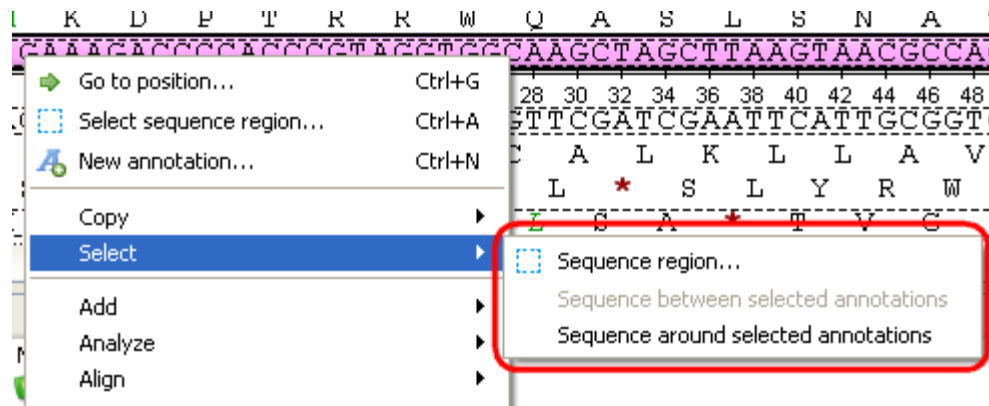
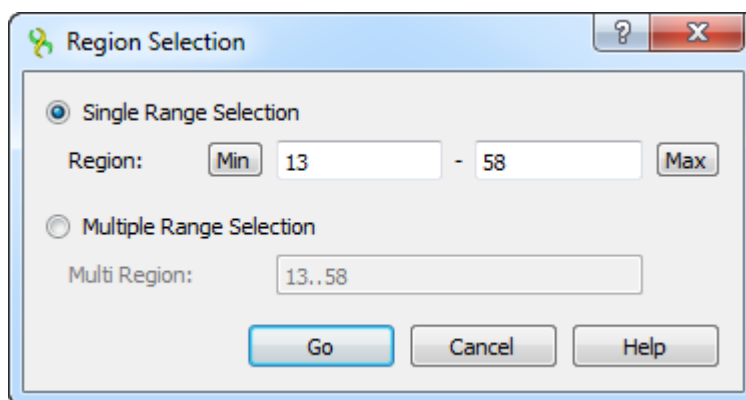


Selecting Sequence

You can use different items from the *Select* submenu of the context menu to select a sequence.



Selecting the *Sequence region* context menu item opens the *Select range* dialog:



Here you can specify the sequence range you would like to select.

You can open the same dialog using the *Select sequence region* button on a sequence toolbar or using the Ctrl-A key sequence.

To use the *Sequence between selected annotations* item, select two annotations in the *Annotations editor* (holding the Ctrl key at the same time):

The screenshot displays a bioinformatics software interface. At the top, a sequence alignment is shown with amino acid residues (N, E, R, P, H, P, V, A, S, L, K, R, H, F, A) and their corresponding DNA codons (M, K, D, P, T, R, R, W, Q, A, S, L, S, N, A, T, L, Q). Below the alignment, a table with 'Name' and 'Value' columns is visible. The 'Name' column lists features: NC_001363 features [murine_copy2.gb], CDS (0, 4), misc_feature (0, 2), and source (0, ...). The 'Value' column shows the corresponding genomic coordinates. A context menu is open over the 'misc_feature (0, 2)' entry, displaying options such as 'Go to position...', 'Select sequence region...', 'New annotation...', 'Copy', 'Select', 'Add', 'Analyze', 'Align', 'Export', 'Edit sequence', 'Remove', 'Rulers...', and 'Annotations highlighting...'. The 'Select' option is highlighted, and a sub-menu is open, showing 'Sequence region...', 'Sequence between selected annotations', and 'Sequence around selected annotations'.

And select the *Select Sequence between selected annotations* item in the context menu.

The *Sequence around selected annotations* item selects the selected annotations and the sequences between these annotations.

