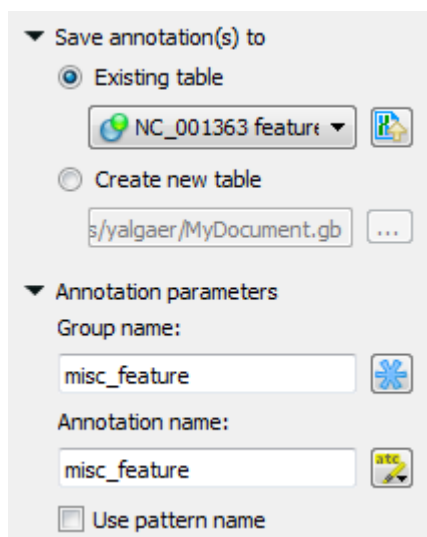


# Annotations Settings



The screenshot shows the 'Annotations Settings' dialog box. It has two main sections. The first section, 'Save annotation(s) to', has two radio buttons: 'Existing table' (selected) and 'Create new table'. Below 'Existing table' is a dropdown menu showing 'NC\_001363 feature' and a file icon. Below 'Create new table' is a text field containing 's/yalgaer/MyDocument.gb' and an ellipsis button. The second section, 'Annotation parameters', has two text fields: 'Group name:' with 'misc\_feature' and a snowflake icon, and 'Annotation name:' with 'misc\_feature' and a yellow arrow icon. At the bottom is a checkbox labeled 'Use pattern name' which is unchecked.

In the *Save annotation(s) to* group of parameters you can set up a file to store annotations. It could be either an existing annotation table object or a new document (file).

In the *Annotation parameters* group you can specify

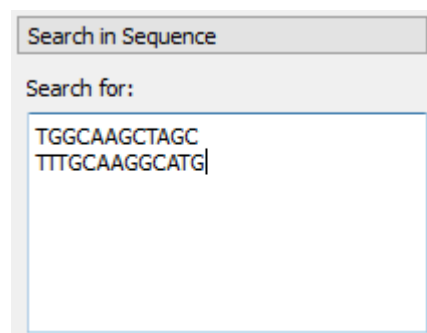
- A group that the found annotations will be stored in (this affects the name of the folder in the [Annotations Editor](#))
- The way name(s) of the found annotations are assigned (see below)

## 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 the 'Search in Sequence' dialog box. It has a title bar 'Search in Sequence'. Below it is a label 'Search for:' followed by a text area. The text area contains two lines of DNA sequence: 'TGGCAAGCTAGC' and 'TTTGAAGGCATG'.

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

Search in Sequence

Search for:

```
>pattern1
TGGCAAGCTAGC

>pattern2
TTTGCAAGGCATG|
```

- [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