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.

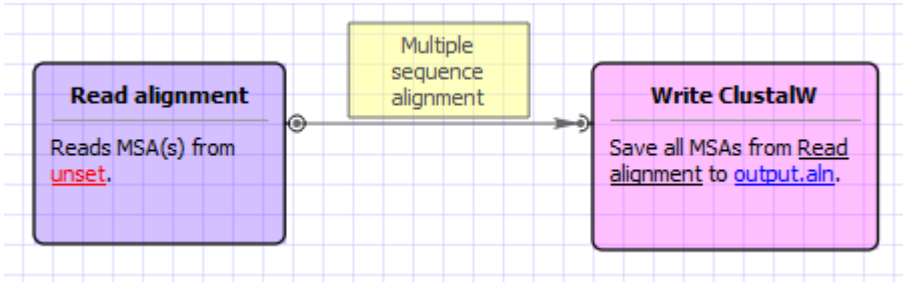
> **How to Use This Sample**
>
> If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

Workflow Sample Location

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

Workflow Image

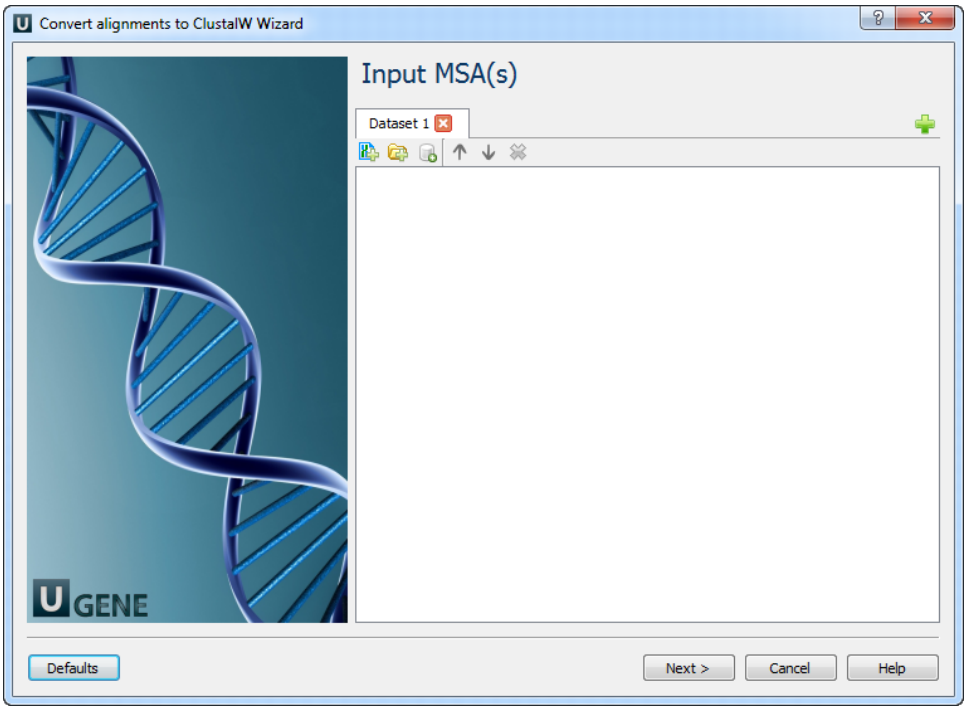
The workflow looks as follows:



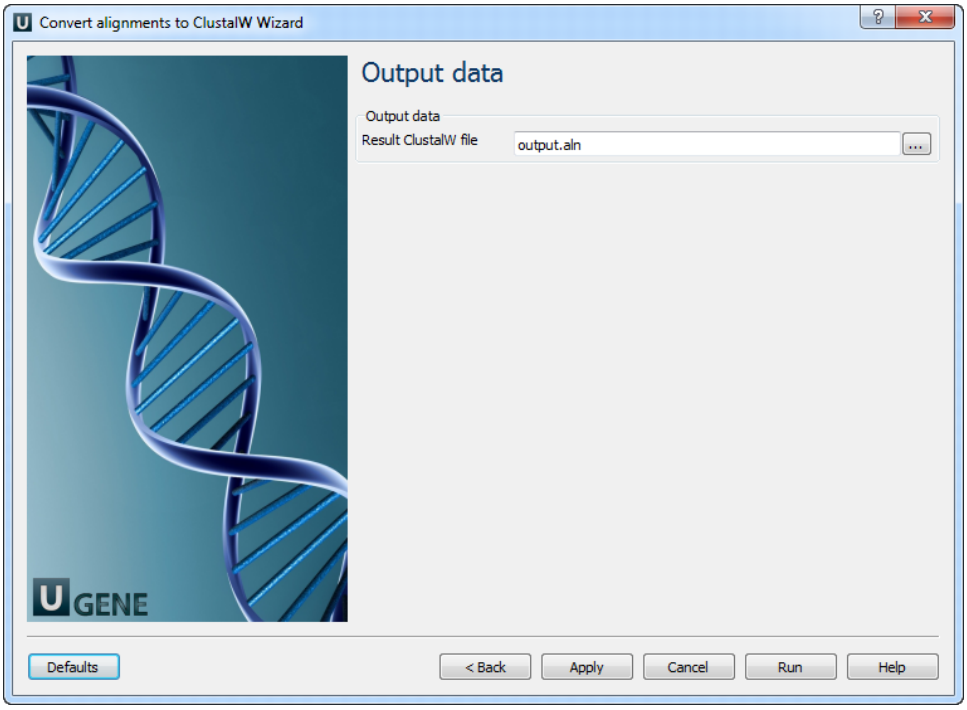
Workflow Wizard

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.


Convert alignments to ClustalW Wizard
Output data
Output data
Result ClustalW file
output.aln
...
UGENE
Defaults
< Back
Apply
Cancel
Run
Help