

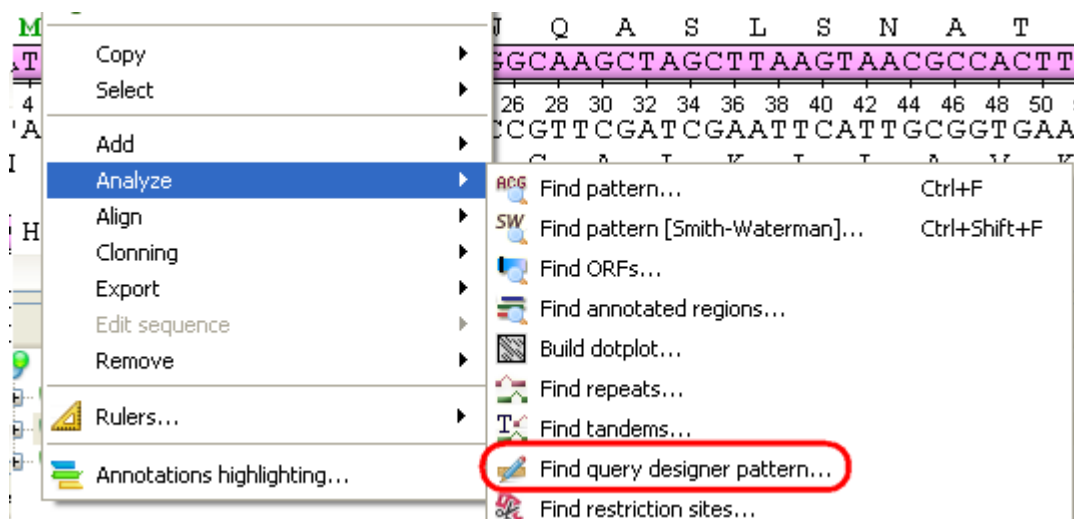
Running Schema from the Sequence View

Prepare a query *schema* and [save](#) it to a file.

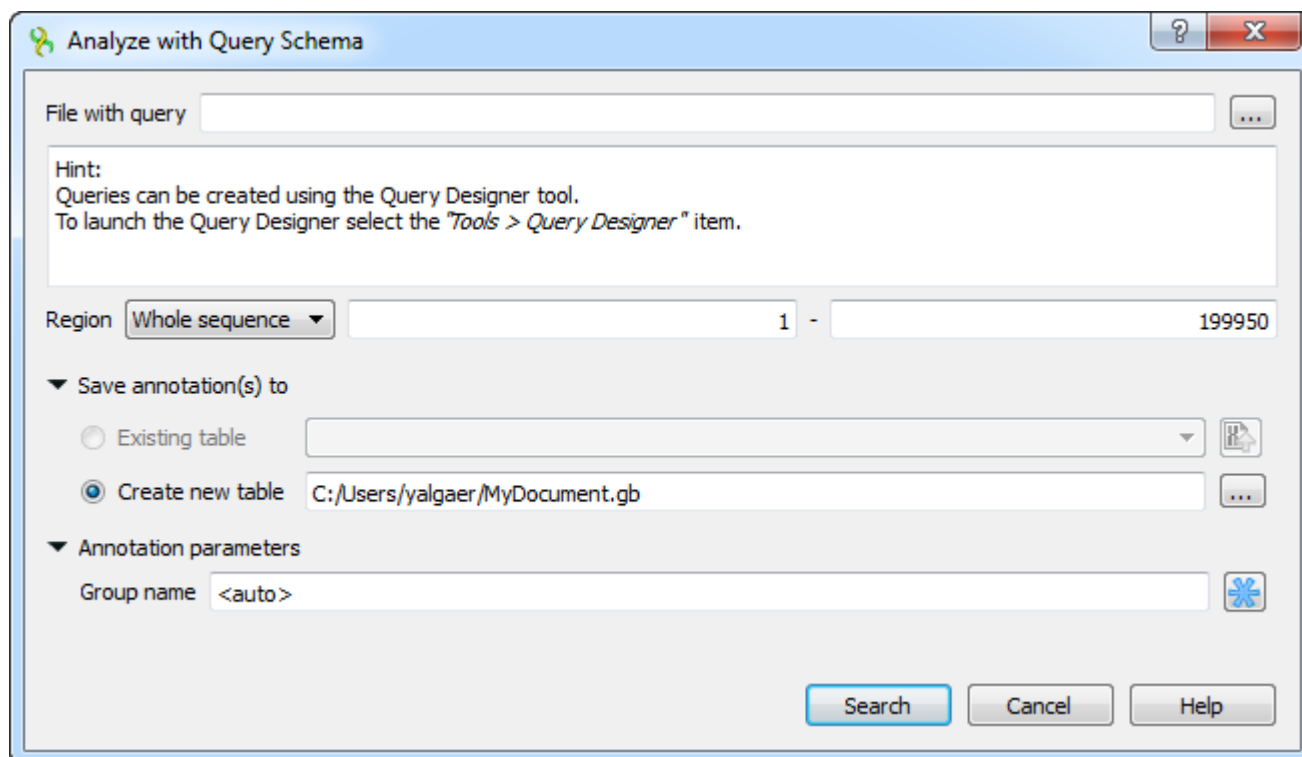
Open a nucleotide sequence that you want to analyze with this query schema. You can see the sequence displayed in the **Sequence view**.

