IVTDesigner v1.1 Report for FUS

Result Summary

🏆 Top 8 Candidates Summary

The detailed analysis corresponds to the Rank #1 candidate, but **Secondary Structure Plots** are provided for all 8 candidates below.

Rank	Final Score	Length (bp)	5' Sequence Preview
#1	0.8126	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#2	0.8097	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#3	0.8097	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#4	0.8085	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#5	0.8066	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#6	0.8065	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#7	0.8053	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`
#8	0.8037	1789	`AGCAAGCTTCAGGGTGCCACCATGGCTTCT...`

Metric (Rank #1)	Before	After
CAI Score	0.9915	**0.7319**
GC Content (%)	68.2	**52.3** ▼
5' UTR MFE (kcal/mol)	-1.85	**-1.85**
Poly-T Tracts (T>=5)	0	**0**
ARE Elements (ATTTA)	0	**0**
Complex DNA Repeats	384	**10** ▼
Immunogenicity Score	0.07	**0.00**

Interpretation

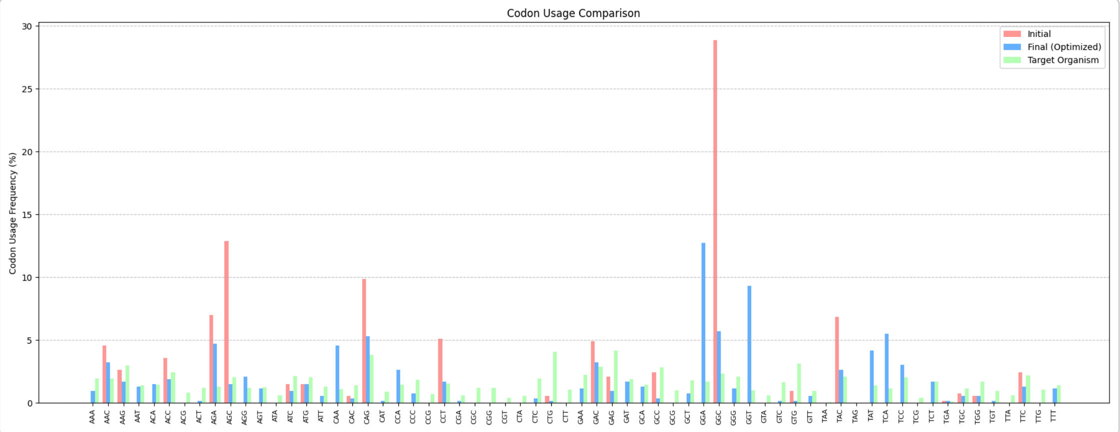
- ⚠️ **Primary Goal Note (Maximize):** The target metric 'CAI Score' did not increase (0.99 → 0.73).
- ℹ️ **GC Content Adjusted:** The GC content moved from 68.2% to 52.3%, getting closer to the target of 58.0%.
- ℹ️ **Improvement:** The 'Complex DNA Repeats' score was reduced from 384 to 10.
- ℹ️ **Improvement:** The 'Immunogenicity Score' score was reduced from 0.07 to 0.0.

Detailed Analysis (Rank #1)

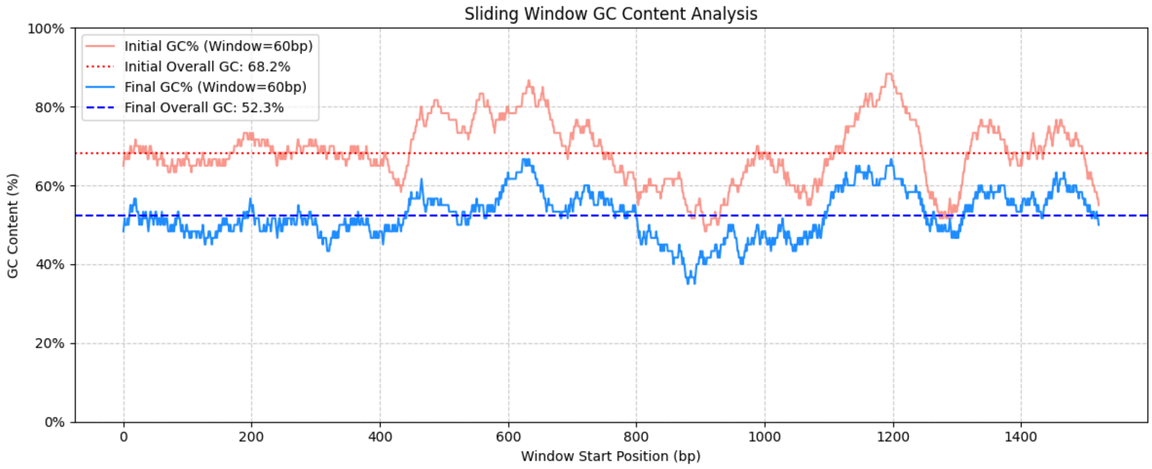
Metric	Initial	Final (Optimized)
Sequence Length	1789	1789
Cds Length	1581	1581
5 Utr Length	21	21
3 Utr Length	76	76
Poly A Length	111	111
Gc Content Percent	68.2	52.3
Cai Score	0.9915	0.7319
Cpb Score	N/A	N/A
Gc Content Full Construct	62.3	48.2
Tfbs Count	1	0
Restricted Enzyme Sites	4	1
Cpg Dinucleotide Count	147	1
Upa Dinucleotide Count	58	46
Immunogenicity Score	0.07	0.00
Immunogenicity Risk	Low	Low
Complex Dna Repeats Count	384	10
Five Prime Mfe Kcal Mol	-1.85	-1.85
Polyt Tracts T5 Plus	0	0
Polyt Tracts Cds Only	0	0
G Tracts G5 Plus	0	0
G Tracts Cds Only	0	0
Are Elements Attta	0	0

Visual Analysis

Codon Usage Analysis (Rank #1)



GC Content Distribution (Rank #1)



RNA Secondary Structure — 2D Visualization

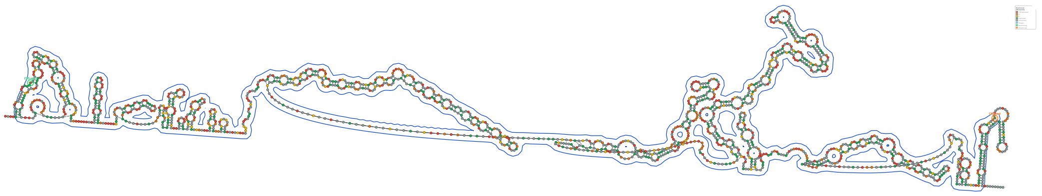
Section 1 — Initial Structure (Pre-optimization)

Initial Structure

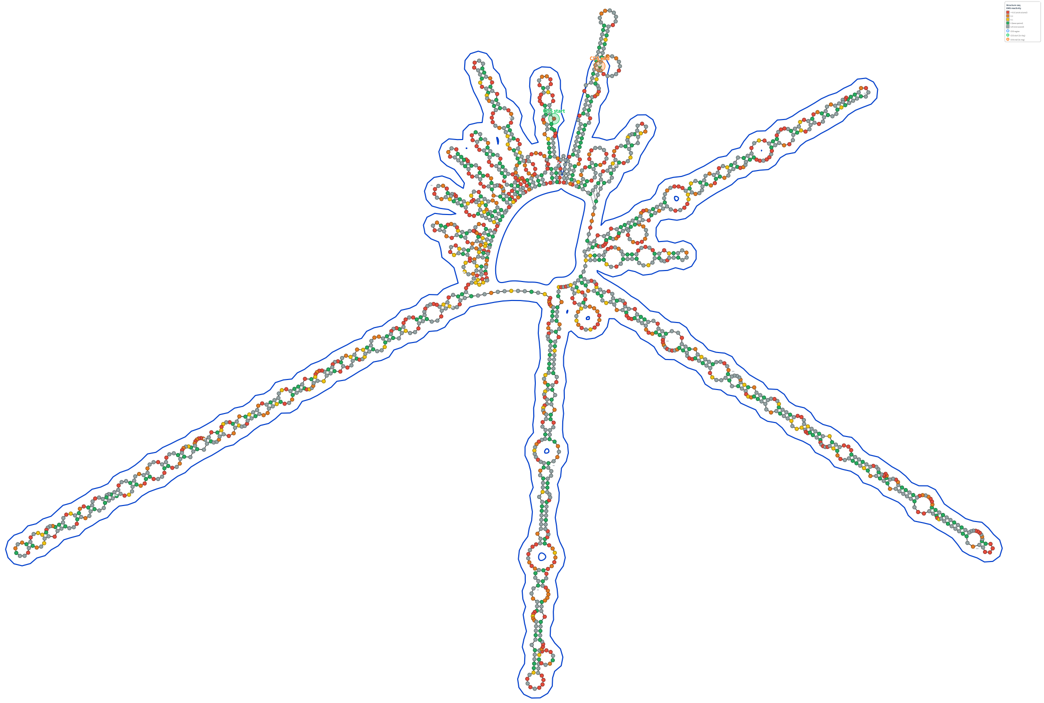
Seeded LinearFold **Layout: RNAplot Puzzler + Refine**

