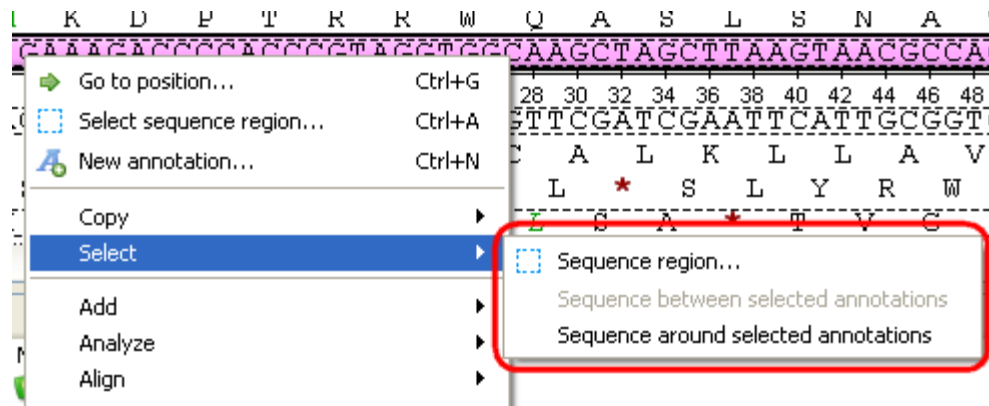
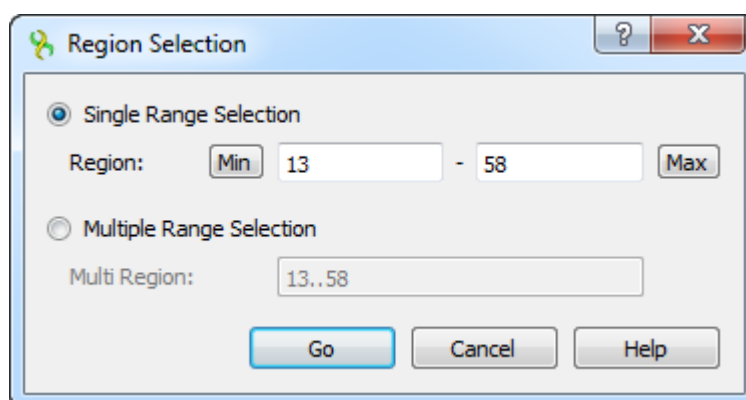


Selecting Sequence

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 two rows. The top row contains amino acid single-letter codes: N, E, R, P, H, P, *, V, A, S, *, L, K, *, R, H, F, A. The bottom row contains amino acid single-letter codes: M, K, D, P, T, R, R, W, Q, A, S, L, S, N, A, T, L, Q. Below the alignment, a DNA sequence is highlighted in pink: AATGAAAGACCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA. Below the DNA sequence, a ruler shows positions from 12 to 54. Below the ruler, a table with columns 'Name' and 'Value' is visible. The table contains the following entries:

Name	Value
NC_001363 features [murine_copy2.gb]	
CDS (0, 4)	
misc_feature (0, 2)	
misc_feature	2, 500
note	Go to position... Ctrl+G
misc_feature	Select sequence region... Ctrl+A
note	New annotation... Ctrl+N
source (0, 2)	

A context menu is open over the 'misc_feature' entry. The menu items are:

- Go to position... Ctrl+G
- Select sequence region... Ctrl+A
- New annotation... Ctrl+N
- Copy
- Select
- Add
- Analyze
- Align
- Export
- Edit sequence
- Remove
- Rulers...
- Annotations highlighting...

The 'Select' item is highlighted, and a sub-menu is open showing the following options:

- Sequence region...
- Sequence between selected annotations
- 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.

NC_001363 sequence

1 500 1k 1.5k 2k 2.5k 3k 3.5k 4k 4.5k 5k 5833

CDS (4)

NP_040335.1 NP_59774 NP_59774 NP_040336.1 NP

5' terminal rep (5) 5' terminal rep

1712 1717 Sequence around selected annotations

G G N G Q L Q Y W P F S S S D L Y N W K N

E E T D S F N T G R S P L T F T T G K I

R K R T A S I L A V L L F * P L Q L E K

GAGGAAACGGACAGCTTCAATACTGGCCGTTCTCCTCTCTGACCTTTACAACCTGGAAAAAT

1700 1705 1710 1715 1720 1725 1730 1735 1740 1745 1750 1755 1761

CTCCTTTGCCTGTTCGAAGTTATGACCGGCAAGAGGAGAAGACTGGAAATGTTGACCTTTT

L F R V A E I S A T R R K Q G K C S S F Y

S S V S L K L V F R R V V V P F I

P F P C S * L Q F F

Sequence between selected annotations

Name	Value
Annotations [MyDocument_11.gb] *	
misc_feature (0, 3)	
misc_feature	1712..1720
misc_feature	1728..1737
misc_feature	1743..1752
NC_001363 features [murine.nh]	

Another way to select a sequence around annotations is to hold Shift and Ctrl keys while clicking on the annotations either in the *Sequence details* view or in the *Sequence zoom* view.