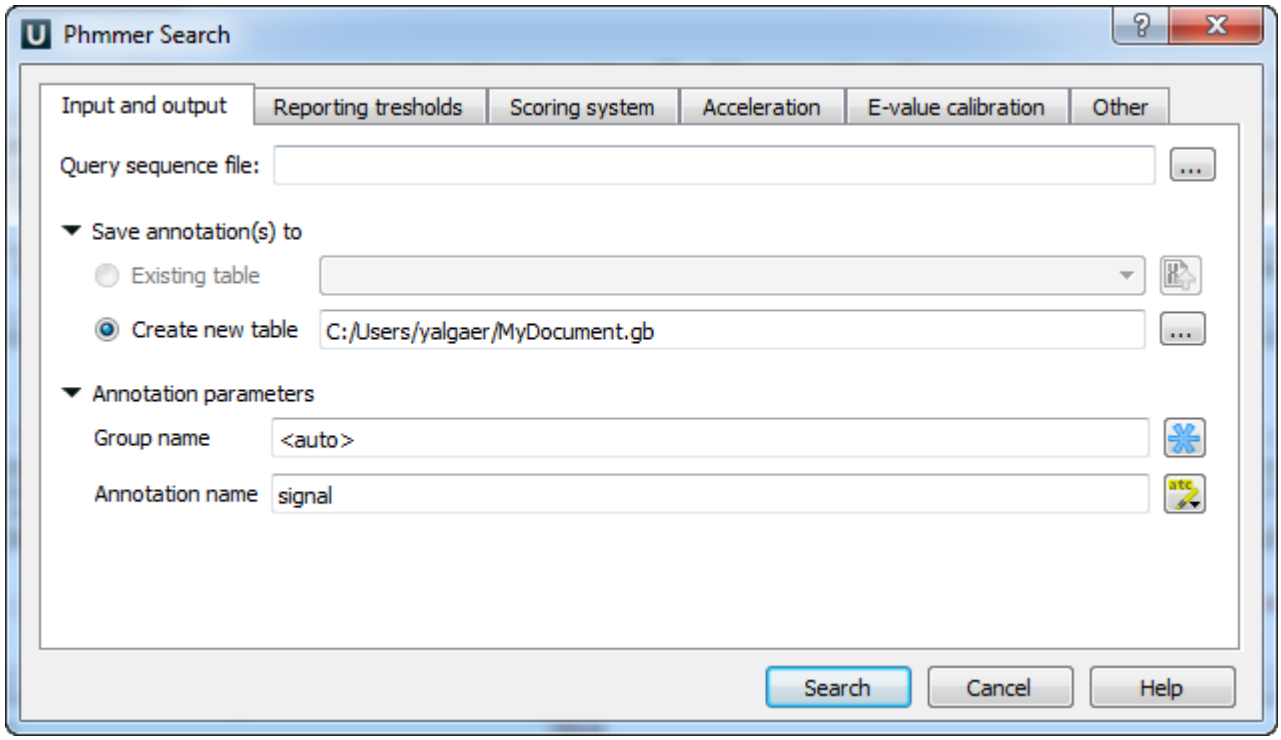
Searching Sequence Against Sequence Database

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

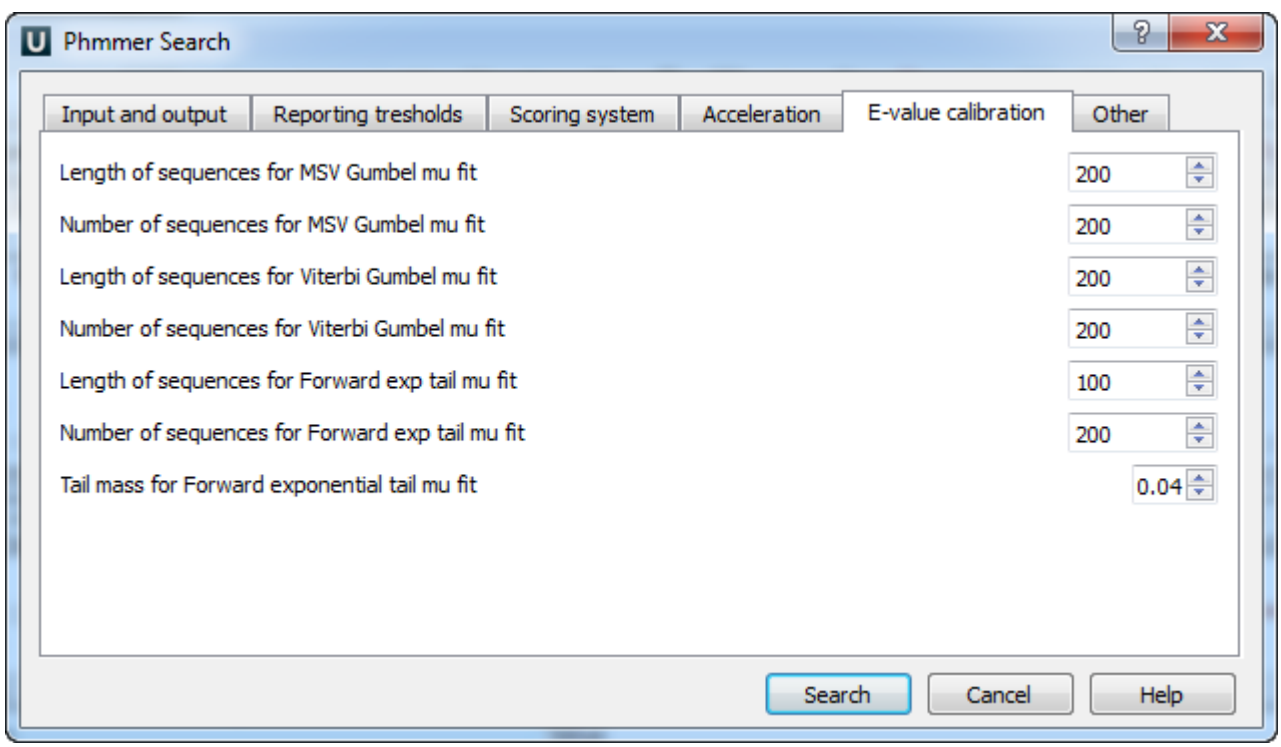
The *Phmmer search* works essentially like the *HMM3 search* does, except you provide a query sequence instead of a query profile HMM.