MFE: -426.80 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 848 / 1,678 nt (50.5%) | **Max depth:** 77 | (12.60s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine



Section 2 — Rank #1 Full Construct (Optimized)

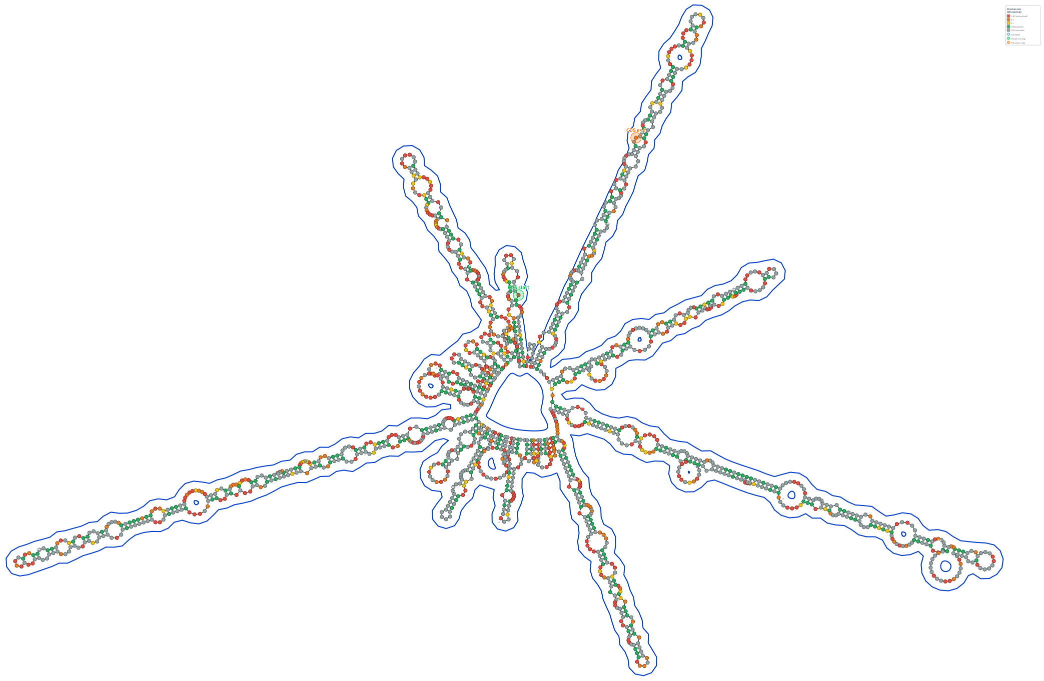
Rank #1 (Score: 0.8126)

Seeded LinearFold **Layout: RNAplot Puzzler + Refine**

MFE: -403.75 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 856 / 1,678 nt (51.0%) | **Max depth:** 74 | (3.12s)

RNAplot Puzzler + Refine

RNAplot Naview + Refine



Section 3 — Optimized Candidates (Full Construct + CDS Highlighted)

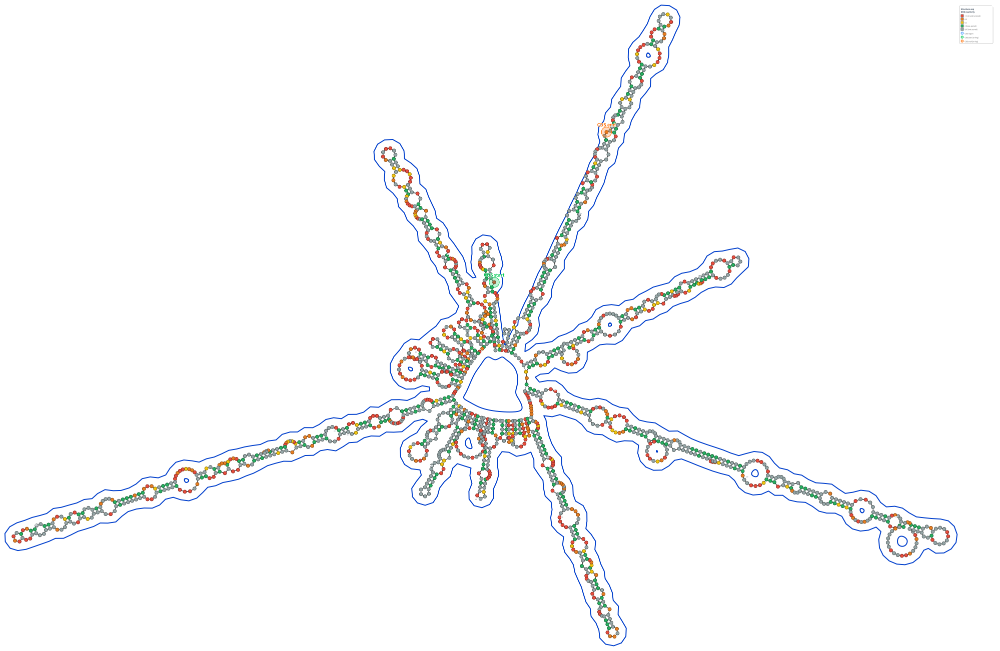
Rank #1

Rank #1 (Score: 0.8126)

Seeded LinearFold Layout: RNAplot Puzzler + Refine

MFE: -403.75 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 856 / 1,678 nt (51.0%) | **Max depth:** 74 | (3.12s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine

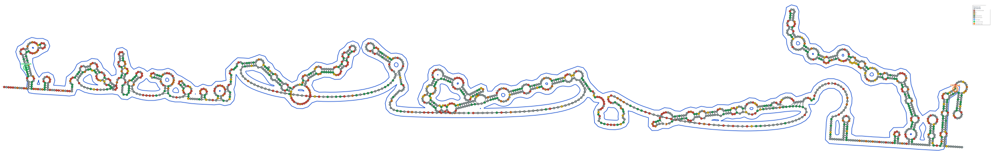
Rank #2

Rank #2 (Score: 0.8097)

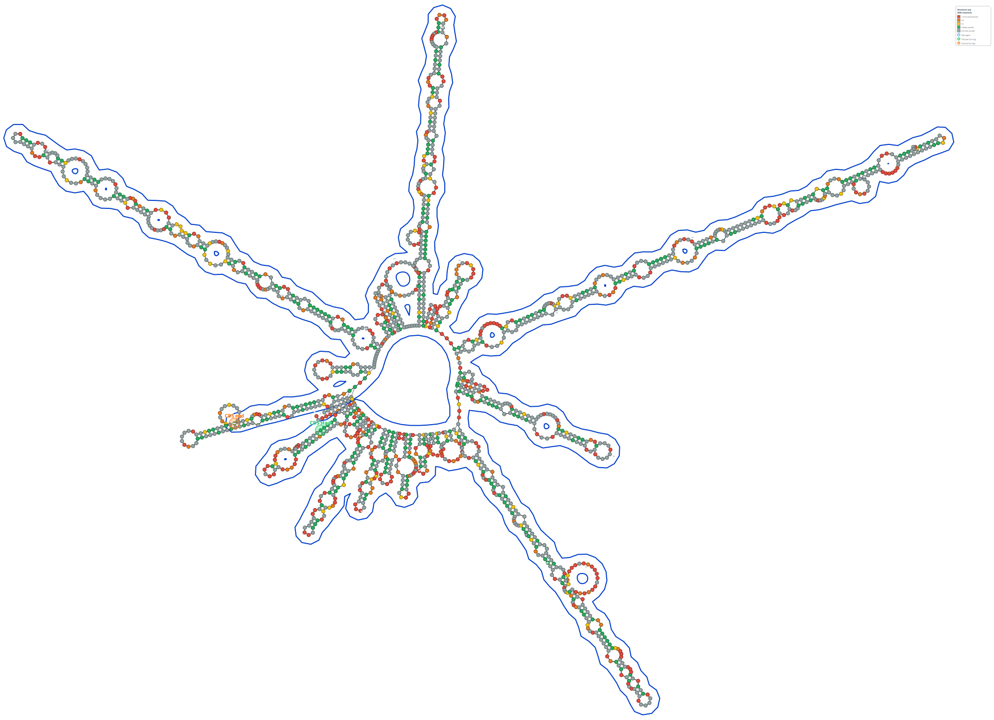
Seeded LinearFold Layout: RNAplot Puzzler + Refine

MFE: -442.00 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 870 / 1,678 nt (51.8%) | **Max depth:** 84 | (3.13s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine

