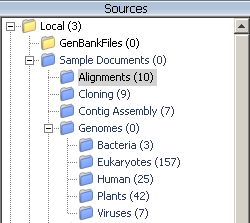
***Sequence view/alignment view switching***

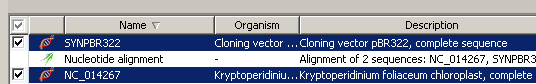
**Geneious**

Geneious has a window “Sources”, divided into different categories:

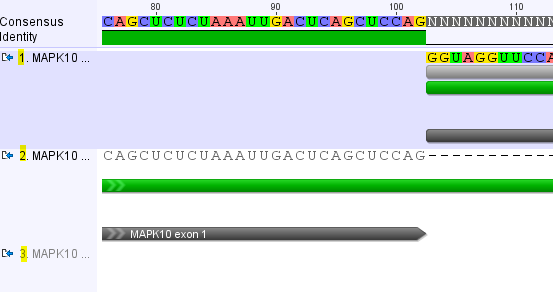


In this window you can choose any of imported sequences. Using context-menu you can perform operation “Pairwise Align” (Alternative: Tools => Align/Assemble). This operation will be available if exactly two sequences are selected and bound on Ctrl+Shift+A. If more than two sequences are selected then operation calls “Multiple Align” (in context menu).

Result alignment saves in category where used sequences are placed.

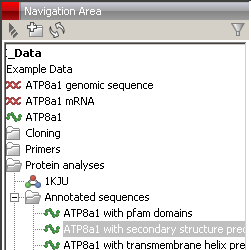


Links to jump to used sequences are available at the beginning of alignment view:

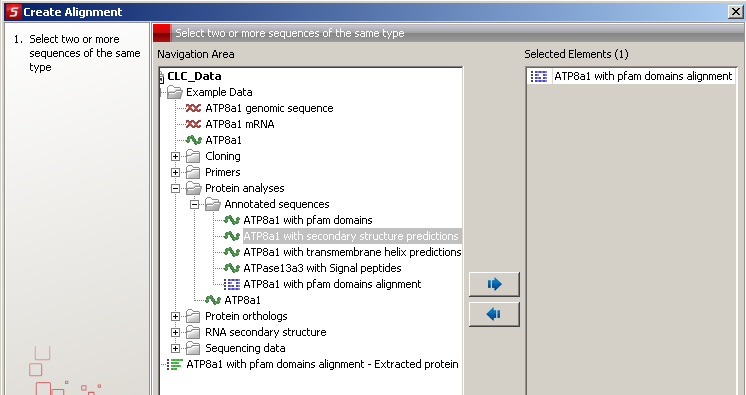


**CLC Sequence Viewer**

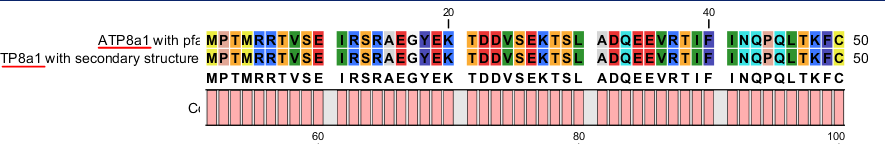
CLC Sequence Viewer has panel “Navigation Area” also divided into different categories:



This window allows importing sequences. Context menu uses to create alignment (also this operation is bound on Ctrl+Shift+A). New window “Create alignment” will be created even if there are no selected sequences:

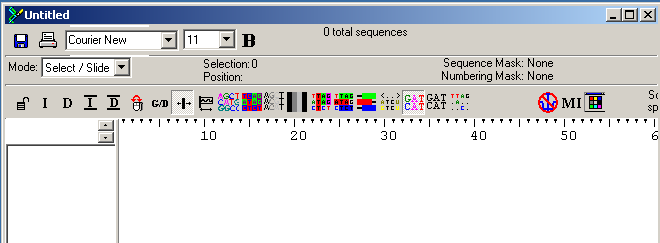
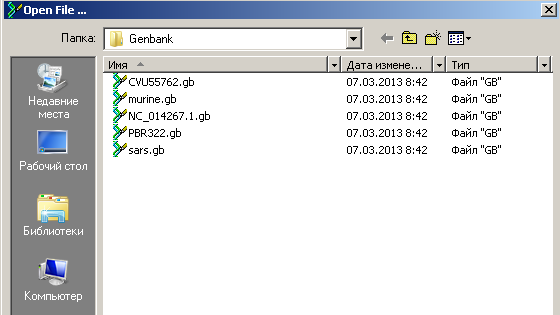


The window “Create alignment” divided into two parts: all loaded data and area for sequences that will be used in alignment. To jump to any of sequences need to select its caption in alignment view and then use context menu.

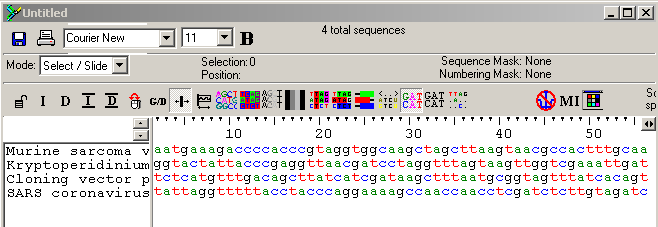


**BioEdit Sequence Alignment Editor**

In this software you can use the following steps to create alignment:

* Choose File/New-alignment menu or just press Ctrl+N to create empty alignment project:
* Use already loaded or import necessary sequences using File/Import/Sequence alignment to get alignment: 

Result is shown in alignment view:



To jump to any sequence need to select it from the list on the left side of alignment.

**Conclusion:**

The presented programs clearly show two main ways of how to create alignment from sequences:

1. Automatic “switching-on” of “alignment operation” button if there are two or more sequences are selected
2. Creating new window specially for this operation where user can choose what sequences need to use in alignment.

First case is more convenient in terms of usability because disappears a necessity of choosing operation “alignment” from context-menu. Need to bind “Create alignment” operation on hotkey to improve access speed (for example, if user worries only about alignment parameters or just changes it very often).

Also jump to any of sequences used in alignment is good way to make fast switching between sequence and alignment views.

Need to store alignment file near with used sequences if that’s possible.