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**	*string*
NCBI database	The database to read from.	nucleotide Available values are: • nucleotide • protein	**database**	*string*

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**	*annotation-table*

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**	*annotation-table*
Sequence	**sequence**	*sequence*