

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 a bioinformatics software interface with a sequence viewer and a configuration panel on the right.

Sequence Viewer: The top part shows a genomic track for NC_001363. A blue arrow indicates a 589 bp region. Below the track, a sequence alignment is shown with various annotations. A red arrow points to a specific annotation in the track.

Annotations Table: Below the sequence viewer, a table lists annotations with their names, types, and values.

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

Annotations Highlighting Panel: On the right, a panel titled "Annotations Highlighting" allows users to select an annotation name and configure its display. A red arrow points to the "Show value of qualifier" checkbox.

Select an annotation name:

Annotation	Color
BadI	Light Green
BaeGI	Orange
BaeI	Purple
CDS	Green
SacII	Light Blue
comment	Pink
misc_feature	Yellow
source	Grey

Configure the annotations:

- ☒ Show annotations
- ☐ Show on translation
- ☒ Show value of qualifier:

note

Buttons: Back, Forward, Help

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