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

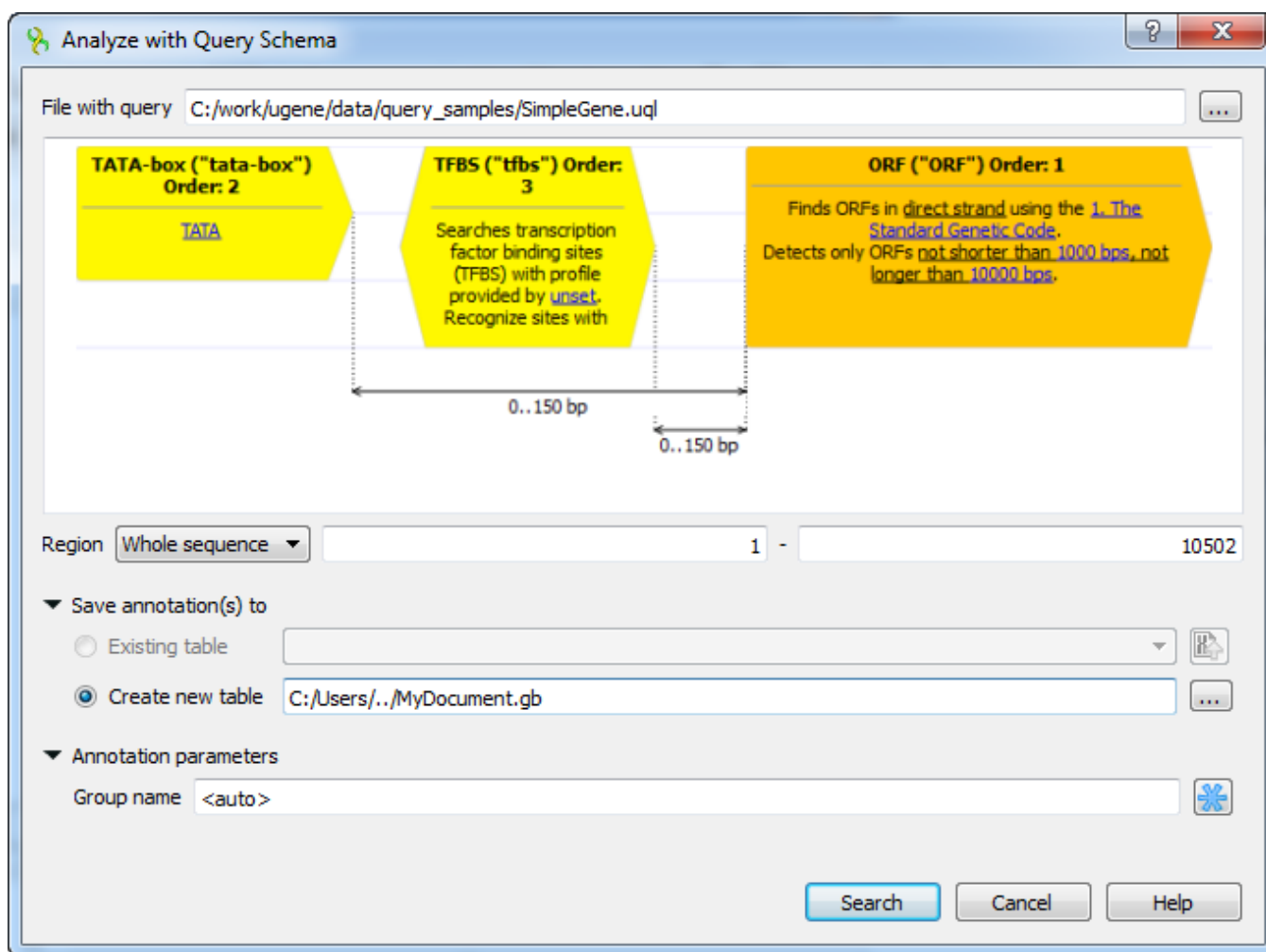
Select the *Analyze > Find query designer pattern* item in the *Actions* main menu or in the context menu:



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:

Range — 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.

Save annotation(s) to — specifies where to save the result annotations:

- *Existing annotation table* — this option is available if there is an existent annotation table and the document is not locked.
- *Create new table* — saves the result annotations to the specified file in GenBank format.

Group name — name of the annotation group. Note, that the annotation name is set in the query schema file.