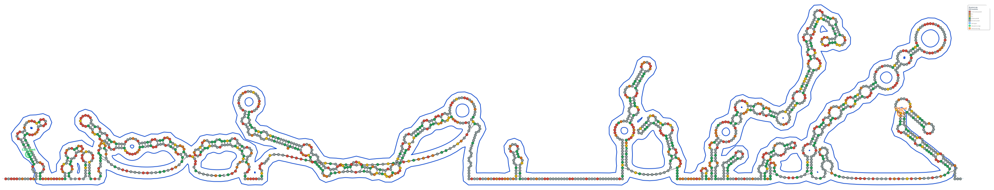


Rank #3

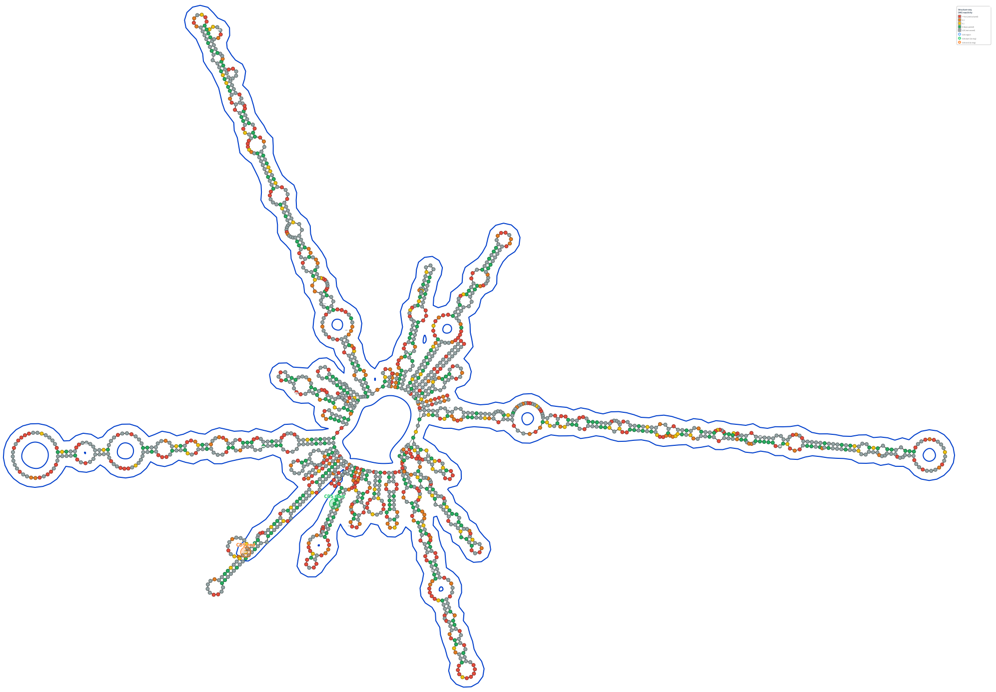
Rank #3 (Score: 0.8097)
Seeded LinearFold **Layout: RNAplot Puzzler + Refine**

MFE: -405.26 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 854 / 1,678 nt (50.9%) | **Max depth:** 83 | (3.10s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine

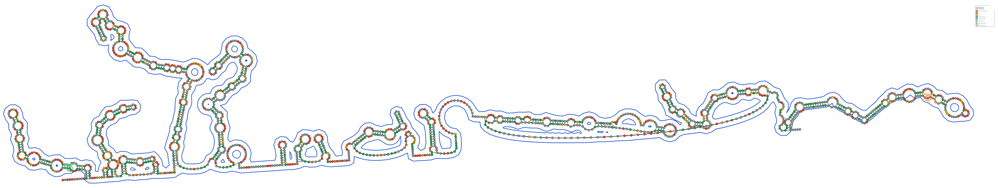


Rank #4

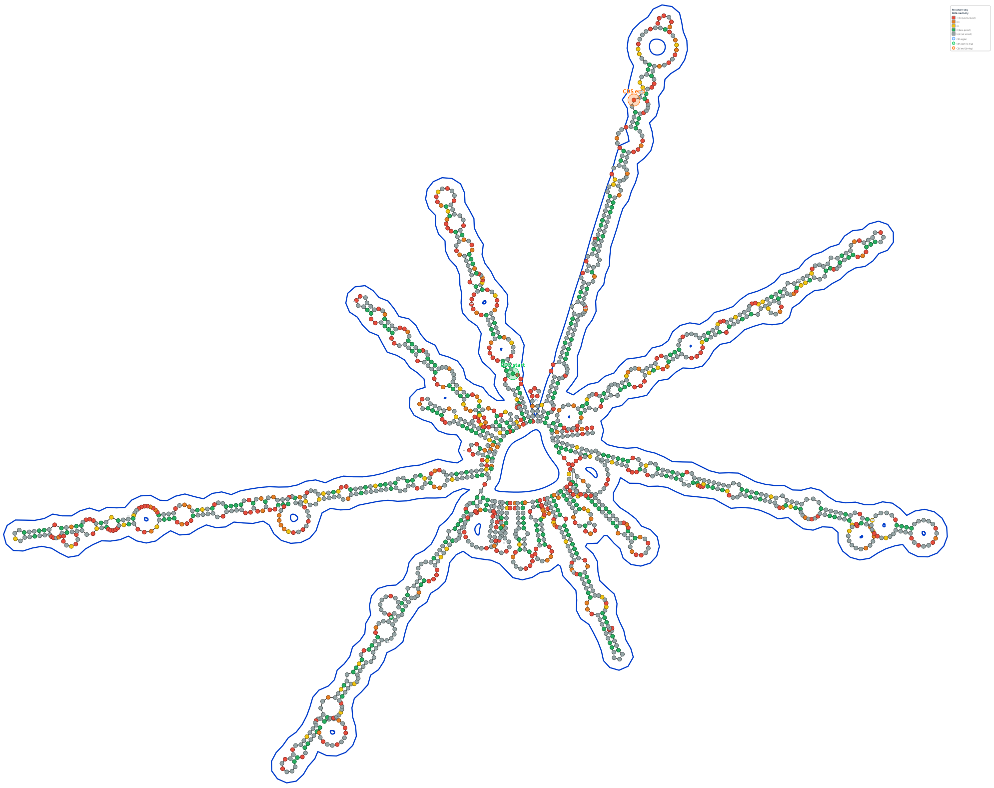
Rank #4 (Score: 0.8085)
Seeded LinearFold Layout: RNAplot Puzzler + Refine

MFE: -432.00 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 880 / 1,678 nt (52.4%) | **Max depth:** 68 | (3.13s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine

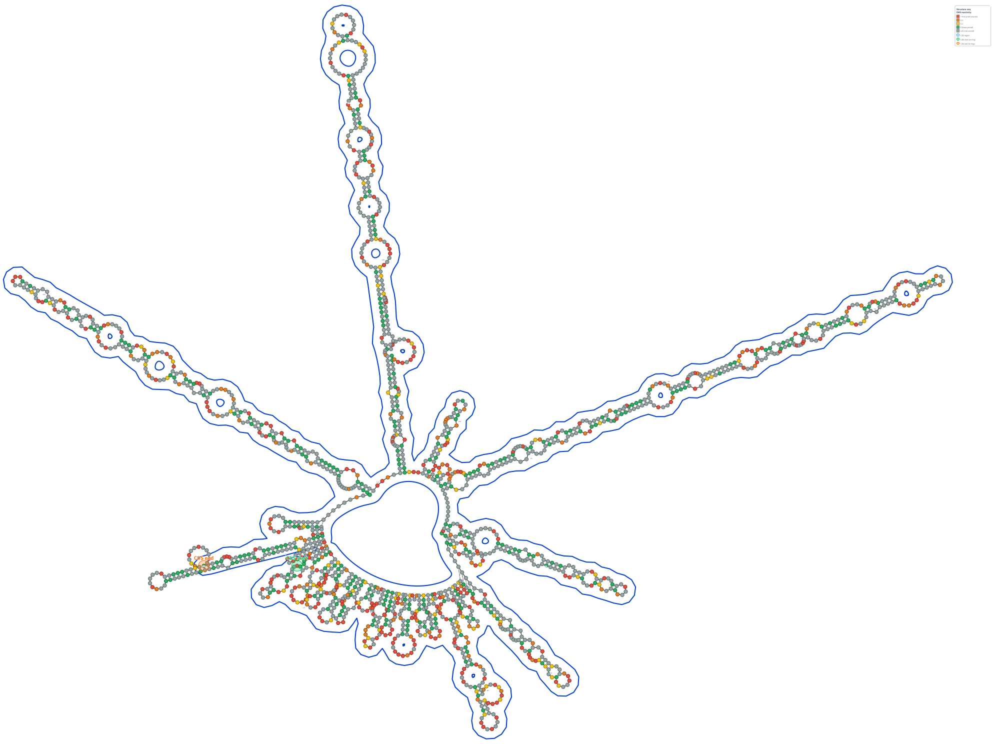


Rank #5

Rank #5 (Score: 0.8066)
Seeded LinearFold Layout: RNAplot Puzzler + Refine
MFE: -428.90 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 862 / 1,678 nt (51.4%) | **Max depth:** 81 | (3.09s)

RNAplot Puzzler + Refine

RNAplot Naview + Refine



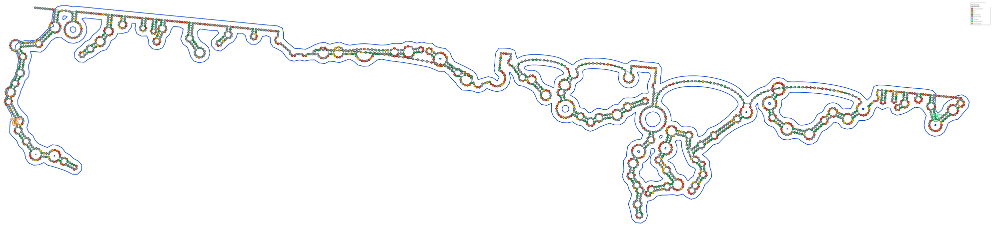
Rank #6

Rank #6 (Score: 0.8065)

