

# 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?	<b>true</b> - absolute mismatches mode is used <b>false</b> - percentage mismatches mode is used 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. 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