

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 this, a sequence of nucleotides is shown with various annotations. A specific region is highlighted with a blue arrow indicating a 1,125 bp segment from position 3,875 to 4,999. The sequence viewer shows multiple lines of nucleotide data with corresponding annotations like 'CDS', 'misc_feature', and 'source'.

The **Annotations Highlighting** panel on the right allows users to select an annotation name and configure its display. The panel includes a table of annotation names and their corresponding 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

[Show all annotation names](#)

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