

Create ScanFold Submission

Submit your sequence (in FASTA format):

```
>hg38|chr6:43784726..43785077(VEGFA_riboswitch_region)
GACTCTGCGCAGAGCACTTTGGGTCCGGAGGGCGAGACTCCGGCGGAAGCATTCCCGGGCGGGTGACCCAGCACGGTC
CCTCTTGGAAATTGGATTGCGCATTTTATTTTCTTGCTGCTAAATCACCGAGCCCGGAAGATTAGAGAGTTTATTTTC
TGGGATTCCGTAGACACACCCACCCACATACATACATTTATATATATATATATATATATATAAAAATAAATATC
TCTATTTATATATATAAAAATATATATATTTCTTTTTTAAATTAACAGTGCTAATGTTATTGGTGTCTTCACTGGATG TATTGACTGCTGTGGACTTGAGTTGGGAGGGGAATGTTCC
```

Sequence must be in FASTA format (i.e. requires a header line before sequence). Or you can upload a FASTA file below. Limit 20,000 nucleotides.

FASTA file upload

 No file chosen

Files must be less than 50 KB.

Allowed file types: **txt fa fasta**.

Input Name

Give a name for this submission to be used for labeling output. No spaces or unique characters allowed. Default = "UserInput"

E-mail address

When your job is complete an email will be sent to this address along with a link to results.

expires

Window Size

This will adjust the window size (in nucleotides) which is used to canvas input sequence (default 120)

Step Size

This will adjust the step size (in nucleotides) of the ScanFold-Scan scanning window analysis. By default this is set to 10 nucleotides. Smaller numbers take longer but increase sequence coverage; larger numbers decrease computational time but reduce sequence coverage.

Randomizations

This will adjust the number of randomizations (number of randomized minimum free energy values) which will be used to calculate the thermodynamic z-score (Default: 30)

Shuffle Type:

ADVANCED SETTING. This will change the method of shuffling used to generate randomized sequence during calculation of the thermodynamic z-score. mono = mononucleotide shuffling; di = dinucleotide shuffling (using Clote's implementation of the Altschul and Erickson algorithm (Mol Bio Evol. 1985)).

Temperature

This will adjust the temperature (in Celsius) at which the minimum free energy RNA secondary structures will be folded (default 37)

Competition

ADVANCED SETTING. 1 = ON (default). 0 = OFF. This field adjusts whether ScanFold will detect and select the most favorable base pairs in regions with competition (when multiple base pairs compete for same partner). ScanFold-Fold results are calculated much faster but are now limited: no CT files or final partner files can be generated; IGV base pair stats are not shown; all base pairs are shown. ScanFold-Scan results are unaffected.

 Global Refold

When checked, this option will refold your entire sequence while constraining the most significant base pairs (with Zavg values < -1 and < -2).