

Results for minimum free energy prediction

The optimal secondary structure in dot-bracket notation with a minimum free energy of **-0.50** kcal/mol is given below.
[\[color by base-pairing probability\]](#) | [\[color by positional entropy\]](#) | [\[no coloring\]](#)

```
1      CACAUACAGCAUAUGGAUCCCC
1      ..((((.....))).....
```

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

Results for thermodynamic ensemble prediction

The free energy of the thermodynamic ensemble is **-0.90** kcal/mol.
The frequency of the MFE structure in the ensemble is **52.06** %.
The ensemble diversity is **2.68** .

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

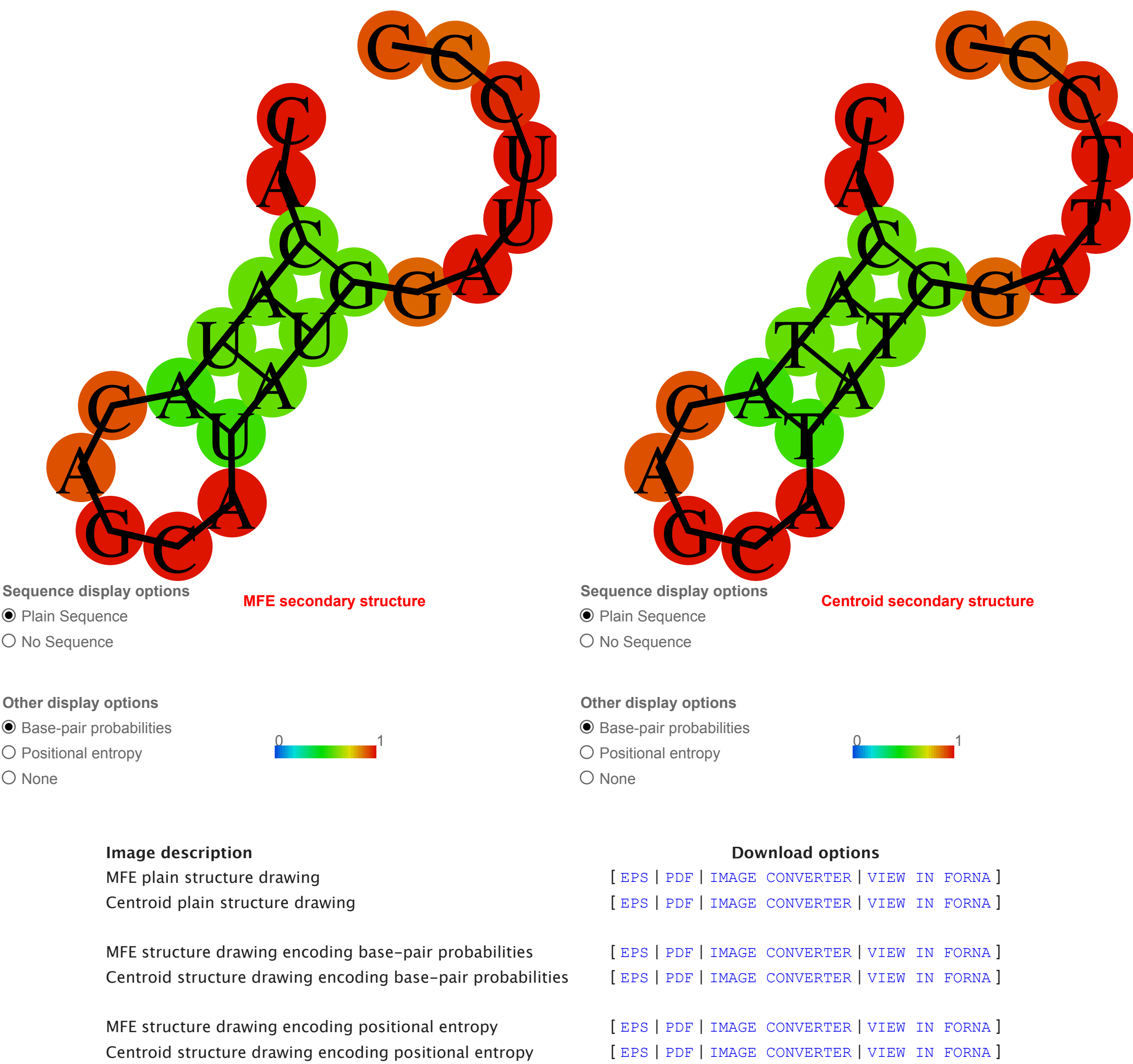
The centroid secondary structure in dot-bracket notation with a minimum free energy of **-0.50** kcal/mol is given below.
[\[color by base-pairing probability\]](#) | [\[color by positional entropy\]](#) | [\[no coloring\]](#)

```
1      CACAUACAGCAUAUGGAUCCCC
1      ..((((.....))).....
```

