

GeneRfold

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fold

Folding routine

Description

Folds the sequence and returns the minimum free energy in 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 <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGTT"  
fold(s)  
dotPlot(s, file="dot.ps")  
rnaPlot(s, file="rna.ps")
```

`rnaPlot`*Plot Rna structure / Dot plot*

Description

Plot (to a postscript 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

<code>s</code>	Sequence (character string)
<code>t</code>	Temperature
<code>struc</code>	Rna structure (given by fold)
<code>file</code>	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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