

# 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 features a title bar with a question mark and a close button. The main area contains several input fields and buttons. At the top, there is a 'Term:' label with a dropdown menu set to 'All fields' and an adjacent text input field. Below this is a second row with a dropdown menu set to 'AND', another 'All fields' dropdown, and a second text input field. A 'Database:' label is followed by a dropdown menu set to 'nucleotide'. Below these is a 'Search query:' label and a large text area. To the right of the text area is a 'History...' button. At the bottom left, there is a 'Result limit:' label with a numeric input field set to '20'. At the bottom right, there are three buttons: 'Search', 'Download', and 'Close'. A 'Help' button is also present near the bottom right.

| ID | Desc | Size |
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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 with a submitter or author name in the following format will produce the best results.

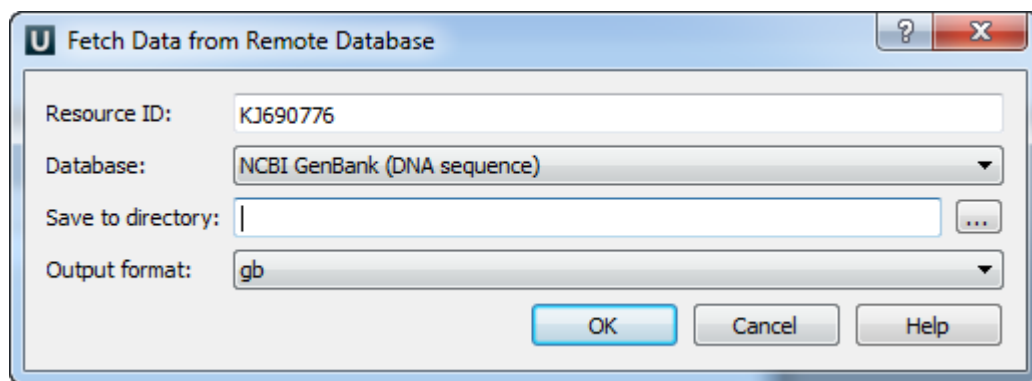
Use the boolean operator *AND* to find records that contain every one of your search terms, the intersection of search results.

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:



The image shows a dialog box titled "Fetch Data from Remote Database" with a blue header bar containing a "U" icon, a question mark, and a close button. The dialog contains four input fields: "Resource ID" with the value "KJ690776", "Database" with a dropdown menu showing "NCBI GenBank (DNA sequence)", "Save to directory" with an empty text box and a browse button "...", and "Output format" with a dropdown menu showing "gb". At the bottom right are three buttons: "OK", "Cancel", and "Help".

|                    |                             |
|--------------------|-----------------------------|
| Resource ID:       | KJ690776                    |
| Database:          | NCBI GenBank (DNA sequence) |
| Save to directory: |                             |
| Output format:     | gb                          |

OK Cancel Help

After you click the *OK* button, UGENE downloads the biological objects and adds it to the current *project*.