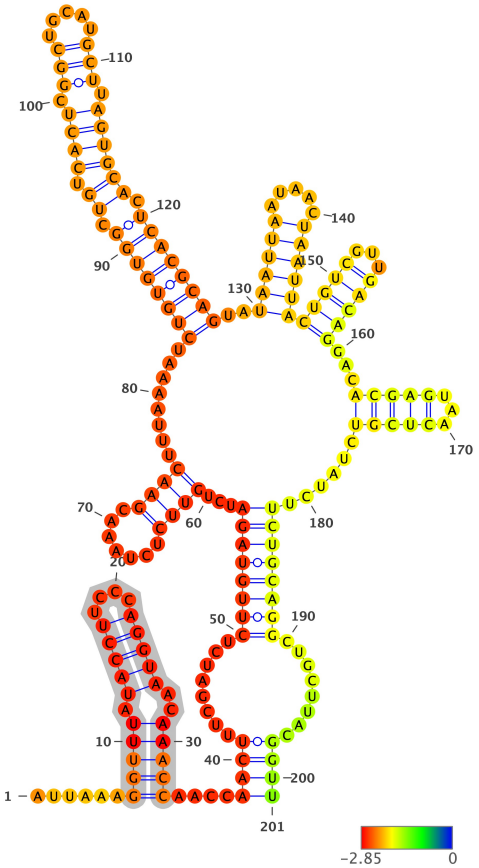
NC_045512.2 (forward strand): Structure number 1 from nt 7 to 33 (nt 7 to 33)

```
5'-GGTTTATACCTTCCCAGGUAACAAACC-3'
5'-(((...(((((....)))))....)))-3'
Motif MFE = -7.0; z-score = -3.28; ED = 1.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1 to 201 (motif highlighted in silver):

```
5'-AUUAAAGGUUUAUACCUUCCCAGGUAACAAACCAACCAACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCU
UAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUU-3
5'-......(((((.(((((....)))))..)))))....((((........(((((((...((((.......)))).......(((((((.((.(((((.(((.....)))
.)))))).)))))))..((((((.....)))))))((((...)))))...(((((...)))))......)))))))........))))-3'
MFE = -51.1; z-score = -2.49; ED = 24.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 201--region, NC_045512.2:1..29903, 1-29903(+)

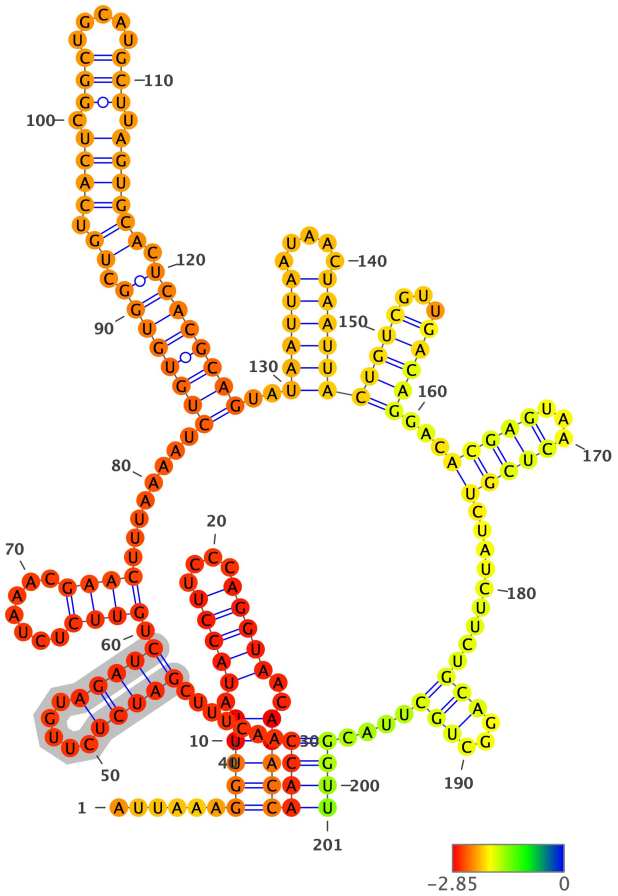
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 201--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

Attributes: ['ID=id-NC_045512.2:1..265', "gbkey=5'UTR"]

NC_045512.2 (forward strand): Structure number 2 from nt 45 to 59 (nt 45 to 59)

```
5'-GATCTCTTGTAGAUC-3'
5'-(((((.....)))))-3'
Motif MFE = -2.3; z-score = -2.43; ED = 0.51
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1 to 201 (motif highlighted in silver):

```
5'-AUUAAAGGUUUAUACCUUCCCAGGUAACAAACCAACCAACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCU
UAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUU-3
5'-......(((((.(((((....)))))..)))))((((.......(((((.....))))).((((.......))))........((((((((.((.((((.(((.....)))
.)))))).))))))))..((((((.....))))))(((((...)))))...(((((...)))))).........(((...)))....))))-3'
MFE = -50.7; z-score = -3.21; ED = 20.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 201--region, NC_045512.2:1..29903, 1-29903(+)

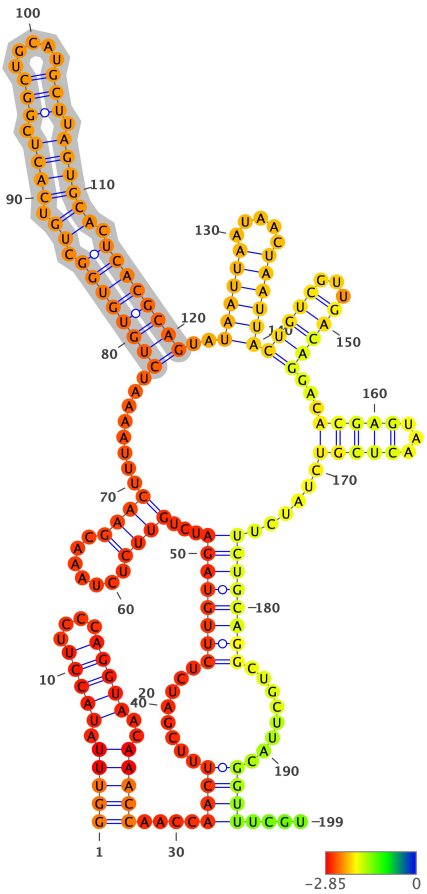
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 201--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

Attributes: ['ID=id-NC_045512.2:1..265', "gbkey=5'UTR"]

NC_045512.2 (forward strand): Structure number 3 from nt 84 to 127 (nt 78 to 121)

```
5'-CTGTGTGGCTGTCACTCGGCTGCATGCUTAGUGCACUCACGCAG-3'
5'-((((((((.((.((((.(((.....)).)))))).))))))))-3'
Motif MFE = -20.1; z-score = -3.44; ED = 1.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7 to 205 (motif highlighted in silver):

```
5'-GGUUUAUACCUUCCCAGGUAACAAACCAACCAACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGC
ACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGU-3
5'-(((((.(((((....)))))..)))))....((((........((((((((...((((.......)))).........((((((((.((.((((.(((.....)))).)))))
).))))))))..((((((.....))))))(((((...)))))...(((((...)))))......))))))))........))))....-3'
MFE = -51.6; z-score = -2.6; ED = 25.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

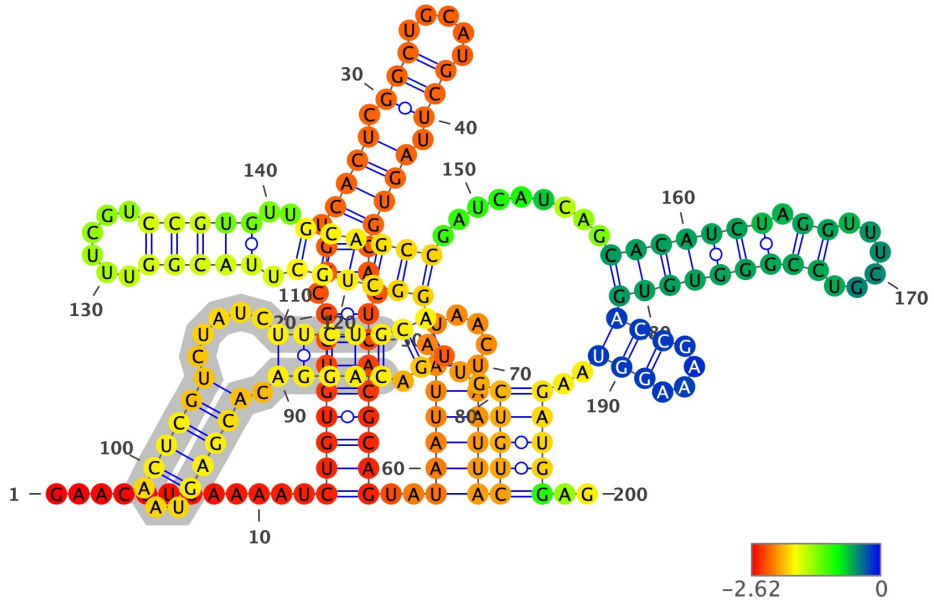
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

Attributes: ['ID=id-NC_045512.2:1..265', "gbkey=5'UTR"]

NC_045512.2 (forward strand): Structure number 4 from nt 157 to 185 (nt 86 to 114)

```
5'-CAGGACACGAGTAACUCGTCTATCUUCUG-3'
5'-(((((...((((...)))).......)))))-3'
Motif MFE = -5.2; z-score = -0.97; ED = 5.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 72 to 271 (motif highlighted in silver):

```
5'-GAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUU
CUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGGAG-3
5'-............((((((((.((.((((.(((.....)).)))))).)))))))))..((((((.....))))))((((..((.(((((.(((((...)))))).....))
)))))((((((.(((((.....)))))..)))))).........(((((((.((.....)))))))))((((....)))..)))))..-3'
MFE = -62.8; z-score = -2.89; ED = 33.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 194--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

Attributes: ['ID=id-NC_045512.2:1..265', "gbkey=5'UTR"]

3-- nt 195 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

4-- nt 195 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

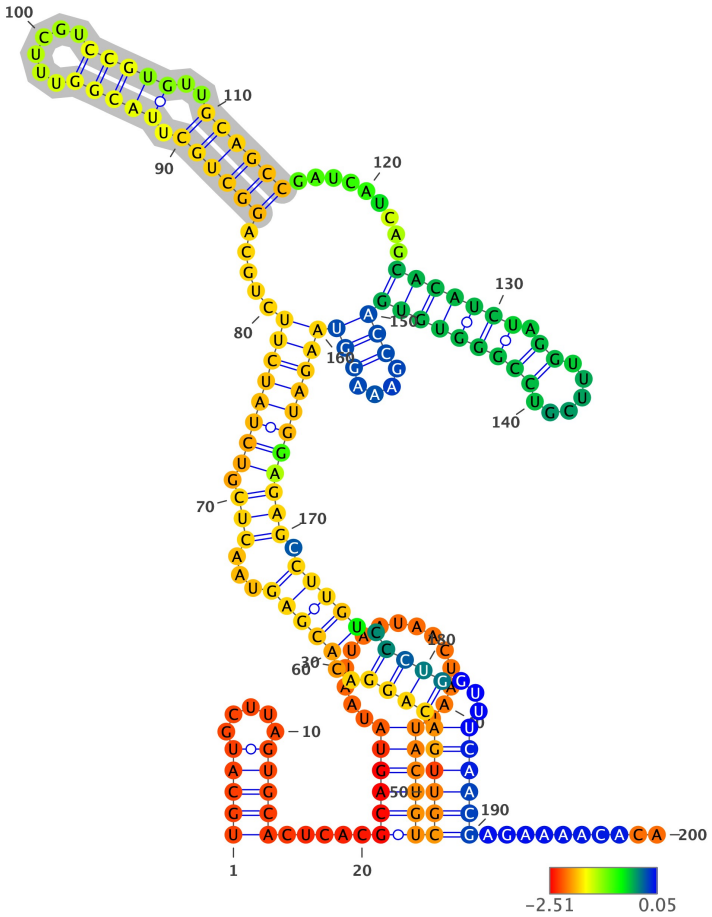
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 195 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 5 from nt 188 to 218 (nt 85 to 115)

```
5'-GGCTGCTTACGGTTTCGTCCGTGTTGCAGCC-3'
5'-((((((...(((......)))....))))))-3'
Motif MFE = -17.2; z-score = -5.2; ED = 0.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 104 to 303 (motif highlighted in silver):

```
5'-UGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGC
AGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGGAGAGCCUUGUCCCUGGUUUCAACGAGAAAACACA-3
5'-(((((.....)))))).....((((((...............))))))((((((((((..(((((...(((.((((((((.....((((((.(((((......)))))..))
))))).........(((((((.((......)))))))))(((....)))))))))))))).))))).))))...))))))..........-3'
MFE = -66.1; z-score = -3.06; ED = 13.42
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 162--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

Attributes: ['ID=id-NC_045512.2:1..265', "gbkey=5'UTR"]

3-- nt 163 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

4-- nt 163 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

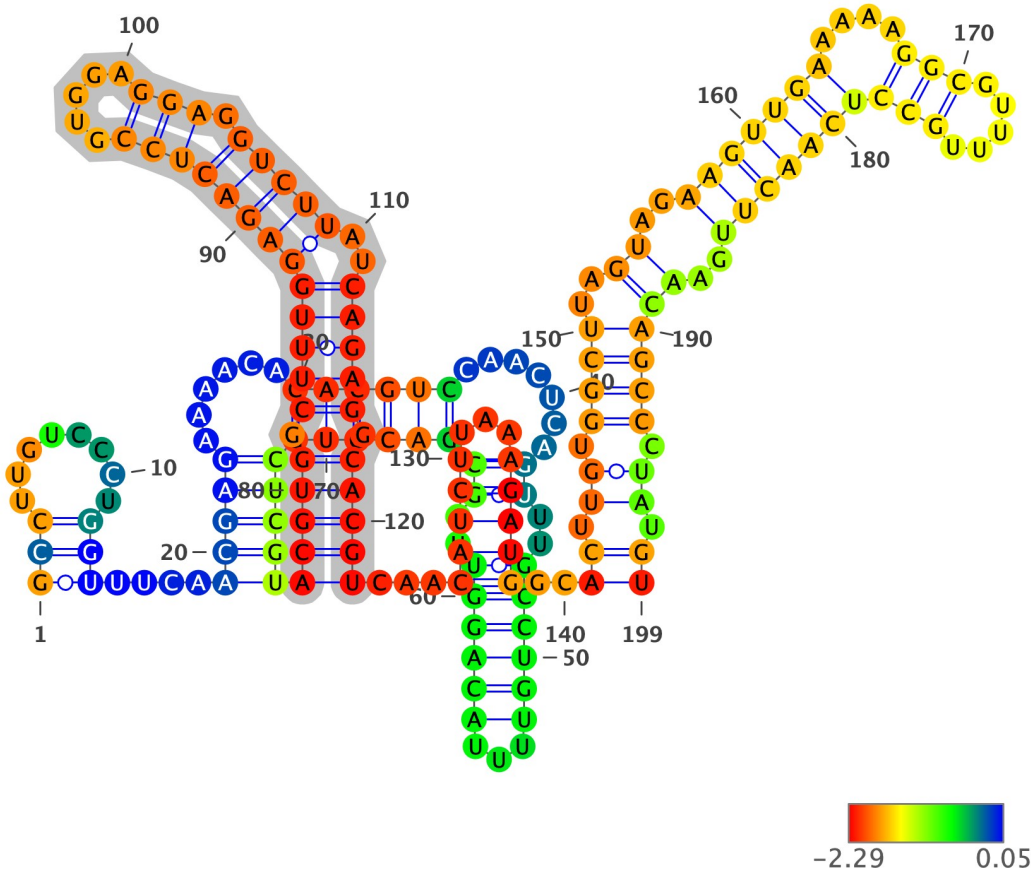
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 163 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 6 from nt 349 to 394 (nt 77 to 122)

```
5'-ACGTGGCTTTGGAGACTCCGTGGAGGAGGUCUUATCAGAGGCACGU-3'
5'-(((((.(((((((((((.....))).)))))..)))))).)))))-3'
Motif MFE = -22.1; z-score = -4.19; ED = 3.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 273 to 471 (motif highlighted in silver):

```
5'-GCCUUGUCCCUGGUUUCAACGAGAAAACACACGUCCAACUCAGUUUGCCUGUUUUACAGGUUCGCGACGUGCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAU
CAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGU-3
5'-(((........)))....((((.....(((((.......((..(((((...)))))).))))))))))))))))))))))))(((((.((((((((((((.....)))).)))))..
)))))).)))))...(((((...)))))..((.((.(((((..((..(((((((....(((.....)))))))))).))))))).)).))-3'
MFE = -62.4; z-score = -1.74; ED = 15.68
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

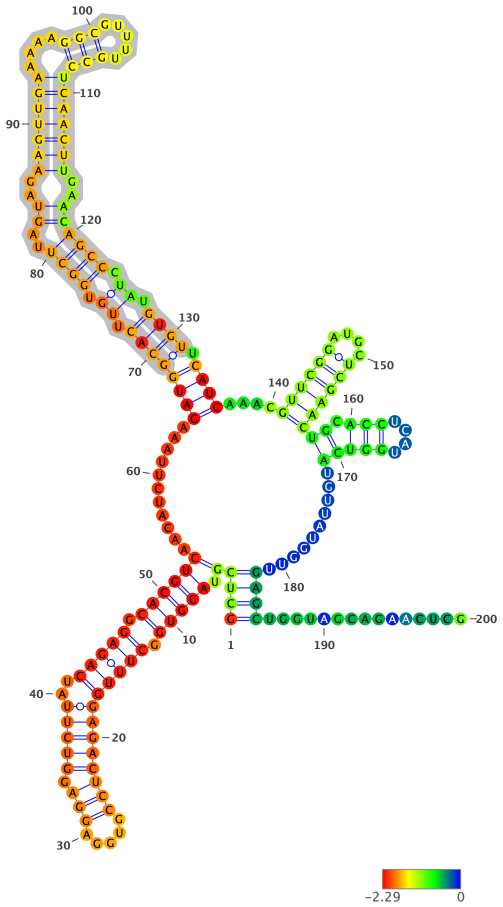
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 7 from nt 411 to 473 (nt 69 to 131)

```
5'-GCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCTCAACUTGAACAGCCCTATGTGU-3'
5'-((.(....((((.......(((((.....(((.....))).)))))).....))))....).))-3'
Motif MFE = -20.8; z-score = -2.74; ED = 3.51
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 343 to 542 (motif highlighted in silver):

```
5'-GCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCA
ACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCG-3
5'-(((((.(((((.(((((((((((((.....))).)))))..)))))).))))))...........((((((((.((.((((..((..(((((((....(((.....))))))
))))..)))))).)).)))).))))....((((((....))))))((.(((....)))))..........))))................-3'
MFE = -63.3; z-score = -1.74; ED = 27.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

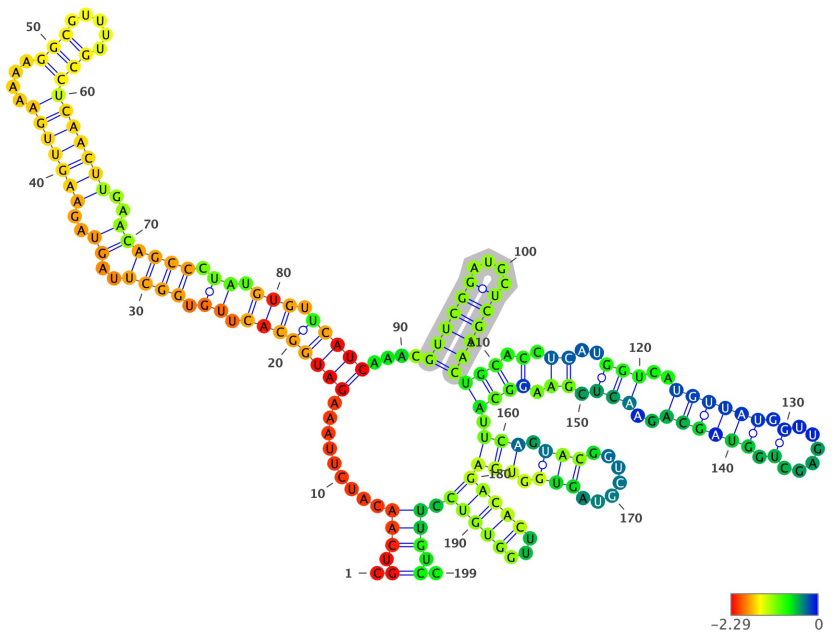
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 8 from nt 483 to 498 (nt 92 to 107)

```
5'-GTTCGGATGCUCGAAC-3'
5'-((((((....))))))-3'
Motif MFE = -4.3; z-score = -2.36; ED = 0.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 392 to 590 (motif highlighted in silver):

```
5'-CGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCA
CCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCC-3
5'-.(.(((.........((((((((.((.((((..((..(((((((....(((.....)))))))))..))))))).)).))).)))))....((((((....))))))(((.
(.((..(((..((((((.(......).))))))..))).)).)))).(((.(((.......))).)))(((((...))))).))).).-3'
MFE = -52.7; z-score = -0.66; ED = 45.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

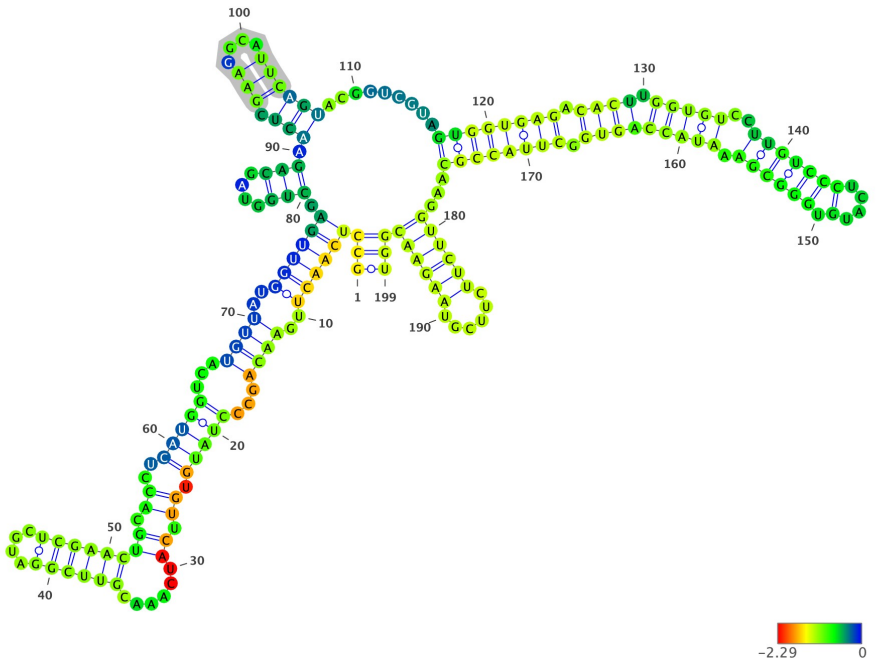
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 9 from nt 542 to 551 (nt 95 to 104)

```
5'-GAAGGCAUUC-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = 0.2; ED = 0.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 448 to 646 (motif highlighted in silver):

```
5'-GCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGG
UCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGU-3
5'-(((((((((..((((...(((((.((.((......((((((....))))))))).))..)))))...))))..)))))).(((....))).(((.(((....))))))....
.....((((((((.((((.(((((..(((((((....).))))))).))))))))).))))))))...((((((......)))))))))-3'
MFE = -60.5; z-score = -1.38; ED = 33.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

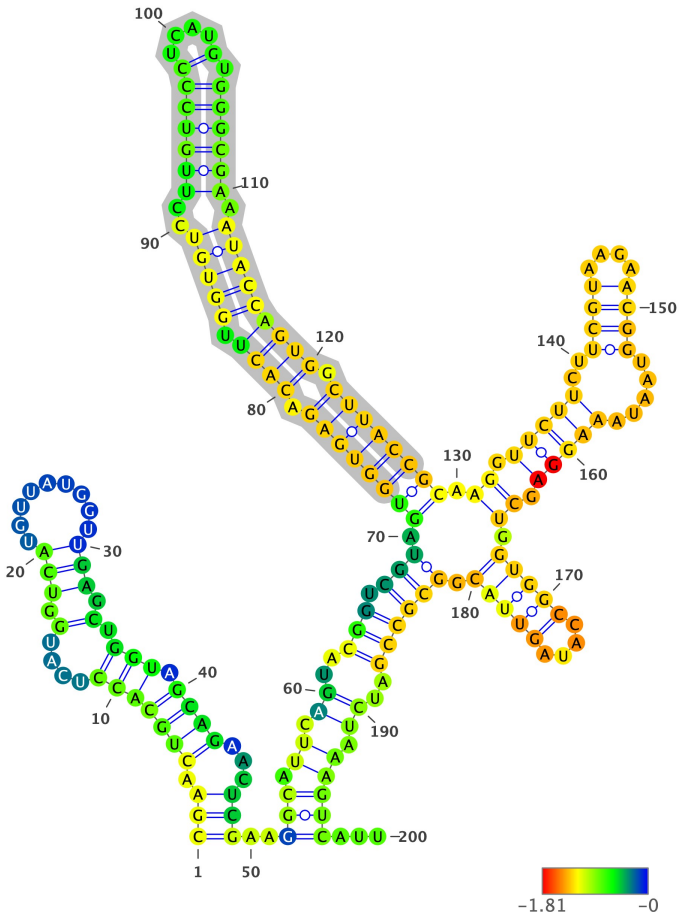
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 10 from nt 566 to 620 (nt 73 to 127)

```
5'-GGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAAUACCAGUGGCUUACC-3'
5'-((((((.(((..(((((.....................)))))).))).))))))-3'
Motif MFE = -24.3; z-score = -3.24; ED = 5.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 494 to 693 (motif highlighted in silver):

```
5'-CGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAA
AUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUU-3
5'-(((.(((((((....(.(((.........))).).))).))))...)))..(((.((.((..(((.(((.(((((((((.((((.(((((..(((((((....).))))))).
))))))))).)))))))).((.(((((..((((....)))).....))))).)).(((((....)))))).))))))..)).)))))...-3'
MFE = -59.2; z-score = -0.38; ED = 60.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

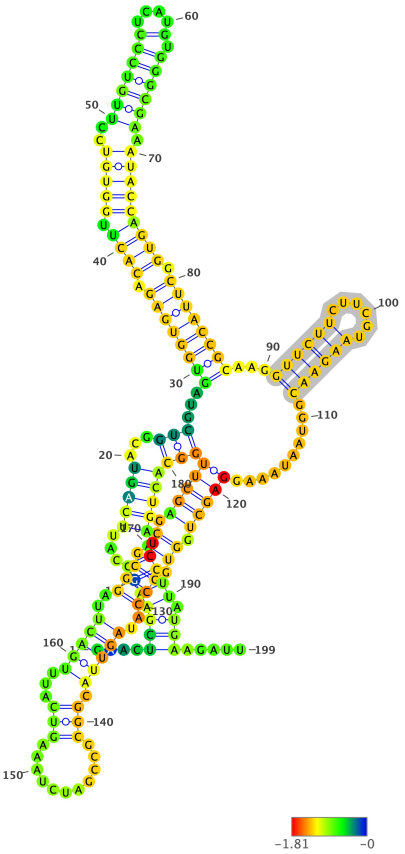
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 11 from nt 626 to 643 (nt 91 to 108)

```
5'-GTTCTTCTTCGTAAGAAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -3.19; ED = 1.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 536 to 734 (motif highlighted in silver):

```
5'-GAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGU
AAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUU-3
5'-....(((((((...(((((...(((((((((.((((.(((((..(((((((....).))))))).))))))))).))))))))...((((((......))))))...
.......(((((.((.(((..(((((.(((...........)))...)))))..))).)).))))))))))))).)))).)))......-3'
MFE = -66.9; z-score = -2.62; ED = 44.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

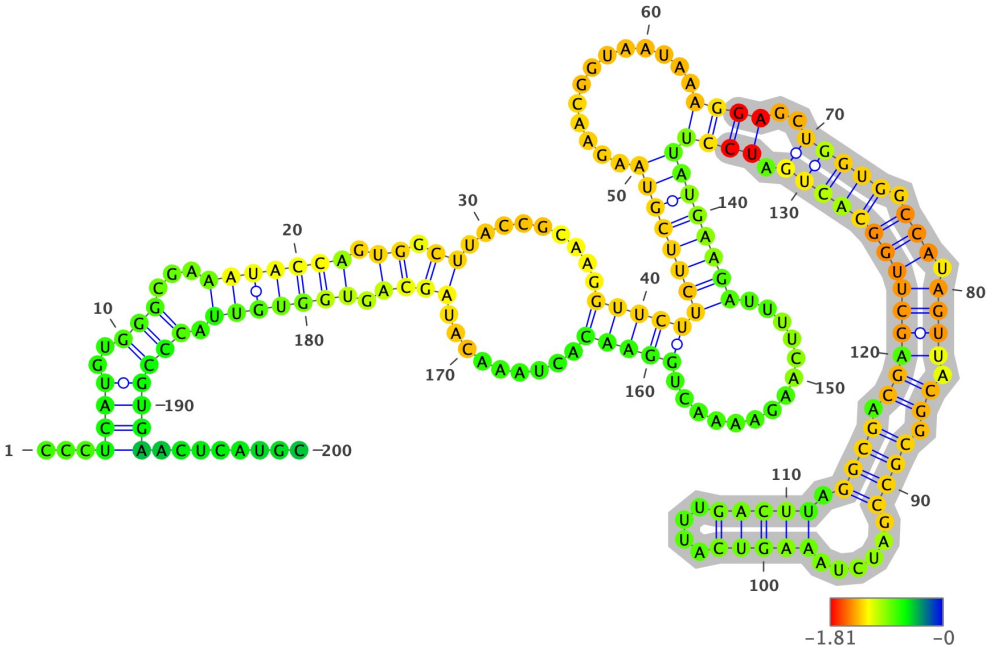
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 12 from nt 654 to 722 (nt 66 to 134)

```
5'-GAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTTGACUTAGGCGACGAGCUUGGCACTGAUC-3'
5'-((........(((.(((..((.((((.....................)))).)).)))))).....))-3'
Motif MFE = -22.4; z-score = -1.36; ED = 18.06
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 589 to 788 (motif highlighted in silver):

