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.

Element type: query

Parameters

Parameter	Description	Default value	Parameter in Workflow File	Type
Workflow (required)	UQL workflow file.		**schema**	*string*
Merge	Merges regions of each result into a single annotation.	False	**merge**	*boolean*
Offset	If the *Merge* parameter is set to *True*, adds left and right offsets of the specified length to the annotation.	0	**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*