

# 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](#).

**Element type:** read-sequence

## Parameters in GUI

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Input files</b>	Semicolon-separated list of datasets to the input files.		<b>url-in</b>	<i>string</i>
<b>Mode</b>	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	<b>mode</b>	<i>numeric</i>  Available values are: <ul style="list-style-type: none"><li>• 0 - for split mode</li><li>• 1 - for merge mode</li></ul>
<b>Merging gap</b>	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	<b>merge-gap</b>	<i>numeric</i>
<b>Sequence count limit</b>	Split mode only. Read only first N sequences from each file. Set 0 value for reading all sequences.	0	<b>sequence-count-limit</b>	<i>numeric</i>
<b>Accession filter</b>	Only reports a sequence with the specified accession (id).		<b>accept-accession</b>	<i>string</i>

## 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
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table</i>
<b>Source URL</b>	<b>url</b>	<i>string</i>