Fetch Sequences by ID From Annotation Element

Parses annotations to find any IDs and fetches corresponding sequences.

Parameters in GUI

Parameter	Description	Default value
Save file to directory	The directory to store sequence files loaded from a database.	default
NCBI database	The database to read from.	nucleotide Available values are: • nucleotide • protein

Parameters in Workflow File

Type: fetch-sequence

Parameter	Parameter in the GUI	Type
save-dir	**Save file to directory**	*string*
database	**NCBI database**	*string*

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*