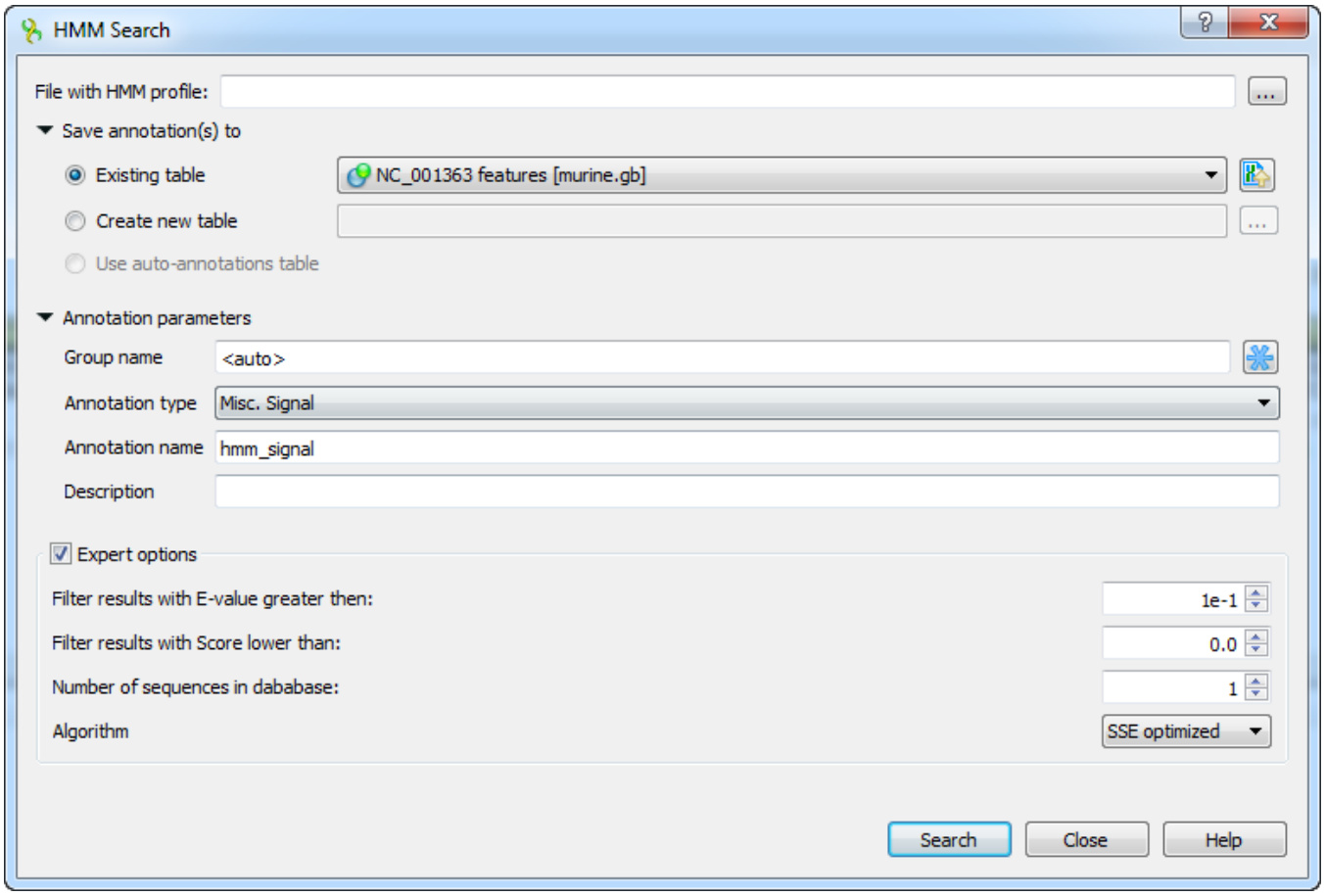
Searching Sequence Using HMM2 Profile

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

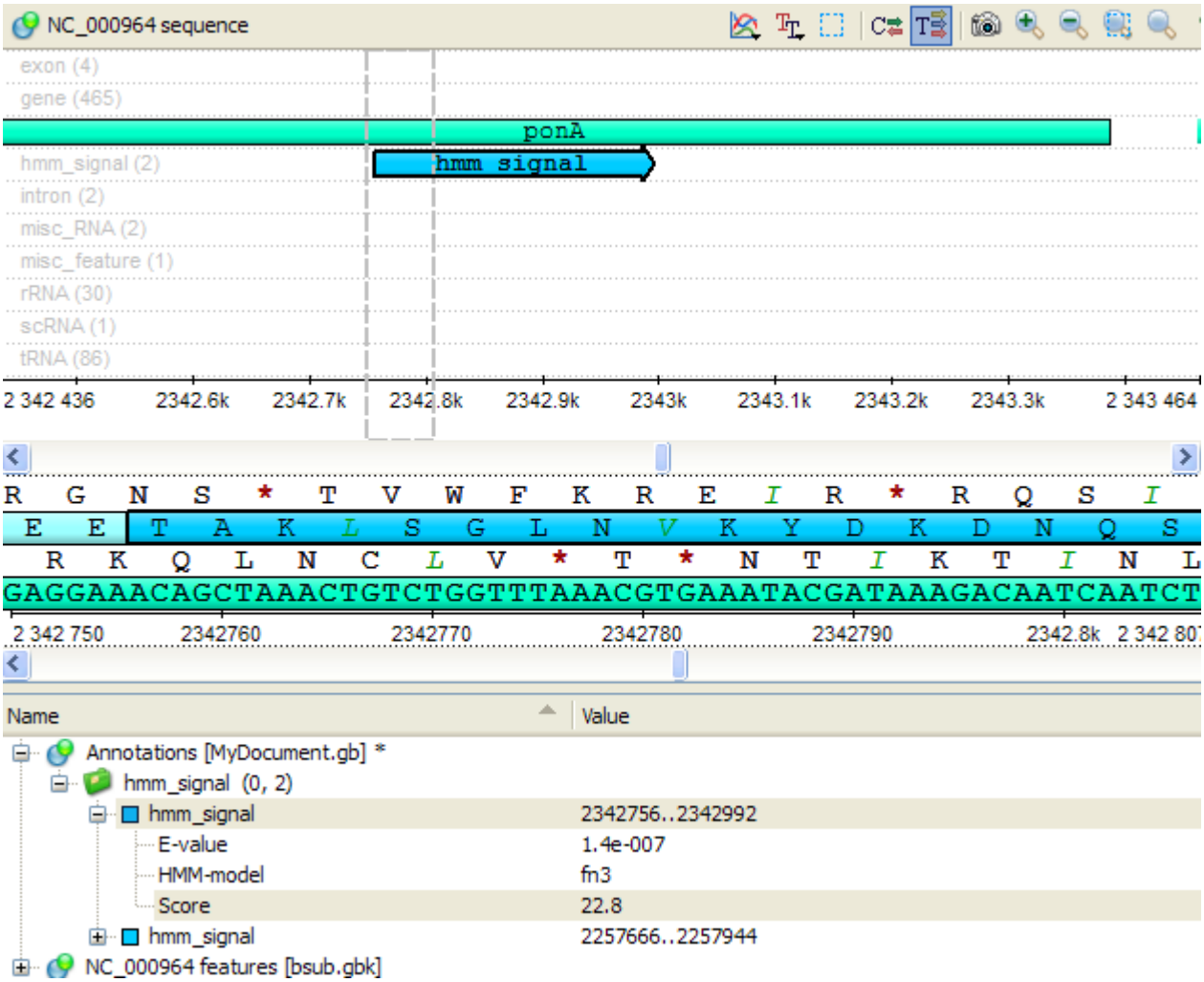
The sequence must be selected in the *Project View* or there must be an active *Sequence View* window opened.

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 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.