

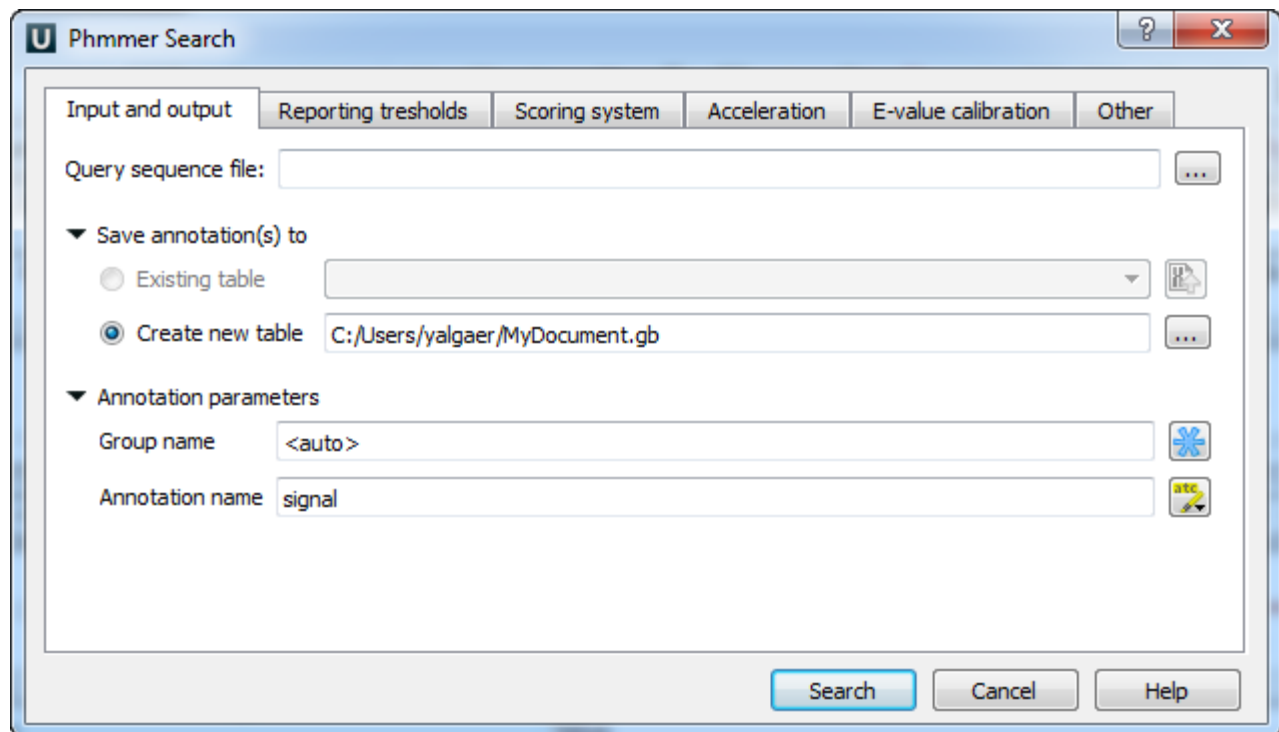
Searching Sequence Against Sequence Database (Phmmer Search)

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:

U Phmmer Search

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

Length of sequences for MSV Gumbel mu fit

Number of sequences for MSV Gumbel mu fit

Length of sequences for Viterbi Gumbel mu fit

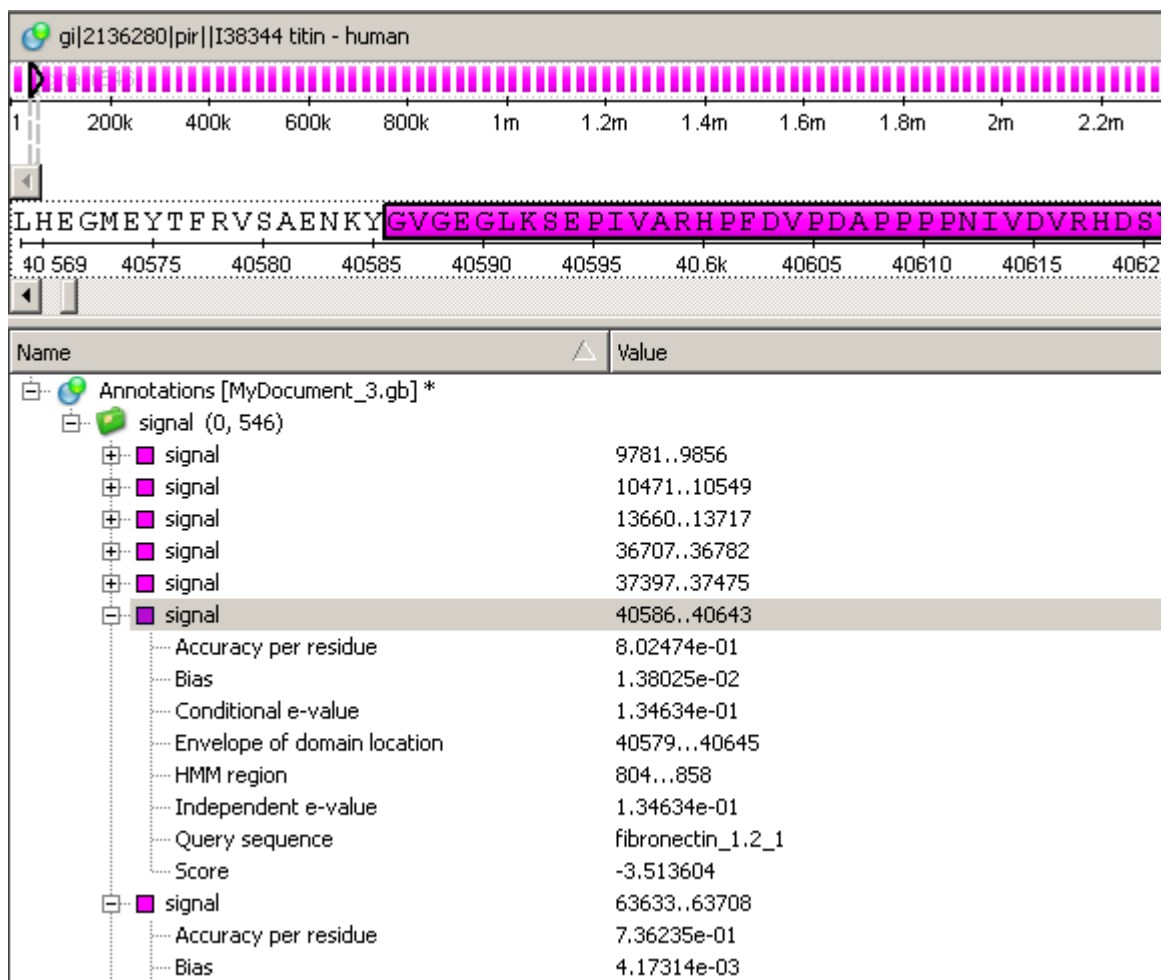
Number of sequences for Viterbi Gumbel mu fit

Length of sequences for Forward exp tail mu fit

Number of sequences for Forward exp tail mu fit

Tail mass for Forward exponential tail mu fit

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





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