```
5'-CCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUU
AGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGC-3
5'-...((((..(((...(((((((.((.((.........((((((((((((.............((((..(((((.(((.((((.((.((((.....((((((....)))))
.)))).))))))))))))))).))))))))))).............)))))........)))).)))))))).)))))))........-3'
MFE = -52.6; z-score = -1.11; ED = 48.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

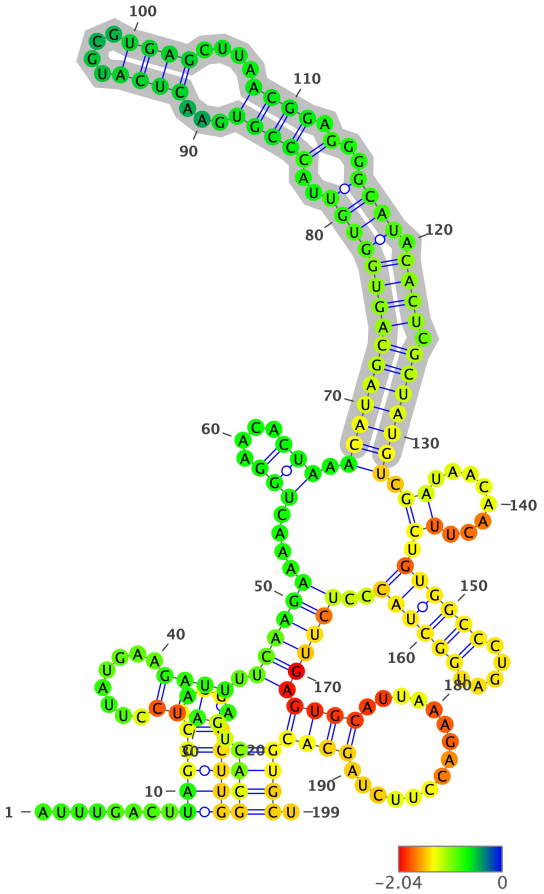
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 13 from nt 758 to 821 (nt 68 to 131)

```
5'-CATAGCAGTGGTGTTACCCGTGAACTCATGCGUGAGCTTAACGGAGGGGCAUACACUCGCUAUG-3'
5'-((((((((((.........................................)))).))))))-3'
Motif MFE = -24.4; z-score = -2.84; ED = 3.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 691 to 889 (motif highlighted in silver):

```
5'-AUUUGACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGG
AGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCU-3
5'-........(((((.....)))))((((.((((........)))).((((((....(((....))).((((((((((((((..(((((...((((....))))....))))
.)..)))).)))).)))))))).((........)).((((((.....))))))..))))))((((...............))))))))).-3'
MFE = -52.0; z-score = -0.65; ED = 22.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

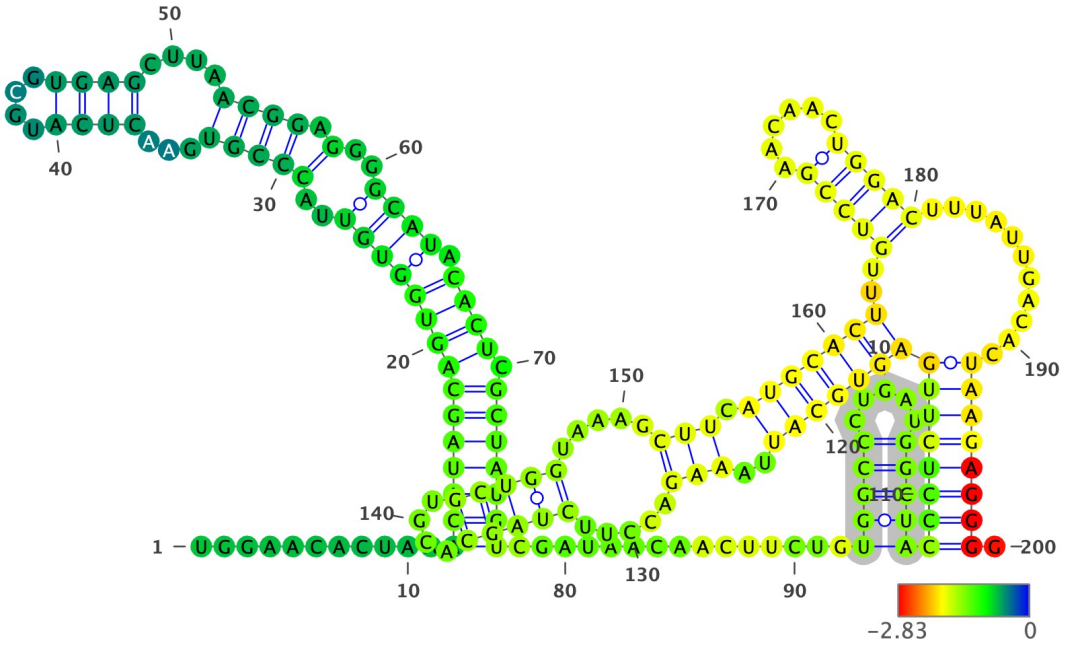
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 14 from nt 838 to 852 (nt 93 to 107)

```
5'-TGGCCCTGATGGCUA-3'
5'-(((((.....)))))-3'
Motif MFE = -4.4; z-score = -2.87; ED = 0.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 746 to 945 (motif highlighted in silver):

```
5'-UGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCU
CUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGG-3
5'-...........((((((((((((((..((((((...((((....))))....)))).)..)))).)))).)))))))..............(((((.....)))))((((
((((((((((..(((.....(((((....)))))).....))).)))))))..(((((......)))))..........)))))))).-3'
MFE = -63.9; z-score = -2.33; ED = 20.82
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

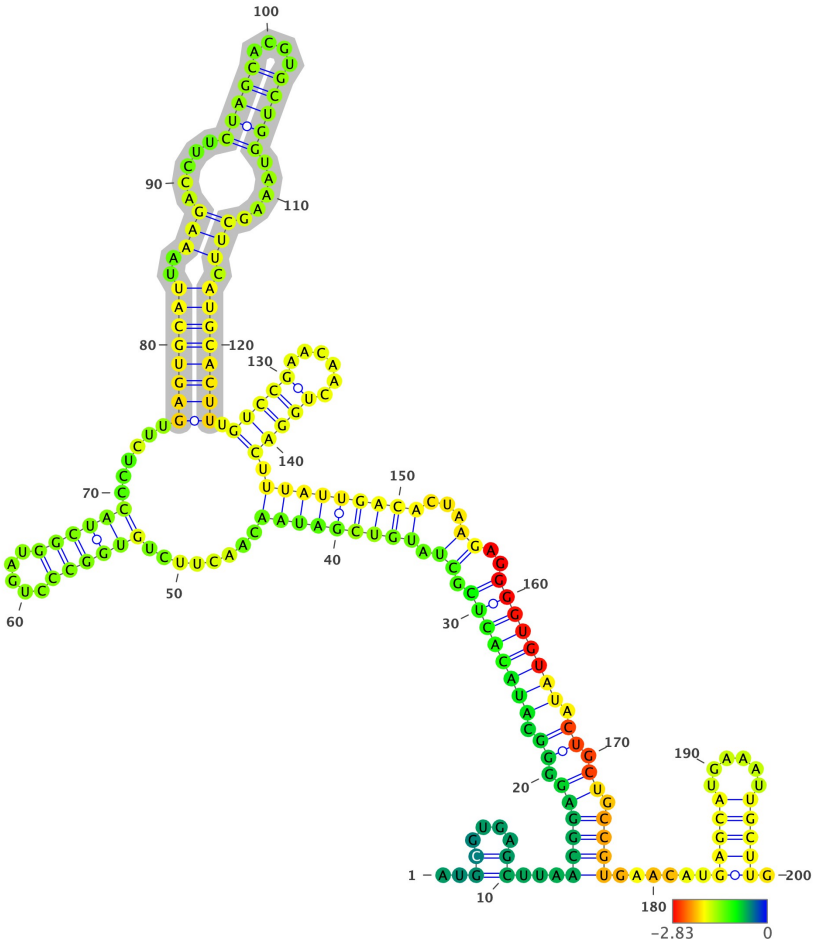
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 15 from nt 860 to 908 (nt 76 to 124)

```
5'-GAGTGCATTAAAGACCTTCTAGCACGTGCUGGTAAAGCUUCAUGCACUU-3'
5'-((((((((..(((.....(((((....)))))).....))).))))))))-3'
Motif MFE = -16.5; z-score = -2.97; ED = 2.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 785 to 984 (motif highlighted in silver):

```
5'-AUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAA
GCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUG-3
5'-..((....))...((((((.((.(((((((((.((.((((((((((.........((((((.....))))))......((((((((..(((.....(((((....)))))....
.))).))))))))).(((((......))))).))))))))))...))..)))))))).)).)).))))......(((((......))))).-3'
MFE = -65.6; z-score = -2.35; ED = 11.41
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

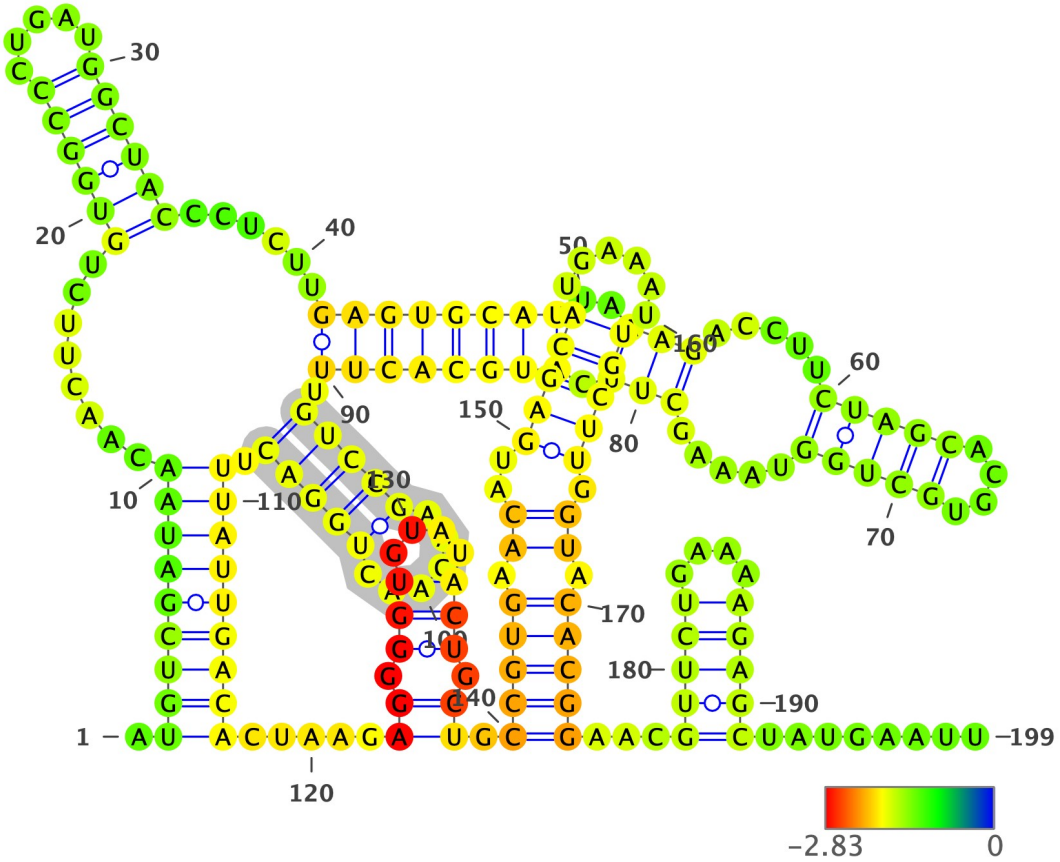
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 16 from nt 910 to 925 (nt 92 to 107)

```
5'-GTCCGAACAACTGGAC-3'
5'-((((........))))-3'
Motif MFE = -4.4; z-score = -2.79; ED = 0.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 819 to 1017 (motif highlighted in silver):

```
5'-AUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUA
UUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACGUUCUGAAAAGAGCUAUGAAUU-3
5'-.(((((((((.........((((((.....))))))......((((((((..(((.....(((((....)))))).....))).)))))))).(((((......))))).)))
))))))).....((.(((....))).)).(((((.((..(((((......))))).)).)))))...(((((....)))))........-3'
MFE = -61.0; z-score = -2.36; ED = 11.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

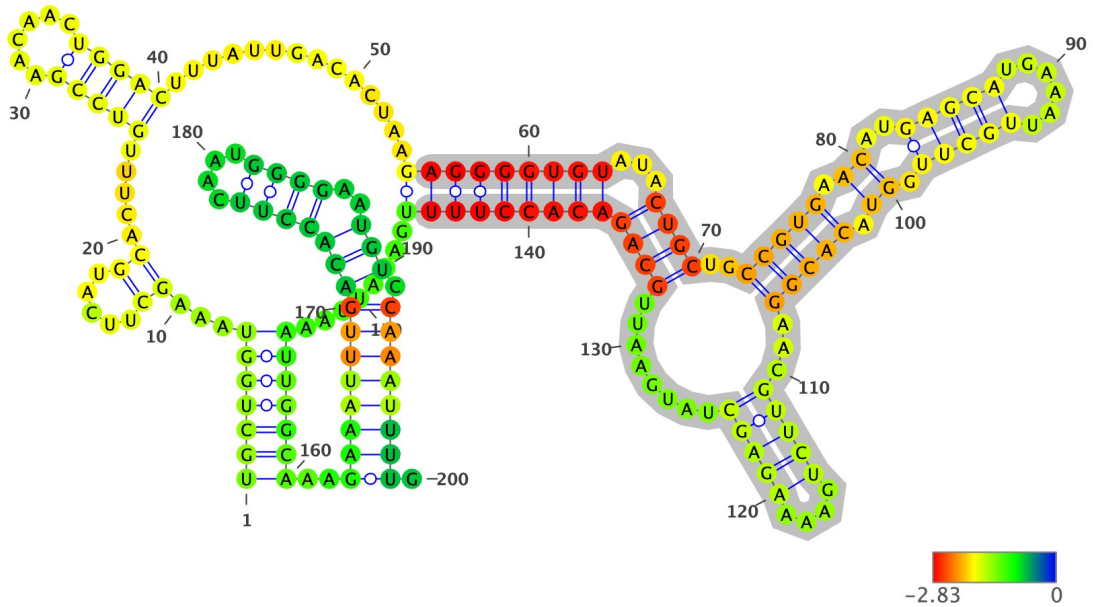
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 17 from nt 941 to 1029 (nt 56 to 144)

```
5'-AGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATUGCUUGGUACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGACACCUUU-3'
5'-(((((((...((((..(((((.((..(((((.....))))).)).)))))...(((((....)))))........)))))))))))-3'
Motif MFE = -31.1; z-score = -3.58; ED = 2.23
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 886 to 1085 (motif highlighted in silver):

```
5'-UGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACG
UUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUG-3
5'-(((((((...((.....)).....(((((.....)))))).............(((((((((...((((..(((((.((..(((((.....)))))).)).)))))...(
((((....)))))........))))))))))))........)))))))..((((((((((((((....)))))..)))).)))))))).-3'
MFE = -52.0; z-score = -1.94; ED = 16.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

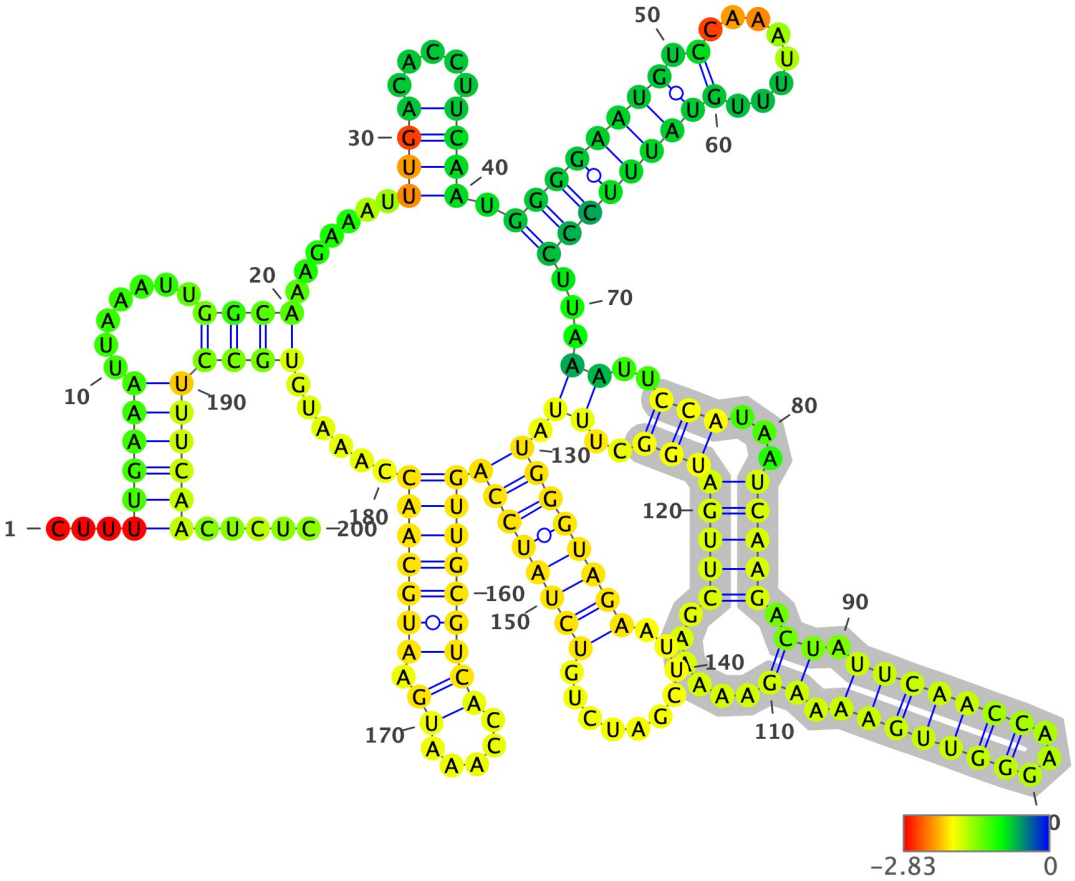
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 18 from nt 1101 to 1149 (nt 76 to 124)

```
5'-CCATAATCAAGACTATTCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGG-3'
5'-(((...(((((....(((((.......)))))..........))))))))-3'
Motif MFE = -10.7; z-score = -2.99; ED = 5.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1026 to 1225 (motif highlighted in silver):

```
5'-CUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGA
AAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUC-3
5'-...((((((.......((((.......((((.....)))).(((((((((.(........)))))))))...((..(((...(((((.((.(((((((...)))))))).)).
.....))))))))..)).((((((((..........))))))))((((((((.....)).)))))))......))))))))))).....-3'
MFE = -41.8; z-score = -2.64; ED = 28.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

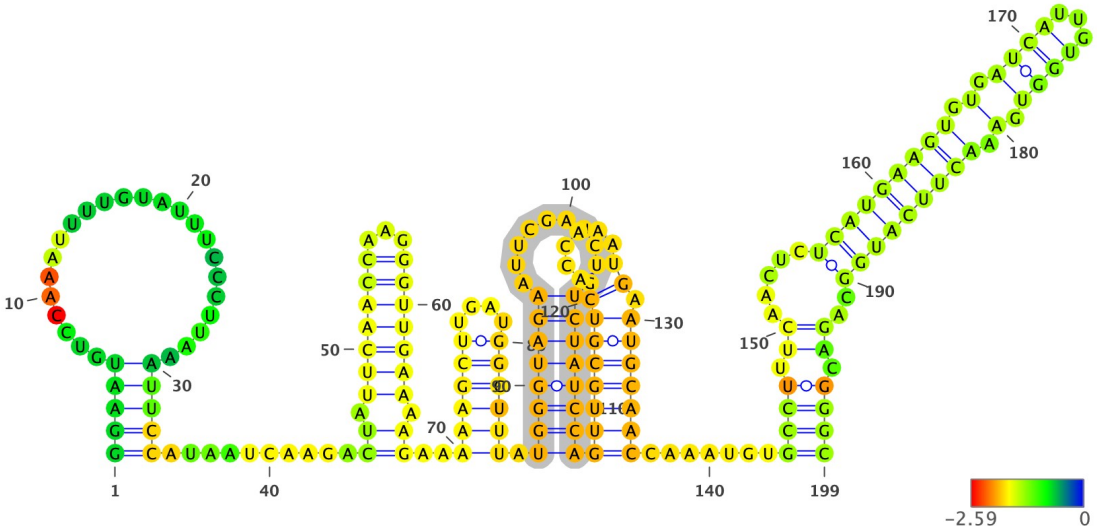
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 19 from nt 1155 to 1180 (nt 87 to 112)

```
5'-TGGGTAGAATTCGATCTGUCUAUCCA-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -7.4; z-score = -2.71; ED = 1.51
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1069 to 1267 (motif highlighted in silver):

```
5'-GGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCC
AGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGC-3
5'-(((((.......................))))).........((.(((((((...)))))))).))..((((((....)))))).(((((((.........)))))))
)(((((((((.....)).)))))))......((((.((.....(((((((((.(.((((...)))).).)))))))))..)).)))))-3'
MFE = -49.1; z-score = -1.82; ED = 30.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

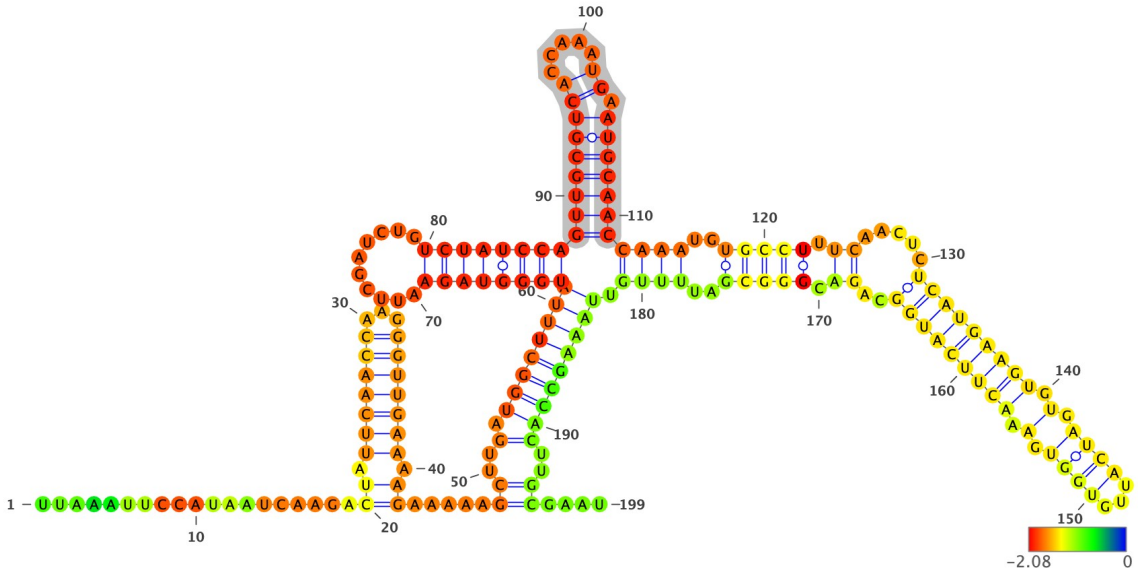
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 20 from nt 1181 to 1204 (nt 88 to 111)

```
5'-GTTGCGTCACCAAATGAAUGCAAC-3'
5'-((((((((.......).)))))))-3'
Motif MFE = -6.5; z-score = -2.82; ED = 1.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1094 to 1292 (motif highlighted in silver):

```
5'-UUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAAC
CAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAU-3
5'-...................((.(((((((...)))))))).)).....((..(.((((((((((((((((.........))))))))((((((((.....)).)))))))
((((..(((((.((.....((((((((((.(.((((...)))).).))))))))))..)).)))))..)))).)))))))))..)).....-3'
MFE = -57.3; z-score = -3.73; ED = 15.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

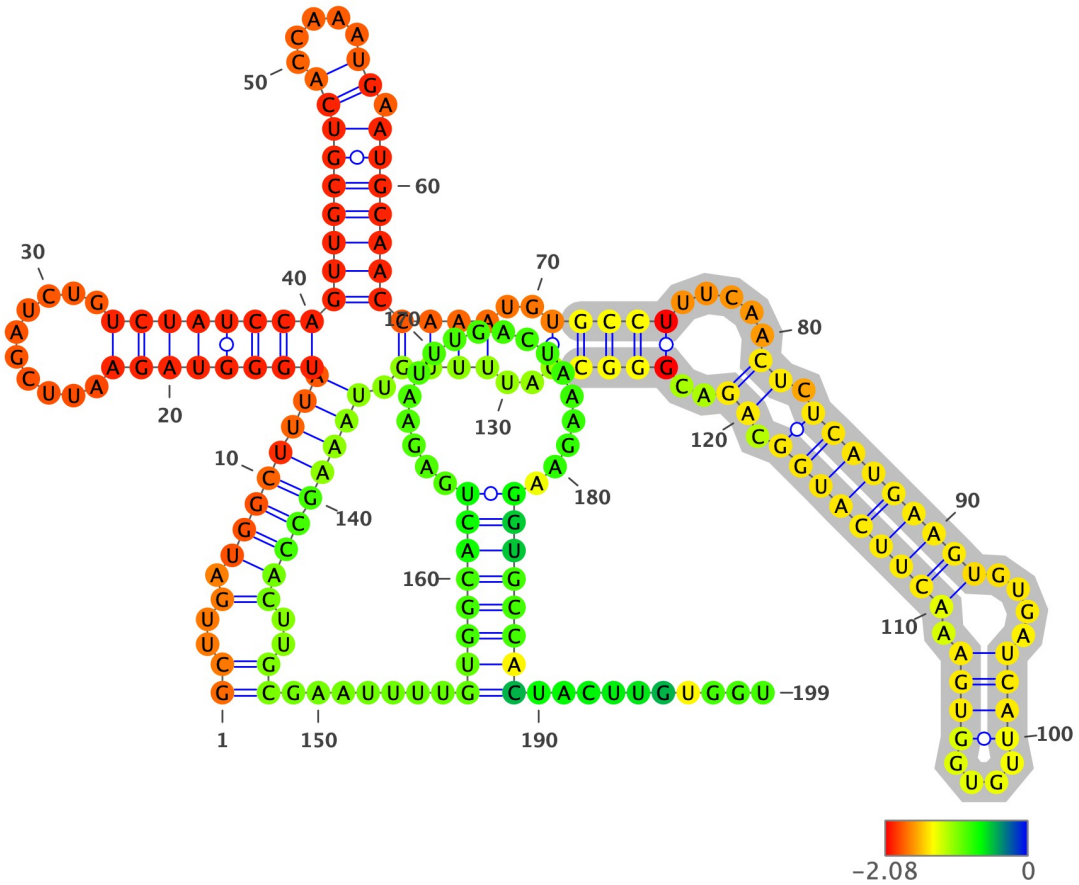
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 21 from nt 1212 to 1267 (nt 72 to 127)

```
5'-GCCTTTCAACTCTCATGAAGTGTGATCATTGTGGUGAAACUUCAUGGCAGACGGGC-3'
5'-(((......((.(((((((((.....(((......)))..)))))))).))...)))-3'
Motif MFE = -17.0; z-score = -1.93; ED = 4.35
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1141 to 1339 (motif highlighted in silver):

```
5'-GCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAAC
UUCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGU-3
5'-((..(.(((((((((((((((((.........))))))))(((((((((.....)).)))))))((((..(((((.....((.(((((((((....((((....)))).))
))))))).))..)))))..)))).))))))))..)).......((((((((.................))))))))..........-3'
MFE = -59.4; z-score = -2.73; ED = 10.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

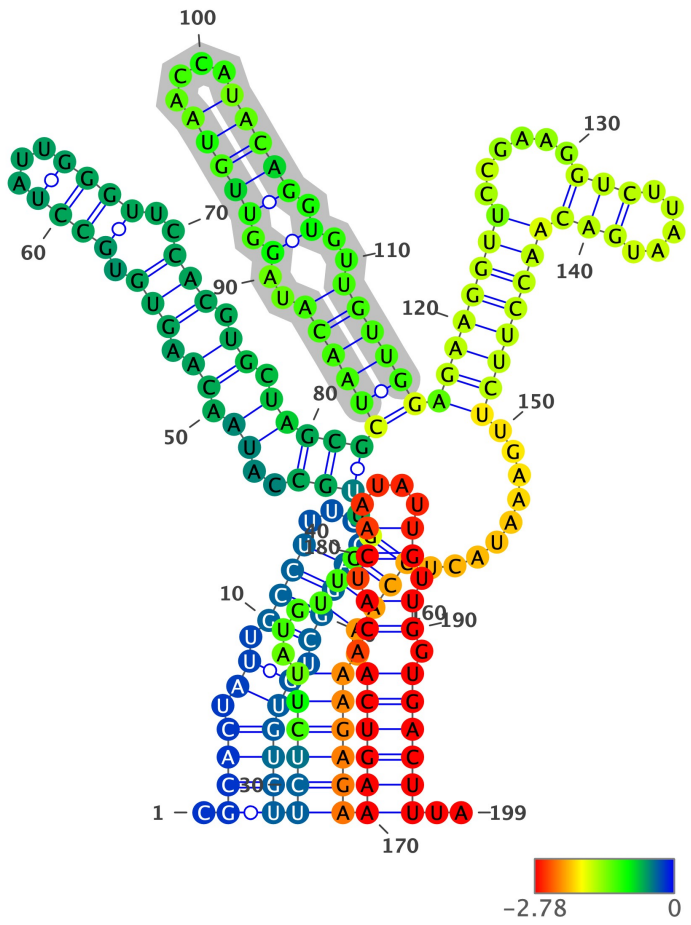
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 22 from nt 1552 to 1583 (nt 84 to 115)

```
5'-TAACATAGGTTGTAACCATACAGGTGTUGUUG-3'
5'-(((((......(........)......)))))-3'
Motif MFE = -7.0; z-score = -1.53; ED = 1.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1469 to 1667 (motif highlighted in silver):

