

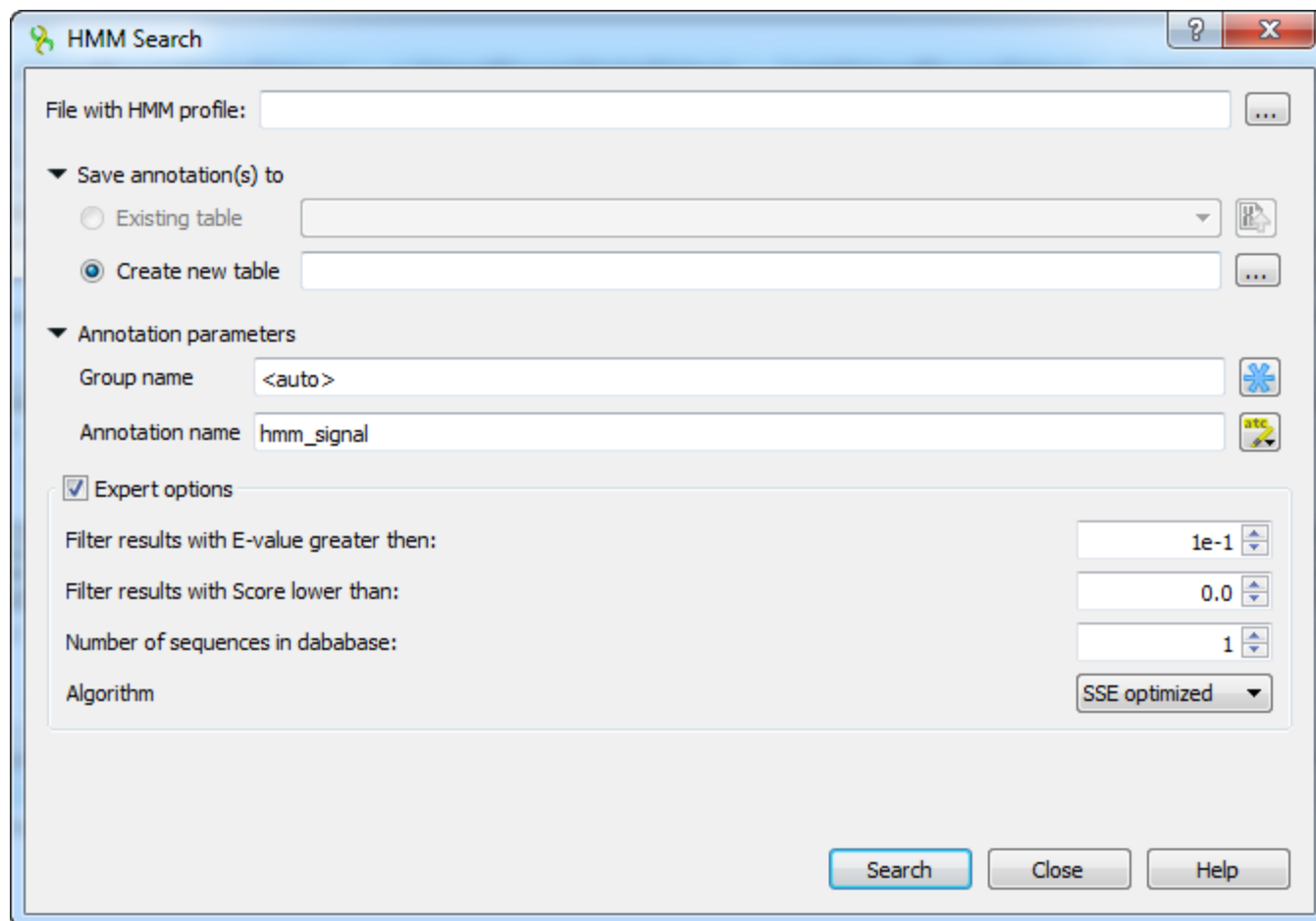
Searching Sequence Using HMM Profile (HMM Search)

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.

