

# Extract Transcript Sequences

This workflow uses input transcripts and genomic sequences to generate a FASTA file with the DNA sequences for the transcripts. Please make sure that contig or chromosome names in the transcript file(s) have corresponding entries in the input sequence(s).



## How to Use This Sample

If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.

## Workflow Sample Location

The workflow sample "Extract Transcript Sequences" can be found in the "NGS" section of the Workflow Designer samples.

## Workflow Image

The workflow looks as follows:

