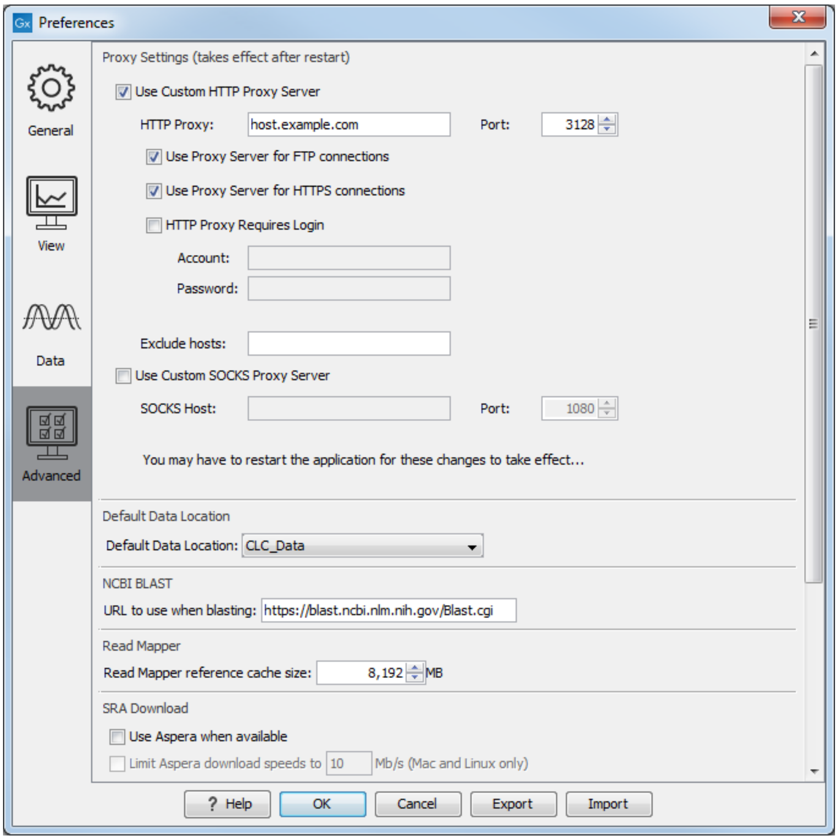
In this list, select which plugins you wish to update, and click **Install Updates**. If you press **Cancel** you will be able to install the plugins later by clicking **Check for Updates** in the Plugin manager (see figure 1.4).

## 1.6 Network configuration

If you use a proxy server to access the Internet you must configure *CLC Sequence Viewer* to use this. Otherwise you will not be able to perform any online activities.

*CLC Sequence Viewer* supports the use of an HTTP-proxy and an anonymous SOCKS-proxy.

To configure your proxy settings, open the workbench, go to **Edit | Preferences** and choose the **Advanced** tab (figure 1.6).



Proxy Settings (takes effect after restart)

☑ Use Custom HTTP Proxy Server

HTTP Proxy: host.example.com Port: 3128

☑ Use Proxy Server for FTP connections

☑ Use Proxy Server for HTTPS connections

□ HTTP Proxy Requires Login

Account:

Password:

Exclude hosts:

□ Use Custom SOCKS Proxy Server

SOCKS Host: Port: 1080

You may have to restart the application for these changes to take effect...

Default Data Location

Default Data Location: CLC_Data

NCBI BLAST

URL to use when blasting: https://blast.ncbi.nlm.nih.gov/Blast.cgi

Read Mapper

Read Mapper reference cache size: 8,192 MB

SRA Download

□ Use Aspera when available

□ Limit Aspera download speeds to 10 Mb/s (Mac and Linux only)

Figure 1.6: *Adjusting proxy preferences.*

You have the choice between an HTTP-proxy and a SOCKS-proxy. The workbench only supports the use of a SOCKS-proxy that does not require authorization.

You can select whether the proxy should be used also for FTP and HTTPS connections.

**Exclude hosts** can be used if there are some hosts that should be contacted directly and not through the proxy server. The value can be a list of hosts, each separated by a `|`, and in addition a wildcard character `*` can be used for matching. For example: `*.foo.com|localhost`.

If you have any problems with these settings you should contact your systems administrator.

## 1.7 Latest improvements

*CLC Sequence Viewer* is being constantly developed and improved. A detailed list of new features, improvements, bug fixes, and changes for the current version of *CLC Sequence Viewer* can be found at http://www.qiagenbioinformatics.com/products/latest-improvements/.

### About the workbenches

In November 2005 CLC bio released two Workbenches: *CLC Free Workbench* and *CLC Protein Workbench*. *CLC Protein Workbench* is developed from the free version, giving it the well-tested user friendliness and look & feel with a range of more advanced analyses.

In March 2006, *CLC DNA Workbench* (formerly *CLC Gene Workbench*) and *CLC Main Workbench* were added to the product portfolio of CLC bio. Like *CLC Protein Workbench*, *CLC DNA Workbench* builds on *CLC Free Workbench*. It shares some of the advanced product features of *CLC Protein Workbench*, and has additional advanced features. *CLC Main Workbench* holds all basic and advanced features of the *CLC Workbenches*.

In June 2007, *CLC RNA Workbench* was released as a sister product of *CLC Protein Workbench* and *CLC DNA Workbench*. *CLC Main Workbench* now also includes all the features of *CLC RNA Workbench*.

In March 2008, the *CLC Free Workbench* changed name to *CLC Sequence Viewer*.

In June 2008, the first version of the *CLC Genomics Workbench* was released due to an extraordinary demand for software capable of handling sequencing data from all new high-throughput sequencing platforms such as Roche-454, Illumina and SOLiD in addition to Sanger reads and hybrid data.

In December 2006, CLC bio released a *Software Developer Kit* which makes it possible for anybody with a knowledge of programming in Java to develop plugins. The plugins are fully integrated with the CLC Workbenches and the Viewer and provide an easy way to customize and extend their functionalities.

In April 2012, *CLC Protein Workbench*, *CLC DNA Workbench* and *CLC RNA Workbench* were discontinued. All customers with a valid license for any of these products were offered an upgrade to the *CLC Main Workbench*.

In February 2014, CLC bio expanded the product repertoire with the release of *CLC Drug Discovery Workbench*, a product that enables studies of protein-ligand interactions for drug discovery.

In April 2014, CLC bio released the CLC Cancer Research Workbench, a product that containing streamlined data analysis workflows with integrated trimming and quality control tailored to meet the requirements of clinicians and researchers working within the cancer field.

In April 2015, the CLC Cancer Research Workbench was renamed to Biomedical Genomics Workbench to reflect the inclusion of tools addressing the requirements of clinicians and researchers working within the hereditary disease field in addition to the tools designed for those working within the cancer field.

# Part II

# Core Functionalities

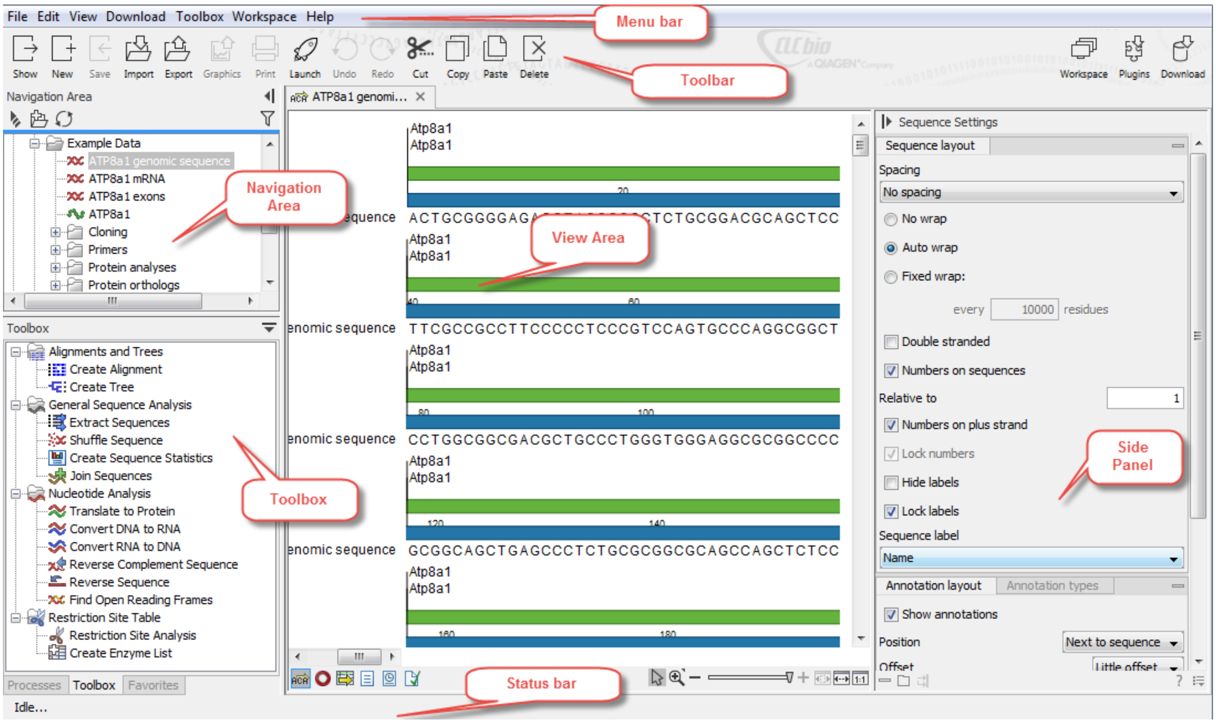
# Chapter 2

# User interface

## Contents

This chapter provides an overview of the different areas in the user interface of *CLC Sequence Viewer*. As can be seen from figure 2.1 this includes:

- a **Navigation Area** where files are sorted;
- a **Toolbox** that can be opened as such, or as a Processes or a Favorites tab;
- a **View Area** with one or more tabs open;
- a **Side Panel** where it is possible to change the settings for the currently opened View;
- a **Menu Bar** to access various function, and a **Toolbar** that highlights the most common actions;
- a **Status Bar** at the bottom of the screen that indicates the status of the workbench (processing a job, or idle) and additional information that are View-dependant.



Sequence Settings

Sequence layout

Spacing: No spacing

○ No wrap

● Auto wrap

○ Fixed wrap: every 10000 residues

□ Double stranded

☑ Numbers on sequences

Relative to 1

☑ Numbers on plus strand

☑ Lock numbers

□ Hide labels

☑ Lock labels

Sequence label: Name

Annotation layout | Annotation types

☑ Show annotations

Position: Next to sequence

Offset: Little offset

Figure 2.1: *The user interface.*

## 2.1 Navigation Area

The **Navigation Area** (see figure 2.2) is used for organizing and navigating data. Its behavior is similar to the way files and folders are usually displayed on your computer.

To provide more space for viewing data, you can hide **Navigation Area** and the **Toolbox** by clicking the hide icon ( ◀| ).

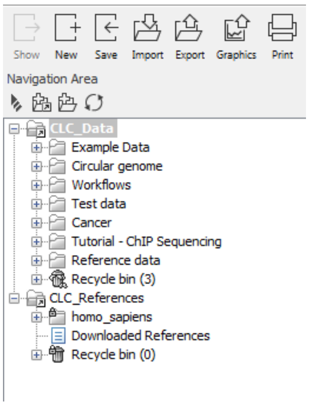


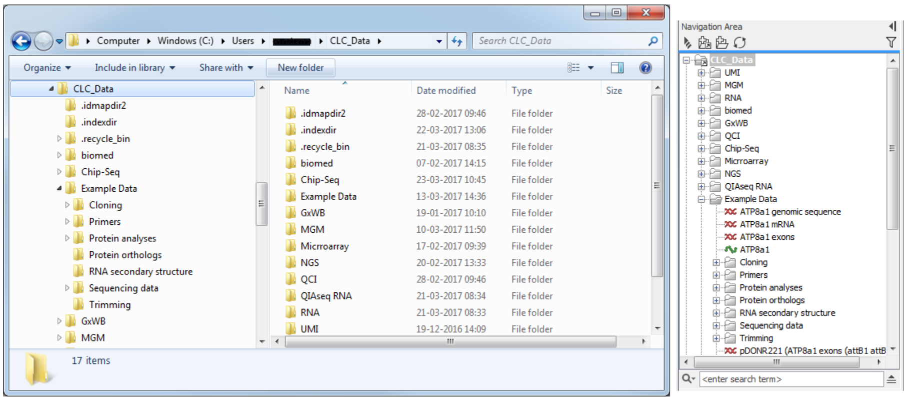
Figure 2.2: *The Navigation Area.*

## 2.1.1 Data structure

The data in the **Navigation Area** is organized into a number of **Locations**. When the *CLC Sequence Viewer* is started for the first time, there is one location called *CLC_Data* (unless your computer administrator has configured the installation otherwise).

A location represents a folder on the computer: The data shown under a location in the **Navigation Area** is stored on the computer in the folder which the location points to.

This is explained visually in figure 2.3. The full path to the system folder can be located by mousing over the data location as shown in figure 2.4.

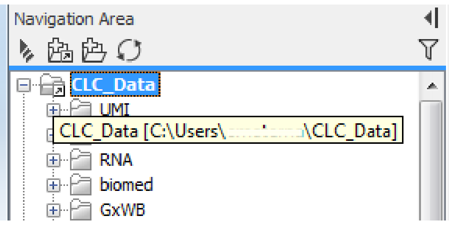


[redacted]

| Name | Date modified | Type | Size |
|---|---|---|---|
| .idmapdir2 | 28-02-2017 09:46 | File folder | |
| .indexdir | 22-03-2017 13:06 | File folder | |
| .recycle_bin | 21-03-2017 08:35 | File folder | |
| biomed | 07-02-2017 14:15 | File folder | |
| Chip-Seq | 23-03-2017 10:45 | File folder | |
| Example Data | 13-03-2017 14:36 | File folder | |
| GxWB | 19-01-2017 10:10 | File folder | |
| MGM | 10-03-2017 11:50 | File folder | |
| Micrroarray | 17-02-2017 09:39 | File folder | |
| NGS | 20-02-2017 13:33 | File folder | |
| QCI | 28-02-2017 09:46 | File folder | |
| QIAseq RNA | 21-03-2017 08:34 | File folder | |
| RNA | 21-03-2017 08:33 | File folder | |
| UMI | 19-12-2016 14:09 | File folder | |

17 items

Figure 2.3: *In this example the location called "CLC_Data" points to the folder at C:\Users\<username>\CLC_Data.*



CLC_Data [C:\Users\ \CLC_Data]

Figure 2.4: *Mousing over the location called 'CLC_Data' shows the full path to the system folder, which in this case is C:\Users\<username>\CLC_Data.*

### Opening data

The elements in the **Navigation Area** are opened by:

**Double-clicking on the element**

or **Clicking once on the element | Show (⇥) in the Toolbar**

or **Clicking once on the element | Right-click on the element | Show (⇥)**

or **Clicking once on the element | Right-click on the element | Show (the one without an icon) | Select the desired way to view the element from the menu that appears when mousing over "Show"**

This will open a view in the **View Area**, which is described in section 2.2.

#### Adding data

Data can be added to the **Navigation Area** in a number of ways. Files can be imported from the file system (see chapter 5). Furthermore, an element can be added by dragging it into the **Navigation Area**. This could be views that are open, elements on lists, e.g. search hits or sequence lists, and files located on your computer.

If a file or another element is dropped on a folder, it is placed at the bottom of the folder. If it is dropped on another element, it will be placed just below that element.

If the element already exists in the **Navigation Area** a copy will be created with the name extension "-1", "-2" etc. if more than one copy exist.

### 2.1.2 Create new folders

In order to organize your files, they can be placed in folders. Creating a new folder can be done in two ways:

**right-click an element in the Navigation Area | New | Folder (📂)**

or **File | New | Folder (📂)**

If a folder is selected in the **Navigation Area** when adding a new folder, the new folder is added at the bottom of this folder. If an element is selected, the new folder is added right above that element.

You can move the folder manually by selecting it and dragging it to the desired destination.

### 2.1.3 Sorting folders

You can sort the elements in a folder alphabetically:

**right-click the folder | Sort Folder**

On Windows, subfolders will be placed at the top of the folder, and the rest of the elements will be listed below in alphabetical order. On Mac, both subfolders and other elements are listed together in alphabetical order.

### 2.1.4 Multiselecting elements

Multiselecting elements means that you select more than one element at the same time. This can be done in the following ways:

- Holding down the <Ctrl> key (⌘ on Mac) while clicking on multiple elements selects the elements that have been clicked.
- Selecting one element, and selecting another element while holding down the <Shift> key selects all the elements listed between the two locations (the two end locations included).
- Selecting one element, and moving the curser with the arrow-keys while holding down the <Shift> key, enables you to increase the number of elements selected.

### 2.1.5 Moving and copying elements

Elements can be moved and copied in several ways:

- Using **Copy** (⧉), **Cut** (✂) and **Paste** (🗋) from the **Edit** menu.
- Using Ctrl + C (⌘ + C on Mac), Ctrl + X (⌘ + X on Mac) and Ctrl + V (⌘ + V on Mac).
- Using **Copy** (⧉), **Cut** (✂) and **Paste** (🗋) in the **Toolbar**.
- Using drag and drop to move elements.
- Using drag and drop while pressing Ctrl / Command to copy elements.

In the following, all of these possibilities for moving and copying elements are described in further detail.

#### Copy, cut and paste functions

Copies of elements and folders can be made with the copy/paste function which can be applied in a number of ways:

**select the files to copy | right-click one of the selected files | Copy (⧉) | right-click the location to insert files into | Paste (🗋)**

or **select the files to copy | Ctrl + C (⌘ + C on Mac) | select where to insert files | Ctrl + P (⌘ + P on Mac)**

or **select the files to copy | Edit in the Menu Bar | Copy (⧉) | select where to insert files | Edit in the Menu Bar | Paste (🗋)**

If there is already an element of that name, the pasted element will be renamed by appending a number at the end of the name.

Elements can also be moved instead of copied. This is done with the cut/paste function:

**select the files to cut | right-click one of the selected files | Cut (✂) | right-click the location to insert files into | Paste (🗋)**

or **select the files to cut | Ctrl + X (⌘ + X on Mac) | select where to insert files | Ctrl + V (⌘ + V on Mac)**

When you have cut the element, it is "grayed out" until you activate the paste function. If you change your mind, you can revert the cut command by copying another element.

Note that if you move data between locations, the original data is kept. This means that you are essentially doing a copy instead of a move operation.

### Move using drag and drop

Using drag and drop in the **Navigation Area**, as well as in general, is a four-step process:

> **click the element | click on the element again, and hold left mouse button | drag the element to the desired location | let go of mouse button**

This allows you to:

- Move elements between different folders in the **Navigation Area**
- Drag from the **Navigation Area** to the **View Area**: A new view is opened in an existing **View Area** if the element is dragged from the **Navigation Area** and dropped next to the tab(s) in that **View Area**.
- Drag from the **View Area** to the **Navigation Area**: The element, e.g. a sequence, alignment, search report etc. is saved where it is dropped. If the element already exists, you are asked whether you want to save a copy. You drag from the **View Area** by dragging the tab of the desired element.

Use of drag and drop is supported throughout the program, also to open and re-arrange views (see section 2.2.6).

Note that if you move data between locations, the original data is kept. This means that you are essentially doing a copy instead of a move operation.

### Copy using drag and drop

To copy instead of move using drag and drop, hold the Ctrl (⌘ on Mac) key while dragging:

> **click the element | click on the element again, and hold left mouse button | drag the element to the desired location | press Ctrl (⌘ on Mac) while you let go of mouse button release the Ctrl/⌘ button**

## 2.1.6 Change element names

This section describes two ways of changing the names of sequences in the **Navigation Area**. In the first part, the sequences themselves are not changed - it's their representation that changes. The second part describes how to change the name of the element.

### Change how sequences are displayed

Sequence elements can be displayed in the **Navigation Area** with different types of information:

- Name (this is the default information to be shown).
- Accession (sequences downloaded from databases like GenBank have an accession number).
- Latin name.
- Latin name (accession).

- Common name.
- Common name (accession).

Whether sequences can be displayed with this information depends on their origin. Sequences that you have created yourself or imported might not include this information, and you will only be able to see them represented by their name. However, sequences downloaded from databases like GenBank will include this information. To change how sequences are displayed:

**right-click any element or folder in the Navigation Area | Sequence Representation | select format**

This will only affect sequence elements, and the display of other types of elements, e.g. alignments, trees and external files, will be not be changed. If a sequence does not have this information, there will be no text next to the sequence icon.

**Rename element**

Renaming a folder or an element in the **Navigation Area** can be done in two different ways:

**select the element | Edit in the Menu Bar | Rename**

or **select the element | F2**

When you can rename the element, you can see that the text is selected and you can move the cursor back and forth in the text. When the editing of the name has finished; press **Enter** or select another element in the **Navigation Area**. If you want to discard the changes instead, press the **Esc**-key.

### 2.1.7 Delete, restore and remove elements

When one deletes data from a data folder in the Workbench, it is moved to the recycle bin in that data location. Each data location has its own recycle bin. From the recycle bin, data can then be restored, or completely removed. Removal of data from the recycle bin frees disk space.

**Deleting a folder or an element from a Workbench data location** can be done in two ways:

**right-click the element | Delete (☒)**

or **select the element | press Delete key**

This will cause the element to be moved to the **Recycle Bin** (🗑) where it is kept until the recycle bin is emptied or until you choose to restore the data object to your data location.

For deleting annotations instead of folders or elements, see section 7.3.2.

**Items in a recycle bin can be restored** in two ways:

Drag the elements with the mouse into the folder where they used to be.

or **select the element | right click and choose the option Restore**.

Once restored, you can continue to work with that data.

**All contents of the recycle bin can be removed** by choosing to empty the recycle bin:

**Edit in the Menu Bar | Empty Recycle Bin (🗑)**

This deletes the data and frees up disk space.

**Note!** This cannot be undone. Data is not recoverable after it is removed by emptying the recycle bin.

### 2.1.8 Show folder elements in a table

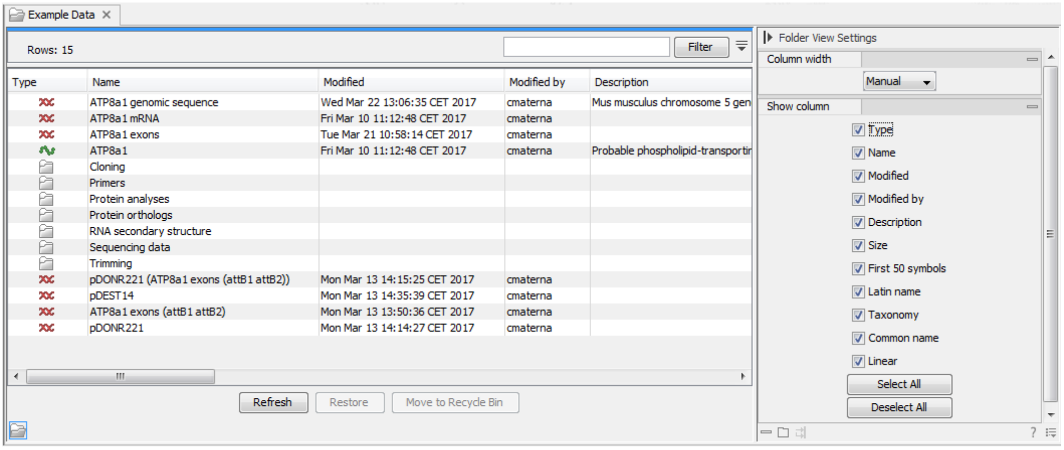
A location or a folder might contain large amounts of elements. It is possible to view their elements in the **View Area**:

> **select a folder or location** | **Show** (→) **in the Toolbar**

or

> **select a folder or location** | right click on the folder and select **Show** (→) | **Contents** (□)

An example is shown in figure 2.5.



Rows: 15

| Type | Name | Modified | Modified by | Description |
|---|---|---|---|---|
| | ATP8a1 genomic sequence | Wed Mar 22 13:06:35 CET 2017 | cmaterna | Mus musculus chromosome 5 gen |
| | ATP8a1 mRNA | Fri Mar 10 11:12:48 CET 2017 | cmaterna | |
| | ATP8a1 exons | Tue Mar 21 10:58:14 CET 2017 | cmaterna | |
| | ATP8a1 | Fri Mar 10 11:12:48 CET 2017 | cmaterna | Probable phospholipid-transportir |
| | Cloning | | | |
| | Primers | | | |
| | Protein analyses | | | |
| | Protein orthologs | | | |
| | RNA secondary structure | | | |
| | Sequencing data | | | |
| | Trimming | | | |
| | pDONR221 (ATP8a1 exons (attB1 attB2)) | Mon Mar 13 14:15:25 CET 2017 | cmaterna | |
| | pDEST14 | Mon Mar 13 14:35:39 CET 2017 | cmaterna | |
| | ATP8a1 exons (attB1 attB2) | Mon Mar 13 13:50:36 CET 2017 | cmaterna | |
| | pDONR221 | Mon Mar 13 14:14:27 CET 2017 | cmaterna | |

Column width: Manual

Show column

☑ Type
☑ Name
☑ Modified
☑ Modified by
☑ Description
☑ Size
☑ First 50 symbols
☑ Latin name
☑ Taxonomy
☑ Common name
☑ Linear

Figure 2.5: *Viewing the elements in a folder.*

When the elements are shown in the view, they can be sorted by clicking the heading of each of the columns. You can further refine the sorting by pressing Ctrl (⌘ on Mac) while clicking the heading of another column.

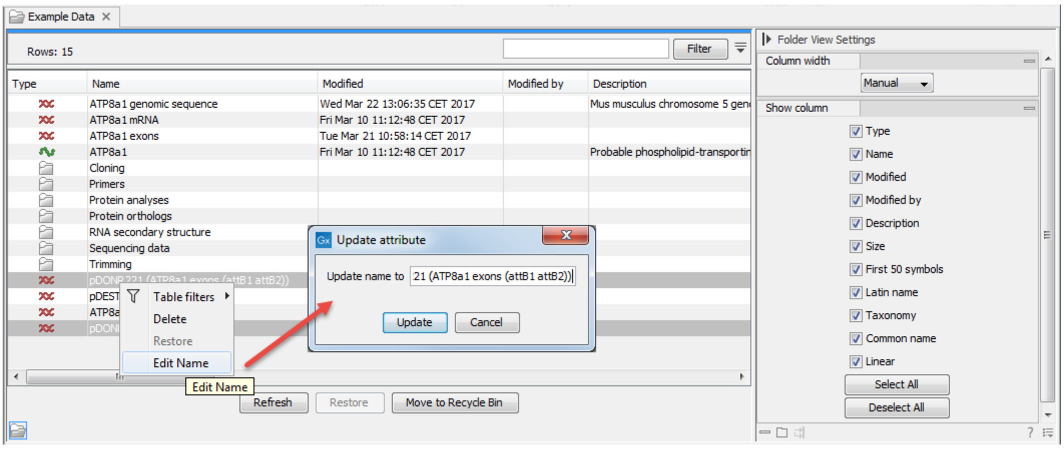
Sorting the elements in a view does not affect the ordering of the elements in the **Navigation Area**.

**Note!** The view only displays one "layer" at a time: the content of subfolders is not visible in this view. Also note that only sequences have the full span of information like organism etc.

#### Batch edit folder elements

You can select a number of elements in the table, right-click and choose **Edit** to batch edit the elements. In this way, you can change for example the description or name of several elements in one go.

In figure 2.6 you can see an example where the name of two sequence are renamed in one go. In this example, a dialog with a text field will be shown, letting you enter a new name for these two sequences.



Example Data

Rows: 15

| Type | Name | Modified | Modified by | Description |
|---|---|---|---|---|
| | ATP8a1 genomic sequence | Wed Mar 22 13:06:35 CET 2017 | | Mus musculus chromosome 5 gen |
| | ATP8a1 mRNA | Fri Mar 10 11:12:48 CET 2017 | | |
| | ATP8a1 exons | Tue Mar 21 10:58:14 CET 2017 | | |
| | ATP8a1 | Fri Mar 10 11:12:48 CET 2017 | | Probable phospholipid-transportin |
| | Cloning | | | |
| | Primers | | | |
| | Protein analyses | | | |
| | Protein orthologs | | | |
| | RNA secondary structure | | | |
| | Sequencing data | | | |
| | Trimming | | | |
| | pDONR221 (ATP8a1 exons (attB1 attB2)) | | | |
| | pDEST | | | |
| | ATP8a | | | |
| | pDON | | | |

Update attribute

Update name to 21 (ATP8a1 exons (attB1 attB2))

Folder View Settings

Column width: Manual

Show column

☑ Type
☑ Name
☑ Modified
☑ Modified by
☑ Description
☑ Size
☑ First 50 symbols
☑ Latin name
☑ Taxonomy
☑ Common name
☑ Linear

Figure 2.6: *Changing the common name of two sequences.*

**Note!** This information is directly saved and you cannot undo.

### Drag and drop folder elements

You can drag and drop objects from the folder editor to the **Navigation area**. This will create a copy of the objects at the selected destination. New elements can be included in the folder editor in the view area by dragging and dropping an element from a destination in the **Navigation Area** to the folder in the **Navigation Area** that you have open in the view area. It is not possible to drag elements directly from the **Navigation Area** to the folder editor in the View area.

## 2.2 View Area

The **View Area** is the central part of the screen, displaying your current work. The View Area may consist of one or more **Views**, represented by **tabs** at the top of the View Area. In figure 2.7, four views are displayed: three as tabs in the upper view, and one in an horizontal split view. The tab currently selected, i.e., active, is indicated by a blue bar underneath the tab (here the bottom tab open in the bottom view).

Switch tabs in View Area using the following shortcuts Ctrl + PageUp or PageDown (or ⌘ + PageUp or PageDown on Mac).

Several operations can be performed by right-click menus that can be activated from the tab, or by using the icon list at the bottom of each view.

### 2.2.1 Open view

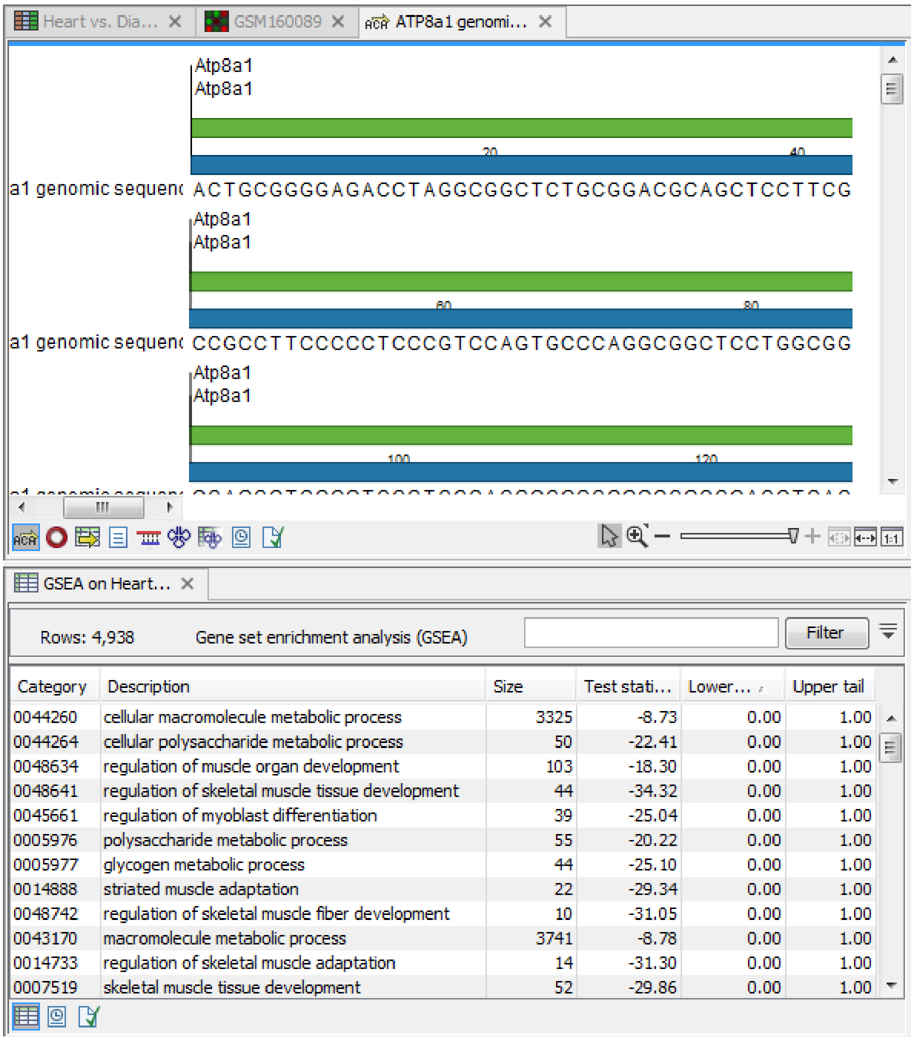
#### Elements

Opening an element can be done in a number of ways:

**double-click an element in the Navigation Area**

or **select an element in the Navigation Area | Show** or **Ctrl + O (⌘ + B on Mac)**

Opening an element while another element is already open in the View Area will show the new element in front of the other. The element that was already open can be brought to front by


Heart vs. Dia...
GSM160089
ATP8a1 genomi...
Atp8a1
Atp8a1
20
40
a1 genomic sequenc ACTGCGGGGAGACCTAGGCGGCTCTGCGGACGCAGCTCCTTCG
Atp8a1
Atp8a1
60
80
a1 genomic sequenc CCGCCTTCCCCCTCCCGTCCAGTGCCCAGGCGGCTCCTGGCGG
Atp8a1
Atp8a1
100
120
GSEA on Heart...
Filter

Rows: 4,938 Gene set enrichment analysis (GSEA)

| Category | Description | Size | Test stati... | Lower... | Upper tail |
|---|---|---|---|---|---|
| 0044260 | cellular macromolecule metabolic process | 3325 | -8.73 | 0.00 | 1.00 |
| 0044264 | cellular polysaccharide metabolic process | 50 | -22.41 | 0.00 | 1.00 |
| 0048634 | regulation of muscle organ development | 103 | -18.30 | 0.00 | 1.00 |
| 0048641 | regulation of skeletal muscle tissue development | 44 | -34.32 | 0.00 | 1.00 |
| 0045661 | regulation of myoblast differentiation | 39 | -25.04 | 0.00 | 1.00 |
| 0005976 | polysaccharide metabolic process | 55 | -20.22 | 0.00 | 1.00 |
| 0005977 | glycogen metabolic process | 44 | -25.10 | 0.00 | 1.00 |
| 0014888 | striated muscle adaptation | 22 | -29.34 | 0.00 | 1.00 |
| 0048742 | regulation of skeletal muscle fiber development | 10 | -31.05 | 0.00 | 1.00 |
| 0043170 | macromolecule metabolic process | 3741 | -8.78 | 0.00 | 1.00 |
| 0014733 | regulation of skeletal muscle adaptation | 14 | -31.30 | 0.00 | 1.00 |
| 0007519 | skeletal muscle tissue development | 52 | -29.86 | 0.00 | 1.00 |

Figure 2.7: *A View Area can enclose several views, each view indicated with a tab.*

clicking its tab.

**Views**

Each element can be shown in different ways. A sequence, for example, can be shown as linear, circular, text, etc.

For example, to see a linear sequence in a circular view, open the sequence as linear in the View Area and

**Click Show As Circular (○) at the lower left part of the view**

The buttons used for switching views are shown in figure 2.8. They are element-dependent, meaning that different elements may have different buttons available. You can switch from one to the other sequentially by clicking Ctrl + Shift + PageUp or Ctrl + Shift + PageDown.

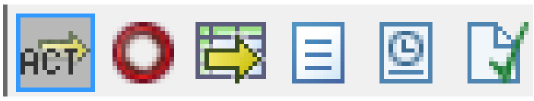


Figure 2.8: *The buttons shown at the bottom of a view of a nucleotide sequence. You can click the buttons to change the view to a circular view or a history view.*

### Split views

If the sequence is already open in a linear view (ACT), and you wish to see both a circular and a linear view, you can split the views very easily:

> **Press Ctrl (⌘ on Mac) while you | Click Show As Circular (○) at the lower left part of the view**

This will open a split view with a linear view at the bottom and a circular view at the top (see 7.5).

You can also show a circular view of a sequence without opening the sequence first:

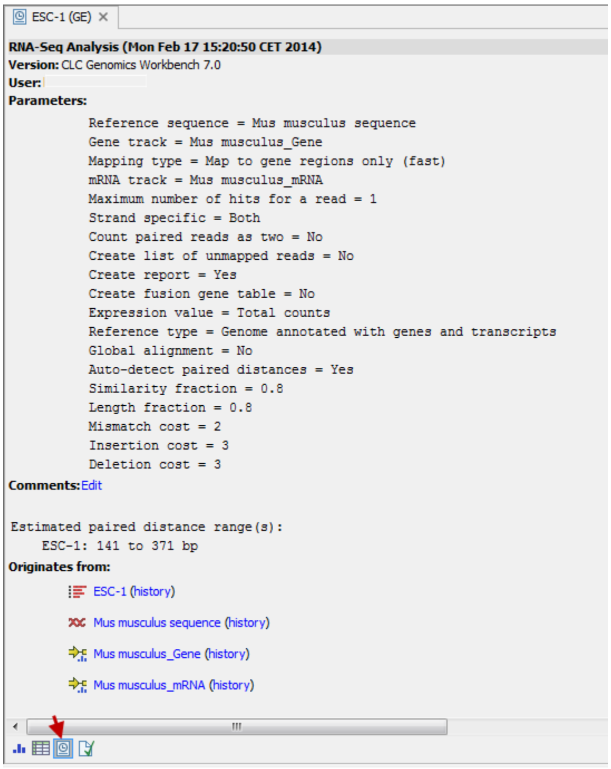
> **Select the sequence in the Navigation Area | Show (⇥) | As Circular (○)**

## 2.2.2 History and Info views

The two buttons to the right hand side of the toolbar are **Show History (◷)** and **Show Element Info (✓)**.

The History view is a textual log of all operations you make in the program. If for example you rename a sequence, align sequences, create a phylogenetic tree or translate a sequence, you can always go back and check what you have done. In this way, you are able to document and reproduce previous operations.

When an element's history is opened, the newest change is submitted in the top of the view (figure 2.9).



**RNA-Seq Analysis (Mon Feb 17 15:20:50 CET 2014)**
**Version:** CLC Genomics Workbench 7.0
**User:**
**Parameters:**

```
          Reference sequence = Mus musculus sequence
          Gene track = Mus musculus_Gene
          Mapping type = Map to gene regions only (fast)
          mRNA track = Mus musculus_mRNA
          Maximum number of hits for a read = 1
          Strand specific = Both
          Count paired reads as two = No
          Create list of unmapped reads = No
          Create report = Yes
          Create fusion gene table = No
          Expression value = Total counts
          Reference type = Genome annotated with genes and transcripts
          Global alignment = No
          Auto-detect paired distances = Yes
          Similarity fraction = 0.8
          Length fraction = 0.8
          Mismatch cost = 2
          Insertion cost = 3
          Deletion cost = 3
```

**Comments:** Edit

```
Estimated paired distance range(s):
    ESC-1: 141 to 371 bp
```

**Originates from:**

- ESC-1 (history)
- Mus musculus sequence (history)
- Mus musculus_Gene (history)
- Mus musculus_mRNA (history)

Figure 2.9: *An element's history.*

The following information is available:

- **Originates from workflow** (optional). In cases where the file was generated by a workflow, the first line will state the Name and Version number of that workflow.
- **Title**. The action that the user performed.
- **Date and time**. Date and time for the operation. The date and time are displayed according to your locale settings (see section 3.1).
- **Version**. The workbench type and version that has been used.
- **User**. The user who performed the operation. If you import some data created by another person in a CLC Workbench, that person's name will be shown.
- **Parameters**. Details about the action performed. This could be the parameters that were chosen for an analysis.
- **Comments**. By clicking **Edit** you can enter your own comments regarding this entry in the history. These comments are saved.
- **Originates from**. This information is usually shown at the bottom of an element's history. Here, you can see which elements the current element originates from. For example, if you have created an alignment of three sequences, the three sequences are shown here. Clicking the element selects it in the Navigation Area, and clicking the "history" link opens the element's own history.

When an element's info is open you can check current information about the element, and in particular the potential association of the data you are looking at with metadata. To learn more about the **Show Element Info** button, see section 7.4 and see section **??**.

### 2.2.3 Close views

When a view is closed, the **View Area** remains open as long as there is at least one open view.

A view is closed by:

**Right-click the tab** | **Close** or **Select the view** | **Ctrl + W**

By right-clicking a tab, the following close options exist (figure 2.10).

- **Close.** See above.
- **Close Other Tabs.** Closes all other tabs, in all tab areas, except the one that is selected.
- **Close Tab Area.** Closes all tabs in the tab area, but not the tabs that are in split view.
- **Close All Tabs.** Closes all tabs, in all tab areas. Leaves an empty workspace.

### 2.2.4 Save changes in a view

When a new view is created, an * in front of the name of the view in the tab indicates that the element has not been saved yet. Similarly, when changes to an element are made in a view, an * is added before the element name on the tab and the element name is shown in *bold and italic* in the Navigation Area (figure 2.11).

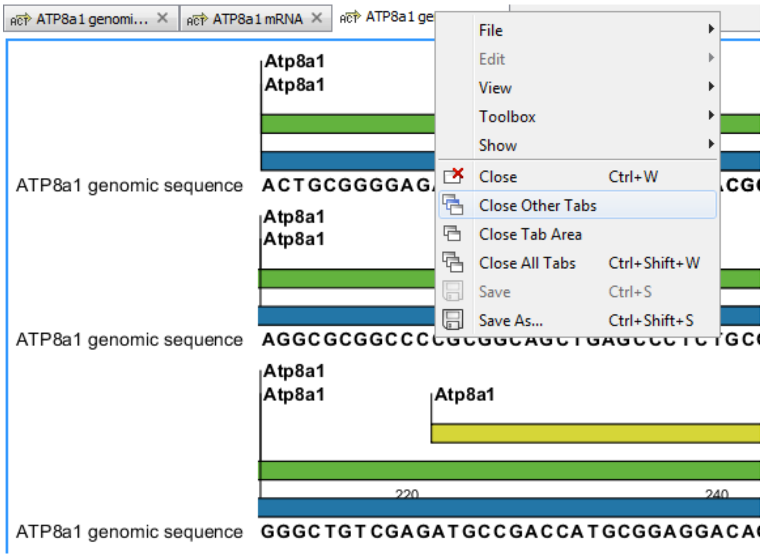


Figure 2.10: *By right-clicking a tab, several close options are available.*

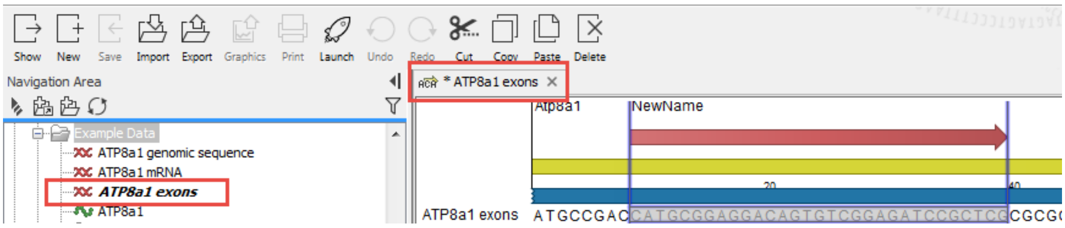


Figure 2.11: *An * on a tab name always indicates that the view is unsaved. In this case, an existing element was edited but not saved yet, so the element's name is also highlighted in bold and italic in the Navigation Area.*

The **Save** function may be activated in two ways: Select the tab of the view you want to save and

**Save (⇐) or Ctrl + S (⌘ + S on Mac)**

If you close a tab of a view containing an element that was edited, you will be asked if you want to save.

When saving an element from a new view that has not been opened from the Navigation Area, a save dialog appears (figure 2.12). In this dialog, you can name the element and select the folder in which you want to save the element.

### 2.2.5 Undo/Redo

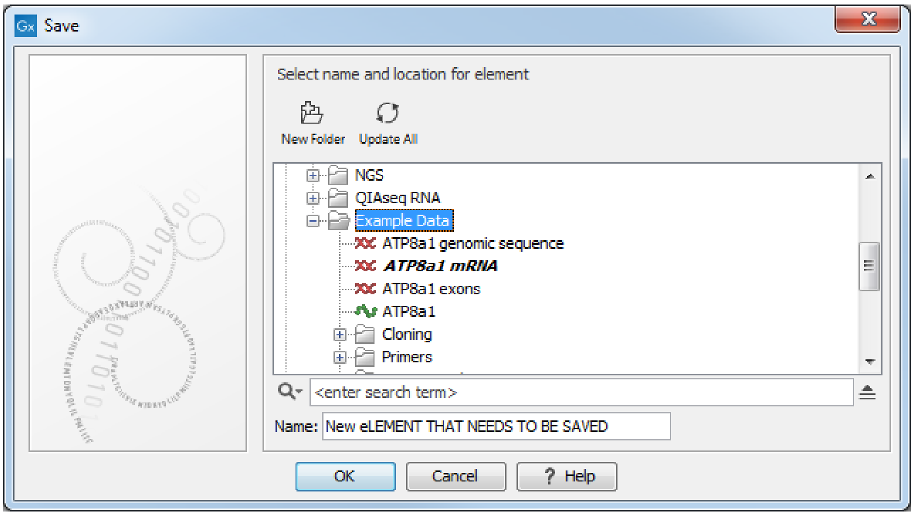
If you make a change to an element in a view, e.g. remove an annotation in a sequence or modify a tree, you can undo the action. In general, **Undo** applies to all changes you can make when right-clicking in a view. **Undo** is done by:

**Click undo (↶) in the Toolbar** or **Ctrl + Z**

If you want to undo several actions, just repeat the steps above.

To reverse the undo action:

**Click the redo icon in the Toolbar** or **Ctrl + Y**



Select name and location for element

Name: New eLEMENT THAT NEEDS TO BE SAVED

Figure 2.12: *Save dialog. The new element has been name "New element that needs to be saved" and will be saved in the "Example Data" folder.*

**Note!** Actions in the Navigation Area, e.g., renaming and moving elements, cannot be undone. However, you can restore deleted elements (see section 2.1.7).

You can set the number of possible undo actions in the Preferences dialog (see section 3).

### 2.2.6 Arrange views in View Area

To provide more space for viewing data, you can hide Navigation Area and Toolbox by clicking the hide icon (◀|) at the top of the Navigation Area. You can also hide the Side Panel using the same icon at the top of the Side Panel.

Views are arranged in the **View Area** by their tabs. The order of the views can be changed using drag and drop.

If a tab is dragged into a view, the area where the tab will be placed is highlighted blue (see figure **??**). The blue area can be a tab bar in another view, or the bottom of an existing view. In that case, the tab will be moved to a new split view.

You can also split a View Area horizontally or vertically using the menus.

Splitting horizontally may be done this way:

**right-click a tab of the view | View | Split Horizontally (⊟)**

This action opens the chosen view below the existing view. When the split is made vertically, the new view opens to the right of the existing view (see figure 2.13).

Splitting the View Area can be undone by dragging the tab of the bottom view to the tab of the top view, or by using the **Maximize/Restore View** function.

Select the view you want to maximize, and click

**View | Maximize/restore View (▭)** or **Ctrl + M**

or **right-click the tab | View | Maximize/restore View (▭)**

or **double-click the tab of view**

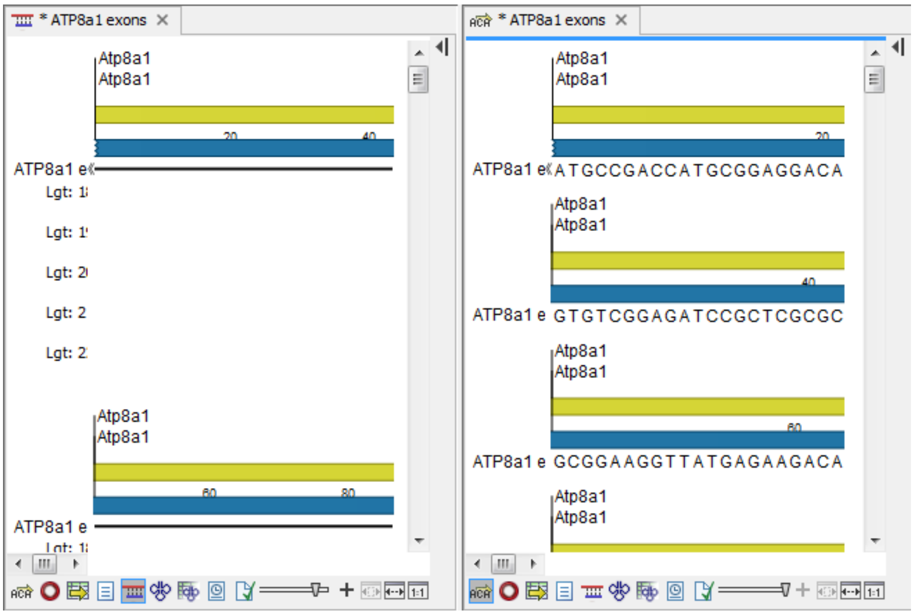


Figure 2.13: *A vertical split screen.*

The following restores the size of the view:

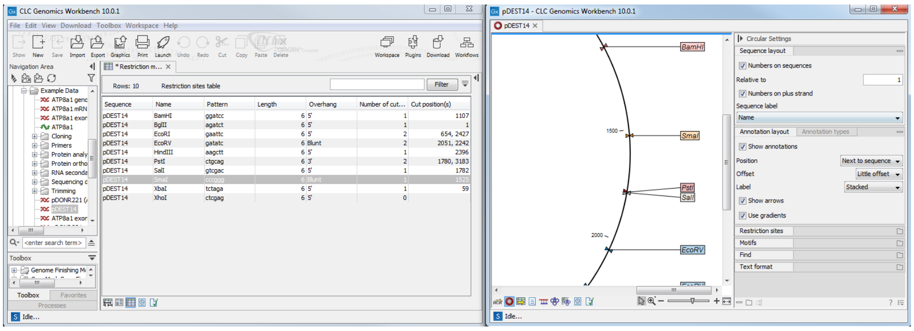
**View** | **Maximize/restore View** (▭) or **Ctrl + M**

or **double-click title of view**

### 2.2.7 Moving a view to a different screen

Using multiple screens can be a great benefit when analyzing data with the *CLC Sequence Viewer*. You can move a view to another screen by dragging the tab of the view and dropping it outside the workbench window. Alternatively, you can right-click in the view area or on the tab itself and select **View | Move to New Window** from the context menu.

An example is shown in figure 2.14, where the main Workbench window shows a table of open reading frames, and the screen to the right is used to display the sequence and annotations.


