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” parameter.
- **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.