

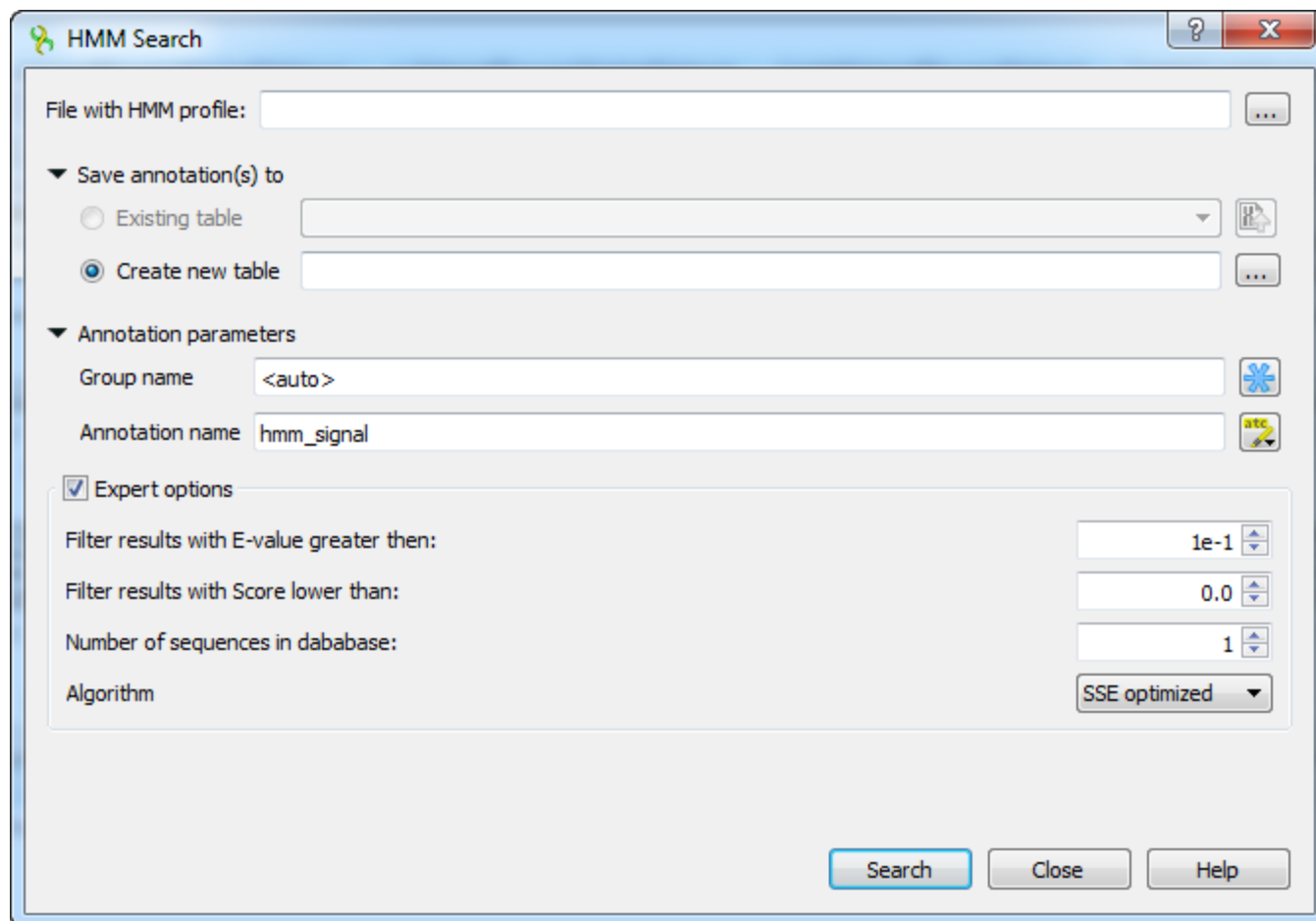
Searching Sequence Using HMM Profile (HMM Search)

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.