CLC Genomics Workbench 10.0.1
pDEST14 - CLC Genomics Workbench 10.0.1
* Restriction m...
BamHI
SmaI
PstI
SalI
EcoRV
1500
2000

Rows: 10 Restriction sites table

| Sequence | Name | Pattern | Length | Overhang | Number of cut... | Cut position(s) |
|---|---|---|---|---|---|---|
| pDEST14 | BamHI | ggatcc | 6 | 5' | 1 | 1107 |
| pDEST14 | BglII | agatct | 6 | 5' | 1 | 1 |
| pDEST14 | EcoRI | gaattc | 6 | 5' | 2 | 654, 2427 |
| pDEST14 | EcoRV | gatatc | 6 | Blunt | 2 | 2051, 2242 |
| pDEST14 | HindIII | aagctt | 6 | 5' | 1 | 2396 |
| pDEST14 | PstI | ctgcag | 6 | 3' | 2 | 1780, 3183 |
| pDEST14 | SalI | gtcgac | 6 | 5' | 1 | 1782 |
| pDEST14 | SmaI | cccggg | 6 | Blunt | 1 | 1525 |
| pDEST14 | XbaI | tctaga | 6 | 5' | 1 | 59 |
| pDEST14 | XhoI | ctcgag | 6 | 5' | 0 | |

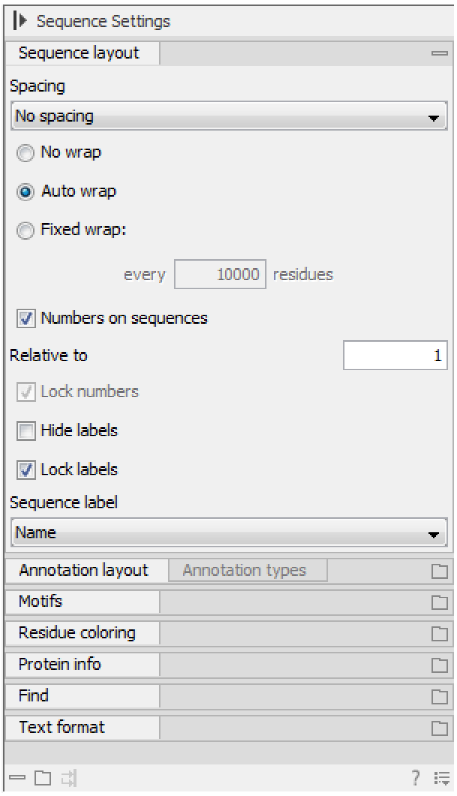
Figure 2.14: *Showing the table on one screen while the sequence is displayed on another screen. Clicking the table of open reading frames causes the view on the other screen to follow the selection.*

You can make more detached windows, by dropping tabs outside the open workbench windows, or you can drag more tabs to a detached window. To get a tab back to the main workbench window, just drag the detached tab back, and drop it next to the other tabs in the top of the view area. **Note:** You should not drag the detached window header, just the tab itself.

### 2.2.8 Side Panel

The **Side Panel** allows you to change the way the content of a view is displayed. The options in the Side Panel depend on the kind of data in the view, and they are described in the relevant sections about sequences, alignments, trees etc.

Figure 2.15 shows the default Side Panel for a protein sequence. It is organized into **palettes**.



Sequence Settings

Sequence layout

Spacing: No spacing

○ No wrap
● Auto wrap
○ Fixed wrap: every 10000 residues

☑ Numbers on sequences

Relative to: 1

☑ Lock numbers
□ Hide labels
☑ Lock labels

Sequence label: Name

Figure 2.15: *The default view of the Side Panel when opening a protein sequence.*

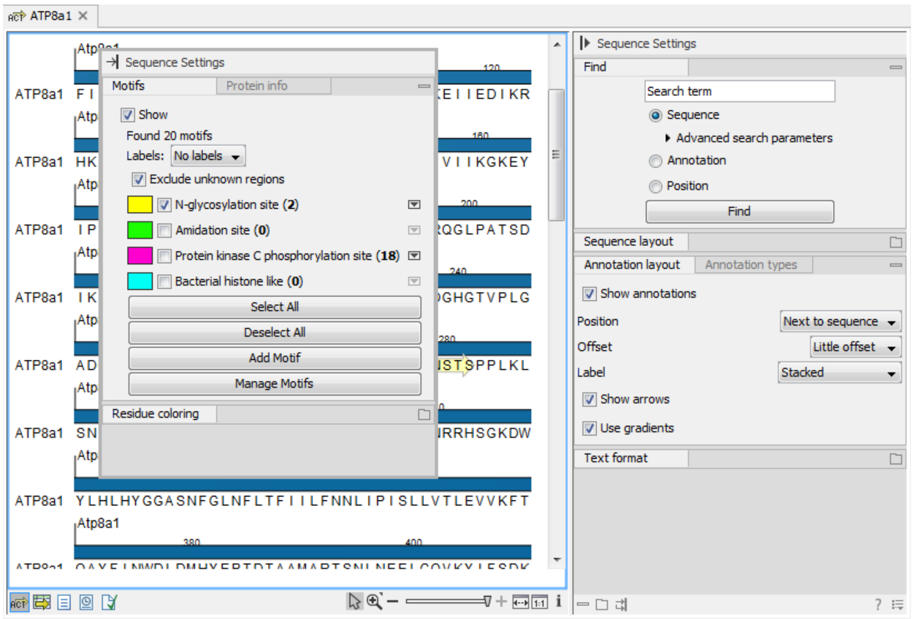
In this example, there is one palette for Sequence layout, one for Annotation Layout etc. These palettes can be re-organized by dragging the palette name with the mouse and dropping it where you want it to be. They can either be situated next to each other, so that you can switch between them, or they can be listed on top of each other, so that expanding one of the palettes will push the palettes below further down.

In addition, they can be moved away from the Side Panel and placed anywhere on the screen as shown in figure 2.16.

In this example, the Motifs palette has been placed on top of the sequence view together with the the Residue coloring palette. In the Side Panel to the right, the Find palette has been put on top.

In order to make all palettes dock in the Side Panel again, click the **Dock Side Panel** icon (⇥).

You can completely hide the Side Panel by clicking the **Hide Side Panel** icon (|▶).



ATP8a1

Sequence Settings

Motifs | Protein info

☑ Show

Found 20 motifs

Labels: No labels

☑ Exclude unknown regions

🟨 ☑ N-glycosylation site (2)

🟩 ☐ Amidation site (0)

🟪 ☐ Protein kinase C phosphorylation site (18)

🟦 ☐ Bacterial histone like (0)

Select All | Deselect All | Add Motif | Manage Motifs

Residue coloring

Sequence Settings

Find

Search term

● Sequence

Advanced search parameters

○ Annotation

○ Position

Find

Sequence layout

Annotation layout | Annotation types

☑ Show annotations

Position: Next to sequence

Offset: Little offset

Label: Stacked

☑ Show arrows

☑ Use gradients

Text format

Figure 2.16: *Palettes can be organized in the Side Panel as you like or placed anywhere on the screen.*

At the bottom of the Side Panel (see figure 2.17) there are a number of icons used to:

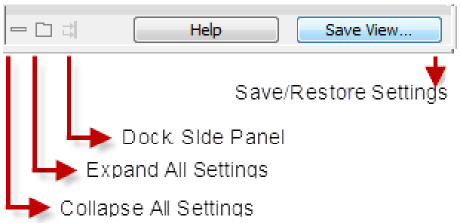


Figure 2.17: *Functionalities found at the bottom of the Side Panel.*

- Collapse all settings (▭).
- Expand all settings (□).
- Dock all palettes (⇥)
- Get **Help** for the particular view and settings
- Save the settings of the Side Panel or apply already saved settings. Changes made to the Side Panel, including the organization of palettes, will not be saved when you save the view. Learn how to save Side Panel settings in section 3.5.

## 2.3 Zoom and selection in View Area

All views except tabular and text views support zooming. Figure 2.18 shows the zoom tools, located at the bottom right corner of the view.

The zoom tools consist of some shortcuts for zooming to fit the width of the view (⟷), zoom to 100 % to see details (1:1), zoom to a selection (⬚), a zoom slider, and two mouse mode buttons (↖) (🔍).

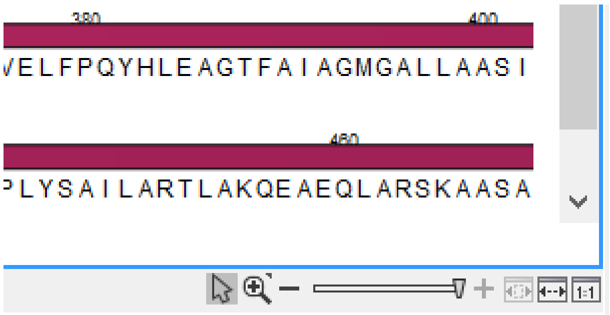


Figure 2.18: *The zoom tools are located at the bottom right corner of the view.*

The slider reflects the current zoom level and can be used to quickly adjust this. For more fine-grained control of the zoom level, move the mouse upwards while sliding.

The sections below describes how to use these tools as well as other ways of zooming and navigating data.

### 2.3.1 Zoom in

There are six ways of **zooming in**:

**Click Zoom in mode (🔍) in the zoom tools (or press Ctrl+2) | click the location in. the view that you want to zoom in on**

or **Click Zoom in mode (🔍) in the zoom tools | click-and-drag a box around a part of the view | the view now zooms in on the part you selected**

or **Press '+' on your keyboard**

or **Move the zoom slider located in the zoom tools**

or **Click the plus icon in the zoom tools**

The last option for zooming in is only available if you have a mouse with a scroll wheel:

or **Press and hold Ctrl (⌘ on Mac) | Move the scroll wheel on your mouse forward**

**Note!** You might have to click in the view before you can use the keyboard or the scroll wheel to zoom.

If you press the **Shift** button on your keyboard while in zoom mode, the zoom function is reversed.

If you want to zoom in to 100 % to see the data at base level, click the **Zoom to base level** (1:1) icon.

### 2.3.2 Zoom out

It is possible to zoom out in different ways:

**Click Zoom out mode (🔍) in the zoom tools (or press Ctrl+3) | click in the view**

or **Press '-' on your keyboard**

or **Move the zoom slider located in the zoom tools**

or **Click the minus icon in the zoom tools**

The last option for zooming out is only available if you have a mouse with a scroll wheel:

or **Press and hold Ctrl (⌘ on Mac) | Move the scroll wheel on your mouse backwards**

**Note!** You might have to click in the view before you can use the keyboard or the scroll wheel to zoom.

If you want to zoom out to see all the data, click the **Zoom to Fit** () icon.

If you press **Shift** while clicking in a **View**, the zoom function is reversed. Hence, clicking on a sequence in this way while the **Zoom out** mode toolbar item is selected, zooms in instead of zooming out.

### 2.3.3 Selecting, panning and zooming

In the zoom tools, you can control which mouse mode to use. The default is **Selection mode** () which is used for selecting data in a view. Next to the selection mode, you can select the **Zoom in mode** as described in section 2.3.1. If you press and hold this button, two other modes become available as shown in figure 2.19:

- **Panning** () is used for dragging the view with the mouse as a way of scrolling.
- **Zoom out** () is used to change the mouse mode so that whenever you click the view, it zooms out.

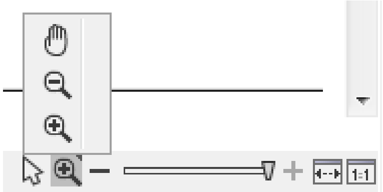


Figure 2.19: *Additional mouse modes can be found in the zoom tools.*

If you hold the mouse over the selection and zoom tools, tooltips will appear that provide further information about how to use the tools.

The mouse modes only apply when the mouse is within the view where they are selected.

The **Selection mode** can also be invoked with the keyboard shortcut Ctrl+1, while the **Panning mode** can be invoked with Ctrl+4.

For some views, if you have made a selection, there is a **Zoom to Selection** () button, which allows you to zoom and scroll directly to fit the view to the selection.

## 2.4 Toolbox and Status Bar

The **Toolbox** is placed in the left side of the user interface of *CLC Sequence Viewer* below the Navigation Area. It can be seen as a **Processes tab**, a **Toolbox tab** and a **Favorites tab**.

The Toolbox can be hidden, so that the Navigation Area is enlarged:

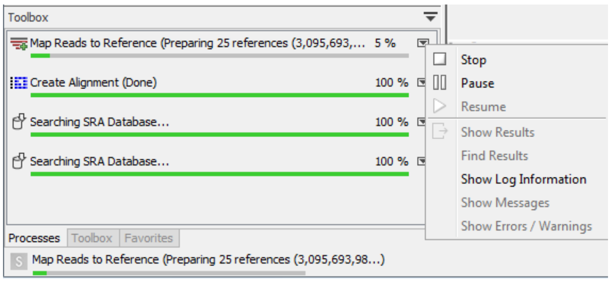
Click the **Hide Toolbox** () button or

**View | Show/Hide Toolbox**

This path gives you the choice to hide the Toolbox, or to selectively hide any of the tabs associated to the Toolbox.

### 2.4.1 Processes

By clicking the **Processes** tab, the Toolbox displays previous and running processes. The running processes can be stopped, paused, and resumed by clicking the small icon (▾) next to the process (see figure 2.20).



Map Reads to Reference (Preparing 25 references (3,095,693,... 5 %
Create Alignment (Done) 100 %
Searching SRA Database... 100 %
Searching SRA Database... 100 %
Map Reads to Reference (Preparing 25 references (3,095,693,98...)

Figure 2.20: *A database search and an alignment calculation are running. Clicking the small icon next to the process allow you to stop, pause and resume processes.*

Stopped and paused processes are not deleted. Processes can be removed by:

**View** | **Remove Finished Processes (✕)** .

Besides the options to stop, pause and resume processes, there are some extra options for *a selected number* of the tools running from the Toolbox:

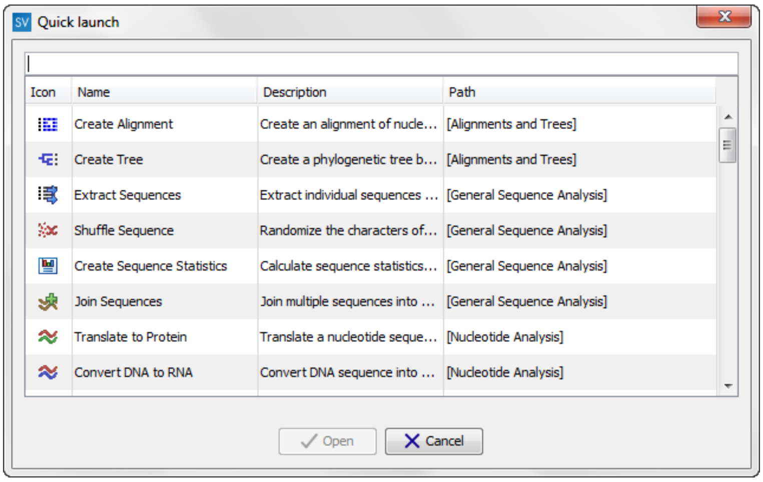
- **Show results**. If you have chosen to save the results (see section **??**), you will be able to open the results directly from the process by clicking this option.
- **Find results**. If you have chosen to save the results (see section **??**), you will be able to highlight the results in the Navigation Area.
- **Show Log Information**. This will display a log file showing progress of the process. The log file can also be shown by clicking **Show Log** in the "handle results" dialog where you choose between saving and opening the results.
- **Show Messages**. Some analyses will give you a message when processing your data. The messages are the black dialogs shown in the lower left corner of the Workbench that disappear after a few seconds. You can reiterate the messages that have been shown by clicking this option.

If you close the program while there are running processes, a dialog will ask if you are sure that you want to close the program. Closing the program will stop the process, and it cannot be restarted when you open the program again.

### 2.4.2 Toolbox

The tools in the toolbox can be accessed by double-clicking, right clicking and choosing "Run", or by dragging elements from the Navigation Area to an item in the Toolbox.

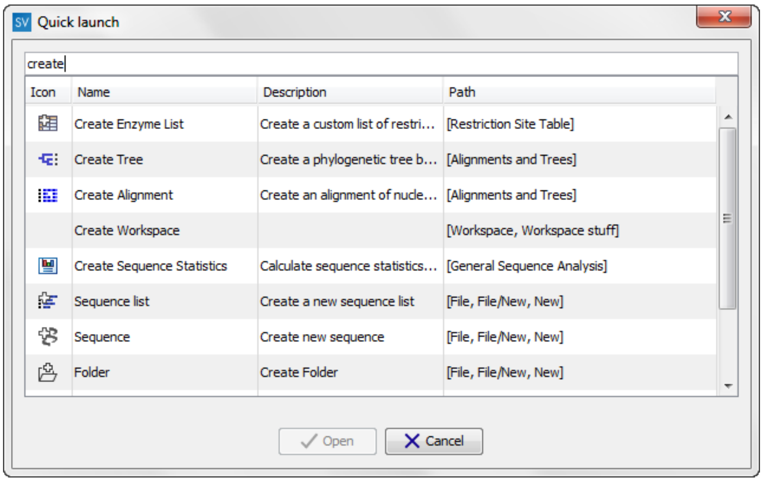
In addition, a **Launch** button (🚀) enables quick launch of tools in *CLC Sequence Viewer*. You can also press Ctrl + Shift + T (⌘ + Shift + T on Mac) to show the quick launch dialog (see figure 2.21).



| Icon | Name | Description | Path |
|---|---|---|---|
| | Create Alignment | Create an alignment of nucle... | [Alignments and Trees] |
| | Create Tree | Create a phylogenetic tree b... | [Alignments and Trees] |
| | Extract Sequences | Extract individual sequences ... | [General Sequence Analysis] |
| | Shuffle Sequence | Randomize the characters of... | [General Sequence Analysis] |
| | Create Sequence Statistics | Calculate sequence statistics... | [General Sequence Analysis] |
| | Join Sequences | Join multiple sequences into ... | [General Sequence Analysis] |
| | Translate to Protein | Translate a nucleotide seque... | [Nucleotide Analysis] |
| | Convert DNA to RNA | Convert DNA sequence into ... | [Nucleotide Analysis] |

Figure 2.21: *Quick access to all tools in* **CLC Sequence Viewer**.

When the dialog is opened, you can start typing search text in the text field at the top. This will bring up the list of tools that match this text either in the name, description or location in the Toolbox. In the example shown in figure 2.22, typing `create` shows a list of tools involving the word "create", and the arrow keys or mouse can be used for selecting and starting a tool.



create

| Icon | Name | Description | Path |
|---|---|---|---|
| | Create Enzyme List | Create a custom list of restri... | [Restriction Site Table] |
| | Create Tree | Create a phylogenetic tree b... | [Alignments and Trees] |
| | Create Alignment | Create an alignment of nucle... | [Alignments and Trees] |
| | Create Workspace | | [Workspace, Workspace stuff] |
| | Create Sequence Statistics | Calculate sequence statistics... | [General Sequence Analysis] |
| | Sequence list | Create a new sequence list | [File, File/New, New] |
| | Sequence | Create new sequence | [File, File/New, New] |
| | Folder | Create Folder | [File, File/New, New] |

Figure 2.22: *Typing in the search field at the top will filter the list of tools to launch.*

### 2.4.3 Favorites

Next to the Toolbox tab, you find the **Favorites** tab. This can be used for organizing and getting quick access to the tools you use the most. It consists of two parts as shown in figure 2.23.

**Favorites** You can manually add tools to the favorites menu simply by right-clicking the tool in the Toolbox. You can also right-click the Favorites folder itself and select **Add Tool**. To remove a tool, right-click and select **Remove from Favorites**. Note that you can also add complete folders to the favorites.

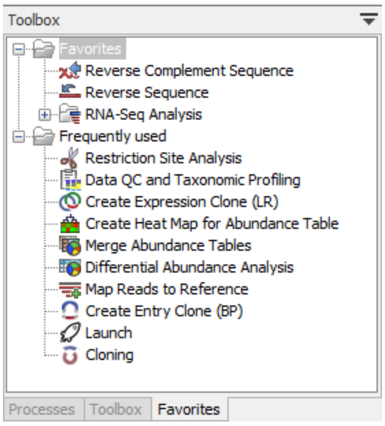

Toolbox
Favorites
Reverse Complement Sequence
Reverse Sequence
RNA-Seq Analysis
Frequently used
Restriction Site Analysis
Data QC and Taxonomic Profiling
Create Expression Clone (LR)
Create Heat Map for Abundance Table
Merge Abundance Tables
Differential Abundance Analysis
Map Reads to Reference
Create Entry Clone (BP)
Launch
Cloning
Processes
Toolbox
Favorites

Figure 2.23: *Favorites toolbox.*

**Frequently used** The list of tools in this folder is automatically populated as you use the Workbench. The most frequently used tools are listed at the top.

### 2.4.4 Status Bar

As can be seen from figure 2.1, the Status Bar is located at the bottom of the window. In the left side of the bar is an indication of whether the computer is making calculations or whether it is idle. The right side of the Status Bar indicates various information depending on the context: it can be the size of a region selected on a sequence, the variant at the position where the cursor stands, or how many rows are selected in a table.

## 2.5 Workspace

If you are working on a project and have arranged the views for this project, you can save this arrangement using **Workspaces**. A Workspace remembers the way you have arranged the views, and you can switch between different workspaces.

The Navigation Area always contains the same data across workspaces. It is, however, possible to open different folders in the different workspaces. Consequently, the program allows you to display different clusters of the data in separate workspaces.

All workspaces are automatically saved when closing down *CLC Sequence Viewer*. The next time you run the program, the workspaces are reopened exactly as you left them.

**Note!** It is not possible to run more than one version of *CLC Sequence Viewer* at a time. Use two or more workspaces instead.

**Create Workspace** When working with large amounts of data, it might be a good idea to split the work into two or more workspaces. As default the *CLC Sequence Viewer* opens one workspace. Additional workspaces are created in the following way:

**Workspace in the Menu Bar** | **Create Workspace** | **enter name of Workspace** | **OK**

Initially, the folders of the **Navigation Area** are collapsed and the View Area is empty and ready to work with.

**Select Workspace** When there is more than one workspace in the *CLC Sequence Viewer*, there are two ways to switch between them:

**Workspace ( ) in the Toolbar | Select the Workspace to activate**

or **Workspace in the Menu Bar | Select Workspace ( ) | choose which Workspace to activate | OK**

**Delete Workspace** Deleting a workspace can be done in the following way:

**Workspace in the Menu Bar | Delete Workspace | choose which Workspace to delete | OK**

**Note!** Be careful to select the right Workspace when deleting. The delete action cannot be undone. (However, no data is lost, because a workspace is only a representation of data.)

It is not possible to delete the default workspace.

## 2.6 List of shortcuts

The keyboard shortcuts in *CLC Sequence Viewer* are listed below.

| Action | Windows/Linux | macOS |
|---|---|---|
| Adjust selection | Shift + arrow keys | Shift + arrow keys |
| Adjust workflow layout | Shift + Alt + L | ⌘ + Shift + Alt + L |
| Back to Navigation Area | Alt + Home<br>or Alt + fn + left arrow | ⌘ + Home<br>or ⌘ + fn + left arrow |
| BLAST | Ctrl + Shift + L | ⌘ + Shift + L |
| BLAST at NCBI | Ctrl + Shift + B | ⌘ + Shift + B |
| Close | Ctrl + W | ⌘ + W |
| Close all views | Ctrl + Shift + W | ⌘ + Shift + W |
| Copy | Ctrl + C | ⌘ + C |
| Create alignment | Ctrl + Shift + A | ⌘ + Shift + A |
| Create track list | Ctrl + L | ⌘ + L |
| Cut | Ctrl + X | ⌘ + X |
| Delete | Delete | Delete or ⌘ + Backspace |
| Exit | Alt + F4 | ⌘ + Q |
| Export | Ctrl + E | ⌘ + E |
| Export graphics | Ctrl + G | ⌘ + G |
| Find Next Conflict | '.' (dot) | '.' (dot) |
| Find Previous Conflict | ',' (comma) | ',' (comma) |
| Help | F1 | F1 |
| Import | Ctrl + I | ⌘ + I |
| Launch tools | Ctrl + Shift + T | ⌘ + Shift + T |
| Maximize/restore View size | Ctrl + M | ⌘ + M |
| Move gaps in alignment | Ctrl + arrow keys | ⌘ + arrow keys |
| New Folder | Ctrl + Shift + N | ⌘ + Shift + N |
| New Sequence | Ctrl + N | ⌘ + N |
| Panning Mode | Ctrl + 4 | ⌘ + 4 |
| Paste | Ctrl + V | ⌘ + V |
| Print | Ctrl + P | ⌘ + P |
| Redo | Ctrl + Y | ⌘ + Y |
| Rename | F2 | F2 |
| Save | Ctrl + S | ⌘ + S |
| Save As | Ctrl + Shift + S | ⌘ + Shift + S |
| Scrolling horizontally | Shift + Scroll wheel | Shift + Scroll wheel |
| Search local data | Ctrl + Shift + F | ⌘ + Shift + F |
| Search via Side Panel | Ctrl + F | ⌘ + F |
| Search NCBI | Ctrl + B | ⌘ + B |
| Search UniProt | Ctrl + Shift + U | ⌘ + Shift + U |
| Select All | Ctrl + A | ⌘ + A |
| Select Selection Mode | Ctrl + 1 (one) | ⌘ + 1 (one) |
| Show folder content | Ctrl + O | ⌘ + O |
| Show/hide Side Panel | Ctrl + U | ⌘ + U |
| Sort folder | Ctrl + Shift + R | ⌘ + Shift + R |
| Split Horizontally | Ctrl + T | ⌘ + T |
| Split Vertically | Ctrl + J | ⌘ + J |
| Switch tabs in View Area | Ctrl + PageUp/PageDown<br>or Ctrl + fn + arrow up/down | Ctrl + PageUp/PageDown<br>or Ctrl + fn + arrow up/down |
| Switch views | Ctrl + Shift + PageUp/arrow up<br>Ctrl + Shift + PageDown/arrow down | Ctrl + Shift + PageUp/arrow up<br>Ctrl + Shift + PageDown/arrow down |
| Translate to Protein | Ctrl + Shift + P | ⌘ + Shift + P |
| Undo | Ctrl + Z | ⌘ + Z |
| Update folder | F5 | F5 |
| User Preferences | Ctrl + K | ⌘ + , |

### Scroll and Zoom shortcuts

| Action | Windows/Linux | macOS |
|---|---|---|
| Vertical scroll in read tracks | Alt + Scroll wheel | Alt + Scroll wheel |
| Vertical scroll in reads tracks, fast | Shift+Alt+Scroll wheel | Shift+Alt+Scroll wheel |
| Vertical zoom in graph tracks | Ctrl + Scroll wheel | ⌘ + Scroll wheel |
| Zoom | Ctrl + Scroll wheel | ⌘ + Scroll wheel |
| Zoom In Mode | Ctrl + 2 | ⌘ + 2 |
| Zoom In (without clicking) | ’+’ (plus) | ’+’ (plus) |
| Zoom Out Mode | Ctrl + 3 | ⌘ + 3 |
| Zoom Out (without clicking) | ’-’ (minus) | ’-’ (minus) |
| Zoom to base level | Ctrl + 0 | ⌘ + 0 |
| Zoom to fit screen | Ctrl + 6 | ⌘ + 6 |
| Zoom to selection | Ctrl + 5 | ⌘ + 5 |
| Reverse zoom mode | press and hold Shift | press and hold Shift |

### Workflows related shortcuts

| Action | Windows/Linux | macOS |
|---|---|---|
| Workflow, add element | Alt + Shift + E | Alt + Shift + E |
| Workflow, collapse if its expanded | Alt + Shift + ’-’ (minus) | Alt + Shift + ’-’ |
| Workflow, create installer | Alt + Shift + I | Alt + Shift + I |
| Workflow, execute | Ctrl + enter | ⌘ + enter |
| Workflow, expand if its collapsed | Alt + Shift + ’+’ (plus) | Alt + Shift + ’-’ |
| Workflow, highlight used elements | Alt + Shift + U | Alt + Shift + U |
| Workflow, remove all elements | Alt + Shift + R | Alt + Shift + R |

### Combinations of keys and mouse movements

| Action | Windows/Linux | macOS | Mouse movement |
|---|---|---|---|
| Maximize View | | | Double-click the tab of the View |
| Restore View | | | Double-click the View title |
| Reverse zoom mode | Shift | Shift | Click in view |
| Select multiple elements not grouped together | Ctrl | ⌘ | Click elements |
| Select multiple elements grouped together | Shift | Shift | Click elements |
| Select Editor and highlight the corresponding element in the Navigation Area | Alt or Ctrl | ⌘ | Click tab |

"Elements" in this context refers to elements and folders in the **Navigation Area** selections on sequences, and rows in tables.

# Chapter 3

# User preferences and settings

**Contents**

The first three sections in this chapter deal with the general preferences that can be set for *CLC Sequence Viewer* using the **Preferences** dialog. The next section explains how the settings in the **Side Panel** can be saved and applied to other views. Finally, you can learn how to import and export the preferences.

The **Preferences** dialog offers opportunities for changing the default settings for different features of the program.

The **Preferences** dialog is opened in one of the following ways and can be seen in figure 3.2:

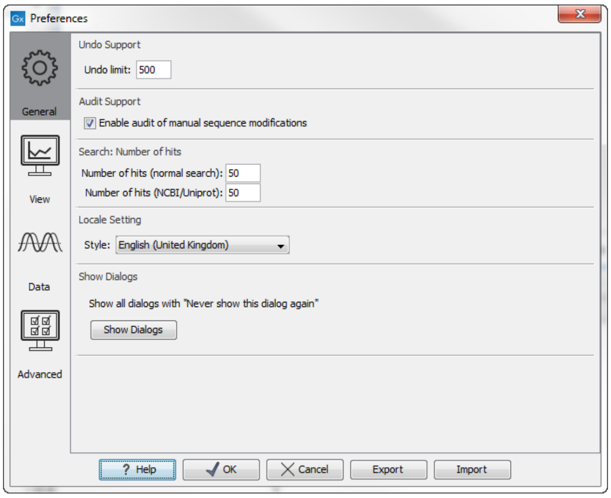
**Edit | Preferences ( )**

or **Ctrl + K (⌘ + ; on Mac)**

## 3.1 General preferences

The **General preferences** include:

- **Undo Limit.** As default the undo limit is set to 500. By writing a higher number in this field, more actions can be undone. Undo applies to all changes made on molecules, sequences, alignments or trees. See section 2.2.5 for more on this topic.
- **Audit Support.** If this option is checked, all manual editing of sequences will be marked with an annotation on the sequence (see figure 3.3). Placing the mouse on the annotation will reveal additional details about the change made to the sequence (see figure 3.4). Note that no matter whether **Audit Support** is checked or not, all changes are also recorded in the **History** ( ) (see section **??**).



Undo Support

Undo limit: 500

Audit Support

☑ Enable audit of manual sequence modifications

Search: Number of hits

Number of hits (normal search): 50

Number of hits (NCBI/Uniprot): 50

Locale Setting

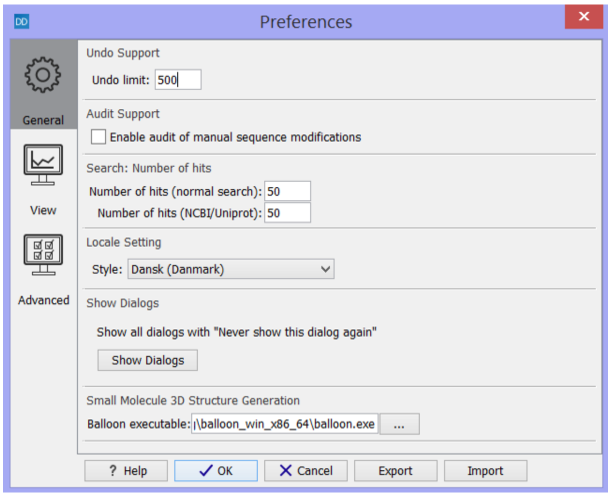
Style: English (United Kingdom)

Show Dialogs

Show all dialogs with "Never show this dialog again"

Show Dialogs

Figure 3.1: *Preferences include General preferences, View preferences, Data preferences, and Advanced settings.*



Undo Support

Undo limit: 500

Audit Support

□ Enable audit of manual sequence modifications

Search: Number of hits

Number of hits (normal search): 50

Number of hits (NCBI/Uniprot): 50

Locale Setting

Style: Dansk (Danmark)

Show Dialogs

Show all dialogs with "Never show this dialog again"

Show Dialogs

Small Molecule 3D Structure Generation

Balloon executable: ;\balloon_win_x86_64\balloon.exe ...

Figure 3.2: *Preferences include General preferences, View preferences, Data preferences, and Advanced settings.*

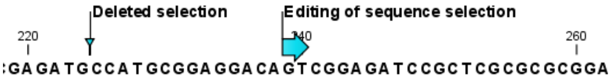
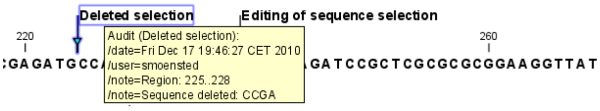

Deleted selection
Editing of sequence selection
220
240
260
:GAGATGCCATGCGGAGGACAGTCGGAGATCCGCTCGCGCGCGGA

Figure 3.3: *Annotations added when the sequence is edited.*



Audit (Deleted selection):
/date=Fri Dec 17 19:46:27 CET 2010
/user=smoensted
/note=Region: 225..228
/note=Sequence deleted: CCGA

Figure 3.4: *Details of the editing.*

- **Number of hits.** The number of hits shown in *CLC Sequence Viewer*, when e.g. searching NCBI. (The sequences shown in the program are not downloaded, until they are opened or dragged/saved into the Navigation Area).
- **Locale Setting.** Specify which country you are located in. This determines how punctation is used in numbers all over the program.

- **Show Dialogs.** A lot of information dialogs have a checkbox: "Never show this dialog again". When you see a dialog and check this box in the dialog, the dialog will not be shown again. If you regret and wish to have the dialog displayed again, click the button in the General Preferences: **Show Dialogs**. Then all the dialogs will be shown again.

- **Usage information.** When this item is checked, anonymous information is shared with QIAGEN about how the Workbench is used. This option is enabled by default.

  The information shared with QIAGEN is:

  - Launch information (operating system, product, version, and memory available)
  - The names of the tools and workflows launched (but not the parameters or the data used)
  - Errors (but without any information that could lead to loss of privacy: file names and organisms will not be logged)
  - Installation and removal of plugins and modules

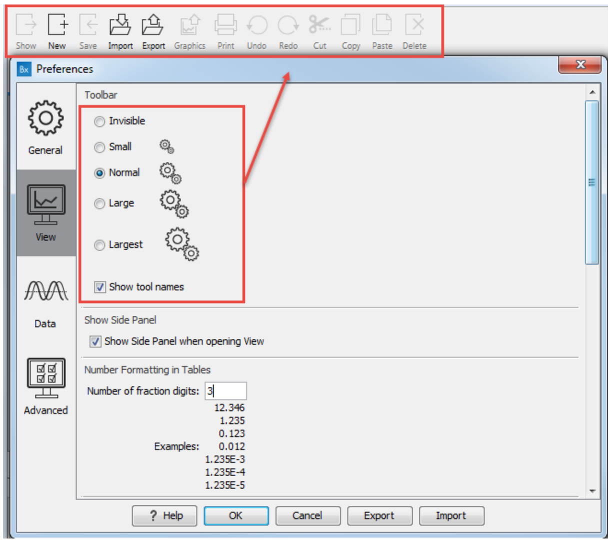
  The following information is also sent:

  - An installation ID. This allows us to group events coming from the same installation. It is not possible to connect this ID to personal or license information.
  - A geographic location. This is predicted based on the IP-address. We do not store IP-addresses after location information has been extracted.
  - A time stamp

## 3.2 View preferences

There are six groups of default **View** settings:

1. **Toolbar** lets you choose the size of the toolbar icons, and whether to display names below the icons (figure 3.5).



Toolbar

○ Invisible
○ Small
● Normal
○ Large
○ Largest

☑ Show tool names

Show Side Panel

☑ Show Side Panel when opening View

Number Formatting in Tables

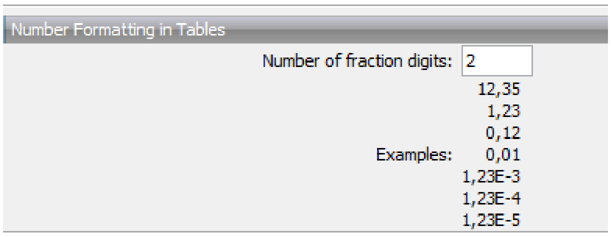
Number of fraction digits: 3

```
           12.346
            1.235
            0.123
Examples:   0.012
         1.235E-3
         1.235E-4
         1.235E-5
```

Figure 3.5: *Number formatting of tables.*

2. **Show Side Panel** allows you to choose whether to display the side panel when opening a new view. Note that for any open view, the side panel can be collapsed by clicking on the small triangle at the top left side of the settings area or by using the key combination Ctrl + U (⌘ + U on Mac).

3. **Number formatting in tables** specifies how the numbers should be formatted in tables (see figure 3.6). The examples below the text field are updated when you change the value so that you can see the effect. After you have changed the preference, you have to re-open your tables to see the effect.



Number Formatting in Tables

Number of fraction digits: 2

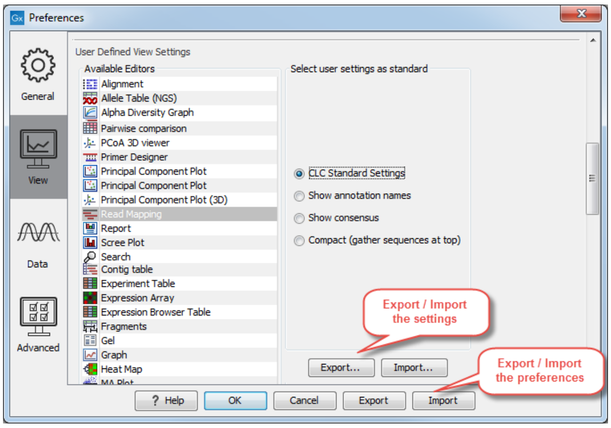
Examples:
12,35
1,23
0,12
0,01
1,23E-3
1,23E-4
1,23E-5

Figure 3.6: *Number formatting of tables.*

4. **Sequence Representation** allows you to change the way the elements appear in the Navigation Area. The following text can be used to describe the element:

   - Name (this is the default information to be shown).
   - Accession (sequences downloaded from databases like GenBank have an accession number).
   - Latin name.
   - Latin name (accession).
   - Common name.
   - Common name (accession).

5. **User Defined View Settings** gives you an overview of the different Side Panel settings that are saved for each view. See section 3.5 to learn more about how to create and save style sheets. If there are other settings beside CLC Standard Settings, you can use this overview to choose which of the settings should be used per default when you open a view (see an example in figure 3.7).



Select user settings as standard

● CLC Standard Settings
○ Show annotation names
○ Show consensus
○ Compact (gather sequences at top)

Export / Import the settings

Export / Import the preferences

Figure 3.7: *Selecting the default view setting.*

Note that the content of this list depends on the nature of the elements that are saved in the Navigation Area. When the list grows, you may have to scroll up or down to find the relevant settings.

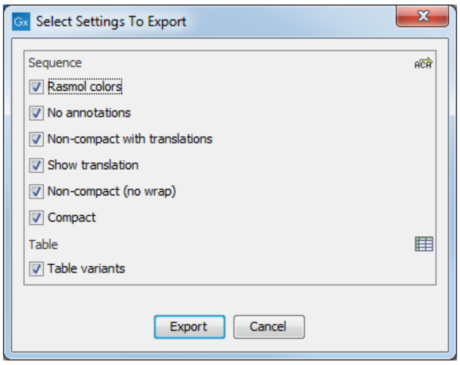
6. **Molecule Project 3D Editor** gives you the option to turn off the modern OpenGL rendering for **Molecule Projects** (see section 8.2).

### 3.2.1 Import and export Side Panel settings

If you have created a special set of settings in the **Side Panel** that you wish to share with other CLC users, you can export the settings in a file. The other user can then import the settings.

To export the **Side Panel** settings, first select the views that you wish to export settings for. Use Ctrl+click (⌘ + click on Mac) or Shift+click to select multiple views. Next click the **Export...** button that is situated below the list of possible settings (see figure 3.7), and not the Export button at the very bottom of the dialog, as this one will export the **Preferences** (see section 3.4).

A dialog will be shown (see figure 3.8) that allows you to select which of the settings you wish to export.



Sequence

☑ Rasmol colors

☑ No annotations

☑ Non-compact with translations

☑ Show translation

☑ Non-compact (no wrap)

☑ Compact

Table

☑ Table variants

Figure 3.8: *Exporting all settings for circular views.*

When multiple views are selected for export, all the view settings for the views will be shown in the dialog. Click **Export** and you will now be able to define a save folder and name for the exported file. The settings are saved in a file with a .vsf extension (View Settings File).

Similarly, to import a **Side Panel** settings file, make sure you are at the bottom of the **View** panel of the **Preferences dialog**, and click the **Import...** button. Note that there is also another import button at the very bottom of the dialog, but this will import the other settings of the **Preferences** dialog (see section 3.4).

Select the *.vsf file where the settings are saved. The following dialog asks if you wish to overwrite existing **Side Panel** settings, or if you wish to merge the imported settings into the existing ones (see figure 3.9).

**WARNING!** If you choose to overwrite the existing settings, you will loose ALL the Side Panel settings that were previously saved.

To avoid confusion of the different import and export options, here is an overview:

- Import and export of **bioinformatics data** such as sequences, alignments etc. (described in section 5.1).

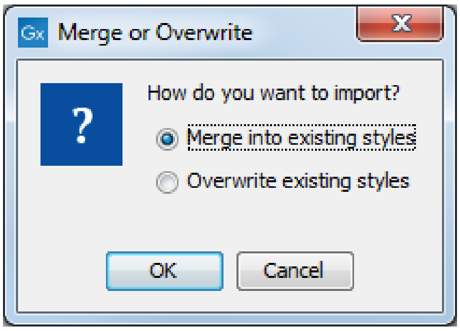

Merge or Overwrite
How do you want to import?
● Merge into existing styles
○ Overwrite existing styles
OK
Cancel

Figure 3.9: *When you import settings, you are asked if you wish to overwrite existing settings or if you wish to merge the new settings into the old ones.*

- **Graphics** export of the views which creates image files in various formats (described in section 5.3).
- Import and export of **Side Panel Settings** as described above.
- Import and export of all the **Preferences** except the Side Panel settings. This is described in the previous section.

## 3.3 Advanced preferences

**Proxy Settings** The Advanced settings include the possibility to set up a proxy server. This is described in section 1.6.

**Default data location** The default location is used when you import a file without selecting a folder or element in the Navigation Area first. It is set to the folder called CLC_Data in the Navigation Area, but can be changed to another data location using a drop down list of data locations already added (see section **??**). Note that the default location cannot be removed, but only changed to another location.

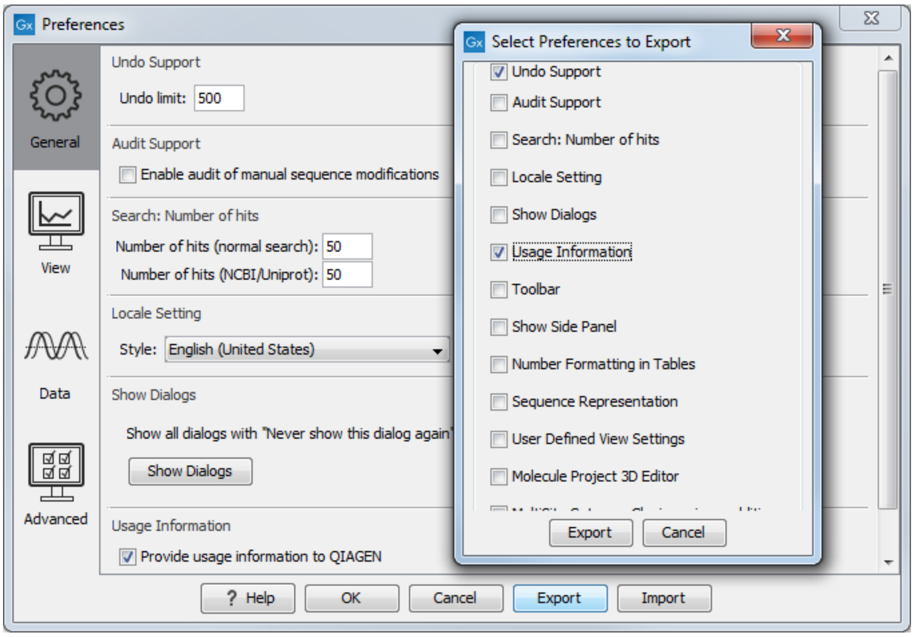
## 3.4 Export/import of preferences

The user preferences of the *CLC Sequence Viewer* can be exported to other users of the program, allowing other users to display data with the same preferences as yours. You can also use the export/import preferences function to backup your preferences.

To export preferences, open the **Preferences** dialog and click on the Export bottom at the bottom of the Preferences dialog. Select the relevant preferences and click Export to choose a location to save the exported file(see figure 3.10).

**Note!** The format of exported preferences is *.cpf. This notation must be submitted to the name of the exported file in order for the exported file to work.

Before exporting, you are asked about which of the different settings you want to include in the exported file. One of the items in the list is "User Defined View Settings". If you export this, only the information about which of the settings is the default setting for each view is exported. If you wish to export the **Side Panel Settings** themselves, see section 3.2.1.



Preferences

Undo Support

Undo limit: 500

Audit Support

□ Enable audit of manual sequence modifications

Search: Number of hits

Number of hits (normal search): 50

Number of hits (NCBI/Uniprot): 50

Locale Setting

Style: English (United States)

Show Dialogs

Show all dialogs with "Never show this dialog again"

Usage Information

☑ Provide usage information to QIAGEN

Select Preferences to Export

☑ Undo Support

□ Audit Support

□ Search: Number of hits

□ Locale Setting

□ Show Dialogs

☑ Usage Information

□ Toolbar

□ Show Side Panel

□ Number Formatting in Tables

□ Sequence Representation

□ User Defined View Settings

□ Molecule Project 3D Editor

Figure 3.10: *Select which of the preferences you want to export.*

The process of importing preferences is similar to exporting: click the Import button and browse to the *.cpf file.

To avoid confusion of the different import and export options, you can find an overview here:

- Import and export of **bioinformatics data** such as molecules, sequences, alignments etc. (described in section 5.1).
- **Graphics** export of the views that create image files in various formats (described in section 5.3).
- Import and export of **Side Panel Settings** as described in the next section.
- Import and export of all the **Preferences** except the Side Panel settings. This is described above.

## 3.5 View settings for the Side Panel

The **Side Panel** is shown to the right of all views that are opened in the View Area. Settings are specific to the type of view. Hence, when you save settings of a circular view, they will not be available if you open the sequence in a linear view (see section 2.2.8).

The options for saving and applying are available at the bottom of the **Side Panel** (see figure 3.11).

Opening a view type (e.g., a circular sequence, a variant table, or a PCA) for the first time will display the element using the CLC Standard Settings for that type of view. You can then adjust the settings using all the options available to you in the side panel. When you have adjusted a view to your preference, the new settings can be saved (see figure 3.12).

Saving can be done two ways. Write a name for the particular settings you just set, and choose to save:

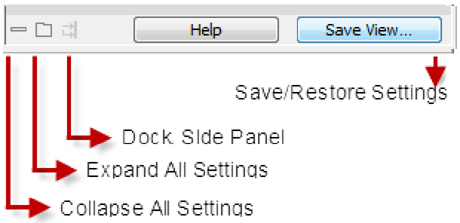
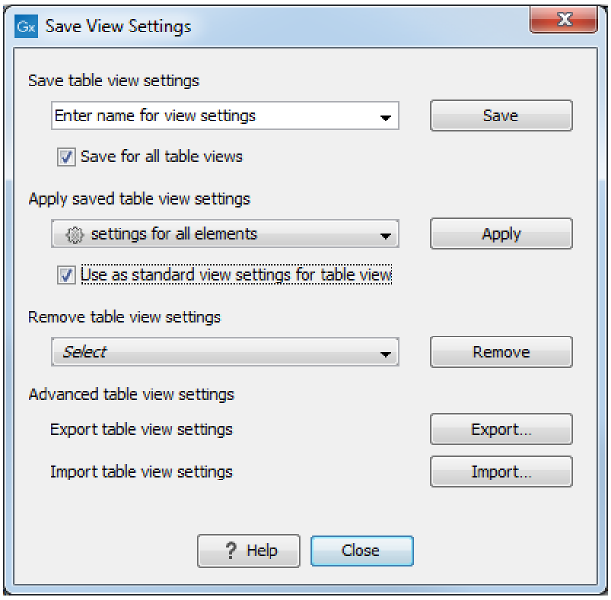


Figure 3.11: *Functionalities found at the bottom of the Side Panel.*


Save View Settings

Save table view settings

Enter name for view settings [Save]

☑ Save for all table views

Apply saved table view settings

settings for all elements [Apply]

☑ Use as standard view settings for table view

Remove table view settings

*Select* [Remove]

Advanced table view settings

Export table view settings [Export...]

Import table view settings [Import...]

[? Help] [Close]

Figure 3.12: *Functionalities found at the bottom of the Side Panel.*

- For that view alone, so that the settings will be available to you the next time you open this particular element. The settings are saved with only this element, and will be exported with the element if you later select to export the element to another destination.
- For all other views, when the option "Save for all element views" is checked, so that the settings will be available to you the next time you open any element for which this type of view is available.

Similarly, applying can be done two ways:

- For that view alone, so that the settings are applied the next time you open this particular element.
- For all other elements, when the option "Use as standard view settings for element view" is checked, so that the settings are applied each time you open any element for which this type of view is available. These "general" settings are user specific and will not be saved with or exported with the element.

"General" settings can be shared and imported with other workbench users using the **Export** and **Import** buttons at the bottom of the dialog. Exporting and importing saved settings can also be done in the **Preferences** dialog under the **View** tab (see section 3.2.1).

It is possible to remove a saved setting using the saved settings list from the drop-down menu and clicking **Remove**.

# Chapter 4

# Printing

## Contents

*CLC Sequence Viewer* offers different choices of printing the result of your work.

This chapter deals with printing directly from *CLC Sequence Viewer*. Another option for using the graphical output of your work, is to export graphics (see chapter 5.3) in a graphic format, and then import it into a document or a presentation.

All the kinds of data that you can view in the **View Area** can be printed. The *CLC Sequence Viewer* uses a WYSIWYG principle: What You See Is What You Get. This means that you should use the options in the Side Panel to change how your data, e.g. a sequence, looks on the screen. When you print it, it will look exactly the same way on print as on the screen.

For some of the views, the layout will be slightly changed in order to be printer-friendly.

It is not possible to print elements directly from the **Navigation Area**. They must first be opened in a view in order to be printed. To print the contents of a view:

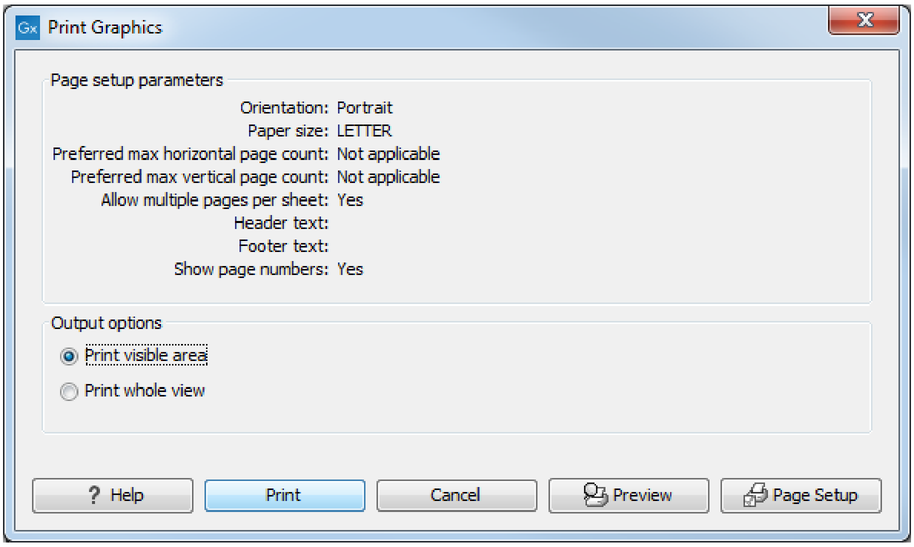
**select relevant view | Print (🖶) in the toolbar**

This will show a print dialog (see figure 4.1).

In this dialog, you can:

- Select which part of the view you want to print.
- Adjust **Page Setup**.
- See a print **Preview** window.

These three options are described in the three following sections.



