

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	<i>string</i>
Merge	Merges regions of each result into a single annotation.	False	merge	<i>boolean</i>
Offset	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	offset	<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
Sequence	sequence	<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
Set of annotations	annotations	<i>annotation-table</i>