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

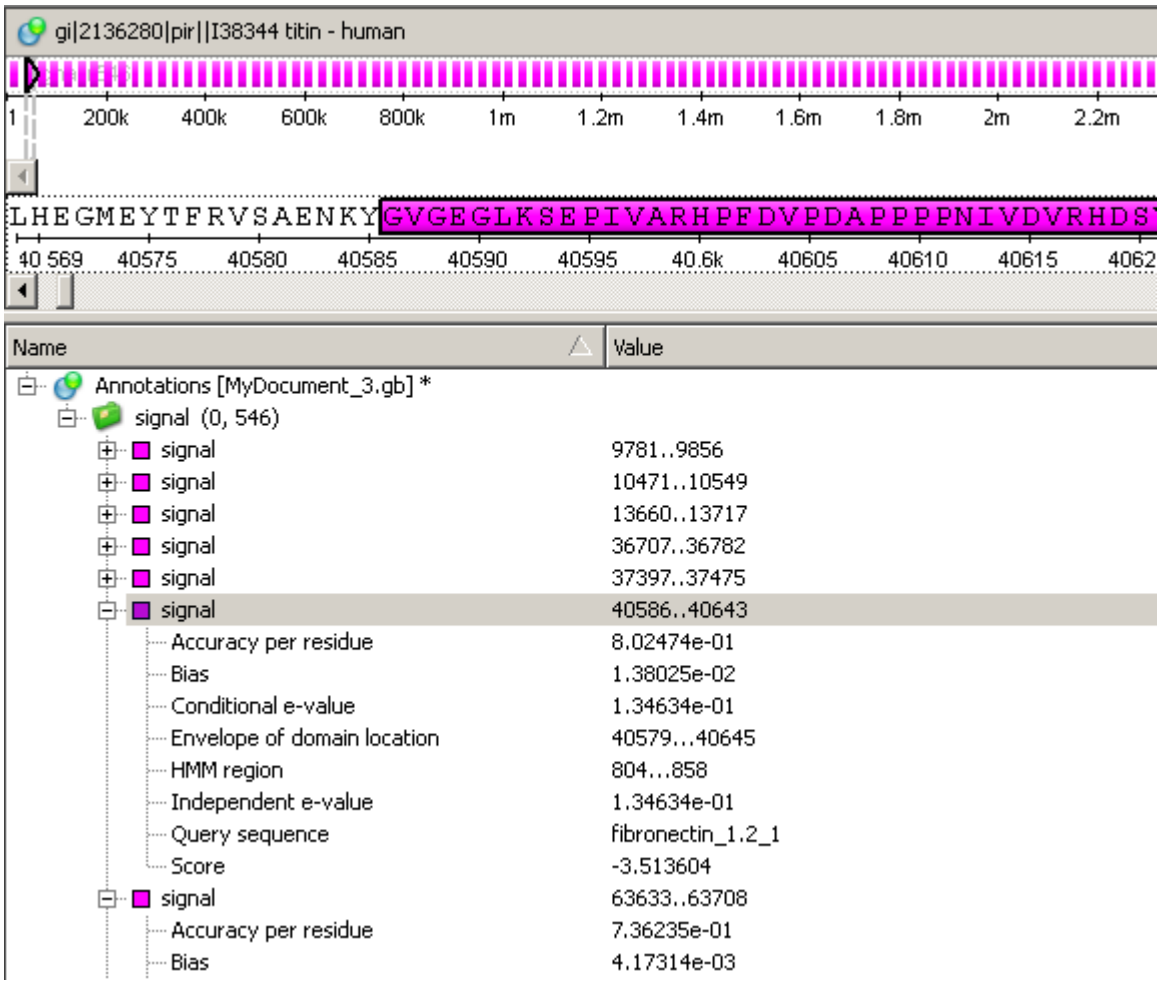
Select the query sequence in the *Phmmer search* dialog:



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



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



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