```
5'-CGCACUAUUGCCUUUGGAGGCUGUGUGUUCUCUUAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUU
GUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUA-3
5'-.((((.((.((((....)))).))))))((((((...((((.(((..((.((.(((.((((...))))..))).)).)))))((((((..(.(((((....))))).)..)
)))))((((((((......(((.....)))))))))))).........)))).))))))((((((.((.((....)).)).))))))..-3'
MFE = -51.8; z-score = -2.64; ED = 28.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

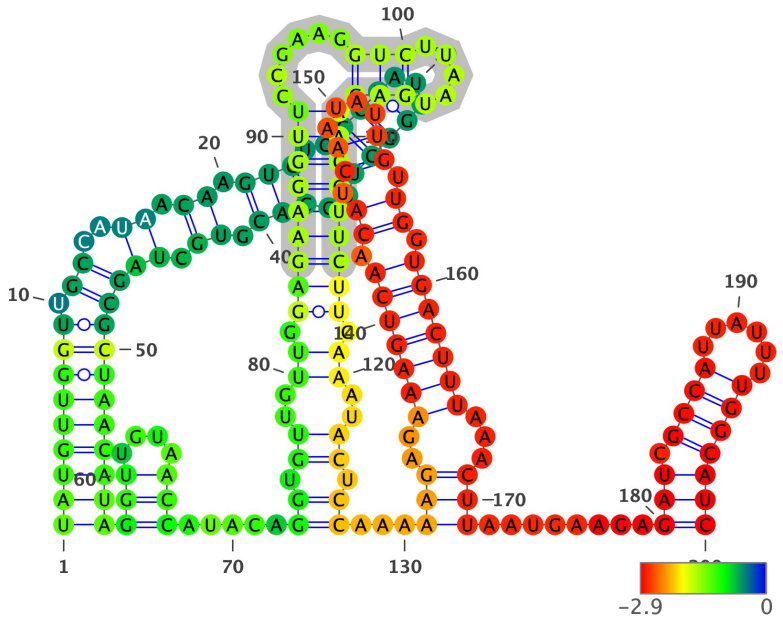
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 23 from nt 1586 to 1616 (nt 85 to 115)

```
5'-GAAGGTTCCGAAGGTCTTAATGACAACCUUC-3'
5'-((((((.......(((.....))).))))))-3'
Motif MFE = -7.9; z-score = -1.96; ED = 0.87
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1502 to 1701 (motif highlighted in silver):

```
5'-UAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAAC
CUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUC-3
5'-(((((((((.((..((.((.(((.((((...)))).)).)))))))))))))(((....))).....((.((..((.(((((((((.....(((.....))))))
))))))).))..)).))...(((..(((((((.((.((....)).)).)))))))...))).........(((.((((......)))))))-3'
MFE = -51.5; z-score = -2.14; ED = 26.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

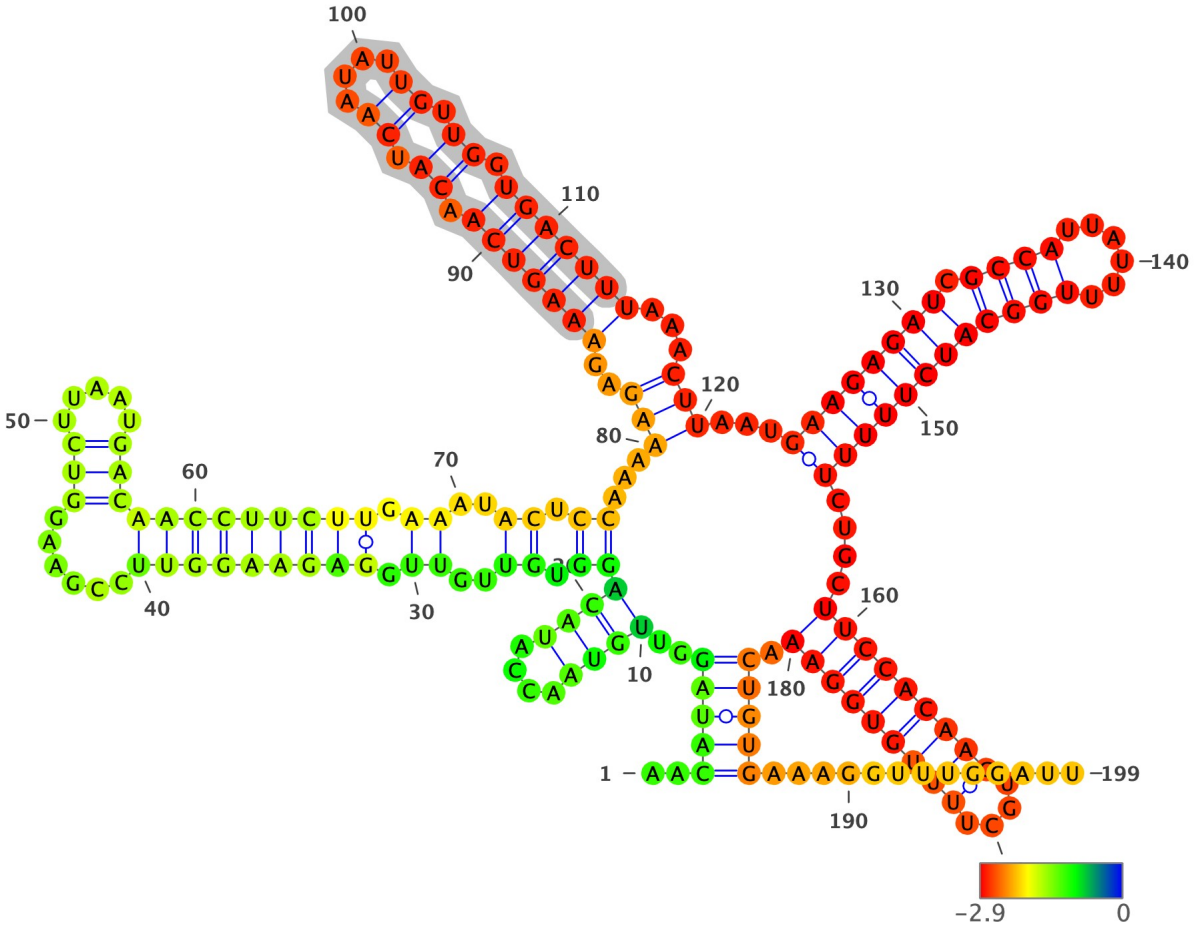
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 24 from nt 1638 to 1665 (nt 86 to 113)

```
5'-AAGTCAACATCAATATTGTUGGUGACUU-3'
5'-((((((.((.(......).)).))))))-3'
Motif MFE = -6.3; z-score = -2.59; ED = 4.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1553 to 1751 (motif highlighted in silver):

```
5'-AACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGAC
UUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUU-3
5'-..(((((..((((....))))((.((..((.(((((((((.....(((.....)))))))))))).))..)).))...(((..(((((((.((.((....)).)).))))
)))...)))...((((((((.((((.....)))))))))))....(((((((((....)))))))))).)))))............-3'
MFE = -56.2; z-score = -3.28; ED = 31.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

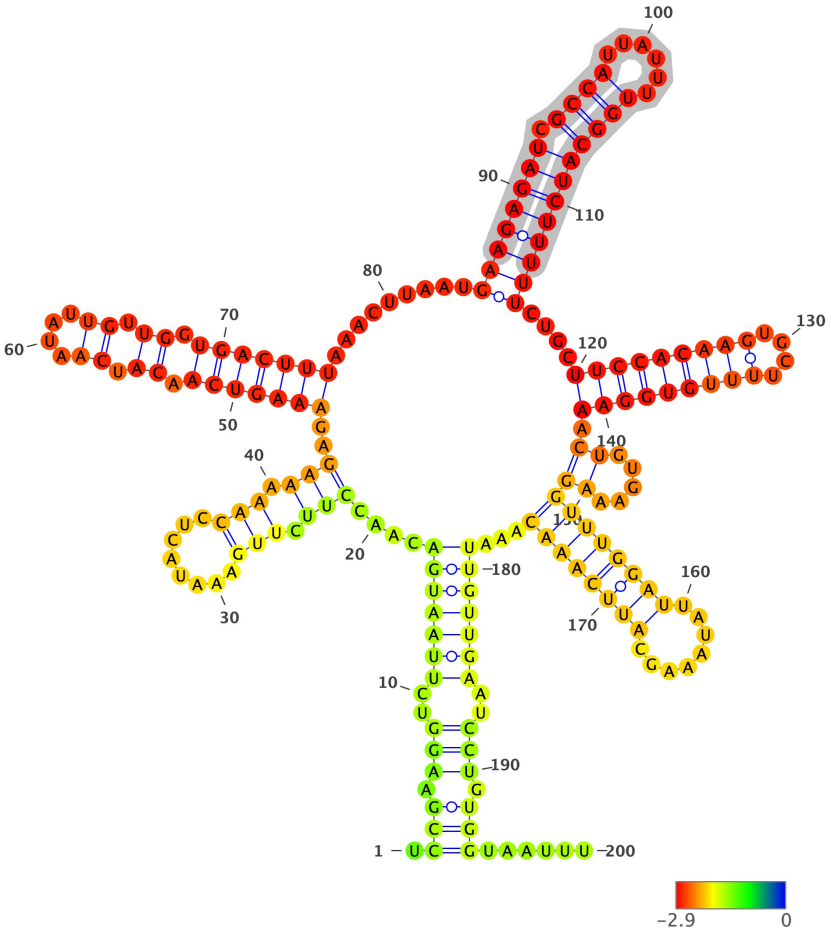
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 25 from nt 1678 to 1704 (nt 87 to 113)

```
5'-AGAGATCGCCATTATTTUGGCAUCUUU-3'
5'-((((((.((((......))))))))))-3'
Motif MFE = -10.0; z-score = -4.86; ED = 0.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1592 to 1791 (motif highlighted in silver):

```
5'-UCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCU
UUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUU-3
5'-.(((.(((..(((((((....(((.(((........))).)))..(((((((.((.((....)).)).)))))))..........((((((((.((((......))))))))
))))....((((((((((....)))))))))).((.....))((((((((........))))))))...)))))))..))).)))......-3'
MFE = -49.0; z-score = -2.98; ED = 44.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

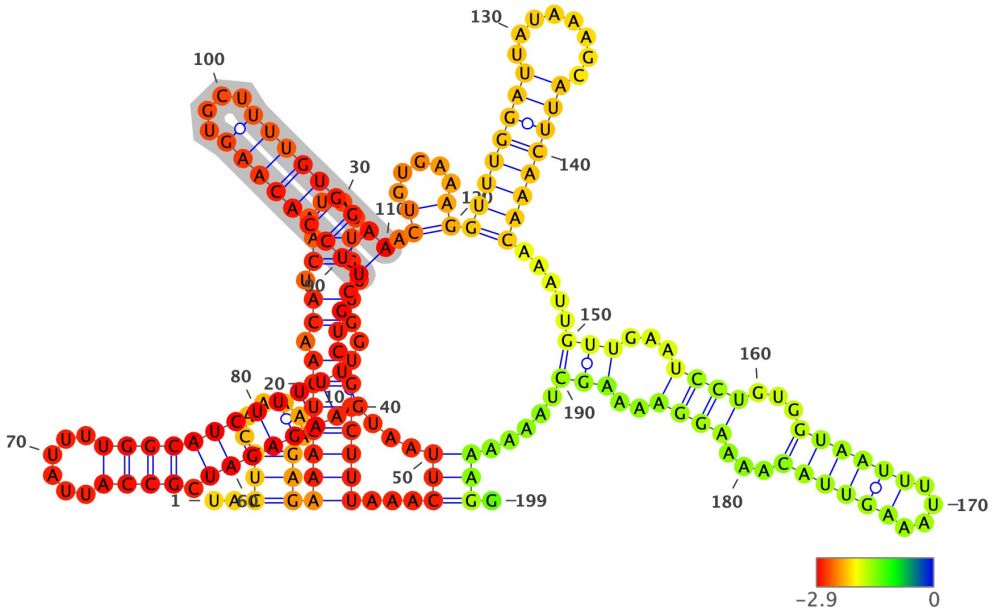
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 26 from nt 1711 to 1732 (nt 89 to 110)

```
5'-TTCCACAAGTGCTTTTGUGGAA-3'
5'-((((((..........))))))-3'
Motif MFE = -9.5; z-score = -4.22; ED = 1.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1623 to 1821 (motif highlighted in silver):

```
5'-UACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAA
CUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGG-3
5'-..(((......)))(((((((.((.((....)).)).)))))))...(((...((((((((.((((......)))))))))))).....((((((((....))))))))).
((.....))((((((((........))))))))).....(((...((((...((((((....))))))...))))..)))).....))).-3'
MFE = -48.5; z-score = -3.22; ED = 33.39
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

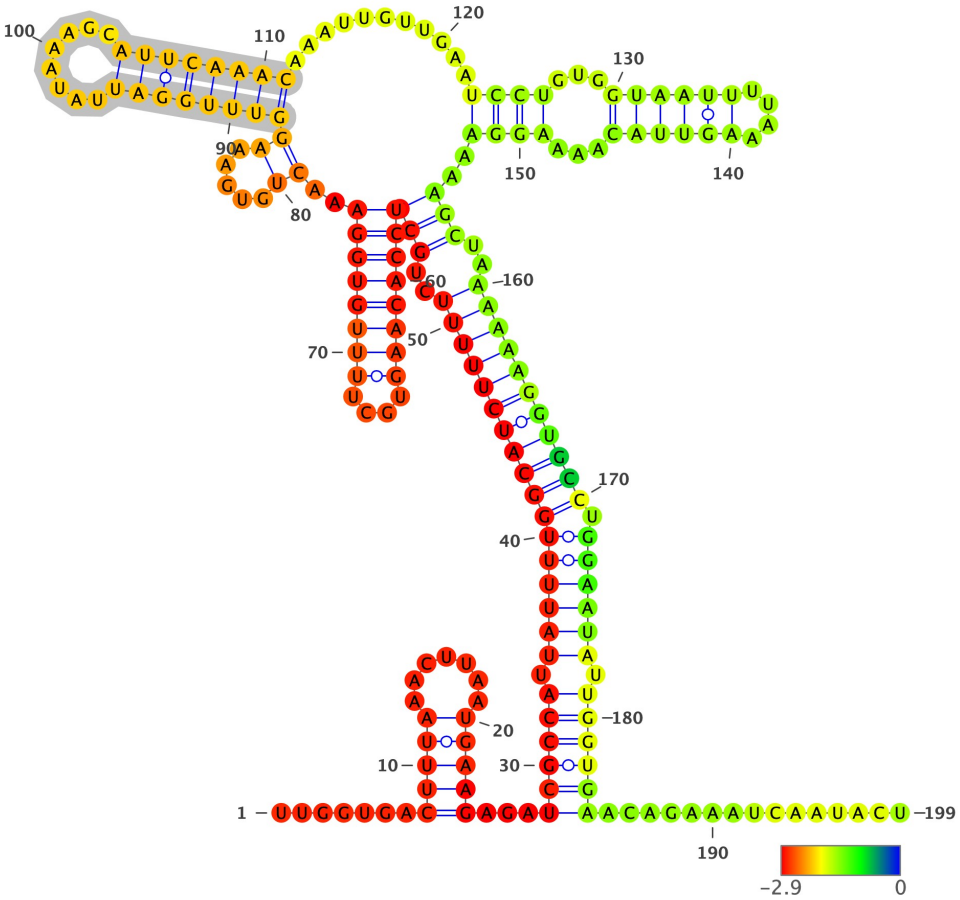
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 27 from nt 1743 to 1766 (nt 88 to 111)

```
5'-GTTTGGATTATAAAGCAUUCAAAC-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -4.6; z-score = -3.19; ED = 0.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1656 to 1854 (motif highlighted in silver):

```
5'-UUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAAC
AAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACU-3
5'-.......(((((.......)))))...((((((.(((((((((((((((..(((((((((((....)))))))))..((.....))(((((((((.......)))))))))
...........((((...((((((....))))))...))))..))))..))))))))))).)))))).))))))...............-3'
MFE = -55.0; z-score = -3.79; ED = 25.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

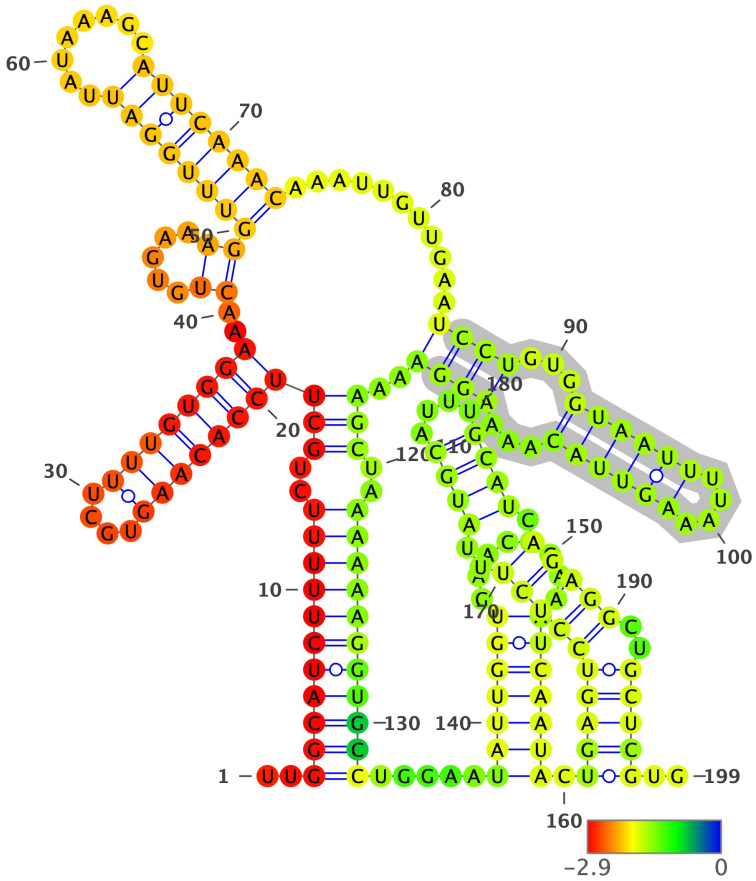
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 28 from nt 1779 to 1806 (nt 86 to 113)

```
5'-CCTGTGGTAATTTTAAAGUUACAAAAGG-3'
5'-(((....((((......))))....)))-3'
Motif MFE = -5.5; z-score = -1.71; ED = 0.85
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1694 to 1892 (motif highlighted in silver):

```
5'-UUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAA
GGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUG-3
5'-..(((((((((((..(((((((((((....))))))))..((.....))((((((((.........))))))))...........((((...((((((....))))))...)
)))..)))..))))))))))).....(((((((.........)))))))..((((((((((..((((....)))).)))))..)))))..-3'
MFE = -60.5; z-score = -4.2; ED = 17.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

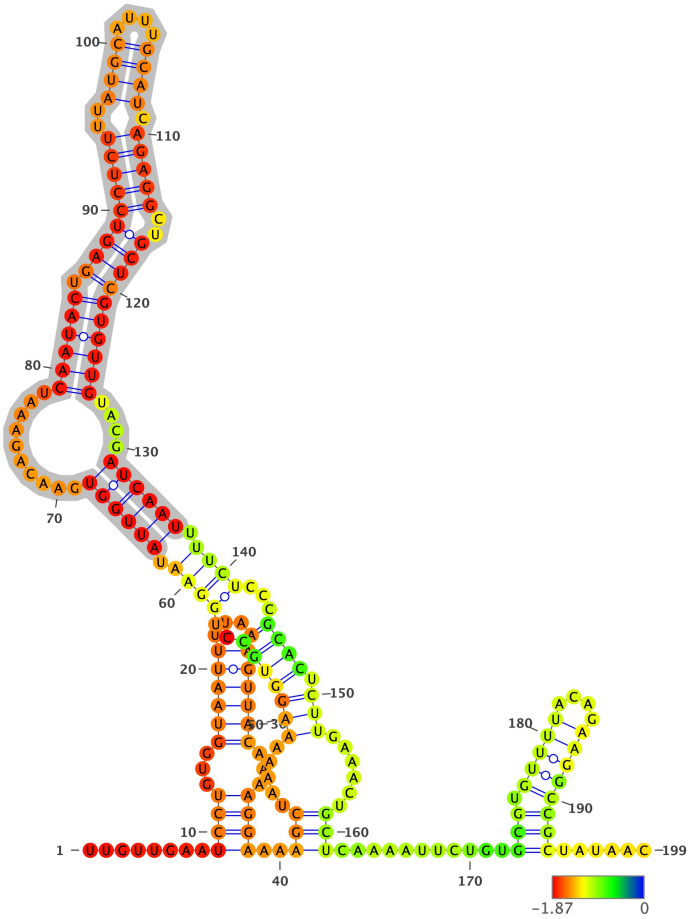
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 29 from nt 1832 to 1905 (nt 63 to 136)

```
5'-ATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCAUCAGAGGCTGCUCGUGUUGTACGAUCAAU-3'
5'-((((((..........((((((..(((((((((..((((....)))).)))))..))).)))))).....))))))-3'
Motif MFE = -20.1; z-score = -2.76; ED = 7.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1770 to 1968 (motif highlighted in silver):

```
5'-UUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAG
AGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAAC-3
5'-........((((...((((((....))))))...))))..(((.....(((((((..((((.((((((..........((((((.(((((((((..((((....)))).))
)))..))))))))))....)))))).))))...)))).)))......)))...........(((.(((((....))))))))......-3'
MFE = -48.9; z-score = -1.56; ED = 28.5
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

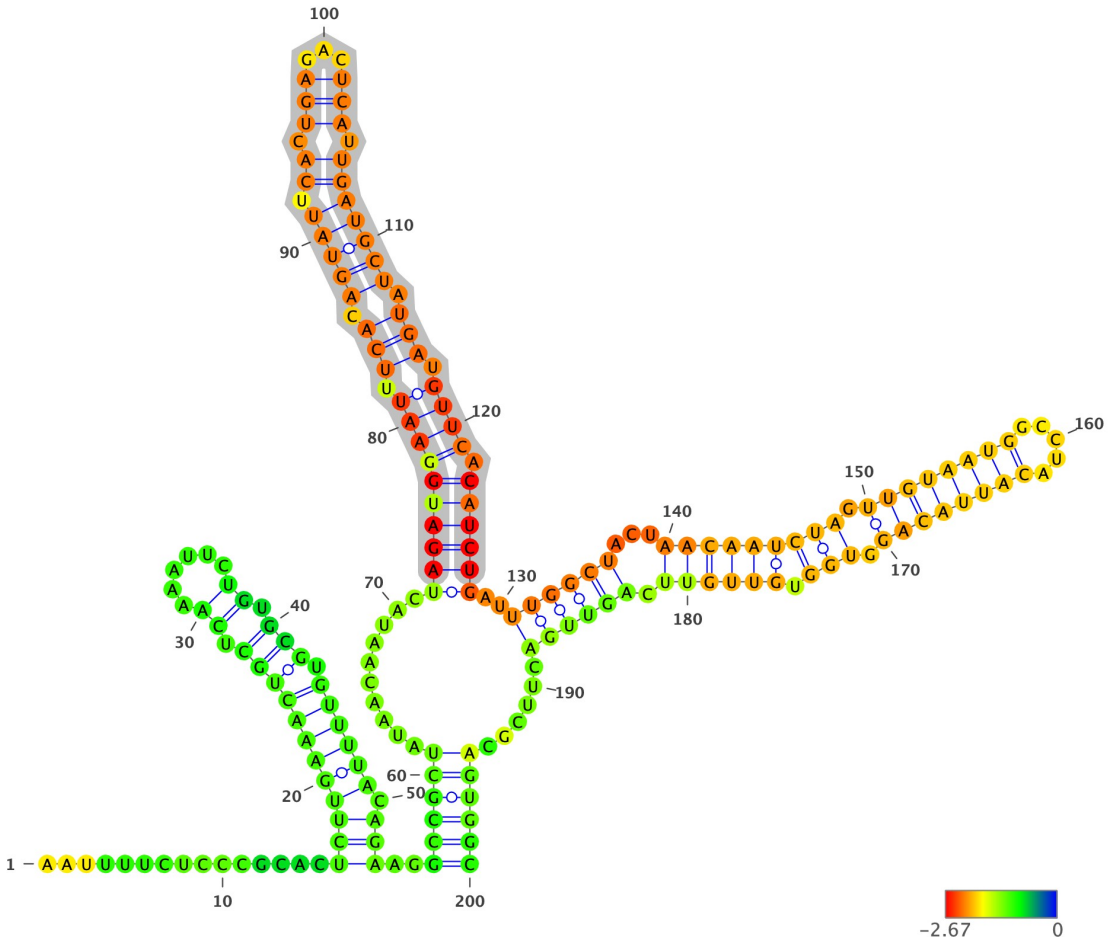
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 30 from nt 1975 to 2029 (nt 73 to 127)

```
5'-AGATGGAATTTCACAGTATTCACTGAGACUCATUGAUGCUAUGATGUUCACAUCU-3'
5'-(((.(.(((.(((.(((((.((.(((...))).)))))))).))).)))..).)))-3'
Motif MFE = -16.5; z-score = -3.32; ED = 2.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1903 to 2102 (motif highlighted in silver):

```
5'-AAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGC
UAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGC-3
5'-...............(((((((((((.((......)).))).)))))).)))..((((((..........((((((((((.(((.(((((.((.(((...))).))))))
).))).)))).)))))).((((((...((((((((.((((((((.....)))))))).))).)))))).))))))......))))))-3'
MFE = -52.4; z-score = -2.63; ED = 26.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

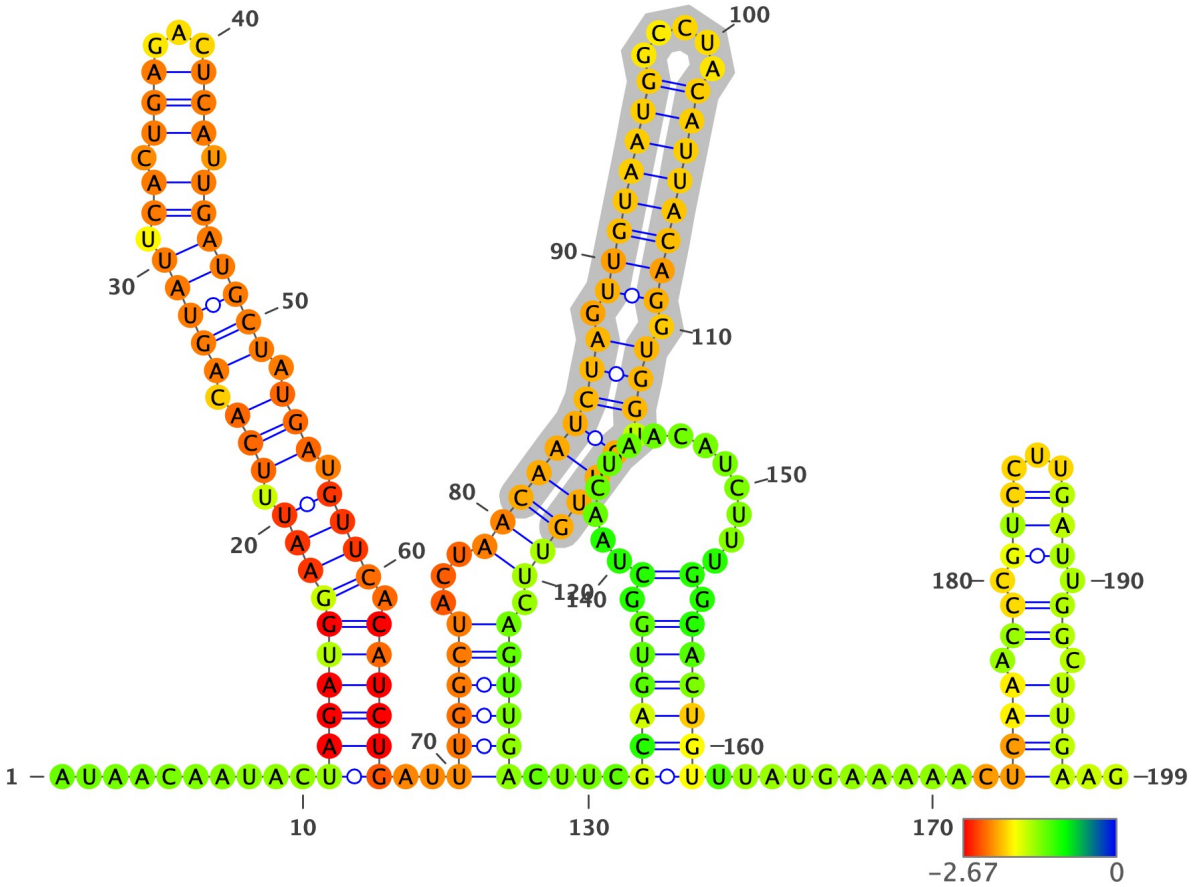
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 31 from nt 2044 to 2081 (nt 81 to 118)

```
5'-CAATCTAGTTGTAATGGCCTACAUUACAGGUGGTGUUG-3'
5'-(((((((.((((((((.....)))))))).))).))))-3'
Motif MFE = -13.0; z-score = -2.85; ED = 1.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 1964 to 2162 (motif highlighted in silver):

