

# 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<br><br>Available values are: <ul style="list-style-type: none"><li>• nucleotide</li><li>• protein</li></ul> |

## Parameters in Workflow File

**Type:** fetch-sequence

| Parameter | Parameter in the GUI   | Type          |
|-----------|------------------------|---------------|
| save-dir  | Save file to directory | <i>string</i> |
| database  | NCBI database          | <i>string</i> |

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>         |