Sequence

- - type
- - seq
- - _encoding_type
- - _header
- - _iupac
- - legalDNA
- - legalRNA
- - legalAmino
- - validType

- + 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()

FastaRelated

- - legalMultiHeaderChar
- - legalMonoHeaderChar
- - legalCommentChar
- - blankChar

- + isHeaderChar()
- + isMonoHeaderChar()
- + isMultiHeaderChar()
- + isCommentChar()
- + isBlankChar()

FastaSequence

- - comments

- + getAllComment()
- + FastaSequence()
- + insert()
- + eraseSeq()
- + addComment()
- + loadComments()
- + removeComment()
- + displaceComment()
- + isCommentedPos()
- + getComment()