

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 scale from 1 to 5,833 bp. Below the scale, a sequence is shown with various annotations. A specific CDS annotation is highlighted in green, spanning from position 3875 to 4999 (1125 bp). The amino acid sequence for this CDS is shown below the nucleotide sequence: D H P L D * M A H S T P C. The configuration panel on the right, titled "Annotations Highlighting", allows users to select an annotation name and configure its display. The "Select an annotation name:" section lists various annotations with their corresponding colors: BadI (light green), BaeGI (orange), BaeI (purple), CDS (green), SacII (cyan), comment (pink), misc_feature (tan), and source (grey). The "Configure the annotations:" section includes checkboxes for "Show annotations" (checked), "Show on translation" (unchecked), and "Show value of qualifier:" (checked). A text input field contains "label,note". Navigation buttons for "Previous annotation" and "Next annotation" are located at the bottom of the panel, along with a "Help" button.

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

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