

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: <ul style="list-style-type: none">nucleotideprotein | 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 |