

# Pairwise Alignment

To align two sequences go to the *Pairwise Alignment* tab of the *Options Panel*:

Pairwise Alignment

Sequences

> Select and add X

> Select and add X

Algorithm:

Kalign3

Algorithm settings

Gap open penalty 8.00

Gap extension penalty 6.00

Terminal gap extension penalty 0.00

Output settings

In new window

Output file:

uments/UGENE\_Data/pairwise-alignment.aln ...

Align

Select two sequence from the original alignment, select the parameters and click on the *Align* button. The following parameters are available:

## Sequences

The first and the second sequences for the *Pairwise Alignment*.

## Algorithm

The algorithm of the *Pairwise Alignment*. There are two algorithms:

1. *KAlign* - the algorithm, provided by the Kalign tool (integrated as an External Tool, check [the Data Analysis Tools page](#) for details). This tool uses the **Wu-Manber** string-matching algorithm. The algorithm details are described in the corresponding publication [Lassmann T, Sonnhammer EL. Kalign--an accurate and fast multiple sequence alignment algorithm. BMC Bioinformatics. 2005 Dec 12;6:298. doi: 10.1186/1471-2105-6-298. PMID: 16343337; PMCID: PMC1325270 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1325270/>].

The algorithm has the following parameters:

- *Gap open penalty* - indicates the penalty applied for opening a gap. The penalty must be negative.
  - *Gap extension penalty* - indicates the penalty applied for extending a gap.
  - *Terminal gap penalty* - the penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.
2. *Smith-Waterman* - the same algorithm, which is used for the [Smith-Waterman Search](#) (check the page for the algorithm details - the alignment process works in a same way as the searching process).  
The following parameters are available:
    - *Algorithm version* - version of the algorithm implementation. Non-classic versions produce the same results as classic but much faster. To use these optimizations our system must support [SSE2](#).
    - *Scoring matrix* - scoring matrix.
    - *Gap open penalty* - penalty for opening a gap.
    - *Gap extension penalty* — penalty for extending a gap.

## Output settings

Settings of the output file:

- *In the new window* - create a new alignment and open it if checked or just align two sequences of the current alignment if it is not.
- *Output file* - the result file path.