```
5'-AUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGU
GGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAG-3
5'-..........((((((((((.(((.((((((.((.(((...)))).)))))))).))).)))).)))))).((((((...(((((((((.(((((((((.....)))))))))).)
)).)))))).)))))).....((((((.(.............).)))))).........((((.((.(((...))).)).)))).-3'
MFE = -51.0; z-score = -2.38; ED = 19.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

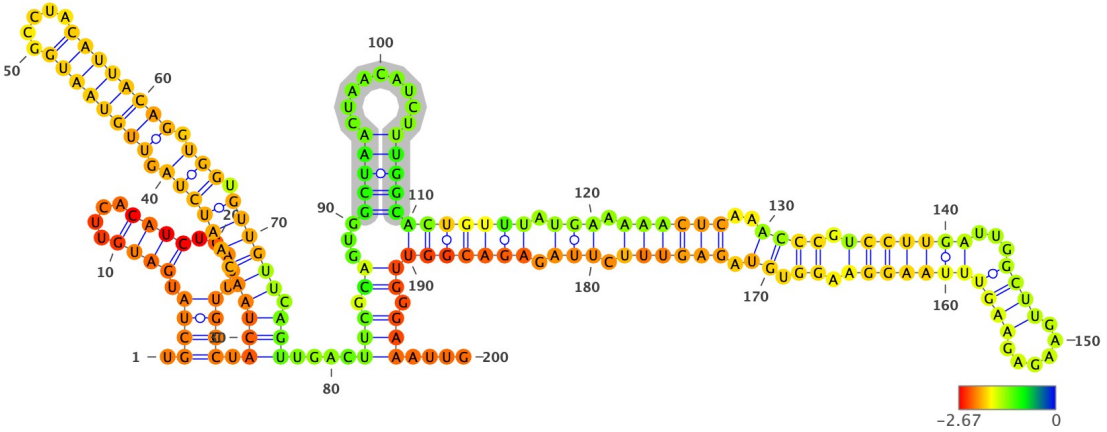
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 32 from nt 2101 to 2119 (nt 91 to 109)

```
5'-GCTAACTAACATCTTUGGC-3'
5'-((((...........))))-3'
Motif MFE = -1.2; z-score = -0.66; ED = 2.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2011 to 2210 (motif highlighted in silver):

```
5'-UGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCAC
UGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUG-3
5'-.((((.((((....)))).....)))).((((((((((((.((((((((.....))))))))).))).)))))).))).....(((.((...(((((.........)))))((
(((((.(((.((((((..((((.(((((((...((((......)))))))))))).)).)).)))))).))).))))))))).))).....-3'
MFE = -52.3; z-score = -2.77; ED = 31.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

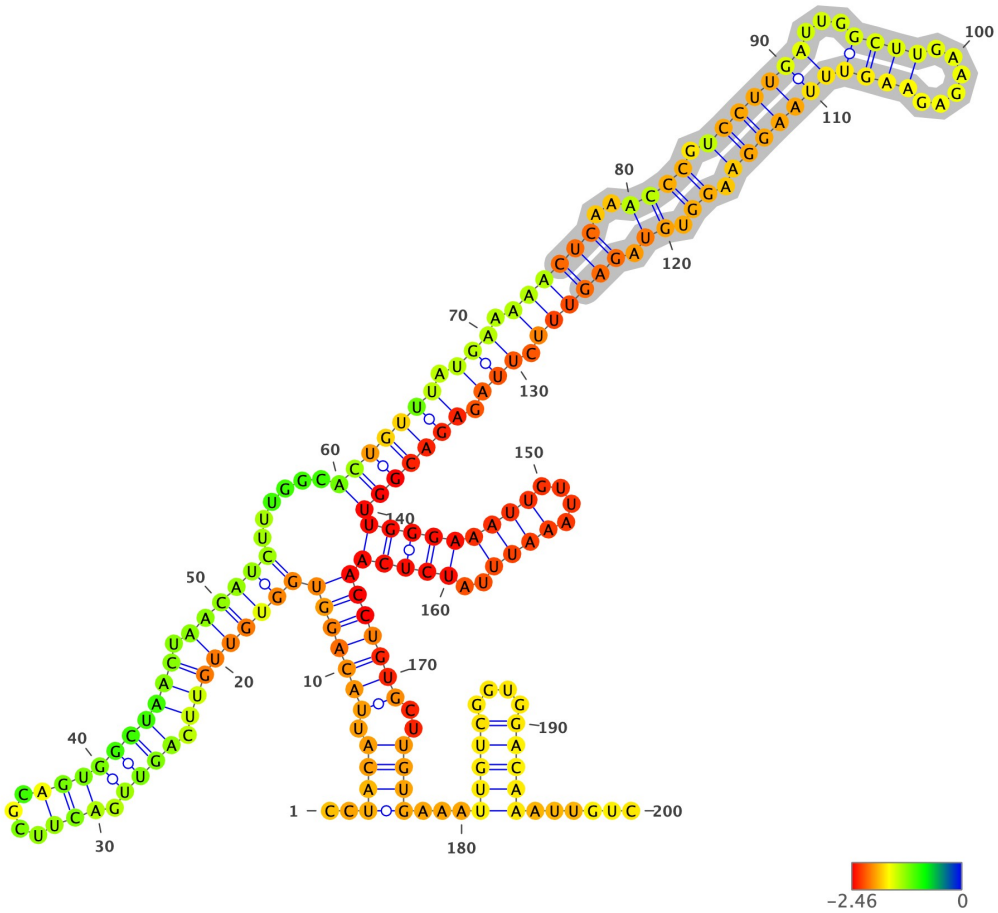
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 33 from nt 2135 to 2185 (nt 75 to 125)

```
5'-CTCAAACCCGTCCTTGATTGGCTTGAAGAGAAGTTTAAGGAAGGTGTAGAG-3'
5'-(((....((..((((.....................))))..))....)))-3'
Motif MFE = -13.7; z-score = -1.79; ED = 8.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2061 to 2260 (motif highlighted in silver):

```
5'-CCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUA
AGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUC-3
5'-..((((.((((((((((((((((.((((.(((....)))))))))).))))))......(((((((.(((.((((((..((((.(((((((...((((......)))))))
))))).)).)).)))))).))).)))))))((((((((....))))..))))))))))))..))))...(((((....)))))......-3'
MFE = -54.3; z-score = -1.86; ED = 47.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

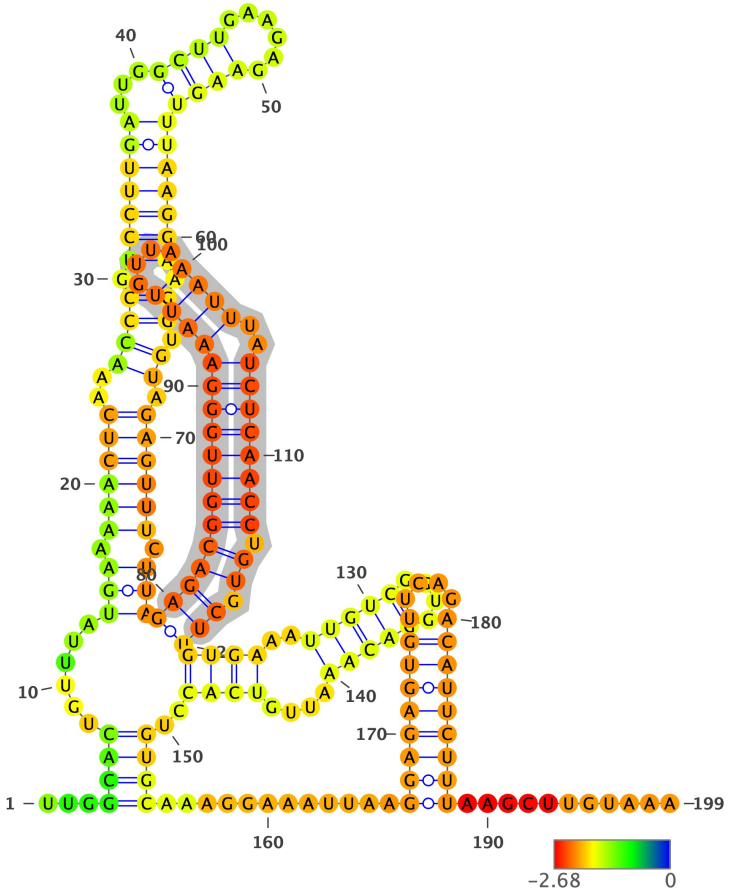
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 34 from nt 2194 to 2233 (nt 80 to 119)

```
5'-AGACGGTTGGGAAATTGTTAAATTTAUCUCAACCTGUGCU-3'
5'-(((((((((((.............))))))))).)).))-3'
Motif MFE = -11.0; z-score = -2.48; ED = 3.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2115 to 2313 (motif highlighted in silver):

```
5'-UUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAA
CCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAA-3
5'-...((((......(((.((((((..((((.(((((((...((((......))))))))))).)).)).)))))).)))((((((((((((((((....))))..))))))
)).)).)))((((..(((((....)))))....))))..))))............(((((((((....)))))))))...........-3'
MFE = -51.1; z-score = -3.39; ED = 40.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

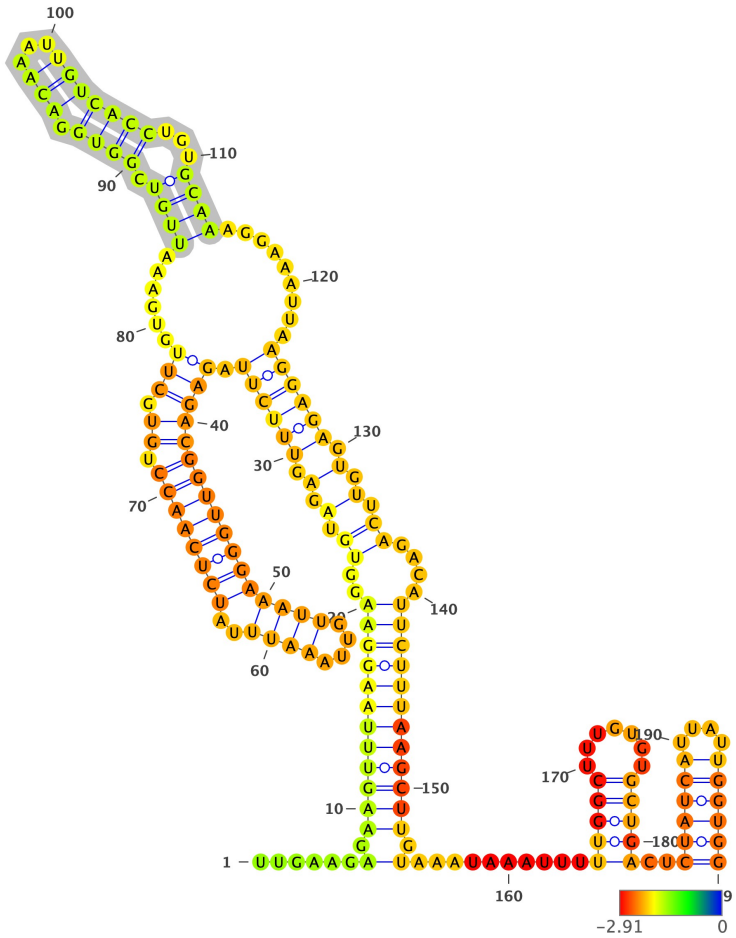
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 35 from nt 2241 to 2270 (nt 85 to 114)

```
5'-TTGTCGGTGGACAAATTGUCACCTGTGCAA-3'
5'-((((.(((((.((.....)))))))...))))-3'
Motif MFE = -6.7; z-score = -1.12; ED = 5.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2157 to 2355 (motif highlighted in silver):

```
5'-UUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUG
CAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGG-3
5'-......(.(((((((((((..((.(.(.((((((.((((((((((((((((((....)))).)))))))).)).)))).....((((.((((.((((...)))))))...)
)))).........)))))).).).)).....))))))))))).).........(((((.......)))))..((((((....))))))-3'
MFE = -43.4; z-score = -1.88; ED = 40.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

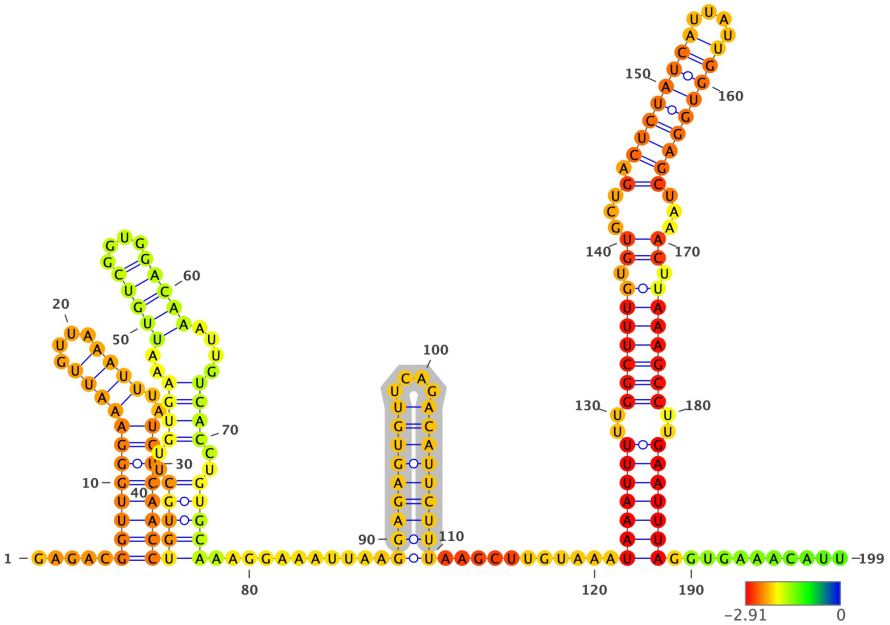
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 36 from nt 2282 to 2301 (nt 90 to 109)

```
5'-GAGAGTGTTCAGACAUUCUU-3'
5'-((((((((....))))))))-3'
Motif MFE = -6.2; z-score = -3.6; ED = 0.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2193 to 2391 (motif highlighted in silver):

```
5'-GAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUA
AGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUU-3
5'-.....(((((((((((....))))..))))))))(((((..((((..(((((....)))))....))))..)))))...........(((((((((....))))))))).
..........(((((((..(((((((.((...(.(((((((((....)))))))))...)).)))))))..)))))))...........-3'
MFE = -57.6; z-score = -3.44; ED = 14.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

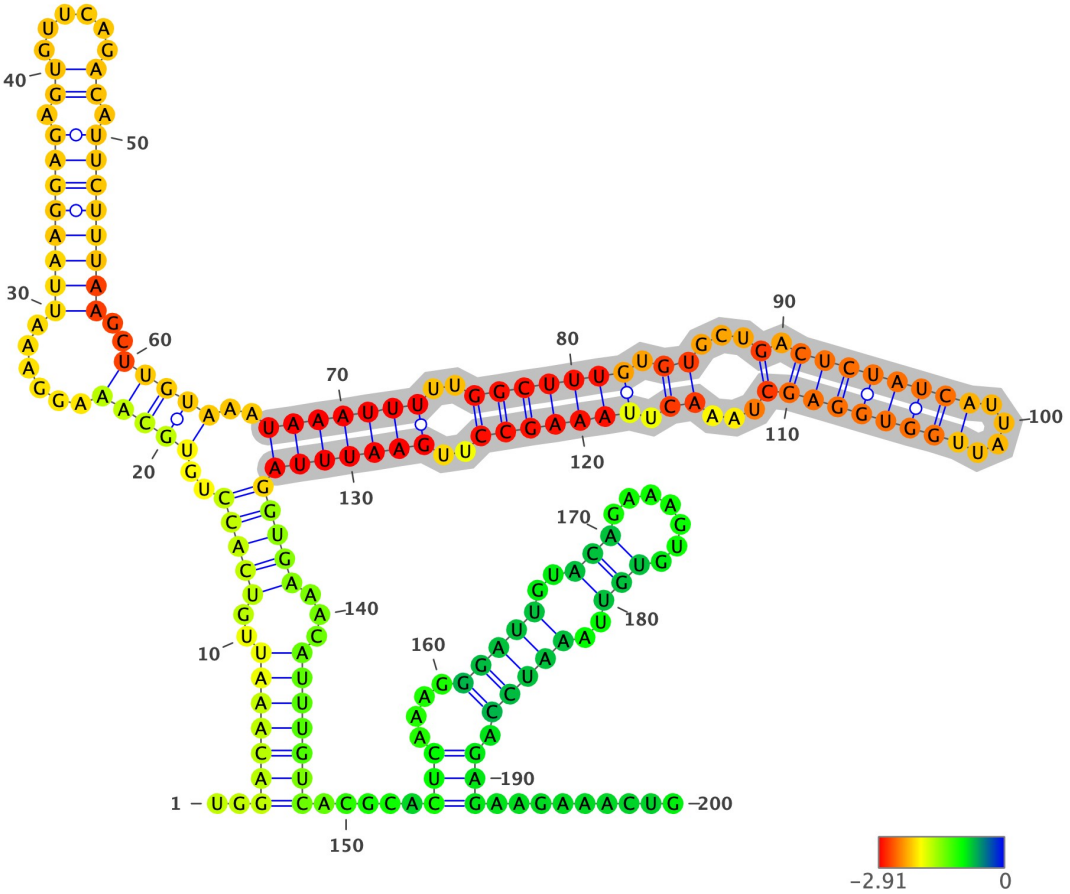
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 37 from nt 2314 to 2380 (nt 67 to 133)

```
5'-TAAATTTTTGGCTTTGTGTGCTGACTCTATCATTATTGGUGGAGCTAAACTTAAAGCCTTGAAUUUA-3'
5'-(((((((..((((((..((...(.(((((((......))))))))...))..))))))..)))))))-3'
Motif MFE = -24.1; z-score = -4.9; ED = 2.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2248 to 2447 (motif highlighted in silver):

```
5'-UGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGC
UAAACUUAAAGCCUUGAAUUUAGGUGAAACAUUUGUCACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUG-3
5'-..(((((((..(((((..(((((......((((((((.((......)).))))))))..)))))..(((((((..(((((((.((...(.((((((((....)))))))))
...)).)))))))..))))))))))))...)))))))).....(((....(((((..(((.......)))..)))))).)))..........-3'
MFE = -52.5; z-score = -2.61; ED = 24.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

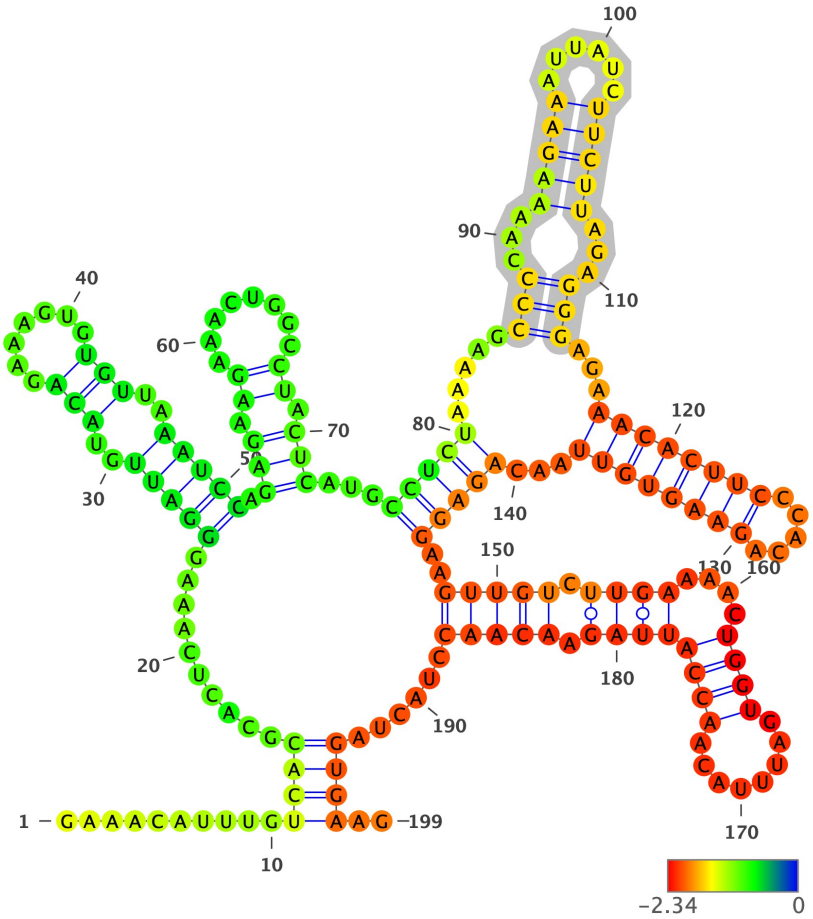
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 38 from nt 2469 to 2496 (nt 86 to 113)

```
5'-CCCCAAAAGAAATTATCUUCTTAGAGGG-3'
5'-(((.....(((......)))).....)))-3'
Motif MFE = -5.3; z-score = -2.33; ED = 3.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2384 to 2582 (motif highlighted in silver):

```
5'-GAAACAUUUGUCACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAG
GGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAG-3
5'-..........((((..........(((((..(((.......)))..))))).(((.((........)).)))...(((((.....(((...(((((......)))))...)
))...(((((((.....))))))))...)))))..(((((.((((....((((........)))))))).)))))......))))..-3'
MFE = -42.6; z-score = -1.63; ED = 22.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

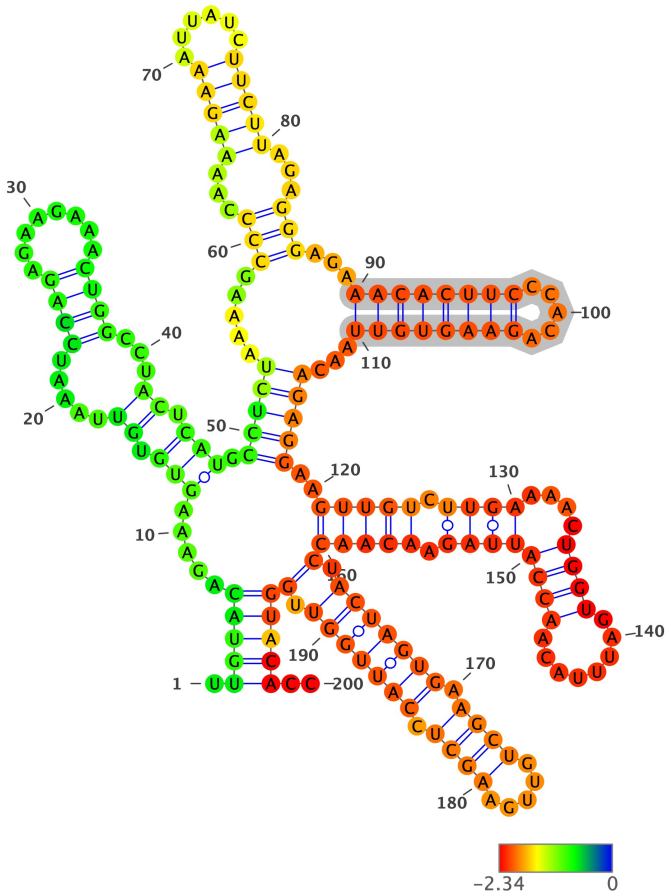
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 39 from nt 2500 to 2520 (nt 90 to 110)

```
5'-AACACTTCCCACAGAAGUGUU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.6; z-score = -5.42; ED = 0.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2411 to 2610 (motif highlighted in silver):

```
5'-UUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUA
ACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACC-3
5'-.(((((.....(((.((.....((((........))))...)).))).(((((.....(((...(((((......)))))...)))...(((((((.....)))))))).
..)))))..(((((.((((....((((........)))))))).)))))(.(((((((.((((.....)))).))))))).)))))..-3'
MFE = -50.3; z-score = -3.04; ED = 26.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

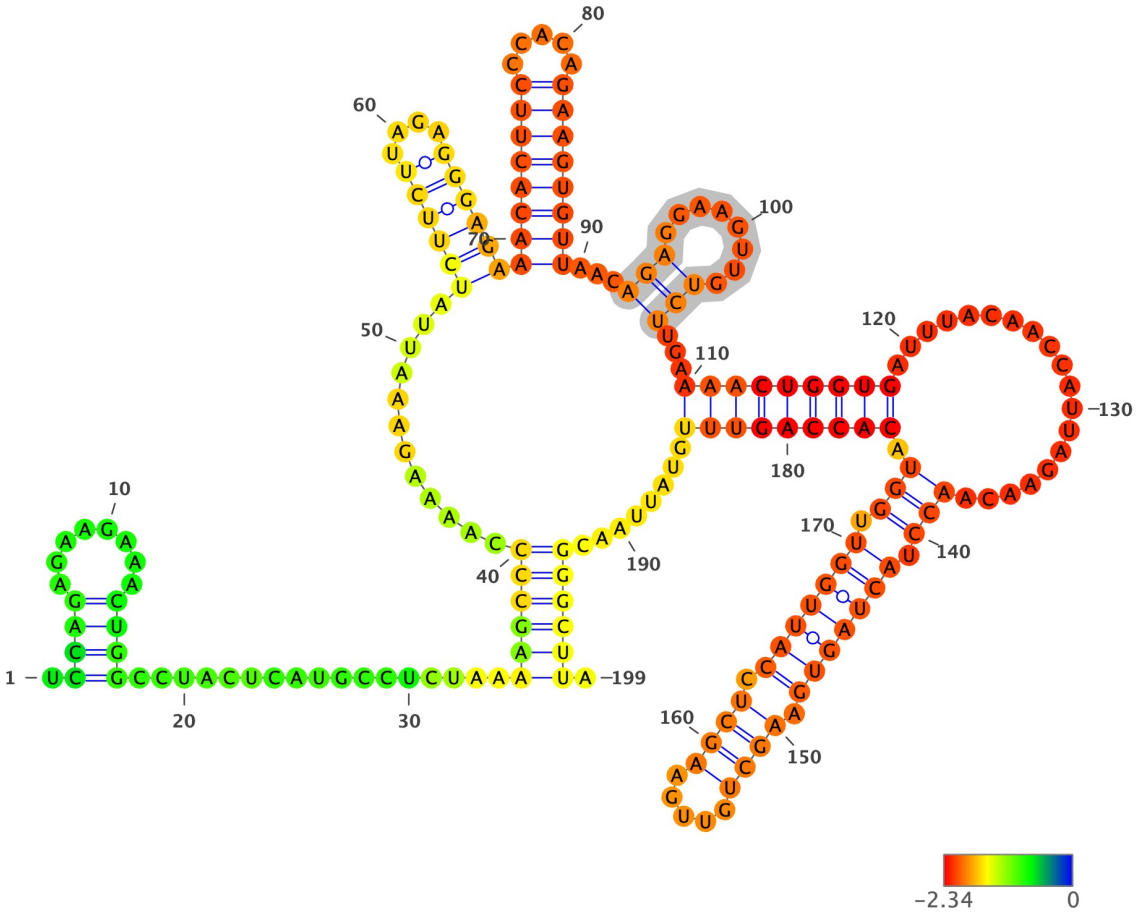
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 40 from nt 2524 to 2537 (nt 93 to 106)

```
5'-AGAGGAAGTTGUCU-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.34; ED = 2.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2432 to 2630 (motif highlighted in silver):

```
5'-UCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAA
ACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUA-3
5'-.((((........))))..................((((((............((((((....))))))((((((((.....))))))))...(((........)))...((
(((((((...................(((.(((((((.((((.....)))).)))))))).))).))))))))).......))))))).-3'
MFE = -51.8; z-score = -2.79; ED = 26.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

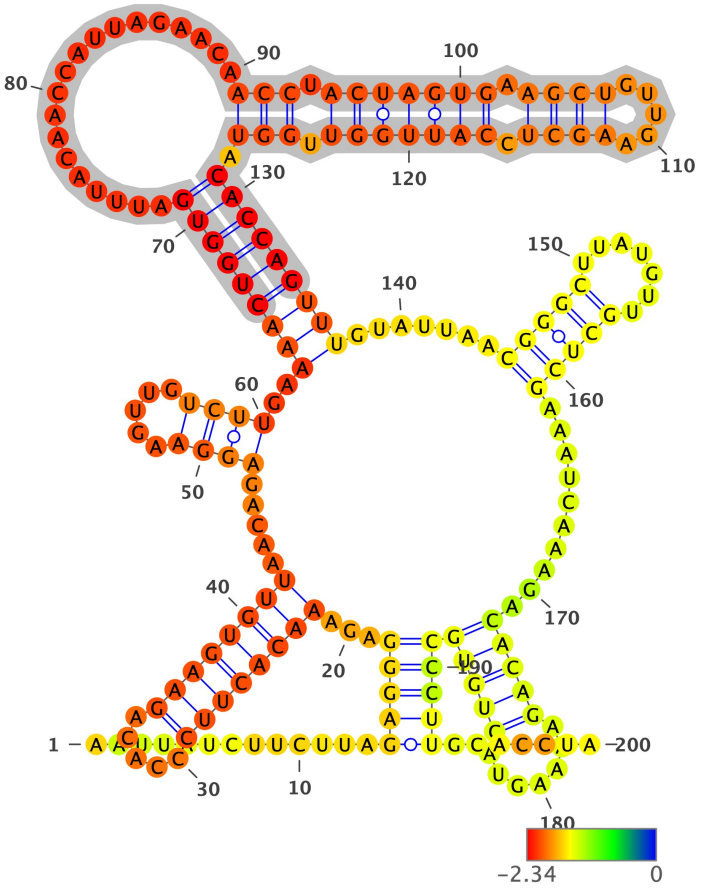
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 41 from nt 2544 to 2612 (nt 66 to 134)

```
5'-CTGGTGATTTACAACCATTAGAACAACCTACTAGTGAAGCTGTTGAAGCUCCAUUGGUTGGUACACCAG-3'
5'-((((((...................(((.(((((((.((((.....)))).)))))))).))).))))))-3'
Motif MFE = -20.7; z-score = -2.82; ED = 10.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2479 to 2678 (motif highlighted in silver):