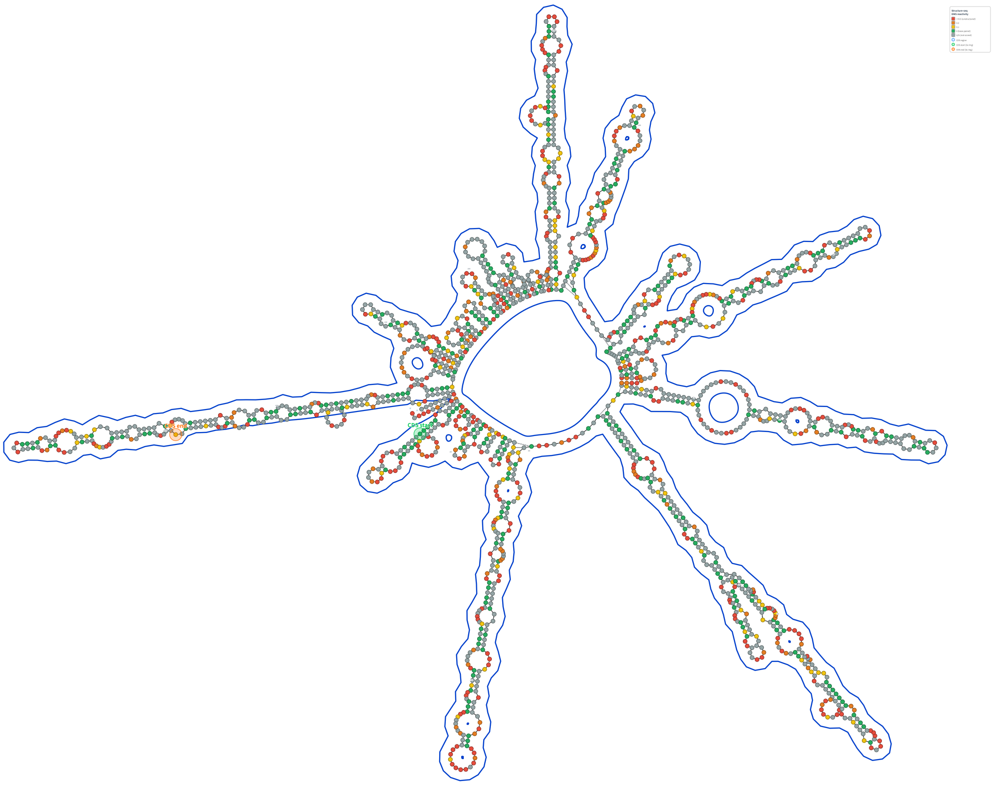
Seeded LinearFold **Layout: RNAplot Puzzler + Refine**

MFE: -384.25 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 868 / 1,678 nt (51.7%) | **Max depth:** 68 | (3.07s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine



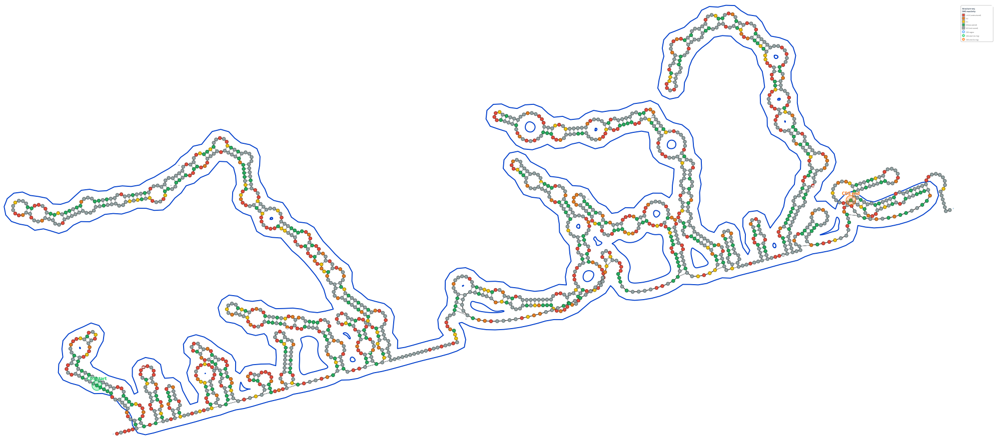
Rank #7

Rank #7 (Score: 0.8053)

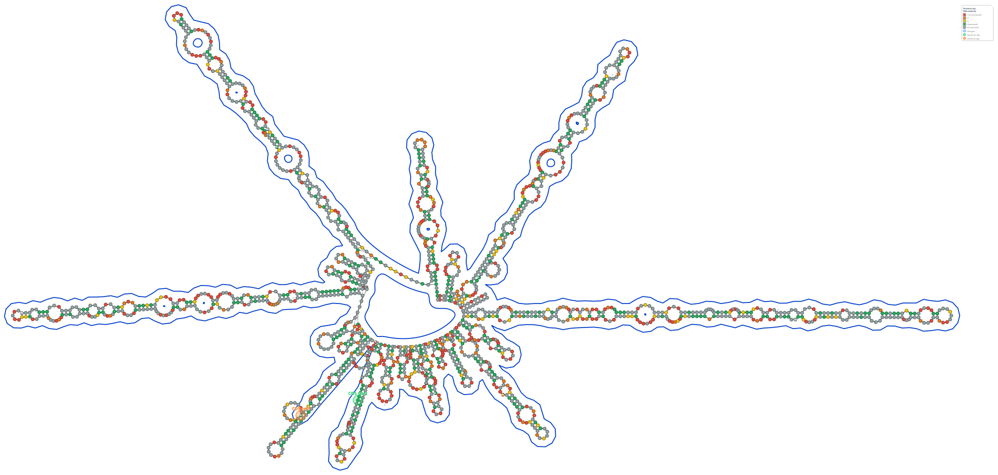
Seeded LinearFold **Layout: RNAplot Puzzler + Refine**

MFE: -428.25 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 892 / 1,678 nt (53.2%) | **Max depth:** 82 | (3.04s)

RNAplot Puzzler + Refine



RNAplot Naview + Refine



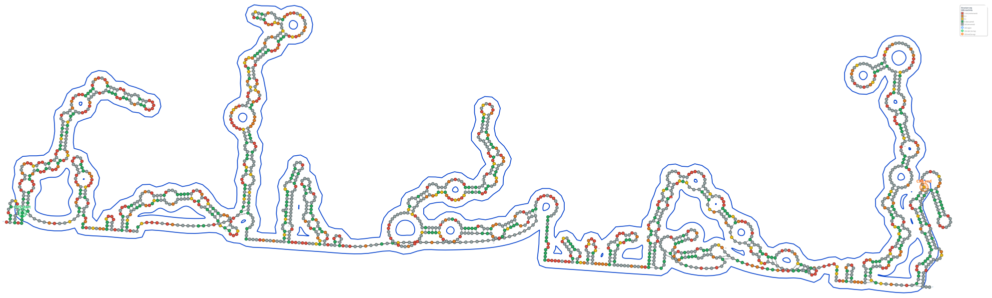
Rank #8

Rank #8 (Score: 0.8037)

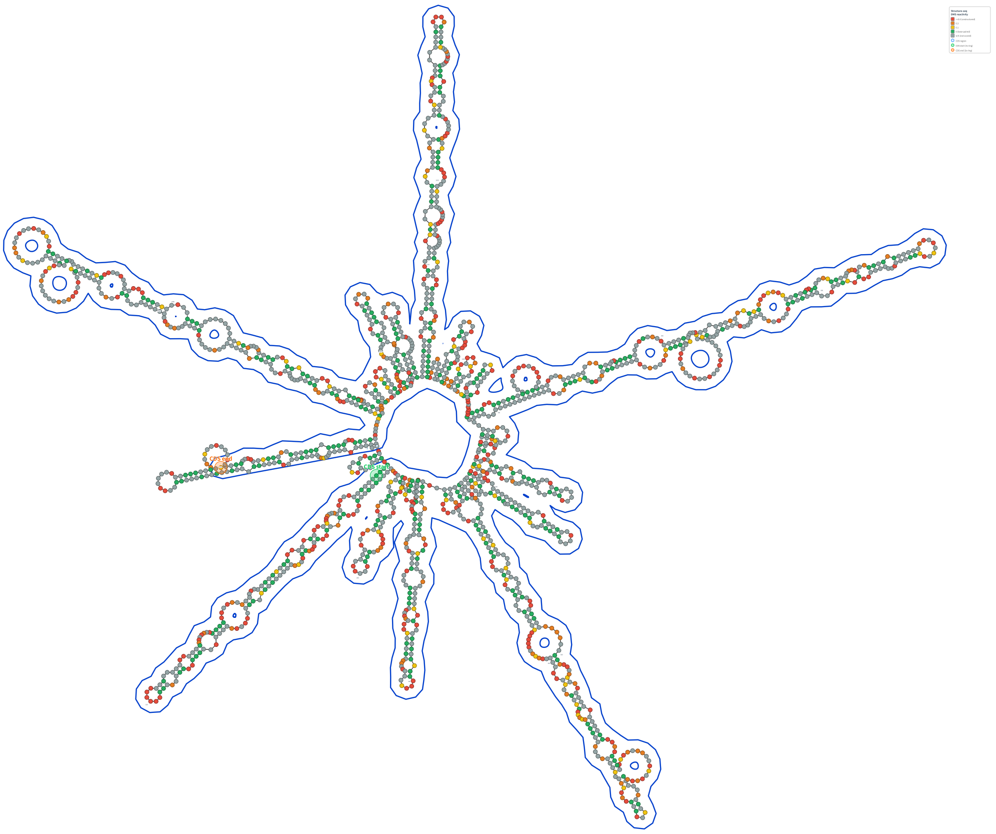
Seeded LinearFold Layout: RNAplot Puzzler + Refine

