

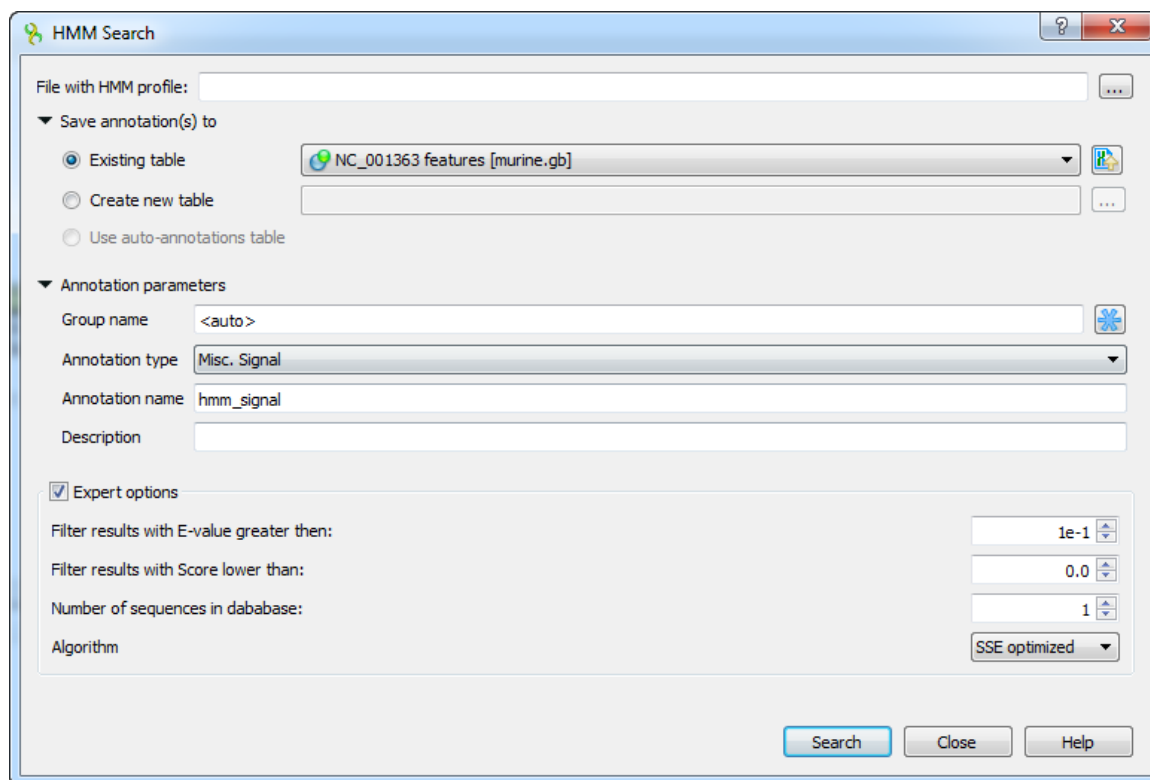
Searching Sequence Using HMM2 Profile

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.

NC_000964 sequence

exon (4)
gene (465)

ponA

hmm_signal (2)

hmm signal

intron (2)
misc_RNA (2)
misc_feature (1)
rRNA (30)
scRNA (1)
tRNA (86)

2 342 436 2342.6k 2342.7k 2342.8k 2342.9k 2343k 2343.1k 2343.2k 2343.3k 2 343 464

R G N S * T V W F K R E I R * R Q S I
E E T A K L S G L N V K Y D K D N Q S
R K Q L N C L V * T * N T I K T I N L
GAGGAAACAGCTAAACTGTCTGGTTTAAACGTGAAATACGATAAAGACAATCAATCT

2 342 750 2342760 2342770 2342780 2342790 2342.8k 2 342 80

Name	Value
Annotations [MyDocument.gb] *	
hmm_signal (0, 2)	
hmm_signal	2342756..2342992
E-value	1.4e-007
HMM-model	fn3
Score	22.8
hmm_signal	2257666..2257944
NC_000964 features [bsub.gbk]	

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