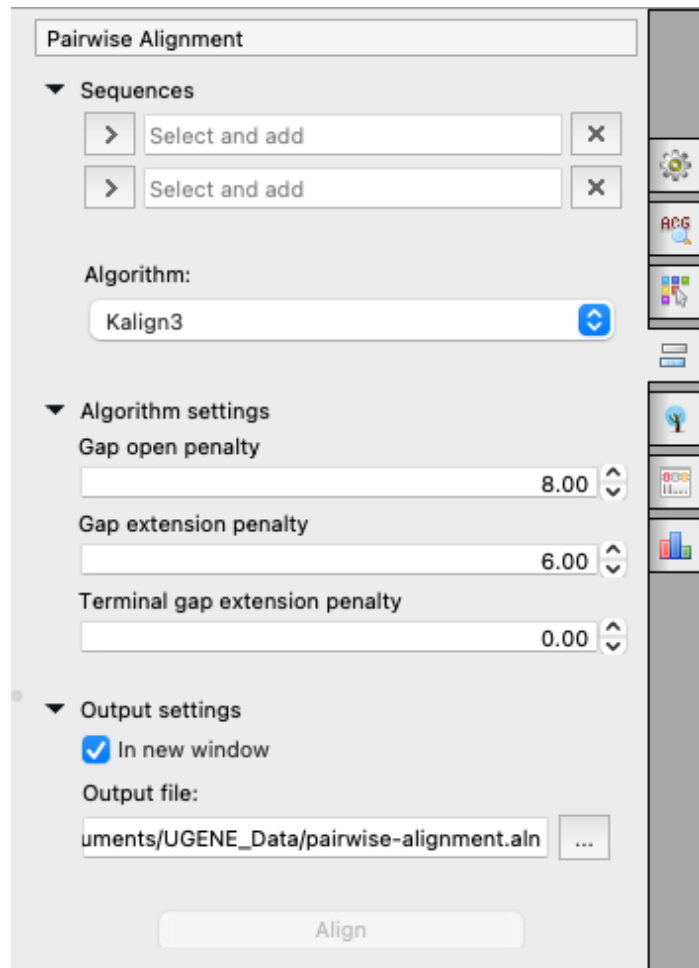# Pairwise Alignment

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

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.