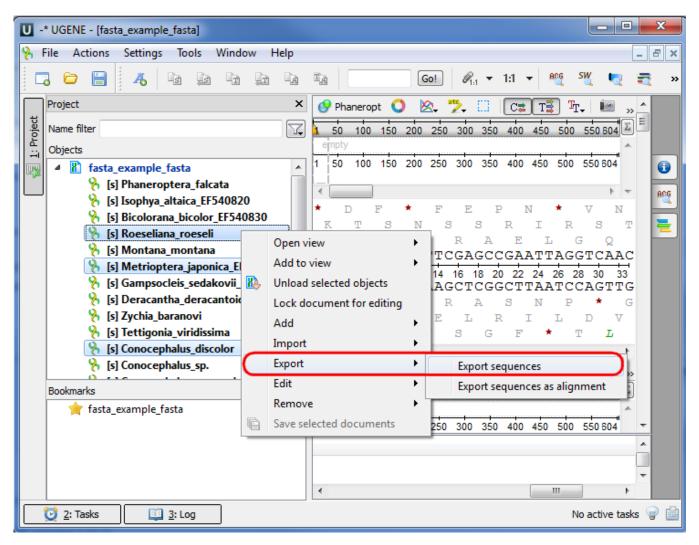
Exporting Sequences to Sequence Format

Select a single or several sequence objects in the Project View window and click the Export Export sequences context menu item:



The Export Selected Sequences dialog will appear:

U Export Selected Sequences		? X
Export to file	C:/work/ugene/data/samples/FASTA/human_T1_region_new.fa	
File format to use	FASTA	•
Export with annotations		
Add document to the project		
Use custom sequence name	human_T1_region	
Convertion options		
Save direct strand	Save complement strand	
Translate to amino alphabet	✓ Save all amino frames	
Use custom translation table	1. The Standard Genetic Code	-
Merge options		
	Marga acquiances	
Save as separate sequences		
Add gap symbols between sequences 0		
	Export Cancel	Help

Here you can select the location of the result file and a sequence file format. You can choose to add newly created document to the current project, export sequence with annotations or without annotations and use custom sequence name. To do it check the corresponding checkboxes.

Use the Conversion options to choose a strand for saving sequence(s). Also you can translate sequence(s) to amino alphabet.

Also it is possible to specify whether to merge the exported sequences into a single sequence or store them as separate sequences. If you merge the sequences, you're allowed to select the gap symbols between sequences. This is the length of the insertion region between sequences that contain N sym bols for nucleic or X for protein sequences.