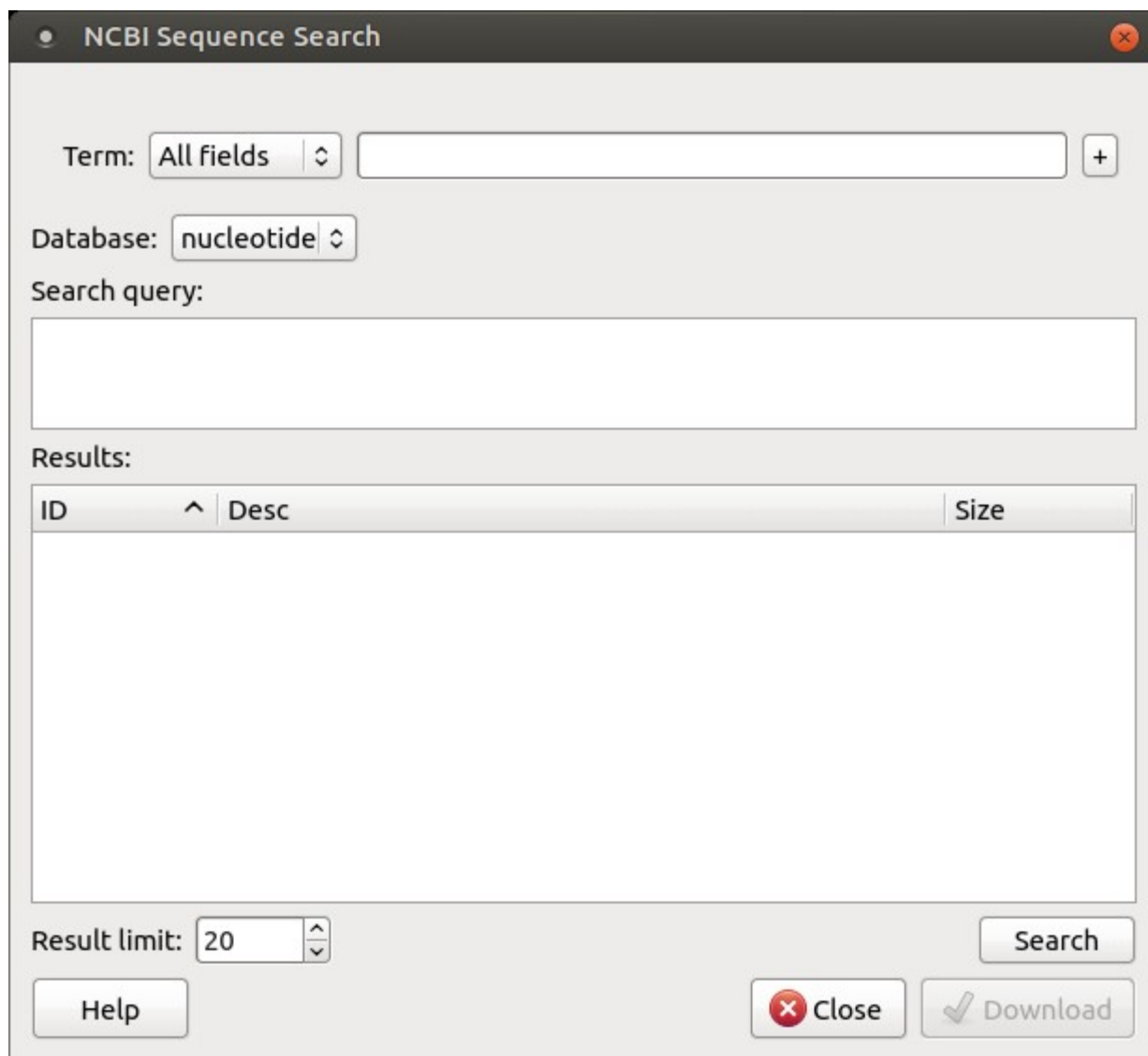


Searching NCBI Genbank

UGENE allows searching data in NCBI GenBank remote database. To do this open the following dialog by *File->Search NCBI Genbank* main menu:



The screenshot shows the "NCBI Sequence Search" dialog box. It has a title bar with a close button. The main area contains the following elements:

- Term:** A dropdown menu set to "All fields" and a text input field with a "+" button.
- Database:** A dropdown menu set to "nucleotide".
- Search query:** A large text input field.
- Results:** A table with columns "ID", "Desc", and "Size". The table is currently empty.
- Result limit:** A dropdown menu set to "20".
- Buttons:** "Help", "Search", "Close" (with a red X icon), and "Download" (with a green checkmark icon).

To search data in the nucleotide or protein databases enter a general text query to the search field, select the database and click on the *Search* button. You can use a protein name, gene name, or gene symbol directly. Searching for a submitter or author name in the following format will produce the best results.

Use the boolean operator AND to find records that contain every one of your search terms, the intersection of search results.

Use the boolean operator OR to find records that include one of several search terms, the union of search results.

Use the boolean operator NOT to exclude records matching a search term.

To limit results use the *Result limit* field.

After you click the *Search* button, UGENE searches the biological objects and shows it in the *Results* field. You can download the object(s). Select one or several objects (for selecting several objects use the *Ctrl* button) and click the *Download* button. The dialog will appear:

U Fetch Data from Remote Database ? X

Resource ID:

Database:

Save to directory: ...

Output format:
 gb
 fasta

☒ Add to project

☒ Force download the appropriate sequence

OK Cancel Help

The meanings of all parameters are similar to the parameters from the dialog *Fetch Data from Remote Database* which is called through *FileAccess Remote Database*.

You can save the downloaded file in one of two formats: fasta or GenBank.

Force download appropriate sequence parameter is not available if you select fasta format.

After you click the *OK* button, UGENE downloads the biological objects and adds it to the current project if *Add to project option* is checked.