

# 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 red arrow points to the 'Show value of qualifier' label above a blue arrow indicating a 589 bp region. The sequence is shown in multiple tracks, including a protein translation track (A R Q D I C G K Q F L P R L) and a DNA sequence track (G G C C A A A C A G G A T A T C T G T G G T A A G C A G T T C C T G C C C C G G C T C G). Below the sequence, a table lists 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, the 'Annotations Highlighting' panel shows a list of annotation types with corresponding colors. The 'Show value of qualifier' checkbox is checked, and a red arrow points to it. Below this, a text field contains the word 'note'. The 'Show on translation' checkbox is unchecked.

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