Print Graphics

Page setup parameters

Orientation: Portrait
Paper size: LETTER
Preferred max horizontal page count: Not applicable
Preferred max vertical page count: Not applicable
Allow multiple pages per sheet: Yes
Header text:
Footer text:
Show page numbers: Yes

Output options

● Print visible area
○ Print whole view

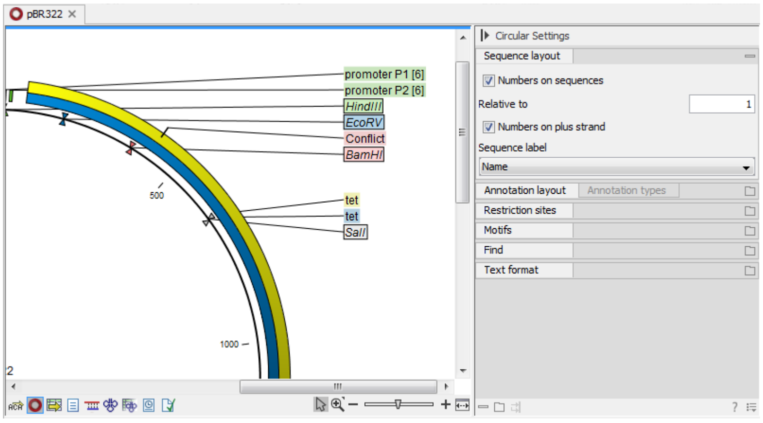
Figure 4.1: *The Print dialog.*

## 4.1 Selecting which part of the view to print

In the print dialog you can choose to:

- **Print visible area**, or
- **Print whole view**

These options are available for all views that can be zoomed in and out. In figure 4.2 is a view of a circular sequence which is zoomed in so that you can only see a part of it.



☑ Numbers on sequences
Relative to 1
☑ Numbers on plus strand
Sequence label: Name

Figure 4.2: *A circular sequence as it looks on the screen.*

When selecting **Print visible area**, your print will reflect the part of the sequence that is *visible* in the view. The result from printing the view from figure 4.2 and choosing **Print visible area** can be seen in figure 4.3.

On the other hand, if you select **Print whole view**, you will get a result that looks like figure 4.4. This means that you also print the part of the sequence which is not visible when you have zoomed in.

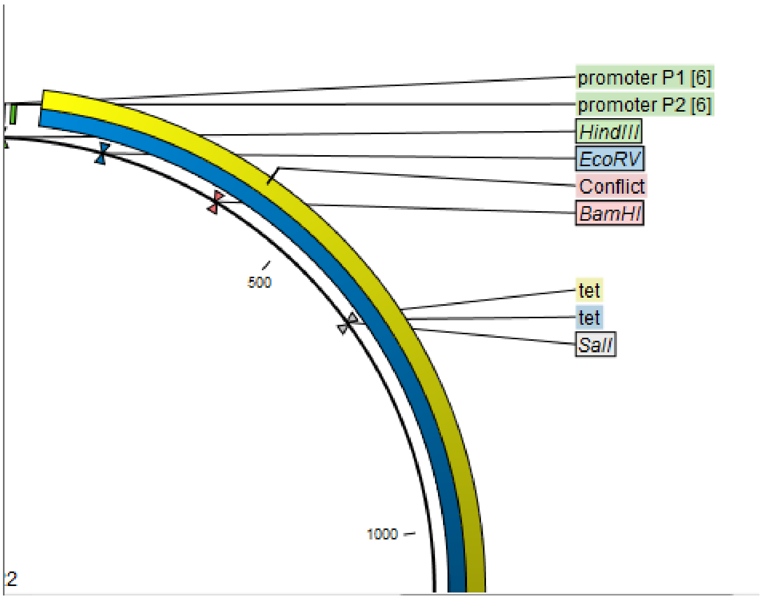


Figure 4.3: *A print of the sequence selecting Print visible area.*

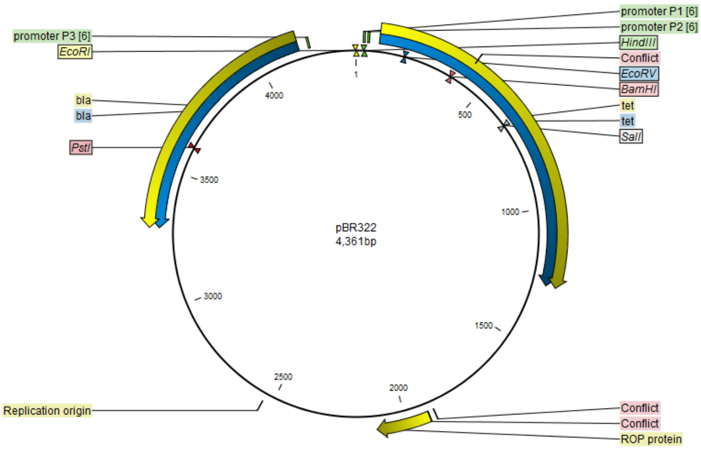


Figure 4.4: *A print of the sequence selecting Print whole view. The whole sequence is shown, even though the view is zoomed in on a part of the sequence.*

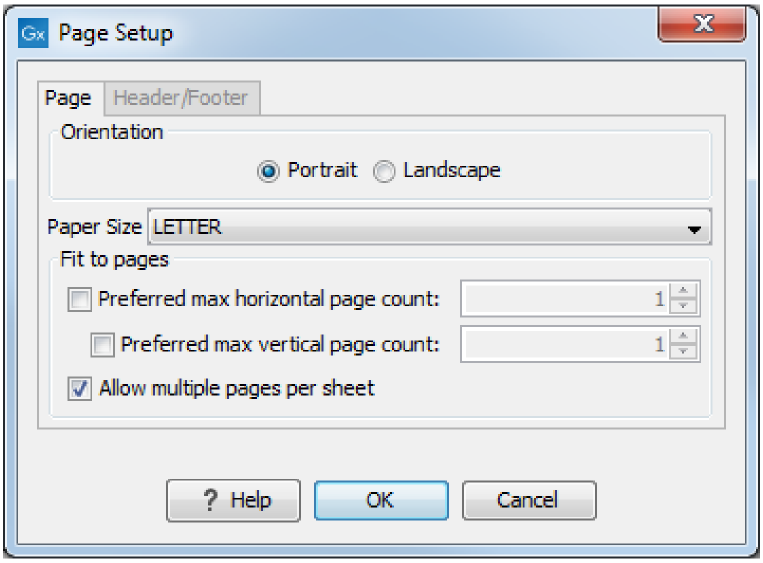
## 4.2 Page setup

No matter whether you have chosen to print the visible area or the whole view, you can adjust page setup of the print. An example of this can be seen in figure 4.5

In this dialog you can adjust both the setup of the pages and specify a header and a footer by clicking the tab at the top of the dialog.

You can modify the layout of the page using the following options:

- **Orientation**.
  - **Portrait**. Will print with the paper oriented vertically.
  - **Landscape**. Will print with the paper oriented horizontally.
- **Paper size**. Adjust the size to match the paper in your printer.



Orientation

● Portrait ○ Landscape

Paper Size LETTER

Fit to pages

□ Preferred max horizontal page count: 1

□ Preferred max vertical page count: 1

☑ Allow multiple pages per sheet

Figure 4.5: *Page Setup.*

- **Fit to pages**. Can be used to control how the graphics should be split across pages (see figure 4.6 for an example).
  - **Horizontal pages**. If you set the value to e.g. 2, the printed content will be broken up horizontally and split across 2 pages. This is useful for sequences that are not wrapped
  - **Vertical pages**. If you set the value to e.g. 2, the printed content will be broken up vertically and split across 2 pages.

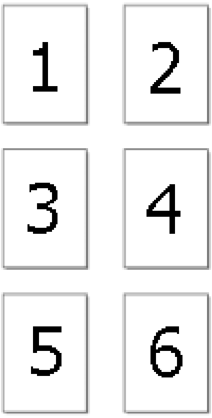


Figure 4.6: *An example where Fit to pages horizontally is set to 2, and Fit to pages vertically is set to 3.*

**Note!** It is a good idea to consider adjusting view settings (e.g. **Wrap** for sequences), in the **Side Panel** before printing. As explained in the beginning of this chapter, the printed material will look like the view on the screen, and therefore these settings should also be considered when adjusting **Page Setup**.

**Header and footer** Click the **Header/Footer** tab to edit the header and footer text. By clicking in the text field for either **Custom header text** or **Custom footer text** you can access the auto formats for header/footer text in **Insert a caret position**. Click either **Date**, **View name**, or **User name** to include the auto format in the header/footer text.

Click **OK** when you have adjusted the **Page Setup**. The settings are saved so that you do not have to adjust them again next time you print. You can also change the **Page Setup** from the **File** menu.

## 4.3 Print preview

The preview is shown in figure 4.7.

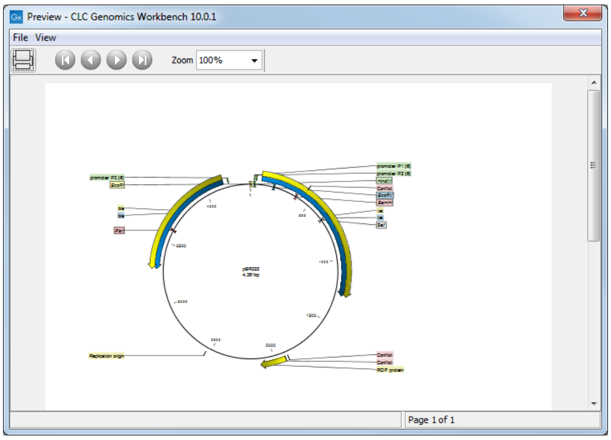


Figure 4.7: *Print preview.*

The **Print preview** window lets you see the layout of the pages that are printed. Use the arrows in the toolbar to navigate between the pages. Click Print (🖶) to show the print dialog, which lets you choose e.g. which pages to print.

The **Print preview** window is for preview only - the layout of the pages must be adjusted in the **Page setup**.

# Chapter 5

# Import/export of data and graphics

**Contents**

*CLC Sequence Viewer* handles a large number of different data formats. In order to work with data in the Workbench, it has to be imported (📥). Data types that are not recognized by the Workbench are imported as "external files" which means that when you open these, they will open in the default application for that file type on your computer (e.g. Word documents will open in Word).

This chapter first deals with importing and exporting data in bioinformatic data formats and as external files. Next comes an explanation of how to export graph data points to a file, and how to export graphics.

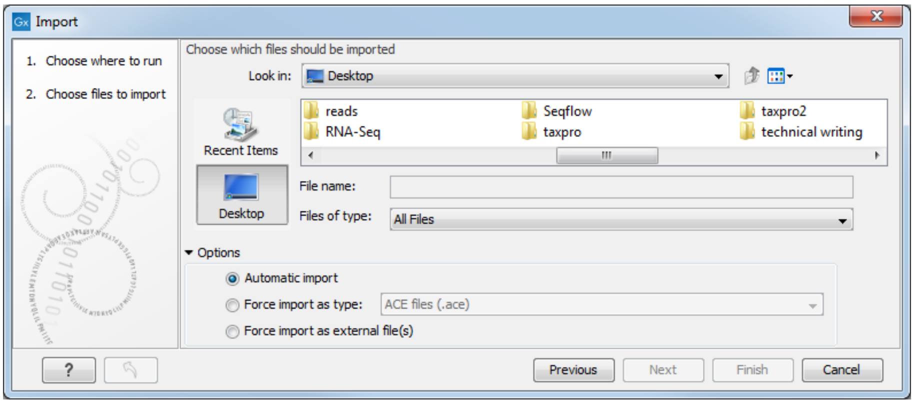
## 5.1 Standard import

*CLC Sequence Viewer* has support for a wide range of bioinformatic data such as molecules, sequences, alignments etc. See a full list of the data formats in section C.1.

These data can be imported through the Import dialog, using drag/drop or copy/paste as explained below.

**Import using the import dialog** To start the import using the import dialog: **click Import ( ) in the Tool**

This will show a dialog similar to figure 5.1. You can change which kind of file types that should be shown by selecting a file format in the **Files of type** box.



Look in: Desktop

Files of type: All Files

● Automatic import

Figure 5.1: *The import dialog.*

Next, select one or more files or folders to import and click **Next** to select a place for saving the result files. If you import one or more folders, the contents of the folder is automatically imported and placed in that folder in the Navigation Area. If the folder contains subfolders, the whole folder structure is imported.

In the import dialog (figure 5.1), there are three import options:

**Automatic import** This will import the file and *CLC Sequence Viewer* will try to determine the format of the file. The format is determined based on the file extension (e.g. SwissProt files have .swp at the end of the file name) in combination with a detection of elements in the file that are specific to the individual file formats. If the file type is not recognized, it will be imported as an external file. In most cases, automatic import will yield a successful result, but if the import goes wrong, the next option can be helpful:

**Force import as type** This option should be used if *CLC Sequence Viewer* cannot successfully determine the file format. By forcing the import as a specific type, the automatic determination of the file format is bypassed, and the file is imported as the type specified.

**Force import as external file** This option should be used if a file is imported as a bioinformatics file when it should just have been external file. It could be an ordinary text file which is imported as a sequence.

**Import using drag and drop** It is also possible to drag a file from e.g. the desktop into the **Navigation Area** of *CLC Sequence Viewer*. This is equivalent to importing the file using the **Automatic import** option described above. If the file type is not recognized, it will be imported as an external file.

**Import using copy/paste of text** If you have e.g. a text file or a browser displaying a sequence in one of the formats that can be imported by *CLC Sequence Viewer*, there is a very easy way to get this sequence into the **Navigation Area**:

**Copy the text from the text file or browser | Select a folder in the Navigation Area | Paste ( )**

This will create a new sequence based on the text copied. This operation is equivalent to saving the text in a text file and importing it into the *CLC Sequence Viewer*.

If the sequence is not formatted, i.e. if you just have a text like this: "ATGACGAATAGGAGTTC-TAGCTA" you can also paste this into the **Navigation Area**.

**Note!** Make sure you copy all the relevant text - otherwise *CLC Sequence Viewer* might not be able to interpret the text.

### 5.1.1 External files

In order to help you organize your research projects, *CLC Sequence Viewer* lets you import all kinds of files. E.g. if you have Word, Excel or pdf-files related to your project, you can import them into the **Navigation Area** of *CLC Sequence Viewer*. Importing an external file creates a copy of the file which is stored at the location you have chosen for import. The file can now be opened by double-clicking the file in the **Navigation Area**. The file is opened using the default application for this file type (e.g. Microsoft Word for .doc-files and Adobe Reader for .pdf).

External files are imported and exported in the same way as bioinformatics files (see section 5.1). Bioinformatics files not recognized by *CLC Sequence Viewer* are also treated as external files.

## 5.2 Data export

The exporter can be used to:

- Export bioinformatic data in most of the formats that can be imported. There are a few exceptions (see section C.1).
- Export one or more data elements at a time to a given format. When multiple data elements are selected, each is written out to an individual file, unless compression is turned on, or "Output as single file" is selected.

The standard export functionality can be launched using the Export button on the toolbar, or by going to the menu:

**File | Export ( )**

An additional export tool is available from under the File menu:

**File | Export with Dependent Elements**

This tool is described further in section 5.2.2.

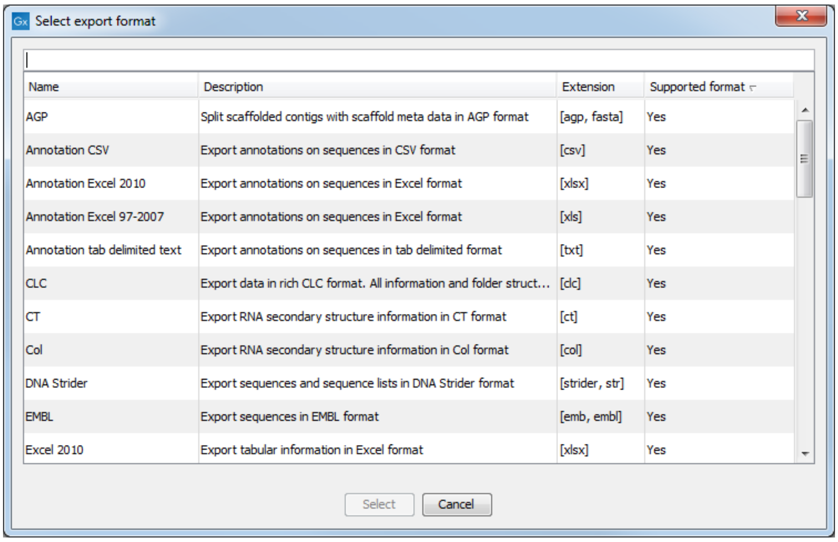
The general steps when configuring a standard export job are:

- (Optional) Select the data to export in the **Navigation Area**.
- Start up the exporter tool via the Export button in the toolbar or using the **Export** option under the File menu.

- Select the format the data should be exported to.
- Select the data to export, or confirm the data to export if it was already selected via the **Navigation Area**.
- Configure the parameters. This includes compression, multiple or single outputs, and naming of the output files, along with other format-specific settings where relevant.
- Select where the data should be exported to.
- Click on the button labeled **Finish**.

**Selecting data for export - part I.** You can select the data elements to export **before** you run the export tool **or after** the format to export to has been selected. If you are not certain which formats are supported for the data being exported, we recommend selecting the data in the **Navigation Area** before launching the export tool.

**Selecting a format to export to.** When data is pre-selected in the **Navigation Area** before launching the export tool you will see a column in the export interface called **Supported formats**. Formats that the selected data elements can be exported to are indicated by a "Yes" in this column. Supported formats will appear at the top of the list of formats (figure 5.2).



Select export format

| Name | Description | Extension | Supported format |
|---|---|---|---|
| AGP | Split scaffolded contigs with scaffold meta data in AGP format | [agp, fasta] | Yes |
| Annotation CSV | Export annotations on sequences in CSV format | [csv] | Yes |
| Annotation Excel 2010 | Export annotations on sequences in Excel format | [xlsx] | Yes |
| Annotation Excel 97-2007 | Export annotations on sequences in Excel format | [xls] | Yes |
| Annotation tab delimited text | Export annotations on sequences in tab delimited format | [txt] | Yes |
| CLC | Export data in rich CLC format. All information and folder struct... | [clc] | Yes |
| CT | Export RNA secondary structure information in CT format | [ct] | Yes |
| Col | Export RNA secondary structure information in Col format | [col] | Yes |
| DNA Strider | Export sequences and sequence lists in DNA Strider format | [strider, str] | Yes |
| EMBL | Export sequences in EMBL format | [emb, embl] | Yes |
| Excel 2010 | Export tabular information in Excel format | [xlsx] | Yes |

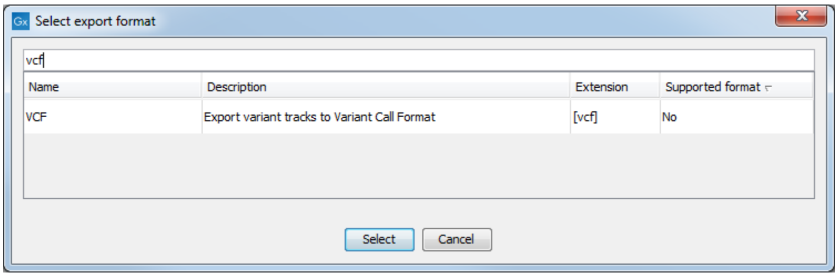
Figure 5.2: *The Select exporter dialog where sequence lists were pre-selected in the Navigation Area before launching the export tool. Here, the formats sequence lists can be exported to are listed at the top, with a Yes in the Selected formats column. Other formats are found below, with No in this column.*

Formats that cannot be used for export of the selected data have a "No" listed in the **Supported formats** column. If you have selected multiple data elements of different types, then formats which can be used for some of the selected data elements but not all of them are indicated by the text "For some elements" in this column.

Please note that the information in the **Supported formats** column only refers to the data already selected in the **Navigation Area**. If you are going to choose your data later in the export process, then the information in this column will not be pertinent.

Only one export format is available if you select a folder to be exported. This is described in more detail in section 5.2.1.

**Finding a particular format in the list.** You can quickly find a particular format by using the text box at the top of the exporter window as shown in figure 5.3, where formats that include the term VCF are searched for. This search term will remain in place the next time the Export tool is launched. Just delete the text from the search box if you no longer wish only the formats with that term to be listed.



Select export format

vcf

| Name | Description | Extension | Supported format |
|---|---|---|---|
| VCF | Export variant tracks to Variant Call Format | [vcf] | No |

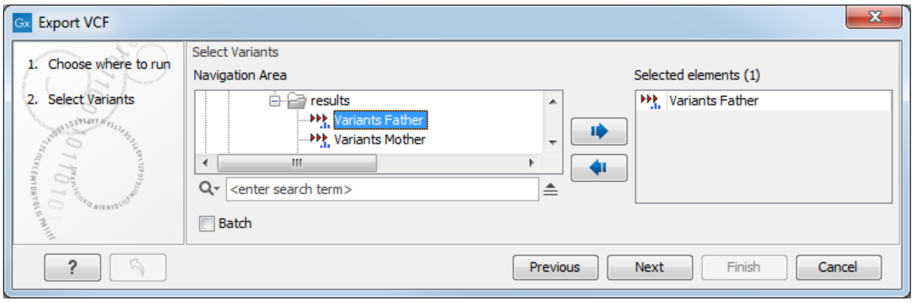
Figure 5.3: *The text field has been used to search for VCF format in the Select exporter dialog.*

When the desired export format has been identified, click on the button labeled **Open**.

**Selecting data for export - part II.** A dialog appears, with a name reflecting the format you have chosen. For example if the "Variant Call Format" (VCF format) was selected, the window is labeled "Export VCF".

If you are logged into a CLC Server, you will be asked whether to run the export job using the Workbench or the Server. After this, you are provided with the opportunity to select or de-select data to be exported.

In figure 5.4 we show the selection of a variant track for export to VCF format.



Export VCF

1. Choose where to run
2. Select Variants

Select Variants

Navigation Area

- results
  - Variants Father
  - Variants Mother

<enter search term>

□ Batch

Selected elements (1)

- Variants Father

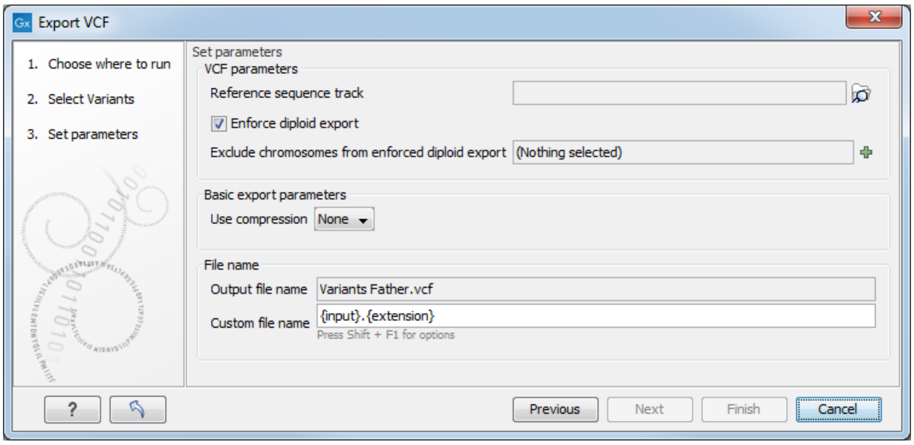
Figure 5.4: *The Select exporter dialog. Select the data element(s) to export.*

The parameters under **Basic export parameters** and **File name** are offered when exporting to any format.

There may be additional parameters for particular export formats. This is illustrated here with the VCF exporter, where a reference sequence track must be selected (see figure 5.5).

**Paired reads settings.** In the case of Fastq Export, the option "Export paired sequence lists to two files" is selected by default: it will export paired-end reads to two fastq files rather than a single interleaved file.

**Compression options.** Within the **Basic export parameters** section, you can choose to compress the exported files. The options are no compression (None), gzip or zip format. Choosing zip format results in all data files being compressed into a single file. Choosing gzip compresses the exported file for each data element individually.



Export VCF

1. Choose where to run
2. Select Variants
3. Set parameters

Set parameters

VCF parameters

Reference sequence track

☑ Enforce diploid export

Exclude chromosomes from enforced diploid export (Nothing selected)

Basic export parameters

Use compression None

File name

Output file name Variants Father.vcf

Custom file name {input}.{extension}

Press Shift + F1 for options

Figure 5.5: *Set the export parameters. When exporting in VCF format, a reference sequence track must be selected.*

**Exporting multiple files.** If you have selected multiple files of the same type, you can choose to export them in one single file (only for certain file formats) by selecting "Output as single file" in the **Basic export parameters** section. If you wish to keep the files separate after export, make sure this box is not ticked. **Note:** Exporting in zip format will export only one zipped file, but the files will be separated again when unzipped.

**Choosing the exported file name(s)** The default setting for the **File name** is to use the original data element name as the basename and the export format as the suffix.

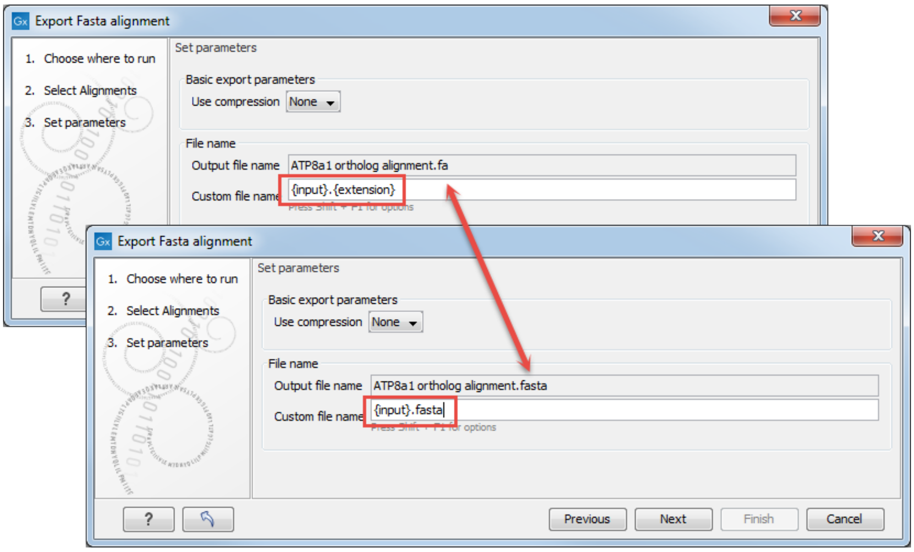
When exporting just one data element, or exporting to a zip file, the desired filename could just be typed in the Custom file name box.

When working with the export of multiple files, using some combination of the terms shown by default in this field and in figure 5.8 are recommended. Clicking in the **Custome file name** field with the mouse and then simultaneously pressing the Shift + F1 keys bring up a list of the available terms that can be included in this field.

The following placeholders are available:

- **{input}** or **{1}** - default name of the data element being exported
- **{extension}** or **{2}** - default extension for the chosen export format
- **{counter}** or **{3}** - a number that is incremented per file exported. i.e. If you export more than one file, counter is replaced with 1 for the first file, 2 for the next and so on.
- **{user}** - name of the user who launched the job
- **{host}** - name of the machine the job is run on
- **{year}**, **{month}**, **{day}**, **{hour}**, **{minute}**, and **{second}** - timestamp information based on the time an output is created. Using these placeholders, items generated by a workflow at different times can have different filenames.

We will look at an example to illustrate this: In this example we would like to change the export file format to .fasta in a situation where .fa was the default format that would be used if you kept the default file extension suggestion ("{2}"). To do this replace "{2}" with ".fasta" in the "Custom file name field". You can see that when changing "{2}" to ".fasta" , the file name extension in the "Output file name" field automatically changes to the new format (see figure 5.6).

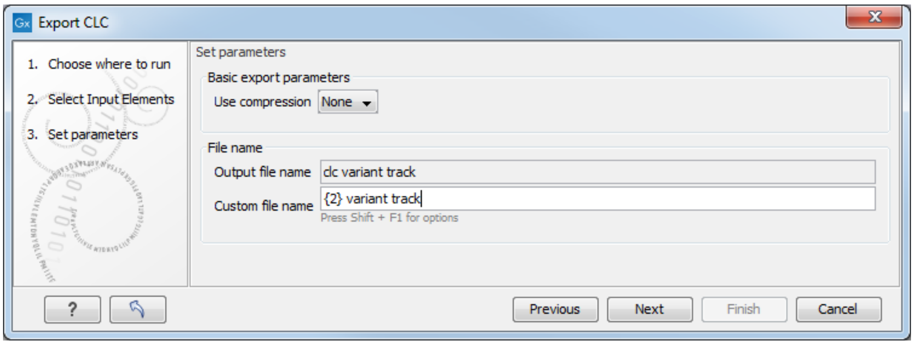


Use compression: None
Output file name: ATP8a1 ortholog alignment.fa
Custom file name: {input}.{extension}
Press Shift + F1 for options

Use compression: None
Output file name: ATP8a1 ortholog alignment.fasta
Custom file name: {input}.fasta
Press Shift + F1 for options

Figure 5.6: *The file name extension can be changed by typing in the preferred file name format.*

When deciding on an output name, you can choose any combination of the different placeholders as well as custom names and punctuation, as in `{input}({day}-{month}-{year})`. Another example of a meaningful name to a variant track could be `{2} variant track` as shown in figure 5.7. If your workflow input is named `Sample 1`, the result would be "Sample 1 variant track".



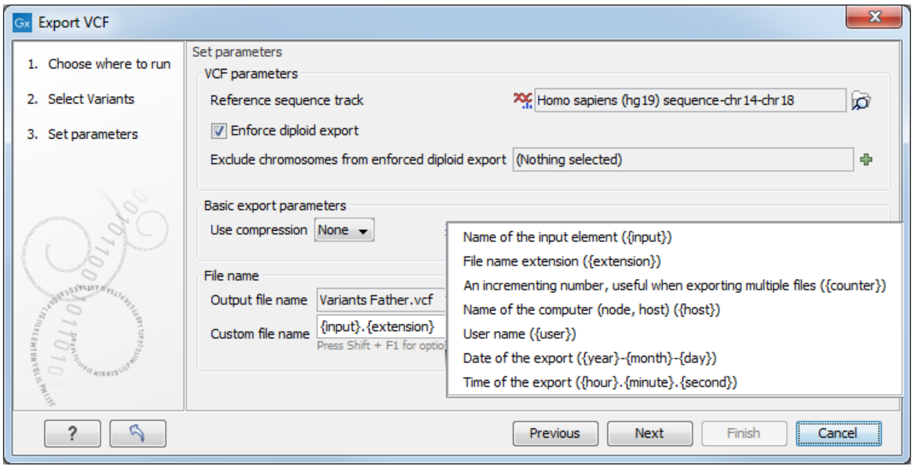
Use compression: None
Output file name: clc variant track
Custom file name: {2} variant track
Press Shift + F1 for options

Figure 5.7: *Providing a custom name for the result.*

As you add or remove text and terms in the **Custom file name** field, the text in the **Output file name** field will change so you can see what the result of your naming choice will be for your data. When working with multiple files, only the name of the first one is shown. Just move the mouse cursor over the name shown in the **Output file name** field to show a listing of the all the filenames.

The last step is to specify the exported data should be saved.

**A note about decimals and Locale settings**. When exporting to CSV and tab delimited files, decimal numbers are formatted according to the Locale setting of the Workbench (see section 3.1). If you open the CSV or tab delimited file with spreadsheet software like Excel, you should make sure that both the Workbench and the spreadsheet software are using the same Locale.


Export VCF

1. Choose where to run
2. Select Variants
3. Set parameters

Set parameters

VCF parameters

Reference sequence track: Homo sapiens (hg19) sequence-chr14-chr18

☑ Enforce diploid export

Exclude chromosomes from enforced diploid export: (Nothing selected)

Basic export parameters

Use compression: None

File name

Output file name: Variants Father.vcf

Custom file name: {input}.{extension}

Press Shift + F1 for optio

- Name of the input element ({input})
- File name extension ({extension})
- An incrementing number, useful when exporting multiple files ({counter})
- Name of the computer (node, host) ({host})
- User name ({user})
- Date of the export ({year}-{month}-{day})
- Time of the export ({hour}.{minute}.{second})

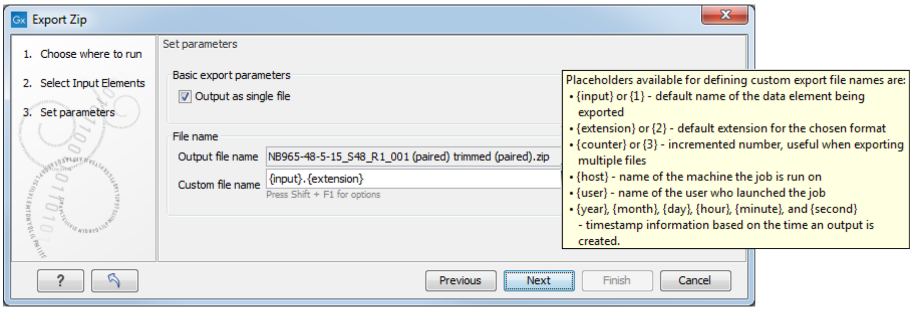
Figure 5.8: *Use the custom file name pattern text field to make custom names.*

### 5.2.1 Export of folders and multiple elements in CLC format

In the list of export formats presented is one called zip format. Choosing this format means that you wish to export the selected data element(s) or folders to a single, compressed CLC format file. This is useful in cases where you wish to exchange data between workbenches or as part of a simple backup procedure.

A zip file generated this way can be imported directly into a workbench using the Standard Import tool and leaving the import type as Automatic.

**Note!** When exporting multiple files, the names will be listed in the "Output file name" text field with only the first file name being visible and the rest being substituted by "...", but will appear in a tool tip if you hover the mouse over that field (figure 5.9).


Export Zip

1. Choose where to run
2. Select Input Elements
3. Set parameters

Set parameters

Basic export parameters

☑ Output as single file

File name

Output file name: NB965-48-5-15_S48_R1_001 (paired) trimmed (paired).zip

Custom file name: {input}.{extension}

Press Shift + F1 for options

Placeholders available for defining custom export file names are:
- {input} or {1} - default name of the data element being exported
- {extension} or {2} - default extension for the chosen format
- {counter} or {3} - incremented number, useful when exporting multiple files
- {host} - name of the machine the job is run on
- {user} - name of the user who launched the job
- {year}, {month}, {day}, {hour}, {minute}, and {second} - timestamp information based on the time an output is created.

Figure 5.9: *The output file names are listed in the "Output file name" text field.*

### 5.2.2 Export of dependent elements

Sometimes it can be useful to export the results of an analysis and its dependent elements. That is, the results along with the data that was used in the analysis. For example, one might wish to export an alignment along with all the sequences that were used in generating that alignment.

To export a data element with its dependent elements:

- Select the parent data element (like an alignment) in the **Navigation Area**.
- Start up the exporter tool by going to **File** | **Export with Dependent Elements**.

- Edit the output name if desired and select where the resulting zip format file should be exported to.

The file you export contains compressed CLC format files containing the data element you chose and all its dependent data elements.

A zip file created this way can be imported directly into a CLC workbench by going to

**File** | **Import** | **Standard Import**

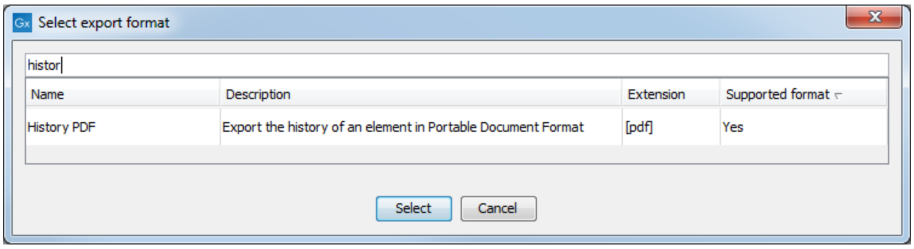
In this case, the import type can be left as Automatic.

### 5.2.3 Export history

Each data element in the Workbench has a history. The history information includes things like the date and time data was imported or an analysis was run, the parameters and values set, and where the data came from. For example, in the case of an alignment, one would see the sequence data used for that alignment listed. You can view this information for each data element by clicking on the Show History view ( ) at the bottom of the viewing area when a data element is open in the Workbench.

This history information can be exported to a pdf document or to a CSV file. To do this:

- (Optional, but preferred) Select the data element (like an alignment) in the **Navigation Area**.
- Start up the exporter tool via the Export button in the toolbar or using the **Export** option under the File menu.
- Select the **History PDF** or History CSV as the format to export to (figure 5.10).
- Select the data to export, or confirm the data to export if it was already selected via the **Navigation Area**.
- Edit any parameters of interest, such as the Page Setup details, the output filename(s) and whether or not compression should be applied (figure 5.11).
- Select where the data should be exported to.
- Click on the button labeled **Finish**.

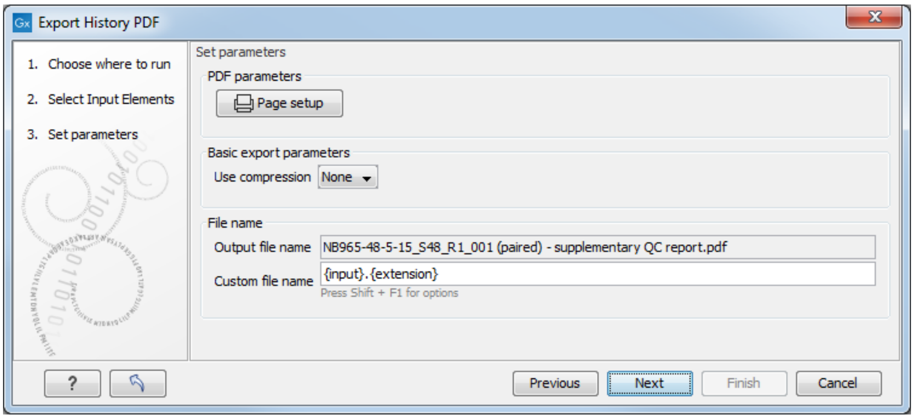


Select export format

histor

| Name | Description | Extension | Supported format |
|---|---|---|---|
| History PDF | Export the history of an element in Portable Document Format | [pdf] | Yes |

Figure 5.10: *Select "History PDF" for exporting the history of an element as a PDF file.*



Use compression None

Output file name NB965-48-5-15_S48_R1_001 (paired) - supplementary QC report.pdf

Custom file name {input}.{extension}

Figure 5.11: *When exporting the history in PDF, it is possible to adjust the page setup.*

### 5.2.4 The CLC format

The *CLC Sequence Viewer* stores bioinformatic data in CLC format. The CLC format contains data, as well as information about that data like history information and comments you may have added.

A given data element in the Workbench can contain different types of data. This is reflected when exporting data, as the choice of different export formats can lead to the extraction of some parts of that data object rather than others. The part of the data exported reflects the type of data a given format can support. As a simple example, if you export the results of an alignment to Annotation CSV format, you will get just the annotation information. If you exported to Fasta alignment format, you would get the aligned sequences in fasta format, but no annotations.

The CLC format holds all the information for a given data object. Thus if you plan to share the data with colleagues who also have a CLC Workbench or you are communicating with the QIAGEN Bioinformatics Technical Service team and you wish to share the data from within the Workbench, exporting to CLC format is usually the best choice as all information associated with that data object in your Workbench will then be available to the other person who imports that data.

If you are planning to share your data with someone who does not have access to a CLC Workbench, then you will wish to export to another data format. Specifically, one they can use with the software they are working with.

### 5.2.5 Backing up data from the CLC Workbench

Regular backups of your data are advisable.

The data stored in your CLC Workbench is in the areas defined as CLC Data Locations. Whole data locations can be backed up directly (option 1) or, for smaller amounts of data, you could export the selected data elements to a zip file (option 2).

**Option 1: Backing up each CLC Data Location**

The easiest way for most people to find out where their data is stored is to put the mouse cursor over the top level directories, that is, the ones that have an icon like (📁), in the **Navigation Area** of the Workbench. This brings up a tool tip with the system location for that data location.

To back up all your CLC data, please ensure that all your CLC Data Locations are backed up.

Here, if you needed to recover the data later, you could put add the data folder from backup as a data location in your Workbench. If the original data location is not present, then the data should be usable directly. If the original data location is still present, the Workbench will re-index the (new) data location. For large volumes of data, re-indexing can take some time.

Information about your data locations can also be found in an xml file called model_settings_300.xml This file is located in the settings folder in the user home area. Further details about this file and how it pertains to data locations in the Workbench can be found in the Deployment Manual: http://resources.qiagenbioinformatics.com/manuals/workbenchdeployment/current/index.php?manual=Changing_default_location.html.

**Option 2: Export a folder of data or individual data elements to a CLC zip file**

This option is for backing up smaller amounts of data, for example, certain results files or a whole data location, where that location contains smaller amounts of data. For data that takes up many gigabases of space, this method can be used, but it can be very demanding on space, as well as time.

Select the data items, including any folders, in the Navigation area of your Workbench and choose to export by going to:

**File** | **Export** ()

and choosing ZIP format.

The zip file created will contain all the data you selected. You can later re-import the zip file into the Workbench by going to:

**File** | **Import** ()

The only data files associated with the *CLC Sequence Viewer* not within a specified data location are BLAST databases. It is unusual to back up BLAST databases as they are usually updated relatively frequently and in many cases can be easily re-created from the original files or re-downloaded from public resources. If you do wish to backup your BLAST database files, they can be found in the folders specified in the BLAST Database Manager, which is started by going to:
**Toolbox | BLAST | Manage BLAST databases** .

### 5.2.6 Export of tables

Tables can be exported in four different formats; CSV, tab-separated, Excel, or html.

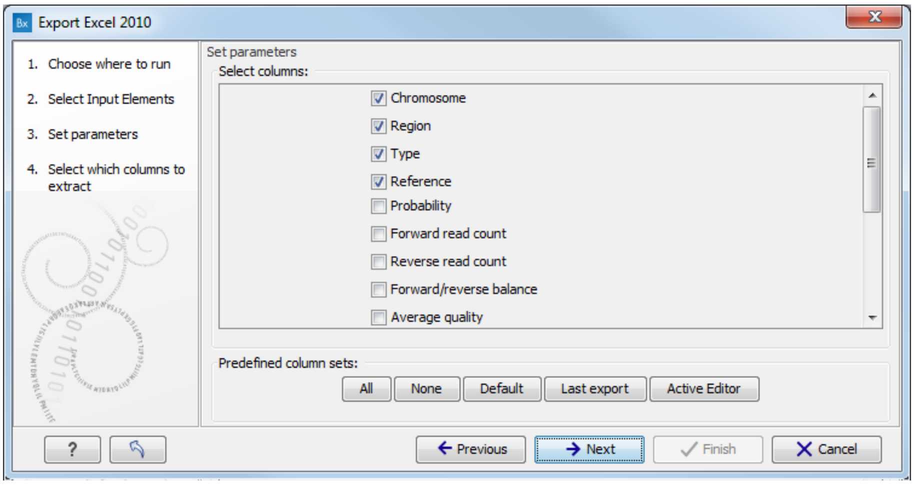
When exporting a table in CSV, tab-separated, or Excel format, numbers with many decimals are printed in the exported file with 10 decimals, or in 1.123E-5 format when the number is close to zero.

Excel limits the number of hyperlinks in a worksheet to 66,530. When exporting a table of more than 66,530 rows, Excel will "repair" the file by removing all hyperlinks. If you want to keep the hyperlinks valid, you will need to export your data to several worksheets in batches smaller than 66,530 rows.

When exporting a table in html format, data are exported with the number of decimals that have been defined in the workbench preference settings. When tables are exported in html format from the server or using command line tools, the default number of exported decimals is 3.

The Excel exporters, the CSV and tab delimited exporters, and the HTML exporter have been extended with the ability to export only a sub-set of columns from the object being exported. Uncheck the option "Export all columns" and click next to see a new dialog window in which columns to be exported can be selected (figure 5.12). You can choose them one by one or choose a predefined subset:

- All: will select all possible columns.
- None: will clear all preselected column.
- Default: will select the columns preselected by default by the software.
- Last export: will select all windows that were selected during the last export.
- Active editor (only if an active editor is currently open): the columns selected are the same than in the active editor window.



Export Excel 2010

1. Choose where to run
2. Select Input Elements
3. Set parameters
4. Select which columns to extract

Set parameters

Select columns:

☑ Chromosome
☑ Region
☑ Type
☑ Reference
□ Probability
□ Forward read count
□ Reverse read count
□ Forward/reverse balance
□ Average quality

Predefined column sets:

Figure 5.12: *Selecting columns to be exported.*

After selecting columns, the user will be directed to the output destination wizard page.

## 5.3 Export graphics to files

*CLC Sequence Viewer* supports export of graphics into a number of formats. This way, the visible output of your work can easily be saved and used in presentations, reports etc. The **Export Graphics** function ( ) is found in the **Toolbar**.

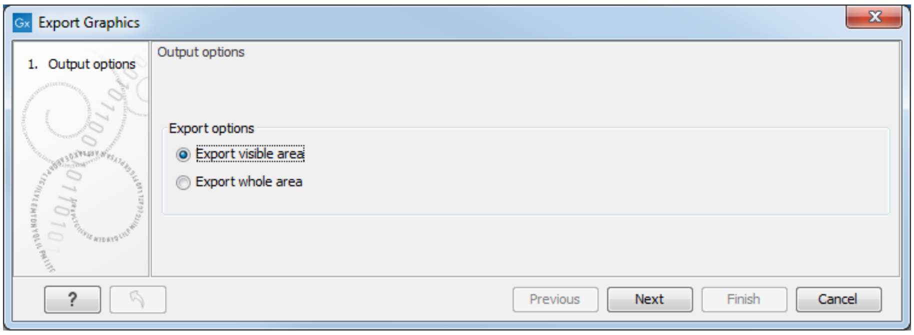
*CLC Sequence Viewer* uses a WYSIWYG principle for graphics export: What You See Is What You Get. This means that you should use the options in the Side Panel to change how your data, e.g. a sequence, looks in the program. When you export it, the graphics file will look exactly the same way.

It is not possible to export graphics of elements directly from the **Navigation Area**. They must first be opened in a view in order to be exported. To export graphics of the contents of a view:

**select tab of View | Graphics ( ) on Toolbar**

This will display the dialog shown in figure 5.13.

In the following dialog, you can choose to:



Export Graphics

1. Output options

Output options

Export options

● Export visible area

○ Export whole area

Figure 5.13: *Selecting to export whole view or to export only the visible area.*

- **Export visible area**, or
- **Export whole view**

These options are available for all views that can be zoomed in and out. In figure 5.14 is a view of a circular sequence which is zoomed in so that you can only see a part of it.

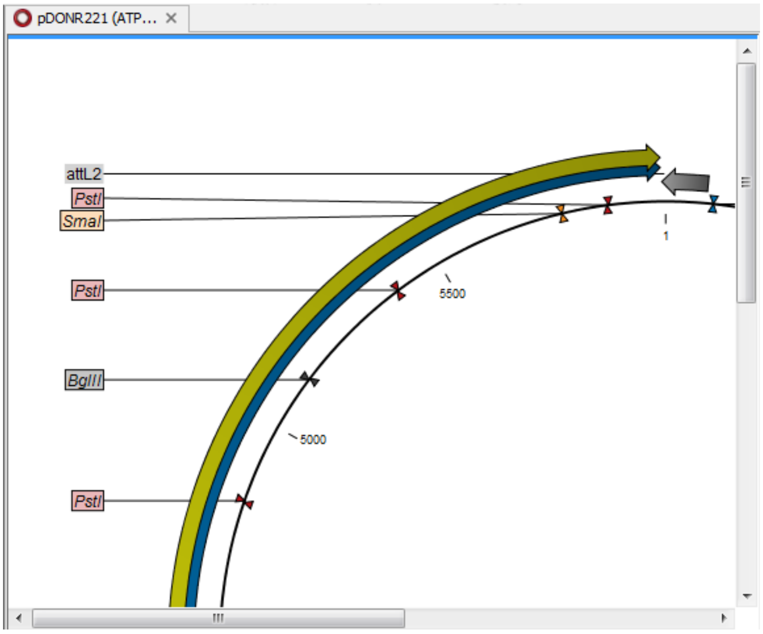


Figure 5.14: *A circular sequence as it looks on the screen when zoomed in.*

When selecting **Export visible area**, the exported file will only contain the part of the sequence that is *visible* in the view. The result from exporting the view from figure 5.14 and choosing **Export visible area** can be seen in figure 5.15.

On the other hand, if you select **Export whole view**, you will get a result that looks like figure 5.16. This means that the graphics file will also include the part of the sequence which is not visible when you have zoomed in.

Finally, choose a name and save location for the graphics file. Then you can either click **Next** or **Finish**, depending on what is available: clicking **Next** allows you to set further parameters for the graphics export, whereas clicking **Finish** will export using the parameters that you have set last time you made a graphics export in that file format (if it is the first time, it will use default parameters).

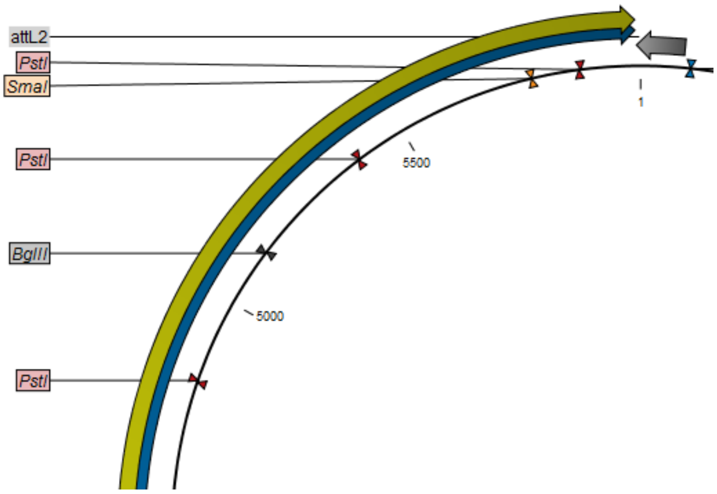


Figure 5.15: *The exported graphics file when selecting Export visible area.*

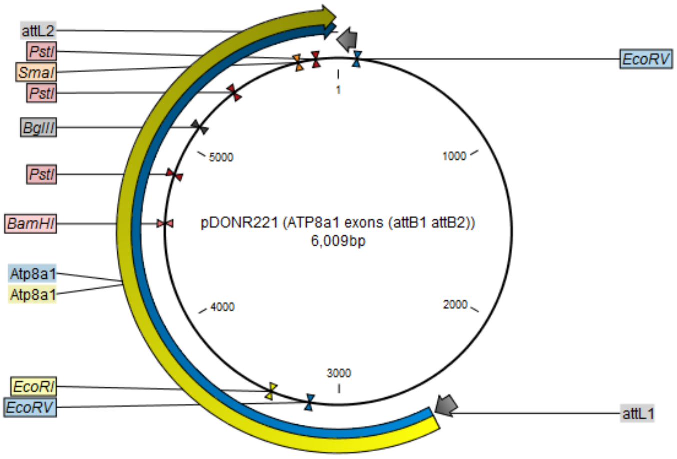


Figure 5.16: *The exported graphics file when selecting Export whole view. The whole sequence is shown, even though the view is zoomed in on a part of the sequence.*

### 5.3.1 File formats

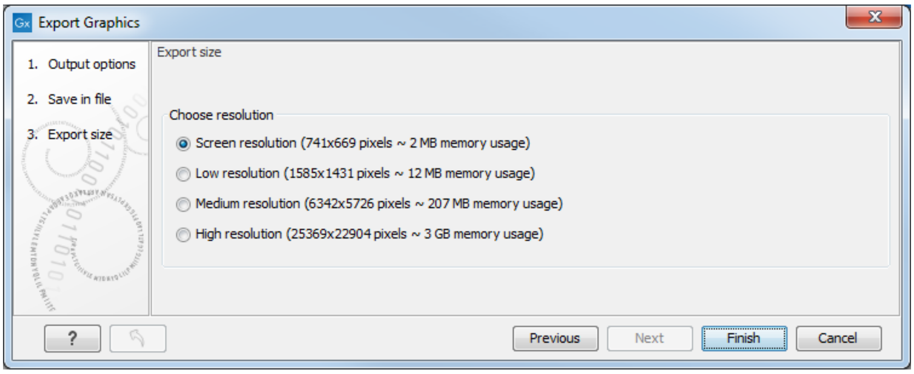
*CLC Sequence Viewer* supports the following file formats for graphics export:

| Format | Suffix | Type |
|---|---|---|
| Portable Network Graphics | .png | bitmap |
| JPEG | .jpg | bitmap |
| Tagged Image File | .tif | bitmap |
| PostScript | .ps | vector graphics |
| Encapsulated PostScript | .eps | vector graphics |
| Portable Document Format | .pdf | vector graphics |
| Scalable Vector Graphics | .svg | vector graphics |

These formats can be divided into bitmap and vector graphics. The difference between these two categories is described below:

**Bitmap images** In a bitmap image, each dot in the image has a specified color. This implies, that if you zoom in on the image there will not be enough dots, and if you zoom out there will be too many. In these cases the image viewer has to interpolate the colors to fit what is actually looked at. A bitmap image needs to have a high resolution if you want to zoom in. This format is a good choice for storing images without large shapes (e.g. dot plots). It is also appropriate if you don't have the need for resizing and editing the image after export.

