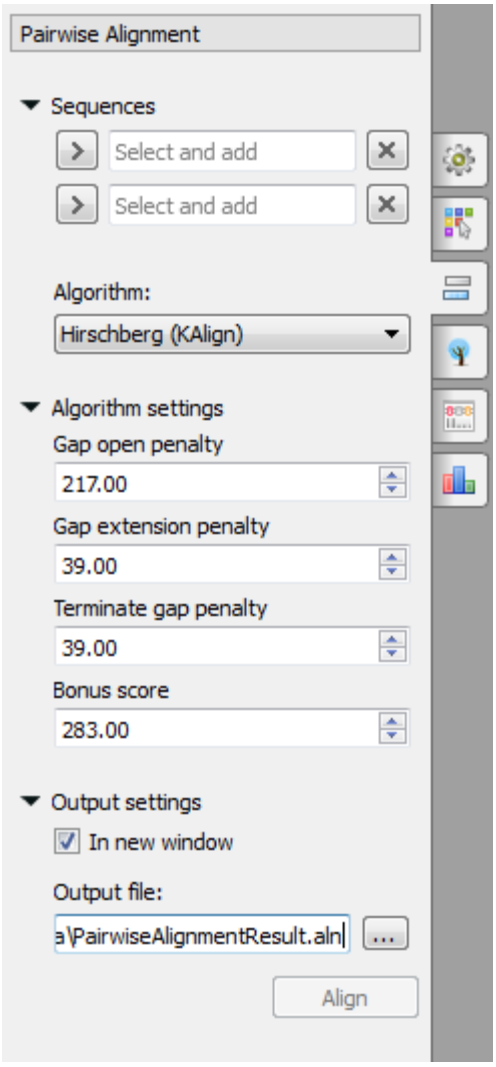
Pairwise Aligning

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 otput file.