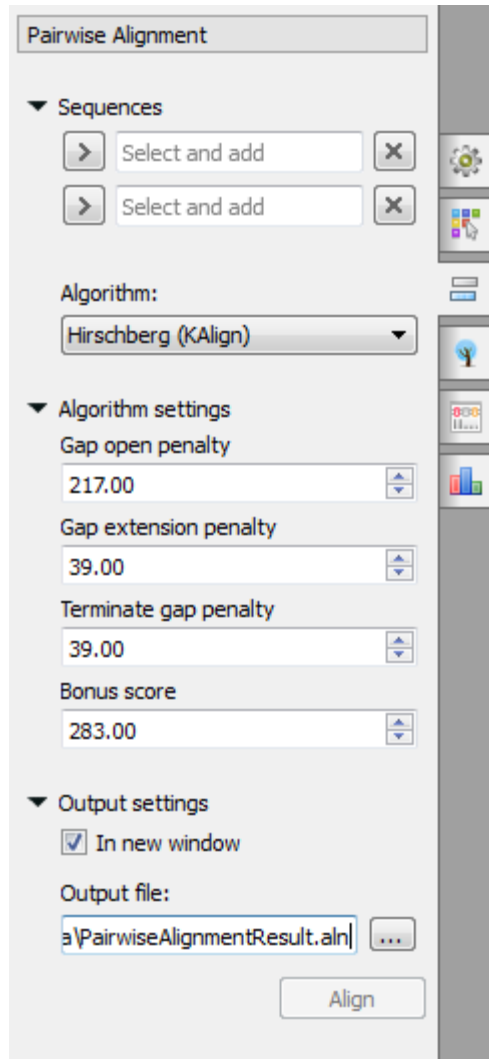


# Pairwise Alignment

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:

*Algorithm* - algorithm of the pairwise alignment. There are two algorithms:

*Hirschberg (KAlign)* - 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.

*Terminate gap penalty* - the penalty to extend gaps from the N/C terminal of protein or 5'/3' terminal of nucleotide sequences.

*Bonus score* - a bonus score that is added to each pair of aligned residues.

*Smith-Waterman* - 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 these capabilities: OPENCL, SSE2 or SW\_classic.

*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.

