

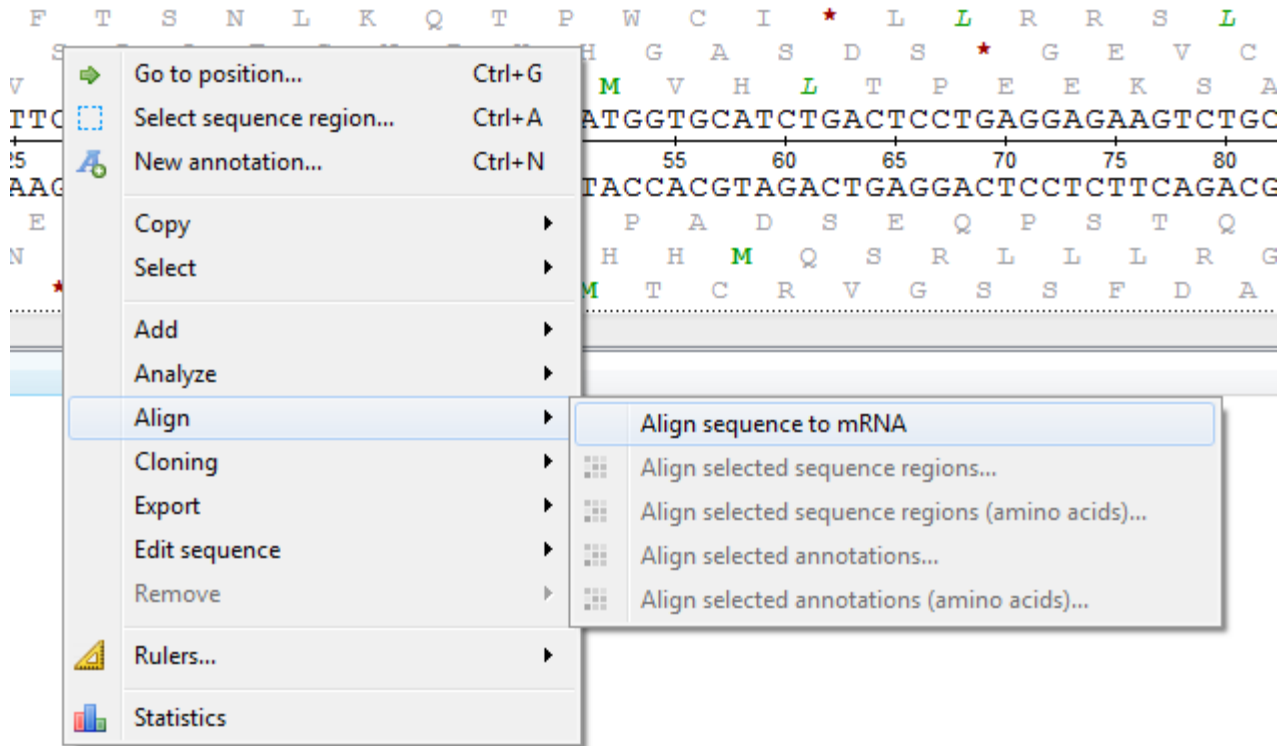
Spliced Alignment (mRNA to genomic)

UGENE allows to align spliced mRNA/cDNA sequence to genomic sequences.

The default underlying algorithm which is used for the alignment is an external tool called [Spidey](#).

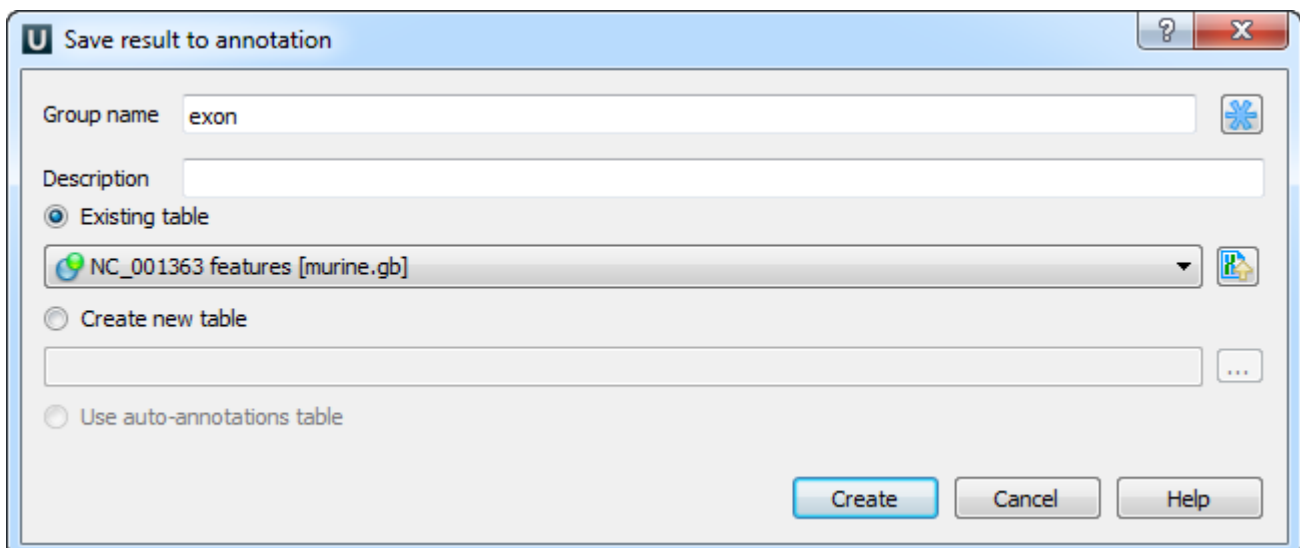
Before running the alignment make sure that Spidey is available and validated in the list of [External Tools](#).

To perform the alignment of a mRNA sequence to a genomic sequence open the the genomic sequence in the *Sequence View*. Next activate context menu item *Align -> Align to sequence to mRNA*.



In the list of sequences select the corresponding mRNA sequence and click OK.

The following dialog will appear:



Here you can set up a file to store annotations. It could be either an existing annotation table object or a new annotation table or auto-annotations table (if it is possible). Also you can modify the group name parameter and add a description.

The resulting alignment will be saved as an annotation with the corresponding name:

The screenshot displays the UGENE software interface. At the top, the title bar reads '* UGENE - [dna [s] dna]'. Below it is a menu bar with 'File', 'Actions', 'Settings', 'Tools', 'Window', and 'Help'. A toolbar contains various icons for file operations and analysis. The main workspace shows a DNA sequence alignment. The top part of the workspace has a scale from 1 to 1608 bp. Three regions are highlighted with pink boxes and labeled 'exon'. Below the scale, the DNA sequence is shown in multiple lines, with some letters highlighted in green. A specific region of the sequence is highlighted in pink, corresponding to one of the exons. At the bottom of the workspace, there is a project panel with a table of annotations:

Name	Value
Annotations [MyDocument.gb] *	
exon (0, 1)	
exon	join(1..142,273..495,1346..1608)
Auto-annotations [dna.txt dna]	

At the bottom of the interface, there are buttons for '2: Tasks' and '3: Log', and a status bar on the right that says 'No active tasks'.