


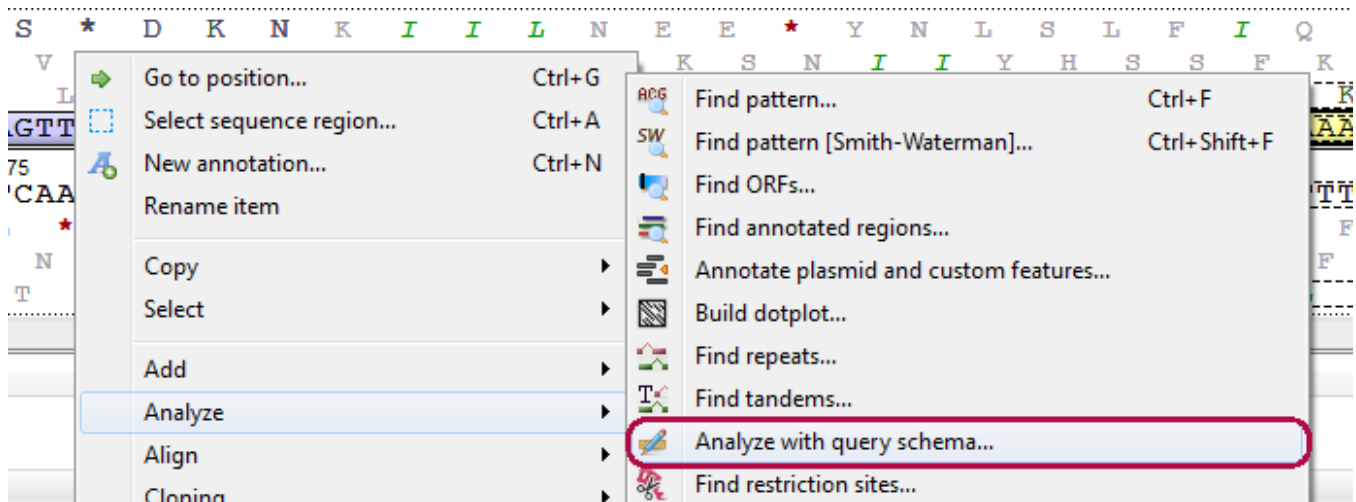
Running Schema from the Sequence View

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:


Analyze with Query Schema

File with query

Hint:
Queries can be created using the Query Designer tool.
To launch the Query Designer select the "Tools > Query Designer" item.

Region Selected region ▼ -


▼ Save annotation(s) to

☒ Existing table NC_014267 features [NC_014267.1.gb] ▼ 

☐ Create new table ...

☐ Use auto-annotations table

▼ Annotation parameters

Group name 

Description

Search Cancel Help

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

Analyze with Query Schema

File with query

TATA-box ("tata-box")
Order: 2
[TATA](#)

TFBS ("tfbs") Order: 3
 Searches transcription factor binding sites (TFBS) with profile provided by [unset](#). Recognize sites with

ORF ("ORF") Order: 1
 Finds ORFs in [direct strand](#) using the [1. The Standard Genetic Code](#). Detects only ORFs [not shorter than 1000 bps](#), [not longer than 10000 bps](#).


0..150 bp 0..150 bp

Region Selected region -

▼ Save annotation(s) to

☒ Existing table
☐ Create new table
☐ Use auto-annotations table

▼ Annotation parameters

Group name 

Description

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.