

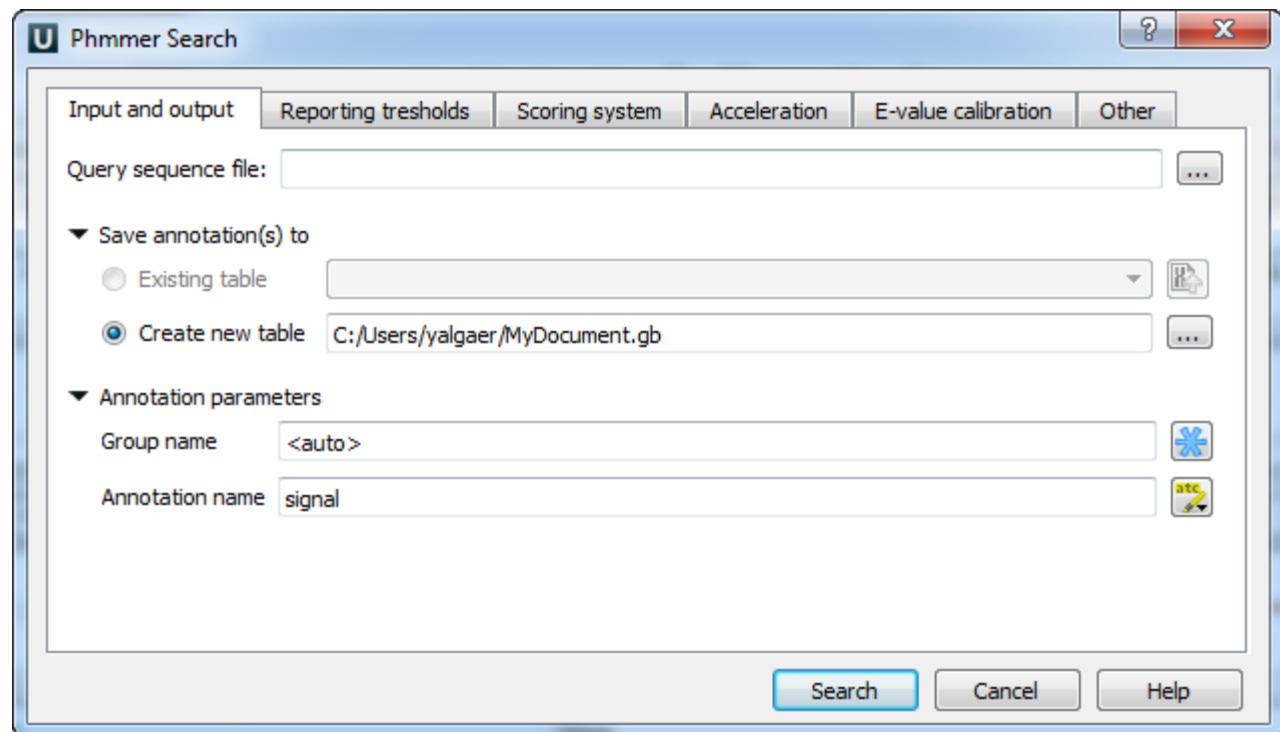
Searching Sequence Against Sequence Database (Phmmer Search)

The *Phmmer search* tool searches for query sequence matches in sequence database, much as BLASTP or FASTA would do.

The *Phmmer search* works essentially like the *HMM3 search* does, except you provide a query sequence instead of a query profile HMM.