MFE: -423.95 kcal/mol | **Shape:** Multi-domain (Dumbbell) | **Paired:** 866 / 1,678 nt (51.6%) | **Max depth:** 68 | (3.07s)

RNAplot Puzzler + Refine

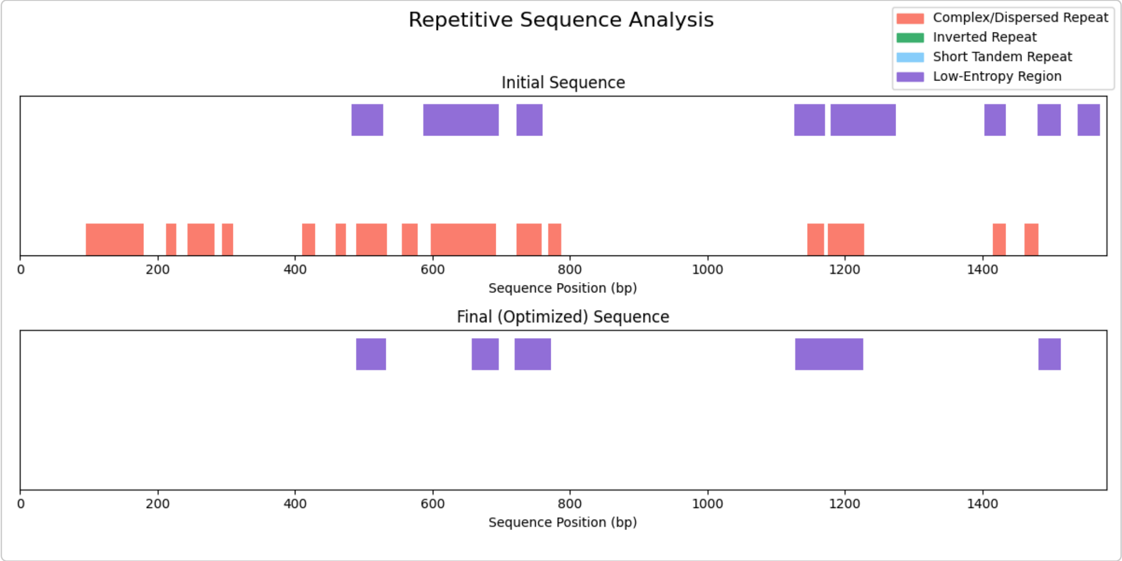


RNAplot Naview + Refine



Repetitive Sequence Analysis (Rank #1)

This plot shows locations of complex repeats.



Input Sequence Breakdown

Initial Sequence Breakdown

Common Components (Matches Optimized Design)

```
>5' UTR (21 bp)
AGCAAGCTTCAGGGTGCCACC

>3' UTR + PolyA (187 bp)
GCTTTATTATACTAGTAACTGCTGTTCCTTCAGTTATTATTAGTTCCTTTCATTTCTGTTCATTTTGTATGTTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

>Initial CDS (1581 bp)

```
ATGGCCAGCAACGACTACACCCAGCAGGCCACCCAGAGCTACGGCGCCTACCCTACCCAGCCTGGCCAGGGCTACAGCCAGCAGAGCAGCCAGCCTTACGGCCAGCAGAGCTACAGCGGCTA
CAGCCAGAGCACCGACACCAGCGGCTACGGCCAGAGCAGCTACAGCAGCTACGGCCAGAGCCAGAACACCGGCTACGGCACCCAGAGCACCCCTCAGGGCTACGGCAGCACCGGCGGCTACG
GCAGCAGCCAGAGCAGCCAGAGCAGCTACGGCCAGCAGAGCAGCTACCCTGGCTACGGCCAGCAGCCTGCCCCTAGCAGCACCAGCGGCAGCTACGGCAGCAGCAGCCAGAGCAGCAGCTAC
GGCCAGCCTCAGAGCGGCAGCTACAGCCAGCAGCCTAGCTACGGCGGCCAGCAGCAGAGCTACGGCCAGCAGCAGAGCTACAACCCTCCTCAGGGCTACGGCCAGCAGAACCAGTACAACAG
CAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCAACTACGGCCAGGACCAGAGCAGCATGAGCAGCGGCGGCGGCAGCGGCGGCGGCTACGGCAACCAGGACCAGAGCGGCGGCGGCG
GCAGCGGCGGCTACGGCCAGCAGGACAGAGGCGGCAGAGGCAGAGGCGGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTACAACAGAAGCAGCGGCGGCTACGAGCCTAGAGGCAGA
GGCGGCGGCAGAGGCGGCAGAGGCGGCATGGGCGGCAGCGACAGAGGCGGCTTCAACAAGTTCGGCGGCCCTAGAGACCAGGGCAGCAGACACGACAGCGAGCAGGACAACAGCGACAACAA
CACCATCTTCGTGCAGGGCCTGGGCGAGAACGTGACCATCGAGAGCGTGGCCGACTACTTCAAGCAGATCGGCATCATCAAGACCAACAAGAAGACCGGCCAGCCTATGATCAACCTGTACA
CCGACAGAGAGACCGGCAAGCTGAAGGGCGAGGCCACCGTGAGCTTCGACGACCCTCCTAGCGCCAAGGCCGCCATCGACTGGTTCGACGGCAAGGAGTTCAGCGGCAACCCTATCAAGGTG
AGCTTCGCCACCAGAAGAGCCGACTTCAACAGAGGCGGCGGCAACGGCAGAGGCGGCAGAGGCAGAGGCGGCCCTATGGGCAGAGGCGGCTACGGCGGCGGCGGCAGCGGCGGCGGCGGCAG
AGGCGGCTTCCCTAGCGGCGGCGGCGGCGGCGGCGGCCAGCAGAGAGCCGGCGACTGGAAGTGCCCTAACCCTACCTGCGAGAACATGAACTTCAGCTGGAGAAACGAGTGCAACCAGTGCA
AGGCCCCTAAGCCTGACGGCCCTGGCGGCGGCCCTGGCGGCAGCCACATGGGCGGCAACTACGGCGACGACAGAAGAGGCGGCAGAGGCGGCTACGACAGAGGCGGCTACAGAGGCAGAGGC
GGCGACAGAGGCGGCTTCAGAGGCGGCAGAGGCGGCGGCGACAGAGGCGGCTTCGGCCCTGGCAAGATGGACAGCAGAGGCGAGCACAGACAGGACAGAAGAGAGAGACCTTACTGA
```

Final Optimized Candidates (FASTA)

1. Common mRNA Components (Shared)

>5' UTR (21 bp)

```
AGCAAGCTTCAGGGTGCCACC
```

>3' UTR (76 bp)

```
GCTTTATTATACTAGTAACTGCTGTTCCTTCAGTTATTATTAGTTCCTTTCATTTCTGTTCATTTTGTATGTTTGG
```

>Poly(A) Tail (111 nt)

```
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
```

2. Optimized CDS Candidates (Variable)

Rank #1 (Score: 0.8126)

```
>Optimized_CDS_FUS_Rank1_Score0.8126_CAI0.7319_MFE-93.9
ATGGCTTCTAATGATTACACCCAGCAGGCAACCCAGTCCTATGGAGCTTATCCAACCCAACCAGGACAGGGATACTCACAACAATCCTCCCAGCCATATGGCCAACAGTCTTACTCAGGCTACTCCCA
```

