

# Write Sequence Element

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

## Parameters in GUI

Parameter	Description	Default value
<b>Data storage</b>	Place to store workflow results: local file system or a database.	
<b>Output file</b>	Location of the output data file. If this attribute is set, then the "Location" slot is not taken into account.	
<b>Output file suffix</b>	This suffix will be used for generating the output file name.	
<b>Existing file</b>	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
<b>Document format</b>	Format of the output file.	fasta
<b>Accumulate objects</b>	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
<b>Split sequence</b>	Split each incoming sequence on several parts.	1

## Parameters in Workflow File

Type: write-sequence

Parameter	Parameter in the GUI	Type
<b>data-storage</b>	<b>Data storage</b>	<i>string</i>
<b>url-out</b>	<b>Output file</b>	<i>string</i>
<b>url-suffix</b>	<b>Output file suffix</b>	<i>string</i>
<b>write-mode</b>	<b>Existing file</b>	<i>numeric</i>  Available values are: <ul style="list-style-type: none"><li>• 0 - for overwrite</li><li>• 1 - for append</li><li>• 2 - for rename</li></ul>
<b>document-format</b>	<b>Document format</b>	<i>string</i>  Available values are: <ul style="list-style-type: none"><li>• fasta</li><li>• fastq</li><li>• genbank</li><li>• raw</li></ul>
<b>accumulate</b>	<b>Accumulate objects</b>	<i>boolean</i>
<b>split</b>	<b>Split sequence</b>	<i>numeric</i>

## 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
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>
<b>Location</b>	<b>url</b>	<i>string</i>
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table-list</i>