

A protocol for entering sequences into UGENE

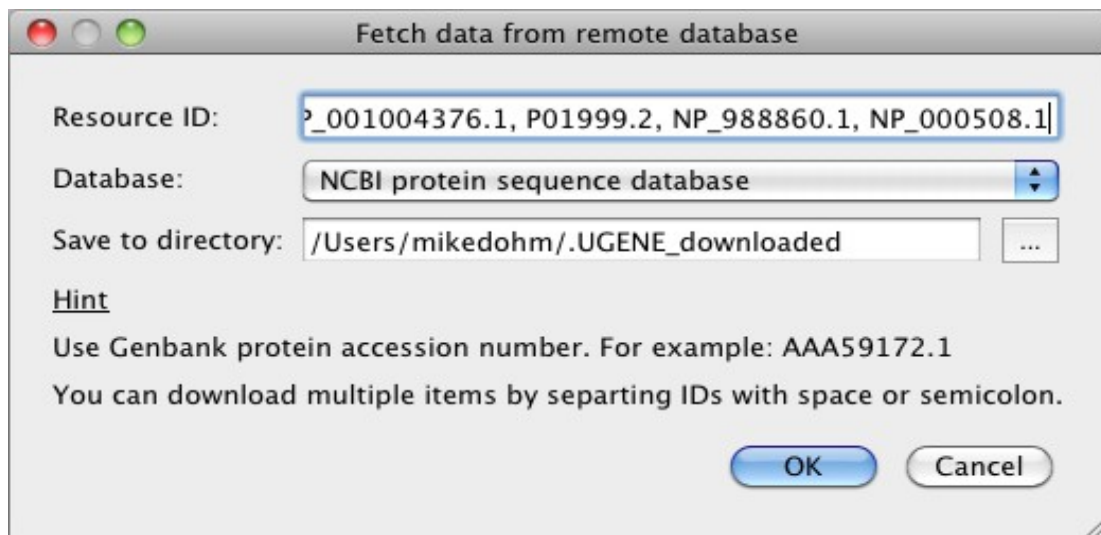
UGENE SOP 1
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For simplicity, this SOP pertains to protein sequences. The protocol for nucleotide sequences would be similar.

This SOP assumes you already have obtained accession numbers of all sequences you want to work with.

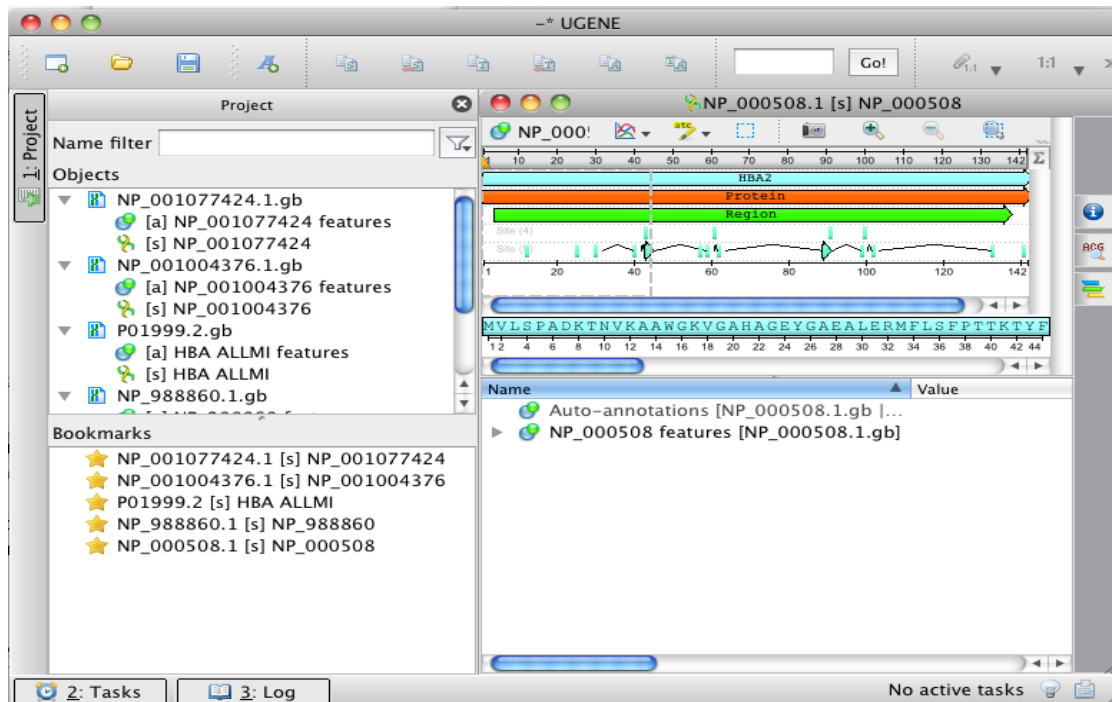
Images of UGENE are from the Mac version.

