

Write Alignment Element

The element gets message(s) with alignment data and saves the data to the specified file(s) in one of the multiple sequence alignment formats, supported by UGENE (ClustalW, FASTA, etc.).

Element type: write-msa

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Data storage	Place to store workflow results: local file system or a database.		data-storage	<i>string</i>
Document format	Format of the output file.	clustal	document-format	<i>string</i> Available values are: • clustal • mega • msf • sam • srfasta • stockholm
Output file	Location of the output data file. If this parameter is set, then the "Location" slot is not taken into account.		url-out	<i>string</i>
Output file suffix	This suffix will be used for generating the output file name.		url-suffix	<i>string</i>
Existing file	If a target file already exists, you can specify how it should be handled: either overwritten, renamed or appended (if supported by file format).	Rename	write-mode	<i>numeric</i> Available values are: • 0 - for overwrite • 1 - for append • 2 - for rename

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Multiple sequence alignment*

Name in Workflow File: in-msa

Slots:

Slot In GUI	Slot in Workflow File	Type
MSA	msa	<i>msa</i>
Location	url	<i>string</i>