

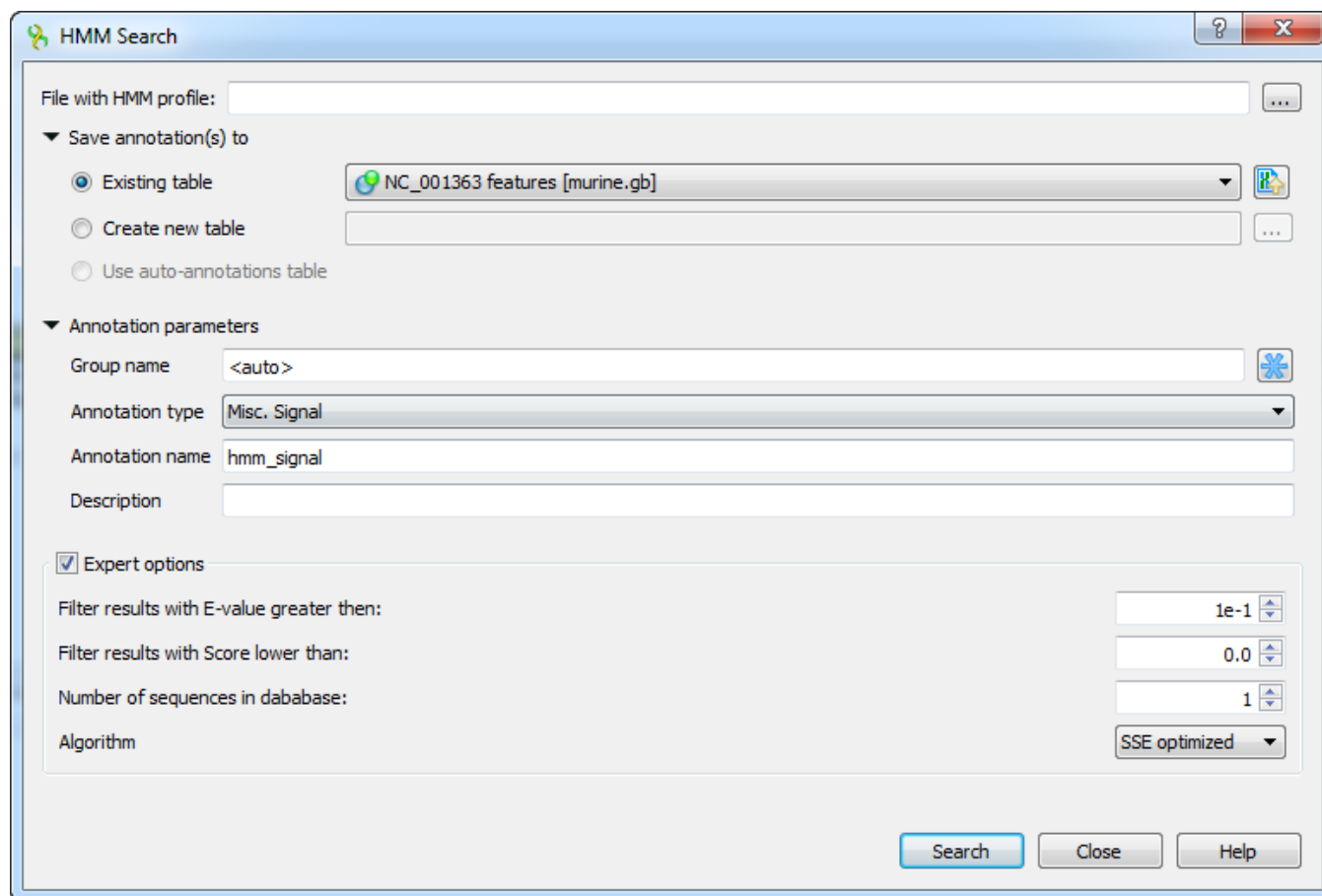
Searching Sequence Using HMM2 Profile

The *HMM search* tool reads a HMM profile from a file and searches the sequence for significantly similar sequence matches.

The sequence must be selected in the *Project View* or there must be an active *Sequence View* window opened.

If the selected sequence is nucleic and the HMM profile is built for amino alignment, the sequence is automatically translated and all 6 translations are used to search in.

If a HMM profile is built for nucleic alignment, the search is performed for both strands (direct and complement).

