

# Convert Alignments to ClustalW

This workflow converts multiple alignment file(s) of any format to ClustalW document(s). If source file is a sequence format (e.g. FASTA), all contained sequences are added to the result alignment. Yet no real alignment is performed, this particular workflow illustrates pure data format conversion.

## How to Use This Sample

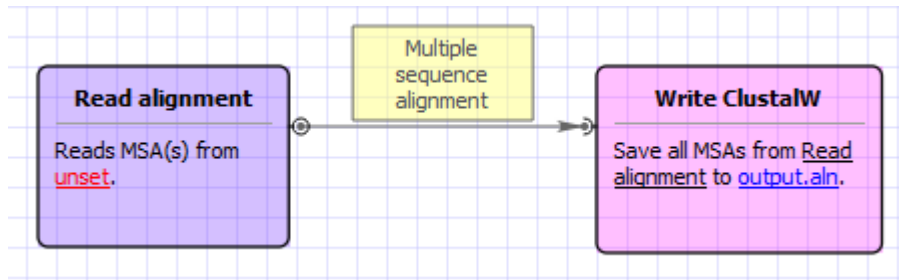
If you haven't used the workflow samples in UGENE before, look at the "[How to Use Sample Workflows](#)" section of the documentation.

## Workflow Sample Location

The workflow sample "Convert Alignments to ClustalW" can be found in the "Conversions" section of the Workflow Designer samples.

## Workflow Image

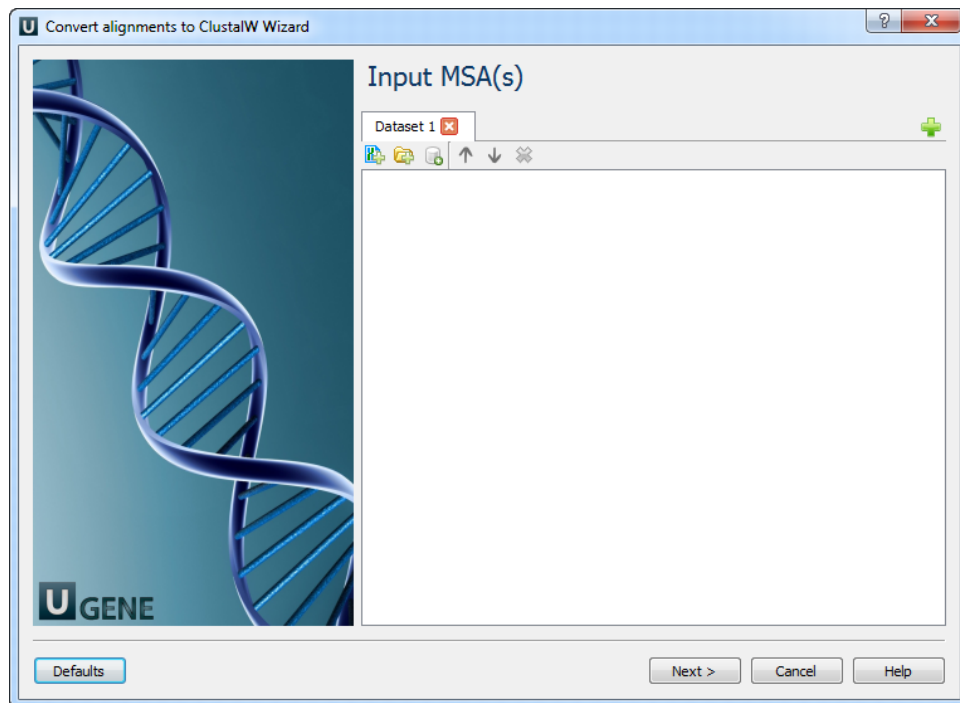
The workflow looks as follows:



## Workflow Wizard

The wizard has 2 pages.

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



2. Output data: On this page you can modify output settings.

