Functions Supported for Multiple Alignment Data

- createAlignment (Sequence seq1, Sequence seq2, ...) returns the alignment created from the sequences.
- addToAlignment (MAlignment aln, Sequence seq, int row = -1) adds the sequence to the specified row of the alignment. If the "row" parameter is not specified the sequence is added to the end of the alignment.
- sequenceFromAlignment (MAlignment aln, int row) returns the sequence from the specified row of the alignment. findInAlignment (MAlignment aln, Sequence seq) searches the alignment for the specified string. Return the number of the row if the sequence has been found or "-1" if it hasn't been found.
- findInAlignment (MAlignment aln, QString name) searches the alignment for a sequence with the specified name.
 removeFromAlignment (MAlignment aln, int row) removes a sequence from the specified row of the alignment.
- **rowNum** (MAlignment aln) returns the number of rows in the alignment.
- **columnNum** (MAlignment aln) returns the length of the alignment. **alignmentAlphabetType** (MAlignment aln) returns the alignment's alphabet.