

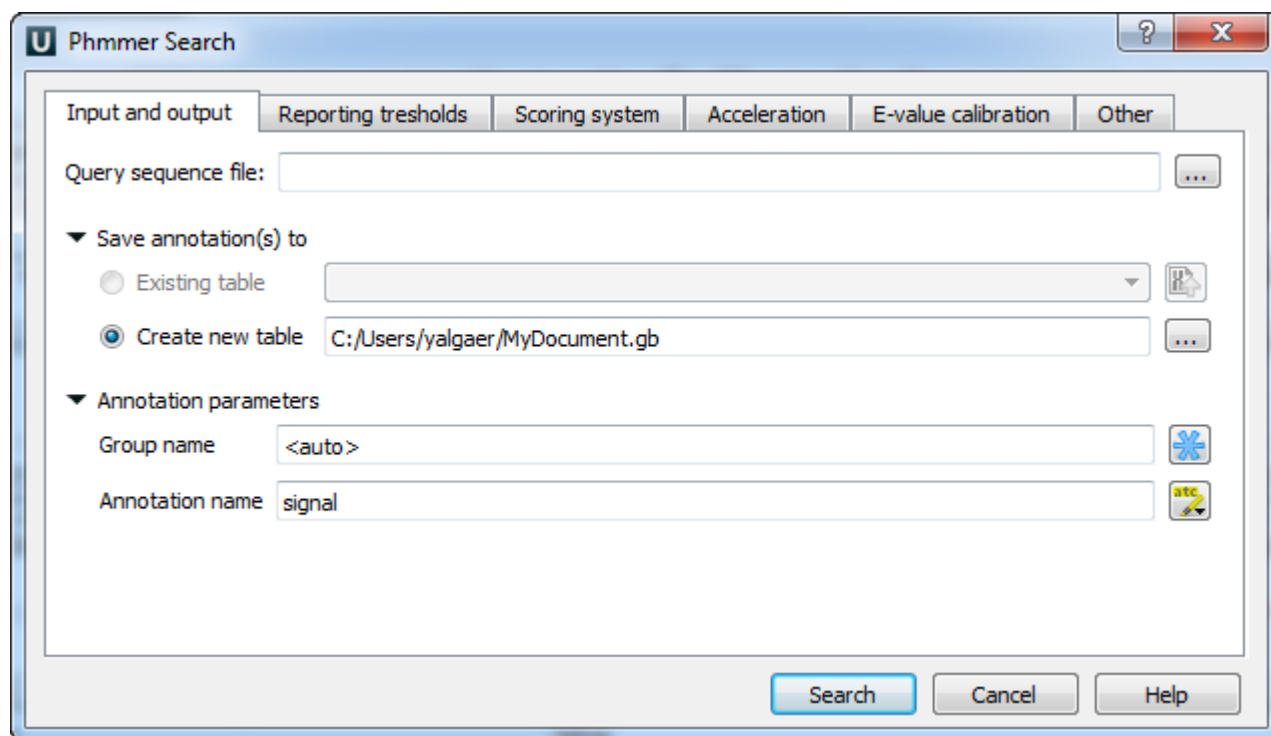
# Searching Sequence Against Sequence Database

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.

