

# Filter Sequence That Match a Pattern

Using this workflow you can select (or reject) only those sequence that match any pattern you input.



## How to Use This Sample

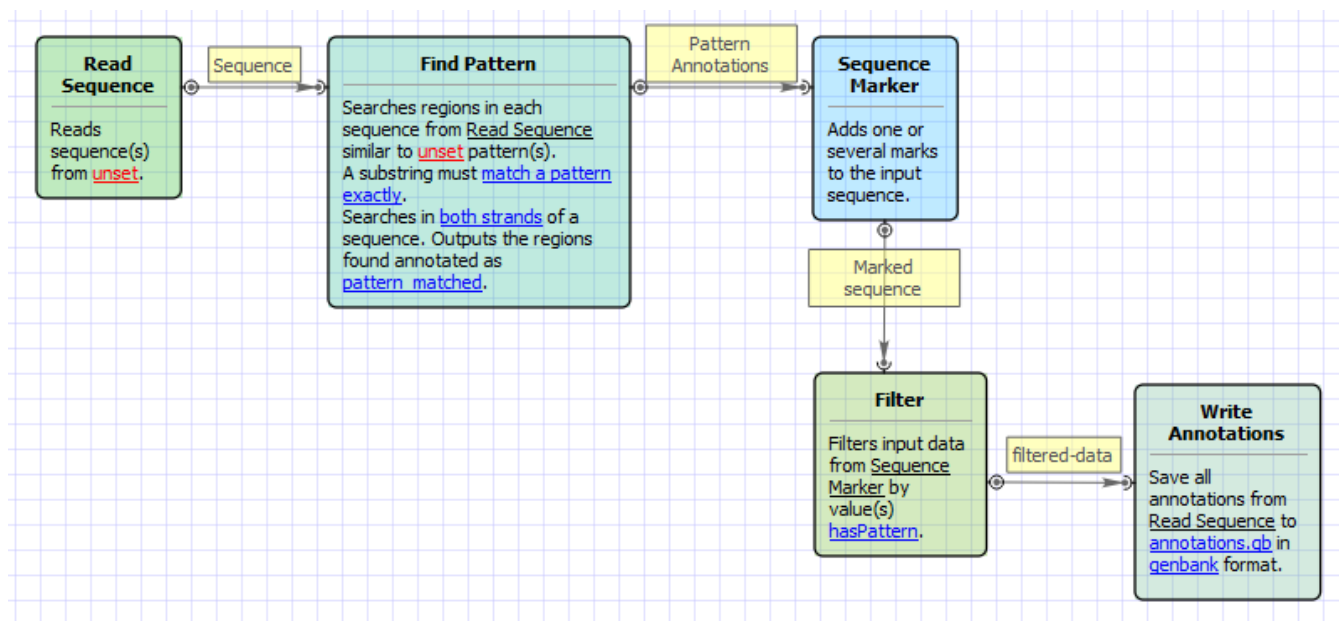
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

The workflow sample "Filter Sequence That Match a Pattern" can be found in the "Scenarios" section of the Workflow Designer samples.

## Workflow Image

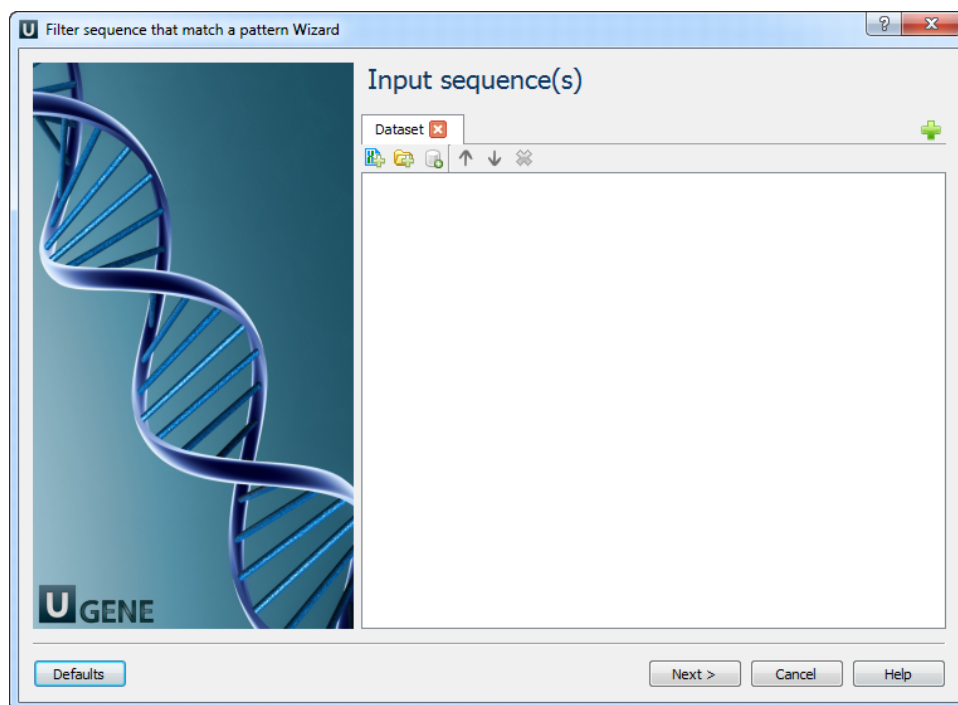
The workflow looks as follows:



