# Map Reads with UGENE Genome Aligner Element

Unique UGENE algorithm for aligning short reads to reference genome.

**Element type:** genome-aligner

## Parameters

| Parameter | Description | Default value | Parameter in Workflow File | Type |
|---|---|---|---|---|
| **Output file name** | Base name of the output file. 'out.sam' by default. | out.sam | **outname** | *string* |
| **Reference genome** | Path to an indexed reference genome. | | **reference** | *string* |
| **Is absolute mismatches values?** | **true** - absolute mismatches mode is used<br><br>**false** - percentage mismatches mode is used<br><br>You can choose absolute or percentage mismatches values mode. | True | **if-absolute-mismatches-value** | *boolean* |
| **Absolute mismatches** | Number of mismatches allowed while aligning reads. | 0 | **absolute-mismatches** | *numeric* |
| **Align reverse complement reads** | Set this option to align both direct and reverse complement reads. | False | **reverse** | *boolean* |
| **Use "best"-mode** | Report only the best alignment for each read (in terms of mismatches). | True | **best** | *boolean* |
| **Omit reads with qualities lower than** | Omit reads with qualities lower than the specified value. Reads that have no qualities are not omitted.<br><br>Set "0" to switch off this option. | 0 | **quality-threshold** | *numeric* |

## Input/Output Ports

The element has 1 *input port*:

**Name in GUI:** Genome aligner data

**Name in Workflow File:** in-data

**Slots:**

| Slot In GUI | Slot in Workflow File | Type |
|---|---|---|
| **URL of a file with mate reads** | **readsurl** | *string* |
| **URL of a file with reads** | **readspairedurl** | *string* |

And 1 *output port*:

**Name in GUI:** Genome aligner output data

**Name in Workflow File:** out-data

**Slots:**

| Slot In GUI | Slot in Workflow File | Type |
|---|---|---|
| **Assembly URL** | **assembly-out** | *string* |