1. Start UGENE application
2. Select File --> Access Remote database ...

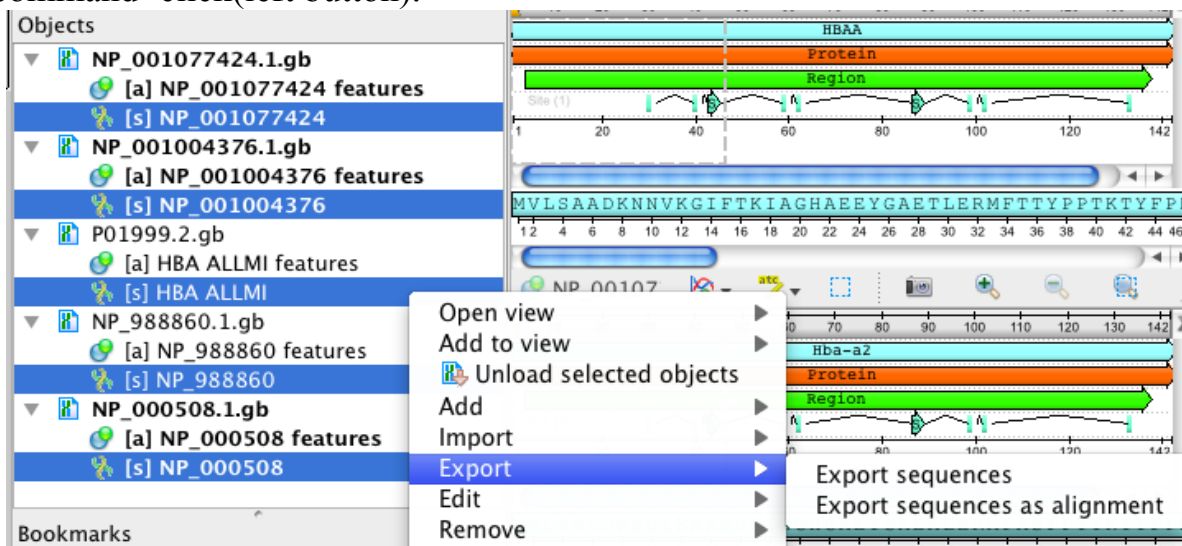


3. Enter accession numbers separated by comma in the Resource ID window.
4. Select the correct NCBI database; protein sequence, in this case.
5. Select a directory you wish to save the file to, then click "OK" button to proceed. You should see something that looks like the following image: in the upper left pane, a list of objects, in the lower left pane, a list of bookmarks, and in the main window, a view of the highlighted sequence (look in the left pane for the bold-type face object = highlighted sequence). UGENE will not allow you to do much of anything at this point (see step 6), but you can click on each object then view that object by right-clicking on it and making a selection (e.g, open view).

