Tutorial

Getting Started
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Getting Started

This tutorial will take you through the most basic steps of working with the CLC Workbenches.

The user interface of a Workbench looks like figure 1.

![Figure 1: The user interface as it looks when you start the program for the first time.](image)

The important features are the **Navigation Area**, the Toolbox and the **View Area**.

The **Navigation Area** is where you keep all your data for use in the program. When **CLC Genomics Workbench** is started there is one element in the Navigation Area called **CLC_Data**: this element is a **Location**. A location points to a folder on your computer where your data for use with the workbench is stored.

The data in the location can be organized into folders. Create a folder using the button of the Toolbar:

- **New | Folder**
- **Ctrl + Shift + N (⌘ + Shift + N on Mac)**

The Toolbox is where most analysis tools are listed. To start an analysis, you can double click on a tool name from the Toolbox, or use the Launch button in the Toolbar to search for the tool by name or key word. More functionalities are available from the Toolbar, such as Save, Import, Export, etc.

The **View Area** is the main area, where the data can be visualized. The View Area can include several Views represented by tabs. The View Area can also be "split" to display two views simultaneously.
View a DNA sequence

This section will take you through some different ways to display a sequence in the program. The tutorial introduces zooming on a sequence, dragging tabs, and opening selection in new view.

We will be working with the sequence called pcDNA3-atp8a1 located in the 'Cloning' folder in the Example data.

1. First, download the Example Data folder by clicking on "Import Example Data" in the Help menu.

2. Double-click on the pcDNA3-atp8a1 sequence in the Navigation Area to open it. The sequence is displayed with annotations above it (see figure 2).

   ![Figure 2: Sequence pcDNA3-atp8a1 opened in a view.](image)

   As default, CLC Genomics Workbench displays a sequence with annotations (colored arrows on the sequence like the green CMV promoter region annotation) and zoomed in to see the residues.

3. In this tutorial we want to have an overview of the whole sequence. There are different ways to zoom out: for example, right click on the magnifier (🔍) in the Toolbar and select the Zoom out mode (🔍) (figure 3). Click on the sequence until you can see the whole sequence.

   You can also directly use the Zoom to a selection icon (🔍) (figure 4). You can switch back to a view where you can see the residues by clicking on the Zoom to base level icon (🔍).

4. This sequence is circular, which is indicated by << and >> at the beginning and the end of the sequence. We can see a circular view of the sequence by clicking on Show as Circular (_circle_icon_) at the bottom of the view. You can see both linear and circular view at once by holding the Ctrl button on the keyboard (on Mac) while clicking on the Show as Circular button (figure 5).

5. You may want to change the text size in the top panel to see more of the sequence. Scroll down in the Sequence Settings panel to Text format and change text size to 7. To learn
6. Make a selection on the circular sequence. Because both views (linear and circular) are linked, the selection can be seen in the linear view above. The selection coordinates also appear at the bottom right corner of the screen. In figure 5, the **Ampicillin ORF** was selected.

You can zoom on the selected portion of the sequence by clicking on the Zoom to a selection button ( ), or you can open a third view of just the selected part of the sequence by right-clicking anywhere in the highlighted sequence text in the top panel and choosing **Open Selection in New View** as shown in figure 5.

7. You can rearrange the View Area by dragging tabs of the different Views between the top and bottom panels. You can also save the selection by dragging the tab to the "Example Data" folder in the Navigation Area.
Figure 5: Horizontally split View Area with linear and circular views of the sequence. Both views are linked and selecting a region in one view will select the same region in the other. A new view panel for just the selected sequence can be created by right-clicking the highlighted sequence and choosing Open Selection in New View.
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Running a Tool

In this section we will show you how to run a tool. As an example we will use the Create Alignment tool.

You can open a tool from the Toolbox by double clicking on its name or you can use the Launch button ( ) and type in the name of the tool - in this case the Create Alignment tool (figure 6).

A pop up window opens. Through a succession of windows you will enter the data you want to analyse, the parameters of the analysis you want to perform and how you want to handle the results of the analysis. You can navigate between windows by clicking the buttons Next and Previous at the bottom of the window. If you are not sure what to do, you can also click on the Help button and read the section of the manual relevant to the tool you are using. The Reset button will reset all parameters from the pop up window to their default values.

