Get Sequences by Annotations Element

Extracts annotated regions from input sequence.

Parameters in GUI

Parameter	Description	Default value
Translate	Translates the annotated regions if the corresponding annotation marks a protein subsequence.	False
Complement	Complements the annotated regions if the corresponding annotation is located on the complement strand.	False
Split joined	Split joined annotations to single region annotations.	False
Extend left	Extends the resulted regions to left.	0
Extend right	Extends the resulted regions to right.	0
Gap length	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
translate	**Translate**	*boolean*
complement	**Complement**	*boolean*
split-joined-annotations	**Split joined**	*boolean*
extend-left	**Extend left**	*numeric*
extend-right	**Extend right**	*numeric*
merge-gap-length	**Gap length**	*numeric*

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
Sequence	**sequence**	*sequence*
Set of annotations	**annotations**	*annotation-table*

And 1 *output port*:

Name in GUI: *Annotated regions*

Name in Workflow File: out-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*