Write Sequence Element

Writes all supplied sequences to file(s) in selected format.

Parameters in GUI

Parameter	Description	Default value
Output file (required)	Location of the output data file. If this attribute is set, then the “Location” slot is not taken into account.	
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
Document format	Format of the output file.	fasta
Accumulate objects	Accumulates all incoming data in one file or creates separate files for each input. In the latter case, an incremental numerical suffix is added to a file name.	True

Parameters in Workflow File

Type: write-sequence

Parameter	Parameter in the GUI	Type
url-out	**Output file**	*string*
write-mode	**Existing file**	*numeric* Available values are: • 0 - for overwrite • 1 - for append • 2 - for rename
document-format	**Document format**	*string* Available values are: • fasta • fastq • genbank • raw
accumulate	**Accumulate objects**	*boolean*

Input/Output Ports

The element has 1 *input port*:

Name in GUI: *Sequence*

Name in Workflow File: in-sequence

Slots:

Slot In GUI	Slot in Workflow File	Type
Sequence	**sequence**	*sequence*
Location	**url**	*string*
Set of annotations	**annotations**	*annotation-table-list*