

Annotations Settings

The screenshot shows the 'Annotations Settings' dialog box. It has two main sections: 'Save annotation(s) to' and 'Annotation parameters'. In the 'Save annotation(s) to' section, the 'Existing table:' radio button is selected, and a dropdown menu shows 'NC_014267 features'. In the 'Annotation parameters' section, the 'Group name:' field contains '<auto>', the 'Annotation type:' dropdown is set to 'Misc. Feature', the 'Annotation name:' field contains 'by type', and the 'Description:' field is empty. The 'Use pattern name' checkbox is unchecked.

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 or a new annotation table.

In the *Annotation parameters* group you can specify the name of the group and the name of the annotation. If the group name is set to <auto> UGENE will use the group name as the name for the group. You can use the '/' characters in this field as a group name separator to create subgroups. If the annotation name is set to *by type* UGENE will use the annotation type from the *Annotation type:* table as the name for the annotation. Also you can add a description in the corresponding text field. To use a pattern name for the annotations check the corresponding checkbox.

After that click the *Create annotations* button. The annotations will be created. Also you can see the result statistic and navigation under the *Search for:* field:

The screenshot shows a search results navigation bar. It displays 'Results: 1/1' and has two buttons: 'Previous' and 'Next'.

Searching for one or several patterns and names of the result annotations

If you search for one pattern only, than input the required name into the *Annotation name* field and leave the *Use pattern name* check box unchecked.

You can also search for several patterns at a time by:

- Inputting several patterns into the search field (click <Ctrl> + <Enter> keys to insert to a new line):

The screenshot shows a search field titled 'Search in Sequence'. Below the title is a 'Search for:' label and a text area containing two lines of DNA sequence: 'TGGCAAGCTAGC' and 'TTTGCAAGGCATG'.

- Inputting several patterns into the search filed in FASTA format:

Search in Sequence

Search for:

```
>pattern1
TGGCAAGCTAGC

>pattern2
TTGCAAGGCATG|
```

- [Loading patterns from a FASTA file](#)

Even when you search for several patterns, names of the found annotations will be identical by default (the name is specified in the *Annotation name* field).

If you want to assign different names to annotations found for different patterns, than you should:

- Input the patterns in FASTA format (the latter two cases above)
- Check the *Use pattern name* checkbox in the *Annotation parameters* group

Here is an example of the found annotations in the [Annotations Editor](#):

Annotations [MyDocument_1.gb] *	
misc_feature (0, 4)	
▶ ■ pattern1	24..35
▶ ■ pattern1	5267..5278
▶ ■ pattern2	50..62
▶ ■ pattern2	5293..5305