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
Workflow (required)	UQL workflow file.	
Merge	Merges regions of each result into a single annotation.	False
Offset	If the *Merge* parameter is set to *True*, 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
schema	**Workflow**	*string*
merge	**Merge**	*boolean*
offset	**Offset**	*numeric*

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
Sequence	**sequence**	*sequence*

And 1 *output port*:

Name in GUI: *Result annotations*

Name in Workflow File: out-annotations

Slots:

Slot In GUI	Slot in Workflow File	Type
Set of annotations	**annotations**	*annotation-table*