**Parameters for bitmap formats** For bitmap files, clicking **Next** will display the dialog shown in figure 5.17.



Choose resolution

- ● Screen resolution (741x669 pixels ~ 2 MB memory usage)
- ○ Low resolution (1585x1431 pixels ~ 12 MB memory usage)
- ○ Medium resolution (6342x5726 pixels ~ 207 MB memory usage)
- ○ High resolution (25369x22904 pixels ~ 3 GB memory usage)

Figure 5.17: *Parameters for bitmap formats: size of the graphics file.*

You can adjust the size (the resolution) of the file to four standard sizes:

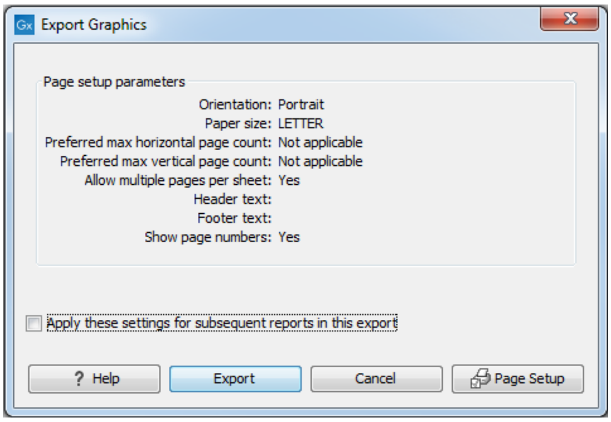
- Screen resolution
- Low resolution
- Medium resolution
- High resolution

The actual size in pixels is displayed in parentheses. An estimate of the memory usage for exporting the file is also shown. If the image is to be used on computer screens only, a low resolution is sufficient. If the image is going to be used on printed material, a higher resolution is necessary to produce a good result.

**Vector graphics** Vector graphic is a collection of shapes. Thus what is stored is information about where a line starts and ends, and the color of the line and its width. This enables a given viewer to decide how to draw the line, no matter what the zoom factor is, thereby always giving a correct image. This format is good for graphs and reports, but less usable for dot plots. If the image is to be resized or edited, vector graphics are by far the best format to store graphics. If you open a vector graphics file in an application such as Adobe Illustrator, you will be able to manipulate the image in great detail.

Graphics files can also be imported into the **Navigation Area**. However, no kinds of graphics files can be displayed in *CLC Sequence Viewer*. See section 5.1.1 for more about importing external files into *CLC Sequence Viewer*.

**Parameters for vector formats** For PDF format, the dialog shown in figure 5.18 will sometimes appear after you have clicked finished (for example when the graphics use more than one page, or there is more than one PDF to export).


Export Graphics

Page setup parameters

Orientation: Portrait
Paper size: LETTER
Preferred max horizontal page count: Not applicable
Preferred max vertical page count: Not applicable
Allow multiple pages per sheet: Yes
Header text:
Footer text:
Show page numbers: Yes

□ Apply these settings for subsequent reports in this export

Figure 5.18: *Page setup parameters for vector formats.*

The settings for the page setup are shown. Clicking the **Page Setup** button will display a dialog where these settings can ba adjusted. This dialog is described in section 4.2.

It is then possible to click the option "Apply these settings for subsequent reports in this export" to apply the chosen settings to all the PDFs included in the export for example.

The page setup is only available if you have selected to export the whole view - if you have chosen to export the visible area only, the graphics file will be on one page with no headers or footers.

**Exporting protein reports** It is possible to export a protein report using the normal **Export** function () which will generate a pdf file with a table of contents:

> **Click the report in the Navigation Area | Export () in the Toolbar | select pdf**

You can also choose to export a protein report using the **Export graphics** function (), but in this way you will not get the table of contents.

## 5.4 Export graph data points to a file

Data points for graphs displayed along the sequence or along an alignment or mapping can be exported to a semicolon-separated text file (csv format). An example of such a graph is shown in figure 5.19. This graph shows the coverage of reads in a read mapping.

To export the data points for the graph, right-click the graph and choose **Export Graph to Comma-separated File**. Depending on what kind of graph you have selected, different options will be shown: If the graph is covering a set of aligned sequences with a main sequence, such as read mappings and BLAST results, the dialog shown in figure 5.20 will be displayed. These kinds of graphs are located under **Alignment info** in the Side Panel. In all other cases, a normal file dialog will be shown letting you specify name and location for the file.

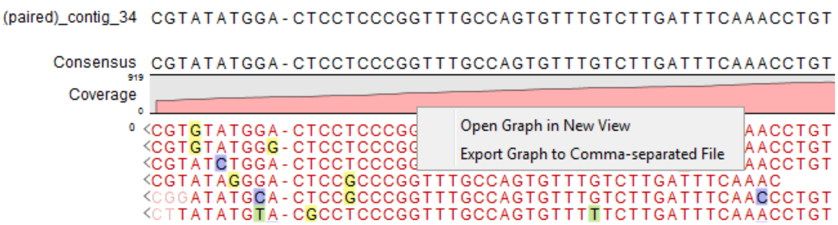
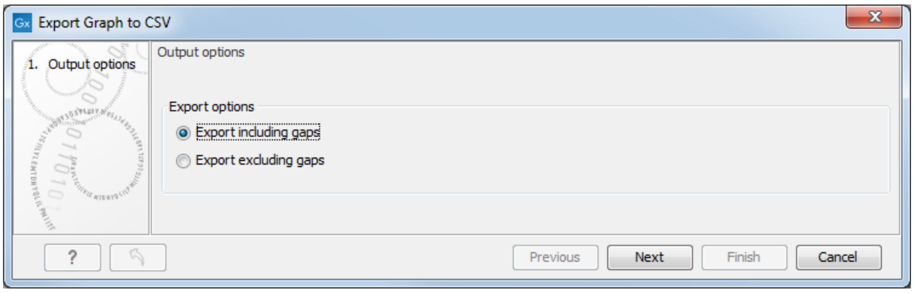


Figure 5.19: *A graph displayed along mapped reads. Right-click the graph to export the data points to a file.*



Output options

Export options

● Export including gaps

○ Export excluding gaps

Figure 5.20: *Choosing to include data points with gaps*

In this dialog, select whether you wish to include positions where the main sequence (the reference sequence for read mappings and the query sequence for BLAST results) has gaps. If you are exporting e.g. coverage information from a read mapping, you would probably want to exclude gaps, if you want the positions in the exported file to match the reference (i.e. chromosome) coordinates. If you export including gaps, the data points in the file no longer corresponds to the reference coordinates, because each gap will shift the coordinates.

Clicking **Next** will present a file dialog letting you specify name and location for the file.

The output format of the file is like this:

```
"Position";"Value";
"1";"13";
"2";"16";
"3";"23";
"4";"17";
...
```

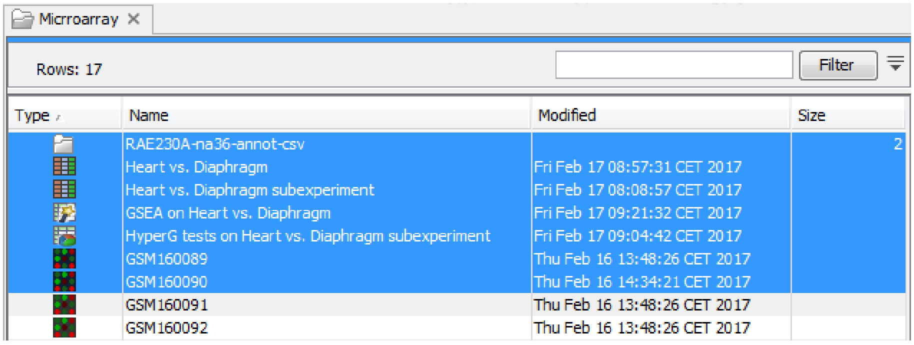
## 5.5 Copy/paste view output

The content of tables (reports, folder lists, and sequence lists) can be copy/pasted into different programs, where it can be edited. *CLC Sequence Viewer* pastes the data in tabulator separated format in various programs in which the copy/paste can be applied. For simplicity, we include one example of the copy/paste function from a **Folder Content** view to Microsoft Excel.

Right click a folder in the Navigation Area and chooses **Show** | **Content**. The different elements saved in that folder are now listed in a table in the View Area. Select one or more of these elements and use the Ctrl + C (or ⌘ + C) command to copy the selected items.

See figure 5.21.

Then, in a new Excel document, right-click in the cell A1 and paste the items previously copied.



Rows: 17

| Type | Name | Modified | Size |
|---|---|---|---|
| | RAE230A-na36-annot-csv | | 2 |
| | Heart vs. Diaphragm | Fri Feb 17 08:57:31 CET 2017 | |
| | Heart vs. Diaphragm subexperiment | Fri Feb 17 08:08:57 CET 2017 | |
| | GSEA on Heart vs. Diaphragm | Fri Feb 17 09:21:32 CET 2017 | |
| | HyperG tests on Heart vs. Diaphragm subexperiment | Fri Feb 17 09:04:42 CET 2017 | |
| | GSM160089 | Thu Feb 16 13:48:26 CET 2017 | |
| | GSM160090 | Thu Feb 16 14:34:21 CET 2017 | |
| | GSM160091 | Thu Feb 16 13:48:26 CET 2017 | |
| | GSM160092 | Thu Feb 16 13:48:26 CET 2017 | |

Figure 5.21: *Selected elements in a Folder Content view.*

The outcome might appear unorganized, but with a few operations the structure of the view in *CLC Sequence Viewer* can be produced. (Except the icons which are replaced by file references in Excel.)

Note that all tables can also be **Exported** (📤) directly in Excel format.

# Chapter 6

# Data download

## Contents

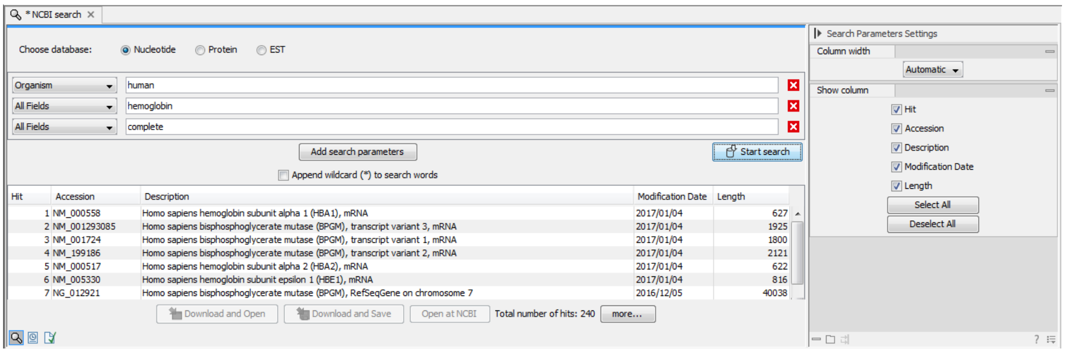
*CLC Sequence Viewer* allows you to search the for sequences on the Internet. You must be online when initiating and performing searches in NCBI.

## 6.1 Search for Sequences at NCBI

This section describes searches for sequences in GenBank - the **NCBI Entrez** database

**Download** | **Search for Sequences at NCBI** (🔍) or **Ctrl + B** (**⌘ + B on Mac)**

This opens the following view (figure 6.1).



Choose database: ● Nucleotide ○ Protein ○ EST

Organism: human

All Fields: hemoglobin

All Fields: complete

□ Append wildcard (*) to search words

| Hit | Accession | Description | Modification Date | Length |
|---|---|---|---|---|
| 1 | NM_000558 | Homo sapiens hemoglobin subunit alpha 1 (HBA1), mRNA | 2017/01/04 | 627 |
| 2 | NM_001293085 | Homo sapiens bisphosphoglycerate mutase (BPGM), transcript variant 3, mRNA | 2017/01/04 | 1925 |
| 3 | NM_001724 | Homo sapiens bisphosphoglycerate mutase (BPGM), transcript variant 1, mRNA | 2017/01/04 | 1800 |
| 4 | NM_199186 | Homo sapiens bisphosphoglycerate mutase (BPGM), transcript variant 2, mRNA | 2017/01/04 | 2121 |
| 5 | NM_000517 | Homo sapiens hemoglobin subunit alpha 2 (HBA2), mRNA | 2017/01/04 | 622 |
| 6 | NM_005330 | Homo sapiens hemoglobin subunit epsilon 1 (HBE1), mRNA | 2017/01/04 | 816 |
| 7 | NG_012921 | Homo sapiens bisphosphoglycerate mutase (BPGM), RefSeqGene on chromosome 7 | 2016/12/05 | 40038 |

Total number of hits: 240

Column width: Automatic

Show column

☑ Hit

☑ Accession

☑ Description

☑ Modification Date

☑ Length

Figure 6.1: *The GenBank search view.*

The search view can be saved either using dragging the search tab and and dropping it in the **Navigation Area** or by clicking **Save** (⇤). When saving the search, only the parameters are saved - not the results of the search. This is useful if you have a special search that you perform from time to time.

Even if you don't save the search, the next time you open the search view, it will remember the parameters from the last time you did a search.

### 6.1.1 NCBI search options

Conducting a search in the **NCBI Database** from *CLC Sequence Viewer* corresponds to conducting the search on NCBI's website. When conducting the search from *CLC Sequence Viewer*, the results are available and ready to work with straight away.

You can choose whether you want to search for nucleotide sequences, protein sequences or EST databases.

As default, *CLC Sequence Viewer* offers one text field where the search parameters can be entered. Click **Add search parameters** to add more parameters to your search.
**Note!** The search is a "and" search, meaning that when adding search parameters to your search, you search for both (or all) text strings rather than "any" of the text strings.

You can append a wildcard character by checking the checkbox at the bottom. This means that you only have to enter the first part of the search text, e.g., searching for "genom" will find both "genomic" and "genome".

The following parameters can be added to the search:

- **All fields** Searches in all parameters in the NCBI database at the same time. It also provide an opportunity to search to parameters which are not listed in the dialog (e.g., `CD9 NOT homo sapiens`).
- **Organism**
- **Definition/Title**
- **Modified Since** Choose one option from the drop-down menu, between 30 days and 10 years.
- **Gene Location** Choose from Genomic DNA/RNA, Mitochondrion, or Chloroplast.
- **Molecule** Choose from Genomic DNA/RNA, mRNA or rRNA.
- **Sequence Length** enter a number for a maximum or minimum length of the sequence.
- **Gene Name**
- **Accession**

**Note!** A "Feature Key" option is available in GenBank when searching for nucleotide sequences: writing `gene[Feature key] AND mouse` will generate hits for one or more genes and where 'mouse' appears somewhere in GenBank file. For more information about how to use this syntax, see `http://www.ncbi.nlm.nih.gov/books/NBK3837/`

When you are satisfied with the parameters you have entered, click **Start search**. When conducting a search, no files are downloaded. Instead, the program produces a list of links to the files in the NCBI database. This ensures a much faster search.

### 6.1.2 Handling of NCBI search results

The search result is presented as a list of links to the files in the NCBI database. The **View** displays 50 hits at a time. This can be changed in the **Preferences** (see chapter 3). More hits can be displayed by clicking the **More...** button at the bottom right of the **View**.

Each sequence hit is represented by text in three columns:

- Accession.
- Description.
- Modification date.
- Length.

It is possible to exclude one or more of these columns by adjust the View preferences for the database search view. Furthermore, your changes in the View preferences can be saved. See section 3.5.

Several sequences can be selected, and by clicking the buttons in the bottom of the search view - or right clicking on the selected sequence(s) - you can do the following:

- **Download and Open** opens the sequence in a new view.
- **Download and Save** lets you choose location for saving sequence.
- **Open at NCBI** opens an internet browser and displays the sequence on NCBI's web page.

Double-clicking a hit will download and open the sequence. The hits can also be downloaded into the **View Area** or the **Navigation Area** from the search results by drag and drop or copy/paste.

**Note!** Search results are downloaded before they are saved. Downloading and saving several files may take some time. However, since the process runs in the background (displayed in the **Status bar**) it is possible to continue other tasks in the program. Like the search process, the download process can be stopped. This is done in the **Toolbox** in the **Processes** tab.

# Part III

# Bioinformatics

# Chapter 7

# Viewing and editing sequences

**Contents**

*CLC Sequence Viewer* offers five different ways of viewing and editing single sequences as described in the first five sections of this chapter. Furthermore, this chapter also explains how to create a new sequence and how to gather several sequences in a sequence list.

## 7.1 View sequence

When you double-click a sequence in the **Navigation Area**, the sequence will open automatically, and you will see the nucleotides or amino acids. The zoom options described in section 2.3 allow you to e.g. zoom out in order to see more of the sequence in one view. There are a number of options for viewing and editing the sequence which are all described in this section.

All the options described in this section also apply to alignments (further described in section 12.2).

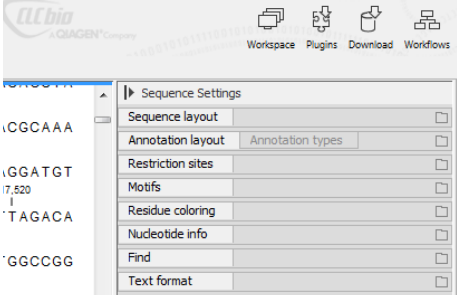


Figure 7.1: *Overview of the Side Panel which is always shown to the right of a view.*

### 7.1.1 Sequence settings in Side Panel

Each view of a sequence has a **Side Panel** located at the right side of the view (see figure 7.1.

When you make changes in the **Side Panel** the view of the sequence is instantly updated. To show or hide the **Side Panel**:

**select the View | Ctrl + U**

or **Click the ( |▸ ) at the top right corner of the Side Panel to hide | Click the ( ◂| ) to the right to show**

Below, each group of settings will be explained. Some of the preferences are not the same for nucleotide and protein sequences, but the differences will be explained for each group of settings.

**Note!** When you make changes to the settings in the **Side Panel**, they are not automatically saved when you save the sequence. Click **Save/restore Settings** ( ☰ ) to save the settings (see section 3.5 for more information).

#### Sequence Layout

These preferences determine the overall layout of the sequence:

- **Spacing.** Inserts a space at a specified interval:
  - **No spacing.** The sequence is shown with no spaces.
  - **Every 10 residues.** There is a space every 10 residues, starting from the beginning of the sequence.
  - **Every 3 residues, frame 1.** There is a space every 3 residues, corresponding to the reading frame starting at the first residue.
  - **Every 3 residues, frame 2.** There is a space every 3 residues, corresponding to the reading frame starting at the second residue.
  - **Every 3 residues, frame 3.** There is a space every 3 residues, corresponding to the reading frame starting at the third residue.
- **Wrap sequences.** Shows the sequence on more than one line.
  - **No wrap.** The sequence is displayed on one line.
  - **Auto wrap.** Wraps the sequence to fit the width of the view, not matter if it is zoomed in our out (displays minimum 10 nucleotides on each line).

  - **Fixed wrap.** Makes it possible to specify when the sequence should be wrapped. In the text field below, you can choose the number of residues to display on each line.

- **Double stranded.** Shows both strands of a sequence (only applies to DNA sequences).

- **Numbers on sequences.** Shows residue positions along the sequence. The starting point can be changed by setting the number in the field below. If you set it to e.g. 101, the first residue will have the position of -100. This can also be done by right-clicking an annotation and choosing **Set Numbers Relative to This Annotation**.

- **Numbers on plus strand.** Whether to set the numbers relative to the positive or the negative strand in a nucleotide sequence (only applies to DNA sequences).

- **Lock numbers.** When you scroll vertically, the position numbers remain visible. (Only possible when the sequence is not wrapped.)

- **Lock labels.** When you scroll horizontally, the label of the sequence remains visible.

- **Sequence label.** Defines the label to the left of the sequence.

  - Name (this is the default information to be shown).
  - Accession (sequences downloaded from databases like GenBank have an accession number).
  - Latin name.
  - Latin name (accession).
  - Common name.
  - Common name (accession).

- **Matching residues as dots** Residues in aligned sequences identical to residues in the first (reference) sequence will be presented as dots. An option that is only available for "Alignments" and "Read mappings".

**Annotation Layout and Annotation Types** See section 7.3.1.

### Restriction sites

See section 7.1.1.

### Residue coloring

These preferences make it possible to color both the residue letter and set a background color for the residue.

- **Non-standard residues.** For nucleotide sequences this will color the residues that are not C, G, A, T or U. For amino acids only B, Z, and X are colored as non-standard residues.

  - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
  - **Background color.** Sets the background color of the residues. Click the color box to change the color.

- **Rasmol colors.** Colors the residues according to the Rasmol color scheme.
  See http://www.openrasmol.org/doc/rasmol.html
  - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
  - **Background color.** Sets the background color of the residues. Click the color box to change the color.
- **Polarity colors (only protein).** Colors the residues according to the following categories:
  - **Green** neutral, polar
  - **Black** neutral, nonpolar
  - **Red** acidic, polar
  - **Blue** basic ,polar
  - As with other options, you can choose to set or change the coloring for either the residue letter or its background:
    - **Foreground color.** Sets the color of the letter. Click the color box to change the color.
    - **Background color.** Sets the background color of the residues. Click the color box to change the color.
- **Trace colors (only DNA).** Colors the residues according to the color conventions of chromatogram traces: A=green, C=blue, G=black, and T=red.
  - **Foreground color.** Sets the color of the letter.
  - **Background color.** Sets the background color of the residues.

### Find

The Find function can be used for searching the sequence and is invoked by pressing Ctrl + Shift + F (⌘ + Shift + F on Mac). Initially, specify the 'search term' to be found, select the type of search (see various options in the following) and finally click on the Find button. The first occurrence of the search term will then be highlighted. Clicking the find button again will find the next occurrence and so on. If the search string is found, the corresponding part of the sequence will be selected.

- **Search term.** Enter the text or number to search for. The search function does not discriminate between lower and upper case characters.
- **Sequence search.** Search the nucleotides or amino acids. For amino acids, the single letter abbreviations should be used for searching. The sequence search also has a set of advanced search parameters:
  - Include negative strand. This will search on the negative strand as well.
  - Treat ambiguous characters as wildcards in search term. If you search for e.g. ATN, you will find both ATG and ATC. If you wish to find literally exact matches for ATN (i.e. only find ATN - not ATG), this option should not be selected.
  - Treat ambiguous characters as wildcards in sequence. If you search for e.g. ATG, you will find both ATG and ATN. If you have large regions of Ns, this option should not be selected.

Note that if you enter a position instead of a sequence, it will automatically switch to position search.

- **Annotation search.** Searches the annotations on the sequence. The search is performed both on the labels of the annotations, but also on the text appearing in the tooltip that you see when you keep the mouse cursor fixed. If the search term is found, the part of the sequence corresponding to the matching annotation is selected. The option "Include translations" means that you can choose to search for translations *which are part of an annotation* (in some cases, CDS annotations contain the amino acid sequence in a "/translation" field). But it will not dynamically translate nucleotide sequences, nor will it search the translations that can enabled using the "Nucleotide info" side panel.

- **Position search.** Finds a specific position on the sequence. In order to find an interval, e.g. from position 500 to 570, enter "500..570" in the search field. This will make a selection from position 500 to 570 (both included). Notice the two periods (..) between the start an end number. If you enter positions including thousands separators like 123,345, the comma will just be ignored and it would be equivalent to entering 123345.

- **Include negative strand.** When searching the sequence for nucleotides or amino acids, you can search on both strands.

- **Name search.** Searches for sequence names. This is useful for searching sequence lists and mapping results for example.

This concludes the description of the **View Preferences**. Next, the options for selecting and editing sequences are described.

#### Text format

These preferences allow you to adjust the format of all the text in the view (both residue letters, sequence name and translations if they are shown).

- **Text size.** Five different sizes.

- **Font.** Shows a list of Fonts available on your computer.

- **Bold residues.** Makes the residues bold.

#### Restriction sites in the Side Panel

Please see section 11.1.

### 7.1.2 Selecting parts of the sequence

You can select parts of a sequence:

> **Click Selection ( ↖ ) in Toolbar | Press and hold down the mouse button on the sequence where you want the selection to start | move the mouse to the end of the selection while holding the button | release the mouse button**

Alternatively, you can search for a specific interval using the find function described above.

If you have made a selection and wish to adjust it:

**drag the edge of the selection (you can see the mouse cursor change to a horizontal arrow**

or **press and hold the Shift key while using the right and left arrow keys to adjust the right side of the selection.**

If you wish to select the entire sequence:

**double-click the sequence name to the left**

**Selecting several parts at the same time (multiselect)** You can select several parts of sequence by holding down the **Ctrl** button while making selections. Holding down the **Shift** button lets you extend or reduce an existing selection to the position you clicked.

To select a part of a sequence covered by an annotation:

**right-click the annotation | Select annotation**

or **double-click the annotation**

To select a fragment between two restriction sites that are shown on the sequence:

**double-click the sequence between the two restriction sites**

(Read more about restriction sites in section 7.1.1.)

**Open a selection in a new view** A selection can be opened in a new view and saved as a new sequence:

**right-click the selection | Open selection in New View ( )**

This opens the annotated part of the sequence in a new view. The new sequence can be saved by dragging the tab of the sequence view into the **Navigation Area**.

The process described above is also the way to manually translate coding parts of sequences (CDS) into protein. You simply translate the new sequence into protein. This is done by:

**right-click the tab of the new sequence | Toolbox | Nucleotide Analysis ( )| Translate to Protein ( )**

A selection can also be copied to the clipboard and pasted into another program:

**make a selection | Ctrl + C (⌘ + C on Mac)**

**Note!** The annotations covering the selection will not be copied.

A selection of a sequence can be edited as described in the following section.

### 7.1.3 Editing the sequence

When you make a selection, it can be edited by:

**right-click the selection | Edit Selection ( )**

A dialog appears displaying the sequence. You can add, remove or change the text and click **OK**. The original selected part of the sequence is now replaced by the sequence entered in the dialog. This dialog also allows you to paste text into the sequence using Ctrl + V (⌘ + V on Mac).

If you delete the text in the dialog and press **OK**, the selected text on the sequence will also be deleted. Another way to delete a part of the sequence is to:

> **right-click the selection | Delete Selection ( )**

If you wish to correct only one residue, this is possible by simply making the selection cover only one residue and then type the new residue.

Before exporting annotated nucleotide sequences in GenBank format, ensure that the annotations in the Annotations Table reflect the edits that have been made to the sequence.

### 7.1.4 Sequence region types

The various annotations on sequences cover parts of the sequence. Some cover an interval, some cover intervals with unknown endpoints, some cover more than one interval etc. In the following, all of these will be referred to as *regions*. Regions are generally illustrated by markings (often arrows) on the sequences. An arrow pointing to the right indicates that the corresponding region is located on the positive strand of the sequence. Figure 7.2 is an example of three regions with separate colors.

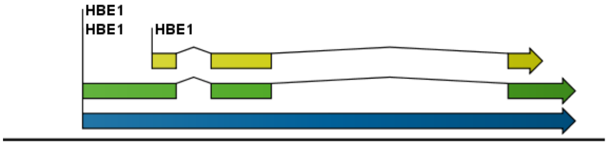


Figure 7.2: *Three regions on a human beta globin DNA sequence (HUMHBB).*

Figure 7.3 shows an artificial sequence with all the different kinds of regions.

## 7.2 Circular DNA

A sequence can be shown as a circular molecule:

> **Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Select "Circular View" ( )**

or **If the sequence is already open | Click "Show Circular View" ( ) at the lower left part of the view**

This will open a view of the molecule similar to the one in figure 7.4.

This view of the sequence shares some of the properties of the linear view of sequences as described in section 7.1, but there are some differences. The similarities and differences are listed below:

- **Similarities**:
  - The editing options.
  - Options for adding, editing and removing annotations.
  - **Restriction Sites**, **Annotation Types**, **Find** and **Text Format** preferences groups.

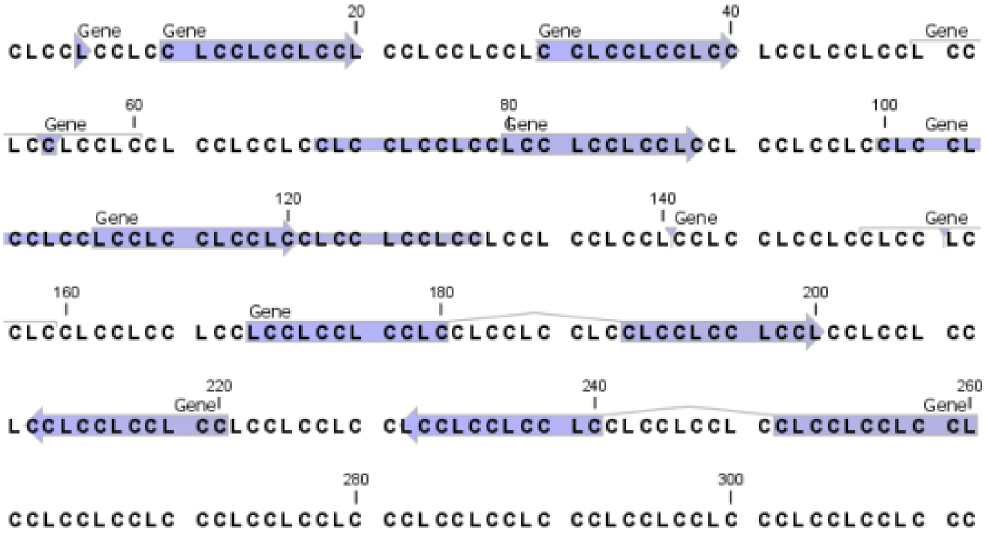

Gene
Gene
20
Gene
40
Gene
CLCCLCCLCC LCCLCCLCCL CCLCCLCCLC CLCCLCCLCC LCCLCCLCCL CC
Gene
60
80
Gene
100
Gene
LCCLCCLCCL CCLCCLCCLC CLCCLCCLCC LCCLCCLCCL CCLCCLCCLC CL
Gene
120
140
Gene
Gene
CCLCCLCCLC CLCCLCCLCC LCCLCCLCCL CCLCCLCCLC CLCCLCCLCC LC
160
Gene
180
200
CLCCLCCLCC LCCLCCLCCL CCLCCLCCLC CLCCLCCLCC LCCLCCLCCL CC
220
Gene
240
260
Gene
LCCLCCLCCL CCLCCLCCLC CLCCLCCLCC LCCLCCLCCL CCLCCLCCLC CL
280
300
CCLCCLCCLC CCLCCLCCLC CCLCCLCCLC CCLCCLCCLC CCLCCLCCLC CC

Figure 7.3: *Region #1: A single residue, Region #2: A range of residues including both endpoints, Region #3: A range of residues starting somewhere before 30 and continuing up to and including 40, Region #4: A single residue somewhere between 50 and 60 inclusive, Region #5: A range of residues beginning somewhere between 70 and 80 inclusive and ending at 90 inclusive, Region #6: A range of residues beginning somewhere between 100 and 110 inclusive and ending somewhere between 120 and 130 inclusive, Region #7: A site between residues 140 and 141, Region #8: A site between two residues somewhere between 150 and 160 inclusive, Region #9: A region that covers ranges from 170 to 180 inclusive and 190 to 200 inclusive, Region #10: A region on negative strand that covers ranges from 210 to 220 inclusive, Region #11: A region on negative strand that covers ranges from 230 to 240 inclusive and 250 to 260 inclusive.*

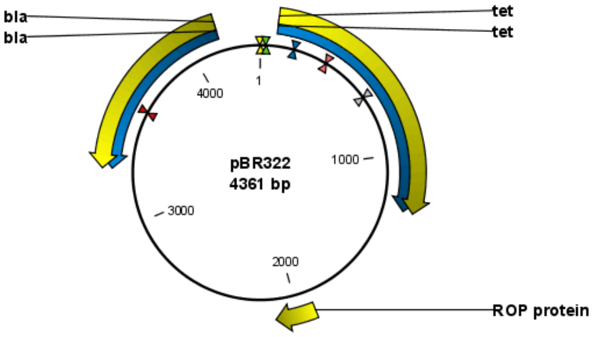


Figure 7.4: *A molecule shown in a circular view.*

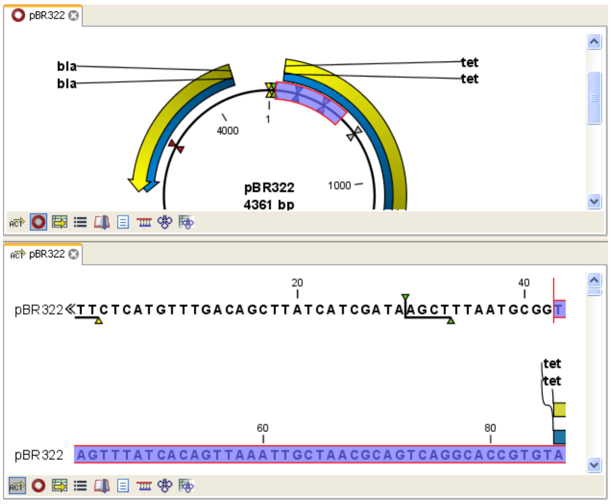
- **Differences**:
  - In the **Sequence Layout** preferences, only the following options are available in the circular view: **Numbers on plus strand**, **Numbers on sequence** and **Sequence label**.
  - You cannot zoom in to see the residues in the circular molecule. If you wish to see these details, split the view with a linear view of the sequence
  - In the **Annotation Layout**, you also have the option of showing the labels as **Stacked**. This means that there are no overlapping labels and that all labels of both annotations and restriction sites are adjusted along the left and right edges of the view.

### 7.2.1 Using split views to see details of the circular molecule

In order to see the nucleotides of a circular molecule you can open a new view displaying a circular view of the molecule:

> **Press and hold the Ctrl button (⌘ on Mac) | click Show Sequence (ACT) at the bottom of the view**

This will open a linear view of the sequence below the circular view. When you zoom in on the linear view you can see the residues as shown in figure 7.5.



```
pBR322«TTCTCATGTTTGACAGCTTATCATCGATAAGCTTTAATGCGGT
pBR322 AGTTTATCACAGTTAAATTGCTAACGCAGTCAGGCACCGTGTA
```

Figure 7.5: *Two views showing the same sequence. The bottom view is zoomed in.*

**Note!** If you make a selection in one of the views, the other view will also make the corresponding selection, providing an easy way for you to focus on the same region in both views.

### 7.2.2 Mark molecule as circular and specify starting point

You can mark a DNA molecule as circular or linear by right-clicking on its name in either the Sequence view or the Circular view. If the sequence is linear, you will see the option to mark it as circular and vice versa (see figure 7.6).

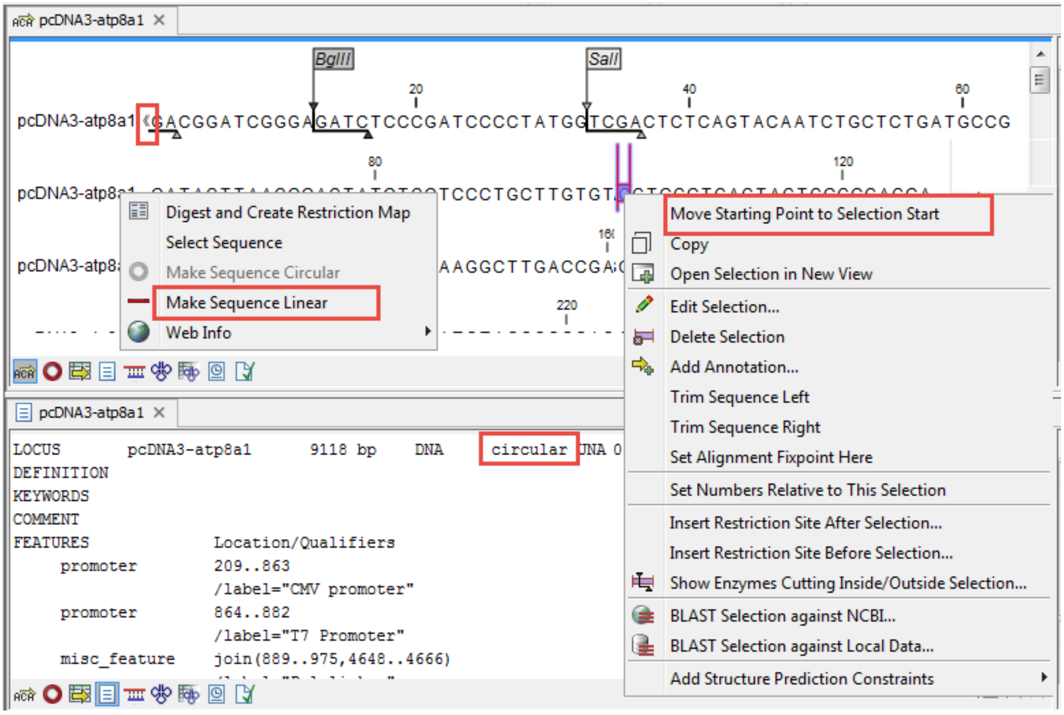
In the Sequence view, a sequence marked as circular is indicated by the use of double angle brackets at the start and end of the sequence. The linear or circular status of a sequence can also be seen in the Locus line of the Text view for a Sequence, or in the Linear column of the Table view of a Sequence List.

The starting point of a circular sequence can be changed by selecting the position of the new starting point and right-clicking on that selection to choose the option **Move Starting Point to Selection Start** (figure 7.7).

.

## 7.3 Working with annotations

Annotations provide information about specific regions of a sequence. A typical example is the annotation of a gene on a genomic DNA sequence.


pcDNA3-atp8a1
BglII
SalI
20
40
60
pcDNA3-atp8a1 «GACGGATCGGGAGATCTCCCGATCCCCTATGGTCGACTCTCAGTACAATCTGCTCTGATGCCG
80
120
pcDNA3-atp8a1
TCCCTGCTTGTGT
pcDNA3-atp8a1
AAGGCTTGACCGA
160
220
Digest and Create Restriction Map
Select Sequence
Make Sequence Circular
Make Sequence Linear
Web Info
Move Starting Point to Selection Start
Copy
Open Selection in New View
Edit Selection...
Delete Selection
Add Annotation...
Trim Sequence Left
Trim Sequence Right
Set Alignment Fixpoint Here
Set Numbers Relative to This Selection
Insert Restriction Site After Selection...
Insert Restriction Site Before Selection...
Show Enzymes Cutting Inside/Outside Selection...
BLAST Selection against NCBI...
BLAST Selection against Local Data...
Add Structure Prediction Constraints
pcDNA3-atp8a1

```
LOCUS       pcDNA3-atp8a1       9118 bp    DNA     circular UNA 0
DEFINITION
KEYWORDS
COMMENT
FEATURES             Location/Qualifiers
     promoter        209..863
                     /label="CMV promoter"
     promoter        864..882
                     /label="T7 Promoter"
     misc_feature    join(889..975,4648..4666)
```

Figure 7.6: *Double angle brackets marks the start and end of a circular sequence seen in linear view. Below, the Text view of the same sequence shows the mention circular in the first line.*

Annotations derive from different sources:

- Sequences downloaded from databases like GenBank are annotated.
- In some of the data formats that can be imported into *CLC Sequence Viewer*, sequences can have annotations (GenBank, EMBL and Swiss-Prot format).
- The result of a number of analyses in *CLC Sequence Viewer* are annotations on the sequence (e.g. finding open reading frames and restriction map analysis).

**Note!** Annotations are included if you export the sequence in GenBank, Swiss-Prot, EMBL or CLC format. When exporting in other formats, annotations are not preserved in the exported file.

### 7.3.1 Viewing annotations

Annotations can be viewed in a number of different ways:

- As arrows or boxes in all views displaying sequences (sequence lists, alignments etc)
- In the table of annotations (⇨).
- In the text view of sequences (☰)

In the following sections, these view options will be described in more detail.

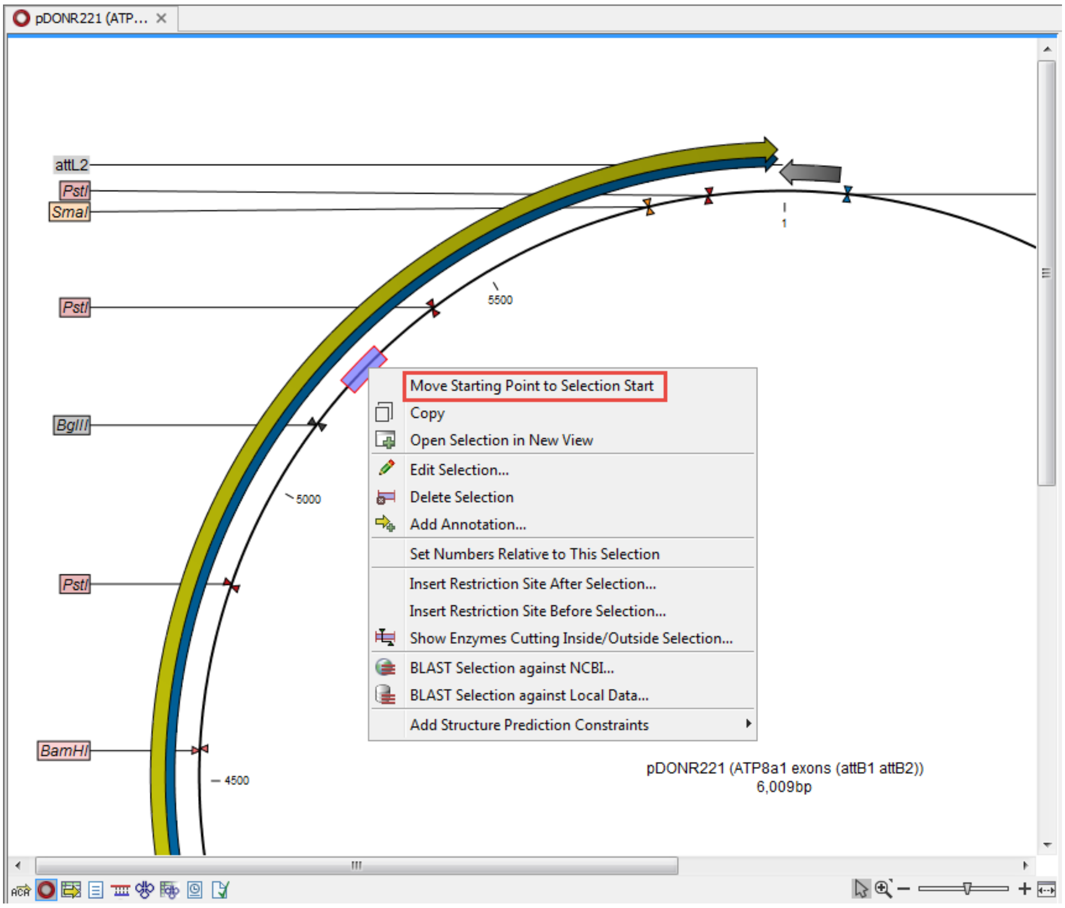

pDONR221 (ATP...
attL2
PstI
SmaI
PstI
BglII
PstI
BamHI
5500
5000
4500
1
Move Starting Point to Selection Start
Copy
Open Selection in New View
Edit Selection...
Delete Selection
Add Annotation...
Set Numbers Relative to This Selection
Insert Restriction Site After Selection...
Insert Restriction Site Before Selection...
Show Enzymes Cutting Inside/Outside Selection...
BLAST Selection against NCBI...
BLAST Selection against Local Data...
Add Structure Prediction Constraints
pDONR221 (ATP8a1 exons (attB1 attB2))
6,009bp

Figure 7.7: *Right-click on a circular sequence to move the starting point to the selected position.*

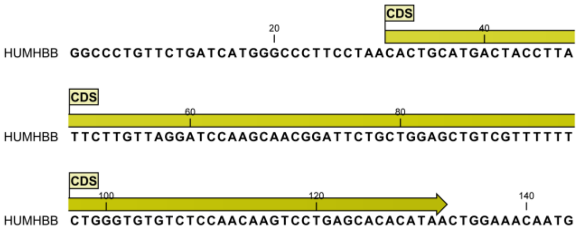

CDS
20
40
HUMHBB GGCCCTGTTCTGATCATGGGCCCTTCCTAACACTGCATGACTACCTTA
CDS
60
80
HUMHBB TTCTTGTTAGGATCCAAGCAACGGATTCTGCTGGAGCTGTCGTTTTTT
CDS
100
120
140
HUMHBB CTGGGTGTGTCTCCAACAAGTCCTGAGCACACATAACTGGAAACAATG

Figure 7.8: *An annotation showing a coding region on a genomic dna sequence.*

### View Annotations in sequence views

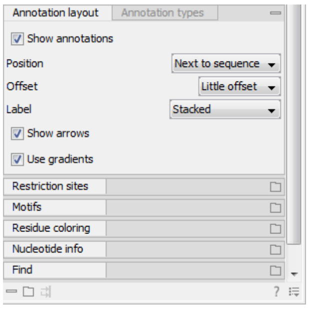
Figure 7.8 shows an annotation displayed on a sequence.

The various sequence views listed in section 7.3.1 have different default settings for showing annotations. However, they all have two groups in the **Side Panel** in common:

- **Annotation Layout**
- **Annotation Types**

The two groups are shown in figure 7.9.

In the **Annotation layout** group, you can specify how the annotations should be displayed (notice



Annotation layout | Annotation types

☑ Show annotations

Position: Next to sequence

Offset: Little offset

Label: Stacked

☑ Show arrows

☑ Use gradients

Restriction sites

Motifs

Residue coloring

Nucleotide info

Find

Figure 7.9: *The annotation layout in the Side Panel. The annotation types can be shown by clicking on the "Annotation types" tab.*

that there are some minor differences between the different sequence views):

- **Show annotations.** Determines whether the annotations are shown.
- **Position.**
  - **On sequence.** The annotations are placed on the sequence. The residues are visible through the annotations (if you have zoomed in to 100%).
  - **Next to sequence.** The annotations are placed above the sequence.
  - **Separate layer.** The annotations are placed above the sequence and above restriction sites (only applicable for nucleotide sequences).
- **Offset.** If several annotations cover the same part of a sequence, they can be spread out.
  - **Piled.** The annotations are piled on top of each other. Only the one at front is visible.
  - **Little offset.** The annotations are piled on top of each other, but they have been offset a little.
  - **More offset.** Same as above, but with more spreading.
  - **Most offset.** The annotations are placed above each other with a little space between. This can take up a lot of space on the screen.
- **Label.** The name of the annotation can shown as a label. Additional information about the sequence is shown if you place the mouse cursor on the annotation and keep it still.
  - **No labels.** No labels are displayed.
  - **On annotation.** The labels are displayed in the annotation's box.
  - **Over annotation.** The labels are displayed above the annotations.
  - **Before annotation.** The labels are placed just to the left of the annotation.
  - **Flag.** The labels are displayed as flags at the beginning of the annotation.
  - **Stacked.** The labels are offset so that the text of all labels is visible. This means that there is varying distance between each sequence line to make room for the labels.
- **Show arrows.** Displays the end of the annotation as an arrow. This can be useful to see the orientation of the annotation (for DNA sequences). Annotations on the negative strand will have an arrow pointing to the left.
- **Use gradients.** Fills the boxes with gradient color.

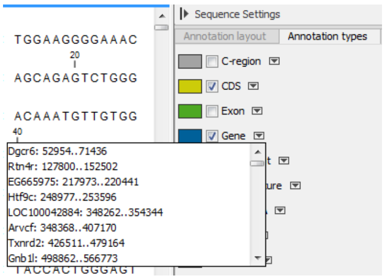
In the **Annotation types** group, you can choose which kinds of annotations that should be displayed. This group lists all the types of annotations that are attached to the sequence(s) in the view. For sequences with many annotations, it can be easier to get an overview if you deselect the annotation types that are not relevant.

Unchecking the checkboxes in the **Annotation layout** will not remove this type of annotations them from the sequence - it will just hide them from the view.

Besides selecting which types of annotations that should be displayed, the **Annotation types** group is also used to change the color of the annotations on the sequence. Click the colored square next to the relevant annotation type to change the color.

This will display a dialog with five tabs: Swatches, HSB, HSI, RGB, and CMYK. They represent five different ways of specifying colors. Apply your settings and click **OK**. When you click **OK**, the color settings cannot be reset. The **Reset** function only works for changes made before pressing **OK**.

Furthermore, the **Annotation types** can be used to easily browse the annotations by clicking the small button (▾) next to the type. This will display a list of the annotations of that type (see figure 7.10).



Dgcr6: 52954..71436
Rtn4r: 127800..152502
EG665975: 217973..220441
Htf9c: 248977..253596
LOC100042884: 348262..354344
Arvcf: 348368..407170
Txnrd2: 426511..479164
Gnb1l: 498862..566773

Figure 7.10: *Browsing the gene annotations on a sequence.*

Clicking an annotation in the list will select this region on the sequence. In this way, you can quickly find a specific annotation on a long sequence.

Note: A waved end on an annotation (figure 7.11) means that the annotation is torn, i.e., it extends beyond the sequence displayed. An annotation can be torn when a new, smaller sequence has been created from a larger sequence. A common example of this situation is when you select a section of a stand alone sequence and open it in a new view. If there are annotations present within this selected region that extend beyond the selection, then the selected sequence shown in the new view will exhibit these torn annotations.

