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	Туре
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	Туре
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	Туре
Sequence	sequence	sequence