```
5'-AAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGA
AGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUA-3
5'-.............(((((...((((((((.....))))))))).....((((.....)))).((((((((((...................(((.(((((((.((((.....
)))).)))))))).))).))))))))).......(((((.......)))))..........(((((.......)))))))))).......-3'
MFE = -53.0; z-score = -2.41; ED = 27.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

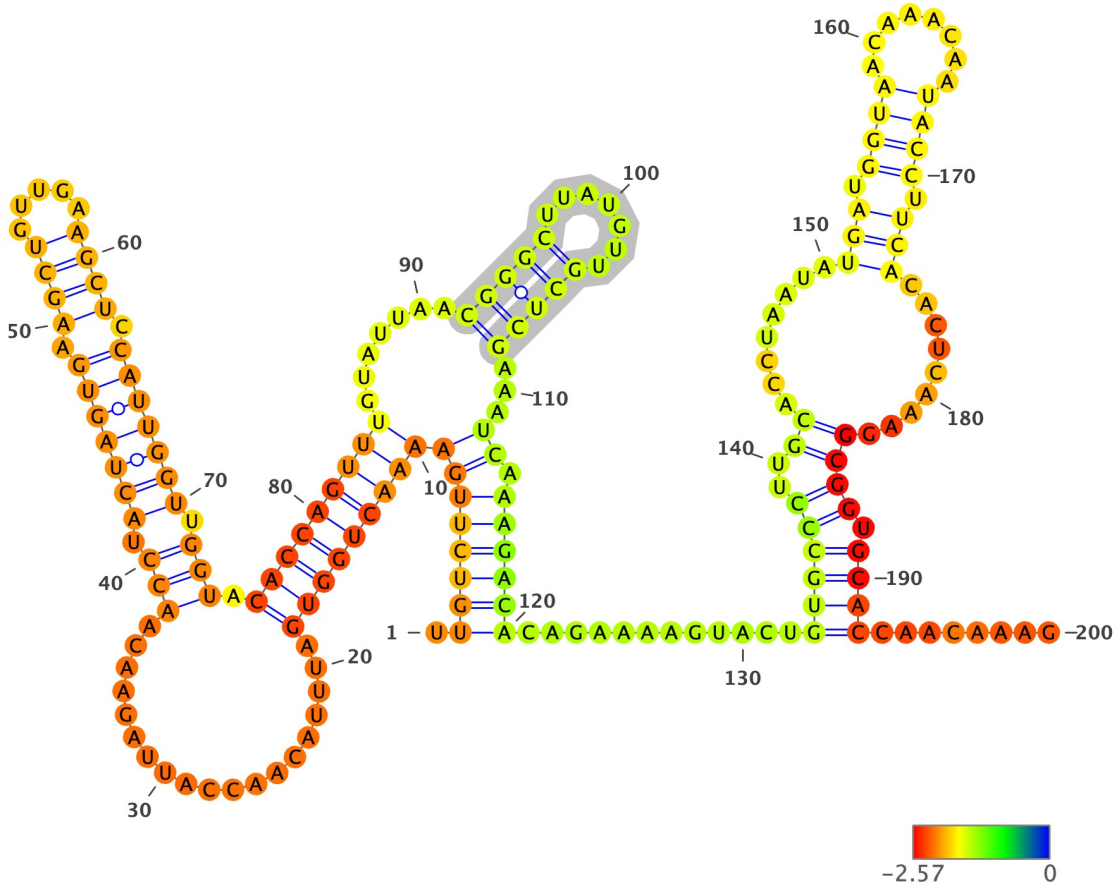
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 42 from nt 2623 to 2639 (nt 92 to 108)

```
5'-CGGGCTTATGTTGCUCG-3'
5'-(((((.......)))))-3'
Motif MFE = -5.5; z-score = -2.66; ED = 0.32
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2532 to 2731 (motif highlighted in silver):

```
5'-UUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAA
UCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAG-3
5'-.((((((((((((((((.....................(((.(((((((.((((.....)))).)))))))).))).)))))))))).......(((((.......)))))...
)).))))))............((((((..((........(((.((((........)))).)))..........)))).))))........-3'
MFE = -49.8; z-score = -2.47; ED = 32.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

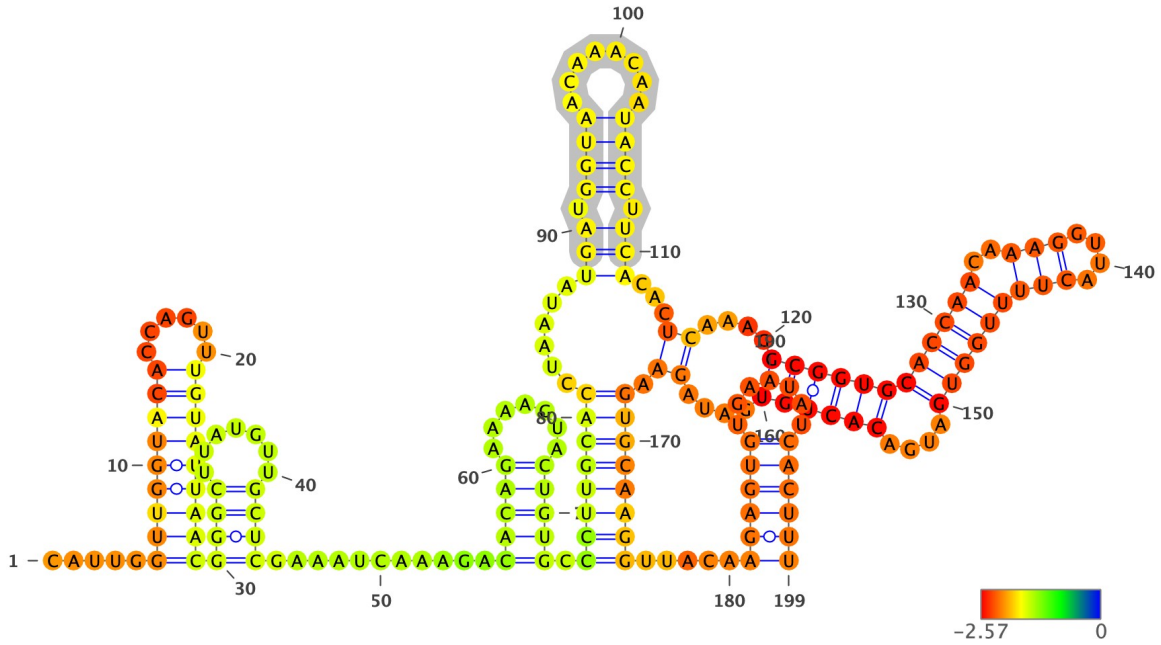
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 43 from nt 2683 to 2704 (nt 89 to 110)

```
5'-GATGGTAACAAACAAUACCTUC-3'
5'-((.((((........)))).))-3'
Motif MFE = -3.2; z-score = -3.81; ED = 1.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2595 to 2793 (motif highlighted in silver):

```
5'-CAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCA
CACUCAAAGGCGGUGCACCAACAAAGGUUACUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUU-3
5'-.....(((((((((.....)))))))))((((.......)))).........(((((.......))))).((((((((.....(((.((((........)))).)))
...((....((((((((((..((((....)))))))))....)))))))....)).)))))))).....((((((.......))))))-3'
MFE = -52.2; z-score = -2.1; ED = 29.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

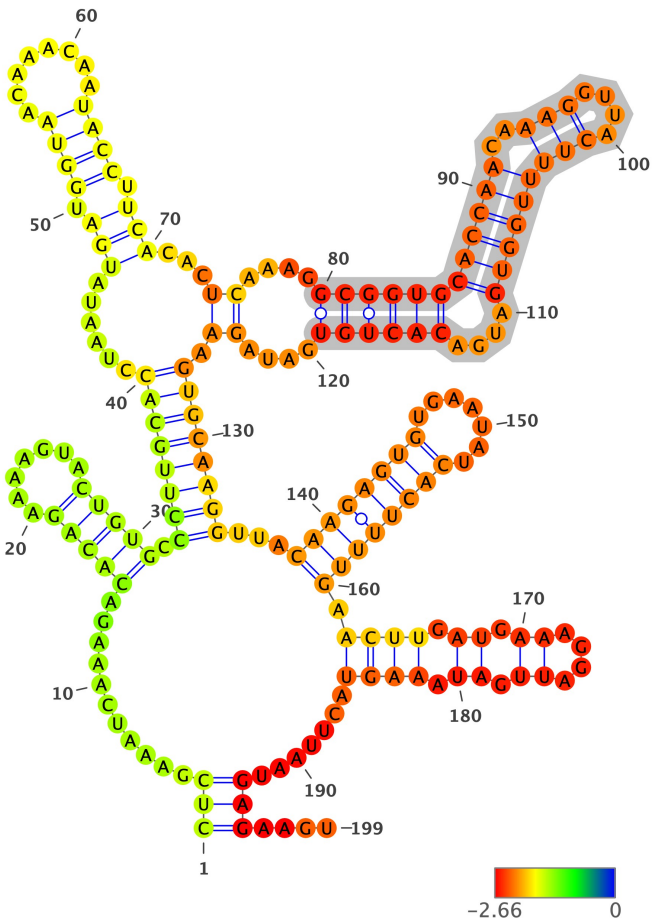
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 44 from nt 2715 to 2754 (nt 80 to 119)

```
5'-GCGGTGCACCAACAAAGGTTACUUUUGGUGATGACACUGU-3'
5'-(((((((((((((..(((....)))))))))....))))))-3'
Motif MFE = -12.9; z-score = -2.33; ED = 3.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2636 to 2834 (motif highlighted in silver):

```
5'-CUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAU
GACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGU-3
5'-(((...........(((((.......))))).((((((((......(((.((((........)))).)))...((....(((((((((((((..(((....)))))))))..
..))))))....)).))))))))...((((((((.......)))))))).((((.((.((....)).)).))))........)))....-3'
MFE = -47.4; z-score = -2.33; ED = 24.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

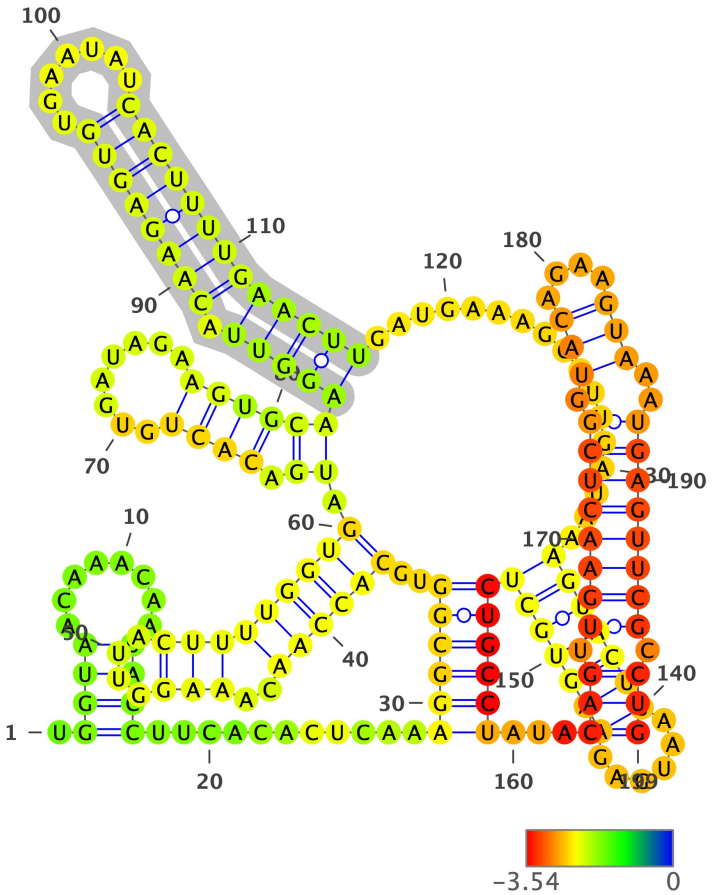
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 45 from nt 2767 to 2800 (nt 83 to 116)

```
5'-AGGTTACAAGAGTGTGAATATCACUUUUGAACUU-3'
5'-(((((.((((((((.......)))))))))))))-3'
Motif MFE = -10.9; z-score = -4.56; ED = 0.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2685 to 2883 (motif highlighted in silver):

```
5'-UGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUG
AACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUG-3
5'-.((((........))))...........((((((..((((((..(((....))))))))).((.((((........))))))(((((.((((((((.......))))))))
)))))..................(((((((......)))))))))))))...(((.((((((((.(((....)))..)))))))).)))-3'
MFE = -55.0; z-score = -3.06; ED = 21.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

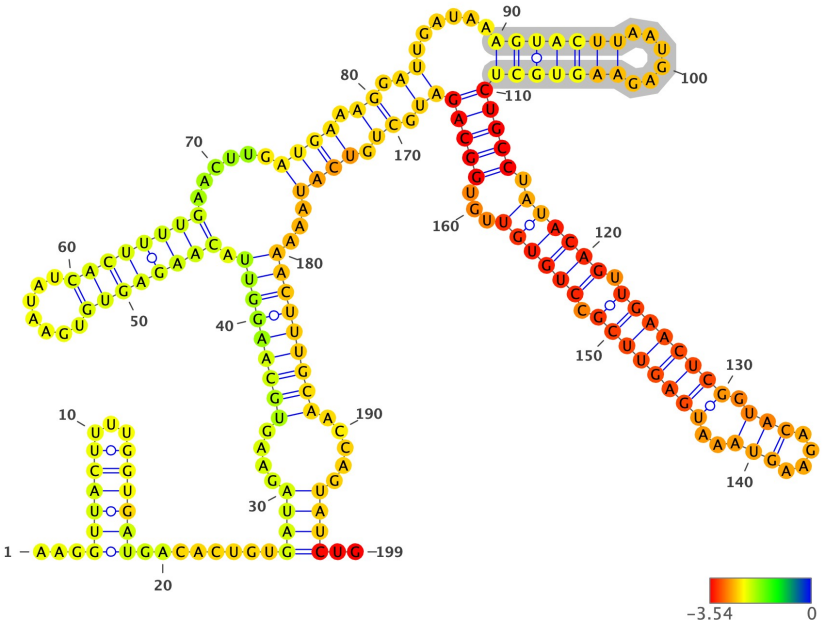
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 46 from nt 2818 to 2837 (nt 90 to 109)

```
5'-AGTACTTAATGAGAAGUGCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.4; z-score = -4.76; ED = 0.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2729 to 2927 (motif highlighted in silver):

```
5'-AAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCU
GCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUG-3
5'-...((((((...)))))).......((((....(((((((((.(((((((((.......)))))))))......((((.((.(((.....((((((.....)))))))))((
(((.((((((.((((((((.(((....)))).. ))))))))..)))))).....))))))).)).)))).....))))))))).....)))).. -3'
MFE = -57.2; z-score = -4.29; ED = 41.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

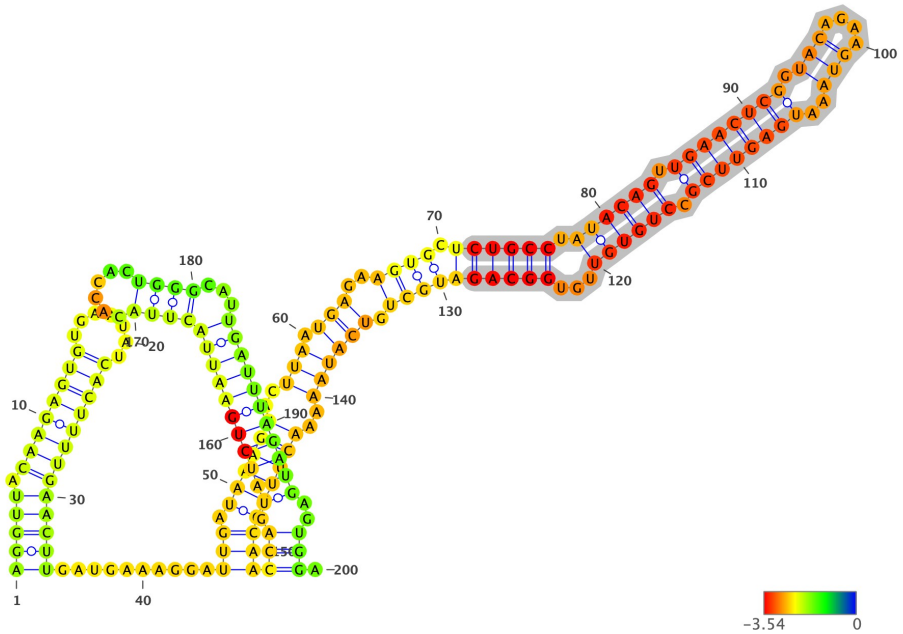
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 47 from nt 2838 to 2894 (nt 72 to 128)

```
5'-CTGCCTATACAGTTGAACTCGGTACAGAAGTAAATGAGUUCGCCUGUGTTGTGGCAG-3'
5'-(((((...((((.(((((((.............))))))).)))).....)))))-3'
Motif MFE = -25.1; z-score = -4.33; ED = 1.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2767 to 2966 (motif highlighted in silver):

```
5'-AGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUU
CGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGA-3
5'-(((((.((((((((.......)))))))))))))..........(((.((((((..(((.(((..((((.((((((.((((((.((((((((.(((....)))..))))))
)).))))))...)))))))))).))))))..)))))))))(((.((((((((((((((.......))))...)))))))))))..))).-3'
MFE = -60.4; z-score = -4.52; ED = 19.76
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

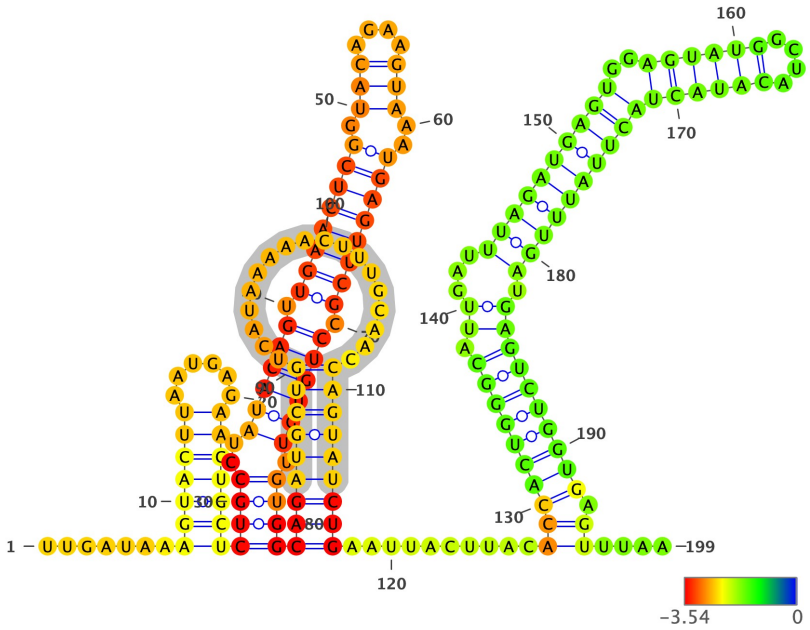
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 48 from nt 2895 to 2924 (nt 85 to 114)

```
5'-ATGCTGTCATAAAAACTTTGCAACCAGUAU-3'
5'-((((((..................))))))-3'
Motif MFE = -2.2; z-score = -0.39; ED = 4.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2811 to 3009 (motif highlighted in silver):

```
5'-UUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAG
UAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAA-3
5'-.......(((((((......)))))))((((..((((((.((((((((.(((....)))..)))))))).)))))).))))((((((((.................)))
))))))..........((((((((((.((...((((((((((..((((((....)))))))))))))))).))))))))))).))....-3'
MFE = -60.2; z-score = -4.39; ED = 19.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

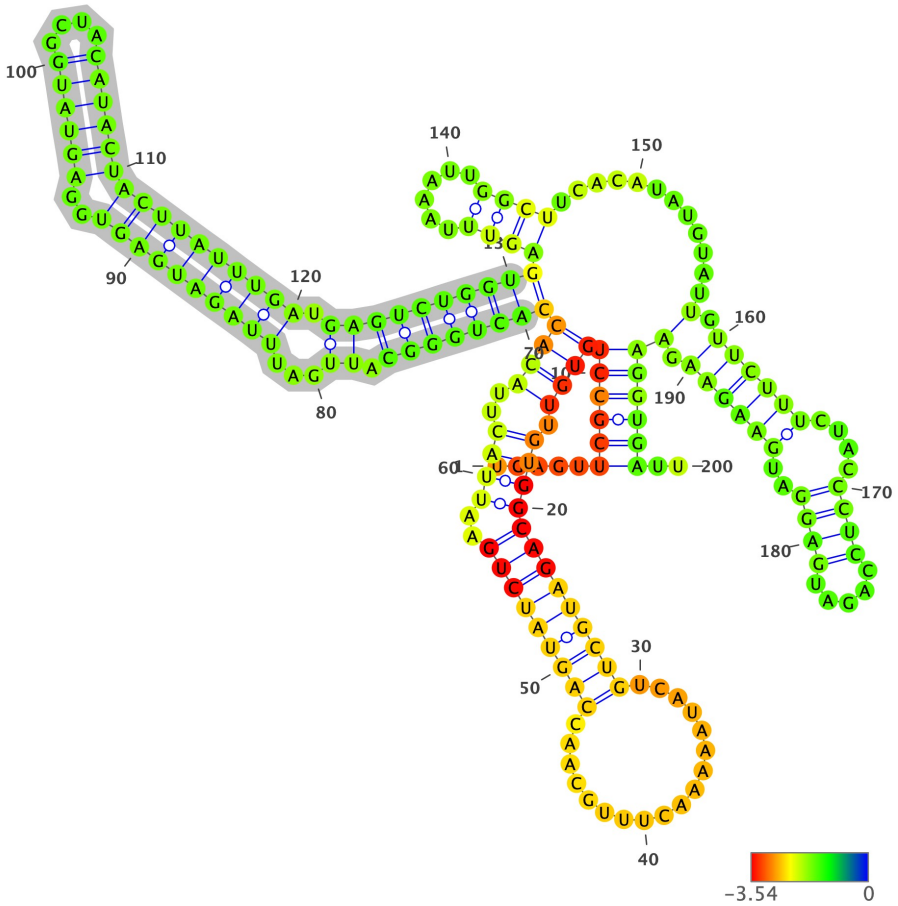
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 49 from nt 2941 to 3001 (nt 70 to 130)

```
5'-ACTGGGCATTGATTTAGATGAGTGGAGTATGGCTACAUACUACUUAUUUGATGAGUCUGGU-3'
5'-(((((((.......((((((((((..(((((.....))))))))))))))....)))))))-3'
Motif MFE = -19.3; z-score = -3.41; ED = 5.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2872 to 3071 (motif highlighted in silver):

```
5'-UGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUA
CUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUU-3
5'-.....((((((((((.((((((((((((((.................)))))))))..))))..))))((((((((.((...((((((((((..((((((....)))))))
))))))))).))))))))))((((......))))............(.((((((....((((.....))))..)))))).)))))))..-3'
MFE = -54.6; z-score = -2.35; ED = 23.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

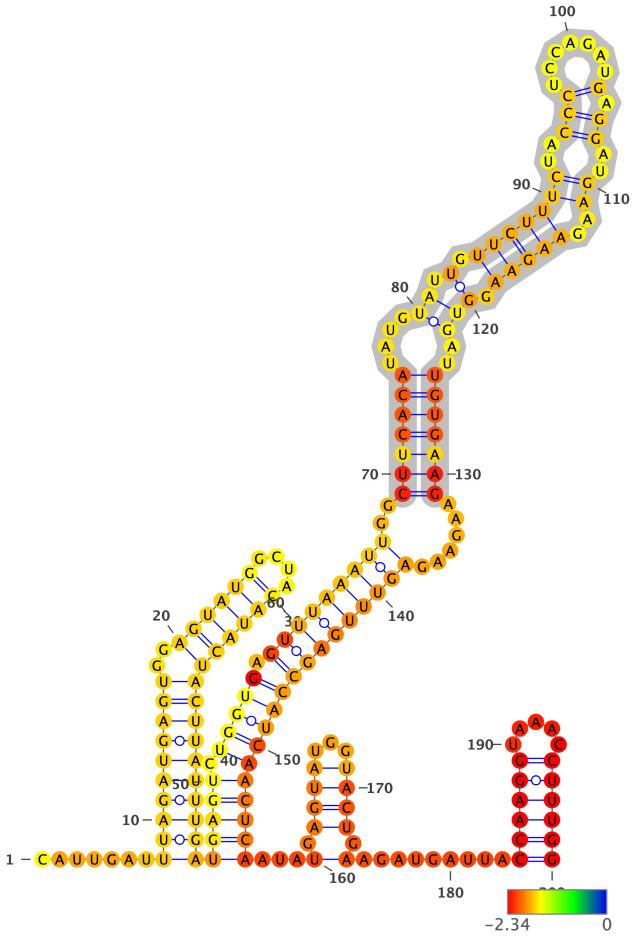
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 50 from nt 3015 to 3077 (nt 69 to 131)

```
5'-CTTCACATATGTATTGTTCTTTCTACCCTCCAGATGAGGATGAAGAAGAAGGTGATUGUGAAG-3'
5'-((.((((.......(.(((((((..(((.......).))..))..))))))..)....)))).))-3'
Motif MFE = -17.5; z-score = -2.6; ED = 8.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 2947 to 3146 (motif highlighted in silver):

```
5'-CAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGA
AGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGG-3
5'-.......((((((((((..((((((....)))))))))))))))))(((((.(((((.(((((((((..(((((((....((.(.(((((((..(((.......).)).))..))
..)))))).)))..)))))))).....))))))))))))))))))...(.((((...)))).).........((((((.....))))))-3'
MFE = -48.3; z-score = -3.43; ED = 21.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

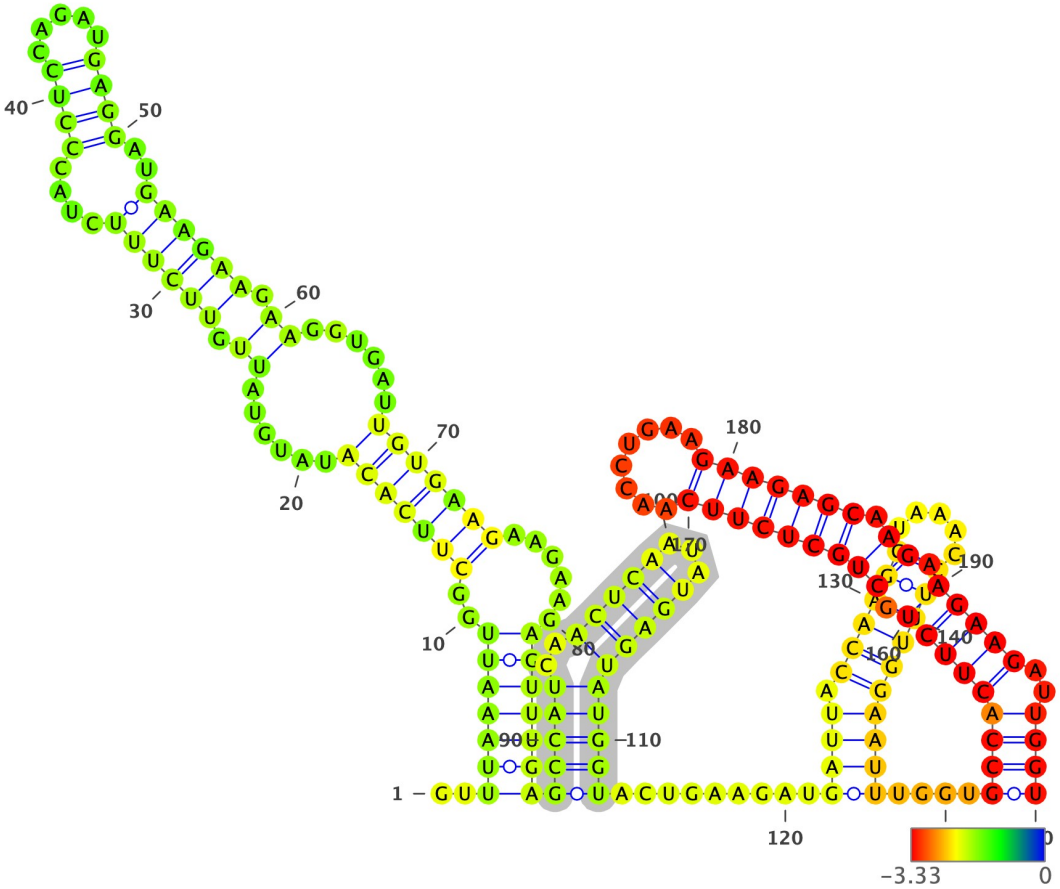
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 51 from nt 3091 to 3115 (nt 88 to 112)

```
5'-GCCATCAACTCAATATGAGUAUGGU-3'
5'-(((((..((((.....)))))))))-3'
Motif MFE = -7.6; z-score = -2.76; ED = 1.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3004 to 3203 (motif highlighted in silver):