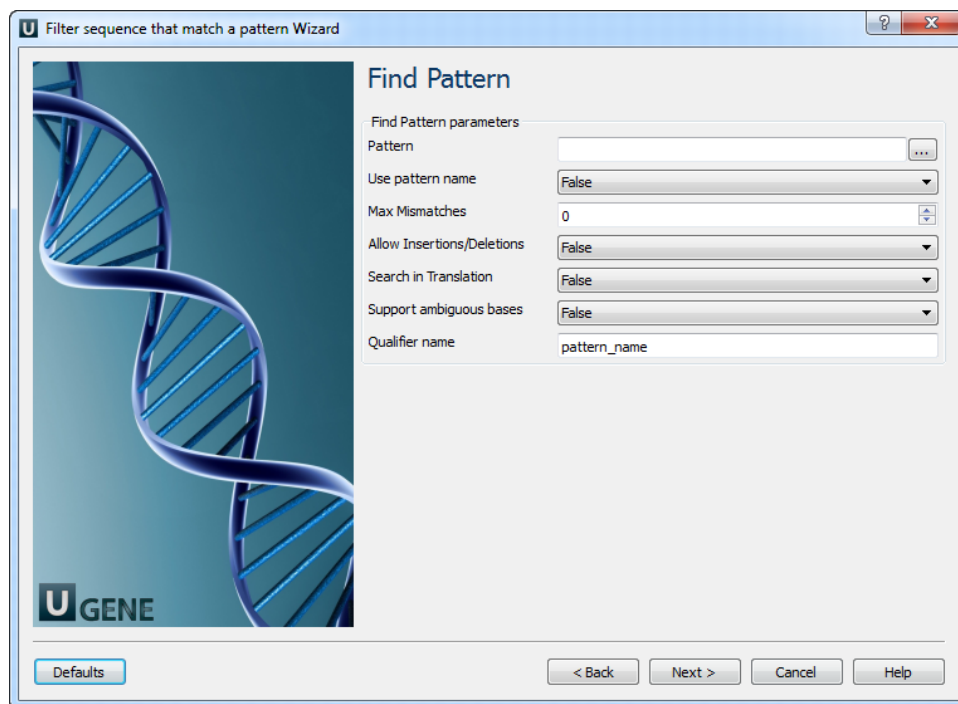
## Workflow Wizard

The wizard has 3 pages.

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



2. Find pattern: On this page you must input pattern(s) and you can modify searching parameters.



The following parameters are available:

|                             |                                                                                                                                          |
|-----------------------------|------------------------------------------------------------------------------------------------------------------------------------------|
| Pattern                     | Semicolon-separated list of patterns to search for.                                                                                      |
| Use pattern name            | If patterns are loaded from a file, use names of pattern sequences as annotation names. The name from the parameters is used by default. |
| Max Mismatches              | Maximum number of mismatches between a substring and a pattern.                                                                          |
| Allow Insertions /Deletions | Takes into account possibility of insertions/deletions when searching. By default substitutions are only considered.                     |
| Search in Translation       | Translates a supplied nucleotide sequence to protein and searches in the translated sequence.                                            |

|                         |                                                                                                                          |
|-------------------------|--------------------------------------------------------------------------------------------------------------------------|
| Support ambiguous bases | Performs correct handling of ambiguous bases. When this option is activated insertions and deletions are not considered. |
| Qualifier name          | Name of qualifier in result annotations which is containing a pattern name.                                              |

3. Output data: On this page you can modify output parameters.