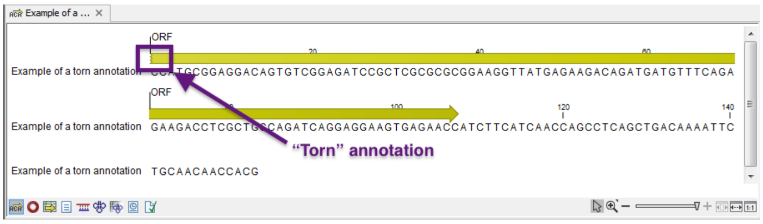

Example of a ...
ORF
20
40
60
Example of a torn annotation CCATGCGGAGGACAGTGTCGGAGATCCGCTCGCGCGGAAGGTTATGAGAAGACAGATGATGTTTCAGA
ORF
100
120
140
Example of a torn annotation GAAGACCTCGCTGCCAGATCAGGAGGAAGTGAGAACCATCTTCATCAACCAGCCTCAGCTGACAAAATTC
"Torn" annotation
Example of a torn annotation TGCAACAACCACG

Figure 7.11: *Example of a torn annotation on a sequence.*

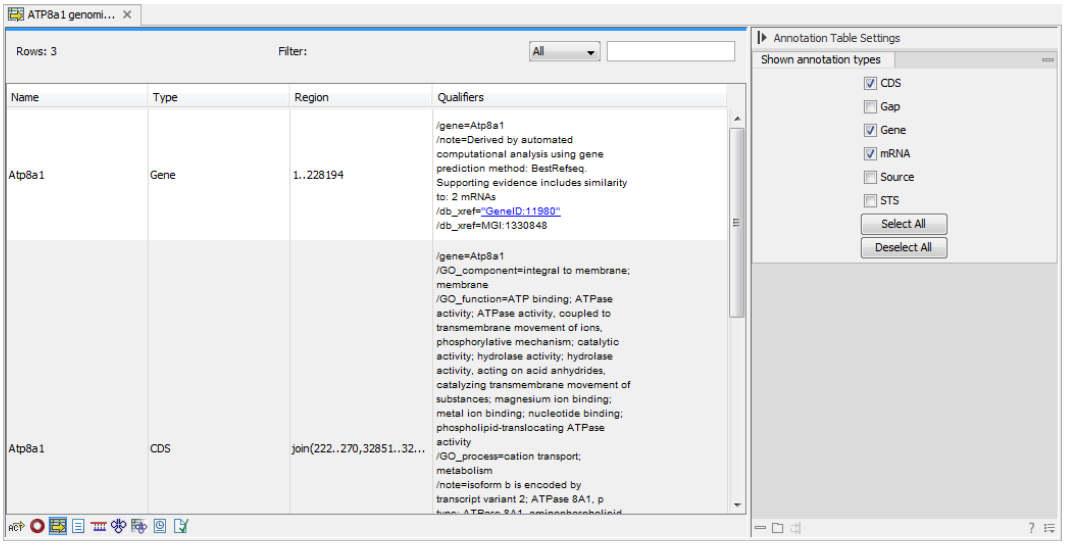
### View Annotations in a table

Annotations can also be viewed in a table:

**Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Annotation Table (  )**

or **If the sequence is already open | Click Show Annotation Table (  ) at the lower left part of the view**

This will open a view similar to the one in figure 7.12).



ATP8a1 genomi...

Rows: 3 Filter: All

| Name | Type | Region | Qualifiers |
|---|---|---|---|
| Atp8a1 | Gene | 1..228194 | /gene=Atp8a1<br>/note=Derived by automated computational analysis using gene prediction method: BestRefseq. Supporting evidence includes similarity to: 2 mRNAs<br>/db_xref="GeneID:11980"<br>/db_xref=MGI:1330848 |
| Atp8a1 | CDS | join(222..270,32851..32... | /gene=Atp8a1<br>/GO_component=integral to membrane; membrane<br>/GO_function=ATP binding; ATPase activity; ATPase activity, coupled to transmembrane movement of ions, phosphorylative mechanism; catalytic activity; hydrolase activity; hydrolase activity, acting on acid anhydrides, catalyzing transmembrane movement of substances; magnesium ion binding; metal ion binding; nucleotide binding; phospholipid-translocating ATPase activity<br>/GO_process=cation transport; metabolism<br>/note=isoform b is encoded by transcript variant 2; ATPase 8A1, p |

Annotation Table Settings

Shown annotation types

☑ CDS
☐ Gap
☑ Gene
☑ mRNA
☐ Source
☐ STS

Figure 7.12: *A table showing annotations on the sequence.*

In the **Side Panel** you can show or hide individual annotation types in the table. E.g. if you only wish to see "gene" annotations, de-select the other annotation types so that only "gene" is selected.

Each row in the table is an annotation which is represented with the following information:

- **Name.**
- **Type.**
- **Region.**
- **Qualifiers.**

### 7.3.2 Removing annotations

Annotations can be hidden using the **Annotation Types** preferences in the **Side Panel** to the right of the view (see section 7.3.1). In order to completely remove the annotation:

**right-click the annotation | Delete Annotation (  )**

If you want to remove all annotations of one type:

**right-click an annotation of the type you want to remove | Delete | Delete Annotations of Type "type"**

If you want to remove all annotations from a sequence:

**right-click an annotation | Delete | Delete All Annotations**

The removal of annotations can be undone using Ctrl + Z or Undo ( ) in the Toolbar.

If you have more sequences (e.g. in a sequence list, alignment or contig), you have two additional options:

> **right-click an annotation | Delete | Delete All Annotations from All Sequences**

> **right-click an annotation | Delete | Delete Annotations of Type "type" from All Sequences**

## 7.4 Element information

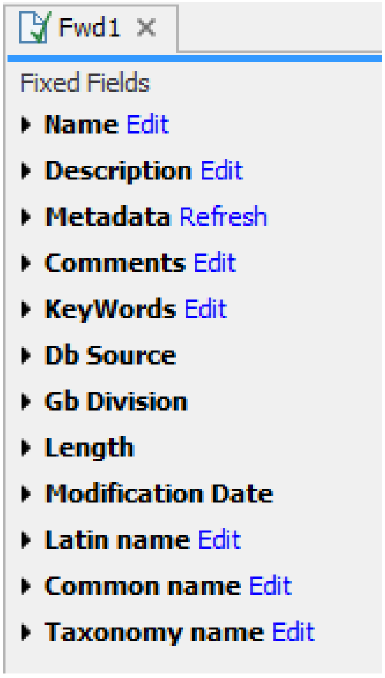
The normal view of a sequence (by double-clicking) shows the annotations as boxes along the sequence, but often there is more information available about sequences. This information is available through the **Element info** view.

To view the sequence information:

> **Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Element Info ( )**

Another way to show the text view is to open the sequence in the **View Area** and click on the "Show Element Info" icon ( ) found at the bottom of the window.

This will display a view similar to fig 7.13.



Fwd1 ×

Fixed Fields

- Name Edit
- Description Edit
- Metadata Refresh
- Comments Edit
- KeyWords Edit
- Db Source
- Gb Division
- Length
- Modification Date
- Latin name Edit
- Common name Edit
- Taxonomy name Edit

Figure 7.13: *The initial display of sequence info for the HUMHBB DNA sequence from the Example data.*

All the lines in the view are headings, and the corresponding text can be shown by clicking the text. The information available depends on the origin of the sequence.

- **Name.** The name of the sequence which is also shown in sequence views and in the **Navigation Area**.

- **Description.** A description of the sequence.
- **Metadata.** The Metadata table and the detailed metadata values associated with the sequence.
- **Comments.** The author's comments about the sequence.
- **Keywords.** Keywords describing the sequence.
- **Db source.** Accession numbers in other databases concerning the same sequence.
- **Gb Division.** Abbreviation of GenBank divisions. See section 3.3 in the GenBank release notes for a full list of GenBank divisions.
- **Length.** The length of the sequence.
- **Modification date.** Modification date from the database. This means that this date does not reflect your own changes to the sequence. See the history (section **??**) for information about the latest changes to the sequence after it was downloaded from the database.
- **Latin name.** Latin name of the organism.
- **Common name.** Scientific name of the organism.
- **Taxonomy name.** Taxonomic classification levels.
- **Read group** Read group identifier "ID", technology used to produced the reads "Platform", and sample name "Sample".
- **Paired Status.** Unpaired or Paired sequences, with in this case the Minimum and Maximum distances as well as the Read orientation set during import.

Some of the information can be edited by clicking the blue **Edit** text. This means that you can add your own information to sequences that do not derive from databases.

## 7.5 View as text

A sequence can be viewed as text without any layout and text formatting. This displays all the information about the sequence in the GenBank file format. To view a sequence as text:

> **Select a sequence in the Navigation Area and right-click on the file name | Hold the mouse over "Show" to enable a list of options | Select "Text View" (☰)**

Another way to show the text view is to open the sequence in the **View Area** and click on the "Show Text View" icon (☰) found at the bottom of the window.

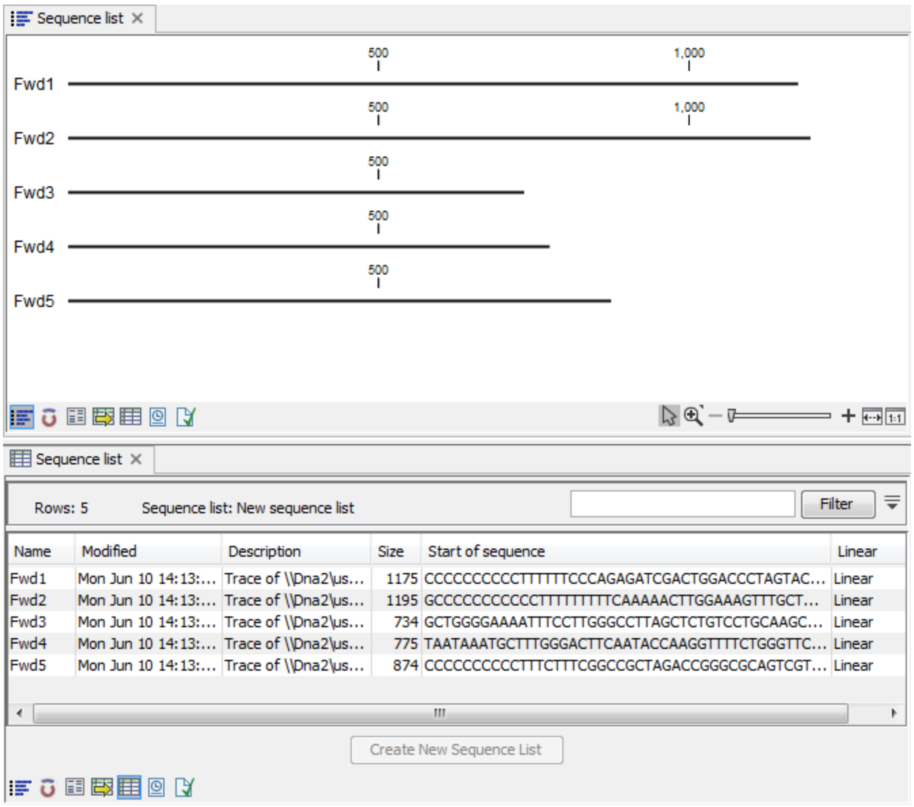
This makes it possible to see background information about e.g. the authors and the origin of DNA and protein sequences. Selections or the entire text of the **Sequence Text View** can be copied and pasted into other programs:

Much of the information is also displayed in the **Sequence info**, where it is easier to get an overview (see section 7.4.)

In the **Side Panel**, you find a search field for searching the text in the view.

## 7.6 Sequence Lists

The **Sequence List** is a file containing a number of sequences. Having sequences in a sequence list can help organizing sequence data. A Sequence List can be displayed in a graphical sequence view or in a tabular format. The two different views of the same sequence list are shown in split screen in figure 7.14.



Rows: 5 Sequence list: New sequence list

| Name | Modified | Description | Size | Start of sequence | Linear |
|---|---|---|---|---|---|
| Fwd1 | Mon Jun 10 14:13:... | Trace of \\Dna2\us... | 1175 | CCCCCCCCCCTTTTTTCCCAGAGATCGACTGGACCCTAGTAC... | Linear |
| Fwd2 | Mon Jun 10 14:13:... | Trace of \\Dna2\us... | 1195 | GCCCCCCCCCCCCTTTTTTTTTTCAAAAACTTGGAAAGTTTGCT... | Linear |
| Fwd3 | Mon Jun 10 14:13:... | Trace of \\Dna2\us... | 734 | GCTGGGGAAAATTTCCTTGGGCCTTAGCTCTGTCCTGCAAGC... | Linear |
| Fwd4 | Mon Jun 10 14:13:... | Trace of \\Dna2\us... | 775 | TAATAAATGCTTTGGGACTTCAATACCAAGGTTTTCTGGGTTC... | Linear |
| Fwd5 | Mon Jun 10 14:13:... | Trace of \\Dna2\us... | 874 | CCCCCCCCCCTTTCTTTCGGCCGCTAGACCGGGCGCAGTCGT... | Linear |

Figure 7.14: *A sequence list containing multiple sequences can be viewed in either a table or in a graphical sequence list. The graphical view is useful for viewing annotations and the sequence itself, while the table view provides other information like sequence lengths, and the number of sequences in the list (number of Rows reported).*

The **graphical view of sequence lists** is almost identical to the view of single sequences (see section 7.1). The main difference is that you now can see more than one sequence in the same view, and additionally have a few extra options for sorting, deleting and adding sequences:

- To add extra sequences to the list, right-click an empty (white) space in the view, and select **Add Sequences**.
- To delete a sequence from the list, right-click the sequence's name and select **Delete Sequence**.
- To sort the sequences in the list, right-click the name of one of the sequences and select **Sort Sequence List by Name** or **Sort Sequence List by Length**.
- To rename a sequence, right-click the name of the sequence and select **Rename Sequence**.

Each sequence in the **table sequence list** is displayed with:

- Name
- Accession
- Description
- Modification date
- Length
- First 50 residues

The number of sequences in the list is reported as the number of Rows at the top of the table view. Adding and removing sequences from the list is easy: adding is done by dragging the sequence from another list or from the Navigation Area and drop it in the table. To delete sequences, simply select them and press **Delete** (). To extract a sequence from a sequence list, drag the sequence directly from the table into the Navigation Area. Another option is to extract all sequences found in the list using the **Extract Sequences** tool. A description of how to use the **Extract Sequences** tool can be found in section 9.1.

Sequence lists are generated automatically when you import files containing more than one sequence. They may also be created as the output from particular Workbench tool, including database searches. For more information about creating sequence lists from a database search, see (chapter 6.1).

You can create a subset of a Sequence List: select the relevant sequences, right-click on the selected elements and choose **Create New Sequence List** from the drop down menu. This will generate a new sequence list that only includes the selected sequences.

A **Sequence List** can also be created from single sequences or by merging already existing sequence lists with the Workbench. To do this, select two or more sequences or sequence lists in the Navigation Area, right click on the selected elements and choose

**New | Sequence List** (**)**

Alternatively, you can launch this tool via the "File" menu system.

This opens the **Sequence List** Wizard (figure 7.15). The dialog allows you to select more sequences to include in the list, or to remove already chosen sequences from the list.

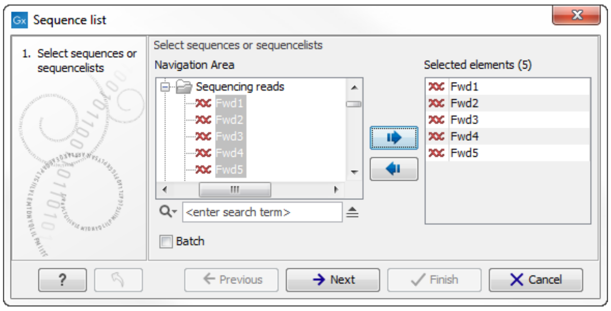
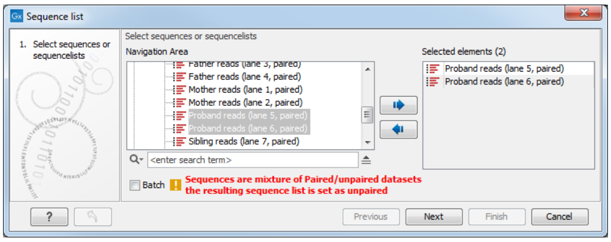


Figure 7.15: *A Sequence List dialog.*

If you are trying to create a new sequence list from a mixture of paired and unpaired datasets, a warning message will let you know that the resulting sequence list will be set as unpaired (figure 7.16).



Sequence list

1. Select sequences or sequencelists

Select sequences or sequencelists

Navigation Area

- Father reads (lane 3, paired)
- Father reads (lane 4, paired)
- Mother reads (lane 1, paired)
- Mother reads (lane 2, paired)
- Proband reads (lane 5, paired)
- Proband reads (lane 6, paired)
- Sibling reads (lane 7, paired)

<enter search term>

Selected elements (2)

- Proband reads (lane 5, paired)
- Proband reads (lane 6, paired)

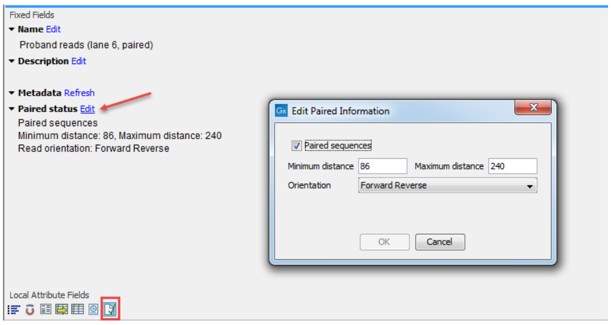
□ Batch

Sequences are mixture of Paired/unpaired datasets
the resulting sequence list is set as unpaired

Figure 7.16: *A warning appears when trying to create a new sequence list from a mixture of paired and unpaired datasets.*

This warning also appears when trying to create a Sequence List out of paired reads lists for which the the Minimum and Maximum distances are different between lists. If that is the case, distances can be edited to be similar for all lists that needs to be merged in a new one.

For this, open all Sequence Lists one after the other and click on the Show Element Info icon at the bottom of the view (figure 7.17). Edit the distances by clicking on the button "Edit" next to the entry "Paired status" and click OK. Save the Sequence lists with the edited Paired statuses before attempting to create a merged sequence List. This final list's status will be set as Paired reads.



Fixed Fields

**Name** Edit

Proband reads (lane 6, paired)

**Description** Edit

**Metadata** Refresh

**Paired status** Edit

Paired sequences
Minimum distance: 86, Maximum distance: 240
Read orientation: Forward Reverse

Local Attribute Fields

Edit Paired Information

☑ Paired sequences

Minimum distance: 86
Maximum distance: 240
Orientation: Forward Reverse

Figure 7.17: *Edit the Minimum and Maximum distances of several sequence lists to be able to merge them into one.*

# Chapter 8

# Viewing structures

## Contents

Proteins are amino acid polymers that are involved in all aspects of cellular function. The structure of a protein is defined by its particular amino acid sequence, with the amino acid sequence being referred to as the primary protein structure. The amino acids fold up in local structural elements; helices and sheets, also called the secondary structure of the protein. These structural elements are then packed into globular folds, known as the tertiary structure or the three dimensional structure.

In order to understand protein function it is often valuable to see the three dimensional structure of the protein. This is possible when the structure of the protein has been resolved and published. Structure files are usually deposited in the Protein Data Bank (PDB) `http://www.rcsb.org/`, where the publicly available protein structure files can be searched and downloaded. The vast majority of the protein structures have been determined by X-ray crystallography (88%) while the rest of the structures predominantly have been obtained by Nuclear Magnetic Resonance techniques.

In addition to protein structures, the PDB entries also contain structural information about molecules that interact with the protein, such as nucleic acids, ligands, cofactors, and water. There are also entries, which contain nucleic acids and no protein structure. The **3D Molecule Viewer** in the *CLC Sequence Viewer* is an integrated viewer of such structure files.

The **3D Molecule Viewer** offers a range of tools for inspection and visualization of molecular structures:

- Automatic sorting of molecules into categories: Proteins, Nucleic acids, Ligands, Cofactors, Water molecules

- Hide/unhide individual molecules from the view
- Four different atom-based molecule visualizations
- Backbone visualization for proteins and nucleic acids
- Molecular surface visualization
- Selection of different color schemes for each molecule visualization
- Customized visualization for user selected atoms
- Browse amino acids and nucleic acids from sequence editors started from within the 3D Molecule Viewer

## 8.1 Importing molecule structure files

Protein Data Bank (PDB) files can be imported from your own file system using Standard Import (section 5.1). Molecule Projects exported as CLC objects from other workbenches can also be imported.

**Import issues** When opening an imported molecule file for the first time, a notification is briefly shown in the lower left corner of the **Molecule Project** editor, with information of the number of issues encountered during import of the file. The issues are categorized and listed in a table view in the Issues view. The Issues list can be opened by selecting **Show | Issues** from the menu appearing when right-clicking in an empty space in the 3D view (figure 8.1).

Alternatively, the issues can be accessed from the lower left corner of the view, where buttons are shown for each available view. If you hold down the Ctrl key (Cmd on Mac) while clicking on the Issues icon ( ), the list will be shown in a split view together with the 3D view. The issues list is linked with the molecules in the 3D view, such that selecting an entry in the list will select the implicated atoms in the view, and zoom to put them into the center of the 3D view.

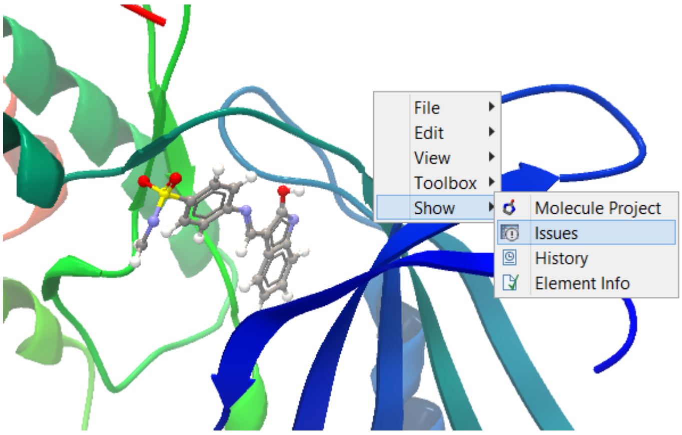
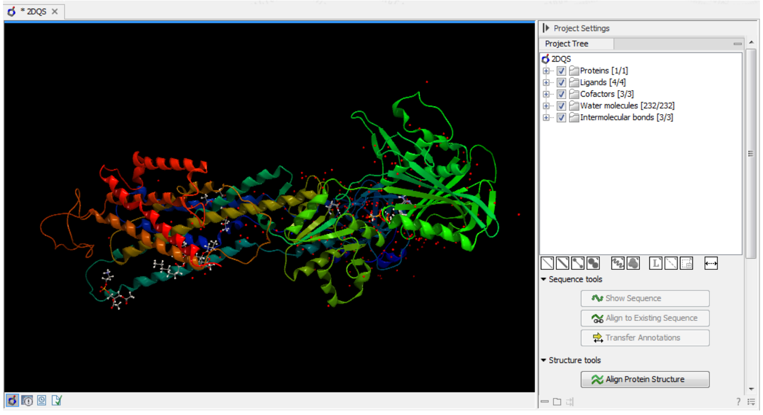


Figure 8.1: *At the bottom of the Molecule Project it is possible to switch to the "Show Issues" view by clicking on the "table-with-exclamation-mark" icon.*

## 8.2 Viewing molecular structures in 3D

An example of a 3D structure that has been opened as a **Molecule Project** is shown in figure 8.2.



2DQS
- ☑ Proteins [1/1]
- ☑ Ligands [4/4]
- ☑ Cofactors [3/3]
- ☑ Water molecules [232/232]
- ☑ Intermolecular bonds [3/3]

Figure 8.2: *3D view of a calcium ATPase. All molecules in the PDB file are shown in the Molecule Project. The Project Tree in the right side of the window lists the involved molecules.*

**Moving and rotating** The molecules can be rotated by holding down the left mouse button while moving the mouse. The right mouse button can be used to move the view.

Zooming can be done with the scroll-wheel or by holding down both left and right buttons while moving the mouse up and down.

All molecules in the **Molecule Project** are listed in categories in the **Project Tree**. The individual molecules or whole categories can be hidden from the view by un-cheking the boxes next to them.

It is possible to bring a particular molecule or a category of molecules into focus by selecting the molecule or category of interest in the **Project Tree** view and double-click on the molecule or category of interest. Another option is to use the zoom-to-fit button (↔) at the bottom of the **Project Tree** view.

**Troubleshooting 3D graphics errors** The 3D viewer uses OpenGL graphics hardware acceleration in order to provide the best possible experience. If you experience any graphics problems with the 3D view, please make sure that the drivers for your graphics card are up-to-date.

If the problems persist after upgrading the graphics card drivers, it is possible to change to a rendering mode, which is compatible with a wider range of graphic cards. To change the graphics mode go to Edit in the menu bar, select "Preferences", Click on "View", scroll down to the bottom and find "Molecule Project 3D Editor" and uncheck the box "Use modern OpenGL rendering".

Finally, it should be noted that certain types of visualization are more demanding than others. In particular, using multiple molecular surfaces may result in slower drawing, and even result in the graphics card running out of available memory. Consider creating a single combined surface (by using a selection) instead of creating surfaces for each single object. For molecules with a large number of atoms, changing to wireframe rendering and hiding hydrogen atoms can also greatly improve drawing speed.

## 8.3 Customizing the visualization

The molecular visualization of all molecules in the Molecule Project can be customized using different visualization styles. The styles can be applied to one molecule at a time, or to a whole category (or a mixture), by selecting the name of either the molecule or the category. Holding down the Ctrl (Cmd on Mac) or shift key while clicking the entry names in the **Project Tree** will select multiple molecules/categories.

The six leftmost quick-style buttons below the **Project Tree** view give access to the molecule visualization styles, while context menus on the buttons (accessible via right-click or left-click-hold) give access to the color schemes available for the visualization styles. Visualization styles and color schemes are also available from context menus directly on the selected entries in the **Project Tree**. Other quick-style buttons are available for displaying hydrogen bonds between Project Tree entries, for displaying labels in the 3D view and for creating custom atom groups. They are all described in detail below.

**Note!** Whenever you wish to change the visualization styles by right-clicking the entries in the **Project Tree**, please be aware that you must first click on the entry of interest, and ensure it is highlighted in blue, before right-clicking.

### 8.3.1 Visualization styles and colors

**Wireframe, Stick, Ball and stick, Space-filling/CPK**

() () () ()

Four different ways of visualizing molecules by showing all atoms are provided: Wireframe, Stick, Ball and stick, and Space-filling/CPK.

The visualizations are mutually exclusive meaning that only one style can be applied at a time for each selected molecule or atom group.

Six color schemes are available and can be accessed via right-clicking on the quick-style buttons:

- Color by Element. Classic CPK coloring based on atom type (e.g. oxygen red, carbon gray, hydrogen white, nitrogen blue, sulfur yellow).
- Color by Temperature. For PDB files, this is based on the b-factors. For structure models created with tools in a CLC workbench, this is based on an estimate of the local model quality. The color scale goes from blue (0) over white (50) to red (100). The b-factors as well as the local model quality estimate are measures of uncertainty or disorder in the atom position; the higher the number, the higher the uncertainty.
- Color Carbons by Entry. Each entry (molecule or atom group) is assigned its own specific color. Only carbon atoms are colored by the specific color, other atoms are colored by element.
- Color by Entry. Each entry (molecule or atom group) is assigned its own specific color.
- Custom Color. The user selects a molecule color from a palette.
- Custom Carbon Color. The user selects a molecule color from a palette. Only carbon atoms are colored by the specific color, other atoms are colored by element.

**Backbone**

()

For the molecules in the Proteins and Nucleic Acids categories, the backbone structure can be visualized in a schematic rendering, highlighting the secondary structure elements for proteins and matching base pairs for nucleic acids. The backbone visualization can be combined with any of the atom-level visualizations.

Five color schemes are available for backbone structures:

- Color by Residue Position. Rainbow color scale going from blue over green to yellow and red, following the residue number.
- Color by Type. For proteins, beta sheets are blue, helices red and loops/coil gray. For nucleic acids backbone ribbons are white while the individual nucleotides are indicated in green (T/U), red (A), yellow (G), and blue (C).
- Color by Backbone Temperature. For PDB files, this is based on the b-factors for the $C\alpha$ atoms (the central carbon atom in each amino acid). For structure models created with tools in the workbench, this is based on an estimate of the local model quality. The color scale goes from blue (0) over white (50) to red (100). The b-factors as well as the local model quality estimate are measures of uncertainty or disorder in the atom position; the higher the number, the higher the uncertainty.
- Color by Entry. Each chain/molecule is assigned its own specific color.
- Custom Color. The user selects a molecule color from a palette.

**Surfaces**

(●)

Molecular surfaces can be visualized.

Five color schemes are available for surfaces:

- Color by Charge. Charged amino acids close to the surface will show as red (negative) or blue (positive) areas on the surface, with a color gradient that depends on the distance of the charged atom to the surface.
- Color by Element. Smoothed out coloring based on the classic CPK coloring of the heteroatoms close to the surface.
- Color by Temperature. Smoothed out coloring based on the temperature values assigned to atoms close to the surface (See the "Wireframe, Stick, Ball and stick, Space-filling/CPK" section above).
- Color by Entry. Each surface is assigned its own specific color.
- Custom Color. The user selects a surface color from a palette.

A surface spanning multiple molecules can be visualized by creating a custom atom group that includes all atoms from the molecules (see section 8.3.1)

It is possible to adjust the opacity of a surface by adjusting the transparency slider at the bottom of the menu.

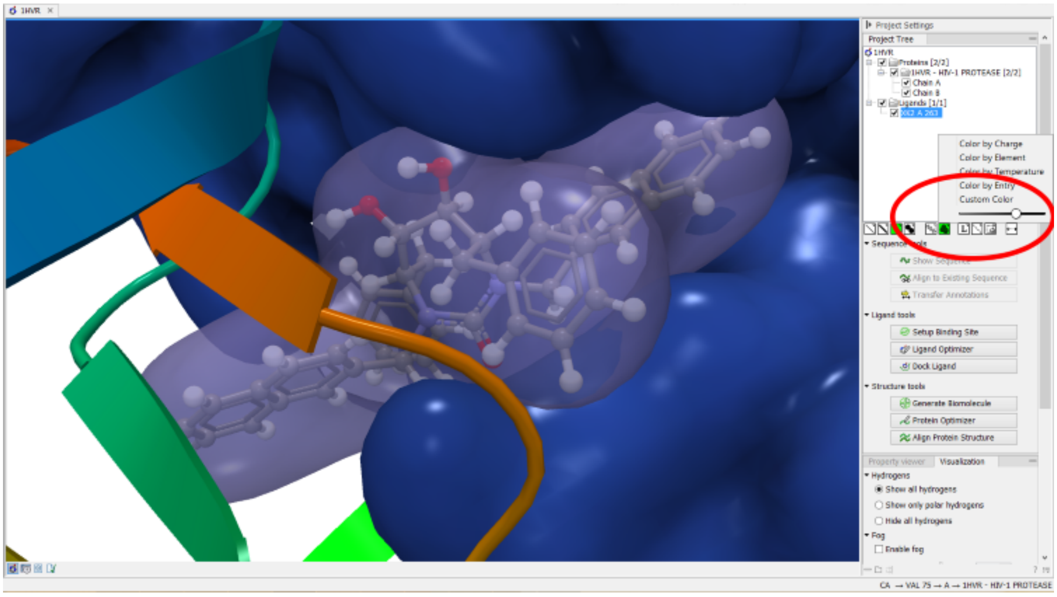


Figure 8.3: *Transparent surfaces*

Notice that visual artifacts may appear when rotating a transparent surface. These artifacts disappear as soon as the mouse is released.

### Labels

( L )

Labels can be added to the molecules in the view by selecting an entry in the Project Tree and clicking the label button at the bottom of the Project Tree view. The color of the labels can be adjusted from the context menu by right clicking on the selected entry (which must be highlighted in blue first) or on the label button in the bottom of the Project Tree view (see figure 8.4).

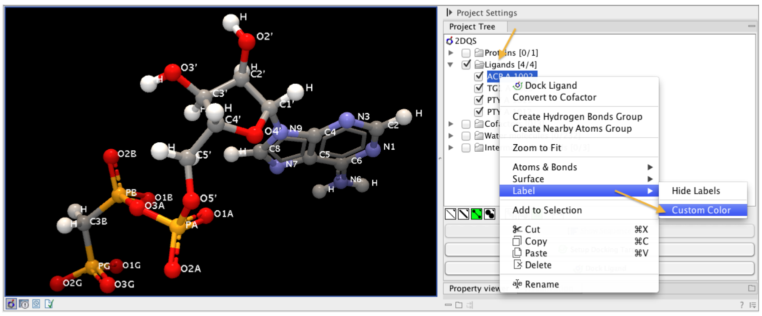


Figure 8.4: *The color of the labels can be adjusted in two different ways. Either directly using the label button by right clicking the button, or by right clicking on the molecule or category of interest in the Project Tree.*

- For proteins and nucleic acids, each residue is labeled with the PDB name and number.
- For ligands, each atom is labeled with the atom name as given in the input.
- For cofactors and water, one label is added with the name of the molecule.
- For atom groups including protein atoms, each protein residue is labeled with the PDB name and number.

- For atom groups not including protein atoms, each atom is labeled with the atom name as given in the input.

Labels can be removed again by clicking on the label button.

### Hydrogen bonds

( )

The Show Hydrogen Bond visualization style may be applied to molecules and atom group entries in the project tree. If this style is enabled for a project tree entry, hydrogen bonds will be shown to all other currently visible objects. The hydrogen bonds are updated dynamically: if a molecule is toggled off, the hydrogen bonds to it will not be shown.

It is possible to customize the color of the hydrogen bonds using the context menu.

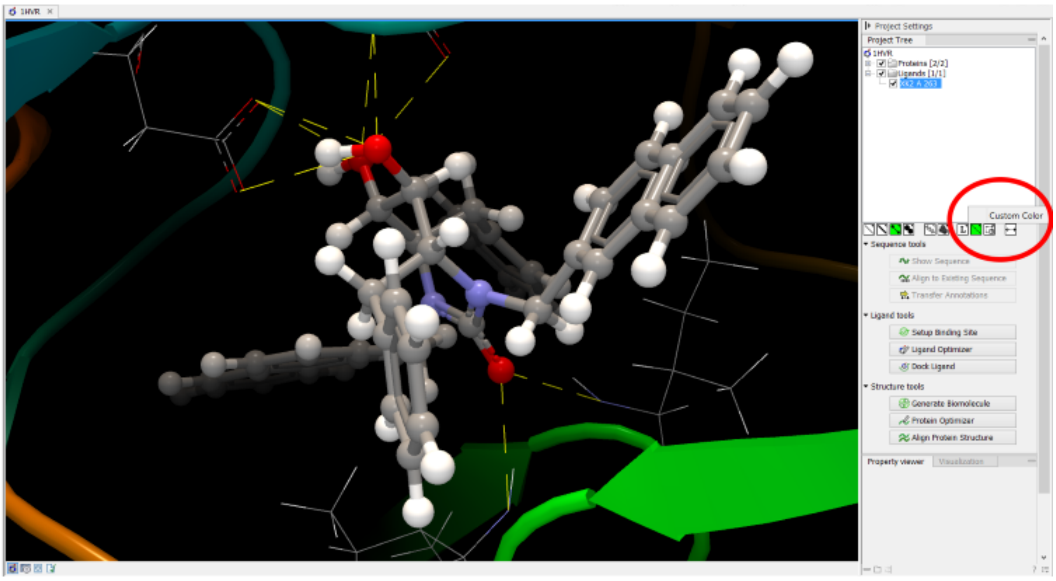


Figure 8.5: *The hydrogen bond visualization setting, with custom bond color*

### Create atom group

( )

Often it is convenient to use a unique visualization style or color to highlight a particular set of atoms, or to visualize only a subset of atoms from a molecule. This can be achieved by creating an atom group. Atom groups can be created based on atoms selected in the 3D view or entries selected in the Project Tree. When an atom group has been created, it appears as an entry in the Project Tree in the category "Atom groups". The atoms can then be hidden or shown, and the visualization changed, just as for the molecule entries in the Project Tree.

Note that an atom group entry can be renamed. Select the atom group in the Project Tree and invoke the right-click context menu. Here, the Rename option is found.

#### Create atom group based on atoms selected in 3D view

When atoms are selected in the 3D view, brown spheres indicate which atoms are included in

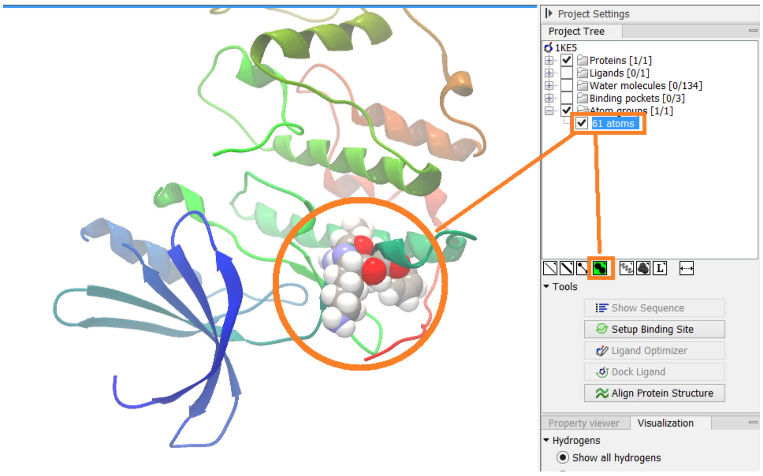


Figure 8.6: *An atom group that has been highlighted by adding a unique visualization style.*

the selection. The selection will appear as the entry "Current" in the Selections category in the Project Tree.

Once a selection has been made, press the "Create Atom Group" button and a context menu will show different options for creating a new atom group based on the selection:

- Selected Atoms. Creates an atom group containing exactly the selected atoms (those indicated by brown spheres). If an entire molecule or residue is selected, this option is not displayed.
- Selected Residue(s)/Molecules. Creates an atom group that includes all atoms in the selected residues (for entries in the protein and nucleic acid categories) and molecules (for the other categories).
- Nearby Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) within 5 Å of the selected atoms. Only atoms from currently visible Project Tree entries are considered.
- Hydrogen Bonded Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) that have hydrogen bonds to the selected atoms. Only atoms from currently visible Project Tree entries are considered.

There are several ways to select atoms in the 3D view:

- Double click to select. Click on an atom to select it. When you double click on an atom that belongs to a residue in a protein or in a nucleic acid chain, the entire residue will be selected. For small molecules, the entire molecule will be selected.
- Adding atoms to a selection. Holding down Ctrl while picking atoms, will pile up the atoms in the selection. All atoms in a molecule or category from the Project Tree, can be added to the "Current" selection by choosing "Add to Current Selection" in the context menu. Similarly, entire molecules can be removed from the current selection via the context menu.
- Spherical selection. Hold down the shift-key, click on an atom and drag the mouse away from the atom. Then a sphere centered on the atom will appear, and all atoms inside the

sphere, visualized with one of the all-atom representations will be selected. The status bar (lower right corner) will show the radius of the sphere.

- Show Sequence. Another option is to select protein or nucleic acid entries in the Project Tree, and click the "Show Sequence" button found below the Project Tree (section 8.4.1). A split-view will appear with a sequence editor for each of the sequence data types (Protein, DNA, RNA) (figure 8.7). If you then select residues in the sequence view, the backbone atoms of the selected residues will show up as the "Current" selection in the 3D view and the Project Tree view. Notice that the link between the 3D view and the sequence editor is lost if either window is closed, or if the sequence is modified.

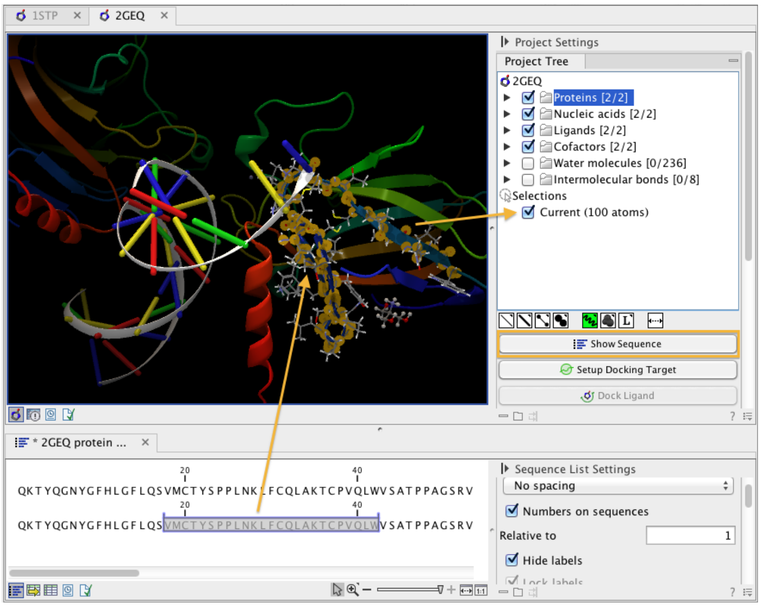


Figure 8.7: *The protein sequence in the split view is linked with the protein structure. This means that when a part of the protein sequence is selected, the same region in the protein structure will be selected.*

### Create atom group based on entries selected in the Project Tree

Select one or more entries in the Project Tree, and press the "Create Atom Group" button, then a context menu will show different options for creating a new atom group based on the selected entries:

- Nearby Atoms. Creates an atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) within 5 Å of the selected entries. Only atoms from currently visible Project Tree entries are considered.

- Hydrogen Bonded Atoms. Creates at atom group that contains residues (for the protein and nucleic acid categories) and molecules (for the other categories) that have hydrogen bonds to the selected entries. Only atoms from currently visible Project Tree entries are considered.

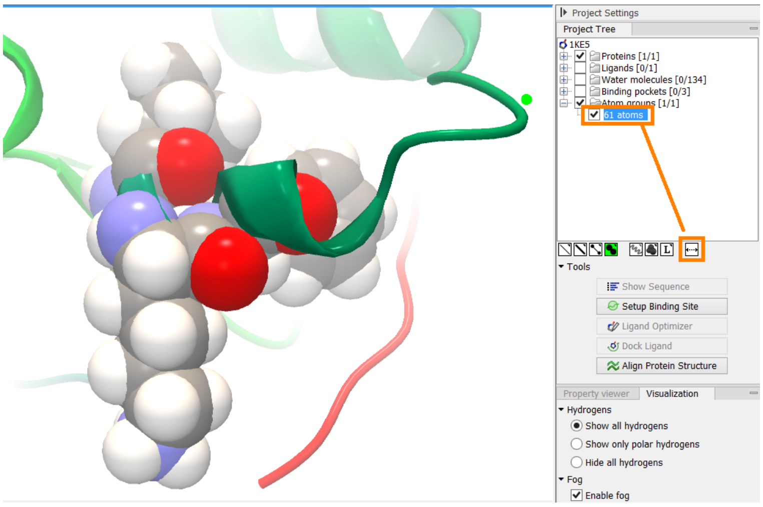
If a Binding Site Setup is present in the Project Tree (A Binding Site Setup could only be created using the now discontinued *CLC Drug Discovery Workbench*), and entries from the Ligands or Docking results categories are selected, two extra options are available under the header **Create**

**Atom Group (Binding Site).** For these options, atom groups are created considering all molecules included in the Binding Site Setup, and thus not taking into account which Project Tree entries are currently visible.

### Zoom to fit

(↔)

The "Zoom to fit" button can be used to automatically move a region of interest into the center of the screen. This can be done by selecting a molecule or category of interest in the Project Tree view followed by a click on the "Zoom to fit" button (↔) at the bottom of the Project Tree view (figure 8.8). Double-clicking an entry in the Project Tree will have the same effect.



1KE5
☑ Proteins [1/1]
□ Ligands [0/1]
□ Water molecules [0/134]
□ Binding pockets [0/3]
☑ Atom groups [1/1]
☑ 61 atoms

Hydrogens
● Show all hydrogens
○ Show only polar hydrogens
○ Hide all hydrogens
Fog
☑ Enable fog

Figure 8.8: *The "Fit to screen" button can be used to bring a particular molecule or category of molecules in focus.*

## 8.3.2 Project settings

A number of general settings can be adjusted from the **Side Panel**. Personal settings as well as molecule visualizations can be saved by clicking in the lower right corner of the **Side Panel** (☰). This is described in detail in section 3.5.

### Project Tree Tools

Just below the Project Tree, the following tools are available

- **Show Sequence** Select molecules which have sequences associated (Protein, DNA, RNA) in the Project Tree, and click this button. Then, a split-view will appear with a sequence list editor for each of the sequence data types (Protein, DNA, RNA). This is described in section 8.4.1.

### Property viewer

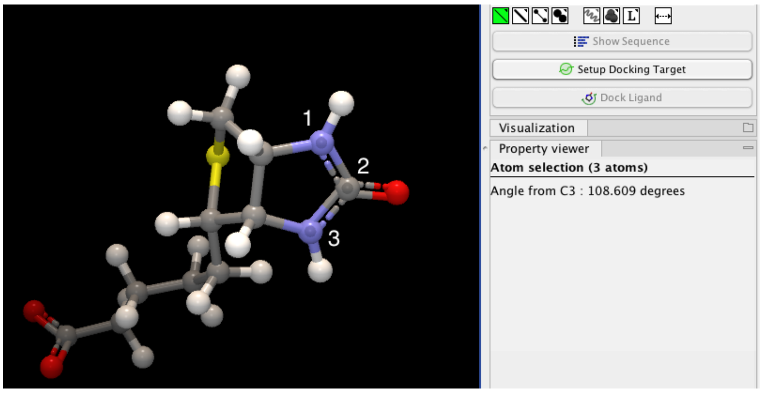
The Property viewer, found in the Side Panel, lists detailed information about the atoms that the mouse hovers over. For all atoms the following information is listed:

- **Molecule** The name of the molecule the atom is part of.
- **Residue** For proteins and nucleic acids, the name and number of the residue the atom belongs to is listed, and the chain name is displayed in parentheses.
- **Name** The particular atom name, if given in input, with the element type (Carbon, Nitrogen, Oxygen...) displayed in parentheses.
- **Hybridization** The atom hybridization assigned to the atom.
- **Charge** The atomic charge as given in the input file. If charges are not given in the input file, some charged chemical groups are automatically recognized and a charge assigned.

For atoms in molecules imported from a PDB file, extra information is given:

- **Temperature** Here is listed the b-factor assigned to the atom in the PDB file. The b-factor is a measure of uncertainty or disorder in the atom position; the higher the number, the higher the disorder.
- **Occupancy** For each atom in a PDB file, the occupancy is given. It is typically 1, but if atoms are modeled in the PDB file, with no foundation in the raw data, the occupancy is 0. If a residue or molecule has been resolved in multiple positions, the occupancy is between 0 and 1.

If an atom is selected, the Property view will be frozen with the details of the selected atom shown. If then a second atom is selected (by holding down Ctrl while clicking), the distance between the two selected atoms is shown. If a third atom is selected, the angle for the second atom selected is shown. If a fourth atom is selected, the dihedral angle measured as the angle between the planes formed by the three first and three last selected atoms is given.



Atom selection (3 atoms)

Angle from C3 : 108.609 degrees

Figure 8.9: *Selecting two, three, or four atoms will display the distance, angle, or dihedral angle, respectively.*

If a molecule is selected in the Project Tree, the Property view shows information about this molecule. Two measures are always shown:

- **Atoms** Number of atoms in the molecule.
- **Weight** The weight of the molecule in Daltons.

**Visualization settings**

Under "Visualization" five options exist:

- **Hydrogens** Hydrogen atoms can be shown (Show all hydrogens), hidden (Hide all hydrogens) or partially shown (Show only polar hydrogens).
- **Fog** "Fog" is added to give a sense of depth in the view. The strength of the fog can be adjusted or it can be disabled.
- **Clipping plane** This option makes it possible to add an imaginary plane at a specified distance along the camera's line of sight. Only objects behind this plane will be drawn. It is possible to clip only surfaces, or to clip surfaces together with proteins and nucleic acids. Small molecules, like ligands and water molecules, are never clipped.
- **3D projection** The view is opened up towards the viewer, with a "Perspective" 3D projection. The field of view of the perspective can be adjusted, or the perspective can be disabled by selecting an orthographic 3D projection.
- **Coloring** The background color can be selected from a color palette by clicking on the colored box.

**Snapshots of the molecule visualization** To save the current view as a picture, right-click in the **View Area** and select "File" and "Export Graphics". Another way to save an image is by pressing the "Graphics" button in the Workbench toolbar (). Next, select the location where you wish to save the image, select file format (PNG, JPEG, or TIFF), and provide a name, if you wish to use another name than the default name.

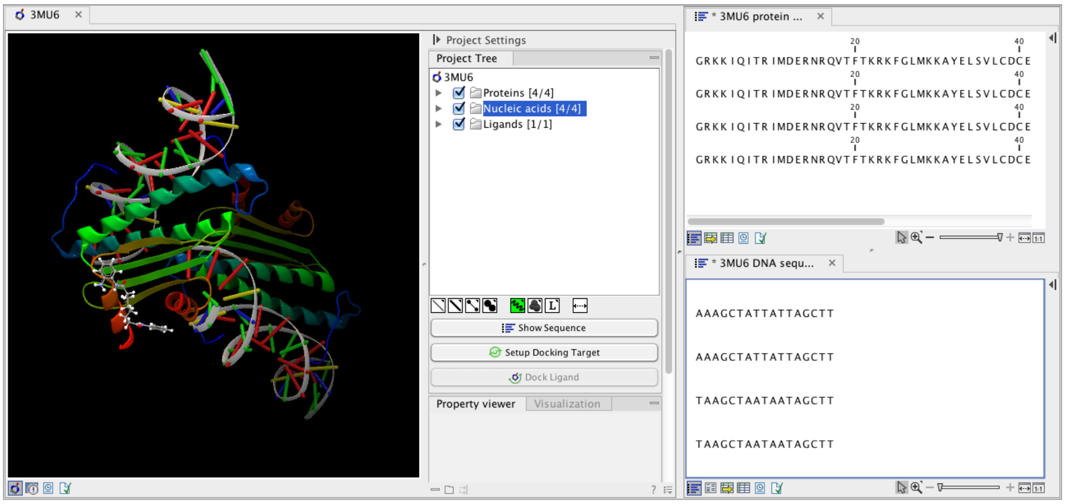
You can also save the current view directly on data with a custom name, so that it can later be applied (see section 3.5).

## 8.4 Tools for linking sequence and structure

The *CLC Sequence Viewer* has functionality that allows you to link a protein sequence to a protein structure. Selections made on the sequence will show up on the structure. This allows you to explore a protein sequence in a 3D structure context.

### 8.4.1 Show sequence associated with molecule

From the Side Panel, sequences associated with the molecules in the Molecule Project can be opened as separate objects by selecting protein or nucleic acid entries in the Project Tree and clicking the button labeled "Show Sequence" (figure 8.10). This will generate a Sequence or Sequence List for each selected sequence type (protein, DNA, RNA). The sequences can be used to select atoms in the Molecular Project as described in section 8.3.1. The sequences can also be used as input for sequence analysis tools or be saved as independent objects.



```
                    20                      40
GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCE
                    20                      40
GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCE
                    20                      40
GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCE
                    20                      40
GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCE
```

```
AAAGCTATTATTAGCTT

AAAGCTATTATTAGCTT

TAAGCTAATAATAGCTT

TAAGCTAATAATAGCTT
```

Figure 8.10: *Protein chain sequences and DNA sequences are shown in separate views.*

# Chapter 9

# General sequence analyses

**Contents**

*CLC Sequence Viewer* offers different kinds of sequence analyses, which apply to both protein and DNA.

## 9.1 Extract sequences

This tool allows the extraction of sequences from other types of data in the Workbench, such as sequence lists or alignments. The data types you can extract sequences from are:

- Alignments
- BLAST result
- BLAST overview tables
- sequence lists
- Contigs and read mappings
- Read mapping tables
- Read mapping tracks
- RNA-Seq mapping results

**Note!** When the Extract Sequences tool is run via the Workbench toolbox on an entire file of one of the above types, **all** sequences are extracted from the data used as input. If only a **subset** of the sequences is desired, for example, the reads from just a small area of a mapping, or the sequences for only a few blast results, then a data set containing just this subsection or subset should be created and the Extract Sequences tool should be run on that.

For extracting a subset of a sequence list, you can highlight the sequences of interest in the table view of the sequence list, right click on the selection and launch the Extract Sequences tool.

The Extract Sequences tool can be launched via the Toolbox menu, by going to:

**Toolbox** | **General Sequence Analysis** ()| **Extract Sequences** ()

Alternatively, on all the data types listed above except sequence lists, the option to run this tool appears by right clicking in the relevant area; a row in a table or in the read area of mapping data. An example is shown in figure 9.1.

Please note that for mappings, only the read sequences are extracted. Reference and consensus sequences are not extracted using this tool. Similarly, when extracting sequences from BLAST results, the sequence hits are extracted, not the original query sequence or a consensus sequence.

