

## Predicting single-stranded regions

**RNAfold WebServer**
1 Enter Input Parameters 2 View Results

[Home][New job][Help]

The **RNAfold web server** will predict secondary structures of single stranded RNA or DNA sequences. Current limits are 7,500 nt for partition function calculations and 10,000 nt for minimum free energy only predictions.

Simply paste or upload your sequence below and click **Proceed**. To get more information on the meaning of the options click the symbols. You can test the server using [this sample sequence](#).

Paste or type your **sequence** here: [clear]

```
AAGCAGATATCCGCCCTTCTCGGGCCCTGCTCGCACCTCAGCCTCTCCTCTCTCGCTCTCTCTCGCTGGCCCTTAGGAGGAAAGGTGC
```

Or upload a file in FASTA format:

**Fold algorithms and basic options**

- minimum free energy (MFE) and partition function
- minimum free energy (MFE) only
- no GU pairs at the end of helices
- avoid isolated base pairs

**Output options**

- interactive RNA secondary structure plot
- RNA secondary structure plots with reliability annotation (Partition function folding only)
- Mountain plot

Notification via e-mail upon completion of the job (optional):

Outcome:  
base-pair probability plot

Questions answered:  
Which pre-mRNA regions are likely single- or double-stranded.

## Predicting if a mutation leads to structural changes

**NIPU server**

splicing motifs and secondary structures

NI & PU VALUES
PU VALUES
REFERENCE
CONTACT

**NIPU web server**

This server allows to display splicing regulatory motifs and single-stranded regions.

For splicing regulatory motifs, we use the **NI** scores [1]. A hexamer with a positive NI score is considered to have ESE function, a hexamer with a negative NI score is considered to have ESS function. Strong ESEs have a score > 0.8, strong ESS a score < -0.8. Hexamers with a score between -0.8 and 0.8 are considered to be splicing-neutral, since their splicing effect is predicted to be weak.

For single-stranded regions, we compute the probability that a hexamer is completely unpaired (denoted as the **PU** value). PU values range between 0 (hexamer is completely base-paired) and 1 (hexamer is completely unpaired). The PU value for one hexamer is determined as the average of all local folding windows that comprise a context up- and downstream of 11 to 30 nt.

NOTE: For analyzing an entire exon, you have to input the exon sequence as well as 30 nt from its upstream and downstream intron flank. For example, input  
 aatgatatttaatttcccttttctttttagagcagatagacaaagatcctgatttggattttatttagacctctccttttggatagctagatgttt  
 (upper case letters are exonic, lower case letters intronic) to analyze human CFTR exon 12.  
 The procedure to compute PU values is illustrated in this figure.

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**Compute NI and PU values.**  
NOTE: computation may take some minutes depending on the input sequence length (two sequences each 160 nt long takes about 2 minutes)

You have to enter one or two RNA sequences (plain sequences, no header)

1. RNA sequence

2. RNA sequence (optional)

Outcome:  
plots showing the single-strandedness of hexamers in the wild-type and mutant sequence

Questions answered:  
Which mutations are likely to result in secondary structure changes and which are not.

## Finding alternative splice events that overlap conserved secondary structures

**Table Browser**

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the [OpenHelix Table Browser tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may want to use [Galaxy](#) or our [public MySQL server](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with these data.

**group:** Genes and Gene Prediction Tracks

**table:** knownAlt

**region:**  genome  ENCODE  position chrX:151073054-151383978

**identifiers (names/accessions):**

**filter:**

**intersection with evofold:**

**correlation:**

**output format:**  hyperlinks to Genome Browser  Send output to Galaxy

**output file:**  (leave blank to keep output in browser)

**file type returned:**  plain text  gzip compressed

Note: The all fields and selected fields output formats are not available when an intersection has been specified.

Outcome:  
a list, an annotation track or Genome Browser links of such alternative splice events

Questions answered:  
Which alternative splice events might be regulated by conserved secondary structures.



