

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 1125 bp segment from position 3875 to 4999. 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, a list of annotation names to show, and configuration options for displaying annotations and their values.

Annotation	Color
BadI	Light Green
BaeGI	Orange
BaeI	Purple
CDS	Green
SacII	Light Blue
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](#)