

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).

HMM Search

File with HMM profile:

▼ Save annotation(s) to

Existing table

Create new table

Use auto-annotations table

▼ Annotation parameters

Group name

Annotation type

Annotation name

Description

Expert options

Filter results with E-value greater than:

Filter results with Score lower than:

Number of sequences in database:

Algorithm

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

NC_000964 sequence

exon (4)
 gene (465)
 ponA
 hmm_signal (2)
 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 2 342 807

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.