```
ATCAACTGACACCTCTGGATATGGACAGTCATCCTACTCCTCATATGGTCAGAGCCAAAACACAGGTTATGGCACCCAGTCAACCCCTCAAGGTTATGGTTCAACAGGAGGCTATGGGTCATCCCAGT
CCTCACAATCCTCATATGGACAGCAAAGCAGTTACCCAGGTTATGGCCAACAGCCTGCTCCCTCATCAACATCAGGCAGTTATGGATCATCCTCCCAAAGTTCTTCATATGGACAGCCACAATCAGGG
TCCTACTCCCAGCAACCTTCCTATGGAGGTCAACAACAAAGCTATGGCCAACAACAGTCATACAACCCACCTCAGGGATATGGCCAGCAGAATCAGTACAACTCCAGCAGTGGTGGAGGTGGAGGAGG
TGGAGGAGGTGGGAATTATGGCCAAGATCAAAGCAGCATGAGCTCTGGAGGAGGATCAGGAGGAGGTTATGGCAACCAAGATCAGTCTGGAGGTGGAGGATCTGGTGGTTATGGCCAGCAGGACAGAG
GTGGACGAGGCAGAGGAGGCTCAGGAGGTGGTGGTGGTGGTGGTGGTGGTGGCTACAACAGATCATCTGGTGGATATGAACCCAGAGGAAGAGGAGGAGGAAGGGGTGGGAGAGGAGGAATGGGTGGA
TCAGACAGAGGAGGCTTCAACAAGTTTGGAGGCCCCAGGGATCAGGGATCAAGACATGACAGTGAGCAGGACAACTCAGACAACAACACCATCTTTGTTCAGGGACTGGGTGAAAATGTCACCATTGA
GTCAGTTGCAGATTACTTCAAACAGATTGGCATCATCAAAACAAACAAGAAGACAGGCCAGCCCATGATCAATCTCTACACAGACAGAGAAACAGGCAAACTCAAGGGTGAAGCAACAGTTTCTTTTG
ATGACCCACCTTCAGCCAAGGCAGCAATTGACTGGTTTGATGGAAAGGAGTTCTCAGGAAACCCAATCAAGGTGTCATTTGCCACCAGAAGAGCTGACTTCAACAGAGGTGGAGGAAATGGAAGGGGT
GGCAGGGGAAGGGGAGGCCCAATGGGAAGAGGTGGATATGGTGGAGGTGGCAGTGGTGGTGGAGGCAGGGGAGGATTCCCATCAGGTGGAGGTGGTGGTGGAGGCCAACAAAGAGCAGGAGACTGGAA
GTGCCCAAACCCAACCTGTGAGAACATGAACTTCAGCTGGAGGAATGAATGCAACCAGTGCAAGGCACCAAAACCAGATGGACCTGGAGGAGGACCTGGTGGATCCCACATGGGAGGCAACTATGGGG
ATGACAGAAGAGGTGGCAGGGGAGGTTATGACAGAGGAGGATACAGAGGCAGAGGAGGTGACAGAGGAGGTTTCAGAGGTGGAAGAGGTGGTGGGGACAGGGGTGGCTTTGGCCCTGGCAAAATGGAC
TCAAGAGGTGAACACAGACAAGACAGGAGAGAGAGGCCTTACTGA
```

Rank #2 (Score: 0.8097)

```
>Optimized_CDS_FUS_Rank2_Score0.8097_CAI0.7463_MFE-56.6
ATGGCTTCTAATGATTACACCCAGCAGGCAACCCAGAGCTATGGTGCCTACCCCACTCAACCAGGCCAAGGTTATTCACAGCAGTCCTCACAGCCTTATGGGCAGCAGTCATACTCAGGGTACTCCCA
GAGCACAGACACCTCAGGTTATGGACAGTCATCCTACAGCTCCTATGGACAGTCACAGAACACTGGATATGGCACCCAGTCAACCCCTCAAGGTTATGGGTCAACAGGAGGCTATGGCTCAAGCCAAT
CATCTCAATCCTCCTATGGACAGCAAAGCTCCTACCCAGGTTATGGACAACAGCCAGCTCCTTCATCAACATCAGGATCATATGGATCATCATCCCAGAGCTCCTCTTATGGCCAGCCTCAGTCAGGG
AGCTATTCCCAGCAGCCTTCCTATGGTGGACAGCAGCAGAGTTATGGTCAGCAGCAAAGTTACAACCCACCACAAGGGTATGGACAACAGAACCAATACAACAGCAGTTCTGGTGGAGGTGGTGGAGG
AGGTGGAGGTGGGAATTATGGACAAGATCAATCATCCATGTCCTCTGGAGGAGGTTCTGGAGGAGGTTATGGCAATCAGGACCAGAGTGGAGGTGGAGGAAGTGGTGGATATGGTCAGCAGGACAGAG
GAGGCAGGGGCAGAGGTGGGTCAGGAGGTGGTGGTGGTGGTGGTGGAGGTGGCTACAACAGGTCTTCTGGTGGCTATGAGCCCAGAGGCAGGGGTGGAGGAAGAGGAGGCAGAGGAGGAATGGGAGGT
TCAGACAGGGGTGGGTTCAACAAGTTTGGTGGTCCAAGGGATCAAGGGTCAAGGCATGACTCAGAACAGGACAACTCTGACAACAACACCATTTTTGTGCAGGGTCTGGGAGAGAATGTCACCATTGA
ATCTGTGGCTGACTACTTCAAGCAGATTGGCATCATCAAGACAAACAAGAAGACAGGCCAACCAATGATCAATCTCTACACAGACAGAGAAACTGGAAAGTTGAAAGGAGAGGCAACTGTTTCTTTTG
ATGACCCCCCATCTGCCAAAGCTGCAATTGATTGGTTTGATGGGAAAGAGTTCTCTGGAAACCCAATCAAGGTGAGCTTTGCAACCAGGAGAGCTGACTTCAACAGAGGAGGAGGAAATGGCAGAGGA
GGAAGGGGAAGGGGTGGACCAATGGGGAGAGGAGGATATGGAGGAGGAGGCAGTGGTGGTGGTGGGAGAGGAGGATTCCCATCAGGTGGAGGAGGCGGAGGAGGACAGCAAAGAGCTGGAGATTGGAA
GTGTCCAAATCCCACCTGTGAGAACATGAACTTCAGCTGGAGGAATGAGTGCAACCAATGCAAAGCTCCAAAGCCTGATGGGCCTGGTGGAGGTCCAGGTGGATCTCACATGGGTGGAAACTATGGTG
ATGACAGGAGGGGAGGCAGGGGTGGTTATGACAGAGGTGGATACAGAGGCAGAGGAGGTGACAGAGGTGGCTTCAGAGGTGGGAGAGGTGGAGGGGACAGGGGTGGTTTTGGACCTGGCAAGATGGAC
TCCAGGGGCGAACACAGACAGGACAGAAGAGAAAGGCCATACTGA
```

Rank #3 (Score: 0.8097)

```
>Optimized_CDS_FUS_Rank3_Score0.8097_CAI0.7441_MFE-84.8
ATGGCTTCTAATGATTACACCCAGCAGGCAACCCAGAGCTATGGTGCCTATCCCACACAACCAGGACAAGGATACTCACAACAGTCTTCCCAGCCTTATGGTCAGCAATCTTACTCTGGCTACTCTCA
GTCCACAGACACCTCTGGATACGGGCAGTCATCCTACTCAAGCTATGGACAGTCACAAAACACTGGATATGGAACACAGTCAACACCACAGGGCTATGGATCAACTGGAGGATATGGCTCATCACAAA
GCTCACAGTCATCATATGGTCAGCAAAGCTCCTATCCTGGTTATGGACAGCAGCCTGCTCCTTCCTCAACCTCTGGATCTTATGGAAGCAGCTCACAGTCCTCAAGTTATGGACAACCTCAATCAGGA
AGCTACTCACAACAGCCTTCATATGGAGGACAACAGCAATCCTATGGCCAGCAACAGAGCTACAACCCACCTCAGGGCTATGGCCAGCAGAACCAATACAACTCATCATCTGGAGGAGGTGGAGGTGG
AGGTGGAGGAGGGAATTATGGACAGGACCAGTCATCCATGTCCTCTGGAGGTGGATCAGGTGGTGGTTATGGCAACCAAGACCAGTCAGGAGGAGGAGGCTCTGGAGGTTATGGCCAGCAGGACAGAG
GTGGAAGAGGAAGAGGAGGATCAGGTGGTGGAGGTGGTGGTGGTGGAGGAGGATACAACAGATCTTCTGGTGGATATGAGCCAAGAGGGAGAGGAGGAGGAAGGGGTGGAAGGGGAGGGATGGGTGGA
TCTGACAGAGGTGGTTTCAACAAATTTGGTGGTCCAAGGGATCAGGGTTCCAGACATGACTCTGAGCAGGACAATTCTGACAACAACACCATCTTTGTGCAGGGTTTGGGAGAGAATGTCACCATTGA
GTCAGTTGCTGATTACTTCAAGCAGATTGGCATCATCAAAACAAACAAGAAAACTGGACAGCCAATGATCAACCTTTACACTGACAGAGAAACTGGCAAATTGAAAGGAGAAGCAACTGTGTCTTTTG
ATGATCCTCCATCTGCAAAAGCTGCAATTGATTGGTTTGACGGCAAGGAGTTCTCAGGCAACCCAATCAAGGTGAGCTTTGCCACCAGAAGAGCAGACTTCAACAGAGGTGGAGGAAATGGCAGAGGT
GGAAGGGGCAGAGGAGGTCCAATGGGGAGAGGAGGATATGGAGGAGGAGGGTCAGGTGGTGGTGGAAGAGGAGGCTTCCCATCAGGAGGAGGAGGTGGTGGTGGACAGCAGAGGGCAGGAGACTGGAA
GTGCCCCAATCCAACATGTGAAAACATGAACTTCTCCTGGAGGAATGAGTGCAACCAGTGCAAGGCTCCAAAGCCTGATGGTCCTGGAGGAGGTCCTGGTGGAAGTCACATGGGAGGAAACTATGGGG
ATGACAGAAGAGGTGGCAGAGGTGGGTATGACAGAGGTGGATACAGAGGCAGAGGAGGTGACAGAGGTGGATTCAGAGGTGGGAGAGGAGGTGGGGACAGAGGTGGTTTTGGACCTGGAAAGATGGAC
AGCAGAGGAGAACACAGACAGGACAGAAGAGAAAGGCCTTACTGA
```

Rank #4 (Score: 0.8085)

