

DNA mfold server : 1996-2008, Michael Zuker, Rensselaer Polytechnic Institute

This is not a *secure* server. Selected submissions may be used as examples in lectures. Click on "Notice" (below left).



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Job submission form for   
*spl1-111.dhcp.uno.edu*

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This web server uses mfold (version 3.2) by Zuker and Turner. Users are requested to cite:

### M. Zuker

Mfold web server for nucleic acid folding and hybridization prediction.

*Nucleic Acids Res.* **31** (13), 3406-15, (2003)

[\[Abstract\]](#) [\[Full Text\]](#) [\[Supplementary Material\]](#) [\[Additional Information\]](#)

The *free energies* used are from the [laboratory](#) of John SantaLucia Jr.

An appropriate citation for these energy rules is

SantaLucia, JJr (1998) A unified view of polymer, dumbbell, and oligonucleotide DNA nearest-neighbor thermodynamics. *Proc. Natl. Acad. Sci. USA* **95**, 1460-1465. [\(Abstract\)](#)

For the salt correction, please cite:

Peyret, N. (2000) Prediction of Nucleic Acid Hybridization: Parameters and Algorithms PhD dissertation, Wayne State University, Department of Chemistry, Detroit, MI



Related servers.

[RNA mfold server.](#)

[D INAMelt](#) Full melting profile prediction for nucleic acids.

[Quikfold server.](#) Fold many short RNA or DNA sequences at once.

[Zipfold server.](#) Compute minimum folding energies only for many RNA or DNA sequences.

[T<sub>m</sub> server.](#) Compute minimum folding energies and T<sub>m</sub> only for many RNA or DNA sequences.

[Hybridizaion server.](#) Compute energies and T<sub>m</sub> for the hybridization of two RNA or DNA sequences.



Enter a name for your sequence:



Enter the sequence to be folded in the box.

All non-alphabet characters will be removed.

FASTA format may be used.

Enter **constraint information** in the box at the right. (optional) You may:

1. force bases  $i, i+1, \dots, i+k-1$  to be double stranded by entering:  
 $F \ i \ 0 \ k$  on 1 line in the constraint box.
2. force consecutive base pairs  $i, j, i+1, j-1, \dots, i+k-1, j-k+1$  by entering:  
 $F \ i \ j \ k$  on 1 line in the constraint box.
3. force bases  $i, i+1, \dots, i+k-1$  to be single stranded by entering:  
 $P \ i \ 0 \ k$  on 1 line in the constraint box.
4. prohibit the consecutive base pairs  $i, j, i+1, j-1, \dots, i+k-1, j-k+1$  by entering:  
 $P \ i \ j \ k$  on 1 line in the constraint box.
5. prohibit bases  $i$  to  $j$  from pairing with bases  $k$  to  $l$  by entering:  
 $P \ i-j \ k-l$  on 1 line in the constraint box.

The DNA sequence is .

Folding temperature (between 0° and 100° C)

**Ionic conditions:** [Na<sup>+</sup>] [Mg<sup>++</sup>]

Units: M mM Correction type: Oligomer Polymer

Enter the **percent suboptimality** number.

Enter an **upper bound** on the number of computed foldings.

Enter the **window** parameter if you wish.

Enter the **maximum distance between paired bases** if you wish.

Your job can be processed while you wait (the default) or can be submitted for batch processing by pressing the button below. In this case, you will be notified at a later time that the job is finished. Please enter your E-mail address in the window below.

**Current limits: 800 bases for an immediate job, 6000 for batch.**

Select: job for:





Choose **image width** for png & jpg files: Small: Regular: Medium: Large: XLarge: Huge:

Choose **structure format:** Automatic: Bases: Outline:

Grid lines in **energy dot plot:** On: Off:

Choose **structure draw mode:** .

Choose **base numbering frequency:** .

-  Choose [sequence numbering offset:](#) .
-  Choose [regularization angle \(in degrees\):](#) (Not used if 0.)
-  Choose [structure rotation angle \(in degrees\):](#)
-  Choose [structure annotation:](#)   None:   p-num:   ss-count:   high-light:

Enter high-light regions(s):

Download the old [mfold](#) software (version 3.2) if you insist, or  
download the much better [UNAFold](#) package.

Please [leave your comments](#)  
or [view the guestbook](#).



Check Input: