

# In Silico PCR Sample

This workflow simulates the PCR process.



## How to Use This Sample

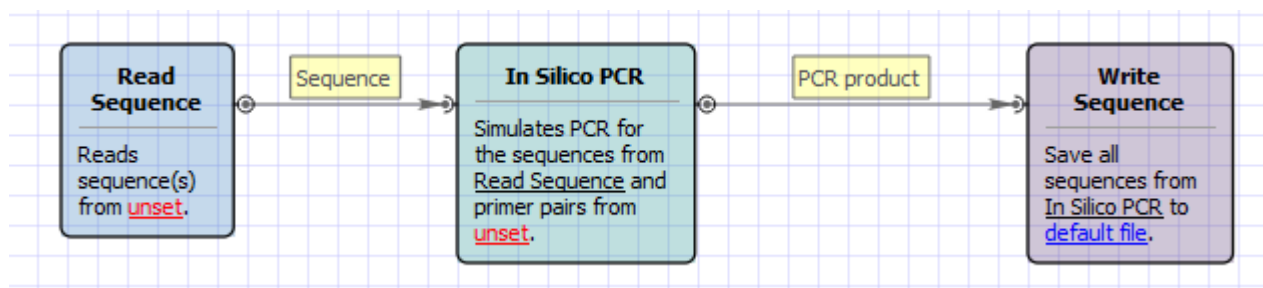
If you haven't used the workflow samples in UGENE before, look at the ["How to Use Sample Workflows"](#) section of the documentation.

## Workflow Sample Location

The workflow sample "In Silico PCR" can be found in the "Scenarios" section of the Workflow Designer samples.

## Workflow Image

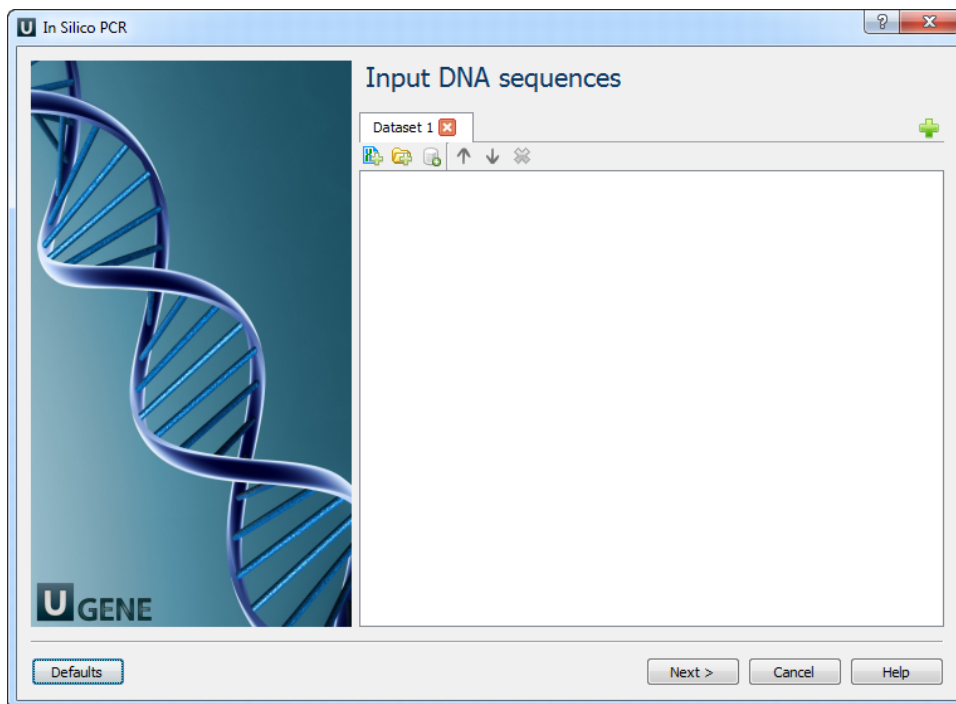
The opened workflow looks as follows:



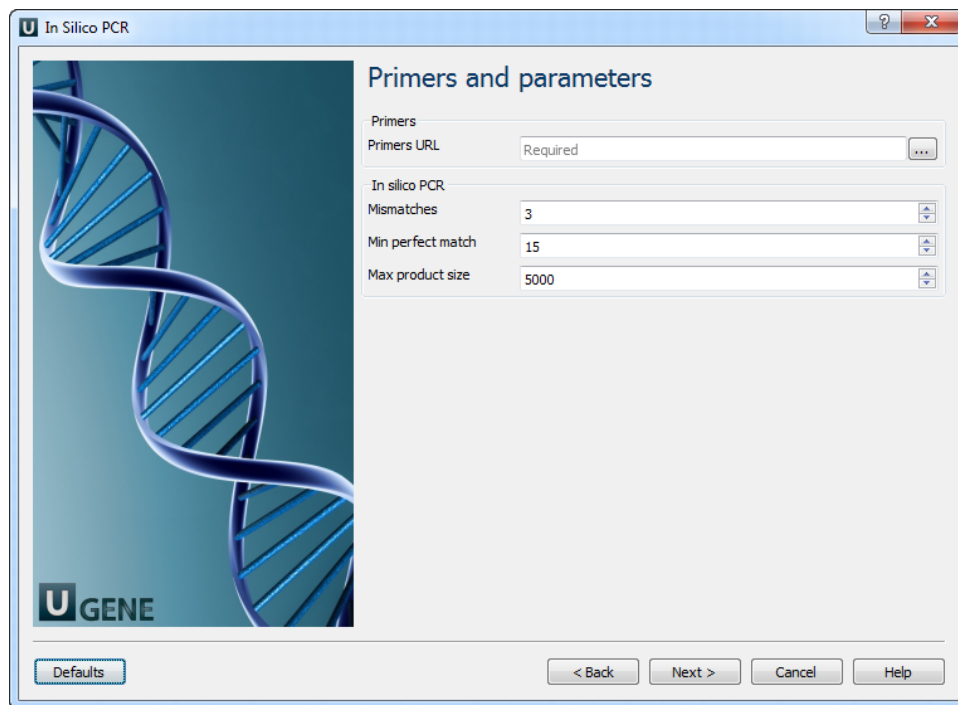
## Workflow Wizard

The wizard has 3 pages.

1. Input DNA Sequences: On this page you must input DNA sequences.



2. Primers and Parameters: Here you must input *Primers* and you can optionally modify *In Silico PCR* parameters.



The following parameters are available:

|                     |  |
|---------------------|--|
| Primers URL         | A URL to the input file with primer pairs.               |
| Mismatches          | Number of allowed mismatches.                            |
| Min perfect match   | Number of bases that match exactly on 3' end of primers. |
| Max product size    | Maximum size of amplified region.                        |
| Use ambiguous bases | Search for ambiguous bases (as "N") if checked.          |

The input primers file should be in the FASTA format and contain an even number of primers (because each pair should have forward and reverse primers).

Example format:

```
>forward
CTTGATGAATGGCCGCACG
>reverse
GATGTAGCGGGTCGTAGTGG
```

3. Output data: Here you can see information about output data.

