

| Sequence |
|--|
| <ul style="list-style-type: none"> - type - seq - _encoding_type - _header - _iupac - legalDNA - legalRNA - legalAmino - validType |
| <ul style="list-style-type: none"> + begin() + end() + Sequence() + Sequence() + Sequence() + getSeq() + getType() + getEncodingType() + getIupac() + getTypeArray() and 19 more... + getSequenceSymbol() + getSymbolDNA() + isLegalNucleic() + isLegalAmino() + isLegalSymbol() + isDNA() + isRNA() + isAmino() + isNucleic() + isDnaSpecificNucleotide() and 14 more... # parseChar() |



| FastaSequence |
|--|
| <ul style="list-style-type: none"> - comments |
| <ul style="list-style-type: none"> + getAllComment() + FastaSequence() + insert() + eraseSeq() + addComment() + loadComments() + removeComment() + displaceComment() + isCommentedPos() + getComment() |