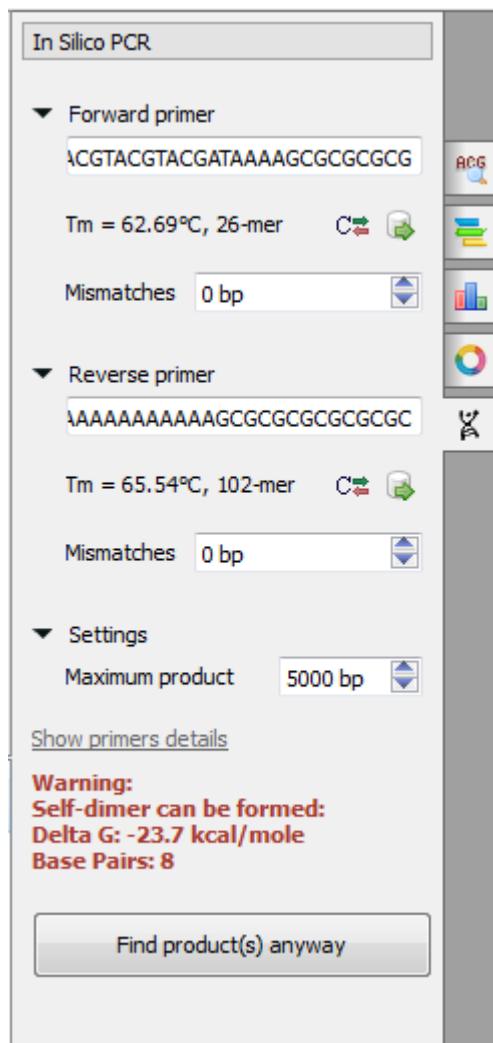


# In Silico PCR

## In Silico PCR Overview

In silico PCR is used to calculate theoretical polymerase chain reaction (PCR) results using a given set of primers (probes) to amplify DNA sequences.

UGENE provides the In silico PCR feature only for nucleic sequences. To use it in UGENE open a DNA sequence and go to the *In silico PCR* tab of the Options Panel:



There are the following parameters:

*Forward primer* - forward primer.

*Reverse primer* - on the opposite strand from the forward primer.

*Mismatches* - mismatches limit.

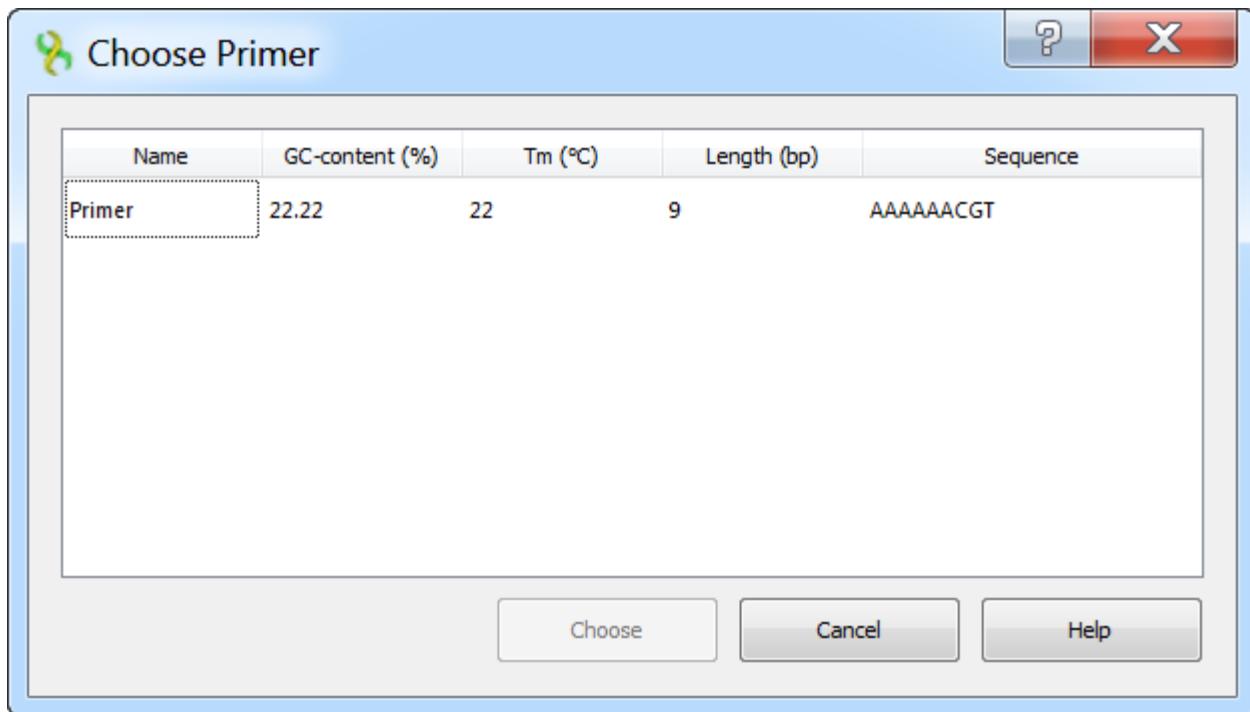
*Maximum product* - maximum size of amplified sequence.

