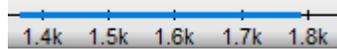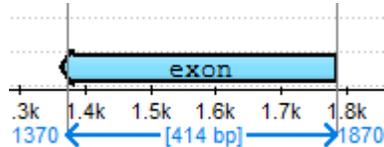# Selecting Sequence Region

Selection in the Sequence View components

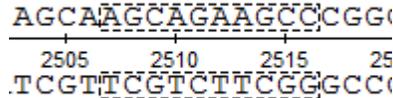Selection of a sequence region is synchronized between different *Sequence View* components.

In the *Sequence Overview* the selection is displayed as a blue line:

In the *Zoom View* a blue line with coordinates and the length of the selected region is shown:

In the *Details View* a rectangle with a dashed border is shown around the selected region:
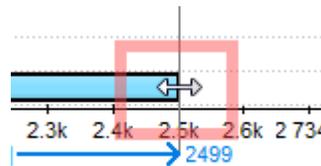

Finally, when one selects an annotation in the *Annotations Editor*, the corresponding region is also selected in the other components and visa versa.
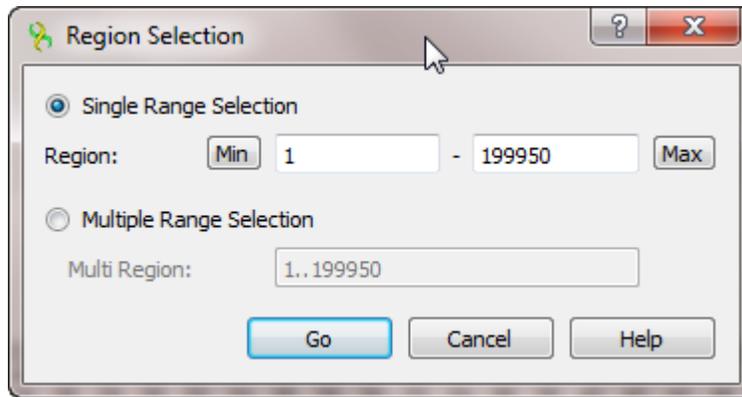
Selecting a region using the mouse

It is possible to select a region of a sequence using the mouse in each component of the *Sequence View*.

In the *Zoom View* and the *Details View* the selection can be adjusted by dragging its left or right border:

Selecting a region using the dialog

If information about exact coordinates of a region is available, click the *Select sequence region* button on the toolbar or *Select–>Sequence region* in the context menu of the *Sequence View*. Input the coordinates in the *Region Selection* dialog:
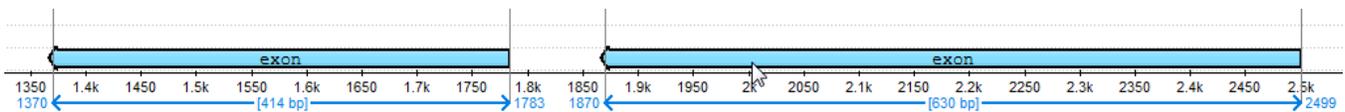
It is possible to input:

- *Single Range Selection* — a common region with a single range. Use the *Min* and *Max* buttons to automatically specify the beginning and the end of the sequence in the corresponding fields.
- *Multiple Range Selection* — a region that consists of several join elements, for example, exons of a gene. See "The DDBJ/ENA/GenBank Feature Table Definition" for details.

Selecting a region around or between annotations

To select a region between two annotations, for example, an intron region between two exons:

- Click on the annotations, holding the *Ctrl*/*Cmd* key:

- Click Select–>*Sequence between selected annotations* in the context menu of the *Sequence View*.

To select a region that contains the annotations in a single range, choose the *Sequence around selected annotations* item in the menu.