

C C A T T 0 1 0 0 0
G A G G A 0 1 1 0 1
G A A T T 0 0 1 1 0
A C A A G 0 0 1 0 0
T A C C A 0 0 1 1 0
T T A C A 0 1 0 0 0
A C C T C 0 0 0 1 0
A A G G A 0 0 0 0 0
G A T G A 0 1 1 0 0
T A G A T 0 0 1 0 0
G A T G A 1 0 1 0 0
T G T A G 1 0 0 0 0
T A G T A 0 0 0 0 0
G A T A T 1 0 0 0 0
G A G T G 0 1 0 0 0
A G A T T 0 1 0 0 0
G A G T A 0 1 0 0 0
T G A T G 0 1 0 0 0
A T T A G 0 0 0 0 0
T A G A T 0 0 0 0 0
G A G A 0 0 0 0 0
G T A 0 0 0 0 0
G A T 0 0 0 0 0
T A G 0 0 0 0 0
A G A 0 0 0 0 0
G A 0 0 0 0 0
A 0 0 0 0 0
T 0 0 0 0 0

Tutorial

Tutorial: Side Panel Settings

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This brief tutorial 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**.

Open the protein alignment located under *Protein orthologs* in the **Example data**. The initial view of the alignment has colored the residues according to the Rasmol color scheme, and the alignment is automatically wrapped to fit the width of the view (shown in figure 1).

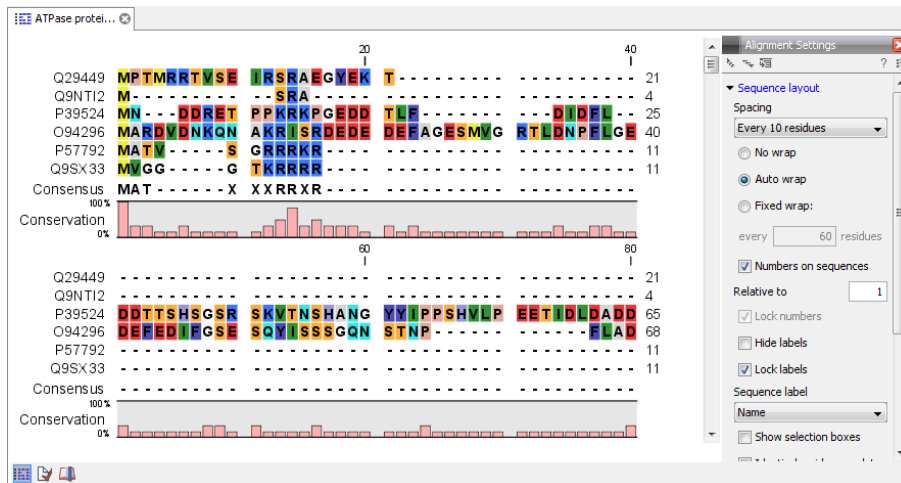


Figure 1: The protein alignment as it looks when you open it with background color according to the Rasmol color scheme and automatically wrapped.

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. The first group is **Sequence Layout** which is expanded by default.

First, 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.

Next, expand the **Annotation Layout** group and select **Show Annotations**. Set the **Offset** to "More offset" and set the **Label** to "Stacked".

Expand the **Annotation Types** group. Here you will see a list of the types annotation that are carried by the sequences in the alignment (see figure 2).

Check the "Region" annotation type, and you will see the regions as red annotations on the sequences.

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.

Saving the settings in the Side Panel

Now the alignment should look similar to figure 3.

At this point, if you just close the view, the changes made to the **Side Panel** will not be saved.

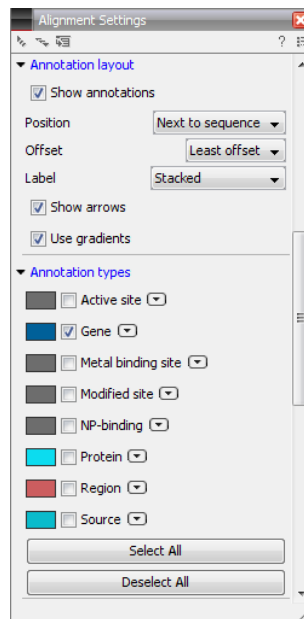


Figure 2: The Annotation Layout and the Annotation Types in the Side Panel.