```
5'-GUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGG
UACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGU-3
5'-..(((((((..(((((((......((.((((((....((((.....))))..)))))).))......)))))))......)))))))(((((..(((((...)))))))))
).........((((.((((((.....)))))))))....((((((((((.(((((((((.........)))))))).)).)))))..))))-3'
MFE = -55.6; z-score = -3.93; ED = 28.76
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

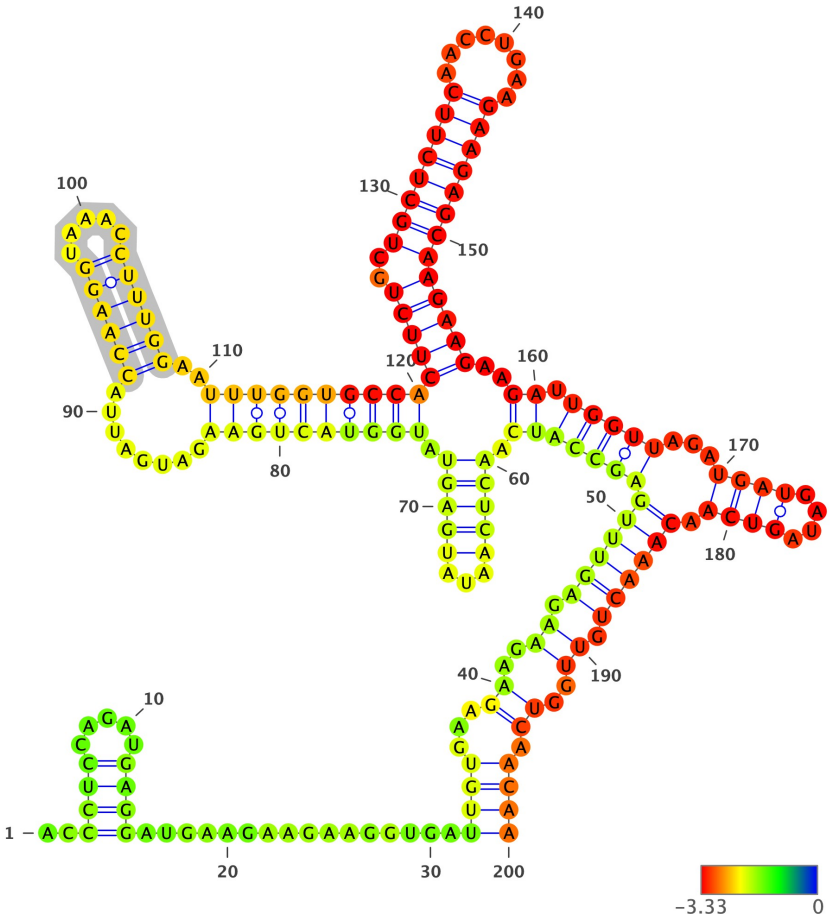
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 52 from nt 3130 to 3146 (nt 92 to 108)

```
5'-CCAAGGTAAACCUUUGG-3'
5'-((((((.....))))))-3'
Motif MFE = -4.3; z-score = -3.2; ED = 3.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3039 to 3238 (motif highlighted in silver):

```
5'-ACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAU
UUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAA-3
5'-..((((.....))))................((((...((..((.(((((((((((((.(((((...))))).((((((((((.........((((((.....))))))..)
))))))))))(((((..((((((((.........)))))))))))))..)).)))))...((((....)))).))))))).))..)).))))-3'
MFE = -51.1; z-score = -2.42; ED = 39.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

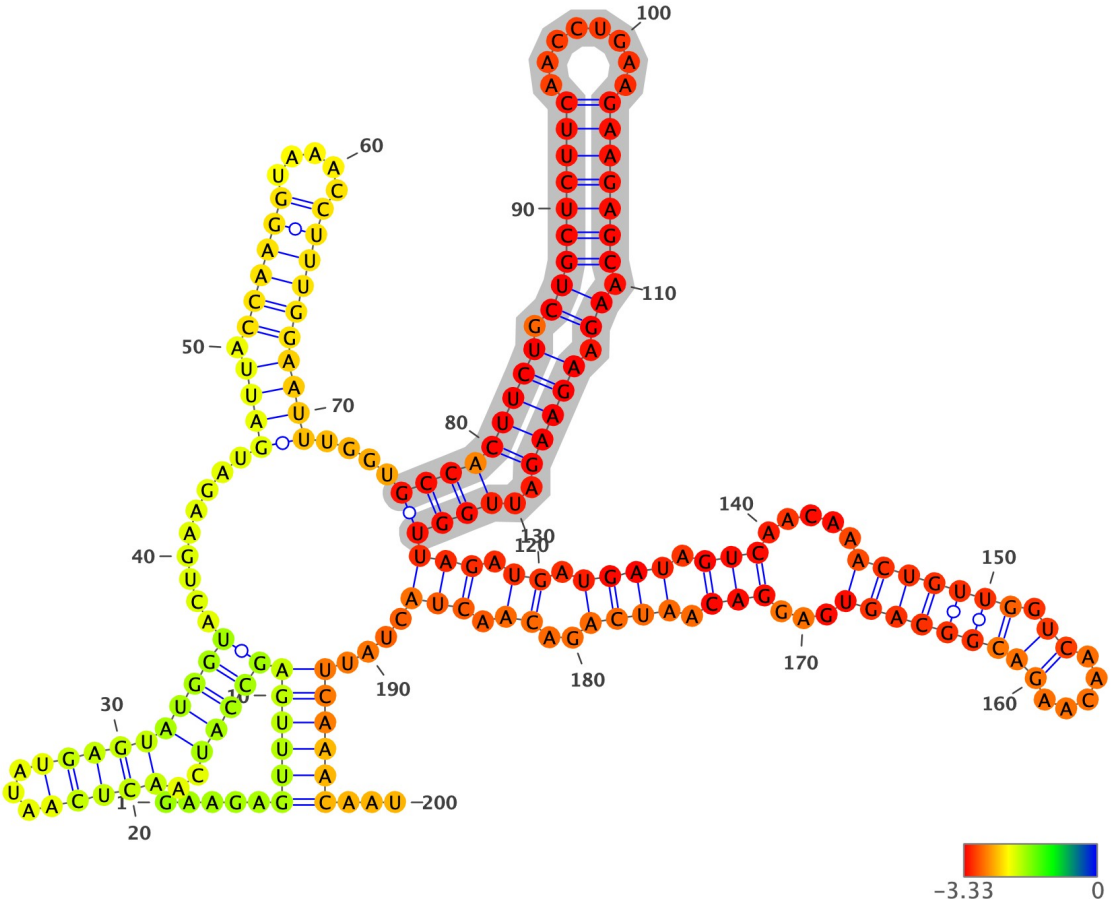
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 53 from nt 3155 to 3203 (nt 76 to 124)

```
5'-GCCACTTCTGCTGCTCTTCAACCTGAAGAAGAGCAAGAAGAAGATTGGU-3'
5'-(((.(((((.(((((((((.........)))))))).)).)))))...)))-3'
Motif MFE = -20.1; z-score = -4.29; ED = 2.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3080 to 3279 (motif highlighted in silver):

```
5'-GAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAA
GAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAU-3
5'-.....(((((((((((..(((((...)))))))))).........((((.((((((.....)))))))))....(((((((((.(((((((((.........)))))))).)
).)))))..))))(((.((.((((.(((.....(((((((.((.....)))))))))...))).))))..)).)))....))))))...-3'
MFE = -57.7; z-score = -4.12; ED = 17.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

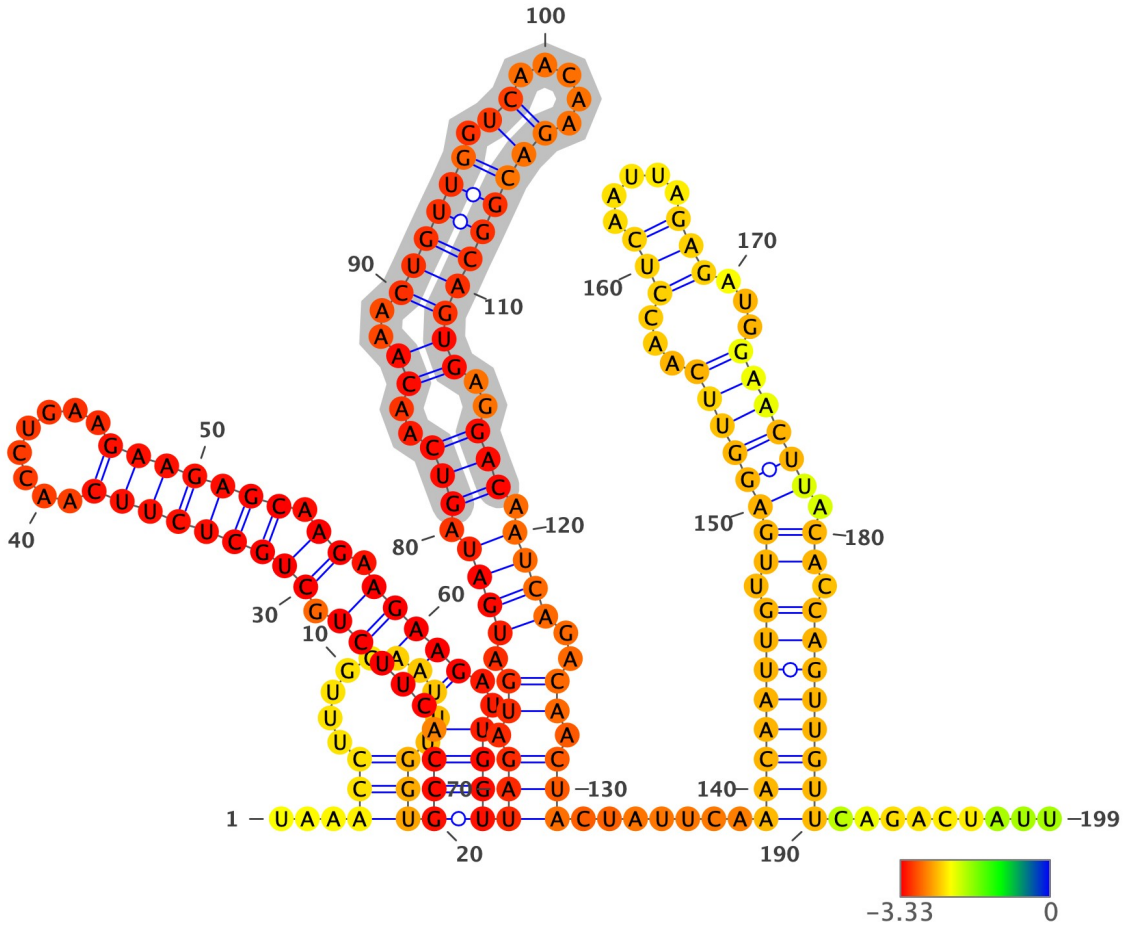
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 54 from nt 3216 to 3253 (nt 81 to 118)

```
5'-GTCAACAAACTGTTGGTCAACAAGACGGCAGUGAGGAC-3'
5'-(((..((..(((((.............)))))))..)))-3'
Motif MFE = -9.6; z-score = -1.89; ED = 3.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3136 to 3334 (motif highlighted in silver):

```
5'-UAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAG
UGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUU-3
5'-...(((..........)))(((((((((.((((((((.........)))))))).)).)))))..))))(((.((.((((.(((..((..((((((.((.....))))))))
))..))).))))..)).)))).......((((((((.((((((((...(((.....)))...)))))).)).))))))))..........-3'
MFE = -55.1; z-score = -3.83; ED = 44.84
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

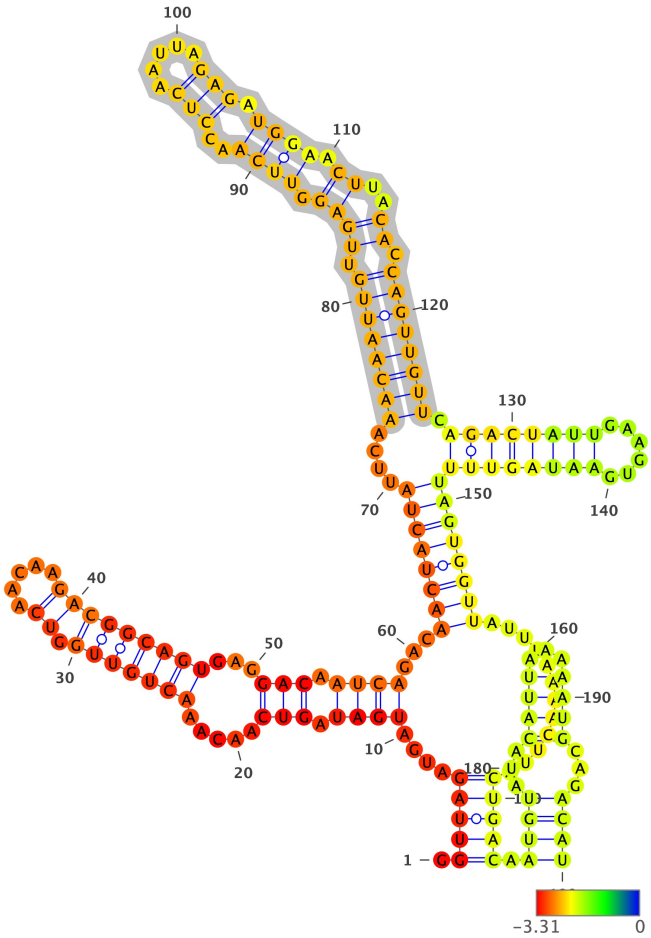
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 55 from nt 3274 to 3325 (nt 74 to 125)

```
5'-AACAATTGTTGAGGTTCAACCTCAATTAGAGAUGGAACUTACACCAGUUGUU-3'
5'-((((((((.((((...((..(((.....))).))...)).)).))))))))-3'
Motif MFE = -16.5; z-score = -3.68; ED = 1.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3201 to 3399 (motif highlighted in silver):

```
5'-GGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAAC
UUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAU-3
5'-.(((((....((((.(((.....(((((((.((.....)))))))))...))).))))...((((((((....((((((((.((((.((((..(((.....))).)))).)
)..)).)))))))).((((((((......)))))))))))))))).............))))).((((...((((...))))...))))-3'
MFE = -40.9; z-score = -2.45; ED = 25.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

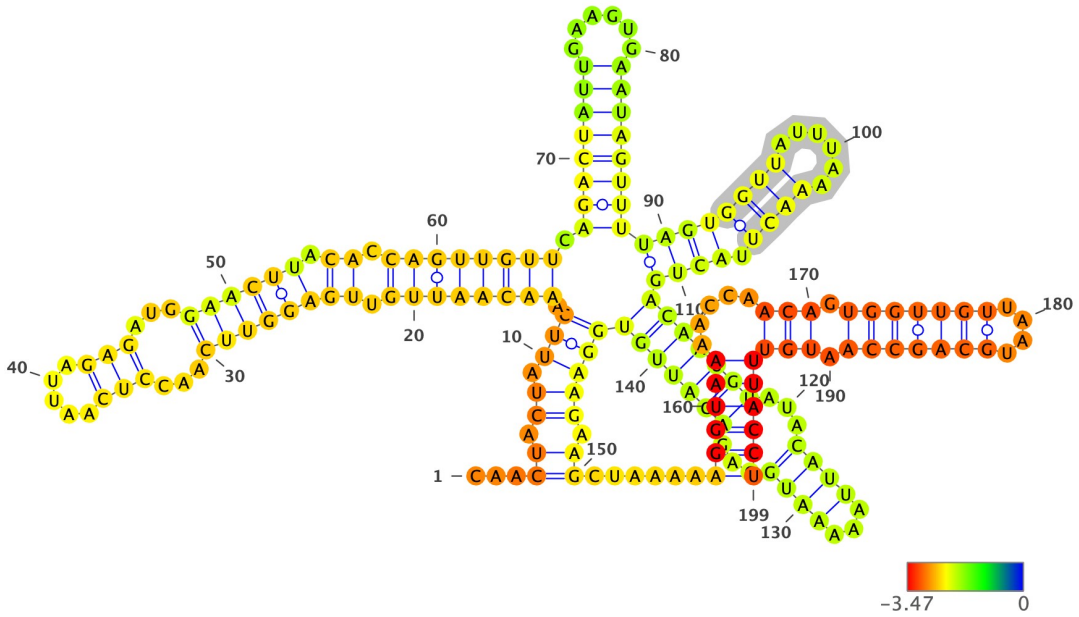
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 56 from nt 3353 to 3366 (nt 93 to 106)

```
5'-GGTTATTTAAAACU-3'
5'-((((......))))-3'
Motif MFE = 0.0; z-score = 0.23; ED = 2.0
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3261 to 3459 (motif highlighted in silver):

```
5'-CAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUG
ACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCU-3
5'-...((.((.(((.((((((((.((((((((...(((.....)))...)))))).)).))))))))).((((((((......))))))))((((((((......)))).))))
(((((((...((((...))))...))))))))))))).)).....((((((.....(((.(((((((....)))))))).)))))))))-3'
MFE = -49.9; z-score = -4.35; ED = 19.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

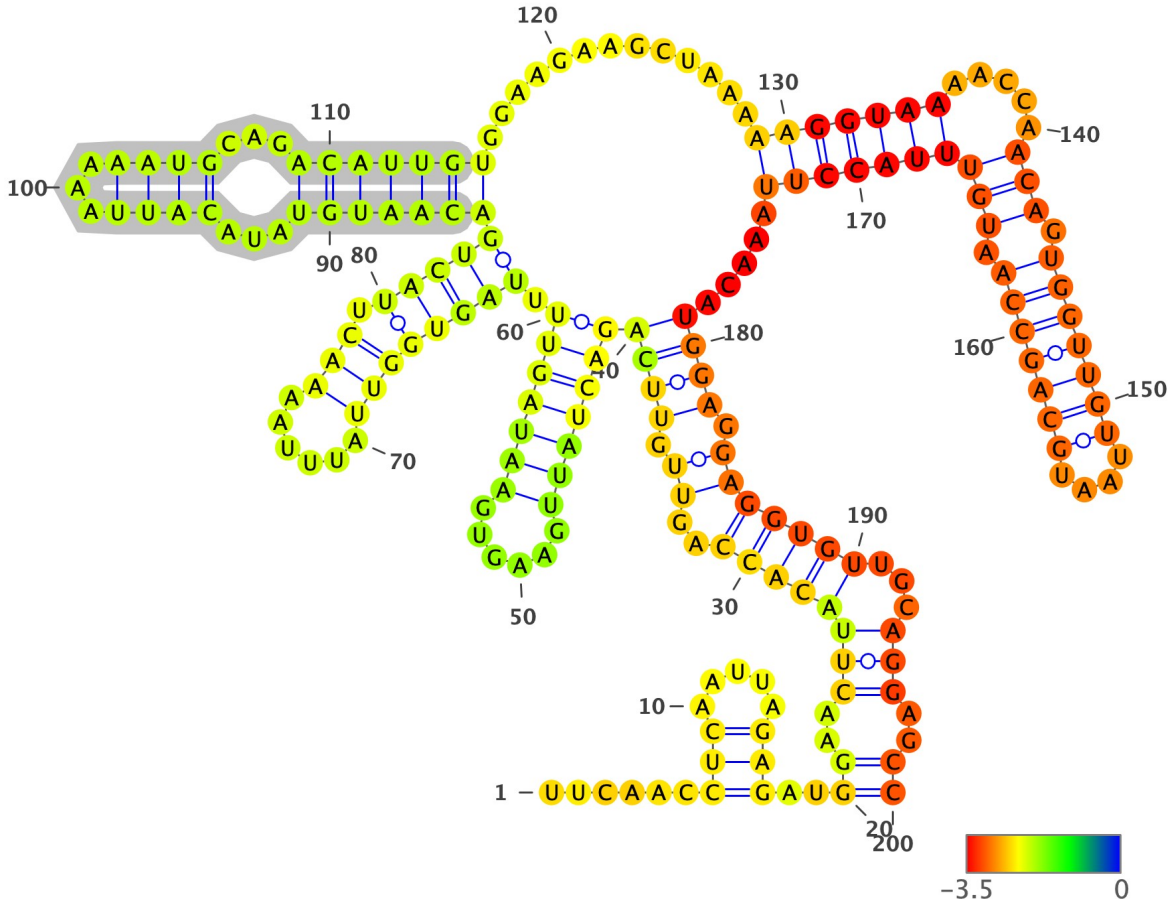
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 57 from nt 3373 to 3401 (nt 86 to 114)

```
5'-CAATGTATACATTAAAAAUGCAGACAUUG-3'
5'-((((((...((.......))...))))))-3'
Motif MFE = -4.7; z-score = -2.6; ED = 1.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3288 to 3487 (motif highlighted in silver):

```
5'-UUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACA
UUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCC-3
5'-......(((.....)))..((..((((((((..((.(((((((((((.......)))))))).((((((((.......))).)))))(((((((...((((...))))...)))
))))).............(((((((.....(((.(((((((....)))))))).))))))))))).....)))).)))))))...)))..))-3'
MFE = -45.5; z-score = -1.96; ED = 38.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

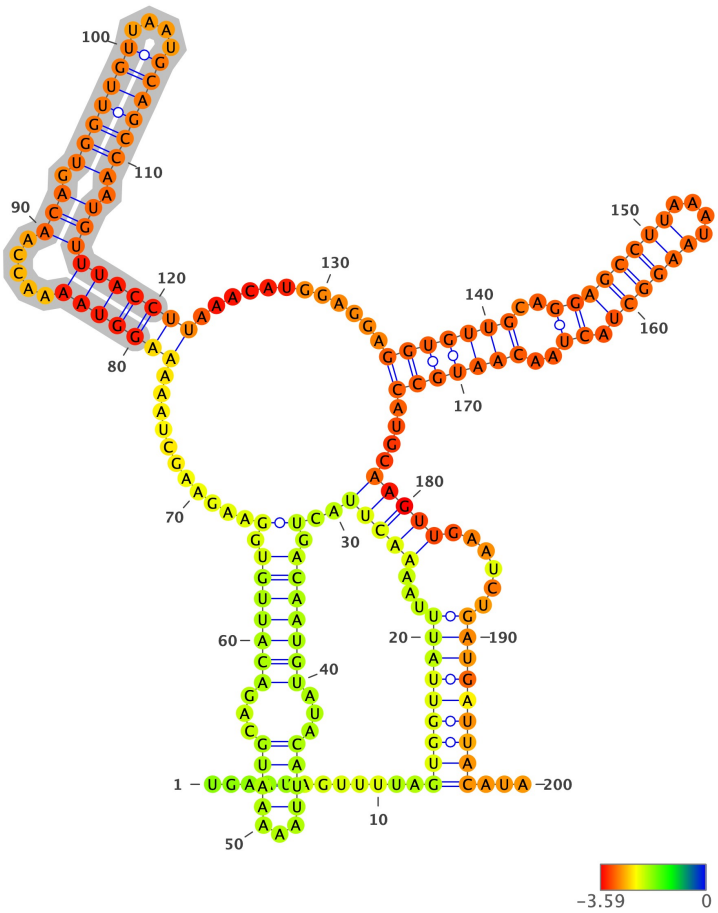
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 58 from nt 3418 to 3458 (nt 80 to 120)

```
5'-GGTAAAACCAACAGTGGTTGTTAATGCAGCCAAUGUUUACC-3'
5'-(((((.....(((.(((((((....)))))))).))))))))-3'
Motif MFE = -13.5; z-score = -2.93; ED = 4.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3339 to 3538 (motif highlighted in silver):

```
5'-UGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCA
AUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUA-3
5'-............((((((((((...(((((..(.(((((((...((((...))))...)))))))).)...........(((((((.....(((.(((((((....)))))))
.))))))))))............(((((((..((((((((....)))))).))..)))))))....)))))......))))))))...-3'
MFE = -50.2; z-score = -3.53; ED = 29.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

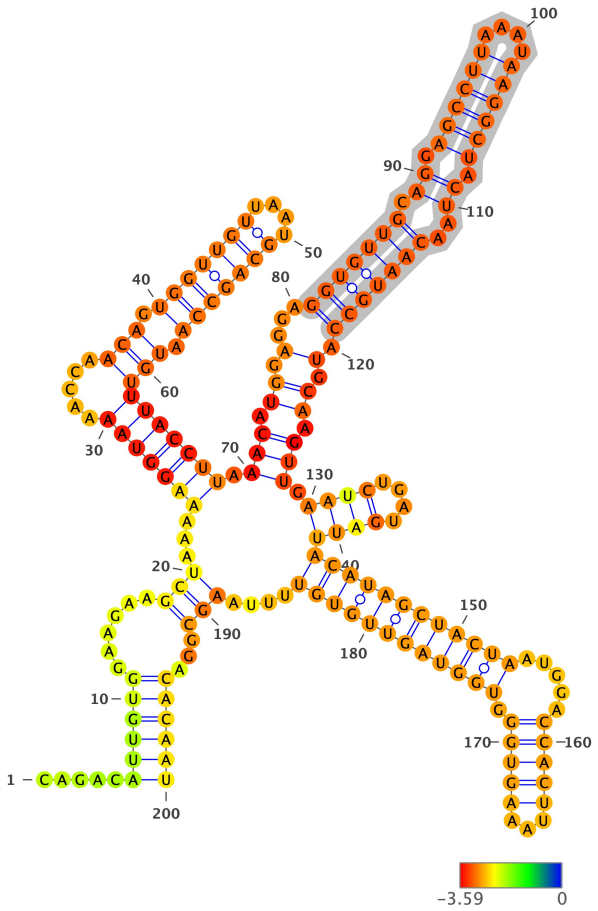
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 59 from nt 3473 to 3511 (nt 81 to 119)

```
5'-GGTGTTGCAGGAGCCTTAAATAAGGCTACUAACAAUGCC-3'
5'-(((((((.((...((((....))))...))..)))))))-3'
Motif MFE = -15.6; z-score = -4.21; ED = 1.87
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3393 to 3592 (motif highlighted in silver):

```
5'-CAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUA
ACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAU-3
5'-.....((((((......(((...(((((((.....(((.(((((((....)))))))).))))))))))).(((.((.(...(((((((.((.((((((....))))))).)).
.)))))))).).)).))).((((....))))((((((((((((.....(((((...))))).)))))))))))....)))...))))))-3'
MFE = -60.2; z-score = -5.04; ED = 19.18
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

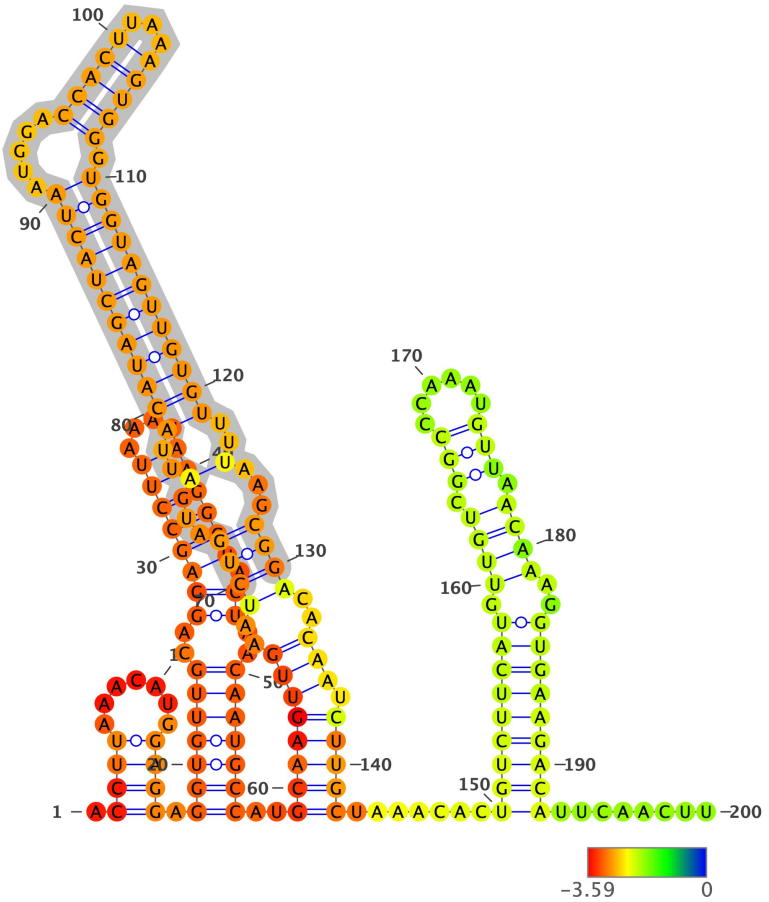
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 60 from nt 3525 to 3585 (nt 70 to 130)

```
5'-CTGATGATTACATAGCTACTAATGGACCACTTAAAGUGGGUGGUAGUUGUGUTTTAAGCGG-3'
5'-(........(((((((((((((.....((((.....)))).))))))))))))........)-3'
Motif MFE = -18.8; z-score = -2.98; ED = 3.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3456 to 3655 (motif highlighted in silver):

```
5'-ACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUG
GUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUU-3
5'-.((((.......)))).(((((((..((((((((....))))))).))..)))))))..((((((((..((((...(..(((((((((((.....(((((...))))).))
))))))))))..)...))))..))).)))))).......(((((((((.((((.(((......))).))))..)))))))))........-3'
MFE = -64.9; z-score = -4.38; ED = 11.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

