

Step 1. Find MFOLD on the web. Enter this URL for MFOLD:

<http://mfold.rna.albany.edu/>

Click the **mfold** link

**THE RNA INSTITUTE**  
COLLEGE OF ARTS AND SCIENCES  
UNIVERSITY AT ALBANY State University of New York

# The UNAFold Web Server

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## Software

- [UNAFold](#)
- [mfold](#)
- [OligoArrayAux](#)
- [OligoArray 2.1 \(external link\)](#)
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## "UNAFold"

- "Unified Nucleic Acid Folding and hybridization package"

The UNAFold web server is currently an amalgamation of two existing web servers: mfold & DINAMelt. The aim of this web site is to integrate the existing servers and to expand by developing algorithms and software that will provide new services to the scientific community.

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Step 2. Then click the [RNA Folding Form](#) link.

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# The mfold Web Server

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## Applications

- [RNA Folding Form](#)
- [DNA Folding Form](#)
- [Structure Display and Free Energy Determination](#)
- [RNA Folding Form \(version 2.3 energies\)](#)

## Download the mfold software.

Note that mfold has been replaced by UNAFold, a software package that is much easier to install and offers many more types of computations. Although UNAFold will install without mfold\_util, the sir\_ programs from the mfold\_util package are required in order to obtain structure plots and dot plots. Install mfold\_util before installing UNAFold. Versions 3.4 and higher of mfold contains all of the non-integer programs from mfold\_util, so a separate download is not required. Download UNAFold [here](#).

Which will open up the following form:

Step 3. To fold an RNA and make structure predictions, minimally you need to:

- (1) Enter a name
- (2) Enter a sequence

**RNA Folding Form**

**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 folding temperature is fixed at 37°. You may still fold with the older *version 2.3* RNA parameters, which allow the temperature to be varied.

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

Enter sequence name:

Enter the sequence to be folded in the box below. All non-alphabet characters will be removed. FASTA format may be used.

**RNA Folding Form**

**M. Zuker**  
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Enter sequence name:

Enter the sequence to be folded in the box below. All non-alphabet characters will be removed. FASTA format may be used.

```
GGAGCCUUAGCUCAGCDGGGAGAGCGCCUGCUU5GC=CGCAGGAG7UCAGCGGTP<GAUCC
CGCUAGGCCUCCACCA
```

Here is an example with a tRNA sequence from *Bacillus subtilis*.

Optional Step. If you click the **Format Sequence** button you get this output, which numbers the alignment, and counts the nucleotides.

Cute. And it verifies you have all the sequence inputted properly.

Step 4. Scroll down past the defaults and click the **Fold RNA** button.

There are many folding parameters you can alter, but ignore them and use the defaults for now.

### RNA Folding Form

**M. Zuker**  
Mfold web server for nucleic acid folding and hybridization prediction.  
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[\[Abstract\]](#) [\[Full Text\]](#) [\[Supplementary Material\]](#) [\[Additional Information\]](#)

The folding temperature is fixed at 37°. You may still fold with the older *version 2.3* RNA parameters, temperature to be varied.

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

Enter sequence name:

Enter the sequence to be folded in the box below. All non-alphabet characters will be removed. FASTA format may be used.

```
      10      20      30      40      50
GGAGCCUJAG CUCAGCDGGG AGAGGCCUUG CUUGCCGCAG GAGUCAGCGG
      60      70      80      90     100
UCCGAIUCCCGC UAGGCUCCAC CA
```

Sequence length = 72.  
12 A's, 24 C's, 24 G's, 11 U/T's, and 1 N's.



Enter high-temperature region(s):

**Current limits: 800 bases for an immediate job, 9000 for batch.**

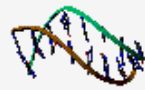
If you wish to make comments, please select an appropriate [forum](#).



After a short wait, you will get this output page. This page has both Energy plots AND images of predicted structures.

Step 5. To get the *energy dot plot*, click on one of the File Formats. I suggest **.jpg link** to start.


Do the same for the 1<sup>st</sup> structure. Click the **.jpg link**



Bsub\_tRNA is the 1709767<sup>th</sup> nucleic acid sequence folded on the RNA Institute mfold server.

- Monday, October 07 14:13:31 EDT 2013 -

## Folding Bsub\_tRNA at 37° C. (3.5)

- Computed for 146.244.235.112  -

Warning! You have used 1 reserved letter in your sequence. Your results may be in error if you do not understand the server conventions. Click [here](#) for an explanation.

```
Linear RNA folding at 5%, window = 2, max folds = 50
12 A's, 25 C's, 24 G's, 11 U/T's and 0 N's.
      10      20      30      40      50
GGAGCCUAG CUCAGCDGGG AGAGCGCCUG CUUGCCGCAG GAGUCAGCGG
      60      70      80
UCGAUCCCGC UAGGCUCCAC CA
```

## Output

The *energy dot plot* for Bsub\_tRNA. ([Definition](#))

File formats: [Text](#), [PostScript](#), [pdf](#), [png](#), [jpg](#)

Computed Structure: ([File Formats](#))

The computed folding contains 20 base pairs out of 21 (95.2%) in the *energy dot plot*.

