Read Alignment Element

Input one or several files in one of the multiple sequence alignment formats, supported by UGENE (ClustalW, FASTA, etc.).

The element outputs message(s) with the alignment data.

See the list of all available formats here.

Parameters in GUI

Parameter	Description	Default value
Input files (required)	Semicolon-separated list of paths to the input files.	

Parameters in Workflow File

Type: read-msa

Parameter	Parameter in the GUI	Type
url-in	**Input files**	*string*

Input/Output Ports

The element has 1 *output port*:

Name in GUI: *Multiple sequence alignment*

Name in Workflow File: out-msa

Slots:

Slot In GUI	Slot in Workflow File	Type
MSA	**msa**	*msa*
Source URL	**url**	*string*