

# Captions on Annotations

It is possible to show a value of a qualifier of an annotation instead of the annotation type name in the Sequence Zoom View. To enable this option for an annotation type check the *Show value of qualifier* check box and input the values of the required qualifiers in the text field nearby this check box. See the image below.

The screenshot shows the Biopython Sequence View interface. On the left, a sequence of DNA (NC\_00136) is displayed with various annotations. A red box highlights the "Show value of qualifier" button in the toolbar at the top. On the right, the "Annotations Highlighting" panel is open, showing configuration for different annotation types (CDS, misc\_feature, source) with their corresponding colors. Below this, the "Configure the annotation type" section includes a checked checkbox for "Show value of qualifier:" and a text input field containing "note". Another red box highlights this configuration area. At the bottom left, a tree view shows the structure of the annotations, with a red box highlighting the "note" value for a misc\_feature entry.

Name	Value
▶ CDS	join(2970..3413,3412..3873)
▶ CDS	3875..4999
▶ CDS	5048..5203
▶ misc_feature (0, 2)	
▶ misc_feature	2.590
note	Show value of qualifier
▶ misc_feature	5245..5833
note	Show value of qualifier
▶ source (0, 1)	
▶ source	1.5833

If you input several qualifiers names (separated by comma), then the first found qualifier is taken into account and shown on the annotation.