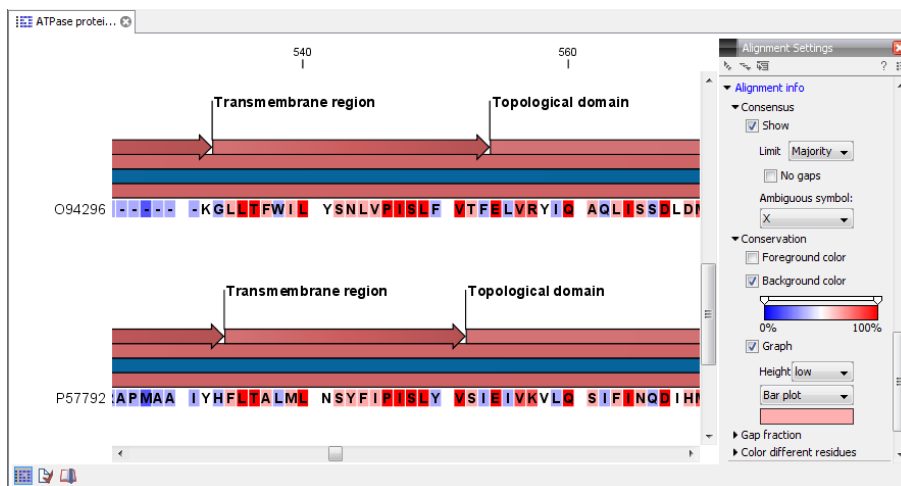


Figure 3: The alignment when all the above settings have been changed.

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/Restore Settings** button (☰) at the top of the **Side Panel** and click **Save Settings** (see figure 4).

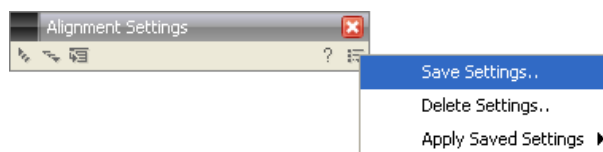


Figure 4: Saving the settings of the Side Panel.

This will open the dialog shown in figure 5.

In this way you can save the current state of the settings in the **Side Panel** so that you can apply them to alignments later on. If you check **Always apply these settings**, these settings will be applied every time you open a view of the alignment.

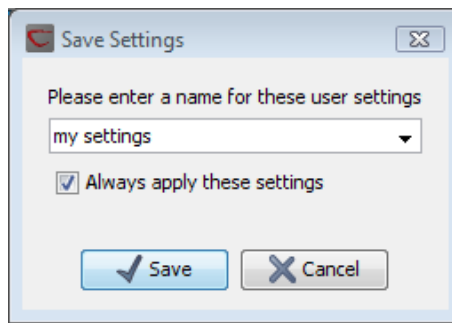


Figure 5: Dialog for saving the settings of the Side Panel.

Type "My settings" in the dialog and click **Save**.

Applying saved settings

When you click the **Save/Restore Settings** button (☰) again and select **Apply Saved Settings**, you will see "My settings" in the menu together with some pre-defined settings that the *CLC Sequence Viewer* has created for you (see figure 6).

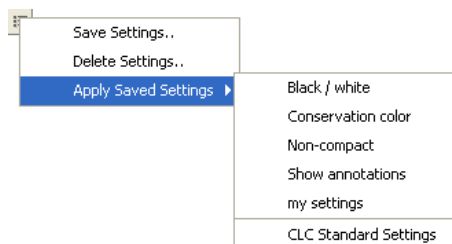


Figure 6: Menu for applying saved settings.

Whenever you open an alignment, you will be able to apply these settings. Each kind of view has its own list of settings that can be applied.

At the bottom of the list you will see the "CLC Standard Settings" which are the default settings for the view.