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

Select the query sequence in the *Phmmer search* dialog:



You can set options of the *Phmmer search* by choosing the needed dialog tab. Here you can see the e-value calibration options:

Phmmer Search

Input and output Reporting thresholds Scoring system Acceleration E-value calibration Other

Length of sequences for MSV Gumbel mu fit: 200

Number of sequences for MSV Gumbel mu fit: 200

Length of sequences for Viterbi Gumbel mu fit: 200

Number of sequences for Viterbi Gumbel mu fit: 200

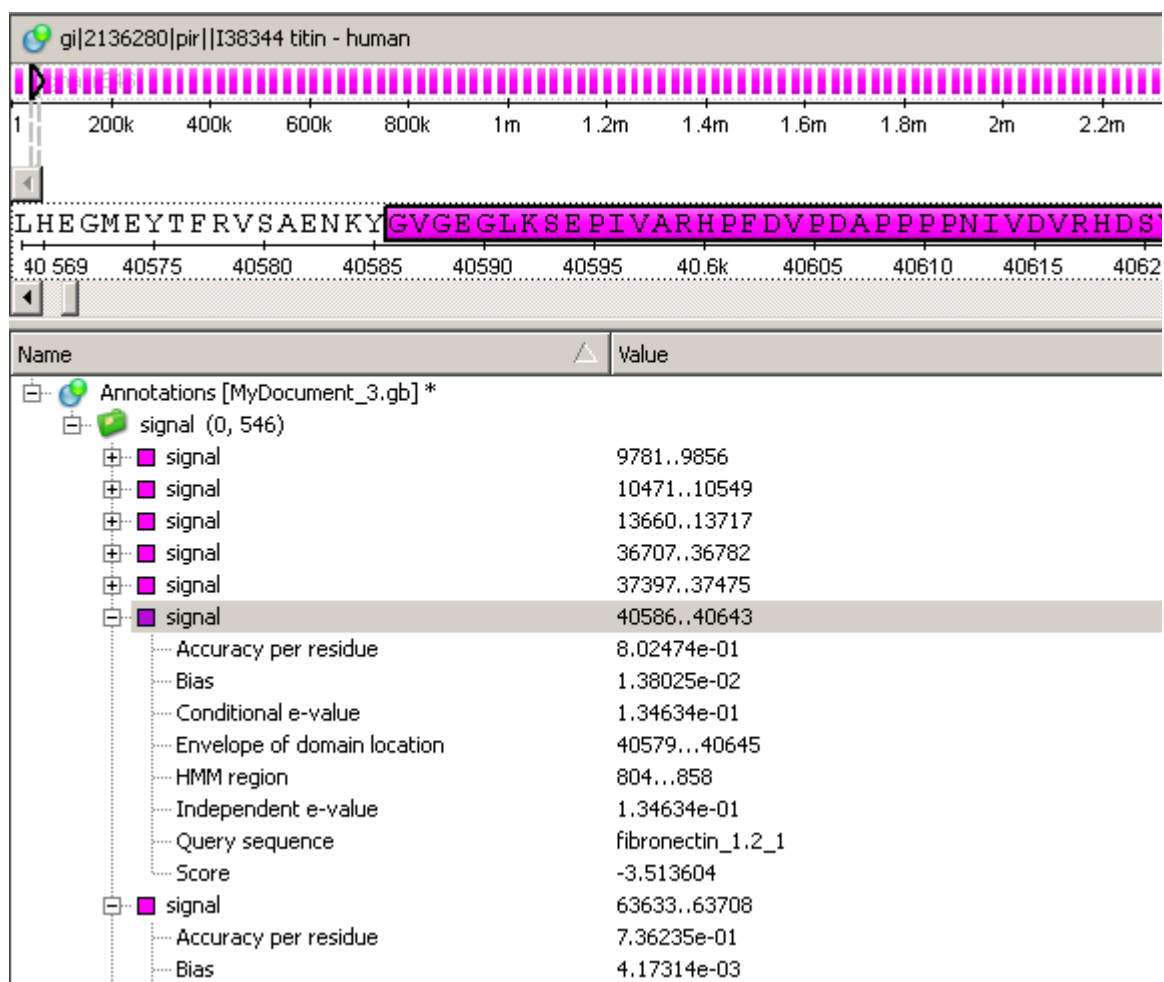
Length of sequences for Forward exp tail mu fit: 100

Number of sequences for Forward exp tail mu fit: 200

Tail mass for Forward exponential tail mu fit: 0.04

Search Cancel Help

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





The *Phmmer* search works only with single-sequence databases.