

# Get Sequences by Annotations Element

Extracts annotated regions from input sequence.

## Parameters in GUI

Parameter	Description	Default value
<b>Translate</b>	Translates the annotated regions if the corresponding annotation marks a protein subsequence.	False
<b>Complement</b>	Complements the annotated regions if the corresponding annotation is located on the complement strand.	False
<b>Split joined</b>	Split joined annotations to single region annotations.	False
<b>Extend left</b>	Extends the resulted regions to left.	0
<b>Extend right</b>	Extends the resulted regions to right.	0
<b>Gap length</b>	Inserts a gap of a specified length between the merged locations of the annotation.	0

## Parameters in Workflow File

**Type:** extract-annotated-sequence

Parameter	Parameter in the GUI	Type
<b>translate</b>	<b>Translate</b>	<i>boolean</i>
<b>complement</b>	<b>Complement</b>	<i>boolean</i>
<b>split-joined-annotations</b>	<b>Split joined</b>	<i>boolean</i>
<b>extend-left</b>	<b>Extend left</b>	<i>numeric</i>
<b>extend-right</b>	<b>Extend right</b>	<i>numeric</i>
<b>merge-gap-length</b>	<b>Gap length</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** *Input sequence*

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

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table</i>

And 1 *output port*:

**Name in GUI:** *Annotated regions*

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

**Slots:**

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