

# 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 sequence is shown with various annotations highlighted in green. A specific region from 3,875 to 4,999 (1,125 bp) is highlighted. The sequence is shown in both DNA and protein format. The protein sequence is: D H P L D \* H G A F N A M T I L \* T D M A H S T P C G P S S R L T W R I Q R H G A C C A T C C T C T A G A C T G A C A T G G C G C A T T C A A C G C C A T G C T G G T A G G A G A T C T G A C T G T A C C G C G T A A G T T G C G G T A C G D E L S V H R M \* R W A V M R \* V S M A C E V G H S W G R S Q C P A N L A M.

The **Annotations Highlighting** panel on the right allows configuration of annotation names. It includes a table of annotation names and their colors, and a section to configure 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](#)