

# GeneRfold

April 19, 2010

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fold

*Folding routine*

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

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`rnaPlot`*Plot Rna structure / Dot plot*

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**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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