## **In Silico PCR Element**

Simulates PCR for input sequences and primer pairs. Creates the table with the PCR statistics.

Element type: in-silico-pcr

## **Parameters**

| Parameter           | Description  | Default value | Parameter in Workflow File | Туре    |
|---------------------|--|---------------|----------------------------|---------|
| Primers URL         | A URL to the input file with primer pairs.               |               | primers-url                | string  |
| Report URL          | A URL to the output file with the PCR report.            |               | report-url                 | string  |
| Mismatches          | Number of allowed mismatches.                            | 3             | mismatches                 | numeric |
| Min perfect match   | Number of bases that match exactly on 3' end of primers. | 15            | perfect-match              | numeric |
| Max product size    | Maximum size of amplified region.                        | 5000          | max-product                | numeric |
| Use ambiguous bases | Search for ambiguous bases (as \"N\") if checked.        | True          | use-ambiguous-bases        | boolean |
| Extract annotations | Extract annotations within a product region.             | Inner         | extract-annotations        | string  |

## Input/Output Ports The element has 1 input port.

Name in GUI: Input sequence

Name in Workflow File: in-sequence

Slots:

| Slot In GUI | Slot in Workflow File | Туре     |
|-------------|-----------------------|----------|
| Sequence    | sequence              | sequence |

And 1 output port:

Name in GUI: PCR product Name in Workflow File: out

Slots:

| Slot In GUI        | Slot in Workflow File | Туре                 |
|--------------------|-----------------------|----------------------|
| Set of annotations | annotations           | annotation-<br>table |
| Sequence           | sequence              | sequence             |