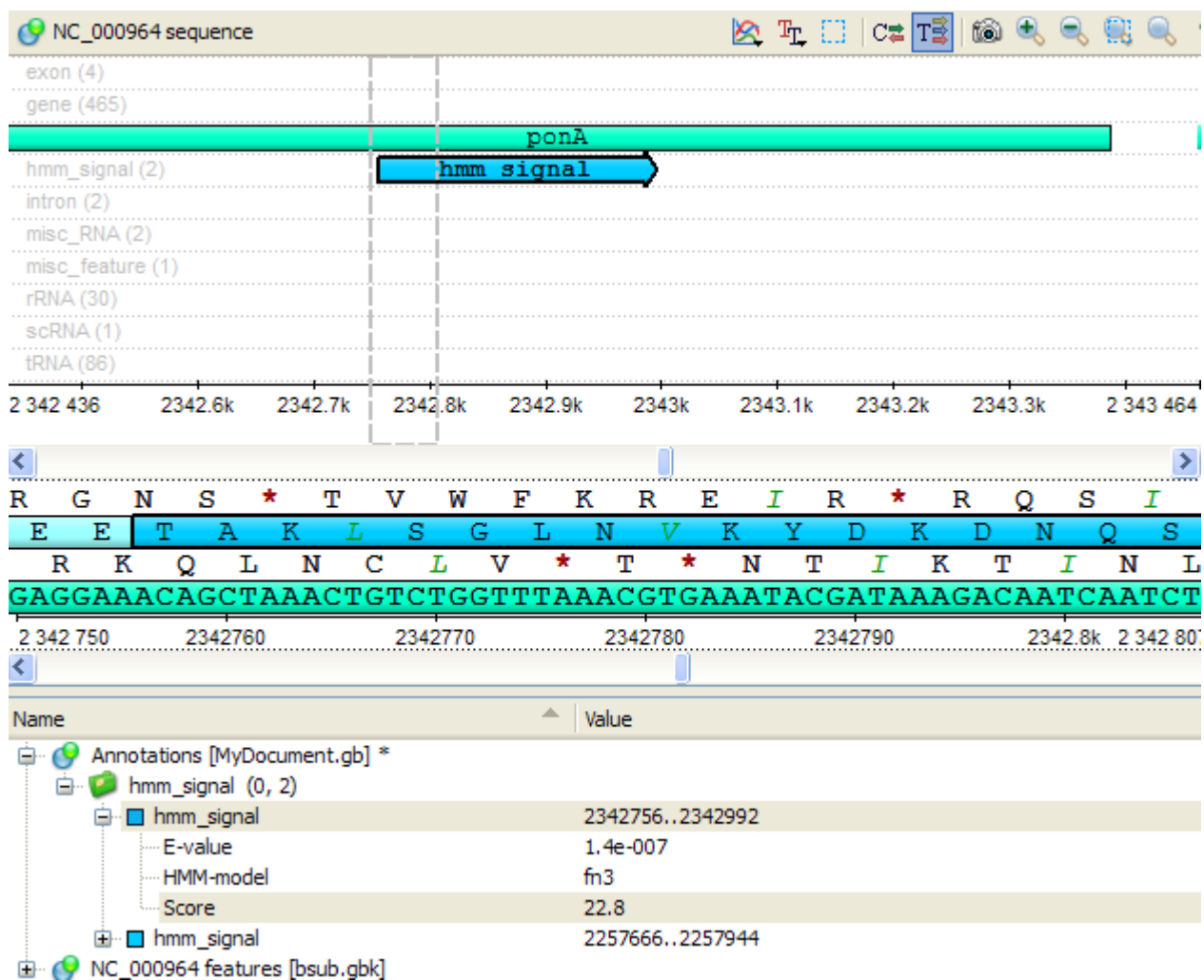
If a HMM profile is built for nucleic alignment, the search is performed for both strands (direct and complement).



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

- File with HMM profile:** A text input field with a browse button (three dots) to its right.
- Save annotation(s) to:** A section with two radio buttons: 'Existing table' and 'Create new table'. The 'Create new table' option is selected. Next to 'Existing table' is a dropdown menu and a save icon. Next to 'Create new table' is a text input field and a save icon.
- Annotation parameters:** A section with two text input fields: 'Group name' (containing '<auto>') and 'Annotation name' (containing 'hmm_signal'). To the right of 'Group name' is a refresh icon, and to the right of 'Annotation name' is a save icon.
- Expert options:** A section with a checked checkbox. It contains four rows of controls:
 - 'Filter results with E-value greater than:' followed by a text input field containing '1e-1' and a spinner button.
 - 'Filter results with Score lower than:' followed by a text input field containing '0.0' and a spinner button.
 - 'Number of sequences in dababase:' followed by a text input field containing '1' and a spinner button.
 - 'Algorithm' followed by a dropdown menu showing 'SSE optimized'.
- Buttons:** At the bottom right are three buttons: 'Search', '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.