

# 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 track shows a scale from 1 to 5,833. Below the scale, a sequence of nucleotides is shown with various annotations. A specific region is highlighted with a blue arrow indicating a 1125 bp segment from position 3875 to 4999. The sequence viewer shows multiple lines of nucleotides with annotations like '5' terminus', '3' terminus', and 'misc\_feature (2)'. Below the sequence, a list of annotations is shown with their names and types. The 'Annotations Highlighting' panel on the right allows users to select an annotation name and configure its color. The panel includes a table with columns 'Annotation' and 'Color'. The 'Configure the annotations' section has checkboxes for 'Show annotations', 'Show on translation', and 'Show value of qualifier', along with a text input field for 'label,note'. Navigation buttons for 'Previous annotation' and 'Next annotation' are also present.

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

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 Visability](#)
- [Show on Translation](#)
- [Captions on Annotations](#)