

Bioinformatics project

Submitted to: Dr. Samina Shakeel

Submitted by: Sayeda Zahra Batool

Department: Biochemistry Bs 7th Morning

Task No: 2

RNA Analysis:

1. DNA To RNA Conversion:

AUGGGAUGCUCACCAGUACUCACACCUCCGGAGUGGAUCCGAGCAGACC
GAGCACCAAACCGGAGGGAGAGCAACGGGCCAGCACACAGGGCGGCC
ACGAGAACGGAA AUGUAGCUGAGGACACUGAAACGCUCCCGAUGAGACA
CCUACUGGAGGCACUGUGGCAGAAC CUGCAGCAGAUGCAACAU CUGCACA
GCCCCACAGCAGGGUGGAACC UCCACCUGCAGCUGCAGCAC CUGUAG
AGGCAACACCACUGCAGAACAGGAACAGCCCC CUGCAGAAGAAGCAGCU
CCACCUGCAGAACAGGU AACACCACUGCAGAACAGAGGCAGCACACCUGC
AGAAGAACGCAGCAGCAGAAAAGCCUUCAGAGGCUGCAACACAAG
AAGCACCAGCAGCUGCAGAGCCAGGGAGCGAGGCCACAGCAGCUGACUCA
GCAGAACGCACCAGCUCCCAGUGAGUGA

2. Manual UTR Identification Results:

The UTRScan and other prediction servers were not opening, then I identified the UTR regions manually from the above RNA sequence.

5' UTR Region:

This is the part of the sequence before the first 'AUG' (Start Codon). It helps the cell start making protein.

3' UTR Region:

This is the part of the sequence after the 'UGA' (Stop Codon). It helps keep the RNA stable.

By finding the Start and Stop signals in the sequence, I identified these non-coding parts manually.

3. RNA fold image:

structure by submitting to our RNAsal web server.

Results for thermodynamic ensemble prediction

The free energy of the thermodynamic ensemble is **-180.39 kcal/mol**.

The frequency of the MFE structure in the ensemble is **0.04 %**.

The ensemble diversity is **62.14**.

You may look at the [dot plot](#) containing the base pair probabilities [EPS|PDF|IMAGE CONVERTER].

The centroid secondary structure in dot-bracket notation with a minimum free energy of **-156.70 kcal/mol** is given below.

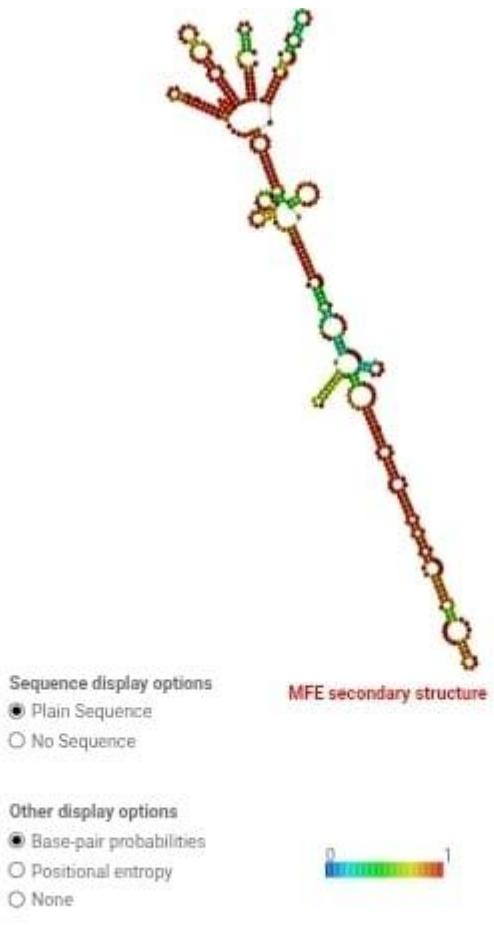
[color by base-pairing probability | color by positional entropy | no coloring]

```
1     AUGGGAUUCUCCACCAUUAUCUACCUUCGGAGUGGAUCCGAGCAGACCGAGCACCAAACGGAGGAGGCAACGGGGGCCAGCAACACAGGGGGGGCCCACGAGAMGGAAAUUGUAGCUGAGGGACACUGAAA  
100    GCACUGUGGCAGAACUCUGCAGCAUGCAACAUUCUCAAGCCCCACAGCAGGGGGUGGAACCUCCACCUUCAGCAGCAGCAGCAGUAGAGGCAACACCACCUCCAGAAACAGGCAACGCCCCUGCAGAAAG  
200    CACCAUCUGAGAAGGGCAGCACCCUCAGAAGAEGACGACCAAGCAGCAGAAAACCCUUCAGAGGGCUCACAAAGAAGCACCAGCAGCUCUGAGCAGGGAGCAGBCCACAGCAGCUCUGACUAGG  
300    ...((.....)).....(((((((((.....((.....))))....))))....(((((.....((.....))))....))))....((.....((.....))))....((.....((.....))))....  
400    (((.....((.....((.....))))....))....(((((.....(((((.....((.....((.....((.....))))....))))....))))....((.....((.....))))....((.....((.....))))....  
500    ))....))))....
```

You can download the minimum free energy (MFE) structure in [[Vienna Format](#)] or [[Ct Format](#)]. You can get thermodynamic details on this structure by submitting to our RNAsal web server.

Graphical output

You may look at the interactive drawing of the MFE structure below. If you do not see the interactive drawing and you are using Internet Explorer, please install the Adobe SVG plugin. **A note on base-pairing probabilities:** The structure below is colored by base-pairing probabilities. For unpaired regions the color denotes the probability of being unpaired.



MFE Value:

The Minimum Free Energy (MFE) is -180.39 kcal/mol. This indicates a stable RNA structure."

Stability Reason:

Because my sequence has a low negative MFE and many stems, it is a stable structure. This stability is important because it allows the mRNA to stay intact long enough to be translated into a protein.