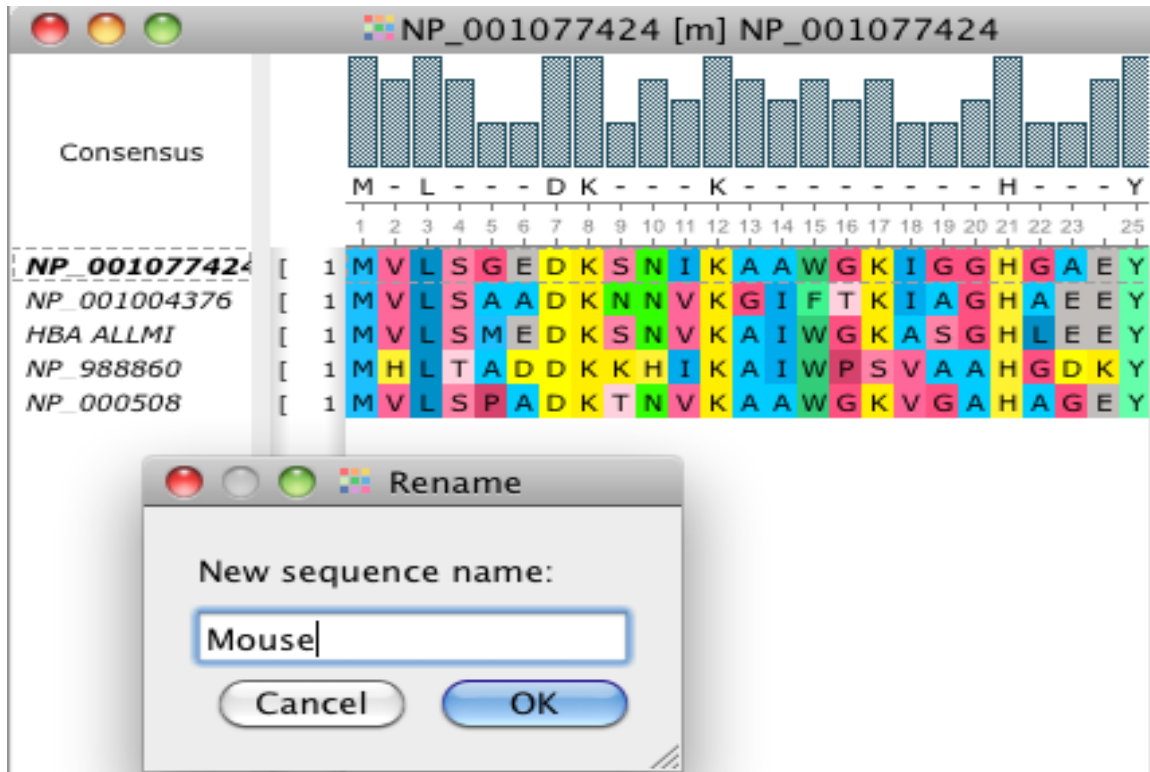
Do save the project at this step by selecting File --> Save project as...



6. In order to work with the sequences in UGENE, you need to work copies of your files. There are a couple of ways to do this in UGENE so I will show you one way. Highlight the sequences marked by [s] in the object pane. To select multiple sequences, use command+click(left button).



7. Once the sequences have been selected, right-click in the Object pane to bring up the sub-menu, select Export then either (a) Export sequences or (b) Export sequences as alignment. Because I want to align the sequences I select the second option (b).
8. A new sub-menu pops up providing export options; I select the filename and directory to save the file. I also select the kind of alignment routine here (default is CLUSTALW). Make sure to include the file in your project (default check box). Click OK and the alignment should show up in the main pane.
9. I want to change the tree tips from the accession numbers to taxon names; I can do this by clicking on the accession text for each row, then renaming the text as shown in the next image.



10. In now wish to generate a neighbor joining distance tree. Select the “tree” icon from the menu bar in UGENE (shown in the next imageand marked by the red arrow).



11. From the tree pop-up menu, the default choice is PHYLIP Neighbor Joining. Select appropriate options (e.g.,substitutions, algorithm) and save the tree in Newick (.nwk) format in the directory of your choice on your computer.

