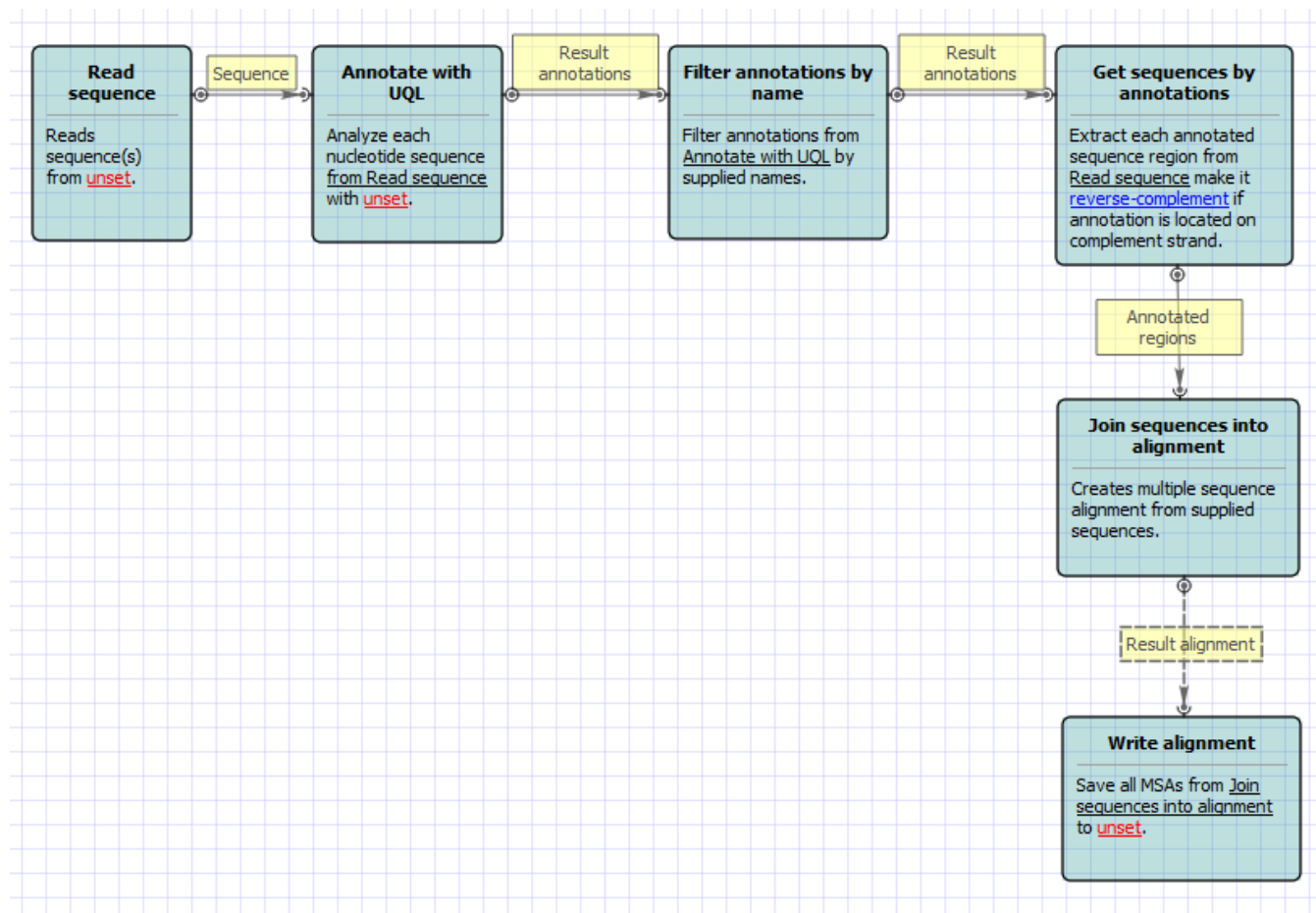


# Convert UQL Schema Results to Alignment

This schema allows to analyze sequence with Query and save results as alignment of selected features.  
To execute the workflow do the following:

1. Select "Sequence Reader" task and specify source file at "URL" field in the Property Editor.
2. Select "Annotate with UQL" task and specify the URL of the UQL schema file.
3. Select "Filter annotations by name" task and specify the name of features to be joined into alignment.
4. Select "Join sequences into alignment" task and specify the URL of the result file.



## 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.