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* Available values are: • 0 - for split mode • 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*