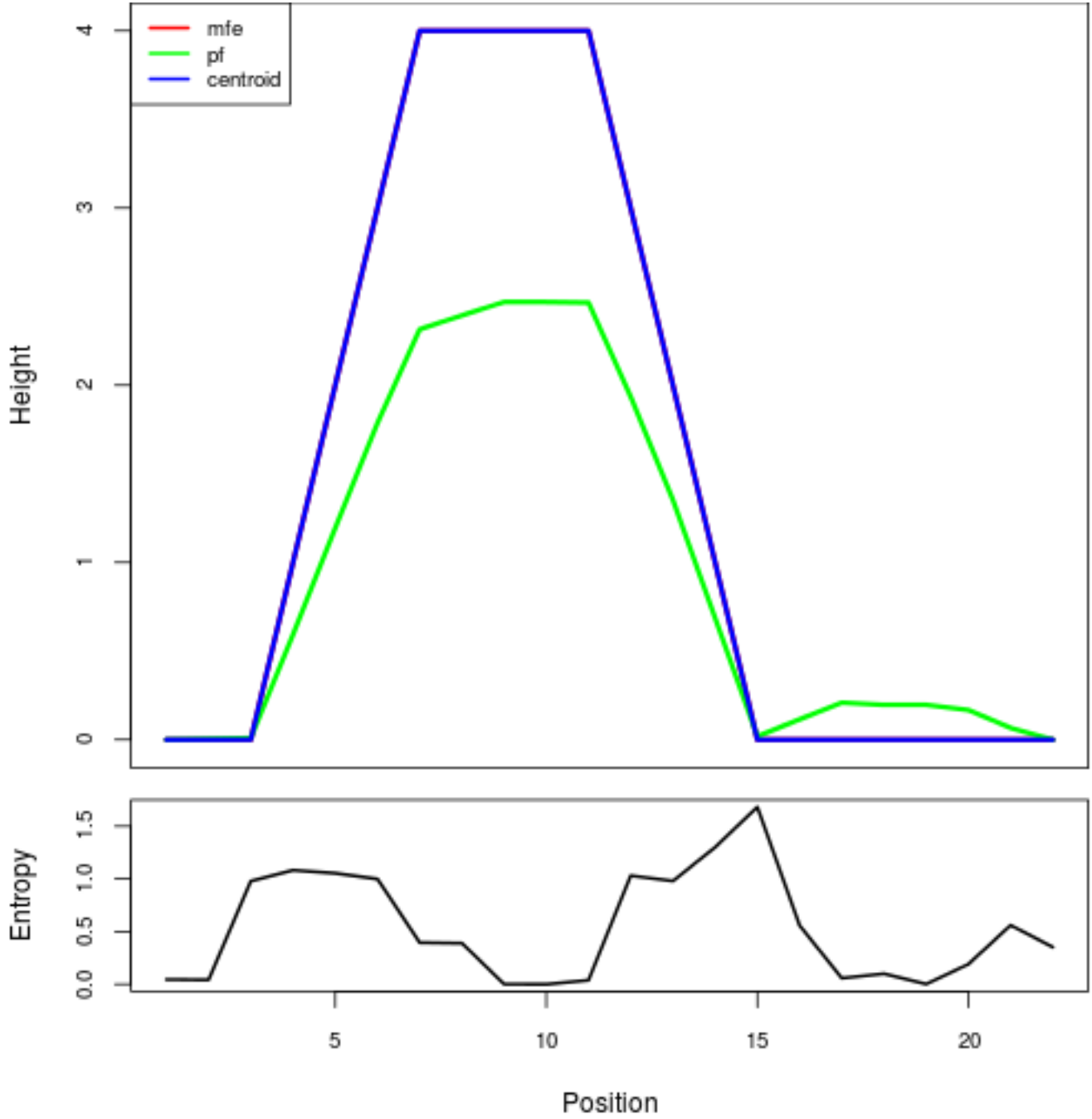
You can download the minimum free energy (MFE) structure in [\[Vienna Format\]](#) [\[Ct Format\]](#). You can get thermodynamic details on this structure by submitting to our [RNAeval web server](#).

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.



Here you find a mountain plot representation of the MFE structure, the thermodynamic ensemble of RNA structures, and the centroid structure. Additionally we present the positional entropy for each position. Download as [\[EPS\]](#)[\[PDF\]](#)[\[IMAGE CONVERTER\]](#).




Results have been computed using RNAfold 2.6.3. An equivalent command line call would have been
RNAfold -p -d2 --noLP < [sequence1.fa](#) > [sequence1.out](#)

RNA parameters are described in

Mathews DH, Disney MD, Childs JL, Schroeder SJ, Zuker M, Turner DH. (2004) Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. *Proc Natl Acad Sci U S A* 101(19):7287–92.

If you find these results helpful for your work you may want to cite:

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Gruber AR, Lorenz R, Bernhart SH, Neuböck R, Hofacker IL.
[The Vienna RNA Website](#). Nucleic Acids Research, Volume 36, Issue suppl_2, 1 July 2008, Pages W70–W74, DOI: 10.1093/nar/gkn188

Lorenz, R. and Bernhart, S.H. and Höner zu Siederdisen, C. and Tafer, H. and Flamm, C. and Stadler, P.F. and Hofacker, I.L. "ViennaRNA Package 2.0", Algorithms for Molecular Biology, 6:1 page(s): 26, 2011