```
>Optimized_CDS_FUS_Rank4_Score0.8085_CAI0.7410_MFE-81.8
ATGGCTTCTAATGATTACACTCAGCAAGCAACCCAATCCTATGGTGCTTATCCCACACAACCAGGTCAGGGTTACTCCCAACAGTCATCCCAACCATATGGGCAGCAGTCCTACTCAGGGTACTCCCA
ATCCACAGACACCTCTGGTTATGGCCAGTCATCCTACAGTTCCTATGGTCAGTCACAGAACACTGGATATGGCACACAGAGCACTCCACAAGGATATGGCTCAACAGGTGGATATGGGTCATCCCAAA
GTTCACAGTCATCATATGGACAGCAGTCCTCCTACCCTGGCTATGGACAGCAGCCTGCTCCATCTTCCACATCTGGATCCTATGGCTCCTCCTCCCAGTCCTCCTCATATGGACAACCACAGTCAGGA
AGCTACAGCCAGCAGCCTTCTTATGGAGGTCAGCAGCAATCCTATGGGCAGCAACAATCCTACAATCCACCCCAGGGGTATGGGCAGCAGAACCAATACAACAGCTCTTCTGGAGGAGGTGGAGGAGG
TGGAGGTGGAGGCAATTATGGTCAGGATCAGTCATCCATGAGTTCTGGTGGTGGATCTGGAGGTGGATATGGCAATCAAGACCAGTCAGGAGGTGGAGGTTCTGGAGGATATGGCCAGCAGGACAGAG
GAGGAAGAGGCAGAGGAGGATCTGGAGGTGGTGGTGGTGGTGGTGGAGGTGGATACAACAGGAGCTCTGGTGGATATGAACCAAGAGGAAGGGGAGGAGGAAGAGGTGGAAGGGGTGGAATGGGTGGA
TCTGACAGAGGTGGATTCAACAAGTTTGGTGGACCAAGGGACCAAGGTTCCAGACATGATTCAGAGCAGGACAACTCTGACAACAACACAATCTTTGTCCAAGGTCTTGGAGAGAATGTCACAATTGA
GTCAGTGGCTGATTACTTCAAGCAGATTGGCATCATCAAGACCAACAAAAAGACAGGTCAGCCAATGATCAACCTGTACACAGACAGAGAAACTGGCAAGTTGAAAGGAGAAGCCACTGTCAGTTTTG
ATGACCCACCTTCAGCAAAAGCTGCAATTGACTGGTTTGATGGCAAAGAGTTCTCTGGCAACCCCATCAAGGTGAGCTTTGCAACCAGGAGAGCTGACTTCAACAGAGGTGGAGGAAATGGAAGAGGT
GGGAGAGGAAGAGGTGGCCCAATGGGCAGAGGAGGTTATGGTGGTGGAGGCTCAGGTGGTGGTGGAAGAGGAGGCTTCCCATCAGGTGGAGGTGGTGGTGGAGGACAACAGAGAGCAGGAGACTGGAA
GTGCCCAAATCCCACCTGTGAAAACATGAACTTCTCTTGGAGGAATGAGTGCAACCAGTGCAAGGCTCCCAAACCTGATGGTCCTGGAGGTGGTCCTGGTGGCTCTCACATGGGAGGAAATTATGGTG
ATGACAGAAGGGGAGGCAGGGGTGGCTATGACAGAGGAGGCTACAGAGGCAGAGGAGGTGACAGAGGTGGTTTCAGGGGAGGAAGGGGTGGAGGGGACAGAGGTGGATTTGGACCAGGAAAGATGGAC
AGCAGAGGAGAGCACAGACAAGACAGGAGGGAAAGGCCTTACTGA
```

Rank #5 (Score: 0.8066)

```
>Optimized_CDS_FUS_Rank5_Score0.8066_CAI0.7359_MFE-56.1
ATGGCTTCTAATGATTACACACAGCAGGCCACCCAGTCCTATGGAGCCTACCCAACTCAACCAGGACAAGGATACTCACAGCAGAGCTCCCAGCCTTATGGGCAGCAGTCTTACTCTGGCTATTCCCA
GTCCACTGACACCTCAGGTTATGGACAGAGCTCATACAGCTCATATGGGCAATCTCAAAACACAGGATATGGCACCCAATCCACCCCACAAGGATATGGATCAACTGGAGGTTATGGCTCATCACAAT
CAAGCCAATCCTCATATGGACAACAGAGCTCTTATCCAGGGTATGGCCAACAGCCAGCTCCATCTTCAACATCAGGTTCATATGGCTCATCTTCCCAGTCCTCATCTTATGGGCAACCACAATCAGGG
TCTTACAGCCAACAACCTTCCTATGGTGGTCAACAGCAATCTTATGGCCAGCAGCAAAGCTACAACCCTCCACAGGGGTATGGGCAGCAAAACCAGTACAATTCAAGTTCTGGAGGAGGTGGCGGTGG
AGGAGGTGGTGGGAACTATGGACAAGATCAAAGTTCCATGAGCTCTGGAGGTGGTTCTGGTGGTGGTTATGGTAATCAGGACCAGTCAGGAGGAGGAGGAAGTGGTGGCTATGGACAGCAGGACAGAG
GTGGGAGAGGCAGGGGTGGGTCAGGTGGTGGTGGTGGTGGTGGAGGAGGTTACAACAGATCATCAGGTGGTTATGAACCCAGAGGCAGAGGTGGAGGAAGGGGTGGAAGAGGAGGAATGGGAGGT
TCAGACAGAGGTGGGTTCAACAAATTTGGAGGACCAAGGGATCAGGGGTCAAGACATGACTCTGAGCAGGACAACTCTGACAACAACACCATTTTTGTGCAGGGCCTGGGAGAGAATGTCACCATTGA
ATCTGTGGCTGACTACTTCAAGCAGATTGGAATCATCAAAACCAACAAGAAGACTGGACAACCCATGATCAATCTCTACACAGACAGAGAGACTGGAAAGTTGAAGGGAGAGGCAACAGTTTCATTTG
ATGATCCTCCTTCTGCCAAAGCAGCAATTGATTGGTTTGATGGAAAGGAGTTCTCAGGAAATCCCATCAAGGTGAGCTTTGCAACCAGGAGAGCTGACTTCAACCGTGGTGGTGGCAATGGCAGGGGA
GGGAGAGGCAGAGGAGGTCCCATGGGAAGAGGTGGATATGGAGGAGGAGGCAGTGGTGGTGGAGGGAGAGGAGGATTCCCATCAGGAGGAGGAGGTGGAGGAGGTCAGCAGAGAGCTGGAGACTGGAA
ATGTCCAAATCCCACTTGTGAAAACATGAACTTCAGCTGGAGGAATGAGTGCAACCAGTGCAAAGCACCAAAGCCAGATGGCCCTGGAGGTGGCCCAGGTGGTTCTCACATGGGAGGAAACTATGGAG
ATGACAGAAGAGGTGGCAGGGGAGGATATGACAGAGGTGGCTACAGAGGCAGAGGAGGAGACAGAGGTGGATTCAGAGGTGGGAGGGGTGGAGGGGACAGAGGTGGTTTTGGTCCTGGAAAGATGGAC
AGCAGAGGTGAGCACAGACAGGACAGAAGAGAAAGGCCATACTGA
```

Rank #6 (Score: 0.8065)