Extra files: [sorted](#) ct file; [h-num](#) values; [p-num](#) values; [log file](#) for main computations.

[Circular structure Plots](#)

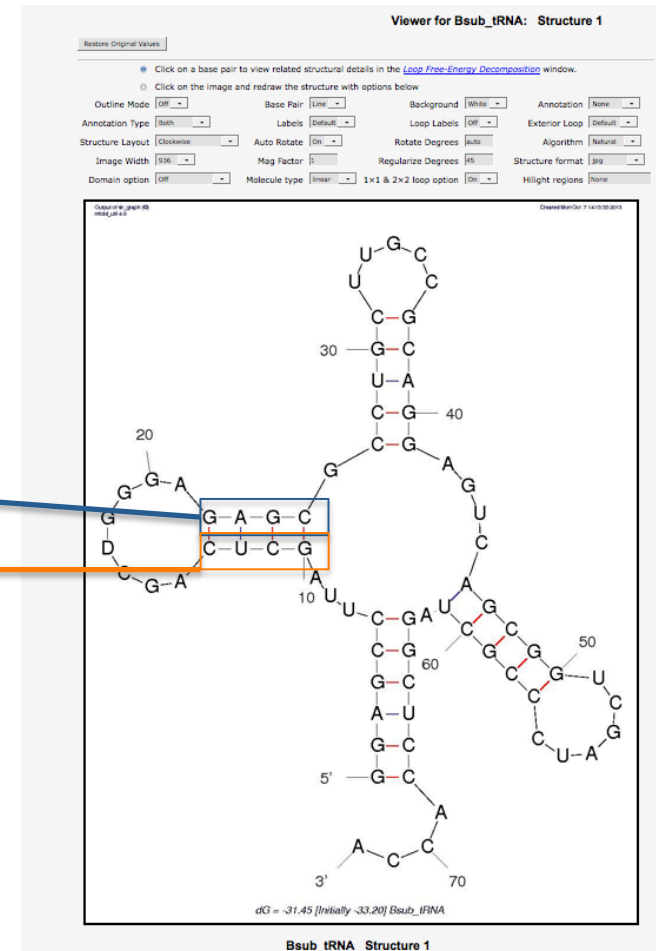
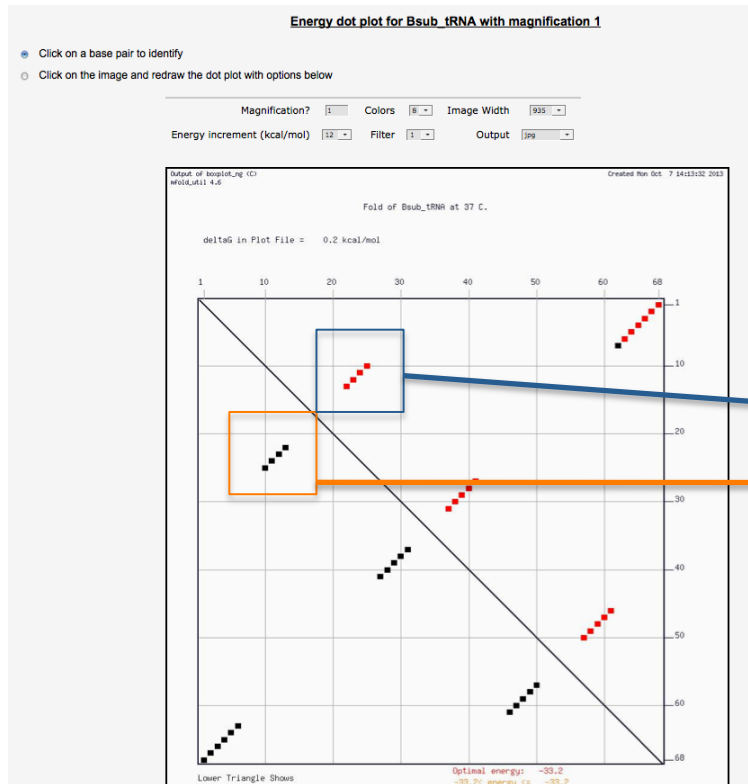
◆ [Structure 1](#) : Initial  $\Delta G = -33.20$  kcal/mol, ([Thermodynamic Details](#)).

Different file formats: [PostScript](#), [pdf](#), [png](#), [jpg](#), [.ct file](#), [Vienna](#), [RNAML](#), [RnaViz ct](#), [Mac ct](#), [RNAdraw](#), [XRNA ss](#).

These computations were performed on maweb1.rit.albany.edu in 0 min. and 1.68 sec. and can be accessed at <http://mfold.ma.albany.edu/cgi-bin/view.cgi?13Oct07-14-13-30-207434c809>

# ENERGY DOT PLOT

# Structure 1



Do you see how they relate to one another?

If you have alternative structure possibilities, you may see different series of dots on the energy dot plot that do not correspond to the 1<sup>st</sup> structure.