Functions Supported for Sequence Data

- subsequence (Sequence seq, int beg, int end) returns the subsequence between the "beg" and "end" parameters.
- complement (Sequence seq) returns the complement sequence.
- translate (Sequence seq, int offset = 0) returns one of the three sequence translations. Which one is returned is determined by the "offset"
- **size** (Sequence seq) returns the length of the sequence.
- getName (Sequence seq) returns the name of the sequence.
- alphabetType (Sequence seq) returns the alphabet of the sequence.
- charAt (Sequence seq, int ind) returns the symbol located in the "ind" position of the sequence.
- hasQuality (Sequence seq) determines whether the sequence has the "Quality" parameter.
- getMinimumQuality (Sequence seq) returns the minimum value of the "Quality".
- isAmino (Sequence seq) returns true if it is amino acid sequence.
- concatSequence (Sequence1 seq1, Sequence2 seq2,...) returns the one sequence consists of the all input sequences.
 sequenceFromText (QString " ") returns the sequence consists of the input text.