# Convert UQL Schema Results to Alignment

This schema allows to analyze sequence with Query and save results as alignment of selected features.

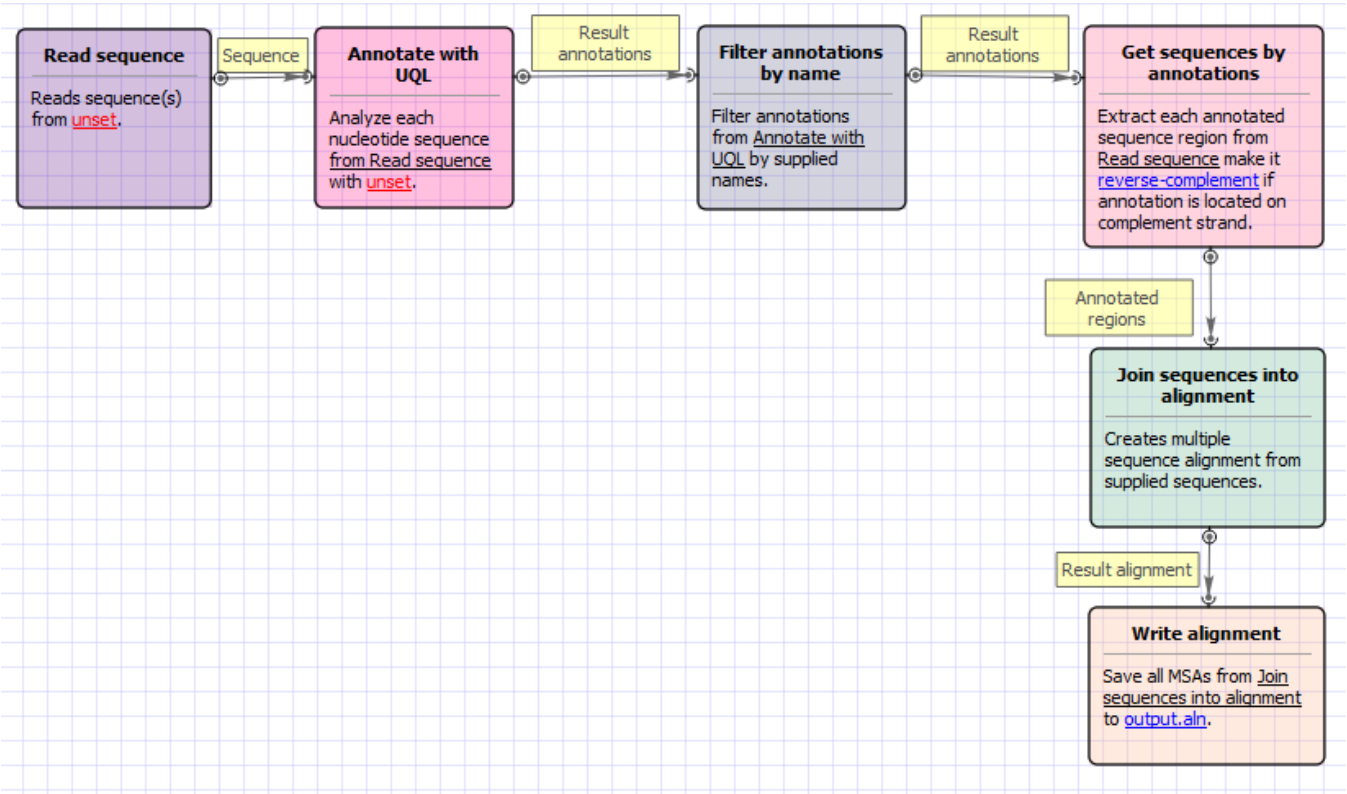
> **How to Use This Sample**
>
> If you haven't used the workflow samples in UGENE before, look at the "How to Use Sample Workflows" section of the documentation.

## Workflow Sample Location

The workflow sample "Convert UQL Schema Results to Alignment" can be found in the "Conversions" section of the Workflow Designer samples.

