

Highlighting Annotations

To configure settings of annotation names go to the *Annotation Highlighting* tab in the *Options Panel*.

By default the tab shows annotations names of the opened *Sequence View*.

The screenshot displays a sequence viewer for NC_00136. The top part shows a genomic map with a scale from 1 to 5,833 bp. A specific region is highlighted with a blue bar, spanning from 3,875 bp to 4,999 bp (1,125 bp). Below this, the DNA sequence is shown with various annotations. A green box highlights a CDS (Coding Sequence) region, and a yellow box highlights a misc_feature region. The amino acid sequence is shown below the DNA sequence, with some residues highlighted in green and yellow.

The right side of the interface shows the **Annotations Highlighting** configuration panel. It includes a table for selecting annotation names and their colors, and a section for configuring the annotations.

Annotation	Color
BadI	Light Green
BaeGI	Orange
BaeI	Purple
CDS	Green
SacII	Cyan
comment	Pink
misc_feature	Yellow
source	Grey

Configure the annotations:

- Show annotations
- Show on translation
- Show value of qualifier:

label,note

Navigation buttons: Previous (left arrow), Next (right arrow), and Help.

If you want to see all annotation names, click the *Show all annotation names* link. The *Previous annotation* and *Next annotation* buttons seek to the previous or to the next annotation of the view correspondingly.

Find below information about annotations names' properties that you can configure.

- Annotations Color
- Annotations Visibility
- Show on Translation
- Captions on Annotations