GeneRfold

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fold   *Folding routine*

Description

Folds the sequence and returns the minimum free energyin kcal/mol; the mfe structure in bracket notation is returned.

Usage

```
fold(s, t=37)
```

Arguments

s   Sequence (character string)

t   Temperature (double)

Value

a list with `Energy` and `Structure`

References

http://www.tbi.univie.ac.at/~ivo/RNA/

See Also

dotPlot,rnaPlot

Examples

```
s <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGGTT"
fold(s)
dotPlot(s,file="dot.ps")
rnaPlot(s,file="rna.ps")
```

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rnaPlot   *Plot Rna structure / Dot plot*

Description

Plot (to a postcript file) a structure (rnaPlot) made by fold or the dot plot.

Usage

```
dotPlot(s,t,file="toto.ps")
rnaPlot(s,struc=fold(s)[[1]],file="toto.ps")
```

Arguments

s	Sequence (character string)
t	Temperature
struc	Rna structure (given by fold)
file	postscript file (output)

Value

A graphic in postscript file

References

http://www.tbi.univie.ac.at/~ivo/RNA/

See Also

fold

Examples

```
s <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGGTT"
fold(s)
dotPlot(s,file="dot.ps")
rnaPlot(s,file="rna.ps")
```

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