

# Amino Acid Translation Element

Translates a sequence into its amino translation or translations.

**Element type:** sequence-translation

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Translate from</b>	Specifies position that should be used to translate the sequence from: first, second, third or all (three output amino sequences would be generated).	all	<b>pos-2-translate</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• all</li><li>• first</li><li>• second</li><li>• third</li></ul>
<b>Auto selected genetic code</b>	Specifies that genetic code should be selected automatically.	True	<b>auto-translation</b>	<i>boolean</i>
<b>Genetic code</b>	Genetic code that should be used to translate the input nucleotide sequence.	The Standard Genetic Code	<b>genetic-code</b>	<i>string</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** *Input Data*

**Name in Workflow File:** in-sequence

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>

And 1 *output port*:

**Name in GUI:** *Amino sequence*

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

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>
<b>Plain text</b>	<b>text</b>	<i>string</i>