

# GeneRfold

April 19, 2009

---

fold	<i>Folding routine</i>
------	------------------------

---

## 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	Temperature (double)
Structure	Temperature (double)

## 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**

<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")
```

# Index

## \*Topic **utilities**

fold, [1](#)

rnaPlot, [2](#)

dotPlot, [1](#)

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

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

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