"Note also, that paired reads will be extracted in accordance with the read group settings, which is specified during the original import of the reads. If the orientation has since been changed (e.g. using the Element Info tab for the sequence list) the read group information will be modified and reads will be extracted as specified by the modified read group. The default read group orientation is forward-reverse."

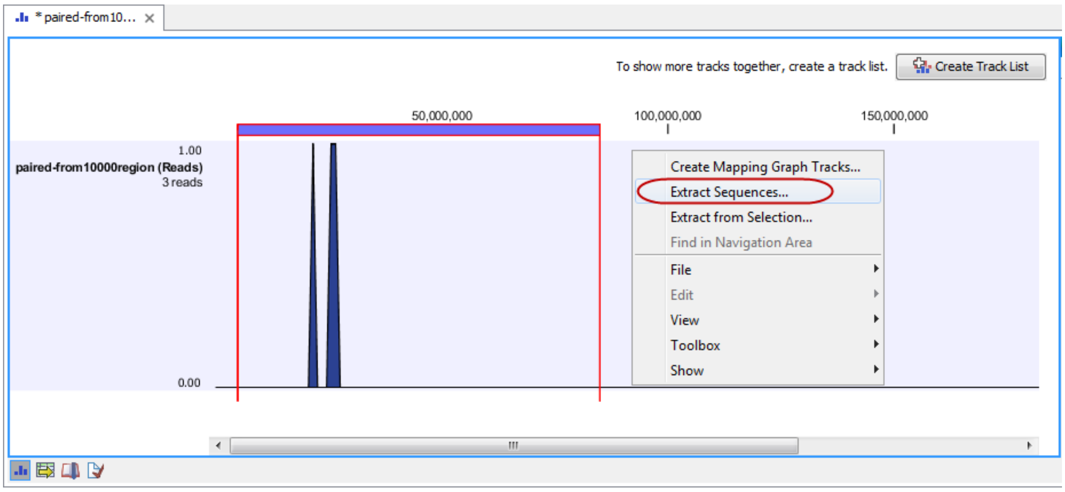
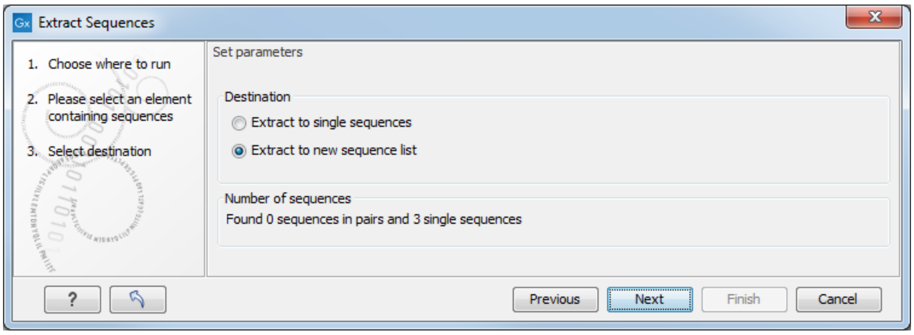


Figure 9.1: *Right click somewhere in the reads track area and select "Extract Sequences".*

The dialog allows you to select the **Destination**. Here you can choose whether the extracted sequences should be extracted as single sequences or placed in a new sequence list. For most data types, it will make most sense to choose to extract the sequences into a sequence list. The exception to this is when working with a sequence list, where choosing to extract to a sequence list would create a copy of the same sequence list. In this case, the other option would generally be chosen. This would then result in the generation of individual sequence objects for each sequence in the sequence list.

Below these options, in the dialog, you can see the number of sequences that will be extracted.



Extract Sequences

1. Choose where to run
2. Please select an element containing sequences
3. Select destination

Set parameters

Destination

○ Extract to single sequences

● Extract to new sequence list

Number of sequences

Found 0 sequences in pairs and 3 single sequences

Figure 9.2: *Choosing whether the extracted sequences should be placed in a new list or as single sequences.*

## 9.2 Shuffle sequence

In some cases, it is beneficial to shuffle a sequence. This is an option in the **Toolbox** menu under **General Sequence Analyses**. It is normally used for statistical analyses, e.g. when comparing an alignment score with the distribution of scores of shuffled sequences.

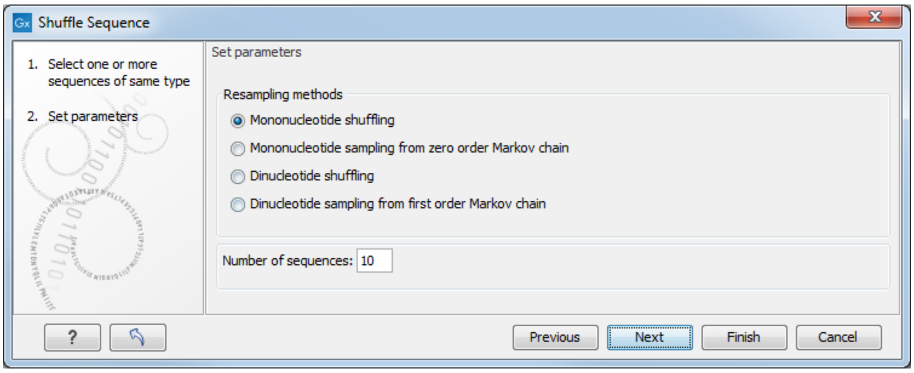
Shuffling a sequence removes all annotations that relate to the residues. To launch the tool, go to:

**Toolbox** | **General Sequence Analysis** ( )| **Shuffle Sequence** ( )

Choose a sequence for shuffling. 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.

Click **Next** to determine how the shuffling should be performed.

In this step, shown in figure 9.3:



Shuffle Sequence

1. Select one or more sequences of same type
2. Set parameters

Set parameters

Resampling methods

● Mononucleotide shuffling

○ Mononucleotide sampling from zero order Markov chain

○ Dinucleotide shuffling

○ Dinucleotide sampling from first order Markov chain

Number of sequences: 10

Figure 9.3: *Parameters for shuffling.*

For nucleotides, the following parameters can be set:

- **Mononucleotide shuffling.** Shuffle method generating a sequence of the exact same mononucleotide frequency
- **Dinucleotide shuffling.** Shuffle method generating a sequence of the exact same dinucleotide frequency
- **Mononucleotide sampling from zero order Markov chain.** Resampling method generating a sequence of the same expected mononucleotide frequency.

- **Dinucleotide sampling from first order Markov chain.** Resampling method generating a sequence of the same expected dinucleotide frequency.

For proteins, the following parameters can be set:

- **Single amino acid shuffling.** Shuffle method generating a sequence of the exact same amino acid frequency.
- **Single amino acid sampling from zero order Markov chain.** Resampling method generating a sequence of the same expected single amino acid frequency.
- **Dipeptide shuffling.** Shuffle method generating a sequence of the exact same dipeptide frequency.
- **Dipeptide sampling from first order Markov chain.** Resampling method generating a sequence of the same expected dipeptide frequency.

For further details of these algorithms, see [Clote et al., 2005]. In addition to the shuffle method, you can specify the number of randomized sequences to output.

Click **Finish** to start the tool.

This will open a new view in the **View Area** displaying the shuffled sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press ctrl + S (⌘ + S on Mac) to activate a save dialog.

## 9.3 Sequence statistics

*CLC Sequence Viewer* can produce an output with many relevant statistics for protein sequences. Some of the statistics are also relevant to produce for DNA sequences. Therefore, this section deals with both types of statistics. The required steps for producing the statistics are the same.

To create a statistic for the sequence, do the following:

**Toolbox** | **General Sequence Analysis ()**| **Create Sequence Statistics ()**

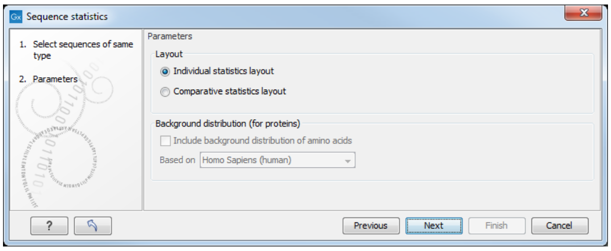
Select one or more sequence(s) or/and one or more sequence list(s). **Note!** You cannot create statistics for DNA and protein sequences at the same time, they must be run separately.

Next (figure 9.4), the dialog offers to adjust the following parameters:

- **Individual statistics layout.** If more sequences were selected in **Step 1**, this function generates separate statistics report for each sequence.
- **Comparative statistics layout.** If more sequences were selected in **Step 1**, this function generates statistics with comparisons between the sequences.

.

You can also choose to include Background distribution of amino acids. If this box is ticked, an extra column with amino acid distribution of the chosen species, is included in the table output. (The distributions are calculated from UniProt `www.uniprot.org` version 6.0, dated September 13 2005.)



Sequence statistics

1. Select sequences of same type
2. Parameters

Parameters

Layout

● Individual statistics layout

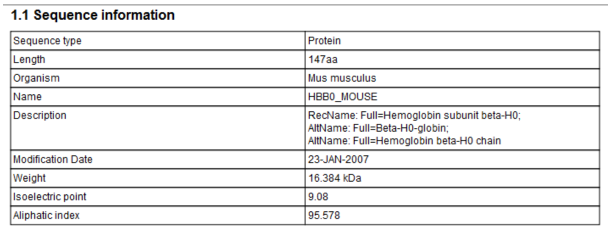
○ Comparative statistics layout

Background distribution (for proteins)

□ Include background distribution of amino acids

Based on Homo Sapiens (human)

Figure 9.4: *Setting parameters for the sequence statistics.*



**1.1 Sequence information**

| | |
|---|---|
| Sequence type | Protein |
| Length | 147aa |
| Organism | Mus musculus |
| Name | HBB0_MOUSE |
| Description | RecName: Full=Hemoglobin subunit beta-H0;<br>AltName: Full=Beta-H0-globin;<br>AltName: Full=Hemoglobin beta-H0 chain |
| Modification Date | 23-JAN-2007 |
| Weight | 16.384 kDa |
| Isoelectric point | 9.08 |
| Aliphatic index | 95.578 |

Figure 9.5: *Example of protein sequence statistics.*

Click **Finish** to start the tool. An example of protein sequence statistics is shown in figure 9.5.

Nucleotide sequence statistics are generated using the same dialog as used for protein sequence statistics. However, the output of Nucleotide sequence statistics is less extensive than that of the protein sequence statistics.

**Note!** The headings of the tables change depending on whether you calculate 'individual' or 'comparative' sequence statistics.

The output of protein sequence statistics includes:

- **Sequence information**:
  - Sequence type
  - Length
  - Organism
  - Name
  - Description
  - Modification Date
  - Weight. This is calculated like this: $sum_{unitsinsequence}(weight(unit)) - links * weight(H2O)$ where `links` is the sequence length minus one and `units` are amino acids. The atomic composition is defined the same way.
  - Isoelectric point
  - Aliphatic index

The output of nucleotide sequence statistics include:

- General statistics:
  - Sequence type
  - Length

  - Organism
  - Name
  - Description
  - Modification Date
  - Weight (calculated as single-stranded and double-stranded DNA)

- Annotation table
- Nucleotide distribution table

If nucleotide sequences are used as input, and these are annotated with CDS, a section on Codon statistics for Coding Regions is included.

### 9.3.1 Bioinformatics explained: Protein statistics

Every protein holds specific and individual features which are unique to that particular protein. Features such as isoelectric point or amino acid composition can reveal important information of a novel protein. Many of the features described below are calculated in a simple way.

- **Molecular weight** The molecular weight is the mass of a protein or molecule. The molecular weight is simply calculated as the sum of the atomic mass of all the atoms in the molecule.

  The weight of a protein is usually represented in Daltons (Da).

  A calculation of the molecular weight of a protein does not usually include additional posttranslational modifications. For native and unknown proteins it tends to be difficult to assess whether posttranslational modifications such as glycosylations are present on the protein, making a calculation based solely on the amino acid sequence inaccurate. The molecular weight can be determined very accurately by mass-spectrometry in a laboratory.

- **Isoelectric point** The isoelectric point (pI) of a protein is the pH where the proteins has no net charge. The pI is calculated from the pKa values for 20 different amino acids. At a pH below the pI, the protein carries a positive charge, whereas if the pH is above pI the proteins carry a negative charge. In other words, pI is high for basic proteins and low for acidic proteins. This information can be used in the laboratory when running electrophoretic gels. Here the proteins can be separated, based on their isoelectric point.

- **Aliphatic index** The aliphatic index of a protein is a measure of the relative volume occupied by aliphatic side chain of the following amino acids: alanine, valine, leucine and isoleucine. An increase in the aliphatic index increases the thermostability of globular proteins. The index is calculated by the following formula.

  $Aliphaticindex = X(Ala) + a * X(Val) + b * X(Leu) + b * (X)Ile$

  *X(Ala)*, *X(Val)*, *X(Ile)* and *X(Leu)* are the amino acid compositional fractions. The constants a and b are the relative volume of valine (a=2.9) and leucine/isoleucine (b=3.9) side chains compared to the side chain of alanine [Ikai, 1980].

- **Estimated half-life** The half life of a protein is the time it takes for the protein pool of that particular protein to be reduced to the half. The half life of proteins is highly dependent on the presence of the N-terminal amino acid, thus overall protein stability [Bachmair et al.,

| **Amino acid** | **Mammalian** | **Yeast** | **E. coli** |
|---|---|---|---|
| Ala (A) | 4.4 hour | >20 hours | >10 hours |
| Cys (C) | 1.2 hours | >20 hours | >10 hours |
| Asp (D) | 1.1 hours | 3 min | >10 hours |
| Glu (E) | 1 hour | 30 min | >10 hours |
| Phe (F) | 1.1 hours | 3 min | 2 min |
| Gly (G) | 30 hours | >20 hours | >10 hours |
| His (H) | 3.5 hours | 10 min | >10 hours |
| Ile (I) | 20 hours | 30 min | >10 hours |
| Lys (K) | 1.3 hours | 3 min | 2 min |
| Leu (L) | 5.5 hours | 3 min | 2 min |
| Met (M) | 30 hours | >20 hours | >10 hours |
| Asn (N) | 1.4 hours | 3 min | >10 hours |
| Pro (P) | >20 hours | >20 hours | ? |
| Gln (Q) | 0.8 hour | 10 min | >10 hours |
| Arg (R) | 1 hour | 2 min | 2 min |
| Ser (S) | 1.9 hours | >20 hours | >10 hours |
| Thr (T) | 7.2 hours | >20 hours | >10 hours |
| Val (V) | 100 hours | >20 hours | >10 hours |
| Trp (W) | 2.8 hours | 3 min | 2 min |
| Tyr (Y) | 2.8 hours | 10 min | 2 min |

Table 9.1: **Estimated half life**. Half life of proteins where the N-terminal residue is listed in the first column and the half-life in the subsequent columns for mammals, yeast and *E. coli*.

1986, Gonda et al., 1989, Tobias et al., 1991]. The importance of the N-terminal residues is generally known as the 'N-end rule'. The N-end rule and consequently the N-terminal amino acid, simply determines the half-life of proteins. The estimated half-life of proteins have been investigated in mammals, yeast and *E. coli* (see Table 9.1). If leucine is found N-terminally in mammalian proteins the estimated half-life is 5.5 hours.

- **Extinction coefficient** This measure indicates how much light is absorbed by a protein at a particular wavelength. The extinction coefficient is measured by UV spectrophotometry, but can also be calculated. The amino acid composition is important when calculating the extinction coefficient. The extinction coefficient is calculated from the absorbance of cysteine, tyrosine and tryptophan using the following equation:

  $Ext(Protein) = count(Cystine) * Ext(Cystine) + count(Tyr) * Ext(Tyr) + count(Trp) * Ext(Trp)$

  where Ext is the extinction coefficient of amino acid in question. At 280nm the extinction coefficients are: Cys=120, Tyr=1280 and Trp=5690. This equation is only valid under the following conditions:

  - pH 6.5
  - 6.0 M guanidium hydrochloride
  - 0.02 M phosphate buffer

  The extinction coefficient values of the three important amino acids at different wavelengths are found in [Gill and von Hippel, 1989]. Knowing the extinction coefficient, the absorbance (optical density) can be calculated using the following formula: $Absorbance(Protein) = \frac{Ext(Protein)}{Molecular\ weight}$

Two values are reported. The first value is computed assuming that all cysteine residues appear as half cystines, meaning they form di-sulfide bridges to other cysteines. The second number assumes that no di-sulfide bonds are formed.

- **Atomic composition** Amino acids are indeed very simple compounds. All 20 amino acids consist of combinations of only five different atoms. The atoms which can be found in these simple structures are: Carbon, Nitrogen, Hydrogen, Sulfur, Oxygen. The atomic composition of a protein can for example be used to calculate the precise molecular weight of the entire protein.

- **Total number of negatively charged residues (Asp + Glu)** At neutral pH, the fraction of negatively charged residues provides information about the location of the protein. Intracellular proteins tend to have a higher fraction of negatively charged residues than extracellular proteins.

- **Total number of positively charged residues (Arg + Lys)** At neutral pH, nuclear proteins have a high relative percentage of positively charged amino acids. Nuclear proteins often bind to the negatively charged DNA, which may regulate gene expression or help to fold the DNA. Nuclear proteins often have a low percentage of aromatic residues [Andrade et al., 1998].

- **Amino acid distribution** Amino acids are the basic components of proteins. The amino acid distribution in a protein is simply the percentage of the different amino acids represented in a particular protein of interest. Amino acid composition is generally conserved through family-classes in different organisms which can be useful when studying a particular protein or enzymes across species borders. Another interesting observation is that amino acid composition variate slightly between proteins from different subcellular localizations. This fact has been used in several computational methods, used for prediction of subcellular localization.

- **Annotation table** This table provides an overview of all the different annotations associated with the sequence and their incidence.

- **Dipeptide distribution** This measure is simply a count, or frequency, of all the observed adjacent pairs of amino acids (dipeptides) found in the protein. It is only possible to report neighboring amino acids. Knowledge on dipeptide composition have previously been used for prediction of subcellular localization.

## 9.4 Join sequences

*CLC Sequence Viewer* can join several nucleotide or protein sequences into one sequence. This feature can for example be used to construct "supergenes" for phylogenetic inference by joining several disjoint genes into one. Note, that when sequences are joined, all their annotations are carried over to the new spliced sequence.

Two (or more) sequences can be joined by:

**Toolbox | General Sequence Analyses | Join sequences ( )**

This opens the dialog shown in figure 9.6.

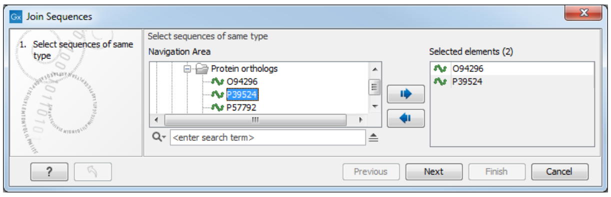


Figure 9.6: *Selecting two sequences to be joined.*

If you have selected some sequences before choosing the Toolbox action, they are now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences from the selected elements. Click **Next** opens the dialog shown in figure 9.7.

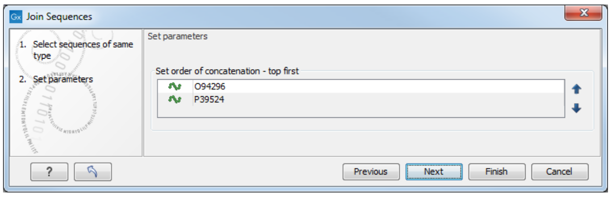


Figure 9.7: *Setting the order in which sequences are joined.*

In step 2 you can change the order in which the sequences will be joined. Select a sequence and use the arrows to move the selected sequence up or down.

Click **Finish** to start the tool.

The result is shown in figure 9.8.

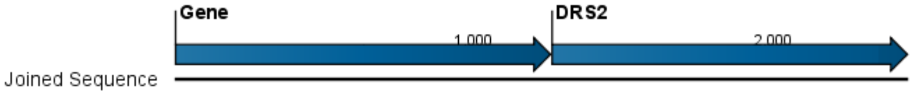


Figure 9.8: *The result of joining sequences is a new sequence containing the annotations of the joined sequences (they each had a HBB annotation).*

# Chapter 10

# Nucleotide analyses

## Contents

*CLC Sequence Viewer* offers different kinds of sequence analyses, which only apply to DNA and RNA.

## 10.1 Convert DNA to RNA

*CLC Sequence Viewer* lets you convert a DNA sequence into RNA, substituting the T residues (Thymine) for U residues (Urasil):

**Toolbox** | **Nucleotide Analysis** ()| **Convert DNA to RNA** ()

This opens the dialog displayed in figure 10.1:

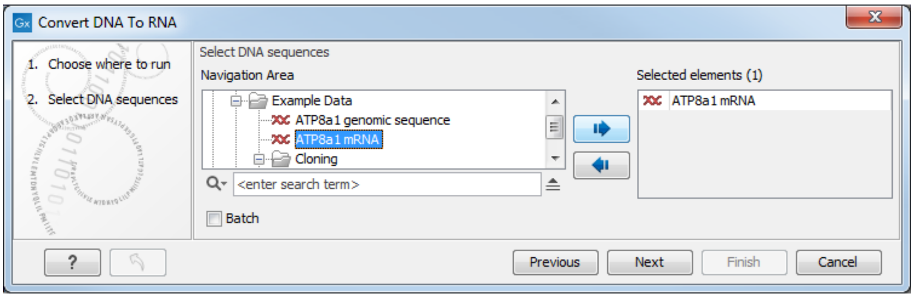


Figure 10.1: *Translating DNA to RNA.*

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.

Click **Finish** to start the tool.

**Note!** You can select multiple DNA sequences and sequence lists at a time. If the sequence list contains RNA sequences as well, they will not be converted.

## 10.2 Convert RNA to DNA

*CLC Sequence Viewer* lets you convert an RNA sequence into DNA, substituting the U residues (Urasil) for T residues (Thymine):

**Toolbox** | **Nucleotide Analysis** ()| **Convert RNA to DNA** ()

This opens the dialog displayed in figure 10.2:

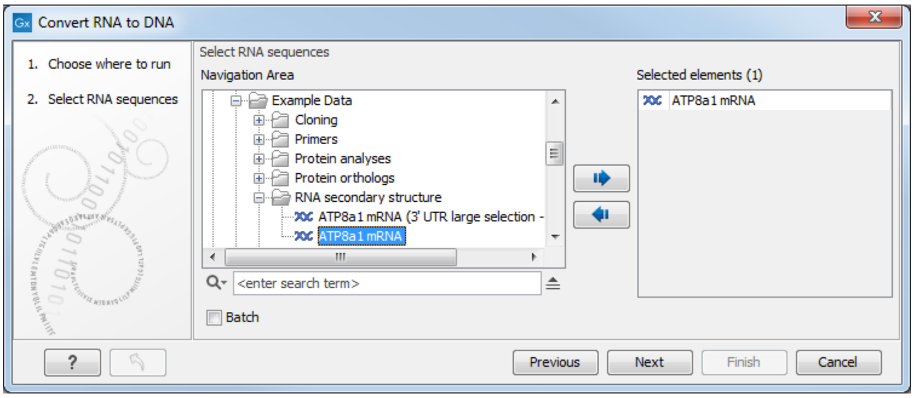


Figure 10.2: *Translating RNA to DNA.*

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.

Click **Finish** to start the tool.

This will open a new view in the **View Area** displaying the new DNA sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

**Note!** You can select multiple RNA sequences and sequence lists at a time. If the sequence list contains DNA sequences as well, they will not be converted.

## 10.3 Reverse complements of sequences

*CLC Sequence Viewer* is able to create the reverse complement of a nucleotide sequence. By doing that, a new sequence is created which also has all the annotations reversed since they now occupy the opposite strand of their previous location.

To quickly obtain the reverse complement of a sequence or part of a sequence, you may select a region on the negative strand and open it in a new view:

**right-click a selection on the negative strand** | **Open selection in New View** ()

By doing that, the sequence will be reversed. This is only possible when the double stranded view option is enabled. It is possible to copy the selection and paste it in a word processing program or an e-mail. To obtain a reverse complement of an entire sequence:

**Toolbox** | **Nucleotide Analysis ()**| **Reverse Complement Sequence ()**

This opens the dialog displayed in figure 10.3:

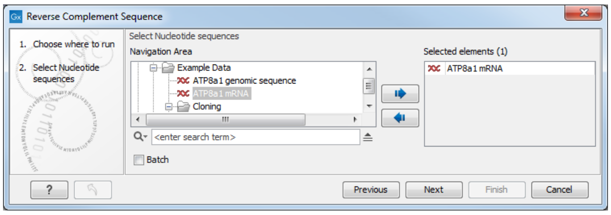


Figure 10.3: *Creating a reverse complement sequence.*

If a sequence was selected before choosing the Toolbox action, the 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.

Click **Finish** to start the tool.

This will open a new view in the **View Area** displaying the reverse complement of the selected sequence. The new sequence is not saved automatically. To save the sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

## 10.4 Reverse sequence

*CLC Sequence Viewer* is able to create the reverse of a nucleotide sequence.

**Note!** This is not the same as a reverse complement. If you wish to create the reverse complement, please refer to section 10.3.

To run the tool, go to:

**Toolbox** | **Nucleotide Analysis ()**| **Reverse Sequence ()**

This opens the dialog displayed in figure 10.4:

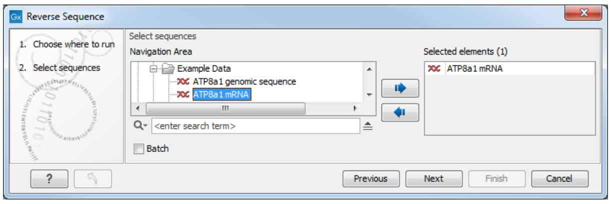


Figure 10.4: *Reversing a sequence.*

If a sequence was selected before choosing the Toolbox action, the 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.

Click **Finish** to start the tool.

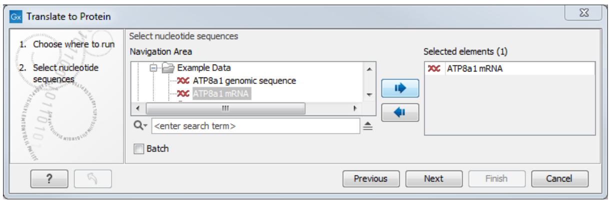
**Note!** This is not the same as a reverse complement. If you wish to create the reverse complement, please refer to section 10.3.

## 10.5 Translation of DNA or RNA to protein

In *CLC Sequence Viewer* you can translate a nucleotide sequence into a protein sequence using the **Toolbox** tools. Usually, you use the +1 reading frame which means that the translation starts from the first nucleotide. Stop codons result in an asterisk being inserted in the protein sequence at the corresponding position. It is possible to translate in any combination of the six reading frames in one analysis. To translate, go to:

**Toolbox** | **Nucleotide Analysis** ()| **Translate to Protein** ()

This opens the dialog displayed in figure 10.5:



Translate to Protein

1. Choose where to run
2. Select nucleotide sequences

Select nucleotide sequences

Navigation Area

- Example Data
  - ATP8a1 genomic sequence
  - ATP8a1 mRNA

<enter search term>

□ Batch

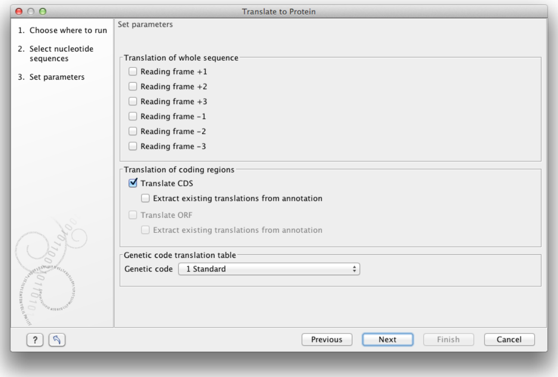
Selected elements (1)

- ATP8a1 mRNA

Figure 10.5: *Choosing sequences for translation.*

If a sequence was selected before choosing the Toolbox action, the 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.

Clicking **Next** generates the dialog seen in figure 10.6:



Translate to Protein

1. Choose where to run
2. Select nucleotide sequences
3. Set parameters

Set parameters

Translation of whole sequence

□ Reading frame +1
□ Reading frame +2
□ Reading frame +3
□ Reading frame -1
□ Reading frame -2
□ Reading frame -3

Translation of coding regions

☑ Translate CDS
□ Extract existing translations from annotation
□ Translate ORF
□ Extract existing translations from annotation

Genetic code translation table

Genetic code: 1 Standard

Figure 10.6: *Choosing translation of CDS's using standard translation table.*

Here you have the following options:

**Reading frames** If you wish to translate the whole sequence, you must specify the reading frame for the translation. If you select e.g. two reading frames, two protein sequences are generated.

**Translate CDS** You can choose to translate regions marked by and CDS or ORF annotation. This will generate a protein sequence for each CDS or ORF annotation on the sequence. The "Extract existing translations from annotation" allows to list the amino acid CDS sequence shown in the tool tip annotation (e.g. interstate from NCBI download) and does therefore not represent a translation of the actual nt sequence.

**Genetic code translation table** Lets you specify the genetic code for the translation. The translation tables are occasionally updated from NCBI. The tables are not available in this printable version of the user manual. Instead, the tables are included in the **Help**-menu in the **Menu Bar** (in the appendix).

Click **Finish** to start the tool. The newly created protein is shown, but is not saved automatically.

To save a protein sequence, drag it into the **Navigation Area** or press Ctrl + S (⌘ + S on Mac) to activate a save dialog.

The name for a coding region translation consists of the name of the input sequence followed by the annotation type and finally the annotation name.

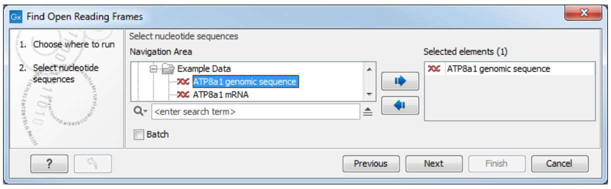
## 10.6 Find open reading frames

The *CLC Sequence Viewer* **Find Open Reading Frames** function can be used to find all open reading frames (ORF) in a sequence, or, by choosing particular start codons to use, it can be used as a rudimentary gene finder. ORFs identified will be shown as annotations on the sequence. You have the option of choosing a translation table, the start codons to use, minimum ORF length as well as a few other parameters. These choices are explained in this section.

To find open reading frames:

**Toolbox** | **Nucleotide Analysis** ()| **Find Open Reading Frames** ()

This opens the dialog displayed in figure 10.7:



Find Open Reading Frames

1. Choose where to run
2. Select nucleotide sequences

Select nucleotide sequences

Navigation Area

Example Data
ATP8a1 genomic sequence
ATP8a1 mRNA

<enter search term>

□ Batch

Selected elements (1)

ATP8a1 genomic sequence

Figure 10.7: *Create Reading Frame dialog.*

If a sequence was selected before choosing the Toolbox action, the 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.

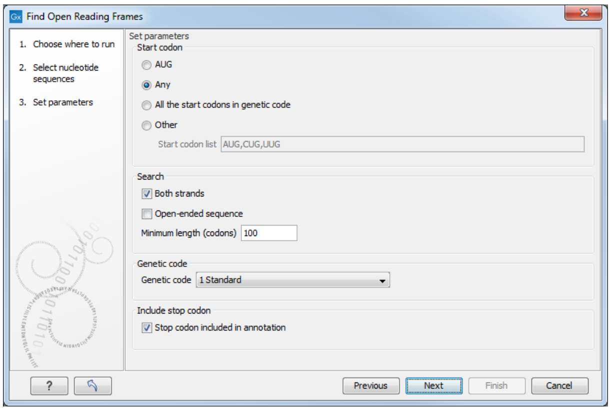
The **Find Open Reading Frames** tool simply looks for start and stop codons and reports any open reading frames that satisfy the parameters. If you want to adjust the parameters for finding open reading frames click **Next**.

### 10.6.1 Open reading frame parameters

This opens the dialog displayed in figure 10.8:

The adjustable parameters for the search are:

- **Start codon**:
  - **AUG**. Most commonly used start codon.



Find Open Reading Frames

1. Choose where to run
2. Select nucleotide sequences
3. Set parameters

Set parameters

Start codon

○ AUG

● Any

○ All the start codons in genetic code

○ Other

Start codon list AUG,CUG,UUG

Search

☑ Both strands

□ Open-ended sequence

Minimum length (codons) 100

Genetic code

Genetic code 1 Standard

Include stop codon

☑ Stop codon included in annotation

Figure 10.8: *Create Reading Frame dialog.*

  - **Any**. Find all open reading frames of specified length. Any combination of three bases that is not a stop-codon is interpreted as a start codon, and translated according to the specified genetic code.
  - **All start codons in genetic code**.
  - **Other**. Here you can specify a number of start codons separated by commas.

- **Both strands**. Finds reading frames on both strands.

- **Open-ended Sequence**. Allows the ORF to start or end outside the sequence. If the sequence studied is a part of a larger sequence, it may be advantageous to allow the ORF to start or end outside the sequence.

- **Genetic code translation table**.

- **Include stop codon in result** The ORFs will be shown as annotations which can include the stop codon if this option is checked. The translation tables are occasionally updated from NCBI. The tables are not available in this printable version of the user manual. Instead, the tables are included in the **Help** menu in the **Menu Bar** (in the appendix).

- **Minimum Length**. Specifies the minimum length for the ORFs to be found. The length is specified as number of codons.

Using open reading frames for gene finding is a fairly simple approach which is likely to predict genes which are not real. Setting a relatively high minimum length of the ORFs will reduce the number of false positive predictions, but at the same time short genes may be missed (see figure 10.9).

Click **Finish** to start the tool.

Finding open reading frames is often a good first step in annotating sequences such as cloning vectors or bacterial genomes. For eukaryotic genes, ORF determination may not always be very helpful since the intron/exon structure is not part of the algorithm.

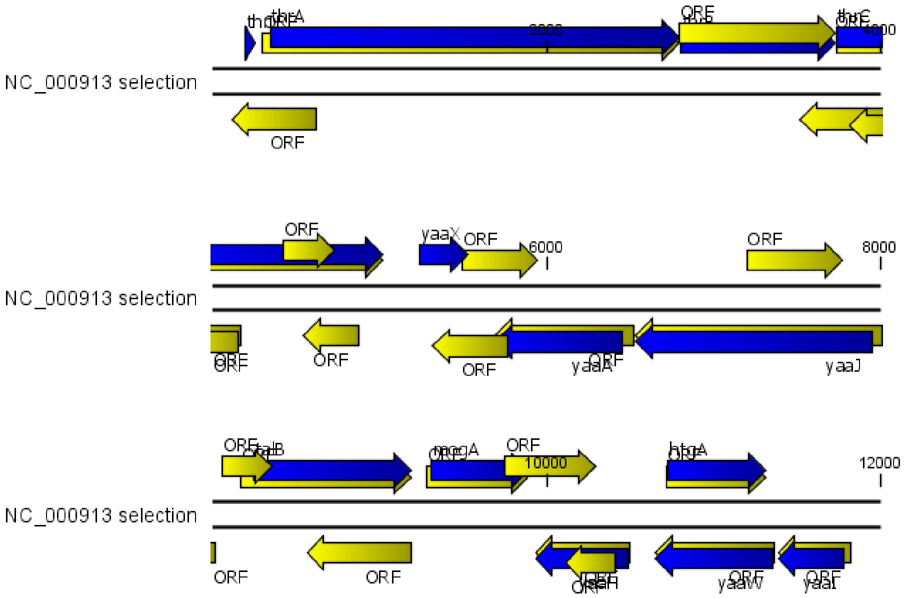


Figure 10.9: *The first 12,000 positions of the* E. coli *sequence NC_000913 downloaded from GenBank. The blue (dark) annotations are the genes while the yellow (brighter) annotations are the ORFs with a length of at least 100 amino acids. On the positive strand around position 11,000, a gene starts before the ORF. This is due to the use of the standard genetic code rather than the bacterial code. This particular gene starts with CTG, which is a start codon in bacteria. Two short genes are entirely missing, while a handful of open reading frames do not correspond to any of the annotated genes.*

# Chapter 11

# Restriction site analyses

**Contents**

There are two ways of finding and showing restriction sites:

- In many cases, the dynamic restriction sites found in the **Side Panel** of sequence views will be useful, since it is a quick and easy way of showing restriction sites.
- In the **Toolbox** you will find the other way of doing restriction site analyses. This way provides more control of the analysis and gives you more output options, e.g. a table of restriction sites and you can perform the same restriction map analysis on several sequences in one step.

## 11.1 Dynamic restriction sites

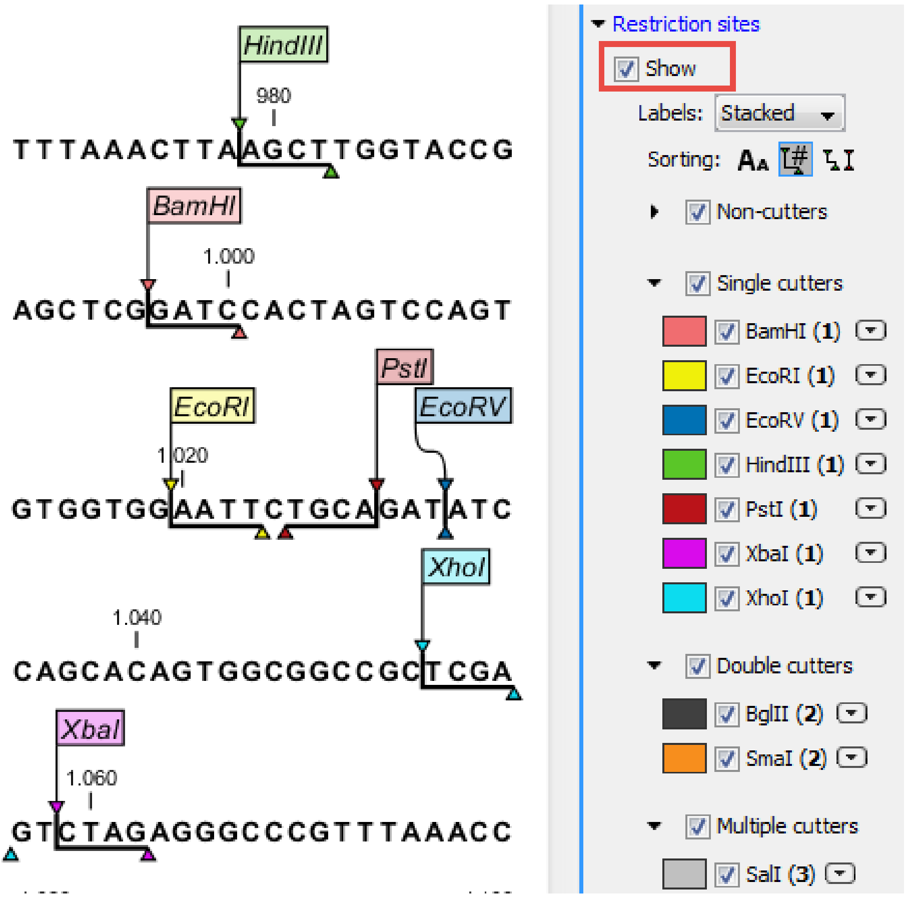
If you open a sequence, a sequence list etc, you will find the **Restriction Sites** group in the **Side Panel**.

Restriction sites can be shown on the sequence as colored triangles and lines (figure 11.1): check the "Show" option on top of the Restriction sites section, then specify the enzymes that should be displayed.

The color of the restriction enzyme can be changed by clicking the colored box next to the enzyme's name. The name of the enzyme can also be shown next to the restriction site by selecting **Show name flags** above the list of restriction enzymes.

There is also an option to specify how the **Labels** shown be shown:

- **No labels**. This will just display the cut site with no information about the name of the enzyme. Placing the mouse button on the cut site will reveal this information as a tool tip.



Restriction sites

☑ Show

Labels: Stacked

Sorting:

☑ Non-cutters

☑ Single cutters

- ☑ BamHI (1)
- ☑ EcoRI (1)
- ☑ EcoRV (1)
- ☑ HindIII (1)
- ☑ PstI (1)
- ☑ XbaI (1)
- ☑ XhoI (1)

☑ Double cutters

- ☑ BglII (2)
- ☑ SmaI (2)

☑ Multiple cutters

- ☑ SalI (3)

Figure 11.1: *Showing restriction sites of ten restriction enzymes.*

- **Flag**. This will place a flag just above the sequence with the enzyme name (see an example in figure 11.2). Note that this option will make it hard to see when several cut sites are located close to each other. In the circular view, this option is replaced by the Radial option.

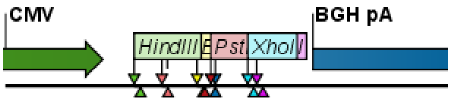


Figure 11.2: *Restriction site labels shown as flags.*

- **Radial**. This option is only available in the circular view. It will place the restriction site labels as close to the cut site as possible (see an example in figure 11.3).

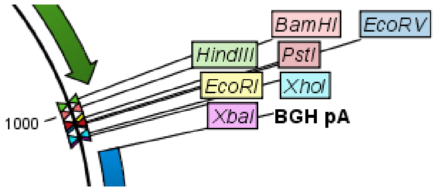


Figure 11.3: *Restriction site labels in radial layout.*

- **Stacked**. This is similar to the flag option for linear sequence views, but it will stack the labels so that all enzymes are shown. For circular views, it will align all the labels on each side of the circle. This can be useful for clearly seeing the order of the cut sites when they are located closely together (see an example in figure 11.4).

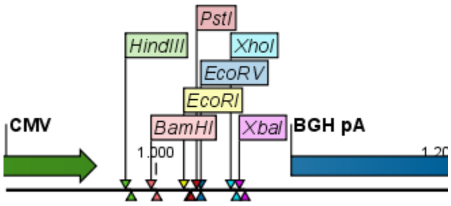


Figure 11.4: *Restriction site labels stacked.*

Note that in a circular view, the **Stacked** and **Radial** options also affect the layout of annotations.

Just above the list of enzymes, three buttons can be used for sorting the list (see figure 11.5).

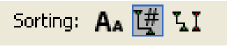


Figure 11.5: *Buttons to sort restriction enzymes.*

- **Sort enzymes alphabetically** (AA). Clicking this button will sort the list of enzymes alphabetically.
- **Sort enzymes by number of restriction sites** (#). This will divide the enzymes into four groups:
  - Non-cutters.
  - Single cutters.
  - Double cutters.
  - Multiple cutters.

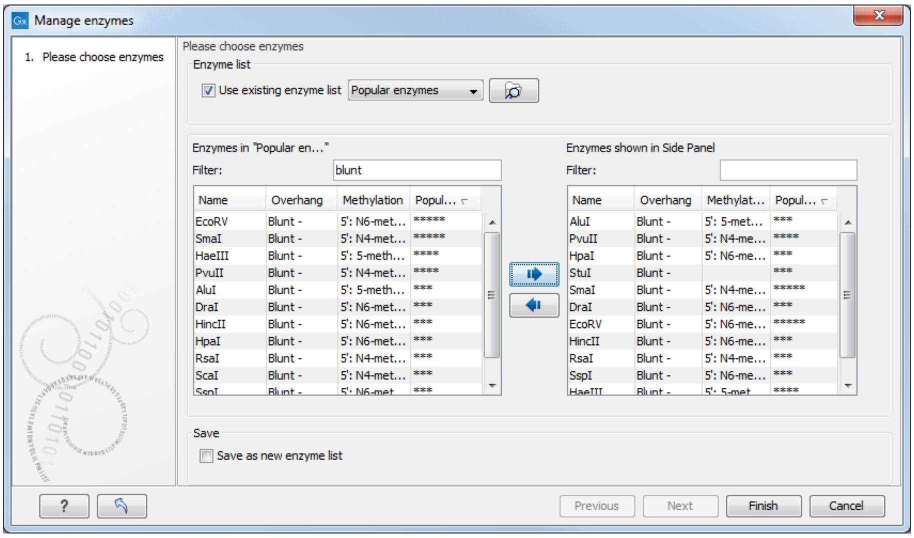
  There is a checkbox for each group which can be used to hide / show all the enzymes in a group.
- **Sort enzymes by overhang** (↳I). This will divide the enzymes into three groups:
  - Blunt. Enzymes cutting both strands at the same position.
  - 3'. Enzymes producing an overhang at the 3' end.
  - 5'. Enzymes producing an overhang at the 5' end.

  There is a checkbox for each group which can be used to hide / show all the enzymes in a group.

### 11.1.1 Manage enzymes

The list of restriction enzymes contains per default some of the most popular enzymes, but you can easily modify this list and add more enzymes by clicking the **Manage enzymes button** at the bottom of the "Restriction sites" palette of the Side Panel.

This will open the dialog shown in figure 11.6.



Manage enzymes

1. Please choose enzymes

Please choose enzymes

Enzyme list

☑ Use existing enzyme list: Popular enzymes

Enzymes in "Popular en..."

Filter: blunt

| Name | Overhang | Methylation | Popul... |
|---|---|---|---|
| EcoRV | Blunt - | 5': N6-met... | ***** |
| SmaI | Blunt - | 5': N4-met... | ***** |
| HaeIII | Blunt - | 5': 5-meth... | **** |
| PvuII | Blunt - | 5': N4-met... | **** |
| AluI | Blunt - | 5': 5-meth... | *** |
| DraI | Blunt - | 5': N6-met... | *** |
| HincII | Blunt - | 5': N6-met... | *** |
| HpaI | Blunt - | 5': N6-met... | *** |
| RsaI | Blunt - | 5': N4-met... | *** |
| ScaI | Blunt - | 5': N4-met... | *** |
| SspI | Blunt - | 5': N6-met... | *** |

Enzymes shown in Side Panel

Filter:

| Name | Overhang | Methylat... | Popul... |
|---|---|---|---|
| AluI | Blunt - | 5': 5-met... | *** |
| PvuII | Blunt - | 5': N4-me... | **** |
| HpaI | Blunt - | 5': N6-me... | *** |
| StuI | Blunt - | | *** |
| SmaI | Blunt - | 5': N4-me... | ***** |
| DraI | Blunt - | 5': N6-me... | *** |
| EcoRV | Blunt - | 5': N6-me... | ***** |
| HincII | Blunt - | 5': N6-me... | *** |
| RsaI | Blunt - | 5': N4-me... | *** |
| SspI | Blunt - | 5': N6-me... | *** |
| HaeIII | Blunt - | 5': 5-met... | **** |

Save

□ Save as new enzyme list

Figure 11.6: *Adding or removing enzymes from the Side Panel.*

At the top, you can choose to **Use existing enzyme list**. Clicking this option lets you select an enzyme list which is stored in the **Navigation Area**. A list of popular enzymes is available in the Example Data folder you can download from the Help menu.

Below there are two panels:

- To the **left**, you can see all the enzymes that are in the list selected above. If you have not chosen to use a specific enzyme list, this panel shows all the enzymes available.
- To the **right**, you can see the list of the enzymes that will be used.

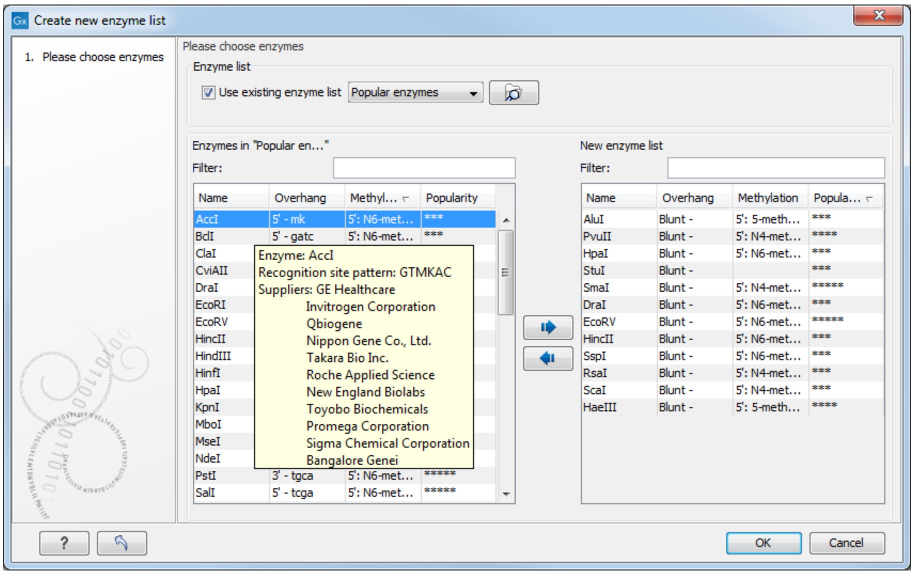
Select enzymes in the left side panel and add them to the right panel by double-clicking or clicking the **Add** button (➡).

The enzymes can be sorted by clicking the column headings, i.e., Name, Overhang, Methylation or Popularity. This is particularly useful if you wish to use enzymes which produce a 3' overhang for example.

When looking for a specific enzyme, it is easier to use the Filter. You can type HindIII or blunt into the filter, and the list of enzymes will shrink automatically to only include respectively only the HindIII enzyme, or all enzymes producing a blunt cut.

If you need more detailed information and filtering of the enzymes, you can hover your mouse on an enzyme (see figure 11.7). You can also open a view of an enzyme list saved in the Navigation Area.

At the bottom of the dialog, you can select to save the updated list of enzymes as a new file. When you click **Finish**, the enzymes are added to the Side Panel and the cut sites are shown on the sequence. If you have specified a set of enzymes which you always use, it will probably be a good idea to save the settings in the Side Panel (see section 3.5) for future use.



Create new enzyme list

1. Please choose enzymes

Please choose enzymes

Enzyme list

☑ Use existing enzyme list Popular enzymes

Enzymes in "Popular en..."

Filter:

| Name | Overhang | Methyl... | Popularity |
|---|---|---|---|
| AccI | 5' - mk | 5': N6-met... | *** |
| BclI | 5' - gatc | 5': N6-met... | *** |
| ClaI | | | |
| CviAII | | | |
| DraI | | | |
| EcoRI | | | |
| EcoRV | | | |
| HincII | | | |
| HindIII | | | |
| HinfI | | | |
| HpaI | | | |
| KpnI | | | |
| MboI | | | |
| MseI | | | |
| NdeI | | | |
| PstI | 3' - tgca | 5': N6-met... | ***** |
| SalI | 5' - tcga | 5': N6-met... | ***** |

Enzyme: AccI
Recognition site pattern: GTMKAC
Suppliers: GE Healthcare
Invitrogen Corporation
Qbiogene
Nippon Gene Co., Ltd.
Takara Bio Inc.
Roche Applied Science
New England Biolabs
Toyobo Biochemicals
Promega Corporation
Sigma Chemical Corporation
Bangalore Genei

New enzyme list

Filter:

| Name | Overhang | Methylation | Popula... |
|---|---|---|---|
| AluI | Blunt - | 5': 5-meth... | *** |
| PvuII | Blunt - | 5': N4-met... | **** |
| HpaI | Blunt - | 5': N6-met... | *** |
| StuI | Blunt - | | *** |
| SmaI | Blunt - | 5': N4-met... | ***** |
| DraI | Blunt - | 5': N6-met... | *** |
| EcoRV | Blunt - | 5': N6-met... | ***** |
| HincII | Blunt - | 5': N6-met... | *** |
| SspI | Blunt - | 5': N6-met... | *** |
| RsaI | Blunt - | 5': N4-met... | *** |
| ScaI | Blunt - | 5': N4-met... | *** |
| HaeIII | Blunt - | 5': 5-meth... | **** |

Figure 11.7: *Showing additional information about an enzyme like recognition sequence or a list of commercial vendors.*

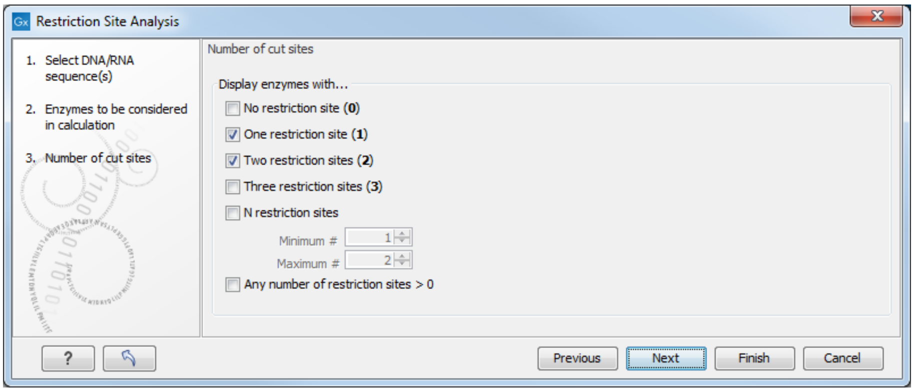
## 11.2 Restriction Site Analysis

Besides the dynamic restriction sites, you can do a more elaborate restriction map analysis with more output formats using the tool:

**Toolbox | Restriction Site Table ( ) | Restriction Site Analysis ( )**

You first specify which sequence should be used for the analysis. Then define which enzymes to use as basis for finding restriction sites on the sequence (see section 11.1.1).

