

# Read Annotations Element

Input one or several files with annotations: a file may also contain a sequence (e.g. GenBank format) or contain annotations only (e.g. GTF format).

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

See the list of all available formats [here](#).

**Element type:** read-annotations

## Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
<b>Input file(s)</b>	Input files.	Dataset 1;	<b>url-in</b>	<i>string</i>
<b>Mode</b>	If the file contains more than one annotation table, Split mode sends them "as is" to the output, while Merge appends all the annotation tables and outputs the sole merged annotation table.  In Merge files is the same as Merge but it operates with all annotation tables from all files of one dataset.	Merge	<b>mode</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *output port*:

**Name in GUI:** Annotations

**Name in Workflow File:** out-annotations

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Set of annotations</b>	<b>annotations</b>	<i>annotation-table-list</i>
<b>Dataset name</b>	<b>dataset</b>	<i>string</i>
<b>Source URL</b>	<b>out-url</b>	<i>string</i>