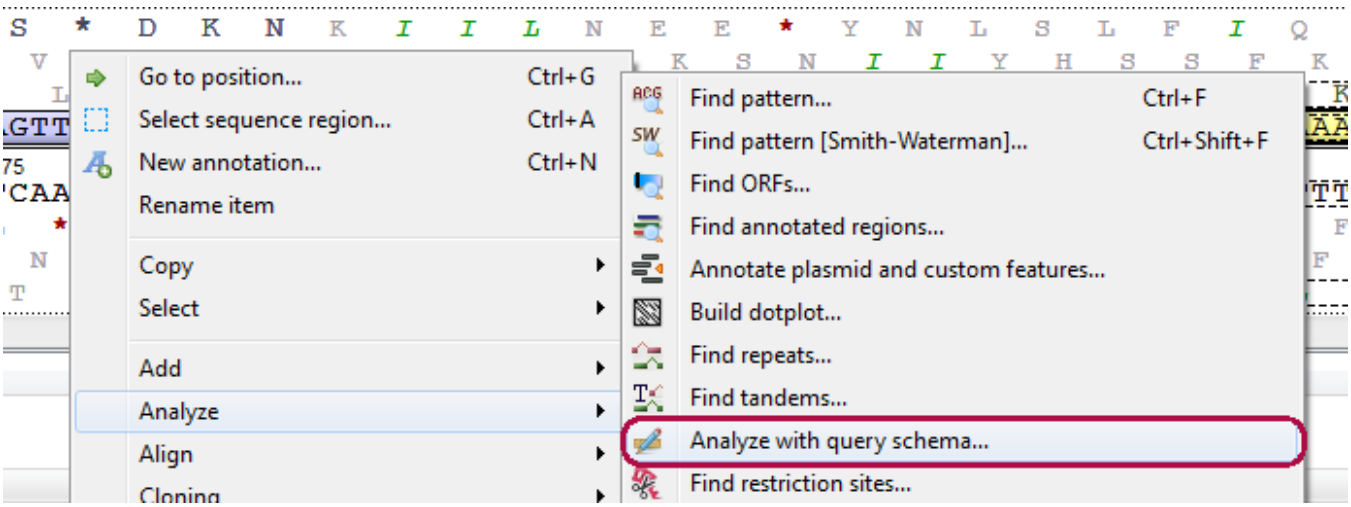
Running Schema from the Sequence View

Prepare a query *schema* and *save* it to a file.

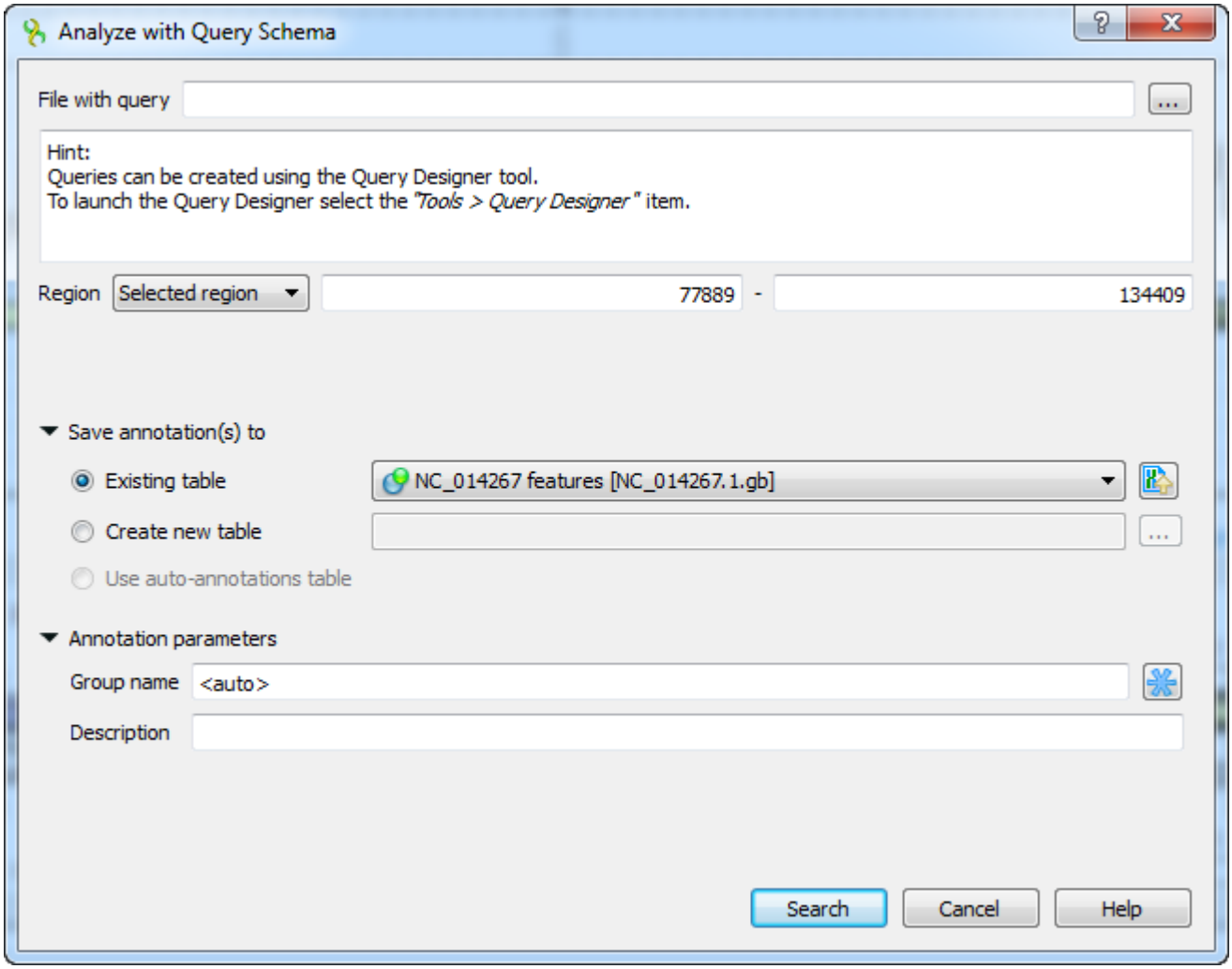
Open a nucleotide sequence that you want to analyze with this query schema. You can see the sequence displayed in the **Sequence view**.