```
>Optimized_CDS_FUS_Rank6_Score0.8065_CAI0.7287_MFE-58.4
ATGGCTTCTAATGATTACACACAGCAAGCCACACAATCATATGGTGCTTACCCCACACAACCAGGTCAAGGATACTCACAGCAGTCATCCCAGCCCTATGGGCAACAGAGCTACTCTGGCTACAGCCA
ATCAACTGACACATCTGGATATGGCCAATCATCTTACTCCTCCTATGGACAATCACAGAACACAGGATATGGAACACAAAGCACACCACAAGGTTATGGTTCAACAGGAGGTTATGGTTCATCACAGT
CATCCCAGTCATCCTATGGCCAGCAATCAAGCTATCCTGGCTATGGACAACAGCCTGCTCCATCTTCAACATCAGGTTCATATGGCAGCTCCTCCCAAAGTTCAAGTTATGGGCAGCCCCAGTCTGGG
AGTTATTCTCAGCAGCCATCCTATGGTGGACAACAGCAGTCTTATGGACAGCAGCAATCATACAACCCACCTCAGGGATATGGACAACAGAACCAATACAACTCATCTTCAGGTGGAGGTGGTGGCGG
AGGTGGAGGAGGAAACTATGGTCAGGATCAGTCTTCAATGTCATCAGGAGGAGGAAGTGGAGGAGGCTATGGAAATCAGGATCAGTCAGGAGGTGGTGGATCAGGAGGATATGGTCAACAGGACAGAG
GTGGAAGGGGCAGAGGTGGGTCTGGAGGAGGAGGTGGTGGTGGAGGAGGCTACAACAGAAGCTCAGGAGGATATGAGCCAAGAGGAAGGGGAGGTGGAAGGGGAGGAAGAGGAGGAATGGGAGGA
TCTGACAGGGGAGGCTTCAACAAGTTTGGAGGACCCAGGGATCAGGGATCAAGACATGACTCAGAACAGGACAACTCAGACAACAACACAATCTTTGTGCAGGGCTTGGGAGAAAATGTCACAATTGA
ATCAGTGGCAGACTATTTCAAGCAGATTGGAATCATCAAGACCAACAAGAAAACTGGACAGCCAATGATCAATCTTTACACTGACAGAGAGACTGGCAAATTGAAGGGGGAAGCAACAGTGAGCTTTG
ATGATCCACCATCTGCCAAGGCTGCAATTGACTGGTTTGATGGCAAGGAGTTCAGTGGAAATCCAATCAAAGTAAGCTTTGCCACCAGAAGAGCAGACTTCAACAGAGGAGGTGGCAATGGAAGGGGT
GGAAGAGGAAGAGGTGGTCCAATGGGGAGAGGAGGATATGGTGGAGGAGGCTCTGGTGGAGGAGGAAGAGGTGGTTTTCCATCTGGTGGAGGTGGTGGTGGAGGCCAACAAAGAGCTGGTGATTGGAA
ATGCCCAAATCCAACATGTGAGAACATGAACTTCAGCTGGAGGAATGAGTGCAATCAGTGCAAGGCACCCAAACCTGATGGACCTGGAGGTGGACCTGGAGGATCTCACATGGGTGGAAATTATGGAG
ATGACAGAAGGGGAGGCAGAGGCGGTTATGACAGAGGAGGCTACAGAGGCAGGGGAGGAGACAGAGGAGGTTTCAGAGGTGGAAGAGGTGGAGGGGACAGGGGTGGTTTTGGACCTGGCAAAATGGAC
TCCAGAGGAGAACACAGGCAGGACAGAAGAGAGAGGCCTTATTGA
```

Rank #7 (Score: 0.8053)

```
>Optimized_CDS_FUS_Rank7_Score0.8053_CAI0.7281_MFE-54.9
ATGGCTTCTAATGATTACACTCAGCAGGCCACTCAGAGCTATGGTGCCTACCCCACACAGCCAGGTCAGGGTTACTCCCAGCAGTCATCCCAGCCTTATGGACAACAGAGTTATTCAGGCTACTCCCA
ATCCACAGACACATCAGGATATGGCCAGTCTTCTTACTCATCATATGGACAGTCACAGAACACTGGATATGGAACACAGTCAACACCACAAGGATATGGTTCAACAGGAGGTTATGGATCAAGCCAGT
CAAGCCAGAGTTCCTATGGACAGCAGAGCAGCTACCCTGGATATGGCCAGCAGCCTGCTCCATCTTCCACTTCAGGATCTTATGGCTCCTCCTCCCAGAGCTCCAGCTATGGACAGCCTCAGTCAGGA
TCATACTCACAGCAGCCTTCTTATGGTGGACAACAACAATCATATGGCCAACAGCAATCTTACAACCCTCCACAAGGTTATGGTCAACAAAATCAGTACAATTCATCCTCTGGTGGAGGTGGTGGTGG
AGGTGGAGGAGGAAATTATGGCCAAGATCAATCATCAATGTCCTCTGGAGGAGGATCTGGTGGTGGTTATGGAAACCAGGATCAATCTGGTGGTGGAGGCTCAGGTGGATATGGCCAACAAGACAGAG
GAGGCAGAGGCAGAGGAGGCTCAGGAGGTGGTGGTGGTGGTGGAGGAGGATACAACAGGTCATCTGGAGGTTATGAGCCCAGAGGAAGGGGTGGTGGAAGGGGAGGAAGAGGAGGAATGGGAGGC
TCTGACAGGGGTGGCTTCAACAAGTTTGGTGGACCCAGGGATCAGGGGTCAAGGCATGACTCAGAACAGGACAACTCAGACAACAACACCATCTTTGTCCAGGGCTTGGGTGAAAATGTGACAATTGA
ATCTGTGGCAGATTACTTCAAACAGATTGGCATCATCAAAACAAACAAGAAAACAGGCCAACCAATGATCAATCTGTACACTGACAGAGAGACTGGAAAACTGAAAGGTGAGGCAACTGTTTCATTTG
ATGACCCTCCATCTGCCAAGGCAGCAATTGATTGGTTTGATGGGAAGGAGTTCTCAGGAAACCCAATCAAAGTGTCATTTGCAACCAGGAGAGCAGATTTCAACAGAGGTGGAGGAAATGGAAGAGGT
GGAAGGGGAAGGGGTGGCCCAATGGGAAGAGGTGGATATGGAGGAGGAGGAAGTGGTGGTGGTGGAAGAGGAGGATTTCCTTCAGGAGGAGGTGGTGGAGGTGGTCAACAGAGAGCTGGAGACTGGAA
GTGTCCAAATCCCACTTGTGAGAACATGAACTTCAGCTGGAGGAATGAATGCAACCAATGCAAAGCCCCTAAACCTGATGGGCCTGGTGGAGGCCCTGGTGGCTCACACATGGGAGGAAACTATGGGG
ATGACAGAAGAGGAGGCAGGGGTGGATATGACAGAGGTGGATACAGAGGCAGAGGAGGTGACAGAGGTGGCTTCAGGGGTGGGAGGGGTGGTGGAGACAGGGGAGGATTTGGCCCTGGCAAAATGGAC
TCAAGAGGAGAGCACAGGCAAGACAGGAGAGAGAGGCCATACTGA
```

Rank #8 (Score: 0.8037)

```
>Optimized_CDS_FUS_Rank8_Score0.8037_CAI0.7530_MFE-67.3
ATGGCTTCTAATGATTACACTCAGCAGGCAACTCAGAGTTATGGAGCATACCCCACTCAGCCAGGTCAGGGTTATTCACAACAATCTTCCCAACCTTATGGGCAGCAGTCCTACTCTGGGTACTCCCA
AAGCACAGACACCTCAGGCTATGGTCAGTCTTCCTACTCCTCATATGGTCAGTCCCAGAACACAGGATATGGAACACAGAGCACCCCACAGGGATATGGAAGCACAGGTGGATATGGCAGTTCCCAGA
GCAGCCAGAGCTCATATGGCCAACAAAGCTCTTACCCTGGGTATGGTCAACAGCCTGCTCCATCTTCCACATCAGGGTCCTATGGATCCTCCTCCCAGTCCAGCAGTTATGGACAACCTCAAAGTGGA
AGCTACTCACAACAACCTTCTTATGGAGGCCAACAGCAGAGCTATGGGCAACAGCAGTCCTACAATCCACCACAAGGTTATGGGCAGCAGAACCAGTACAATTCATCATCTGGTGGAGGTGGAGGAGG
AGGTGGAGGAGGGAATTATGGCCAGGACCAGTCATCAATGTCCTCTGGAGGAGGAAGTGGTGGTGGTTATGGCAATCAGGACCAGTCAGGAGGTGGTGGATCAGGTGGATATGGCCAGCAGGACAGAG
GAGGCAGAGGCAGAGGAGGATCAGGAGGAGGTGGTGGTGGTGGTGGTGGATACAACAGAAGCTCAGGTGGATATGAACCCAGAGGAAGAGGAGGAGGCAGGGGTGGCAGGGGAGGGATGGGTGGA
TCTGACAGAGGTGGCTTCAACAAGTTTGGAGGTCCCAGAGATCAGGGGTCAAGACATGACAGTGAACAGGACAACTCTGACAACAACACAATCTTTGTGCAGGGTCTGGGAGAGAATGTCACCATTGA
AAGTGTTGCTGATTACTTCAAGCAGATTGGCATCATCAAAACCAACAAGAAGACTGGGCAGCCCATGATCAATCTTTACACAGACAGGGAAACAGGCAAGTTGAAAGGAGAGGCCACAGTGTCTTTTG
ATGACCCACCGTCAGCAAAGGCTGCAATTGACTGGTTTGATGGCAAGGAGTTTTCTGGAAACCCCATCAAAGTGAGCTTTGCAACCAGGAGAGCTGACTTCAACAGAGGTGGTGGAAATGGAAGGGGA
GGGAGGGGAAGAGGAGGTCCAATGGGAAGAGGTGGCTATGGAGGCGGTGGCTCTGGTGGTGGAGGGAGAGGAGGATTCCCATCTGGAGGAGGAGGCGGAGGTGGCCAGCAGAGAGCTGGAGACTGGAA
GTGCCCAAACCCAACATGTGAAAACATGAACTTCAGCTGGAGAAATGAGTGCAACCAGTGCAAGGCCCCCAAGCCTGATGGCCCTGGTGGTGGTCCAGGAGGCTCACACATGGGAGGAAACTATGGGG
ATGACAGAAGAGGAGGAAGAGGTGGTTATGACAGAGGTGGATACAGAGGCCGTGGTGGAGACAGGGGTGGGTTCAGAGGTGGAAGGGGAGGTGGGGACAGGGGAGGTTTTGGCCCAGGCAAAATGGAC
TCAAGAGGAGAGCACAGACAAGACAGGAGAGAAAGGCCTTACTGA
```