

Fetch Sequences by ID From Annotation Element

Parses annotations to find any IDs and fetches corresponding sequences.

Element type: fetch-sequence

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Save file to directory	The directory to store sequence files loaded from a database.	default	save-dir	<i>string</i>
NCBI database	The database to read from.	nucleotide Available values are: - nucleotide - protein	database	<i>string</i>

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Input annotations*

Name in Workflow File: in-annotations

Slots:

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

And 1 *output port*:

Name in GUI: *Sequence*

Name in Workflow File: out-sequence

Slots:

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