# 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.

**Element type:** muscle

## Parameters

| Parameter | Description | Default value | Parameter in Workflow File | Type |
|---|---|---|---|---|
| **Mode** | 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 | **mode** | *numeric*<br><br>Availables values are:<br>• 0 - for MUSCLE default<br>• 1 - for Large alignment<br>• 2 - for Refine only |
| **Stable order** | 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 | **stable** | *boolean* |

# 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 |
|---|---|---|
| **MSA** | **msa** | *msa* |

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 |
|---|---|---|
| **MSA** | **msa** | *msa* |