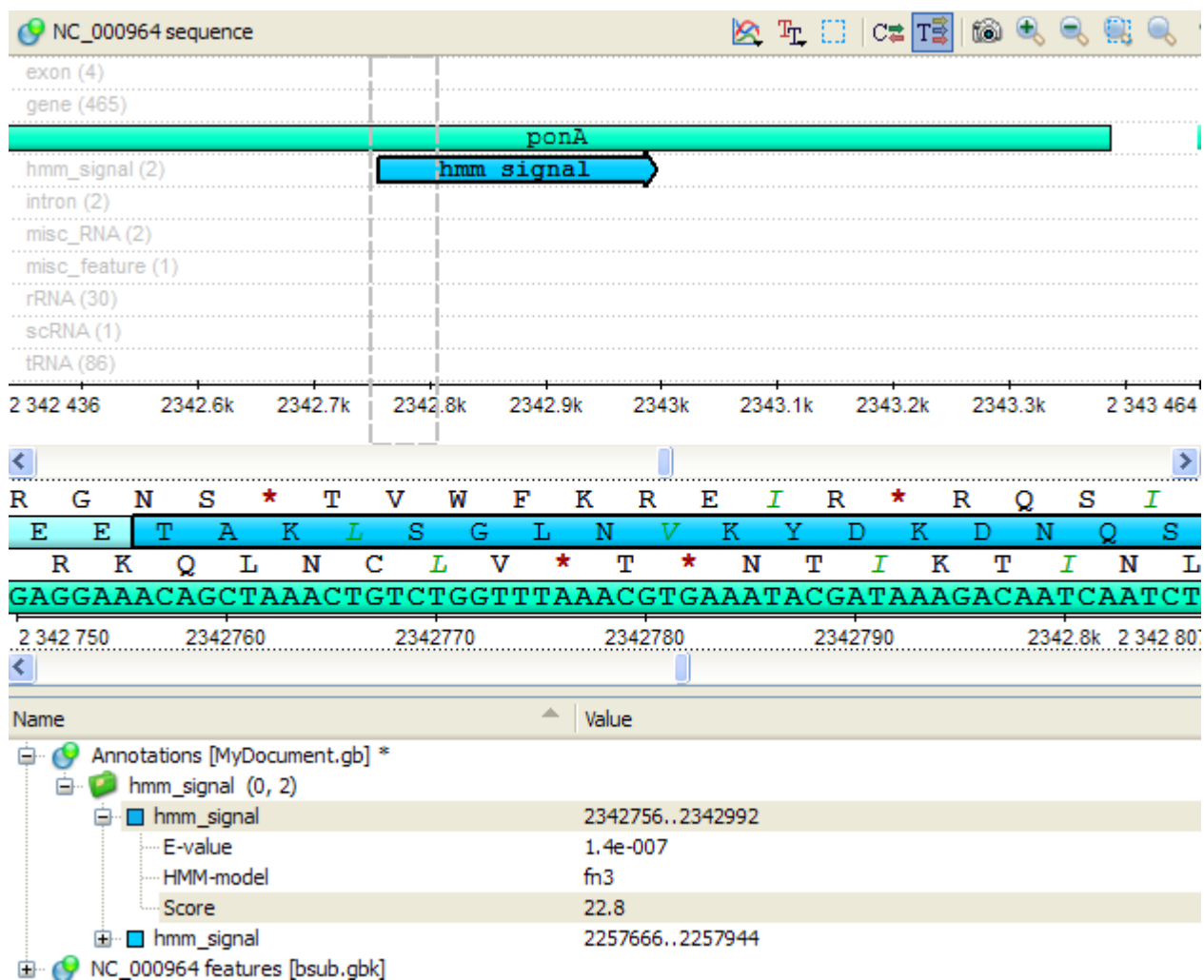


The screenshot shows the 'HMM Search' dialog box with the following fields and options:

- File with HMM profile:** A text input field with a browse button (three dots).
- Save annotation(s) to:**
 - ☒ Existing table: A dropdown menu showing 'NC_001363 features [murine.gb]' with a browse button.
 - ☐ Create new table: A text input field with a browse button.
 - ☐ Use auto-annotations table.
- Annotation parameters:**
 - Group name:** A text input field with '<auto>' and a refresh button (circular arrow).
 - Annotation type:** A dropdown menu showing 'Misc. Signal'.
 - Annotation name:** A text input field with 'hmm_signal'.
 - Description:** A text input field.
- Expert options:** A section with a checked checkbox and several settings:
 - Filter results with E-value greater than:** A text input field with '1e-1' and a spinner.
 - Filter results with Score lower than:** A text input field with '0.0' and a spinner.
 - Number of sequences in database:** A text input field with '1' and a spinner.
 - Algorithm:** A dropdown menu showing 'SSE optimized'.

At the bottom right, there are three buttons: 'Search' (highlighted in blue), 'Close', and 'Help'.

The search results are stored as sequence annotations in the Genbank file format.



! All HMM2 UGENE tools work only with files that contain a single HMM model.