## **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	Туре
Input files	Semicolon-separated list of datasets to the input files.		url-in	string
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	mode	numeric  Available values are:  O - for split mode 1 - for merge mode
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	merge-gap	numeric
Sequence count limit	Split mode only. Read only first N sequences from each file. Set 0 value for reading all sequences.	0	sequence-count- limit	numeric
Accession filter	Only reports a sequence with the specified accession (id).		accept- accession	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	Туре
Sequence	sequence	sequence
Set of annotations	annotations	annotation-table
Source URL	url	string