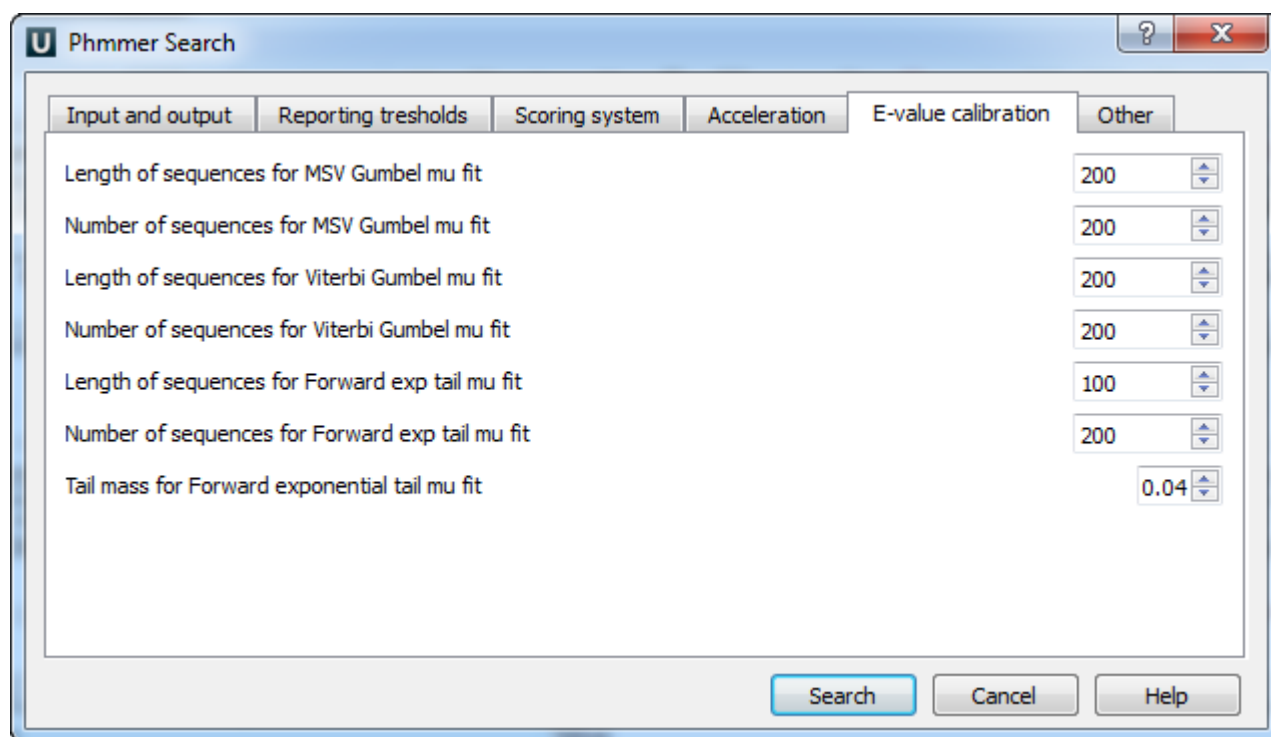
Select the query sequence in the *Phmmer search* dialog:



The image shows the 'Phmmer Search' dialog box with the 'Input and output' tab selected. The dialog has a title bar with a question mark and a close button. Below the title bar are several tabs: 'Input and output', 'Reporting thresholds', 'Scoring system', 'Acceleration', 'E-value calibration', and 'Other'. The 'Input and output' tab is active, showing a 'Query sequence file:' text box with a browse button (...). Below this is a section 'Save annotation(s) to' with two radio buttons: 'Existing table' and 'Create new table'. The 'Create new table' option is selected, and its text box contains 'C:/Users/yalgaer/MyDocument.gb'. Below this is a section 'Annotation parameters' with two text boxes: 'Group name' containing '<auto>' and 'Annotation name' containing 'signal'. At the bottom are three buttons: 'Search', 'Cancel', and 'Help'.

| Tab                   | Field                 | Value                          |
|-----------------------|-----------------------|--------------------------------|
| Input and output      | Query sequence file:  |                                |
|                       | Save annotation(s) to |                                |
|                       | Existing table        |                                |
|                       | Create new table      | C:/Users/yalgaer/MyDocument.gb |
| Annotation parameters | Group name            | <auto>                         |
|                       | Annotation name       | signal                         |

