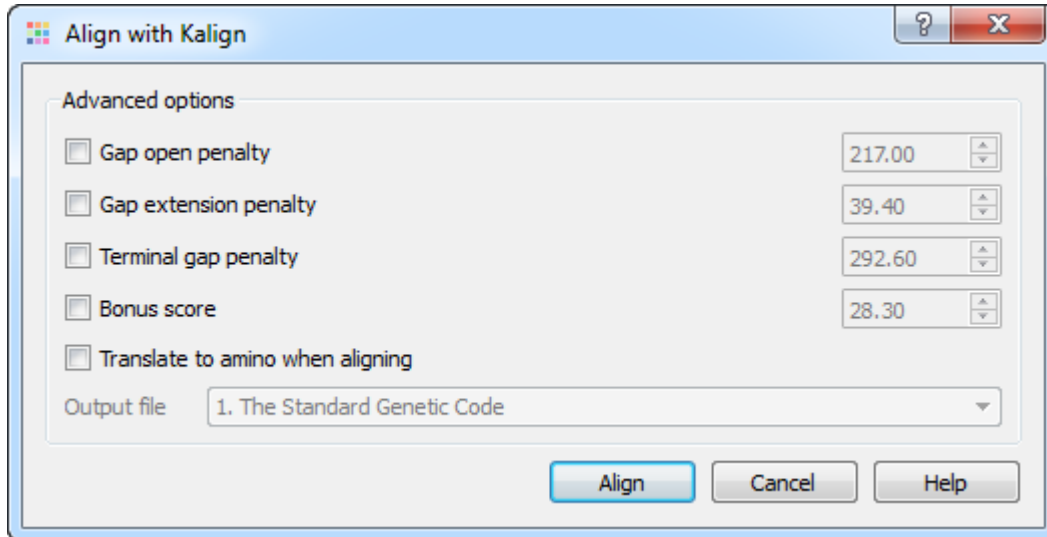


# Kalign Aligning

Kalign is a fast and accurate multiple sequence package designed to align large numbers of protein sequences.

**Kalign home page:** [KAlign](#)

To use *Kalign* open a multiple sequence alignment file and select the *Align with Kalign* item in the context menu or in the *Actions* main menu. The following dialog appears:



The following parameters are available:

*Gap opening 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.

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

*Translate to amino when aligning* - translates an alignment to amino when aligning.