

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 top panel shows a genomic map with a scale from 1 to 5k. A blue arrow indicates a 589 bp region. The sequence is shown in a zoomed-in view with various annotations. A red arrow points to the 'Show value of qualifier' text in the sequence viewer. Below the sequence, a table lists the annotations:

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 and colors, and a 'Configure the annotations:' section with checkboxes for 'Show annotations', 'Show on translation', and 'Show value of qualifier'. The 'Show value of qualifier' checkbox is checked, and a red arrow points to it. Below the checkboxes is a text field labeled 'note'.

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