# Read Sequence Element

Input one or several files with nucleotide or protein sequences.

A file may also contain annotations. Any format, supported by UGENE, is allowed (GenBank, FASTA, etc.).

The element outputs message(s) with the sequence and annotations data.

See the list of all available formats here.

## Parameters in GUI

| Parameter | Description | Default value |
|---|---|---|
| **Input files** | Semicolon-separated list of datasets to the input files. | |
| **Mode** | If the file contains more than one sequence, “split” mode sends them as is to output, while “merge” appends all the sequences and outputs the merged sequence. | Split |
| **Merging gap** | In the “merge” mode, inserts the specified number of gaps between the original sequences. This is helpful e.g. to avoid finding false positives at the merge boundaries. | 10 |
| **Sequence count limit** | Split mode only. Read only first N sequences from each file. Set 0 value for reading all sequences. | 0 |
| **Accession filter** | Only reports a sequence with the specified accession (id). | |

# Parameters in Workflow File

**Type:** read-sequence

| Parameter | Parameter in the GUI | Type |
|---|---|---|
| **url-in** | **Input files** | *string* |
| **mode** | **Mode** | *numeric*<br>Available values are:<br>• 0 - for split mode<br>• 1 - for merge mode |
| **merge-gap** | **Merging gap** | *numeric* |
| **sequence-count-limit** | **Sequence count limit** | *numeric* |
| **accept-accession** | **Accession filter** | *string* |

# Input/Output Ports

The element has 1 *output port*:

**Name in GUI:** *Sequence*

**Name in Workflow File:** out-sequence

**Slots:**

| Slot In GUI | Slot in Workflow File | Type |
|---|---|---|
| **Sequence** | **sequence** | *sequence* |
| **Set of annotations** | **annotations** | *annotation-table* |
| **Source URL** | **url** | *string* |