## Workflow Image

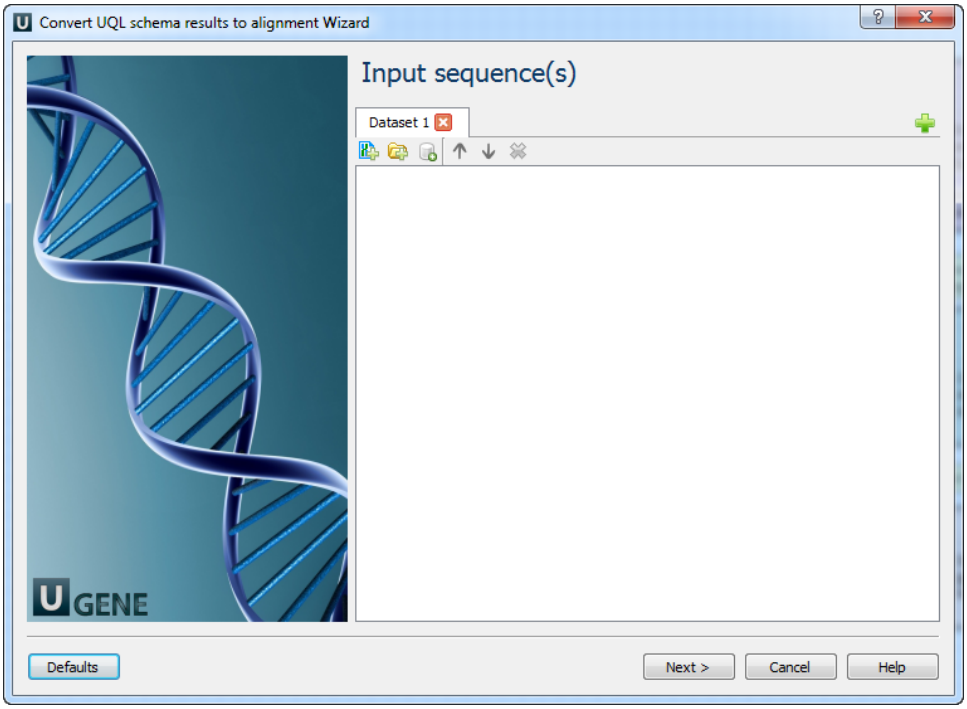
The workflow looks as follows:



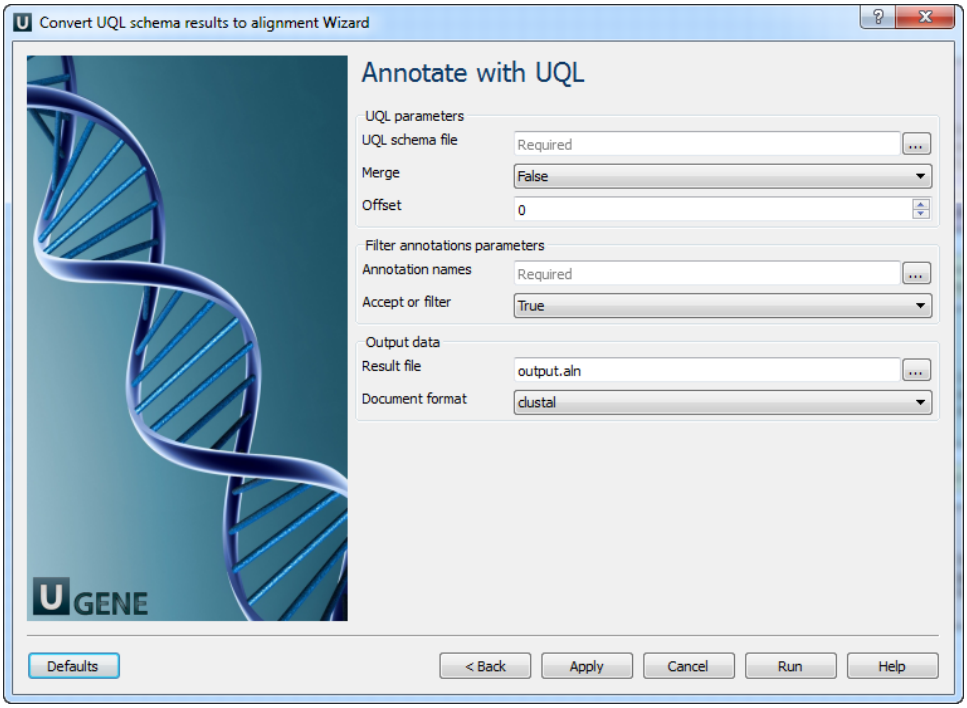

## Workflow Wizard

The wizard has 2 pages.

1. Input sequence(s): On this page you must input sequence(s).




2. Annotate with UQL: On this page you can modify annotation and output settings.




The following parameters are available:

| | |
|---|---|
| UQL schema file | Schema file. |
| Merge | Merges regions of each result into single annotation if true. |
| Offset | Specifies left and right offsets for merged annotation (if 'Merge' parameter is set to true). |
| Annotation names | File with annotation names, separated with whitespaces or list of annotation names which will be accepted or filtered. Use space as the separator. |
| Accept or filter | Selects the name filter: accept specified names or accept all except specified. |

| | |
|---|---|
| Result file | Location of output data file. If this attribute is set, slot "Location" in port will not be used. |
| Document format | Document format of output file. |