In the next dialog, you can use the checkboxes so that the output of the restriction map analysis only include restriction enzymes which cut the sequence a specific number of times (figure 11.8).



Restriction Site Analysis

1. Select DNA/RNA sequence(s)
2. Enzymes to be considered in calculation
3. Number of cut sites

Number of cut sites

Display enzymes with...

☐ No restriction site (**0**)

☑ One restriction site (**1**)

☑ Two restriction sites (**2**)

☐ Three restriction sites (**3**)

☐ N restriction sites

Minimum # 1

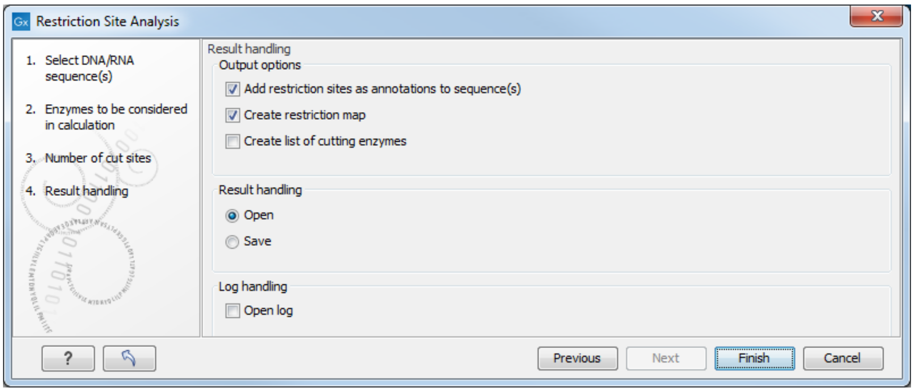
Maximum # 2

☐ Any number of restriction sites > 0

Figure 11.8: *Selecting number of cut sites.*

The default setting is to include the enzymes which cut the sequence one or two times, but you can use the checkboxes to perform very specific searches for restriction sites: e.g. if you wish to find enzymes which do not cut the sequence, or enzymes cutting exactly twice.

The Result handling dialog (figure 11.9) lets you specify how the result of the restriction map analysis should be presented.



Restriction Site Analysis

1. Select DNA/RNA sequence(s)
2. Enzymes to be considered in calculation
3. Number of cut sites
4. Result handling

Result handling

Output options

☑ Add restriction sites as annotations to sequence(s)

☑ Create restriction map

□ Create list of cutting enzymes

Result handling

● Open

○ Save

Log handling

□ Open log

Figure 11.9: *Choosing to add restriction sites as annotations or creating a restriction map.*

**Add restriction sites as annotations to sequence(s)** . This option makes it possible to see the restriction sites on the sequence (see figure 11.10) and save the annotations for later use.

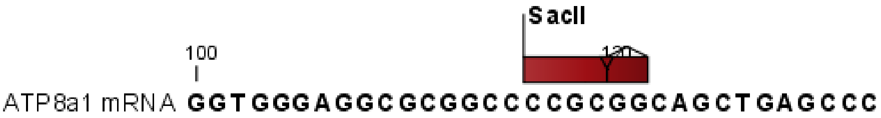
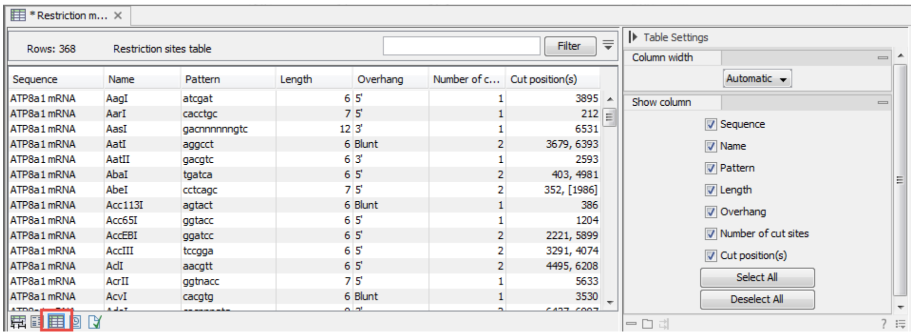


Figure 11.10: *The result of the restriction analysis shown as annotations.*

**Create restriction map** . The restriction map is a table of restriction sites as shown in figure 11.11. If more than one sequence were selected, the table will include the restriction sites of all the sequences. This makes it easy to compare the result of the restriction map analysis for two sequences (or more).



* Restriction m...

Rows: 368 Restriction sites table

| Sequence | Name | Pattern | Length | Overhang | Number of c... | Cut position(s) |
|---|---|---|---|---|---|---|
| ATP8a1 mRNA | AagI | atcgat | 6 | 5' | 1 | 3895 |
| ATP8a1 mRNA | AarI | cacctgc | 7 | 5' | 1 | 212 |
| ATP8a1 mRNA | AasI | gacnnnnnngtc | 12 | 3' | 1 | 6531 |
| ATP8a1 mRNA | AatI | aggcct | 6 | Blunt | 2 | 3679, 6393 |
| ATP8a1 mRNA | AatII | gacgtc | 6 | 3' | 1 | 2593 |
| ATP8a1 mRNA | AbaI | tgatca | 6 | 5' | 2 | 403, 4981 |
| ATP8a1 mRNA | AbeI | cctcagc | 7 | 5' | 2 | 352, [1986] |
| ATP8a1 mRNA | Acc113I | agtact | 6 | Blunt | 1 | 386 |
| ATP8a1 mRNA | Acc65I | ggtacc | 6 | 5' | 1 | 1204 |
| ATP8a1 mRNA | AccEBI | ggatcc | 6 | 5' | 2 | 2221, 5899 |
| ATP8a1 mRNA | AccIII | tccgga | 6 | 5' | 2 | 3291, 4074 |
| ATP8a1 mRNA | AclI | aacgtt | 6 | 5' | 2 | 4495, 6208 |
| ATP8a1 mRNA | AcrII | ggtnacc | 7 | 5' | 1 | 5633 |
| ATP8a1 mRNA | AcvI | cacgtg | 6 | Blunt | 1 | 3530 |

Table Settings

Column width: Automatic

Show column

☑ Sequence

☑ Name

☑ Pattern

☑ Length

☑ Overhang

☑ Number of cut sites

☑ Cut position(s)

Figure 11.11: *The result of the restriction analysis shown as annotations.*

Each row in the table represents a restriction enzyme. The following information is available for each enzyme:

- **Sequence**. The name of the sequence which is relevant if you have performed restriction map analysis on more than one sequence.
- **Name**. The name of the enzyme.
- **Pattern**. The recognition sequence of the enzyme.

- **Overhang**. The overhang produced by cutting with the enzyme (3', 5' or Blunt).
- **Number of cut sites**.
- **Cut position(s)**. The position of each cut.
  - **,** If the enzyme cuts more than once, the positions are separated by commas.
  - **[]** If the enzyme's recognition sequence is on the negative strand, the cut position is put in brackets (as the enzyme TsoI in figure 11.11 whose cut position is [134]).
  - **()** Some enzymes cut the sequence twice for each recognition site, and in this case the two cut positions are surrounded by parentheses.

## 11.3 Restriction enzyme lists

*CLC Sequence Viewer* includes all the restriction enzymes available in the **REBASE** database, with methylation shown as performed by the cognate methylase rather than by Dam/Dcm. If you want to customize the enzyme database for your installation, see section D. However, when performing restriction site analyses, it is often an advantage to use a customized list of enzymes. In this case, the user can create special lists containing for example all enzymes available in the laboratory freezer, or all enzymes used to create a given restriction map or all enzymes that are available form the preferred vendor.

In the example data (see section **??**) under Nucleotide->Restriction analysis, there are two enzyme lists: one with the 50 most popular enzymes, and another with all enzymes that are included in the *CLC Sequence Viewer*.

**Create enzyme list** *CLC Sequence Viewer* uses enzymes from the **REBASE** restriction enzyme database at `http://rebase.neb.com`. If you want to customize the enzyme database for your installation, see section D.

To create an enzyme list of a subset of these enzymes:

**File | New | Enzyme list ()**

This opens the dialog shown in figure 11.12

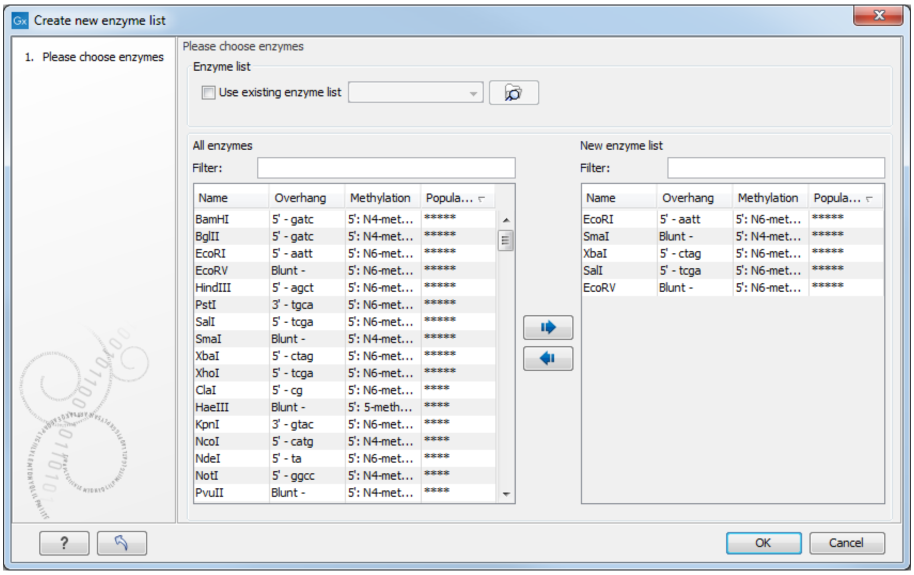
Choose which enzyme you want to include in the new enzyme list (see section 11.1.1), and click **Finish** to open the enzyme list.

**View and modify enzyme list** An enzyme list is shown in figure 11.13. It can be sorted by clicking the columns, and you can use the filter at the top right corner to search for specific enzymes, recognition sequences etc.

If you wish to remove or add enzymes, click the **Add/Remove Enzymes** button at the bottom of the view. This will present the same dialog as shown in figure 11.12 with the enzyme list shown to the right.

If you wish to extract a subset of an enzyme list, open the list, select the relevant enzymes, right-click on the selection and choose to **Create New Enzyme List from Selection** ().

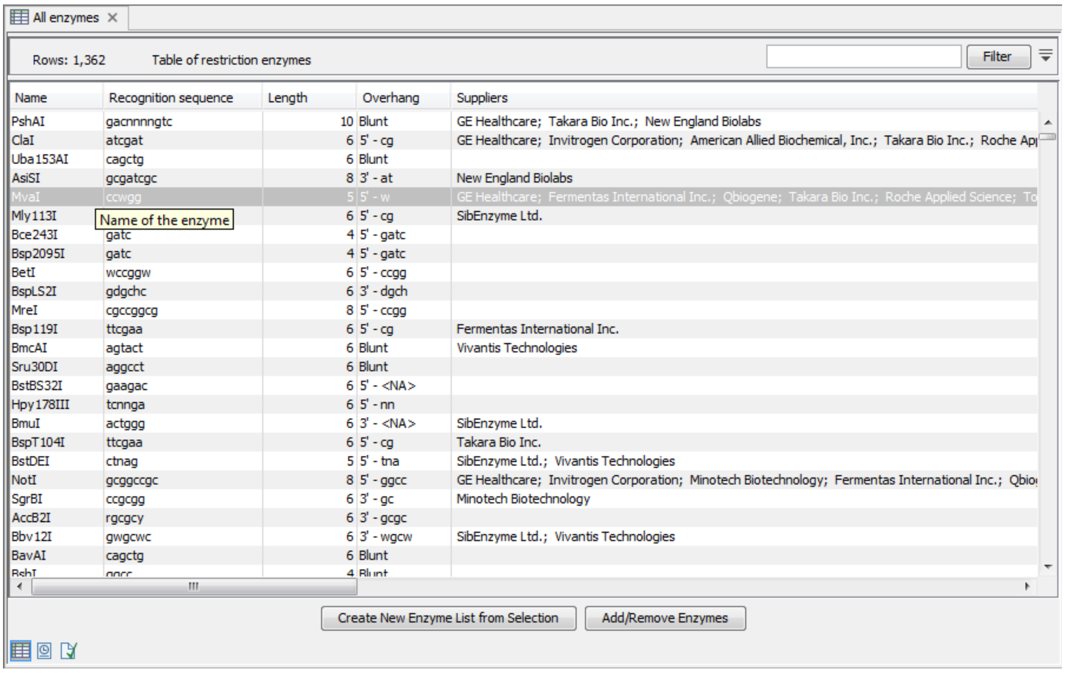
If you combined this method with the filter located at the top of the view, you can extract a very specific set of enzymes. for example, if you wish to create a list of enzymes sold by a particular



| Name | Overhang | Methylation | Popula... |
|---|---|---|---|
| BamHI | 5' - gatc | 5': N4-met... | ***** |
| BglII | 5' - gatc | 5': N4-met... | ***** |
| EcoRI | 5' - aatt | 5': N6-met... | ***** |
| EcoRV | Blunt - | 5': N6-met... | ***** |
| HindIII | 5' - agct | 5': N6-met... | ***** |
| PstI | 3' - tgca | 5': N6-met... | ***** |
| SalI | 5' - tcga | 5': N6-met... | ***** |
| SmaI | Blunt - | 5': N4-met... | ***** |
| XbaI | 5' - ctag | 5': N6-met... | ***** |
| XhoI | 5' - tcga | 5': N6-met... | ***** |
| ClaI | 5' - cg | 5': N6-met... | **** |
| HaeIII | Blunt - | 5': 5-meth... | **** |
| KpnI | 3' - gtac | 5': N6-met... | **** |
| NcoI | 5' - catg | 5': N4-met... | **** |
| NdeI | 5' - ta | 5': N6-met... | **** |
| NotI | 5' - ggcc | 5': N4-met... | **** |
| PvuII | Blunt - | 5': N4-met... | **** |

| Name | Overhang | Methylation | Popula... |
|---|---|---|---|
| EcoRI | 5' - aatt | 5': N6-met... | ***** |
| SmaI | Blunt - | 5': N4-met... | ***** |
| XbaI | 5' - ctag | 5': N6-met... | ***** |
| SalI | 5' - tcga | 5': N6-met... | ***** |
| EcoRV | Blunt - | 5': N6-met... | ***** |

Figure 11.12: *Choosing enzymes for the new enzyme list.*



Rows: 1,362 Table of restriction enzymes

| Name | Recognition sequence | Length | Overhang | Suppliers |
|---|---|---|---|---|
| PshAI | gacnnnngtc | 10 | Blunt | GE Healthcare; Takara Bio Inc.; New England Biolabs |
| ClaI | atcgat | 6 | 5' - cg | GE Healthcare; Invitrogen Corporation; American Allied Biochemical, Inc.; Takara Bio Inc.; Roche Ap |
| Uba153AI | cagctg | 6 | Blunt | |
| AsiSI | gcgatcgc | 8 | 3' - at | New England Biolabs |
| MvaI | ccwgg | 5 | 5' - w | GE Healthcare; Fermentas International Inc.; Qbiogene; Takara Bio Inc.; Roche Applied Science; To |
| Mly113I | Name of the enzyme | 6 | 5' - cg | SibEnzyme Ltd. |
| Bce243I | gatc | 4 | 5' - gatc | |
| Bsp2095I | gatc | 4 | 5' - gatc | |
| BetI | wccggw | 6 | 5' - ccgg | |
| BspLS2I | gdgchc | 6 | 3' - dgch | |
| MreI | cgccggcg | 8 | 5' - ccgg | |
| Bsp119I | ttcgaa | 6 | 5' - cg | Fermentas International Inc. |
| BmcAI | agtact | 6 | Blunt | Vivantis Technologies |
| Sru30DI | aggcct | 6 | Blunt | |
| BstBS32I | gaagac | 6 | 5' - <NA> | |
| Hpy178III | tcnnga | 6 | 5' - nn | |
| BmuI | actggg | 6 | 3' - <NA> | SibEnzyme Ltd. |
| BspT104I | ttcgaa | 6 | 5' - cg | Takara Bio Inc. |
| BstDEI | ctnag | 5 | 5' - tna | SibEnzyme Ltd.; Vivantis Technologies |
| NotI | gcggccgc | 8 | 5' - ggcc | GE Healthcare; Invitrogen Corporation; Minotech Biotechnology; Fermentas International Inc.; Qbio |
| SgrBI | ccgcgg | 6 | 3' - gc | Minotech Biotechnology |
| AccB2I | rgcgcy | 6 | 3' - gcgc | |
| Bbv12I | gwgcwc | 6 | 3' - wgcw | SibEnzyme Ltd.; Vivantis Technologies |
| BavAI | cagctg | 6 | Blunt | |
| BshI | ggcc | 4 | Blunt | |

Figure 11.13: *An enzyme list.*

distributor, type the name of the distributor into the filter and select and create a new enzyme list from the selection.

# Chapter 12

# Sequence alignment

**Contents**

*CLC Sequence Viewer* can align nucleotides and proteins using a *progressive alignment* algorithm (see section 12.3.2.

This chapter describes how to use the program to align sequences, and alignment algorithms in more general terms.

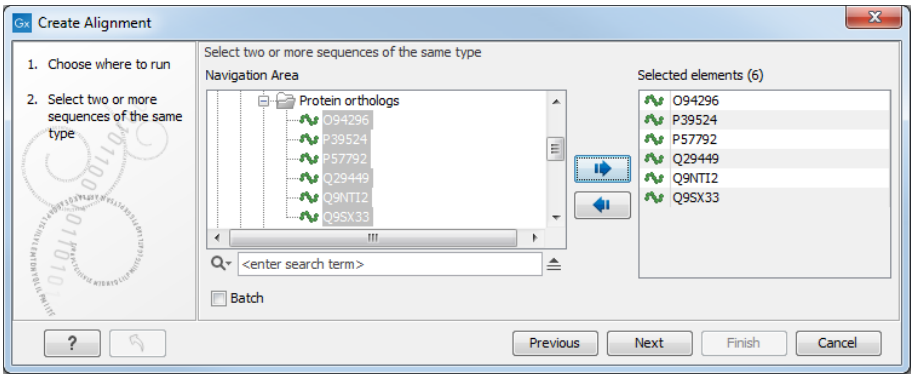
## 12.1 Create an alignment

To create an alignment in *CLC Sequence Viewer*:

**Toolbox** | **Alignments and Trees** ()| **Create Alignment** ()

This opens the dialog shown in figure 12.1.

If you have selected some elements before choosing the Toolbox action, they are now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove sequences, sequence lists or alignments from the selected elements. Click **Next** to adjust alignment algorithm parameters. Clicking **Next** opens the dialog shown in figure 12.2.



Create Alignment

1. Choose where to run
2. Select two or more sequences of the same type

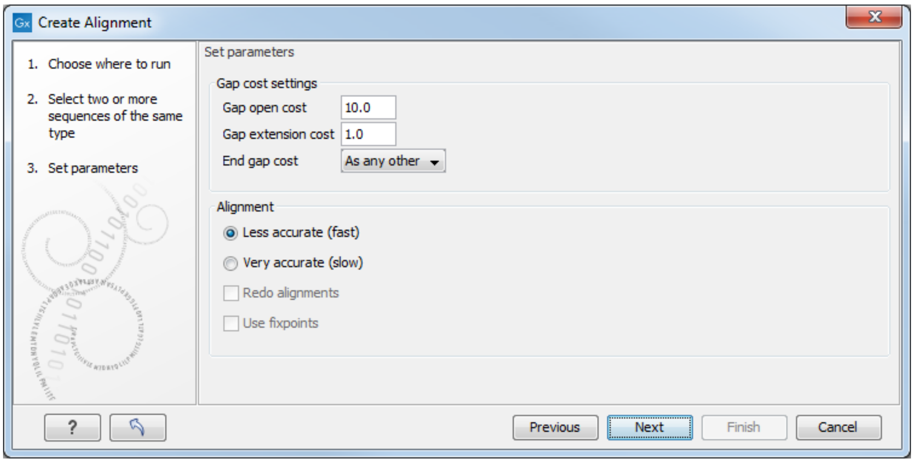
Select two or more sequences of the same type

Navigation Area: Protein orthologs — O94296, P39524, P57792, Q29449, Q9NTI2, Q9SX33

Selected elements (6): O94296, P39524, P57792, Q29449, Q9NTI2, Q9SX33

☐ Batch

Figure 12.1: *Creating an alignment.*



Create Alignment

1. Choose where to run
2. Select two or more sequences of the same type
3. Set parameters

Set parameters

Gap cost settings

Gap open cost: 10.0

Gap extension cost: 1.0

End gap cost: As any other

Alignment

● Less accurate (fast)

○ Very accurate (slow)

☐ Redo alignments

☐ Use fixpoints

Figure 12.2: *Adjusting alignment algorithm parameters.*

### 12.1.1 Gap costs

The alignment algorithm has three parameters concerning gap costs: Gap open cost, Gap extension cost and End gap cost. The precision of these parameters is to one place of decimal.

- **Gap open cost**. The price for introducing gaps in an alignment.
- **Gap extension cost**. The price for every extension past the initial gap.

If you expect a lot of small gaps in your alignment, the Gap open cost should equal the Gap extension cost. On the other hand, if you expect few but large gaps, the Gap open cost should be set significantly higher than the Gap extension cost.

However, for most alignments it is a good idea to make the Gap open cost quite a bit higher than the Gap extension cost. The default values are 10.0 and 1.0 for the two parameters, respectively.

- **End gap cost**. The price of gaps at the beginning or the end of the alignment. One of the advantages of the *CLC Sequence Viewer* alignment method is that it provides flexibility in the treatment of gaps at the ends of the sequences. There are three possibilities:
  - **Free end gaps**. Any number of gaps can be inserted in the ends of the sequences without any cost.

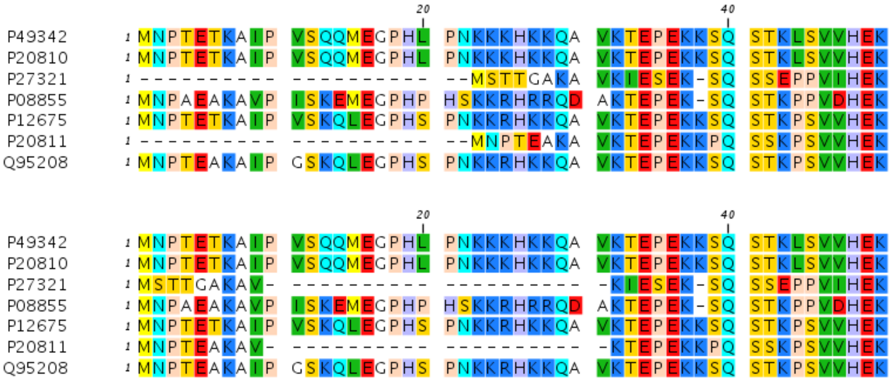
- **Cheap end gaps**. All end gaps are treated as gap extensions and any gaps past 10 are free.
- **End gaps as any other**. Gaps at the ends of sequences are treated like gaps in any other place in the sequences.

When aligning a long sequence with a short partial sequence, it is ideal to use free end gaps, since this will be the best approximation to the situation. The many gaps inserted at the ends are not due to evolutionary events, but rather to partial data.

Many homologous proteins have quite different ends, often with large insertions or deletions. This confuses alignment algorithms, but using the **Cheap end gaps** option, large gaps will generally be tolerated at the sequence ends, improving the overall alignment. This is the default setting of the algorithm.

Finally, treating end gaps like any other gaps is the best option when you know that there are no biologically distinct effects at the ends of the sequences.

Figures 12.3 and 12.4 illustrate the differences between the different gap scores at the sequence ends.



```
                                  20                    40
                                   |                     |
P49342   1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P20810   1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P27321   1 ---------- ---------- --MSTTGAKA VKIESEK-SQ SSEPPVIHEK
P08855   1 MNPAEAKAVP ISKEMEGPHP HSKKRHRRQD AKTEPEK-SQ STKPPVDHEK
P12675   1 MNPTETKAIP VSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
P20811   1 ---------- ---------- --MNPTEAKA VKTEPEKKPQ SSKPSVVHEK
Q95208   1 MNPTEAKAIP GSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK

                                  20                    40
                                   |                     |
P49342   1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P20810   1 MNPTETKAIP VSQQMEGPHL PNKKKHKKQA VKTEPEKKSQ STKLSVVHEK
P27321   1 MSTTGAKAV- ---------- ---------- -KIESEK-SQ SSEPPVIHEK
P08855   1 MNPAEAKAVP ISKEMEGPHP HSKKRHRRQD AKTEPEK-SQ STKPPVDHEK
P12675   1 MNPTETKAIP VSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
P20811   1 MNPTEAKAV- ---------- ---------- -KTEPEKKPQ SSKPSVVHEK
Q95208   1 MNPTEAKAIP GSKQLEGPHS PNKKRHKKQA VKTEPEKKSQ STKPSVVHEK
```

Figure 12.3: *The first 50 positions of two different alignments of seven calpastatin sequences. The top alignment is made with cheap end gaps, while the bottom alignment is made with end gaps having the same price as any other gaps. In this case it seems that the latter scoring scheme gives the best result.*

### 12.1.2 Fast or accurate alignment algorithm

*CLC Sequence Viewer* has two algorithms for calculating alignments:

- **Fast (less accurate).** This allows for use of an optimized alignment algorithm which is very fast. The fast option is particularly useful for data sets with very long sequences.
- **Slow (very accurate).** This is the recommended choice unless you find the processing time too long.

Both algorithms use progressive alignment. The faster algorithm builds the initial tree by doing more approximate pairwise alignments than the slower option.

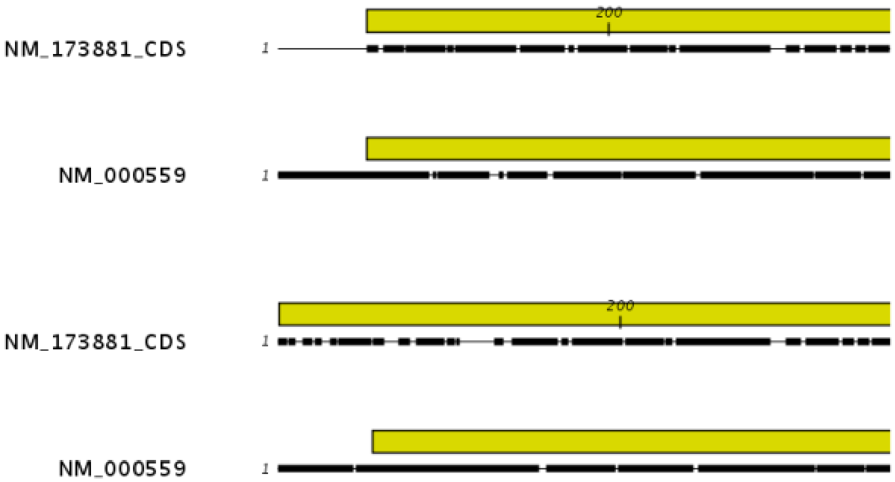


Figure 12.4: *The alignment of the coding sequence of bovine myoglobin with the full mRNA of human gamma globin. The top alignment is made with free end gaps, while the bottom alignment is made with end gaps treated as any other. The yellow annotation is the coding sequence in both sequences. It is evident that free end gaps are ideal in this situation as the start codons are aligned correctly in the top alignment. Treating end gaps as any other gaps in the case of aligning distant homologs where one sequence is partial leads to a spreading out of the short sequence as in the bottom alignment.*

### 12.1.3 Aligning alignments

If you have selected an existing alignment in the first step (12.1), you have to decide how this alignment should be treated.

- **Redo alignment.** The original alignment will be realigned if this checkbox is checked. Otherwise, the original alignment is kept in its original form except for possible extra equally sized gaps in all sequences of the original alignment. This is visualized in figure 12.5.

This feature is useful if you wish to add extra sequences to an existing alignment, in which case you just select the alignment and the extra sequences and choose not to redo the alignment.

It is also useful if you have created an alignment where the gaps are not placed correctly. In this case, you can realign the alignment with different gap cost parameters.

### 12.1.4 Fixpoints

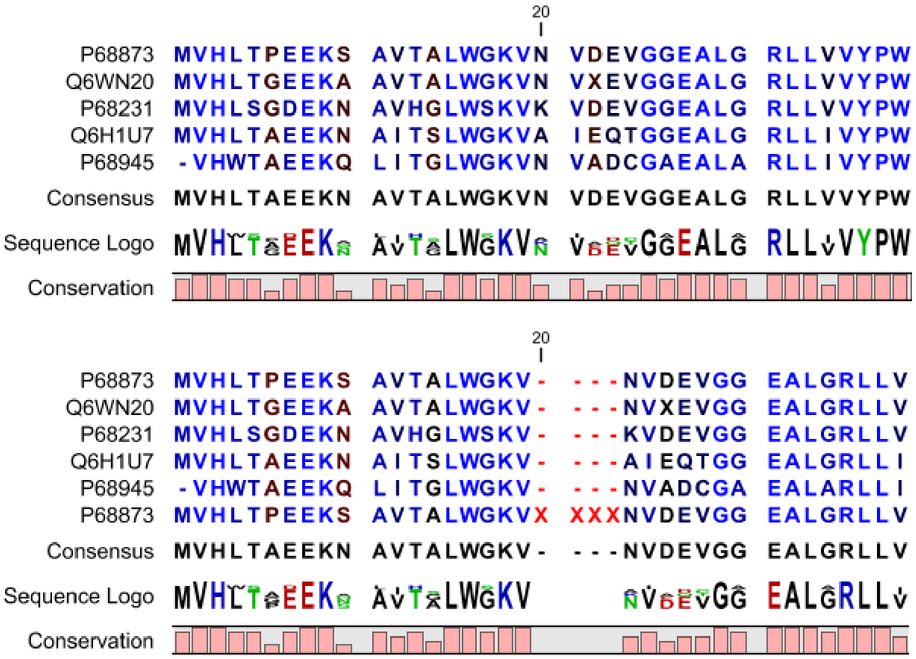
With fixpoints, you can get full control over the alignment algorithm. The fixpoints are points on the sequences that are forced to align to each other.

To add a fixpoint, open the sequence or alignment and:

> **Select the region you want to use as a fixpoint | right-click the selection | Set alignment fixpoint here**

This will add an annotation labeled "Fixpoint" to the sequence (see figure 12.6). Use this procedure to add fixpoints to the other sequence(s) that should be forced to align to each other.

When you click "Create alignment" and go to **Step 2**, check **Use fixpoints** in order to force the



```
                                    20
                                    |
P68873          MVHLTPEEKS AVTALWGKVN VDEVGGEALG RLLVVYPW
Q6WN20          MVHLTGEEKA AVTALWGKVN VXEVGGEALG RLLVVYPW
P68231          MVHLSGDEKN AVHGLWSKVK VDEVGGEALG RLLVVYPW
Q6H1U7          MVHLTAEEKN AITSLWGKVA IEQTGGEALG RLLIVYPW
P68945          -VHWTAEEKQ LITGLWGKVN VADCGAEALA RLLIVYPW
Consensus       MVHLTAEEKN AVTALWGKVN VDEVGGEALG RLLVVYPW
Sequence Logo
Conservation

                                    20
                                    |
P68873          MVHLTPEEKS AVTALWGKV- ---NVDEVGG EALGRLLV
Q6WN20          MVHLTGEEKA AVTALWGKV- ---NVXEVGG EALGRLLV
P68231          MVHLSGDEKN AVHGLWSKV- ---KVDEVGG EALGRLLV
Q6H1U7          MVHLTAEEKN AITSLWGKV- ---AIEQTGG EALGRLLI
P68945          -VHWTAEEKQ LITGLWGKV- ---NVADCGA EALARLLI
P68873          MVHLTPEEKS AVTALWGKVX XXXNVDEVGG EALGRLLV
Consensus       MVHLTAEEKN AVTALWGKV- ---NVDEVGG EALGRLLV
Sequence Logo
Conservation
```

Figure 12.5: *The top figures shows the original alignment. In the bottom panel a single sequence with four inserted X's are aligned to the original alignment. This introduces gaps in all sequences of the original alignment. All other positions in the original alignment are fixed.*

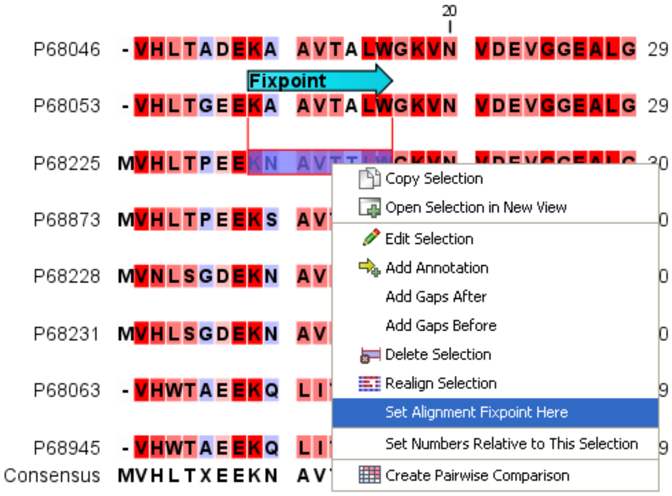

20
P68046 -VHLTADEKA AVTALWGKVN VDEVGGEALG 29
Fixpoint
P68053 -VHLTGEEKA AVTALWGKVN VDEVGGEALG 29
P68225
P68873
P68228
P68231
P68063
P68945
Consensus MVHLTXEEKN
Copy Selection
Open Selection in New View
Edit Selection
Add Annotation
Add Gaps After
Add Gaps Before
Delete Selection
Realign Selection
Set Alignment Fixpoint Here
Set Numbers Relative to This Selection
Create Pairwise Comparison

Figure 12.6: *Adding a fixpoint to a sequence in an existing alignment. At the top you can see a fixpoint that has already been added.*

alignment algorithm to align the fixpoints in the selected sequences to each other.

In figure 12.7 the result of an alignment using fixpoints is illustrated.

You can add multiple fixpoints, e.g. adding two fixpoints to the sequences that are aligned will force their first fixpoints to be aligned to each other, and their second fixpoints will also be aligned to each other.

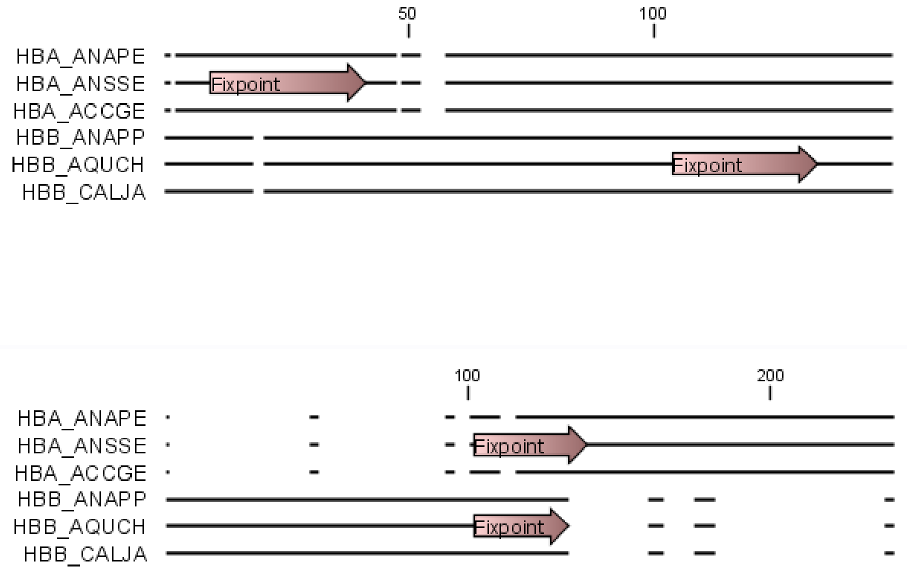


Figure 12.7: *Realigning using fixpoints. In the top view, fixpoints have been added to two of the sequences. In the view below, the alignment has been realigned using the fixpoints. The three top sequences are very similar, and therefore they follow the one sequence (number two from the top) that has a fixpoint.*

## 12.2 View alignments

Since an alignment is a display of several sequences arranged in rows, the basic options for viewing alignments are the same as for viewing sequences. Therefore we refer to section 7.1 for an explanation of these basic options.

However, there are a number of alignment-specific view options in the **Alignment info** in the Side Panel to the right of the view. Below is more information on these view options.

The options in the **Alignment info** relate to each column in the alignment.

**Consensus** Shows a consensus sequence at the bottom of the alignment. The consensus sequence is based on every single position in the alignment and reflects an artificial sequence which resembles the sequence information of the alignment, but only as one single sequence. If all sequences of the alignment is 100% identical the consensus sequence will be identical to all sequences found in the alignment. If the sequences of the alignment differ the consensus sequence will reflect the most common sequences in the alignment. Parameters for adjusting the consensus sequences are described below.

- **Limit** This option determines how conserved the sequences must be in order to agree on a consensus. Here you can also choose **IUPAC** which will display the ambiguity code when there are differences between the sequences. For example, an alignment with **A** and a **G** at the same position will display an **R** in the consensus line if the **IUPAC** option is selected. The IUPAC codes can be found in section F and E. Please note that the IUPAC codes are only available for nucleotide alignments.

- **No gaps** Checking this option will not show gaps in the consensus.

- **Ambiguous symbol** Select how ambiguities should be displayed in the consensus line (as

**N**, **?**, *, . or **-**). This option has no effect if **IUPAC** is selected in the **Limit** list above.

The Consensus Sequence can be opened in a new view, simply by right-clicking the Consensus Sequence and click **Open Consensus in New View**.

**Conservation** Displays the level of conservation at each position in the alignment. The conservation shows the conservation of all sequence positions. The height of the bar, or the gradient of the color reflect how conserved that particular position is in the alignment. If one position is 100% conserved the bar will be shown in full height, and it is colored in the color specified at the right side of the gradient slider.

- **Foreground color** Colors the letters using a gradient, where the right side color is used for highly conserved positions and the left side color is used for positions that are less conserved.
- **Background color.** Sets a background color of the residues using a gradient in the same way as described above.
- **Graph** Displays the conservation level as a graph at the bottom of the alignment. The bar (default view) show the conservation of all sequence positions. The height of the graph reflects how conserved that particular position is in the alignment. If one position is 100% conserved the graph will be shown in full height. Learn how to export the data behind the graph in section 5.4.
  - **Height** Specifies the height of the graph.
  - **Type** The type of the graph: **Line plot**, **Bar plot**, or **Colors**, in which case the graph is seen as a color bar using a gradient like the foreground and background colors.
  - **Color box** Specifies the color of the graph for line and bar plots, and specifies a gradient for colors.

**Gap fraction** Which fraction of the sequences in the alignment that have gaps. The gap fraction is only relevant if there are gaps in the alignment.

- **Foreground color** Colors the letter using a gradient, where the left side color is used if there are relatively few gaps, and the right side color is used if there are relatively many gaps.
- **Background color** Sets a background color of the residues using a gradient in the same way as described above.
- **Graph** Displays the gap fraction as a graph at the bottom of the alignment (Learn how to export the data behind the graph in section 5.4).
  - **Height** Specifies the height of the graph.
  - **Type** The type of the graph: **Line plot**, **Bar plot**, or **Colors**, in which case the graph is seen as a color bar using a gradient like the foreground and background colors.
  - **Color box** Specifies the color of the graph for line and bar plots, and specifies a gradient for colors.

**Color different residues** Indicates differences in aligned residues.

- **Foreground color** Colors the letter.
- **Background color.** Sets a background color of the residues.

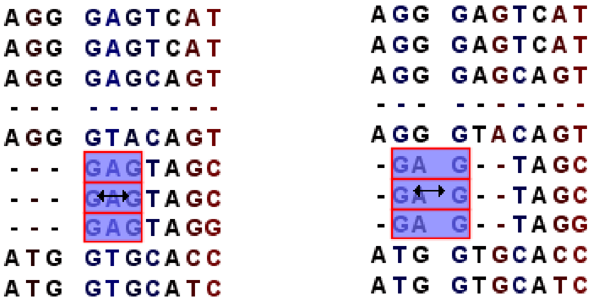
## 12.3 Edit alignments

**Move residues and gaps** The placement of gaps in the alignment can be changed by modifying the parameters when creating the alignment (see section 12.1). However, gaps and residues can also be moved after the alignment is created:

> **select one or more gaps or residues in the alignment | drag the selection to move**

This can be done both for single sequences, but also for multiple sequences by making a selection covering more than one sequence. When you have made the selection, the mouse pointer turns into a horizontal arrow indicating that the selection can be moved (see figure 12.8).

**Note!** Residues can only be moved when they are next to a gap.



```
AGG GAGTCAT        AGG GAGTCAT
AGG GAGTCAT        AGG GAGTCAT
AGG GAGCAGT        AGG GAGCAGT
--- -------        --- -------
AGG GTACAGT        AGG GTACAGT
--- GAGTAGC        -GA G--TAGC
--- GAGTAGC        -GA G--TAGC
--- GAGTAGG        -GA G--TAGG
ATG GTGCACC        ATG GTGCACC
ATG GTGCATC        ATG GTGCATC
```

Figure 12.8: *Moving a part of an alignment. Notice the change of mouse pointer to a horizontal arrow.*

**Insert gaps** The placement of gaps in the alignment can be changed by modifying the parameters when creating the alignment. However, gaps can also be added manually after the alignment is created.

To insert extra gaps:

> **select a part of the alignment | right-click the selection | Add gaps before/after**

If you have made a selection covering five residues for example, a gap of five will be inserted. In this way you can easily control the number of gaps to insert. Gaps will be inserted in the sequences that you selected. If you make a selection in two sequences in an alignment, gaps will be inserted into these two sequences. This means that these two sequences will be displaced compared to the other sequences in the alignment.

**Delete residues and gaps** Residues or gaps can be deleted for individual sequences or for the whole alignment. For individual sequences:

> **select the part of the sequence you want to delete | right-click the selection | Edit Selection (✎) | Delete the text in the dialog | Replace**

The selection shown in the dialog will be replaced by the text you enter. If you delete the text, the selection will be replaced by an empty text, i.e. deleted.

In order to delete entire columns:

> **manually select the columns to delete | right-click the selection | click 'Delete Selection'**

**Move sequences up and down** Sequences can be moved up and down in the alignment:

> **drag the name of the sequence up or down**

When you move the mouse pointer over the label, the pointer will turn into a vertical arrow indicating that the sequence can be moved.

The sequences can also be sorted automatically to let you save time moving the sequences around. To sort the sequences alphabetically:

> **Right-click the name of a sequence | Sort Sequences Alphabetically**

If you change the Sequence name (in the **Sequence Layout** view preferences), you will have to ask the program to sort the sequences again.

If you have one particular sequence that you would like to use as a reference sequence, it can be useful to move this to the top. This can be done manually, but it can also be done automatically:

> **Right-click the name of a sequence | Move Sequence to Top**

### 12.3.1 Delete and rename sequences

Sequences can be removed from the alignment by right-clicking the label of a sequence:

> **right-click label | Delete Sequence**

If you wish to delete several sequences, you can check all the sequences, right-click and choose **Delete Marked Sequences**. To show the checkboxes, you first have to click the **Show Selection Boxes** in the **Side Panel**.

A sequence can also be renamed:

> **right-click label | Rename Sequence**

This will show a dialog, letting you rename the sequence. This will not affect the sequence that the alignment is based on.

### 12.3.2 Bioinformatics explained: Multiple alignments

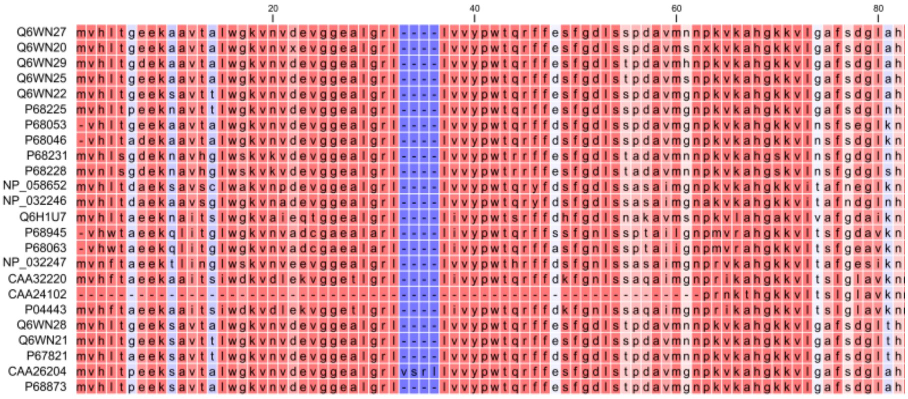
Multiple alignments are at the core of bioinformatical analysis. Often the first step in a chain of bioinformatical analyses is to construct a multiple alignment of a number of homologs DNA or protein sequences. However, despite their frequent use, the development of multiple alignment algorithms remains one of the algorithmically most challenging areas in bioinformatical research.

Constructing a multiple alignment corresponds to developing a hypothesis of how a number of sequences have evolved through the processes of character substitution, insertion and deletion. The input to multiple alignment algorithms is a number of homologous sequences, i.e., sequences that share a common ancestor and most often also share molecular function. The generated alignment is a table (see figure 12.9) where each row corresponds to an input sequence and each column corresponds to a position in the alignment. An individual column in this table represents residues that have all diverged from a common ancestral residue. Gaps in the table (commonly represented by a '-') represent positions where residues have been inserted or deleted and thus do not have ancestral counterparts in all sequences.

### Use of multiple alignments

Once a multiple alignment is constructed it can form the basis for a number of analyses:

- The phylogenetic relationship of the sequences can be investigated by tree-building methods based on the alignment.
- Annotation of functional domains, which may only be known for a subset of the sequences, can be transferred to aligned positions in other un-annotated sequences.
- Conserved regions in the alignment can be found which are prime candidates for holding functionally important sites.
- Comparative bioinformatical analysis can be performed to identify functionally important regions.



```
                              20                  40                  60                  80
                              |                   |                   |                   |
Q6WN27     mvhltgeekaavtalwgkvnvdevggealgrl----lvvypwtqrffesfgdlsspdavmnnpkvkahgkkvlgafsdglah
Q6WN20     mvhltgeekaavtalwgkvnvxevggealgrl----lvvypwtqrffesfgdlsspdavmsnxkvkahgkkvlgafsdglah
Q6WN29     mvhltgdekaavtalwgkvnvdevggealgrl----lvvypwtqrffesfgdlstpdavmhnpkvkahgkkvlgafsdglah
Q6WN25     mvhltgeekaavtalwgkvnvdevggealgrl----lvvypwtqrffdsfgdlstpdavmsnpkvkahgkkvlgafsdglah
Q6WN22     mvhltgeeksavttlwgkvnvdevggealgrl----lvvypwtqrffesfgdlsspdavmgnpkvkahgkkvlgafsdglah
P68225     mvhltpeeknavttlwgkvnvdevggealgrl----lvvypwtqrffesfgdlsspdavmgnpkvkahgkkvlgafsdglnh
P68053     -vhltgeekaavtalwgkvnvdevggealgrl----lvvypwtqrffdsfgdlsspdavmgnpkvkahgkkvlnsfseglkn
P68046     -vhltadekaavtalwgkvnvdevggealgrl----lvvypwtqrffdsfgdlsspdavmgnpkvkahgkkvlnsfsdglkn
P68231     mvhlsgdeknavhglwskvkvdevggealgrl----lvvypwtrrffesfgdlstadavmnnpkvkahgskvlnsfgdglnh
P68228     mvnlsgdeknavhglwskvkvdevggealgrl----lvvypwtrrffesfgdlstadavmnnpkvkahgskvlnsfgdglsh
NP_058652  mvhltdaeksavsclwakvnpdevggealgrl----lvvypwtqryfdsfgdlssasaimgnpkvkahgkkvitafneglkn
NP_032246  mvhltdaekaavsglwgkvnadevggealgrl----lvvypwtqryfdsfgdlssasaimgnakvkahgkkvitafndglnh
Q6H1U7     mvhltaeeknaitslwgkvaieqtggealgrl----livypwtsrffdhfgdlsnakavmsnpkvlahgakvlvafgdaikn
P68945     -vhwtaeekqlitglwgkvnvadcgaealarl----livypwtqrffssfgnlssptaillgnpmvrahgkkvltsfgdavkn
P68063     -vhwtaeekqlitglwgkvnvadcgaealarl----livypwtqrffasfgnlssptaiignpmvrahgkkvltsfgeavkn
NP_032247  mvnftaeektlinglwskvnveevggealgrl----lvvypwthrffdsfgnlssasaimgnprvkahgkkvltafgesikn
CAA32220   mvhftaeekaaitsiwdkvdlekvggetlgrl----livypwtqrffdkfgnlssaqaimgnprikahgkkvltslglavkn
CAA24102   --------------------------------------------------------------prnkthgkkvltslglavkn
P04443     mvhftaeekaaitsiwdkvdlekvggetlgrl----livypwtqrffdkfgnlssaqaimgnprikahgkkvltslglavkn
Q6WN28     mvhltgeeksavtalwgkvnvdevggealgrl----lvvypwtqrffesfgdlstpdavmnnpkvkahgkkvlgafsdglth
Q6WN21     mvhltgeeksavttlwgkvnvdevggealgrl----lvvypwtqrffesfgdlsspdavmnnpkvkahgkkvlgafsdglth
P67821     mvhltaeeksavttlwgkvnvdevggealgrl----lvvypwtqrffdsfgdlstpdavmnnpkvkahgkkvlgafsdglth
CAA26204   mvhltpeeksavtalwgkvnvdevggealgrlvsrllvvypwtqrffesfgdlstpdavmgnpkvkahgkkvlgafsdglah
P68873     mvhltpeeksavtalwgkvnvdevggealgrl----lvvypwtqrffesfgdlstpdavmgnpkvkahgkkvlgafsdglah
```

Figure 12.9: *The tabular format of a multiple alignment of 24 Hemoglobin protein sequences. Sequence names appear at the beginning of each row and the residue position is indicated by the numbers at the top of the alignment columns. The level of sequence conservation is shown on a color scale with blue residues being the least conserved and red residues being the most conserved.*

### Constructing multiple alignments

Whereas the optimal solution to the pairwise alignment problem can be found in reasonable time, the problem of constructing a multiple alignment is much harder.

The first major challenge in the multiple alignment procedure is how to rank different alignments, i.e., which *scoring function* to use. Since the sequences have a shared history they are correlated through their *phylogeny* and the scoring function should ideally take this into account. Doing so is, however, not straightforward as it increases the number of model parameters considerably. It is therefore commonplace to either ignore this complication and assume sequences to be unrelated, or to use heuristic corrections for shared ancestry.

The second challenge is to find the optimal alignment given a scoring function. For pairs of sequences this can be done by *dynamic programming* algorithms, but for more than three sequences this approach demands too much computer time and memory to be feasible.

