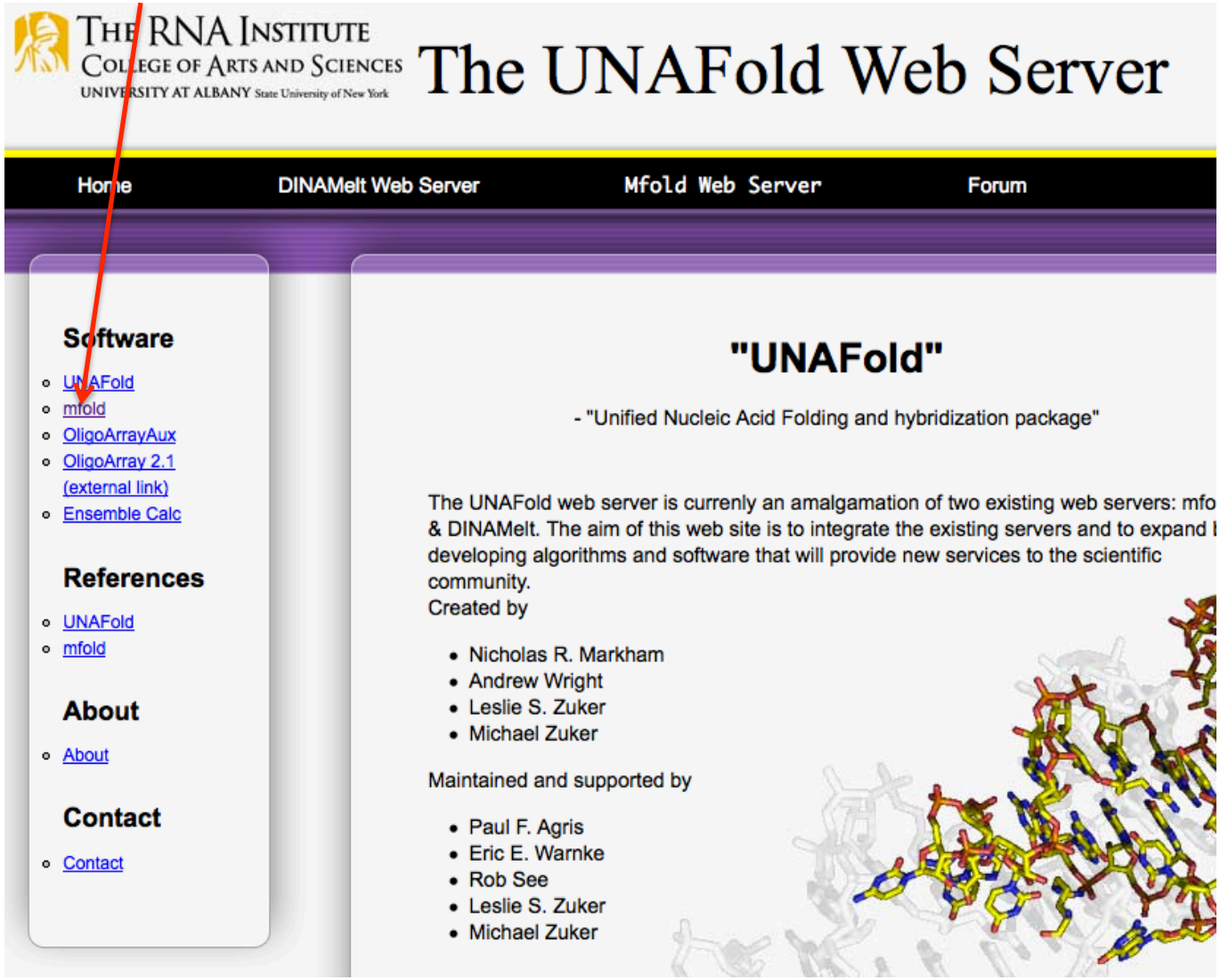
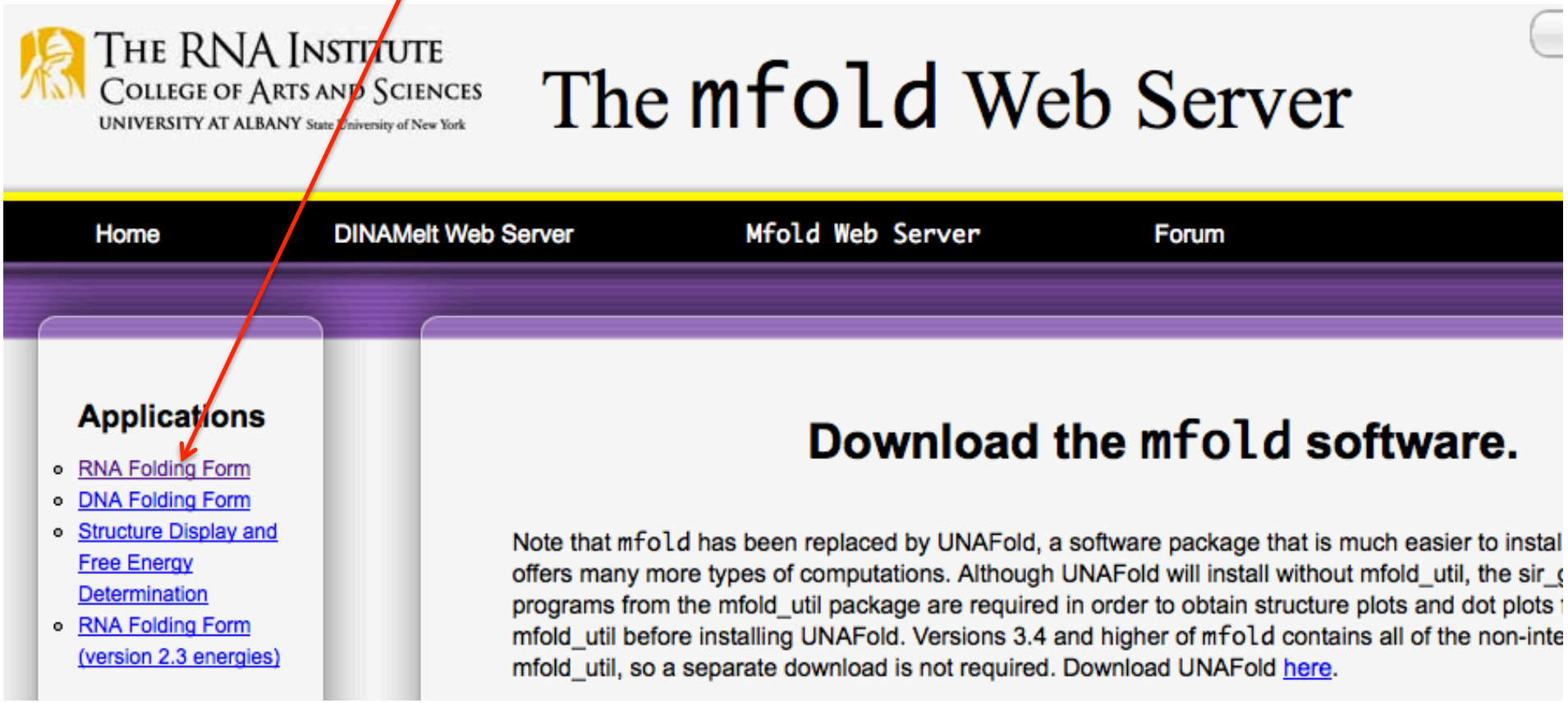
Step 1. Find MFOLD on the web. Enter this URL for MFOLD:

