

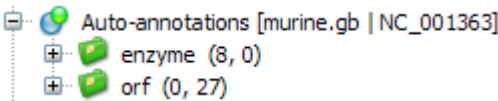
Automatic Annotations Highlighting

Enabling the automatic annotations highlighting allows you to automatically calculate and highlight annotations on each nucleotide sequence opened.

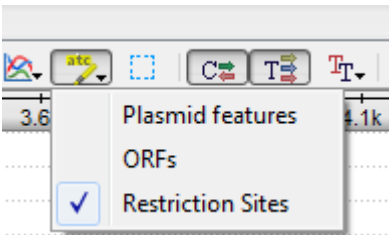
Currently, the following annotations types support the automatic highlighting:

- Open reading frames
- Restriction sites
- Plasmid features

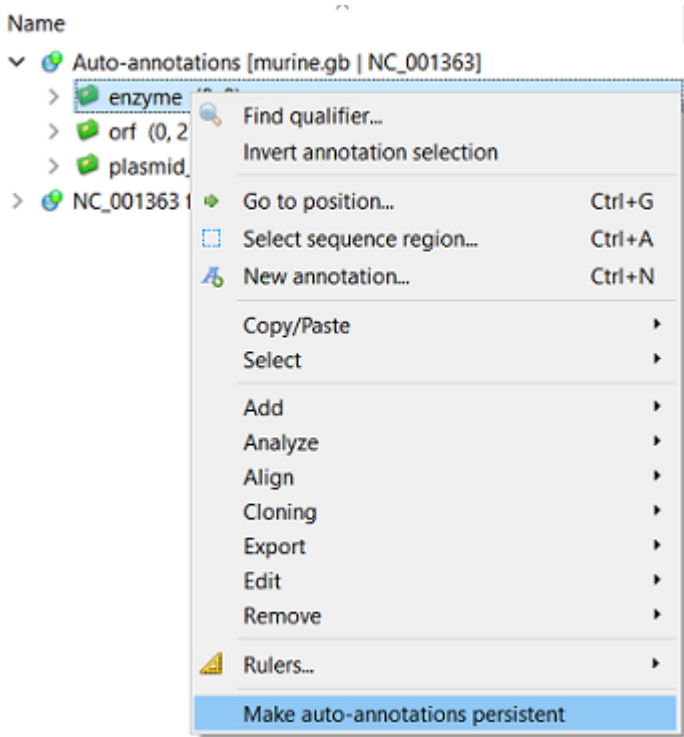
The corresponding groups of annotations found are stored in the *Auto-annotations* object in the *Annotations editor*, for example:



To disable/enable the automatic annotations calculations to use the *Automatic annotations highlighting* menu button on the *Sequence View* toolbar:



To create a permanent annotation click on the *Make auto-annotations persistent* context menu item and choose the annotation parameters in the *Create Permanent Annotation* dialog.



The following dialog will appear:

Create Permanent Annotation

Group name

auto



Description

Save annotation(s) to

☐ Existing document



☒ New document



Help



Cancel



Create