

# Align with Kalign Element

Aligns multiple sequence alignments (MSAs) supplied with Kalign. Kalign is a fast and accurate multiple sequence alignment tool. The original version of the tool can be found on <http://msa.sbc.su.se>.

**Element type:** kalign

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Gap extension penalty</b>	The penalty for extending a gap.	8.52	<b>gap-ext-penalty</b>	<i>numeric</i>
<b>Gap open penalty</b>	The penalty for opening/closing a gap. Half the value will be subtracted from the alignment score when opening, and half when closing a gap.	54.90	<b>gap-open-penalty</b>	<i>numeric</i>
<b>Terminal gap penalty</b>	The penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.	4.42	<b>terminal-gap-penalty</b>	<i>numeric</i>
<b>Bonus score</b>	A bonus score that is added to each pair of aligned residues.	0.02	<b>bonus-score</b>	<i>numeric</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:** *Kalign result MSA*

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

**Slots:**

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