

# Align with MUSCLE Element

MUSCLE is public domain multiple alignment software for protein and nucleotide sequences. MUSCLE stands for MULTiple Sequence Comparison by Log-Expectation.

## Parameters in GUI

Parameter	Description	Default value
<b>Mode</b>	Selector of preset configurations, that give you the choice of optimizing accuracy, speed, or some compromise between the two. The default favors accuracy.	MUSCLE default
<b>Stable order</b>	Do not rearrange aligned sequences (-stable switch of MUSCLE). Otherwise, MUSCLE re-arranges sequences so that similar sequences are adjacent in the output file. This makes the alignment easier to evaluate by eye.	True

## Parameters in Workflow File

Type: muscle

Parameter	Parameter in the GUI	Type
<b>mode</b>	<b>Mode</b>	<i>numeric</i>  Availables values are: <ul style="list-style-type: none"><li>• 0 - for MUSCLE default</li><li>• 1 - for Large alignment</li><li>• 2 - for Refine only</li></ul>
<b>stable</b>	<b>Stable order</b>	<i>boolean</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** *Input MSA*

**Name in Workflow File:** in-msa

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>MSA</b>	<b>msa</b>	<i>msa</i>

And 1 *output port*:

**Name in GUI:** *Multiple sequence alignment*

**Name in Workflow File:** out-msa

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>MSA</b>	<b>msa</b>	<i>msa</i>