

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> |