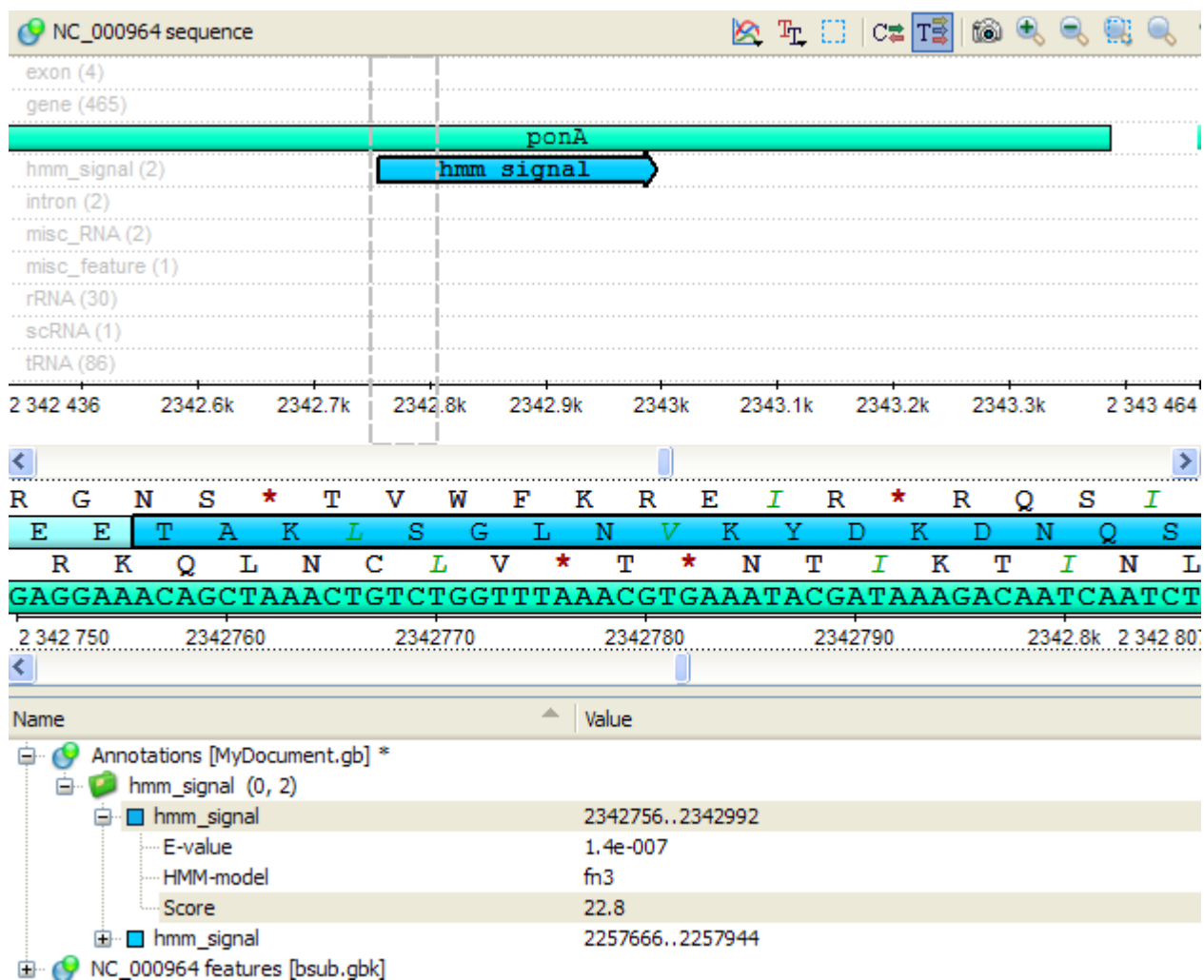
If a HMM profile is built for nucleic alignment, the search is performed for both strands (direct and complement).



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).
- Save annotation(s) to:**
 - ☐ Existing table: A text input field with a dropdown arrow and a save icon.
 - ☒ Create new table: A text input field with a browse button (three dots).
- Annotation parameters:**
 - Group name:** A text input field containing '<auto>' with a refresh icon.
 - Annotation name:** A text input field containing 'hmm_signal' with a save icon.
- Expert options:** A section with a checked checkbox and several controls:
 - Filter results with E-value greater than:** A text input field with a spinner showing '1e-1'.
 - Filter results with Score lower than:** A text input field with a spinner showing '0.0'.
 - Number of sequences in dababase:** A text input field with a spinner showing '1'.
 - Algorithm:** A dropdown menu showing 'SSE optimized'.
- Buttons:** 'Search', 'Close', and 'Help' buttons at the bottom right.

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.