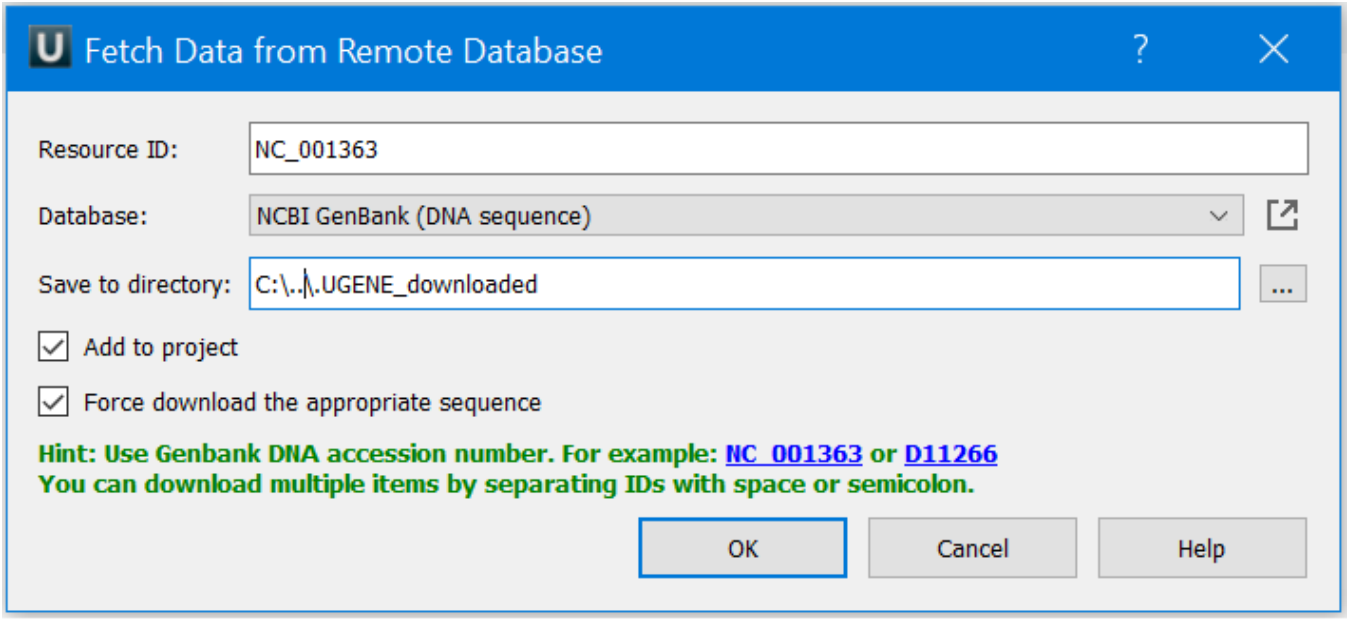
Fetching Data from Remote Database

UGENE allows fetching data from remote biological databases such as NCBI GenBank, NCBI protein sequence database, and some others.

To fetch data select the *File Access remote database...* item in the main menu.

The dialog will appear:



The following parameters are available:

Resource ID: Here you need to enter the unique id of the biological object and choose a database. Unique identifiers are different for various databases. For example, for NCBI GenBank such unique id could be Accession Number or NCBI GI number.

Database: The following databases are available: NCBI Genbank (DNA sequence), NCBI protein sequence database, ENSEMBL, PDB, SWISS-PROT, UniProtKB/Swiss-Prot, UniProtKB/TrEMBL. You can open the database page by clicking on the arrow button at the end where the link to the external database is stored.

Save to directory: Browse for a directory to save the fetched file to.

Add to project: Select this checkbox if you want add the document to a project.

Force download the appropriate sequence: Some entries in NCBI databases contains features without sequences. You can download both sequence and features by clicking this parameter. Note that some sequence are rather big. For for example, only annotations without sequences will be loaded for NC.000853.1 if this parameter is unchecked.

After you click the *OK* button, UGENE downloads the biological object (DNA sequence, protein sequence, 3d model, etc.) and adds it to the current *project*.

Task report with the specified information will be generated after downloading.

If something goes wrong check the *Log View*, it will help you to diagnose the problem.