

# Get Amino Translations of a Sequence

The workflow takes a nucleotide sequence as input and returns two files: translations of the sequence and translations of the complement sequence.

## How to Use This Sample

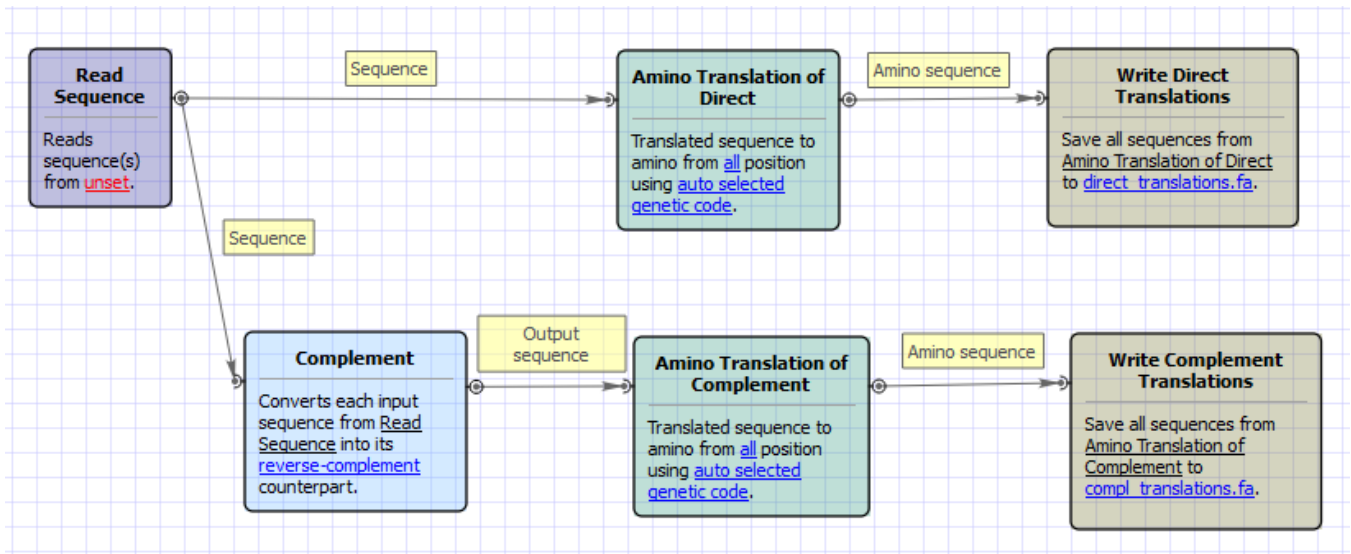
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

The workflow sample "Get Amino Translations of a Sequence" can be found in the "Scenarios" section of the Workflow Designer samples.

## Workflow Image

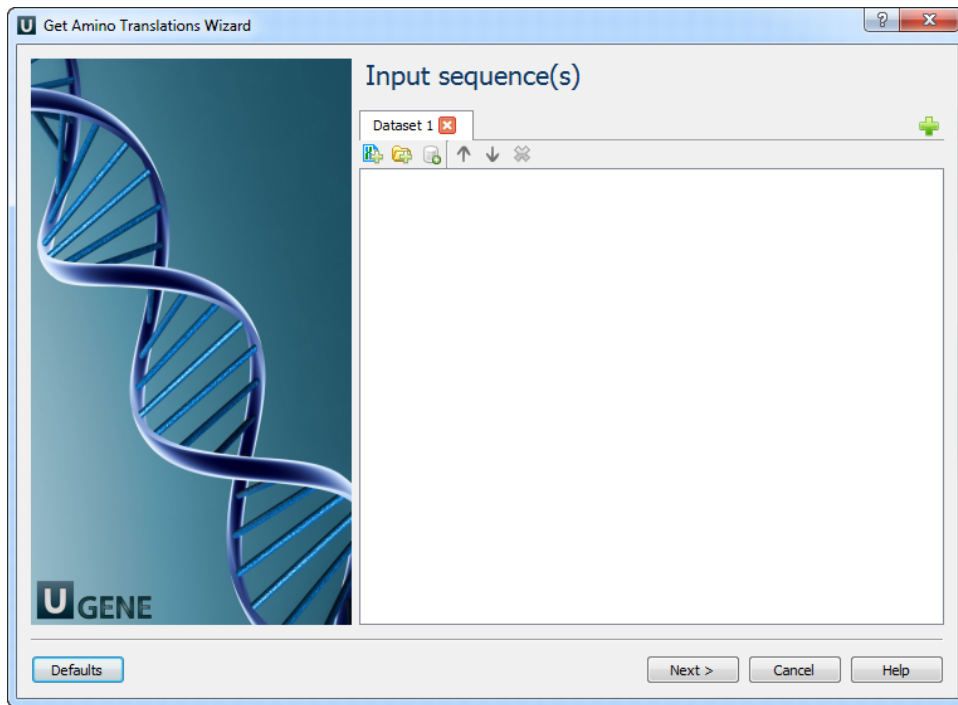
The opened workflow looks as follows:



## Workflow Wizard

The wizard has 2 pages.

1. Input sequence(s): On this page you must input sequence(s).



2. Output Data: On this page you can modify result files settings.