1. In the first window select the Protein orthologs folder in the Example data folder in the Navigation Area and choose the six sequences as shown in figure 7. The arrows can be used to add the sequences as well as remove the sequences from the Selected Elements list. Click on Next.

2. The parameters should be set to default as shown in figure 8. To set all parameters as default click the Reset button. An explanation of the parameters can be found by clicking the Help button. Click on Next.

3. Specify where you would like to save the results. For example you can create a new folder outside the Example data folder.

4. Once you click on Finish, the tool starts. It is usually fast, but for heavier processes you can check on the progress of the tool in the "Processes" area, accessible by clicking on the "Processes" tab below the Toolbox.

Figure 6: Launching a tool can be done from the toolbox or from the Launch dialog.
5. When done, the status of the workbench will be set to "Idle..." in the lower left corner of the workbench. If you had chosen to "Open" the results, the alignment would open automatically in the View Area and you would have to save it manually to the Navigation Area. In this case we chose to Save results, so to check your alignment, double click on the name of the result file in the Navigation Area. If you do not know the name of the file the tool just generated, or do not remember where you saved it, you can use the arrow next to the process that you want to view the results for (in this case the "Create Alignment" process as seen in figure 9) and choose the option "Show results" (the results will open in the View Area) or "Find results" (results will be highlighted in the Navigation Area).

6. Once the alignment is open, it should look like displayed in figure 10.
Figure 9: The results can be viewed by clicking on the recently finished process and clicking Show Results.

Figure 10: The resulting alignment.
**Side Panel Settings**

In this section we will show you how to use the Side Panel to change the way your sequences, alignments and other data are shown. You will also see how to save the changes that you made in the Side Panel.

The initial view of the alignment has colored the residues' background according to the Rasmol color scheme, and the alignment is automatically wrapped to fit the width of the view (figure 11).

![Figure 11: The protein alignment as it looks when you open it with background color according to the Rasmol color scheme and automatically wrapped.](image)

Now, we are going to modify how this alignment is displayed. For this, we use the settings in the Side Panel to the right. All the settings are organized into groups, which can be expanded / collapsed by clicking the name of the group.

1. The first group is **Sequence Layout** which is expanded by default. Select **No wrap** in the Sequence Layout. This means that each sequence in the alignment is kept on the same line. To see more of the alignment, you now have to scroll horizontally.

2. Next, expand the **Annotation Layout** group and select **Show Annotations**. Set the **Offset** to "More offset" and set the **Label** to "Stacked" (see figure 12).

![Figure 12: The Annotation Layout and the Annotation Types tabs in the Side Panel.](image)

3. Click on the **Annotation Types** tab. Here you will see a list of the types annotation that are carried by the sequences in the alignment. Check the "Region" annotation type, and you will see the regions as red annotations on the sequences.
4. Next, we will change the way the residues are colored. Click the **Alignment Info** group and under **Conservation**, check "Background color". This will use a gradient as background color for the residues. You can adjust the coloring by dragging the small arrows above the color box.

5. You can remove the Conservation graph and the Sequence logo by unchecking these in the Alignment info section.

Now the alignment should look similar to figure 13.

**Figure 13: The alignment when all the above settings have been changed.**

**Saving the settings in the Side Panel** At this point, if you just close the view, the changes made to the **Side Panel** will not be saved. This means that you would have to perform the changes again next time you open the alignment. To save the changes to the **Side Panel**, click the **Save view** button () at the bottom of the **Side Panel** (see figure 14).

**Figure 14: Saving the settings of the Side Panel either generally or this particular alignment only.**

In the Save alignment view settings, type in "preferred alignment settings", check the option "Save for alignment views" and click **Save**, then **Close**. This setting will be from now on available from the drop-down menu for Alignment Side Panels.
**Applying saved settings in the Side Panel**  Open the "ATP8a1 ortholog alignment" from the Example data folder in the Navigation Area. Then click on **Save View** in the Side Panel (figure 15).

![Figure 15: Saving the settings of the Side Panel either generally or this particular alignment only.](image)

Select the "preferred alignment settings" from the "Apply saved alignment view settings" field, and click Apply. If you wish all your alignments top open automatically with these settings, check the option "Use as standard view settings for alignment view" before clicking **Apply**.

**Removing alignment view settings**  When you click the **Save View** button and select **Remove Alignments View Settings**, you can choose to remove previously saved settings, or to export or import view settings (VSF files) to share it with other users.