> To learn more about the **Sequence view** read the main UGENE User Manual.

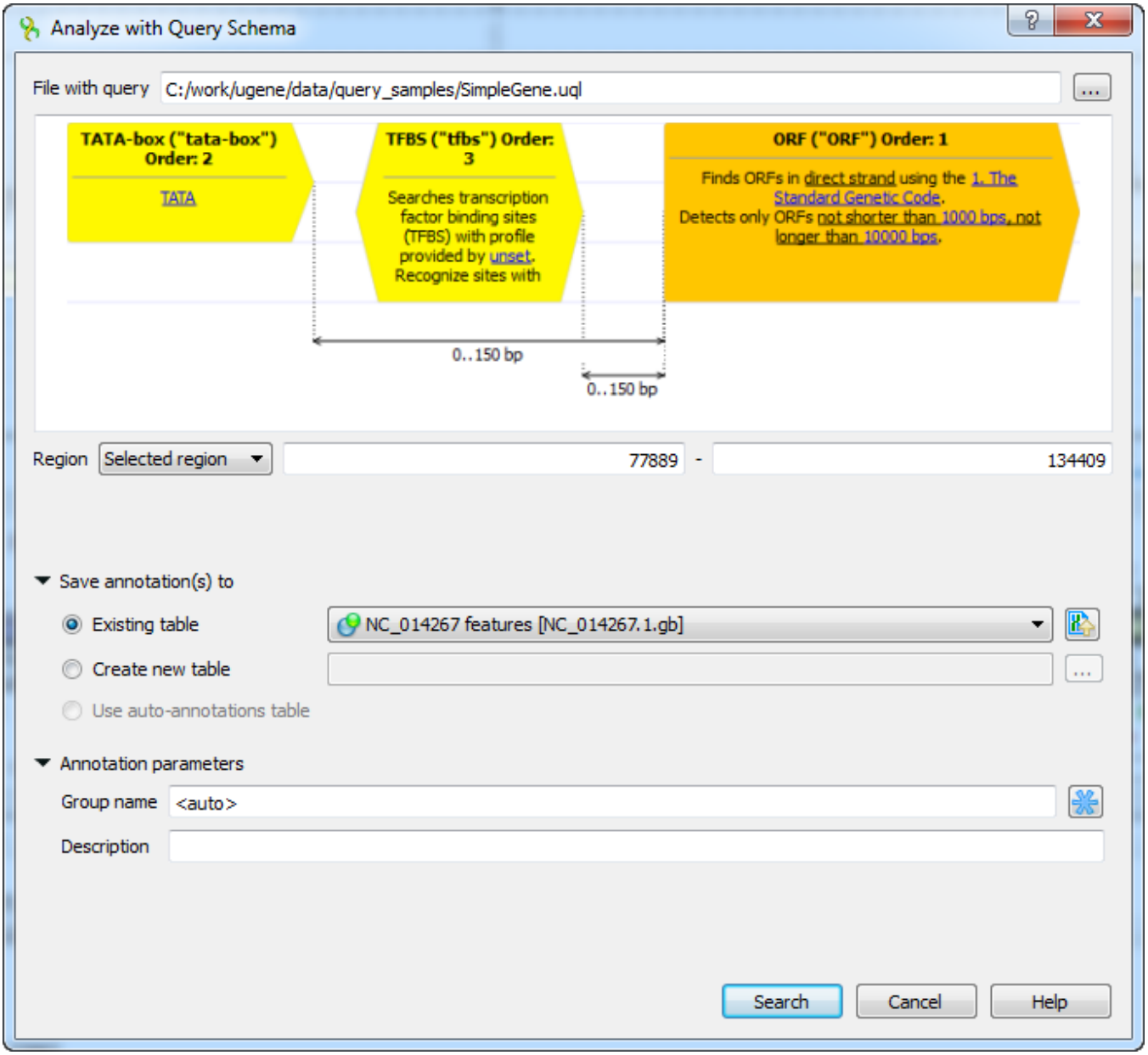
Select the *Analyze Find query designer pattern* item in the *Actions* main menu or in the context menu:



The *Analyze with query schema* dialog appears:



Browse for the file with a query schema. The selected schema preview appears in the dialog, for example:



You can also adjust other parameters:

Region — the sequence range to analyze with the query schema, you can select:

- *Whole sequence* — to analyze the whole sequence.
- *Selected range* — to analyze the currently selected sequence region. This item is disabled if there is no region selected.
- *Custom range* — to specify manually a range to analyze.

In the *Save annotation(s) to* group you can set up a file to store annotations. It could be either an existing annotation table object, a new annotation table or auto-annotations table (if it is available).

In the *Annotation parameters* group you can specify the name of the group. If the group name is set to <auto> UGENE will use the group name as the name for the group. Also you can add a description in the corresponding text field.