## **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:

😵 Get Sequences by ID
The sequences from selected BLAST results will be downloaded from NCBI Genbank by their GI identifier
Save to directory:
OK Cancel Help

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