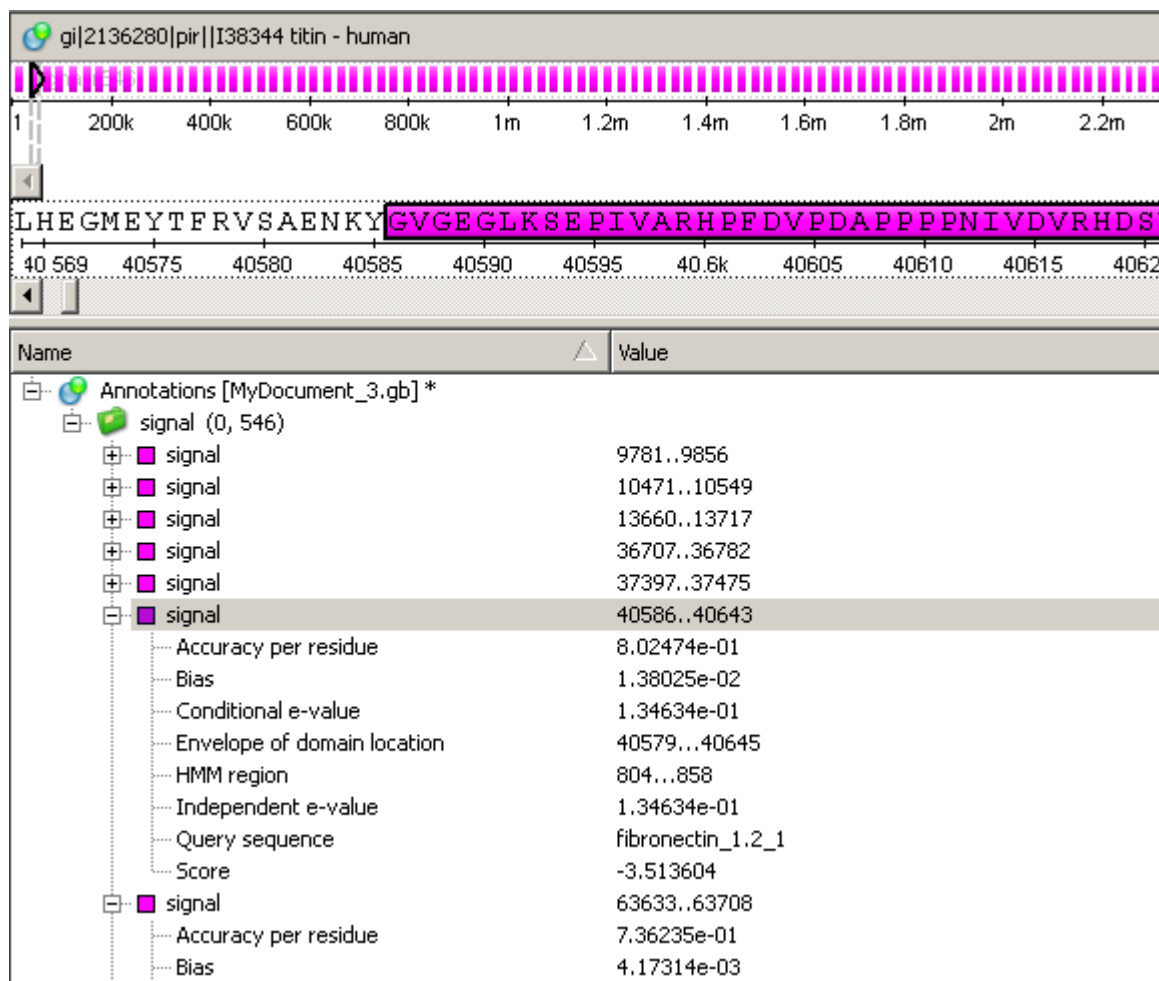
You can set options of the *Phmmer search* by choosing the needed dialog tab. Here you can see the e-value calibration options:



The image shows the 'Phmmer Search' dialog box with the 'E-value calibration' tab selected. The dialog has the same title bar and tabs as the previous image. The 'E-value calibration' tab is active, showing a list of parameters with corresponding spinners. The parameters are: '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), and 'Tail mass for Forward exponential tail mu fit' (0.04). At the bottom are three buttons: 'Search', 'Cancel', and 'Help'.

| Parameter                                       | Value |
|-------------------------------------------------|-------|
| 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  |

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



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