

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 shows the BioEdit software interface. On the left is the Sequence View displaying the nucleotide sequence NC_00136. A CDS feature is highlighted in green, spanning from position 3875 to 4999. The sequence is shown in three lines, with positions 3856 to 3894 indicated below. On the right is the Annotations Highlighting panel. It includes a list of annotations with their corresponding colors: BadI (light green), BaeGI (orange), BaeI (purple), CDS (dark green), SacII (cyan), comment (pink), misc_feature (brown), and source (grey). Below this is a table for configuring annotations:

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

Below the table are checkboxes for "Show annotations" (checked), "Show on translation" (unchecked), and "Show value of qualifier:" (checked), with a text input field containing "label,note". At the bottom are "Help" and navigation buttons.

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