Automatic Annotations Highlighting

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

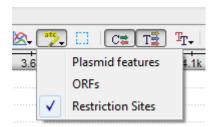
Currently, the following annotations types support the automatic highlighting:

- · 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.