

# Annotate with UQL Element

Analyzes a nucleotide sequence with a UGENE Query Language (UQL) workflow. The workflow specifies a set of features to search for and their positional relationship.

To learn more about UQL workflows read [UGENE Query Designer Manual](#).

## Parameters in GUI

Parameter	Description	Default value
<b>Workflow</b> (required)	UQL workflow file.	
<b>Merge</b>	Merges regions of each result into a single annotation.	False
<b>Offset</b>	If the <i>Merge</i> parameter is set to <i>True</i> , adds left and right offsets of the specified length to the annotation.	0

## Parameters in Workflow File

**Type:** query

Parameter	Parameter in the GUI	Type
<b>schema</b>	<b>Workflow</b>	<i>string</i>
<b>merge</b>	<b>Merge</b>	<i>boolean</i>
<b>offset</b>	<b>Offset</b>	<i>numeric</i>

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** *Input sequences*

**Name in Workflow File:** in-sequence

**Slots:**

Slot In GUI	Slot in Workflow File	Type
<b>Sequence</b>	<b>sequence</b>	<i>sequence</i>

And 1 *output port*:

**Name in GUI:** *Result 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</i>