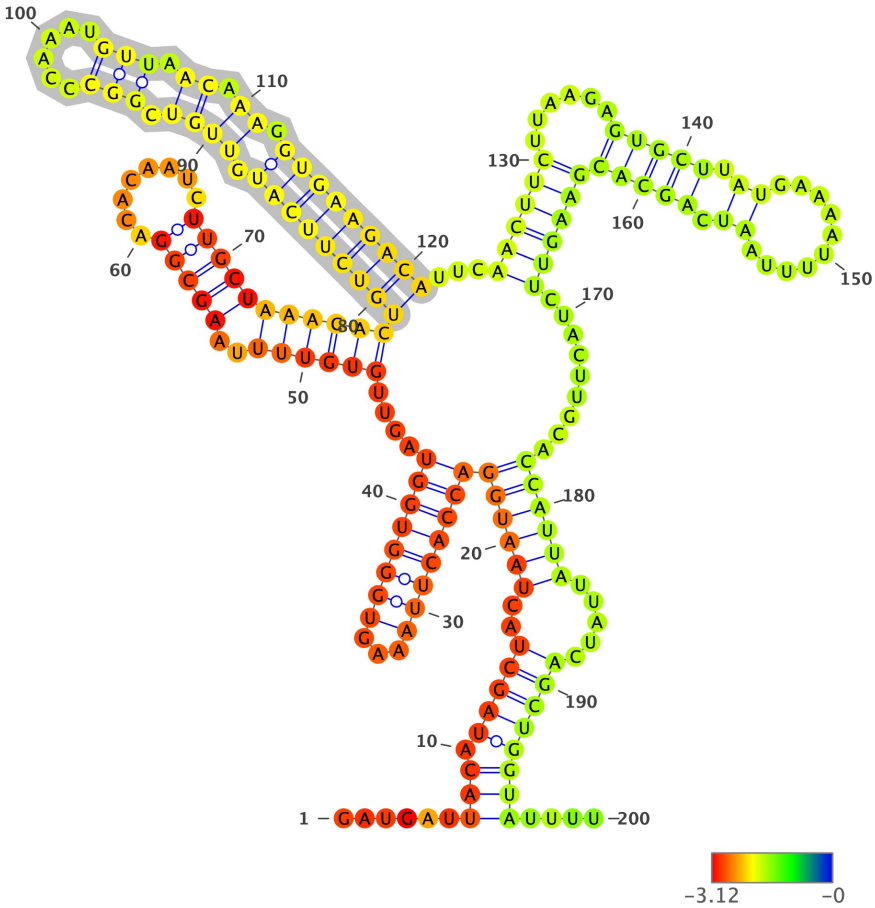
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 61 from nt 3605 to 3647 (nt 79 to 121)

```
5'-TGTCTTCATGTTGTCGGCCCAAATGUTAACAAAGGUGAAGACA-3'
5'-(((((((((.((((..((......))..)).)).)))))))))-3'
Motif MFE = -14.2; z-score = -3.08; ED = 2.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3527 to 3726 (motif highlighted in silver):

```
5'-GAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAA
GGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUU-3
5'-......(((.(((((..((((((((((((((...))))))))....((((((..(((((........)))))))))))(((((((((.((((.(((......))).)).))
.)))))))))...((((((......(((((.((..........)).))))))))))).........))))))).....))))))))....-3'
MFE = -49.3; z-score = -2.19; ED = 33.14
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

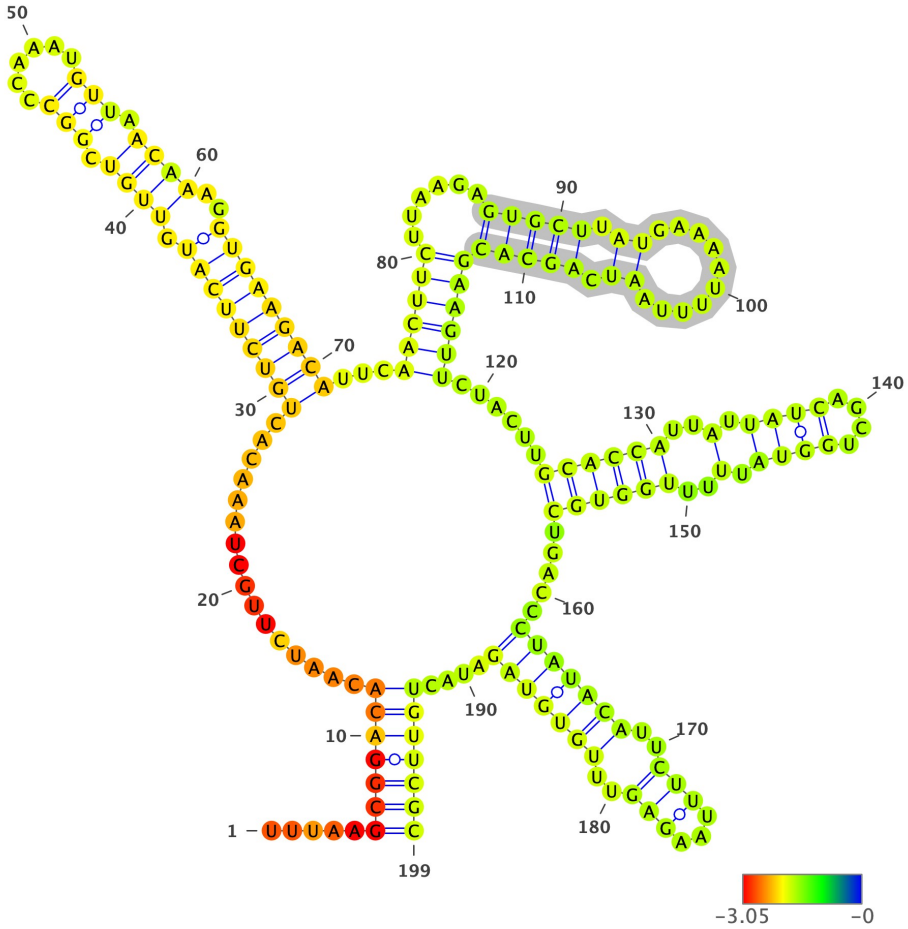
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 62 from nt 3663 to 3688 (nt 87 to 112)

```
5'-GTGCTTATGAAAATTTTAATCAGCAC-3'
5'-(((((................)))))-3'
Motif MFE = -4.0; z-score = -1.67; ED = 3.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3577 to 3775 (motif highlighted in silver):

```
5'-UUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCA
CGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGC-3
5'-.....(((((((.................(((((((((.((((.(((......))).))))..)))))))))...((((((......(((((.((..........)).))))
)))))))......((((((..(.((((....)))).)..))))))).....(((((((..(((...)))..)))))))....)))))))-3'
MFE = -53.2; z-score = -3.42; ED = 20.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

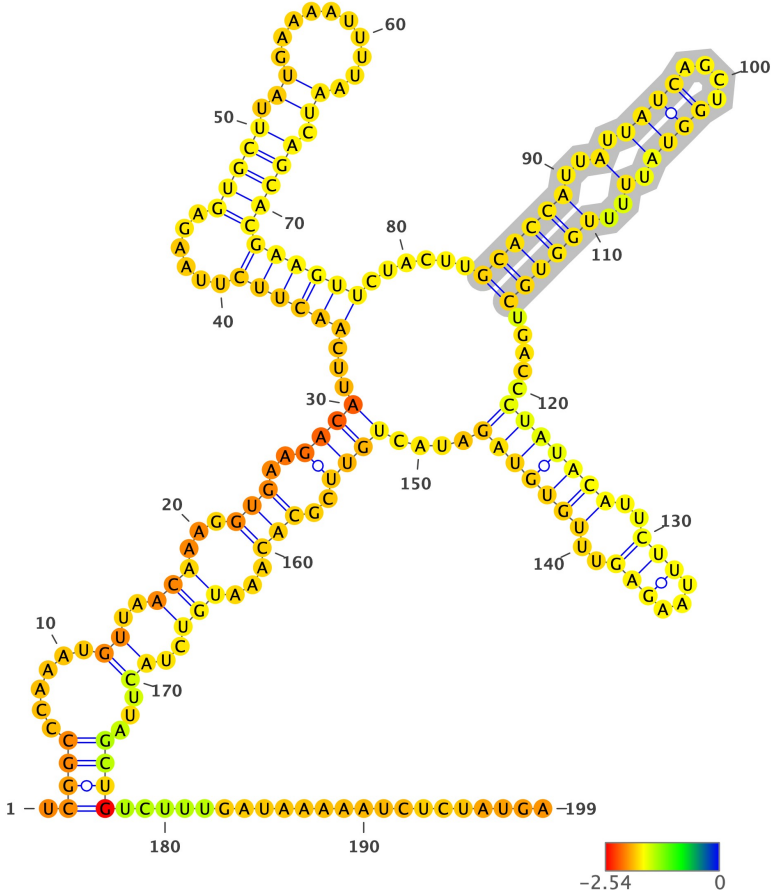
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 63 from nt 3701 to 3732 (nt 84 to 115)

```
5'-GCACCATTATTATCAGCTGGUATUTTUGGUGC-3'
5'-((((((..(..(((....)))..)..))))))-3'
Motif MFE = -11.2; z-score = -3.9; ED = 0.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3618 to 3816 (motif highlighted in silver):

```
5'-UCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUG
GUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGA-3
5'-.((((......((..(((...(((..((((...((((((......(((((.((..........)).)))))))))))......((((((..(.((((....)))).)..))
))))).....(((((((..(((...)))..)))))))....))))..)))...)))..))...))))......................-3'
MFE = -40.6; z-score = -1.07; ED = 36.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

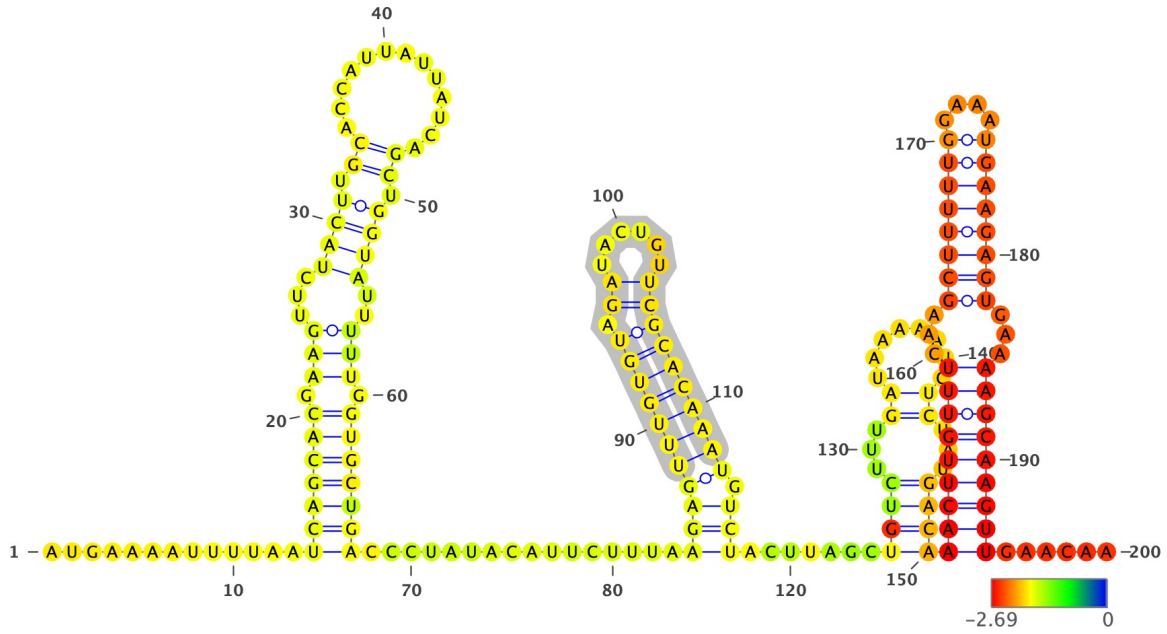
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 64 from nt 3756 to 3780 (nt 88 to 112)

```
5'-TTTGTGTAGATACTGTUCGCACAAA-3'
5'-(((((((.((......)))))))))-3'
Motif MFE = -6.1; z-score = -2.19; ED = 2.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3669 to 3868 (motif highlighted in silver):

```
5'-AUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAA
AUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAA-3
5'-.............(((((((.(((...((((.((.............)).))))..))).)))))))................(((((((((((.((......)))))))))
)).)))......((((...((........))...))))((((((((((...((((((((....))))))))...))))))))).....-3'
MFE = -43.7; z-score = -2.68; ED = 30.6
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

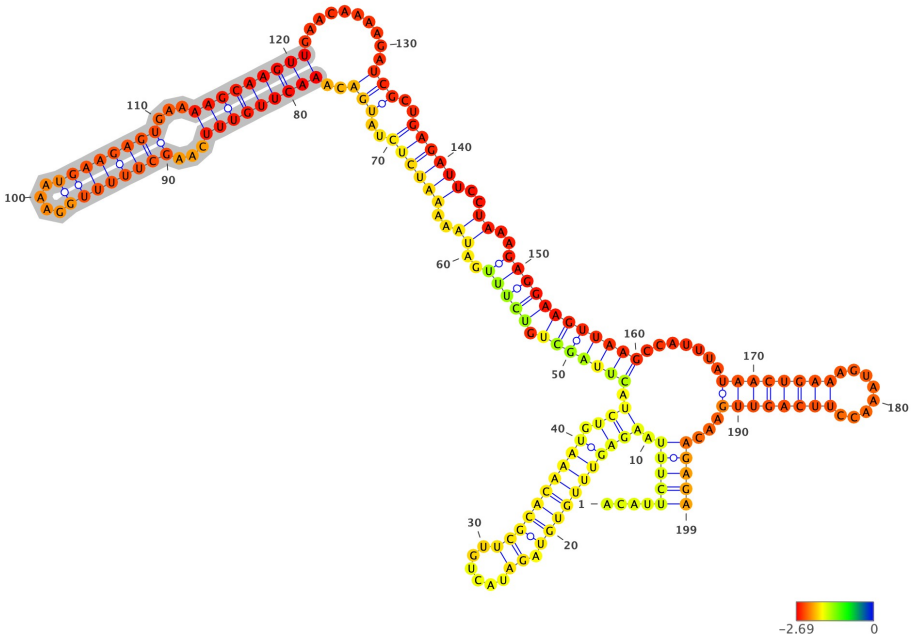
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 65 from nt 3819 to 3862 (nt 78 to 121)

```
5'-AACTTGTTTCAAGCTTTTTGGAAATGAAGAGUGAAAAGCAAGUU-3'
5'-((((((((((...(((((((.....)))))))...)))))))))-3'
Motif MFE = -13.1; z-score = -4.27; ED = 3.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3742 to 3940 (motif highlighted in silver):

```
5'-ACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGA
AAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGA-3
5'-....(((((.((((((((((((.((.....)))))))))).))).(((((((.(((((..((..((((((..(((..((((((((((...((((((((....))))))))..
.)))))))))..........)))..))))))..))..))))))))))))).......((((((((........))))))))...)))))-3'
MFE = -47.3; z-score = -2.96; ED = 34.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

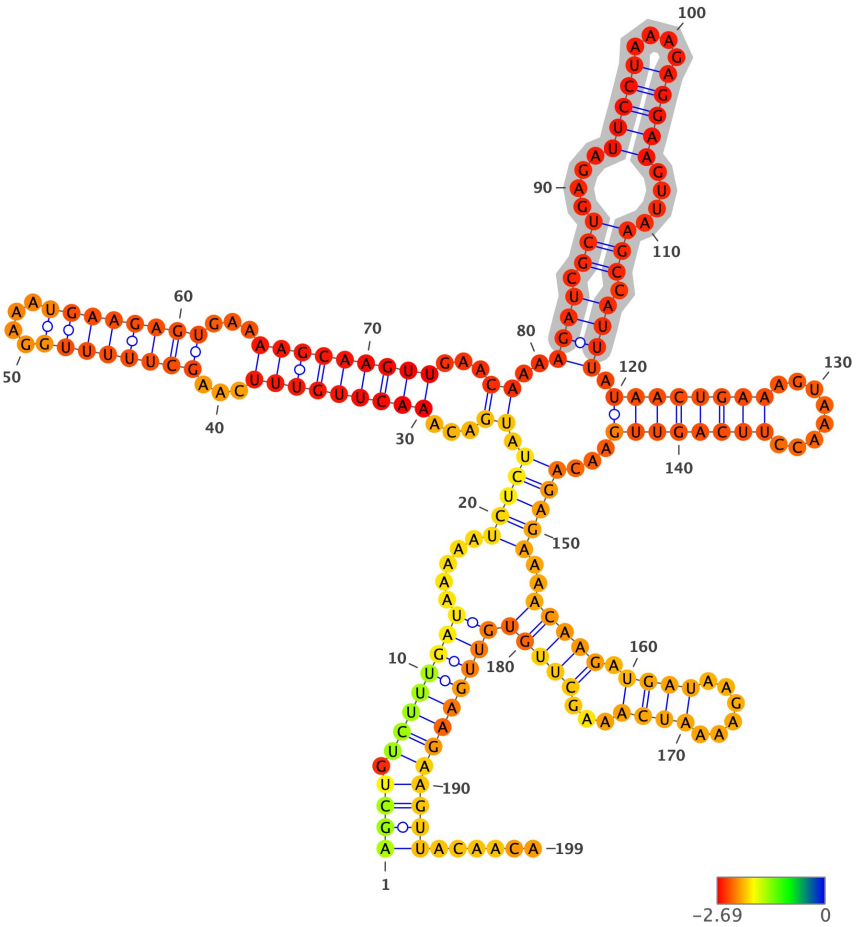
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 66 from nt 3871 to 3906 (nt 82 to 117)

```
5'-GATCGCTGAGATTCCTAAAGAGGAAGTTAAGCCAUU-3'
5'-(((.(((....((((......))))....))).)))-3'
Motif MFE = -8.5; z-score = -1.99; ED = 2.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3790 to 3988 (motif highlighted in silver):

```
5'-AGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAA
GCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACA-3
5'-((((.(((((((.....(((((.((...(((((((((...((((((((....)))))))).....))))))))).....)).)))).((((.(((....((((((....)))))).....)
)).)))).(((((((.........)))))))...)))))..(((((.((((......)))).....))))))))))))))))))).......-3'
MFE = -45.2; z-score = -3.93; ED = 13.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

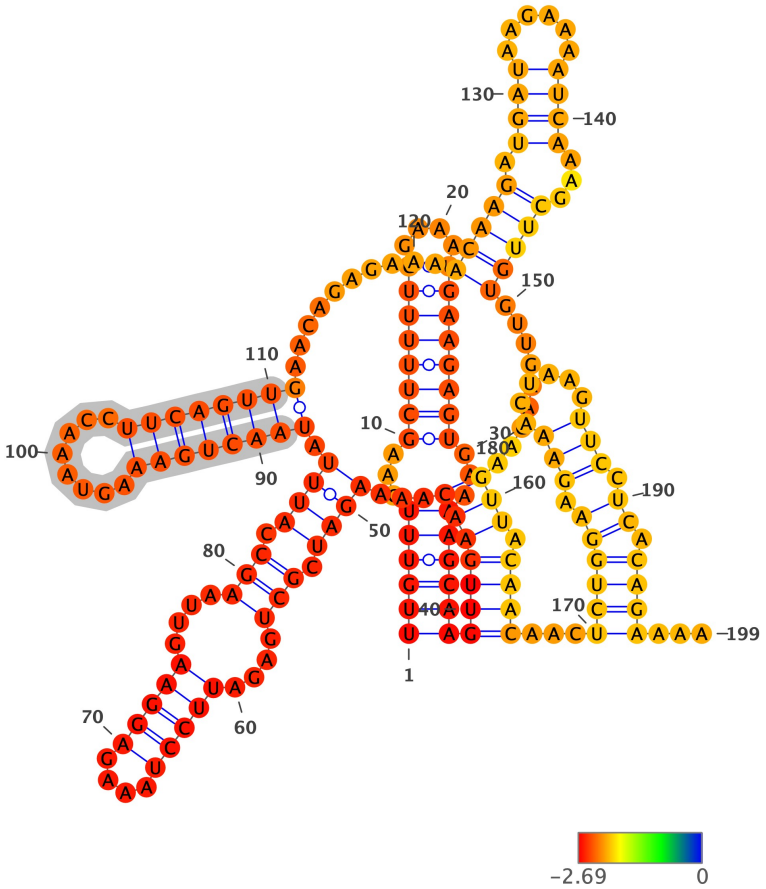
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 67 from nt 3910 to 3931 (nt 89 to 110)

```
5'-AACTGAAAGTAAACCUUCAGUU-3'
5'-(((((((........)))))))-3'
Motif MFE = -5.1; z-score = -4.3; ED = 1.95
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3822 to 4020 (motif highlighted in silver):

```
5'-UUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUG
AACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAA-3
5'-((((((...((((((((....))))))))...))))))(((((((...((((.(((....(((((....)))))....))).)))).((((((((........))))))))
..........(((((.((((......))))...)))))..........))).))))...((((((.(((......))).)).))))...-3'
MFE = -40.6; z-score = -2.94; ED = 28.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

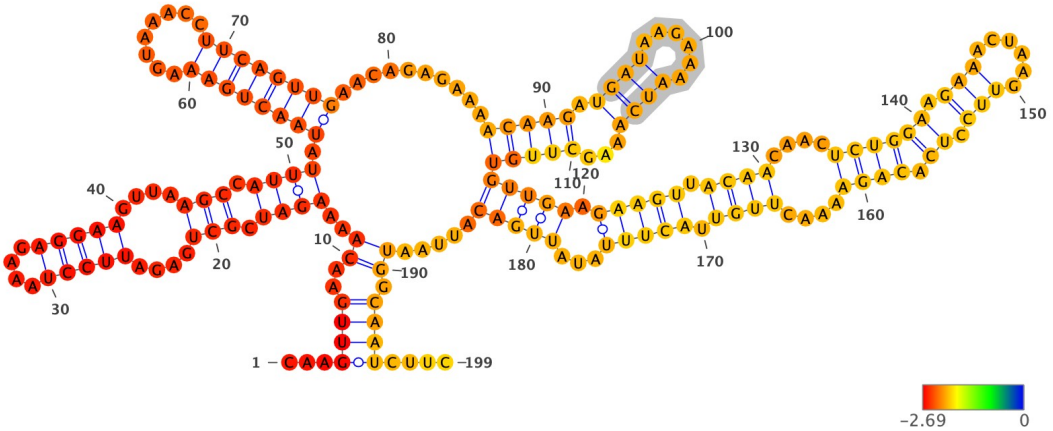
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 68 from nt 3950 to 3961 (nt 94 to 105)

```
5'-GATAAGAAAAUC-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3857 to 4055 (motif highlighted in silver):

```
5'-CAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCU
UGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUC-3
5'-...((((..((..((((.(((....(((((....)))))....))).)))).((((((((........))))))))..........(((((.((((......))))...))
)))(((((.(((((.((((....((((((.(((......))).)).))))....)))).)))))...)))))).....)).))))....-3'
MFE = -36.9; z-score = -1.84; ED = 32.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

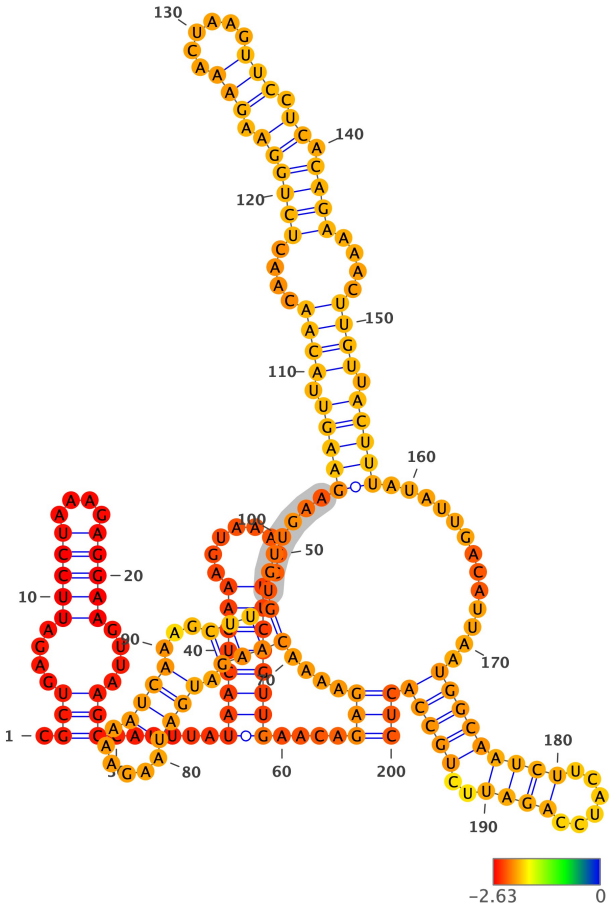
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 69 from nt 3970 to 3976 (nt 97 to 103)

```
5'-TGTTGAA-3'
5'-(.....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3874 to 4073 (motif highlighted in silver):

```
5'-CGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUAC
AACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUC-3
5'-.((((....((((((....))))))....)))).....(((((((((.......)))))))).....(((....((((.((((......)))).)).....)))).......((((((.((
((....((((((.((((......)))).)).)))))....)))).)))))).............(((((((((.....)))))..)))))))-3'
MFE = -38.7; z-score = -2.47; ED = 23.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

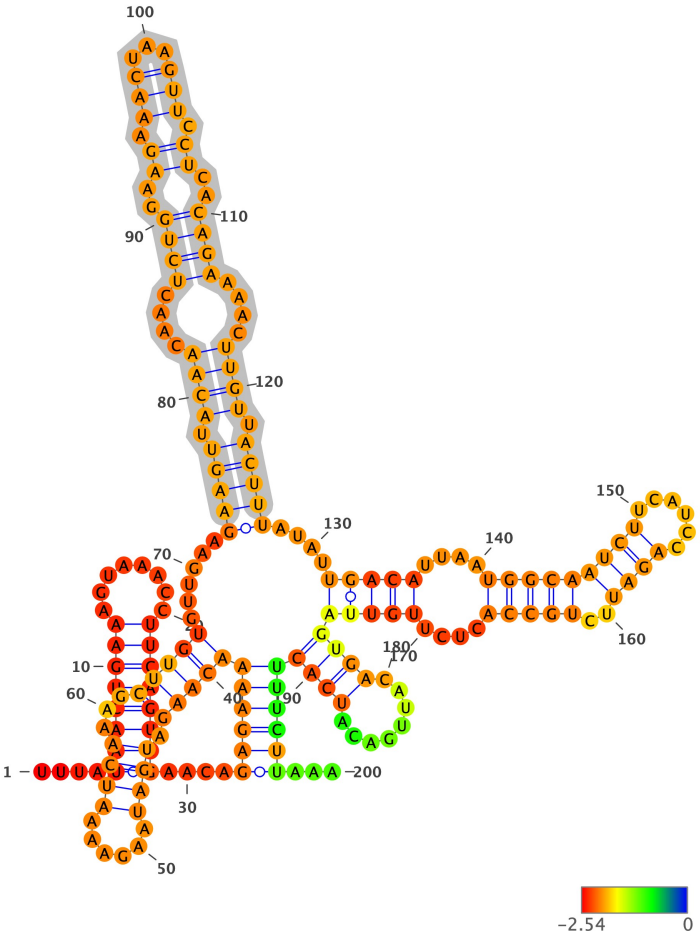
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 70 from nt 3978 to 4030 (nt 74 to 126)

```
5'-AAGTTACAACAACTCTGGAAGAAACTAAGTTCCUCACAGAAAACUUGUTACUU-3'
5'-((((.((((....((((..((...........)).)))).....)))).))))-3'
Motif MFE = -10.0; z-score = -3.07; ED = 6.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3905 to 4104 (motif highlighted in silver):

```
5'-UUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACA
GAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAA-3
5'-....(((((((((.......)))))))).....((((((((((.((((......)))).)))))))).....(((((.((((....((((..((.(((...)))).)).))..))
)).....)))).)))))....((((.....((((((((((.....)))).)).))))).....)))))((((.........)))))))))).....-3'
MFE = -41.8; z-score = -3.17; ED = 26.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

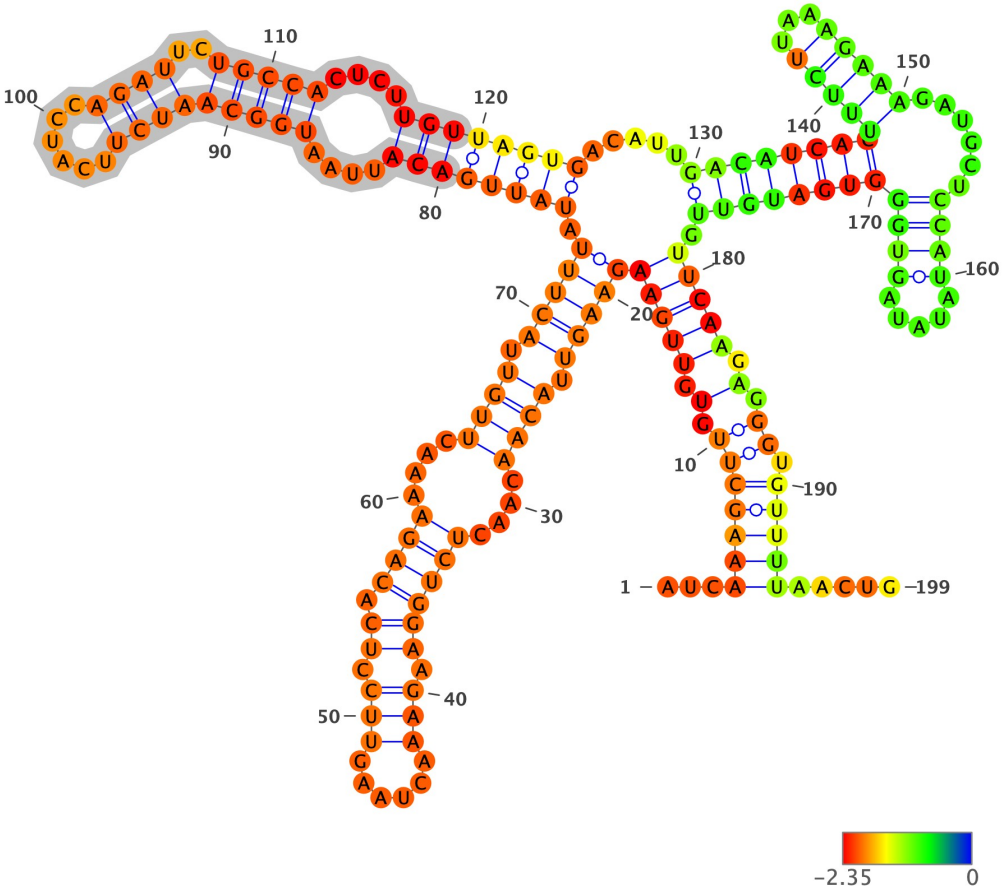
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 71 from nt 4038 to 4077 (nt 80 to 119)

```
5'-ACATTAATGGCAATCTTCATCCAGAUTCUGCCACTCTUGU-3'
5'-(((....(((((((((.....))))..)))))....)))-3'
Motif MFE = -8.1; z-score = -3.09; ED = 3.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 3959 to 4157 (motif highlighted in silver):