A commonly used approach is therefore to do *progressive alignment* [Feng and Doolittle, 1987] where multiple alignments are built through the successive construction of pairwise alignments. These algorithms provide a good compromise between time spent and the quality of the resulting alignment

The method has the inherent drawback that once two sequences are aligned, there is no way of changing their relative alignment based on the information that additional sequences may contribute later in the process. It is therefore important to make the best possible alignments early in the procedure, to avoid accumulating errors. To accomplish this, a tree of the sequences is usually constructed to guide the progressive alignment algorithm. And to overcome the problem of a time consuming tree construction step, we are using word matching, a method that group sequences in a very efficient way, saving much time, without reducing the resulting alignment accuracy significantly.

Our algorithm (developed by QIAGEN Aarhus) has two speed settings: "standard" and "fast". The **standard method** makes a fairly standard progressive alignment using the fast method of generating a guide tree. When aligning two alignments to each other, two matching columns are scored as the average of all the pairwise scores of the residues in the columns. The gap cost is affine, allowing a different cost for the first gapped position and for the consecutive gaps. This ensures that gaps are not spread out too much.

The **fast method** of alignment uses the same overall method, except that it uses fixpoints in the alignment algorithm based on short subsequences that are identical in the sequences that are being aligned. This allows similar sequences to be aligned much more efficiently, without reducing accuracy very much.

# Chapter 13

# Phylogenetic trees

## Contents

Phylogenetics describes the taxonomical classification of organisms based on their evolutionary history i.e. their phylogeny. Phylogenetics is therefore an integral part of the science of systematics that aims to establish the phylogeny of organisms based on their characteristics. Furthermore, phylogenetics is central to evolutionary biology as a whole as it is the condensation of the overall paradigm of how life arose and developed on earth. The focus of this module is the reconstruction and visualization of phylogenetic trees. Phylogenetic trees illustrate the inferred evolutionary history of a set of organisms, and makes it possible to e.g. identify groups of closely related organisms and observe clustering of organisms with common traits. See 13.1.1 for a more detailed introduction to phylogenetic trees.

The viewer for visualizing and working with phylogenetic trees allows the user to create high-quality, publication-ready figures of phylogenetic trees. Large trees can be explored in two alternative tree layouts; circular and radial.

Below is an overview of the main features of the phylogenetic tree editor. Further details can be found in the subsequent sections.

**Main features of the phylogenetic tree editor:**

- Circular and radial layouts.

- Options for collapsing nodes based on bootstrap values.
- Re-ordering of tree nodes.
- Minimap navigation.
- Coloring and labeling of subtrees.
- Curved edges.
- Editable node sizes and line width.
- Intelligent visualization of overlapping labels and nodes.

For a given set of aligned sequences (see section 12.1) it is possible to infer their evolutionary relationships using a distance based method to generate a phylogenetic tree (see "Bioinformatics explained" in section 13.1.1). **Create Tree** ( ) is a tool that uses distance estimates computed from multiple alignments to generate phylogenetic trees. The user can select whether to use Jukes-Cantor distance correction or Kimura distance correction (Kimura 80 for nucleotides/Kimura protein for proteins) in combination with either the neighbor joining or UPGMA method (see section 13.1.1).

## 13.1 Create tree

The "Create tree" tool can be used to generate a distance-based phylogenetic tree with multiple alignments as input:

**Toolbox** | **Alignments and Trees ( )**| **Create Tree ( )**

This will open the dialog displayed in figure 13.1:

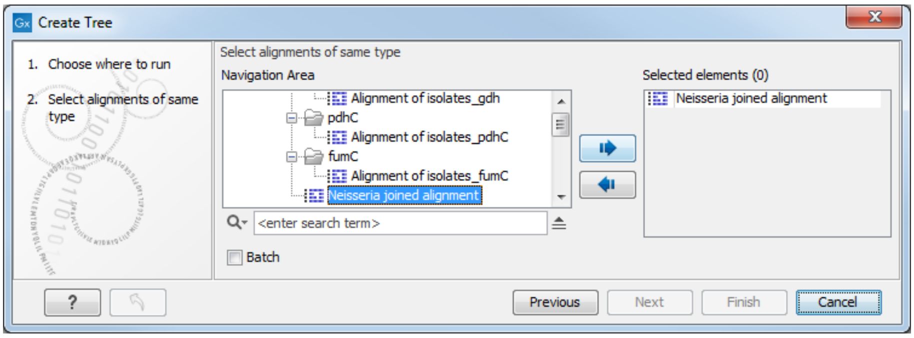
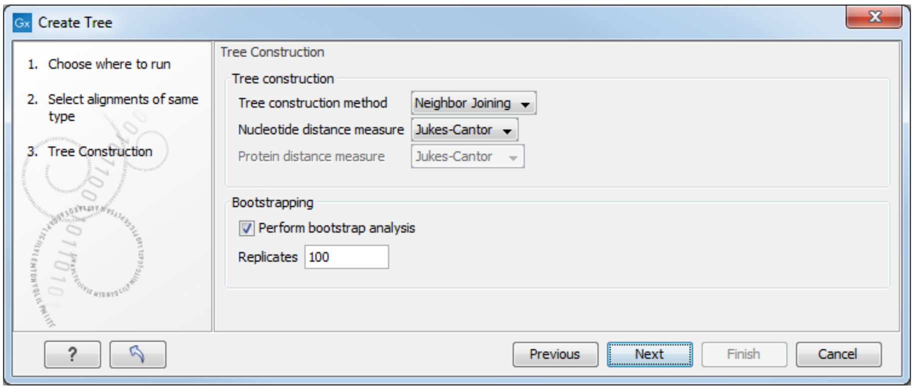

Create Tree
1. Choose where to run
2. Select alignments of same type
Select alignments of same type
Navigation Area
Alignment of isolates_gdh
pdhC
Alignment of isolates_pdhC
fumC
Alignment of isolates_fumC
Neisseria joined alignment
<enter search term>
□ Batch
Selected elements (0)
Neisseria joined alignment
?
Previous
Next
Finish
Cancel

Figure 13.1: *Creating a tree.*

If an alignment was selected before choosing the Toolbox action, this alignment is now listed in the **Selected Elements** window of the dialog. Use the arrows to add or remove elements from the **Navigation Area**. Click **Next** to adjust parameters.

Figure 13.2 shows the parameters that can be set for this distance-based tree creation:

- Tree construction (see section 13.1.1)
  - Tree construction method



1. Choose where to run
2. Select alignments of same type
3. Tree Construction

Tree Construction

Tree construction

Tree construction method: Neighbor Joining

Nucleotide distance measure: Jukes-Cantor

Protein distance measure: Jukes-Cantor

Bootstrapping

☑ Perform bootstrap analysis

Replicates: 100

Figure 13.2: *Adjusting parameters for distance-based methods.*

        - The **UPGMA** method. Assumes constant rate of evolution.
        - The **Neighbor Joining** method. Well suited for trees with varying rates of evolution.
    - Nucleotide distance measure
        - **Jukes-Cantor**. Assumes equal base frequencies and equal substitution rates.
        - **Kimura 80**. Assumes equal base frequencies but distinguishes between transitions and transversions.
    - Protein distance measure
        - **Jukes-Cantor**. Assumes equal amino acid frequency and equal substitution rates.
        - **Kimura protein**. Assumes equal amino acid frequency and equal substitution rates. Includes a small correction term in the distance formula that is intended to give better distance estimates than Jukes-Cantor.

- Bootstrapping.
    - Perform bootstrap analysis. To evaluate the reliability of the inferred trees, *CLC Sequence Viewer* allows the option of doing a **bootstrap** analysis (see section 13.1.1). A bootstrap value will be attached to each node, and this value is a measure of the confidence in the subtree rooted at the node. The number of replicates used in the bootstrap analysis can be adjusted in the wizard. The default value is 100 replicates which is usually enough to distinguish between reliable and unreliable nodes in the tree. The bootstrap value assigned to each inner node in the output tree is the percentage (0-100) of replicates which contained the same subtree as the one rooted at the inner node.

For a more detailed explanation, see "Bioinformatics explained" in section 13.1.1.

### 13.1.1 Bioinformatics explained

#### The phylogenetic tree

The evolutionary hypothesis of a phylogeny can be graphically represented by a phylogenetic tree.

Figure 13.3 shows a proposed phylogeny for the great apes, *Hominidae*, taken in part from Purvis [Purvis, 1995]. The tree consists of a number of nodes (also termed vertices) and branches (also termed edges). These nodes can represent either an individual, a species, or a higher grouping and are thus broadly termed taxonomical units. In this case, the terminal nodes (also called leaves or tips of the tree) represent extant species of *Hominidae* and are the *operational taxonomical units* (OTUs). The internal nodes, which here represent extinct common ancestors of the great apes, are termed *hypothetical taxonomical units* since they are not directly observable.

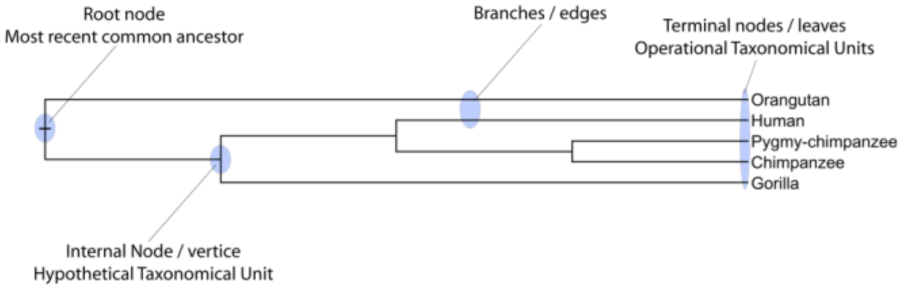


Figure 13.3: *A proposed phylogeny of the great apes (Hominidae). Different components of the tree are marked, see text for description.*

The ordering of the nodes determine the tree *topology* and describes how lineages have diverged over the course of evolution. The branches of the tree represent the amount of evolutionary divergence between two nodes in the tree and can be based on different measurements. A tree is completely specified by its topology and the set of all edge lengths.

The phylogenetic tree in figure 13.3 is rooted at the most recent common ancestor of all *Hominidae* species, and therefore represents a hypothesis of the direction of evolution e.g. that the common ancestor of gorilla, chimpanzee and man existed before the common ancestor of chimpanzee and man. In contrast, an unrooted tree would represent relationships without assumptions about ancestry.

#### Modern usage of phylogenies

Besides evolutionary biology and systematics the inference of phylogenies is central to other areas of research.

As more and more genetic diversity is being revealed through the completion of multiple genomes, an active area of research within bioinformatics is the development of comparative machine learning algorithms that can simultaneously process data from multiple species [Siepel and Haussler, 2004]. Through the comparative approach, valuable evolutionary information can be obtained about which amino acid substitutions are functionally tolerant to the organism and which are not. This information can be used to identify substitutions that affect protein function and stability, and is of major importance to the study of proteins [Knudsen and Miyamoto, 2001]. Knowledge of the underlying phylogeny is, however, paramount to comparative methods of inference as the phylogeny describes the underlying correlation from shared history that exists between data from different species.

In molecular epidemiology of infectious diseases, phylogenetic inference is also an important tool. The very fast substitution rate of microorganisms, especially the RNA viruses, means that these show substantial genetic divergence over the time-scale of months and years. Therefore, the phylogenetic relationship between the pathogens from individuals in an epidemic can be resolved and contribute valuable epidemiological information about transmission chains and epidemiologically significant events [Leitner and Albert, 1999], [Forsberg et al., 2001].

### Distance based reconstruction methods

Distance based phylogenetic reconstruction methods use a pairwise distance estimate between the input organisms to reconstruct trees. The distances are an estimate of the evolutionary distance between each pair of organisms which are usually computed from DNA or amino acid sequences. Given two homologous sequences a distance estimate can be computed by aligning the sequences and then counting the number of positions where the sequences differ. The number of differences is called the observed number of substitutions and is usually an underestimate of the real distance as multiple mutations could have occurred at any position.

To correct for these hidden substitutions a substitution model, such as Jukes-Cantor or Kimura 80, can be used to get a more precise distance estimate.

Alternatively, k-mer based methods or SNP based methods can be used to get a distance estimate without the use of substitution models.

After distance estimates have been computed, a phylogenetic tree can be reconstructed using a distance based reconstruction method. Most distance based methods perform a bottom up reconstruction using a greedy clustering algorithm. Initially, each input organism is put in its own cluster which corresponds to a leaf node in the resulting tree. Next, pairs of clusters are iteratively joined into higher level clusters, which correspond to connecting two nodes in the tree with a new parent node. When a single node remains, the tree is reconstructed.

The *CLC Sequence Viewer* provides two of the most widely used distance based reconstruction methods:

- The **UPGMA** method [Michener and Sokal, 1957] which assumes a constant rate of evolution (molecular clock hypothesis) in the different lineages. This method reconstruct trees by iteratively joining the two nearest clusters until there is only one cluster left. The result of the UPGMA method is a rooted bifurcating tree annotated with branch lengths.

- The **Neighbor Joining** method [Saitou and Nei, 1987] attempts to reconstruct a minimum evolution tree (a tree where the sum of all branch lengths is minimized). Opposite to the UPGMA method, the neighbor joining method is well suited for trees with varying rates of evolution in different lineages. A tree is reconstructed by iteratively joining clusters which are close to each other but at the same time far from all other clusters. The resulting tree is a bifurcating tree with branch lenghts. Since no particular biological hypothesis is made about the placement of the root in this method, the resulting tree is unrooted.

### Bootstrap tests

Bootstrap tests [Felsenstein, 1985] is one of the most common ways to evaluate the reliability of the topology of a phylogenetic tree. In a bootstrap test, trees are evaluated using Efron's re-sampling technique [Efron, 1982], which samples nucleotides from the original set of sequences as follows:

Given an alignment of $n$ sequences (rows) of length $l$ (columns), we randomly choose $l$ columns in the alignment with replacement and use them to create a new alignment. The new alignment has $n$ rows and $l$ columns just like the original alignment but it may contain duplicate columns and some columns in the original alignment may not be included in the new alignment. From this new alignment we reconstruct the corresponding tree and compare it to the original tree. For each subtree in the original tree we search for the same subtree in the new tree and add a score of one to the node at the root of the subtree if the subtree is present in the new tree. This procedure is repeated a number of times (usually around 100 times). The result is a counter for each interior node of the original tree, which indicate how likely it is to observe the exact same subtree when the input sequences are sampled. A bootstrap value is then computed for each interior node as the percentage of resampled trees that contained the same subtree as that rooted at the node.

Bootstrap values can be seen as a measure of how reliably we can reconstruct a tree, given the sequence data available. If all trees reconstructed from resampled sequence data have very different topologies, then most bootstrap values will be low, which is a strong indication that the topology of the original tree cannot be trusted.

### Scale bar

The scale bar unit depends on the distance measure used and the tree construction algorithm used. The trees produced using the Maximum Likelihood Phylogeny tool has a very specific interpretation: A distance of x means that the expected number of substitutions/changes per nucleotide (amino acid for protein sequences) is x. i.e. if the distance between two taxa is 0.01, you expected a change in each nucleotide independently with probability 1 %. For the remaining algorithms, there is not as nice an interpretation. The distance depends on the weight given to different mutations as specified by the distance measure.

## 13.2 Tree Settings

The Tree Settings Side Panel found in the left side of the view area can be used to adjust the tree layout . The following section describes the visualization options available from the Tree Settings side panel.

**The preferred tree layout settings** (user defined tree settings) can be saved and applied via the top right **Save Tree Settings** (figure 13.4). Settings can either be saved **For This Tree Only** or for all saved phylogenetic trees (**For Tree View in General**). The first option will save the layout of the tree for that tree only and it ensures that the layout is preserved even if it is exported and opened by a different user. The second option stores the layout globally in the Workbench and makes it available to other trees through the **Apply Saved Settings** option.

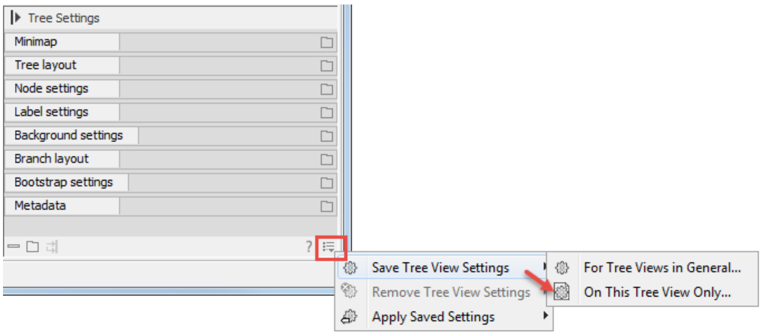


Figure 13.4: *Save, remove or apply preferred layout settings.*

### 13.2.1 Minimap

The Minimap is a navigation tool that shows a small version of the tree. A grey square indicates the specific part of the tree that is visible in the View Area (figure 13.5). To navigate the tree using the Minimap, click on the Minimap with the mouse and move the grey square around within the Minimap.

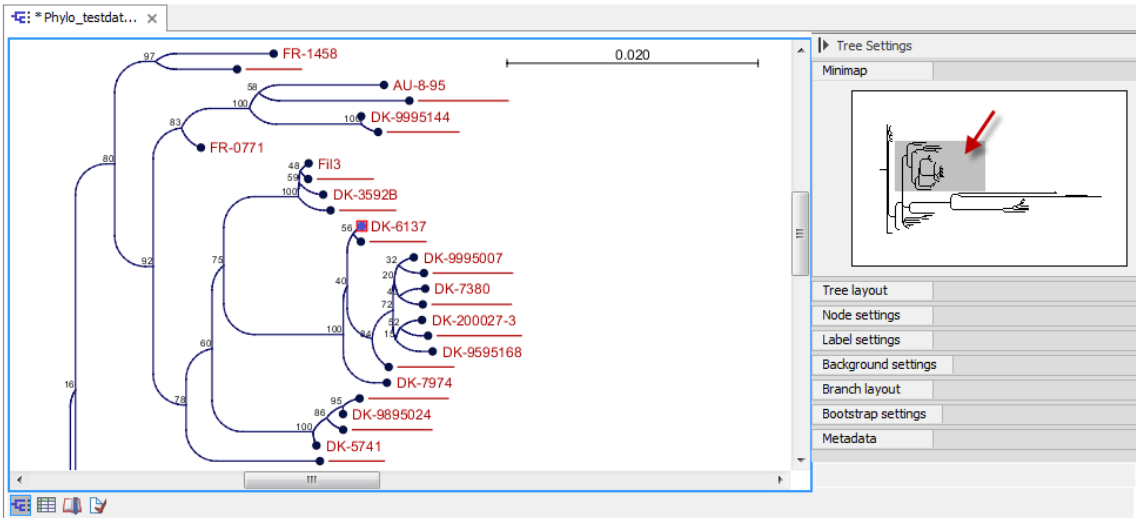


Figure 13.5: *Visualization of a phylogenetic tree. The grey square in the Minimap shows the part of the tree that is shown in the View Area.*

### 13.2.2 Tree layout

The **Tree Layout** can be adjusted in the Side Panel (figure 13.6).

- **Layout** Selects one of the five layout types: Phylogram, Cladogram, Circular Phylogram, Circular Cladogram or Radial. Note that only the Cladogram layouts are available if all branches in the tree have zero length.
  - **Phylogram** is a rooted tree where the edges have "lengths", usually proportional to the inferred amount of evolutionary change to have occurred along each branch.
  - **Cladogram** is a rooted tree without branch lengths which is useful for visualizing the topology of trees.
  - **Circular Phylogram** is also a phylogram but with the leaves in a circular layout.
  - **Circular Cladogram** is also a cladogram but with the leaves in a circular layout.
  - **Radial** is an unrooted tree that has the same topology and branch lengths as the rooted styles, but lacks any indication of evolutionary direction.
- **Ordering** The nodes can be ordered after the branch length; either **Increasing** (shown in figure 13.6) or **Decreasing**.
- **Reset Tree Topology** Resets to the default tree topology and node order (see figure 13.6).
- **Fixed width on zoom** Locks the horizontal size of the tree to the size of the main window. Zoom is therefore only performed on the vertical axis when this option is enabled.
- **Show as unrooted tree** The tree can be shown with or without a root.

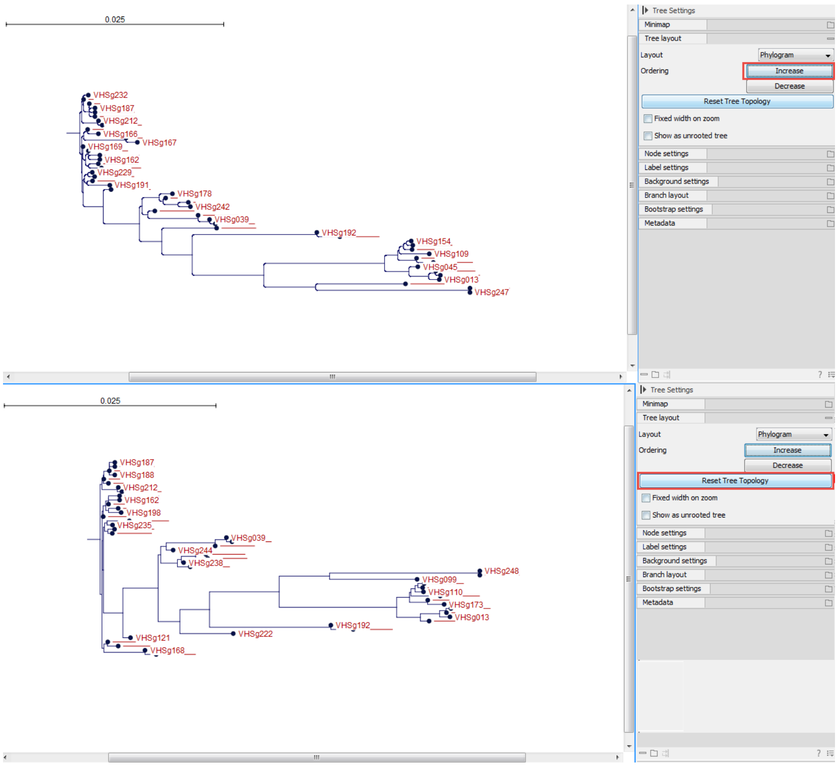


Figure 13.6: *The tree layout can be adjusted in the Side Panel. The top part of the figure shows a tree with increasing node order. In the bottom part of the figure the tree has been reverted to the original tree topology.*

### 13.2.3 Node settings

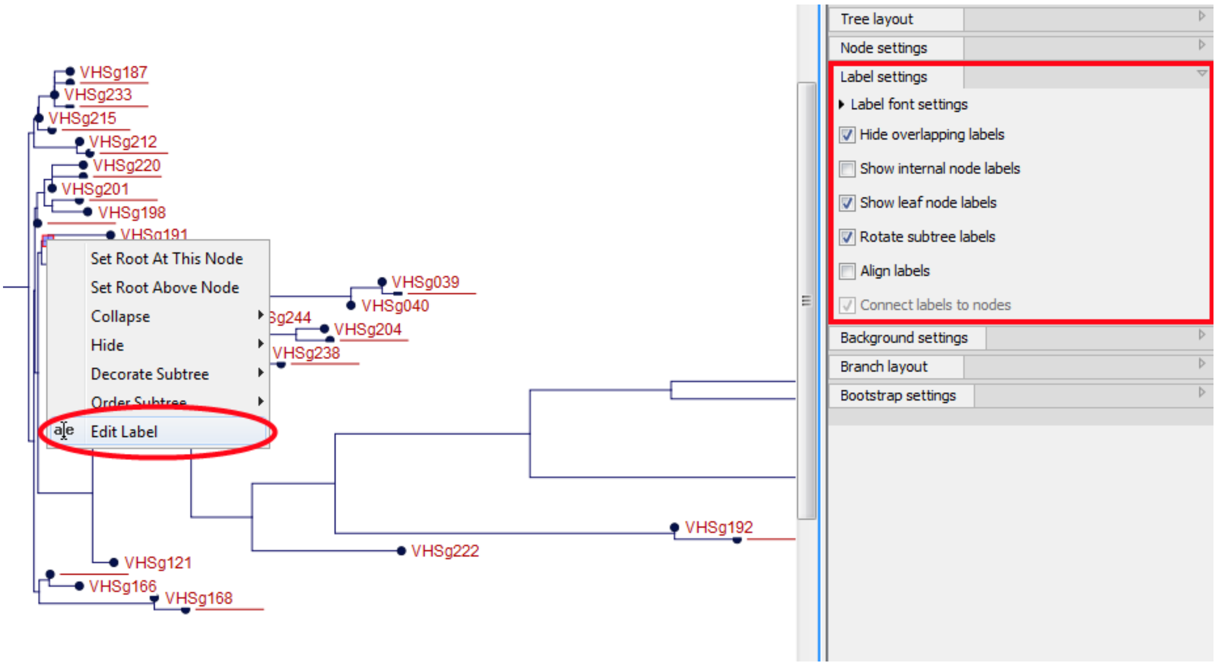
The nodes can be manipulated in several ways.

- **Leaf node symbol** Leaf nodes can be shown as a range of different symbols (Dot, Box, Circle, etc.).
- **Internal node symbols** The internal nodes can also be shown with a range of different symbols (Dot, Box, Circle, etc.).
- **Max. symbol size** The size of leaf- and internal node symbols can be adjusted.
- **Avoid overlapping symbols** The symbol size will be automatically limited to avoid overlaps between symbols in the current view.
- **Node color** Specify a fixed color for all nodes in the tree.

### 13.2.4 Label settings

- **Label font settings** Can be used to specify/adjust font type, size and typography (Bold, Italic or normal).
- **Hide overlapping labels** Disable automatic hiding of overlapping labels and display all labels even if they overlap.

- **Show internal node labels** Labels for internal nodes of the tree (if any) can be displayed. Please note that subtrees and nodes can be labeled with a custom text. This is done by right clicking the node and selecting **Edit Label** (see figure 13.7).
- **Show leaf node labels** Leaf node labels can be shown or hidden.
- **Rotate Subtree labels** Subtree labels can be shown horizontally or vertically. Labels are shown vertically when "Rotate subtree labels" has been selected. Subtree labels can be added with the right click option "Set Subtree Label" that is enabled from "Decorate subtree" (see section 13.2.8).
- **Align labels** Align labels to the node furthest from the center of the tree so that all labels are positioned next to each other. The exact behavior depends on the selected tree layout.
- **Connect labels to nodes** Adds a thin line from the leaf node to the aligned label. Only possible when Align labels option is selected.



☑ Hide overlapping labels
□ Show internal node labels
☑ Show leaf node labels
☑ Rotate subtree labels
□ Align labels
☑ Connect labels to nodes

Figure 13.7: *"Edit label" in the right click menu can be used to customize the label text. The way node labels are displayed can be controlled through the labels settings in the right side panel.*

When working with big trees there is typically not enough space to show all labels. As illustrated in figure 13.7, only some of the labels are shown. The hidden labels are illustrated with thin horizontal lines (figure 13.8).

There are different ways of showing more labels. One way is to reduce the font size of the labels, which can be done under **Label font settings** in the Side Panel. Another option is to zoom in on specific areas of the tree (figure 13.8 and figure 13.9). The last option is to disable **Hide overlapping labels** under "Label settings" in the right side panel. When this option is unchecked all labels are shown even if the text overlaps. When allowing overlapping labels it is usually a good idea to disable **Show label background** under "Background settings" (see section 13.2.5).

**Note!** When working with a tree with hidden labels, it is possible to make the hidden label text appear by moving the mouse over the node with the hidden label.

**Note!** The text within labels can be edited by editing the metadata table values directly.

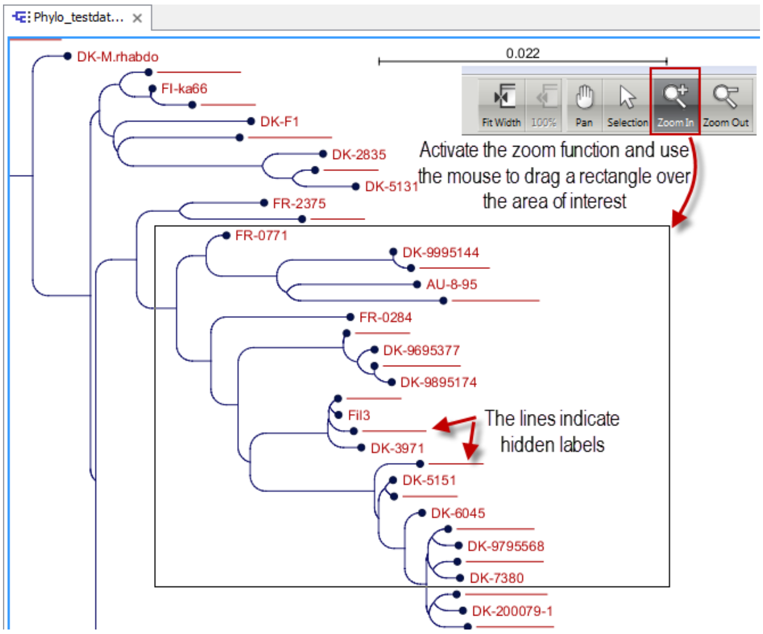


Figure 13.8: *The zoom function in the upper right corner of CLC Genomics Workbench can be used to zoom in on a particular region of the tree. When the zoom function has been activated, use the mouse to drag a rectangle over the area that you wish to zoom in at.*

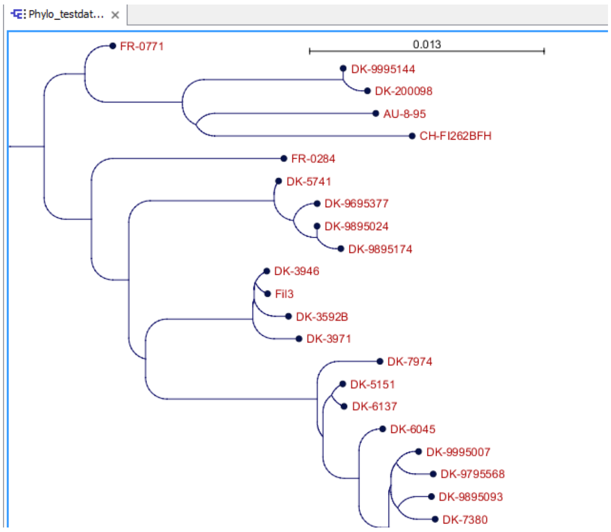


Figure 13.9: *After zooming in on a region of interest more labels become visible. In this example all labels are now visible.*

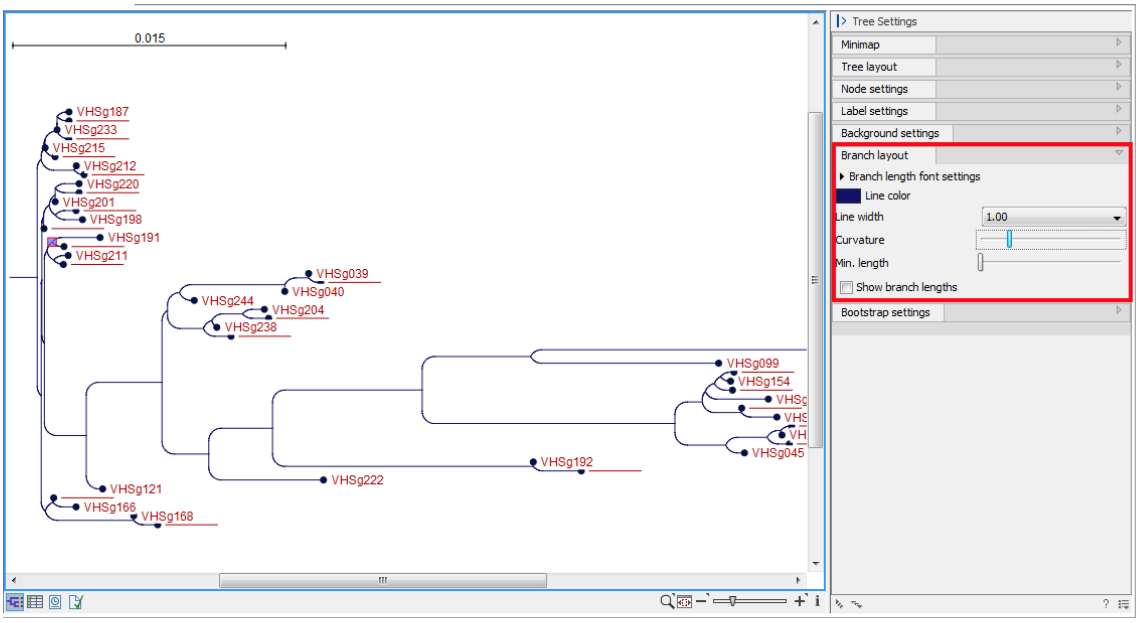
### 13.2.5 Background settings

- **Show label background** Show a background color for each label. Once ticked, it is possible to specify a background color.

### 13.2.6 Branch layout

- **Branch length font settings** Specify/adjust font type, size and typography (Bold, Italic or normal).
- **Line color** Select the default line color.
- **Line width** Select the width of branches (1.0-3.0 pixels).
- **Curvature** Adjust the degree of branch curvature to get branches with round corners.
- **Min. length** Select a minimum branch length. This option can be used to prevent nodes connected with a short branch to cluster at the parent node.
- **Show branch lengths** Show or hide the branch lengths.

The branch layout settings in the Side Panel are shown in figure 13.10.



Line width 1.00

Figure 13.10: *Branch Layout settings.*

### 13.2.7 Bootstrap settings

Bootstrap values can be shown on the internal nodes. The bootstrap values are shown in percent and can be interpreted as confidence levels where a bootstrap value close to 100 indicate a clade, which is strongly supported by the data from which the tree was reconstructed. Bootstrap values are useful for identifying clades in the tree where the topology (and branch lengths) should not be trusted.

Some branches in rooted trees may not have bootstrap values. Trees constructed with neighbour joining are unrooted and to correctly visualize them, the "Radial" view is required. In all other tree views we need a root to visualize the tree. An "artificial node" and therefore an extra branch are created for such visualization to achieve this, which makes it look like a bootstrap value is missing

- **Bootstrap value font settings** Specify/adjust font type, size and typography (Bold, Italic or normal).
- **Show bootstrap values (%)** Show or hide bootstrap values. When selected, the bootstrap values (in percent) will be displayed on internal nodes if these have been computed during the reconstruction of the tree.
- **Bootstrap threshold (%)** When specifying a bootstrap threshold, the branch lengths can be controlled manually by collapsing internal nodes with bootstrap values under a certain threshold.
- **Highlight bootstrap $\geq$ (%)** Highlights branches where the bootstrap value is above the user defined threshold.

### 13.2.8 Node right click menu

Additional options for layout and extraction of subtree data are available when right clicking the nodes (figure 13.7):

- **Set Root At This Node** Re-root the tree using the selected node as root. Please note that re-rooting will change the tree topology.
- **Set Root Above Node** Re-root the tree by inserting a node between the selected node and its parent. Useful for rooting trees using an outgroup.
- **Collapse** Branches associated with a selected node can be collapsed with or without the associated labels. Collapsed branches can be uncollapsed using the *Uncollapse* option in the same menu.
- **Hide** Can be used to hide a node or a subtree. Hidden nodes or subtrees can be shown again using the *Show Hidden Subtree* function on a node which is root in a subtree containing hidden nodes (see figure 13.11). When hiding nodes, a new button appears labeled "Show X hidden nodes" in the Side Panel under "Tree Layout" (figure 13.12). When pressing this button, all hidden nodes are shown again.
- **Decorate Subtree** A subtree can be labeled with a customized name, and the subtree lines and/or background can be colored. To save the decoration, see figure 13.4 and use option: **Save/Restore Settings** | **Save Tree View Settings On This Tree View only**.
- **Order Subtree** Rearrange leaves and branches in a subtree by Increasing/Decreasing depth, respectively. Alternatively, change the order of a node's children by left clicking and dragging one of the node's children.
- **Edit label** Edit the text in the selected node label. Labels can be shown or hidden by using the Side Panel: **Label settings | Show internal node labels**

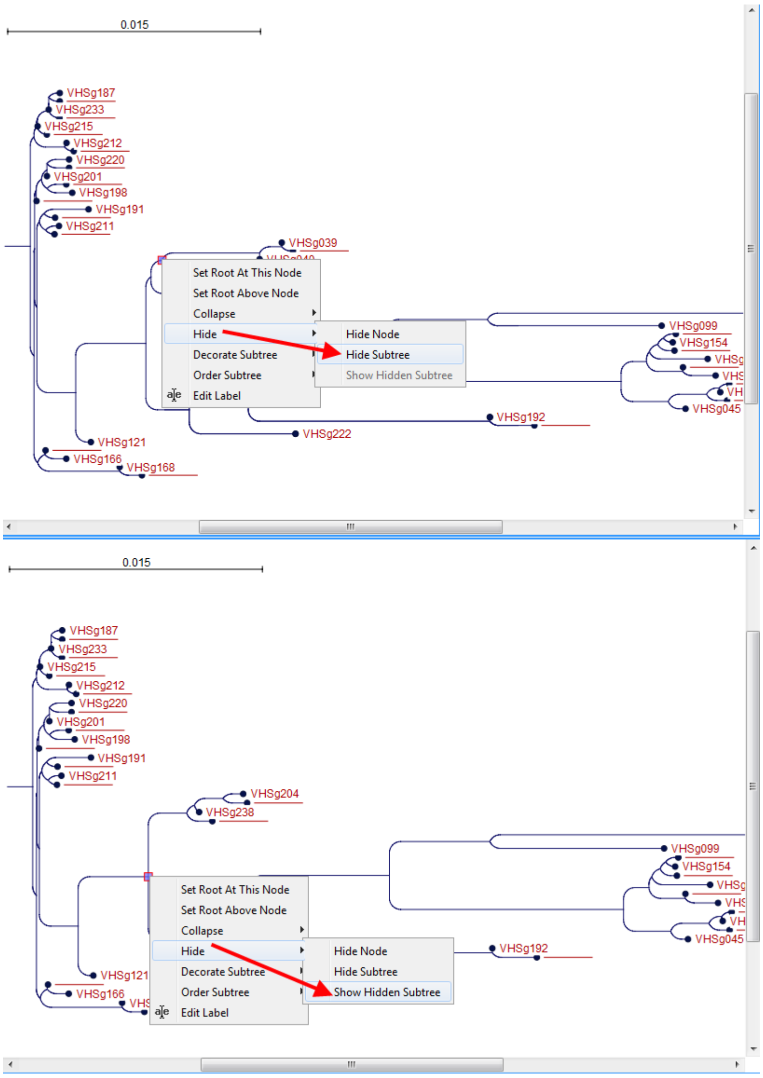
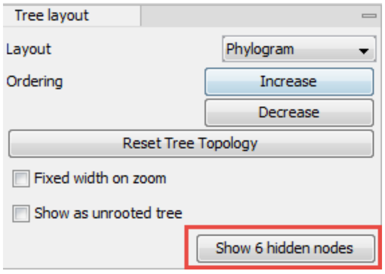


Figure 13.11: *A subtree can be hidden by selecting "Hide Subtree" and is shown again when selecting "Show Hidden Subtree" on a parent node.*



Layout Phylogram

Ordering

□ Fixed width on zoom

□ Show as unrooted tree

Figure 13.12: *When hiding nodes, a new button labeled "Show X hidden nodes" appears in the Side Panel under "Tree Layout". When pressing this button, all hidden nodes are brought back.*

# Part IV

# Appendix

## Appendix A

# More features

# Appendix B

# Graph preferences

This section explains the view settings of graphs. The **Graph preferences** at the top of the **Side Panel** includes the following settings:

- **Lock axes** This will always show the axes even though the plot is zoomed to a detailed level.
- **Frame** Shows a frame around the graph.
- **Show legends** Shows the data legends.
- **Tick type** Determine whether tick lines should be shown outside or inside the frame.
  - Outside
  - Inside
- **Tick lines at** Choosing Major ticks will show a grid behind the graph.
  - None
  - Major ticks
- **Horizontal axis range** Sets the range of the horizontal axis (x axis). Enter a value in **Min** and **Max**, and press Enter. This will update the view. If you wait a few seconds without pressing Enter, the view will also be updated.
- **Vertical axis range** Sets the range of the vertical axis (y axis). Enter a value in **Min** and **Max**, and press Enter. This will update the view. If you wait a few seconds without pressing Enter, the view will also be updated.
- **X-axis at zero**. This will draw the x axis at y = 0. Note that the axis range will not be changed.
- **Y-axis at zero**. This will draw the y axis at x = 0. Note that the axis range will not be changed.
- **Show as histogram**. For some data-series it is possible to see the graph as a histogram rather than a line plot.

The **Lines and plots** below contains the following settings:

- **Dot type**
  - None
  - Cross
  - Plus
  - Square
  - Diamond
  - Circle
  - Triangle
  - Reverse triangle
  - Dot
- **Dot color.** Allows you to choose between many different colors. Click the color box to select a color.
- **Line width**
  - Thin
  - Medium
  - Wide
- **Line type**
  - None
  - Line
  - Long dash
  - Short dash
- **Line color.** Allows you to choose between many different colors. Click the color box to select a color.

For graphs with multiple data series, you can select which curve the dot and line preferences should apply to. This setting is at the top of the **Side Panel** group.

Note that the graph title and the axes titles can be edited simply by clicking with the mouse. These changes will be saved when you **Save** () the graph - whereas the changes in the **Side Panel** need to be saved explicitly (see section 3.5).

# Appendix C

# Formats for import and export

## C.1 List of bioinformatic data formats

Below is a list of bioinformatic data formats, i.e. formats for importing and exporting molecule structures, sequences, alignments and trees.

### C.1.1 Sequence data formats

Note that the "Description" column refers to the file format, and not the viewing modes that are supported by the workbench. In particular, Sequence Viewer does not allow trace data to be shown.

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| AB1 | .ab1 | X | | Including chromatograms |
| ABI | .abi | X | | Including chromatograms |
| CLC | .clc | X | X | Rich format including all information |
| Clone manager | .cm5 | X | | Clone manager sequence format |
| DNAstrider | .str/.strider | X | X | |
| DS Gene | .bsml | X | | |
| EMBL | .emb/.embl | X | X | Rich information incl. annotations (nucs only) |
| FASTA | .fsa/.fasta | X | X | Simple format, name & description |
| GenBank | .gbk/.gb/.gp/.gbff | X | X | Rich information incl. annotations |
| Gene Construction Kit | .gck | X | | |
| Lasergene | .pro/.seq | X | | |
| Nexus | .nxs/.nexus | X | X | |
| Phred | .phd | X | | Including chromatograms |
| PIR (NBRF) | .pir | X | X | Simple format, name & description |
| Raw sequence | any | X | | Only sequence (no name) |
| SCF2 | .scf | X | | Including chromatograms |
| SCF3 | .scf | X | X | Including chromatograms |
| Sequence Comma separated values | .csv | X | X | Simple format. One seq per line: name, description(optional), sequence |
| Staden | .sdn | X | | |
| Swiss-Prot | .swp | X | X | Rich information incl. annotations (only peptides) |
| Tab delimited text | .txt | | X | Annotations in tab delimited text format |
| Vector NTI archives* | .ma4/.pa4/.oa4 | X | | Archives in rich format |
| Vector NTI Database* | | X | | Special import full database |

*Vector NTI import functionality comes as standard within the CLC Main Workbench and can be installed as a plugin via the Plugins Manager of the CLC Genomics Workbench (read more in section **??**).

### C.1.2 Alignment formats

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| Aligned fasta | .fa | X | X | Simple fasta-based format with – for gaps |
| CLC | .clc | X | X | Rich format including all information |
| ClustalW | .aln | X | X | |
| GCG Alignment | .msf | X | X | |
| Nexus | .nxs/.nexus | X | X | |
| Phylip Alignment | .phy | X | X | |

### C.1.3 Tree formats

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| CLC | .clc | X | X | Rich format including all information |
| Newick | .nwk | X | X | |
| Nexus | .nxs/.nexus | X | X | |

### C.1.4 Other formats

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| CLC | .clc | X | X | Rich format including all information |
| PDB | .pdb | X | | 3D structure |

### C.1.5 Table and text formats

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| Excel | .xls/.xlsx | X | X | All tables and reports |
| Table CSV | .csv | X | X | All tables |
| Tab delimited | .txt | | X | All tables |
| Text | .txt | X | X | All data in a textual format |
| CLC | .clc | X | X | Rich format including all information |
| HTML | .html | | X | All tables |
| PDF | .pdf | | X | Export reports in Portable Document Format |

### C.1.6 File compression formats

| File type | Suffix | Import | Export | Description |
|---|---|---|---|---|
| Zip export | .zip | | X | Selected files in CLC format |
| Zip import | .zip/.gz/.tar | X | | Contained files/folder structure |

**Note!** It is possible to import 'external' files into the Workbench and view these in the **Navigation Area**, but it is only the above mentioned formats whose *contents* can be shown in the Workbench.

## C.2 List of graphics data formats

Below is a list of formats for exporting graphics. All data displayed in a graphical format can be exported using these formats. Data represented in lists and tables can only be exported in .pdf format (see section 5.3 for further details).

| Format | Suffix | Type |
|---|---|---|
| Portable Network Graphics | .png | bitmap |
| JPEG | .jpg | bitmap |
| Tagged Image File | .tif | bitmap |
| PostScript | .ps | vector graphics |
| Encapsulated PostScript | .eps | vector graphics |
| Portable Document Format | .pdf | vector graphics |
| Scalable Vector Graphics | .svg | vector graphics |

# Appendix D

# Restriction enzymes database configuration

*CLC Sequence Viewer* uses enzymes from the **REBASE** restriction enzyme database at http://rebase.neb.com. If you wish to add enzymes to this list, you can do this by manually using the procedure described here.

**Note! Please be aware that this process needs to be handled carefully, otherwise you may have to re-install the Workbench to get it to work.**

First, download the following file: http://www.resources.qiagenbioinformatics.com/wbsettings/link_emboss_e_custom. In the Workbench installation folder under `settings`, create a folder named `rebase` and place the extracted `link_emboss_e_custom` file here.

Note that in macOS, the extension file "link_emboss_e_custom" will have a ".txt" extension in its filename and metadata that needs to be removed. Right click the file name, choose "Get info" and remove ".txt" from the "Name & extension" field.

Open the file in a text editor. The top of the file contains information about the format, and at the bottom there are two example enzymes that you should replace with your own.

Please note that the CLC Workbenches only support the addition of 2-cutter enzymes. Further details about how to format your entries accordingly are given within the file mentioned above.

After adding the above file, or making changes to it, you must restart the Workbench for changes take effect.

# Appendix E

# IUPAC codes for amino acids

(Single-letter codes based on International Union of Pure and Applied Chemistry)

The information is gathered from: http://www.insdc.org/documents/feature_table.html

| One-letter abbreviation | Three-letter abbreviation | Description |
|---|---|---|
| A | Ala | Alanine |
| R | Arg | Arginine |
| N | Asn | Asparagine |
| D | Asp | Aspartic acid |
| C | Cys | Cysteine |
| Q | Gln | Glutamine |
| E | Glu | Glutamic acid |
| G | Gly | Glycine |
| H | His | Histidine |
| J | Xle | Leucine or Isoleucineucine |
| L | Leu | Leucine |
| I | ILe | Isoleucine |
| K | Lys | Lysine |
| M | Met | Methionine |
| F | Phe | Phenylalanine |
| P | Pro | Proline |
| O | Pyl | Pyrrolysine |
| U | Sec | Selenocysteine |
| S | Ser | Serine |
| T | Thr | Threonine |
| W | Trp | Tryptophan |
| Y | Tyr | Tyrosine |
| V | Val | Valine |
| B | Asx | Aspartic acid or Asparagine Asparagine |
| Z | Glx | Glutamic acid or Glutamine Glutamine |
| X | Xaa | Any amino acid |

# Appendix F

# IUPAC codes for nucleotides

(Single-letter codes based on International Union of Pure and Applied Chemistry)

The information is gathered from: http://www.iupac.org and http://www.insdc.org/documents/feature_table.html.

| Code | Description |
|---|---|
| A | Adenine |
| C | Cytosine |
| G | Guanine |
| T | Thymine |
| U | Uracil |
| R | Purine (A or G) |
| Y | Pyrimidine (C, T, or U) |
| M | C or A |
| K | T, U, or G |
| W | T, U, or A |
| S | C or G |
| B | C, T, U, or G (not A) |
| D | A, T, U, or G (not C) |
| H | A, T, U, or C (not G) |
| V | A, C, or G (not T, not U) |
| N | Any base (A, C, G, T, or U) |

# Bibliography

[Andrade et al., 1998] Andrade, M. A., O'Donoghue, S. I., and Rost, B. (1998). Adaptation of protein surfaces to subcellular location. *J Mol Biol*, 276(2):517–525.

[Bachmair et al., 1986] Bachmair, A., Finley, D., and Varshavsky, A. (1986). In vivo half-life of a protein is a function of its amino-terminal residue. *Science*, 234(4773):179–186.

[Clote et al., 2005] Clote, P., Ferré, F., Kranakis, E., and Krizanc, D. (2005). Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency. *RNA*, 11(5):578–591.

[Efron, 1982] Efron, B. (1982). *The jackknife, the bootstrap and other resampling plans*, volume 38. SIAM.

[Felsenstein, 1985] Felsenstein, J. (1985). Confidence limits on phylogenies: An approach using the bootstrap. *Journal of Molecular Evolution*, 39:783–791.

[Feng and Doolittle, 1987] Feng, D. F. and Doolittle, R. F. (1987). Progressive sequence alignment as a prerequisite to correct phylogenetic trees. *J Mol Evol*, 25(4):351–360.

[Forsberg et al., 2001] Forsberg, R., Oleksiewicz, M. B., Petersen, A. M., Hein, J., Bøtner, A., and Storgaard, T. (2001). A molecular clock dates the common ancestor of European-type porcine reproductive and respiratory syndrome virus at more than 10 years before the emergence of disease. *Virology*, 289(2):174–179.

[Gill and von Hippel, 1989] Gill, S. C. and von Hippel, P. H. (1989). Calculation of protein extinction coefficients from amino acid sequence data. *Anal Biochem*, 182(2):319–326.

[Gonda et al., 1989] Gonda, D. K., Bachmair, A., Wünning, I., Tobias, J. W., Lane, W. S., and Varshavsky, A. (1989). Universality and structure of the N-end rule. *J Biol Chem*, 264(28):16700–16712.

[Ikai, 1980] Ikai, A. (1980). Thermostability and aliphatic index of globular proteins. *J Biochem (Tokyo)*, 88(6):1895–1898.

[Knudsen and Miyamoto, 2001] Knudsen, B. and Miyamoto, M. M. (2001). A likelihood ratio test for evolutionary rate shifts and functional divergence among proteins. *Proc Natl Acad Sci U S A*, 98(25):14512–14517.

[Leitner and Albert, 1999] Leitner, T. and Albert, J. (1999). The molecular clock of HIV-1 unveiled through analysis of a known transmission history. *Proc Natl Acad Sci U S A*, 96(19):10752–10757.

[Michener and Sokal, 1957] Michener, C. and Sokal, R. (1957). A quantitative approach to a problem in classification. *Evolution*, 11:130–162.

[Purvis, 1995] Purvis, A. (1995). A composite estimate of primate phylogeny. *Philos Trans R Soc Lond B Biol Sci*, 348(1326):405–421.

[Saitou and Nei, 1987] Saitou, N. and Nei, M. (1987). The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Mol Biol Evol*, 4(4):406–425.

[Siepel and Haussler, 2004] Siepel, A. and Haussler, D. (2004). Combining phylogenetic and hidden Markov models in biosequence analysis. *J Comput Biol*, 11(2-3):413–428.

[Tobias et al., 1991] Tobias, J. W., Shrader, T. E., Rocap, G., and Varshavsky, A. (1991). The N-end rule in bacteria. *Science*, 254(5036):1374–1377.

# Part V

# Index

# Index