

GeneRfold

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R topics documented:

fold	1
rnaPlot	2

Index	3
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fold	<i>Folding routine</i>
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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 <- "TTAGCTCAATTGGTAAAGACCCTAGGCGAAGCTTAGAGGTCGCCGGTT"
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

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")
```

Index

*Topic **utilities**

fold, [1](#)

rnaPlot, [2](#)

dotPlot, [1](#)

dotPlot(*rnaPlot*), [2](#)

fold, [1](#), [2](#)

rnaPlot, [1](#), [2](#)