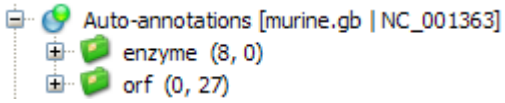
Automatic Annotations Highlighting

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

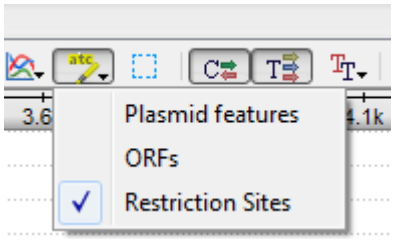
Currently, the following annotations types support the automatic highlighting:

- 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 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.