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

Click the **mfold** link

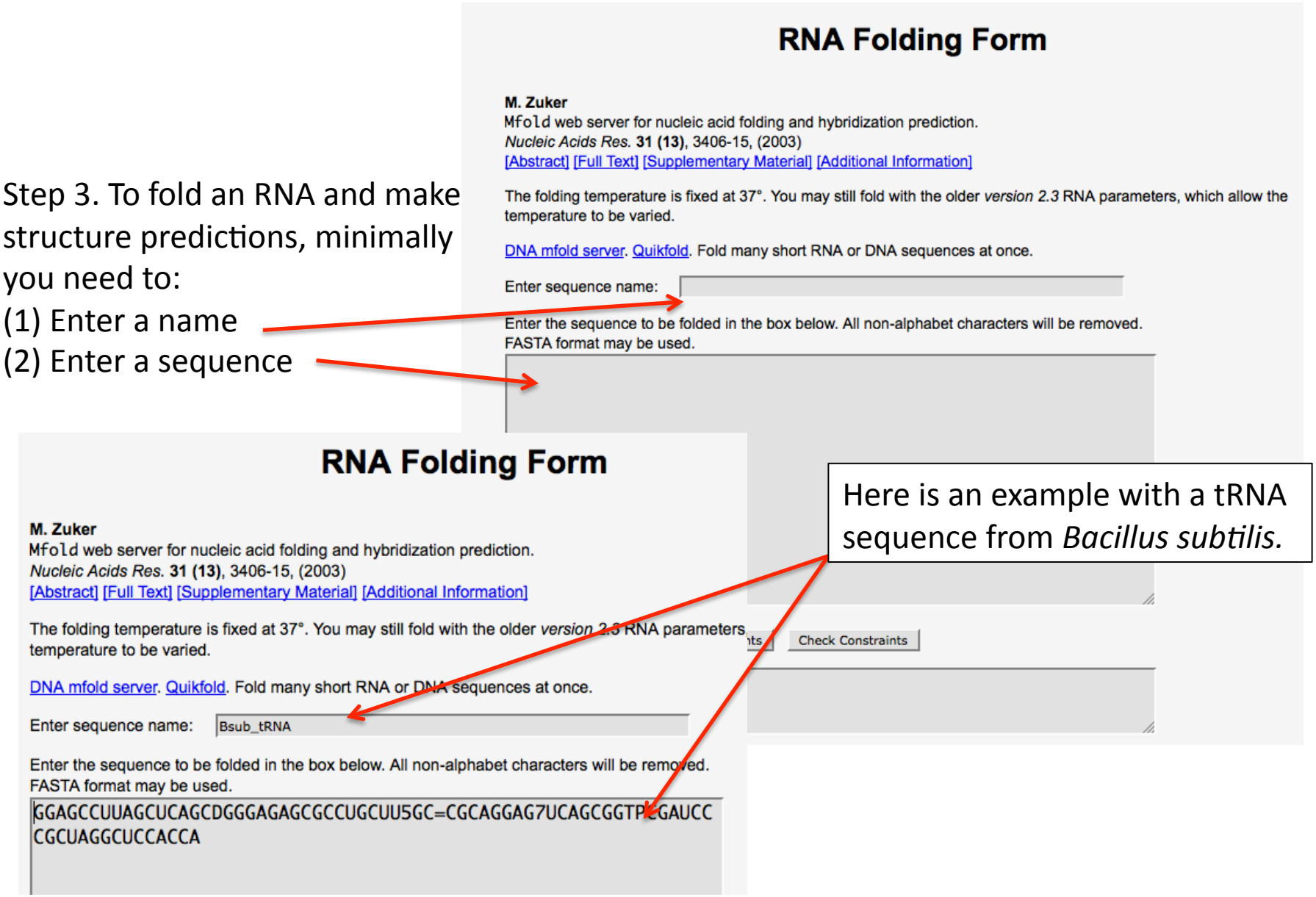


Step 2. Then click the **RNA Folding Form** link.



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

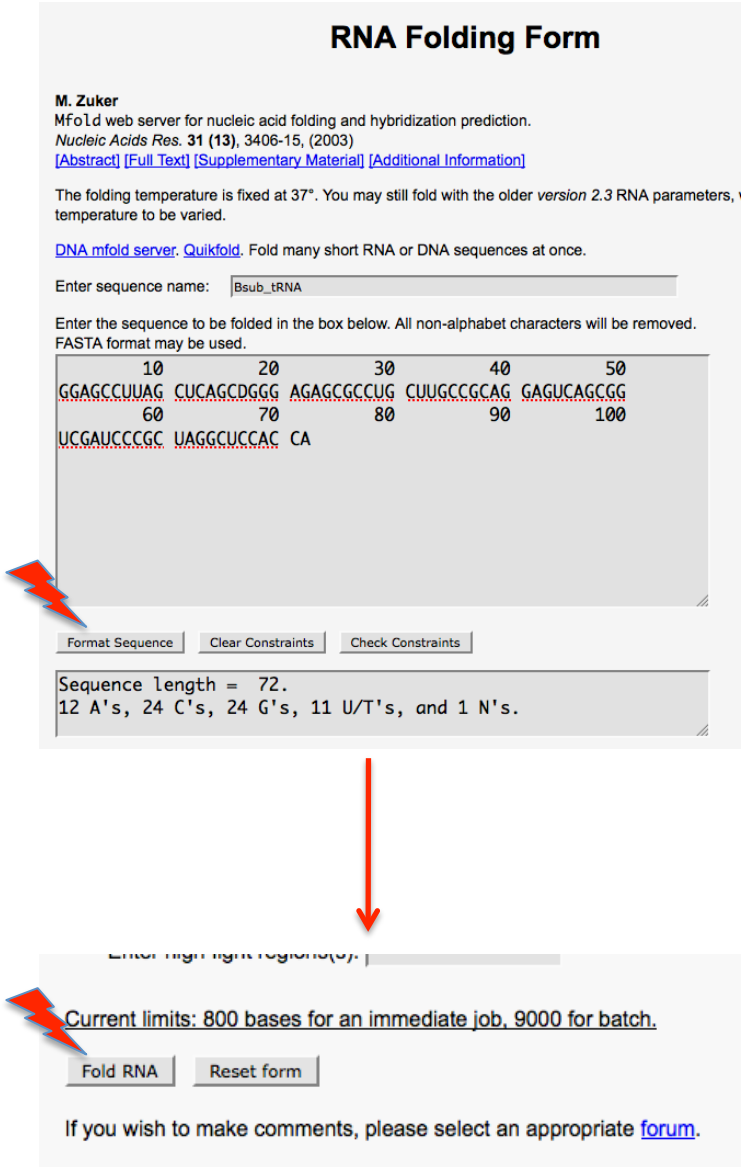


Optional Step. If you click the **Format Sequence** button you get this output, which numbers the alignment, and counts the nucleotides.

