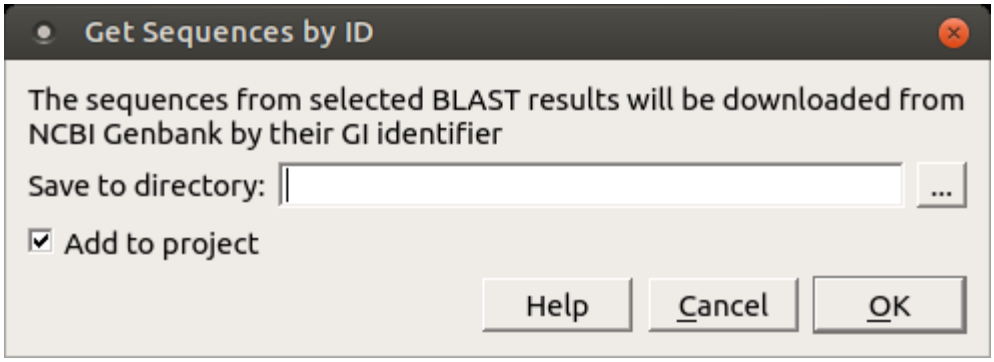
Fetching Sequences from Remote Database

Each result annotation found with the *remote BLAST* in UGENE has "accession" and "id" qualifiers that can be used to fetch the corresponding sequences from the NCBI. The prompt way to fetch the sequences of several annotations is the following:

- Select the annotations in the *Annotations Editor*.
- Open the context menu.
- Choose the *Fetch sequences from remote database->Fetch sequences by 'id' from 'blast result'* item or *Fetch sequences from remote database->Fetch sequences by 'accession' from 'blast result'* item.

The following dialog will appear:



Select an output path in the dialog and click the *OK* button.