

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 from 3,875 to 4,999 (1,125 bp) is highlighted. The 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 GACCATCCTCTAGACTGACATGGCGCATTCAACGCCATGCTGGTAGGAGATCTGACTGTACCGCGTAAGTTGCGGTACG 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 for selecting annotation names and their 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](#)