

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 displays the NC_001363 [d] sequence viewer. The main window shows a genomic track with a scale from 1 to 5k. A specific region is highlighted with a blue arrow and labeled "[589 bp]". Below the scale, the DNA sequence is shown in a multi-line format, with some letters highlighted in green. A red arrow points to the "Show value of qualifier" text in the sequence view.

At the bottom, a table lists the features for NC_001363:

Name	Type	Value
NC_001363 features [m...]		
source (0, 1)		
misc_feature (0, 2)		
misc_feature	Misc. Feature	5245..5833
note		Show value of qualifier
misc_feature	Misc. Feature	2..590
comment (0, 1)		
CDS (0, 4)		
CDS	CDS	5048..5203
CDS	CDS	3875..4999

On the right side, the "Annotations Highlighting" panel is visible. It includes a "Select an annotation name:" dropdown, a table of annotation types with their corresponding colors, and a "Configure the annotations:" section with checkboxes for "Show annotations", "Show on translation", and "Show value of qualifier". A red arrow points to the "Show value of qualifier" checkbox, which is checked. Below this checkbox is a text field containing the word "note".

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