Get Sequences by Annotations Element

Extracts annotated regions from the input sequence.

Element type: extract-annotated-sequence

Parameters

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