## Choosing primers

Type two primers for running In Silico PCR. If the primers pair is invalid for running the PCR process then the warning is shown. Also, primers for the running In silico PCR can be chosen from a [primer library](#). Click the following button to choose a primer from the primers library:

A screenshot of a software interface for primer analysis. It shows a primer sequence: `ACACACGTACTGACAGTCAGCATAACG`. Below the sequence, it says  $Tm = 61.39^{\circ}\text{C}$ , 28-mer. There are two small buttons: one for reverse complement (`CR`) and one for copy (`copy`). At the bottom, it says "Mismatches 7 bp". A red arrow points from the text "Click the Reverse-complement button for making a primer sequence reverse-complement:" to the `CR` button.

The following dialog will appear:



The table consists of the following columns: name, GC-content (%), Tm, Length (bp) and sequence. Select primer in the table and click the *Choose* button.

Click the *Reverse-complement* button for making a primer sequence reverse-complement:

A screenshot of an "In Silico PCR" dialog. It shows a primer sequence: `ACACACGTACTGACAGTCAGCATAACG`. Below the sequence, it says  $Tm = 61.39^{\circ}\text{C}$ , 28-mer. There are two small buttons: one for reverse complement (`CR`) and one for copy (`copy`). A red arrow points from the text "Click the Reverse-complement button for making a primer sequence reverse-complement:" to the `CR` button.

Click *Show primers details* for seeing [statistic details](#) about primers.

When you run the process, the predicted PCR products appear in the products table.

## Products table

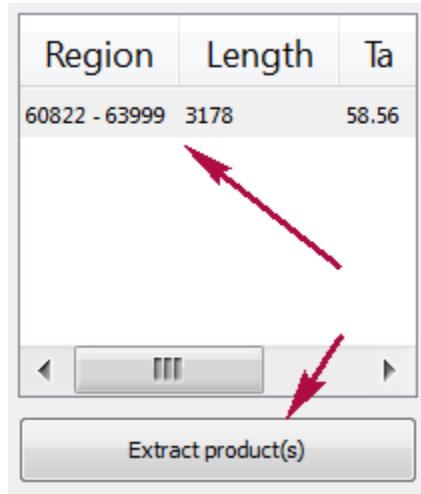
There are three columns in the table:

- region of product in the sequence
- product length
- preferred annealing temperature

Click the product for navigating to its region in the sequence.

Click the *Extract product(s)* button for exporting a product(s) in a file or use double click for that.

Region	Length	Ta
60822 - 63999	3178	58.56



The screenshot shows a software window with a table and some navigation controls. The table has three columns: 'Region', 'Length', and 'Ta'. The first row contains the values '60822 - 63999', '3178', and '58.56'. Below the table are several buttons: a left arrow, a right arrow, a vertical ellipsis, and a horizontal ellipsis. At the bottom is a button labeled 'Extract product(s)'. Red arrows from the accompanying text point to the 'Region' column in the table and the 'Extract product(s)' button.

- Primers Details
- Primer Library