frame

Compressor

+ field: type

+ method(type): type

Decompressor

+ field: type

+ method(type): type

ResultsLabeling

+ field: type

+ method(type): type

LabelActions

+ field: type

+ method(type): type

Nuclotide

+ static validateNuclotide: bool

DNASequence

+ sequence: char[]
+ name: string
+ id: size_t

+ relationalOperators: bool
+ streamingOut: ostream
+ brackets: char
+ length: size_t
+ slice:DNASequence
+ find: size_t
+ count: size_t
+ findAll:vector<size_t>
+ findConsensus: vector<pair<size_t, size_t> >

Codon

+ static string: startingCodon
+ static string[] endingCodons

+ isStartingCodon: bool
+ isEndingCodon: bool

SequenceCreation

+ field: type

+ method(type): type

CLICache

+ vectoor<DNASequence>

+ method(type): type

OnCacheManipulations

+ field: type

+ method(type): type

SequenceManipulation

+ field: type

+ method(type): type

ResultLabeling

+ field: type

+ method(type): type

DataBaseManagement

+ field: type

+ method(type): type

SequenceAnalysis

+ field: type

+ method(type): type

LastReferences

+ field: type

+ method(type): type

CLIControlUnit

+ field: type

+ method(type): type

SequenceManagement

+ field: type

+ method(type): type