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

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

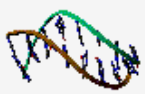
There are many folding parameters you can alter, but ignore them and use the defaults for now.



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 1st structure. Click the **.jpg link**



Bsub_tRNA is the 1709767th 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
 GGAGCCUUAG 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*.

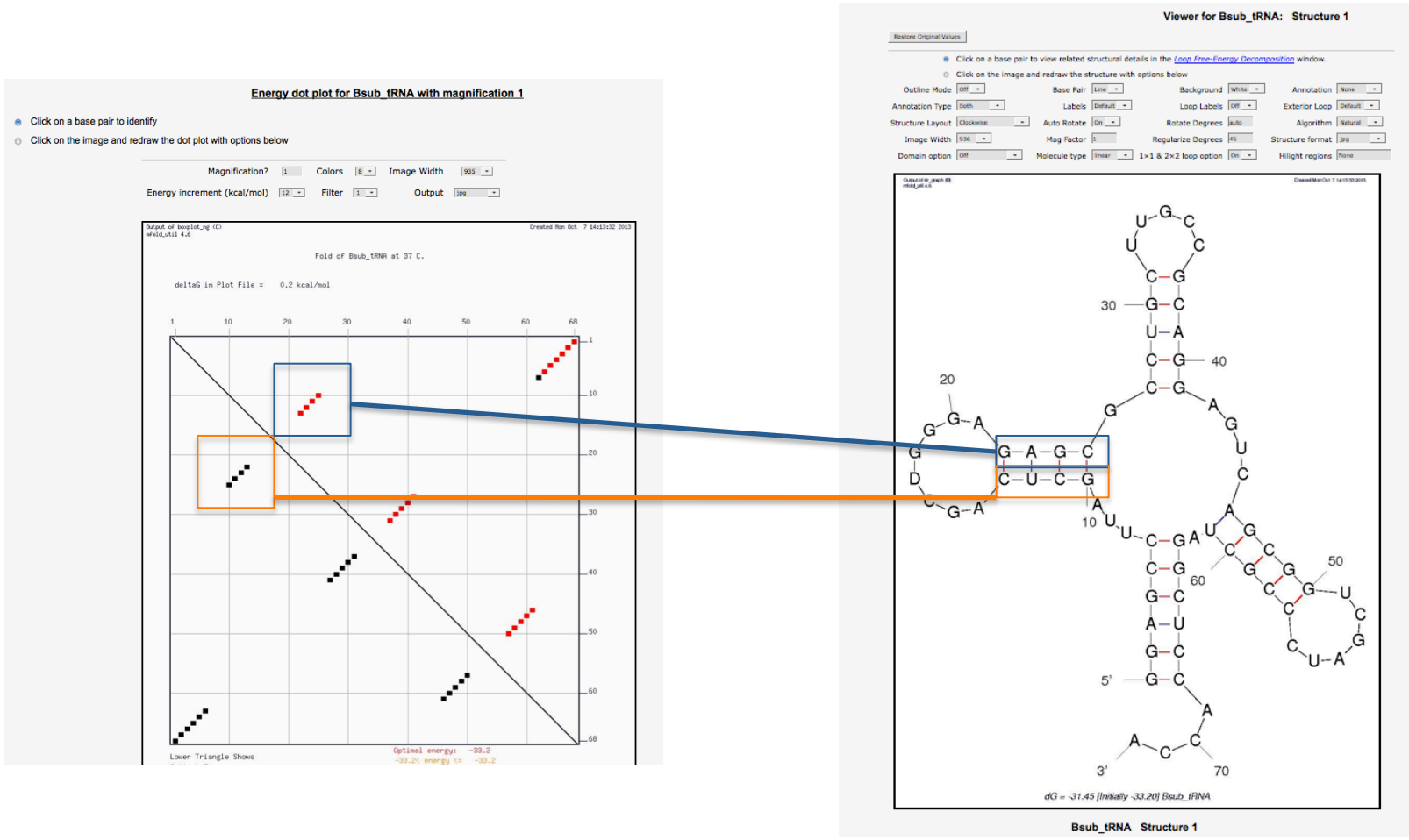
Extra files: sorted ct file; *h-num* values; *p-num* values; *log file* for main computations.
Circular structure Plots

Structure 1 : Initial ΔG = -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 rnaweb1.rit.albany.edu in 0 min. and 1.68 sec. and can be accessed at
http://mfold.rna.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 1st structure.