```
5'-AUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCC
ACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUG-3
5'-...(((((((.(.((((((((((.((((....((((((.(((.....))).)).)))).....)))).)))))).(((((((((....(((((((((.....)))))..))))
)....)))))))).....((((((((((((...)))))).....(((.....)))))))))))).)))))).)).)))))).....-3'
MFE = -44.4; z-score = -1.45; ED = 34.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

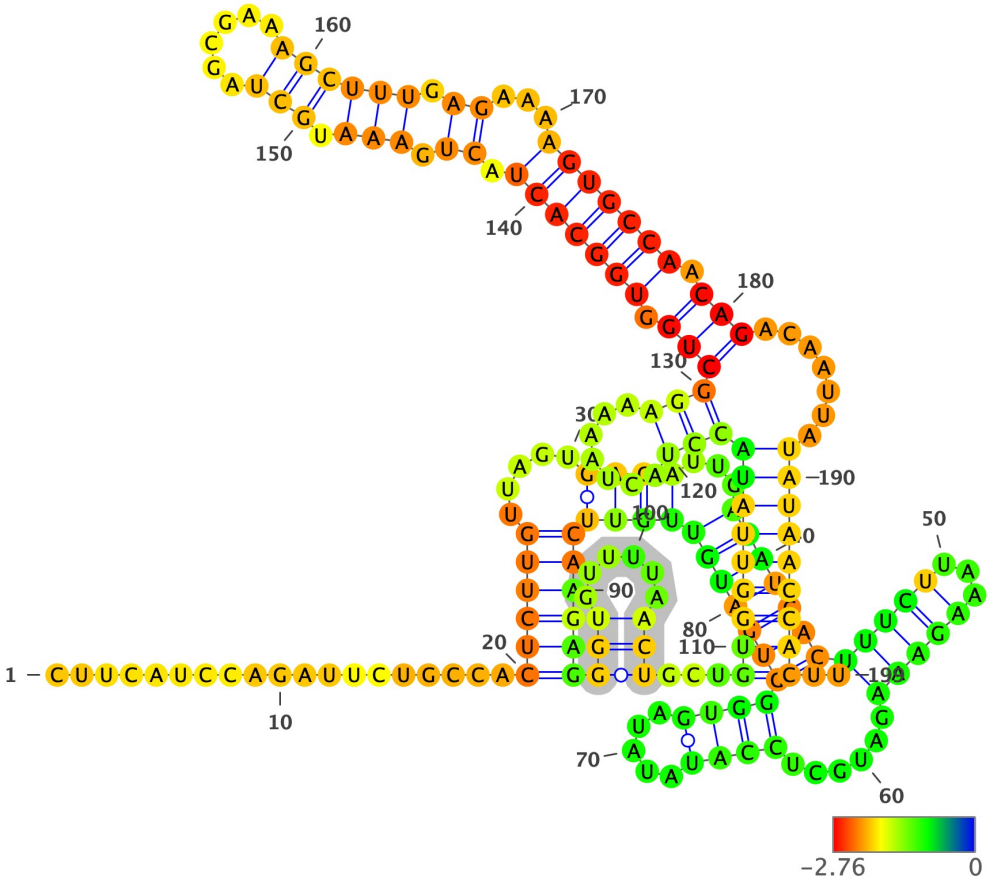
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 72 from nt 4145 to 4156 (nt 94 to 105)

```
5'-GGTGTTTTAACU-3'
5'-((........))-3'
Motif MFE = 0.0; z-score = 0.19; ED = 1.57
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4052 to 4250 (motif highlighted in silver):

```
5'-CUUCAUCCAGAUUCUGCCACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUG
GUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUU-3
5'-...................((((((.....((((...(((((((((((((...)))))).....((((.....)))))))))))))))))))))(((......)))...(((
(((((((((.......)))(((.(((((((.((.(((.(((......))))))).))...)))))))).)))).......)))))))))..-3'
MFE = -49.4; z-score = -2.46; ED = 21.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

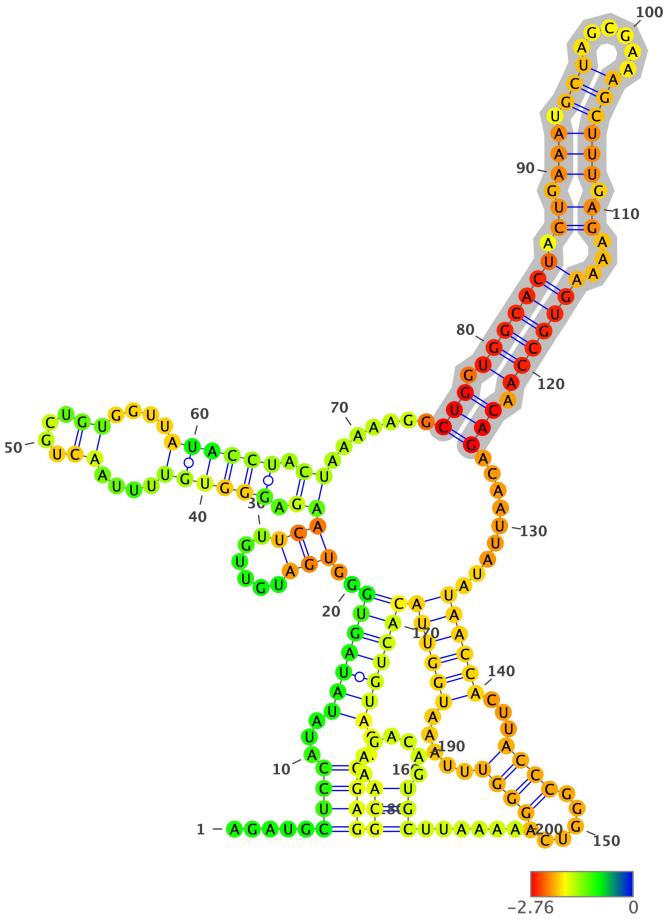
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 73 from nt 4182 to 4232 (nt 75 to 125)

```
5'-CTGGTGGCACTACTGAAATGCTAGCGAAAGCUUUGAGAAAAGUGCCAACAG-3'
5'-(((.((((((..((.(((.(((......)))))).))....)))))).)))-3'
Motif MFE = -18.7; z-score = -3.74; ED = 1.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4108 to 4307 (motif highlighted in silver):

```
5'-AGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAG
AAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAA-3
5'-.....((((...(((((((..(((......)))((.((((((....((....))....)))))).))........(((.(((((((.((.(((.(((......)))))).))
...)))))))).))).........((((((...((((......))))).....))))))))))))..))))(((.......)))......-3'
MFE = -54.2; z-score = -2.38; ED = 18.14
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

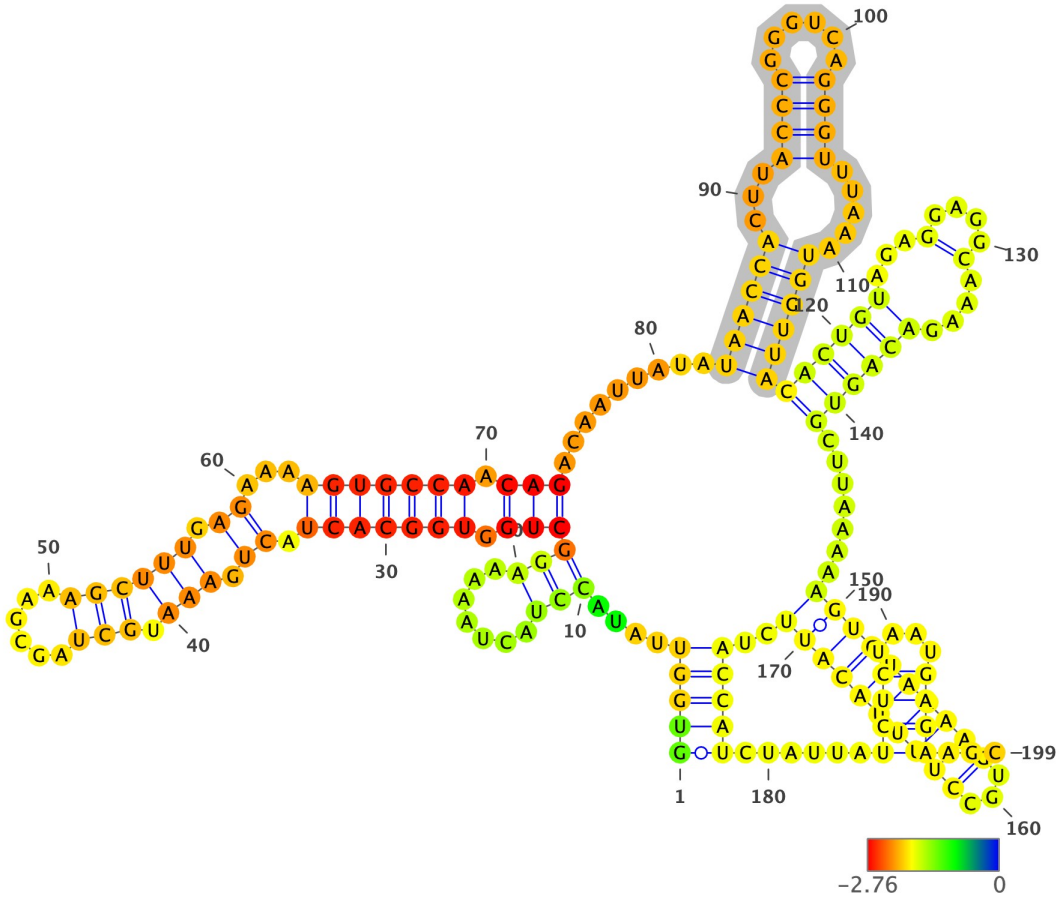
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 74 from nt 4242 to 4275 (nt 83 to 116)

```
5'-TAACCACTTACCCGGGTCAGGGUTTAAAUGGUUA-3'
5'-((((((...(((........)))).....))))))-3'
Motif MFE = -10.7; z-score = -2.37; ED = 2.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4160 to 4358 (motif highlighted in silver):

```
5'-GUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAU
GGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGC-3
5'-(((((....(((.......)))(((.(((((((.((.(((.(((......))))))).))...)))))))).)))........((((((...((((......))))).....)
)))))((((((...(....)....))))))).......((((((((((...)))))))))))..)))))......((((....))))...-3'
MFE = -53.7; z-score = -3.69; ED = 24.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

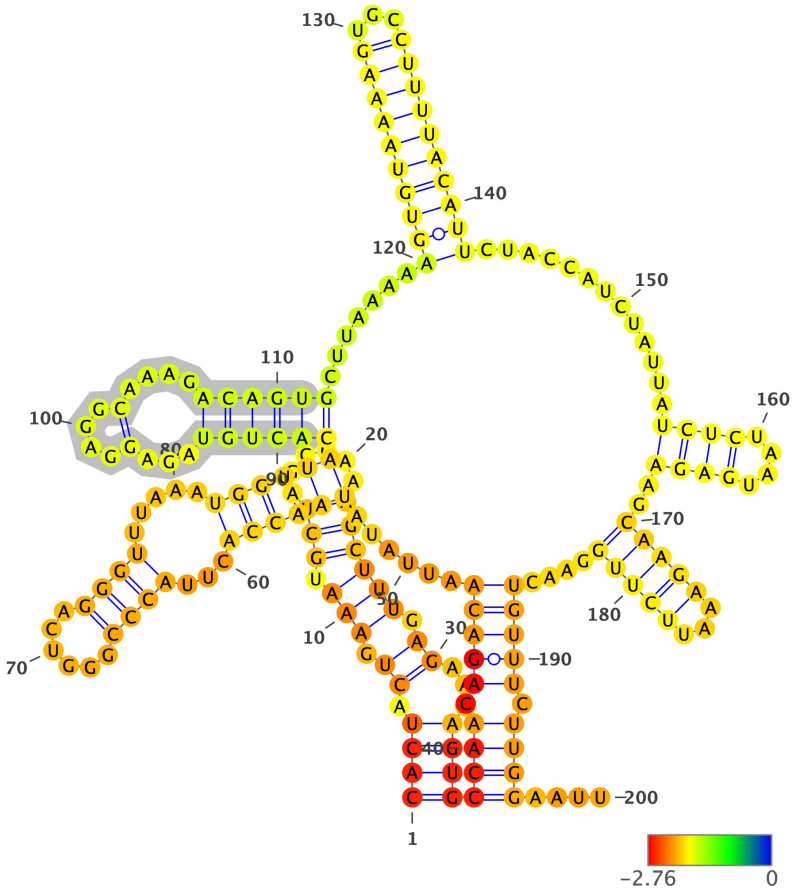
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 75 from nt 4277 to 4299 (nt 89 to 111)

```
5'-ACTGTAGAGGAGGCAAAGACAGU-3'
5'-(((((.............)))))-3'
Motif MFE = -2.1; z-score = -0.78; ED = 1.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4189 to 4388 (motif highlighted in silver):

```
5'-CACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGU
GCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUU-3
5'-((((.((.(((.(((......))))))).))...))))((((.(((((......((((((...((((......))))).....))))))((((((...(....)....)))))
).......((((((((((...))))))))))).............((((....))))..(((((...)))))....)))))).))))....-3'
MFE = -46.8; z-score = -2.34; ED = 10.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

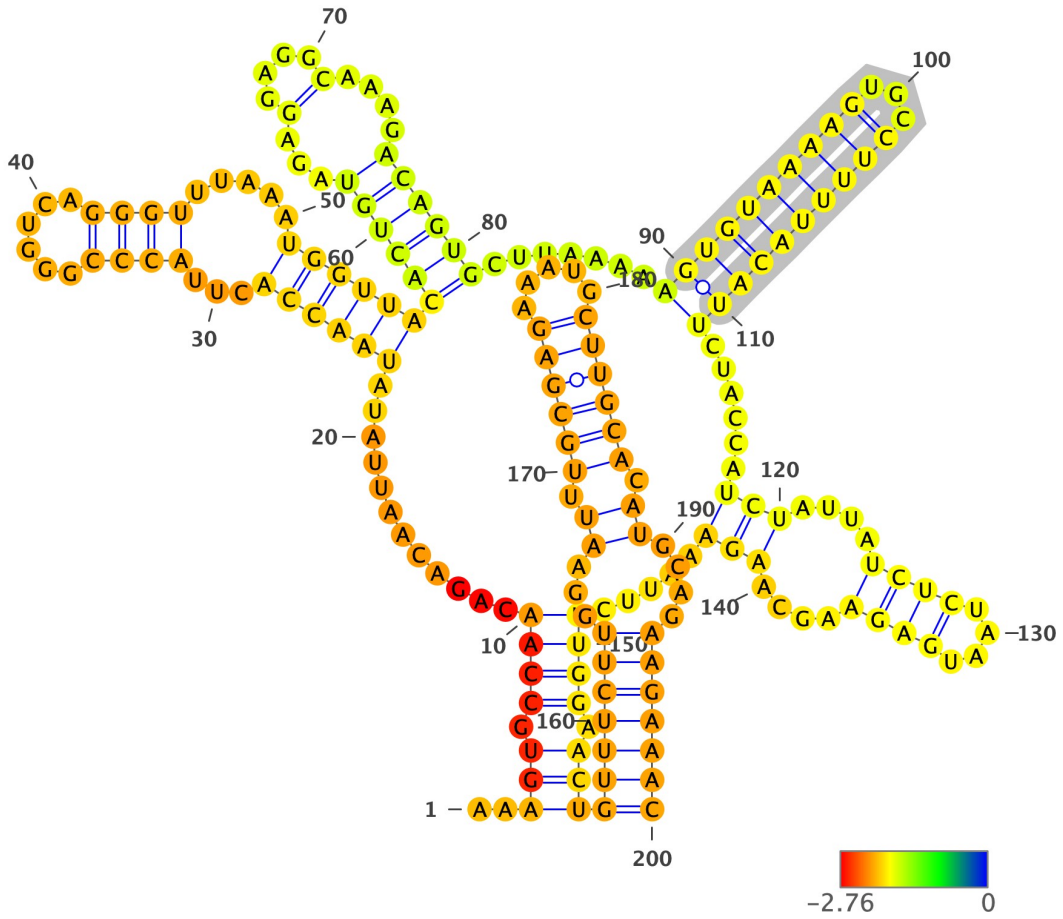
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 76 from nt 4309 to 4329 (nt 90 to 110)

```
5'-GTGTAAAAGTGCCUUUUACAU-3'
5'-((((((((...)))))))))-3'
Motif MFE = -5.9; z-score = -3.51; ED = 0.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4220 to 4419 (motif highlighted in silver):

```
5'-AAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUU
CUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAAC-3
5'-..(((.((((.............((((((...((((......))))).....))))))((((((...(....)....))))))........((((((((((...))))))))))
......(((....((((....))))....)))).....)))).)))(((((((...((.((((((.....)))))).))....)))))))-3'
MFE = -46.6; z-score = -1.99; ED = 32.14
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

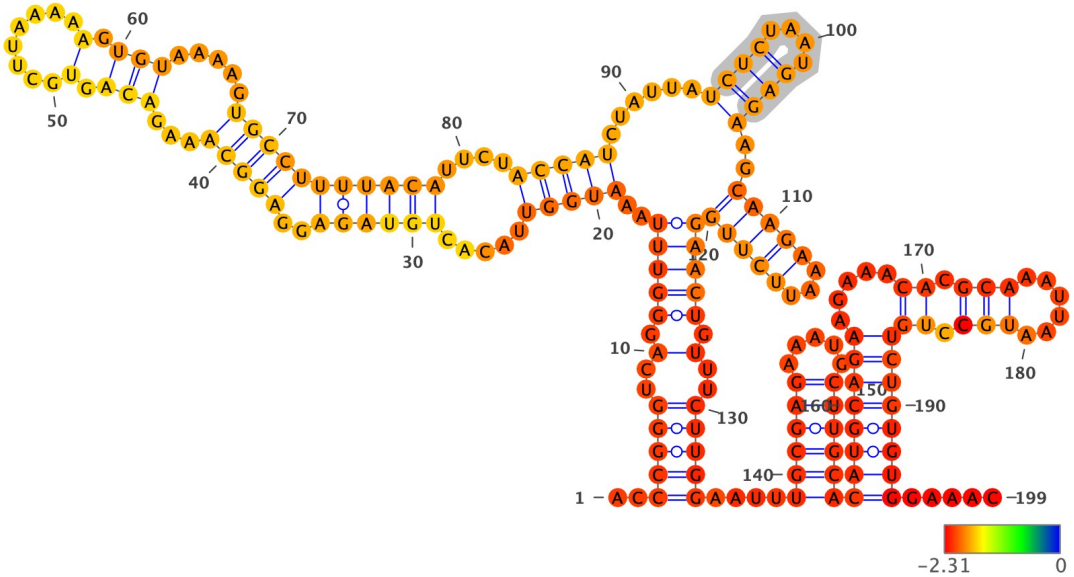
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 77 from nt 4345 to 4354 (nt 95 to 104)

```
5'-CTCTAATGAG-3'
5'-(((....)))-3'
Motif MFE = -1.0; z-score = -8.62; ED = 0.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4251 to 4449 (motif highlighted in silver):

```
5'-ACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAG
AAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAAC-3
5'-..(((((..(.(((((..(((((.....((((((..(((((...(((.(.........).)))).....))))))))))).....)))))......((((....))))..((((
(...)))))))))).)..)))))....((((((.....))))))((((((((.....((.(((......))).)))))))))).....-3'
MFE = -50.7; z-score = -1.93; ED = 51.44
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

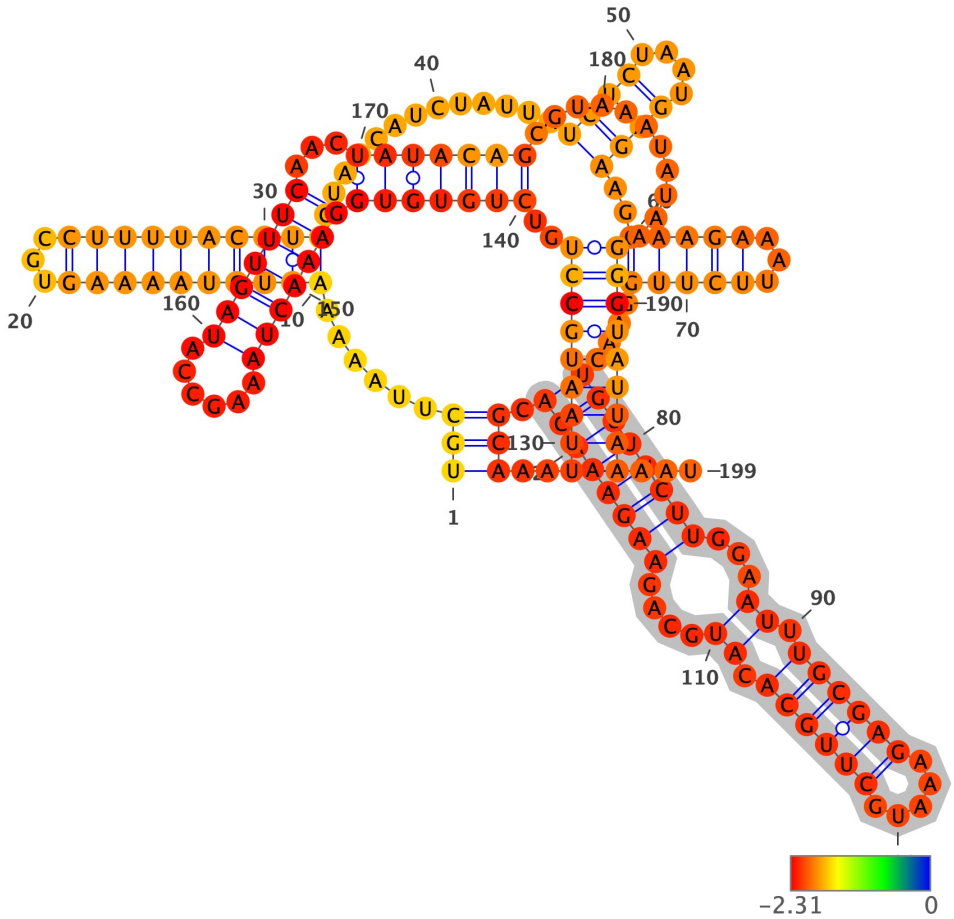
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 78 from nt 4375 to 4420 (nt 77 to 122)

```
5'-TGTTTCTTGGAATTTGCGAGAAATGCUUGCACAUGCAGAAGAAACA-3'
5'-((((((((...((.((((((.....)))))).))....))))))))-3'
Motif MFE = -14.0; z-score = -3.64; ED = 2.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4299 to 4497 (motif highlighted in silver):

```
5'-UGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUG
CAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAU-3
5'-(((......((((((((((...)))))))))).............((((....))))..(((((...)))))....((((((((...((.((((((.....)))))).)).
...))))))))).)))..((((((((((..((((((((((((((.....)))))))...)))))))).........))))))))...-3'
MFE = -49.7; z-score = -3.68; ED = 10.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

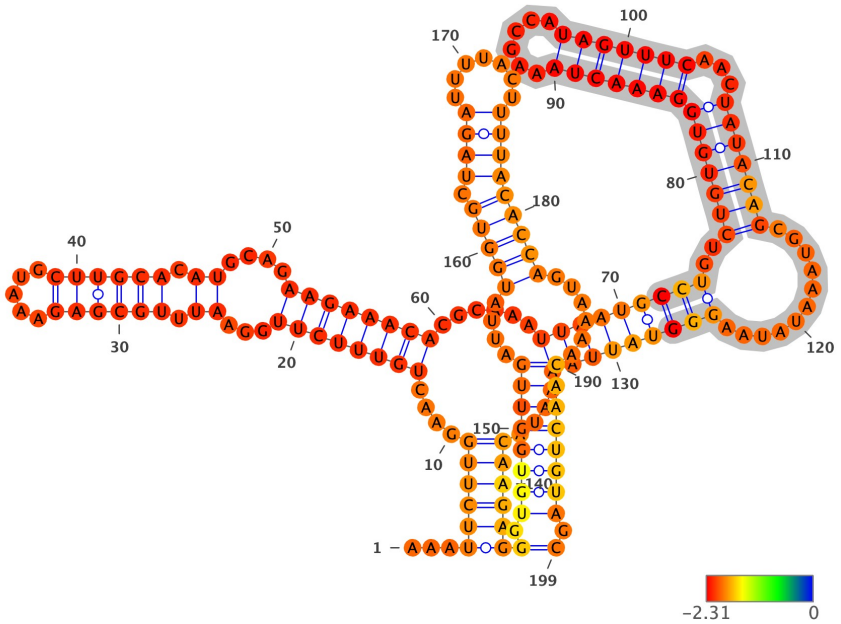
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 79 from nt 4433 to 4488 (nt 72 to 127)

```
5'-CCTGTCTGTGTGGAAACTAAAGCCAUAGUUUCAACTATACAGCGTAAATATAAGGG-3'
5'-(...........(((((((......)))))))......................)-3'
Motif MFE = -12.1; z-score = -1.5; ED = 5.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4362 to 4560 (motif highlighted in silver):

```
5'-AAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUAC
AGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGC-3
5'-...((((((....((((((((...((.((((((.....)))))).)).....))))))))......((((((((..((((((((((((((......)))))))...)))))
))...........))))))))).....))))))(.((((((((....(((((.((((.......)))))))))......))))))))).)-3'
MFE = -47.8; z-score = -2.76; ED = 15.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

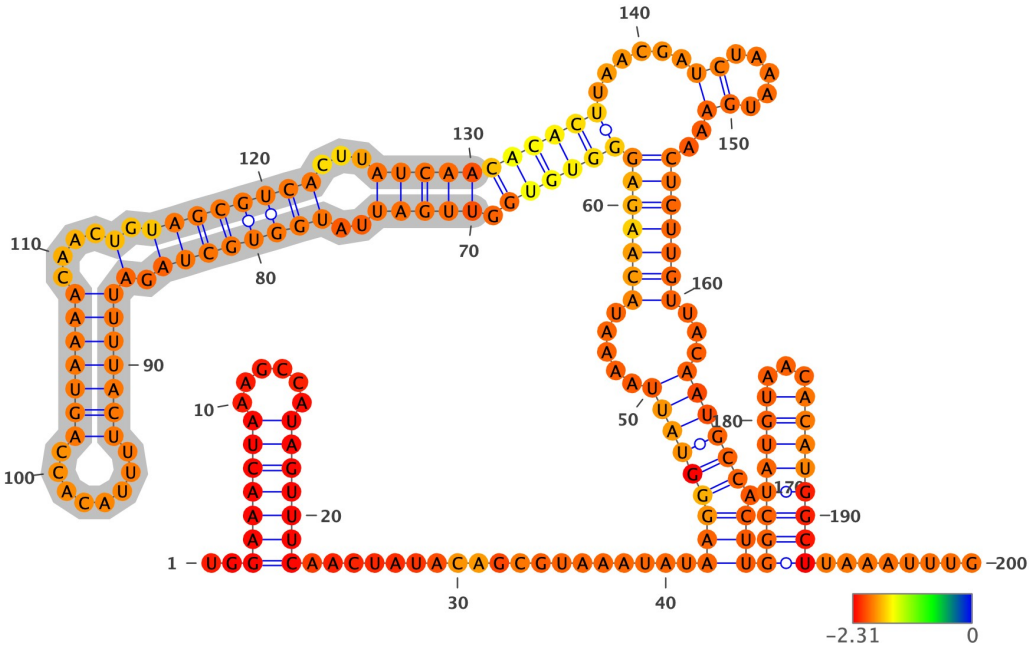
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 80 from nt 4512 to 4572 (nt 70 to 130)

```
5'-TTGATTATGGTGCTAGATTTTACTTTTACACCAGUAAAACAACTGTAGCGUCACTTAUCAA-3'
5'-(((((..(((((((...(((((((.......)))))))).....)))))))...)))))-3'
Motif MFE = -11.9; z-score = -2.56; ED = 9.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4443 to 4642 (motif highlighted in silver):

```
5'-UGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAA
CUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUG-3
5'-..(((((((.....)))))))...................(((((((((.....(((((((((((((.(((((..(((((((((.(((((((.......)))))))...
.).))))))))...))))))))))).....((.....)).)))))))...)))))).)))((((((((((...)))))))))........-3'
MFE = -49.0; z-score = -3.5; ED = 22.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

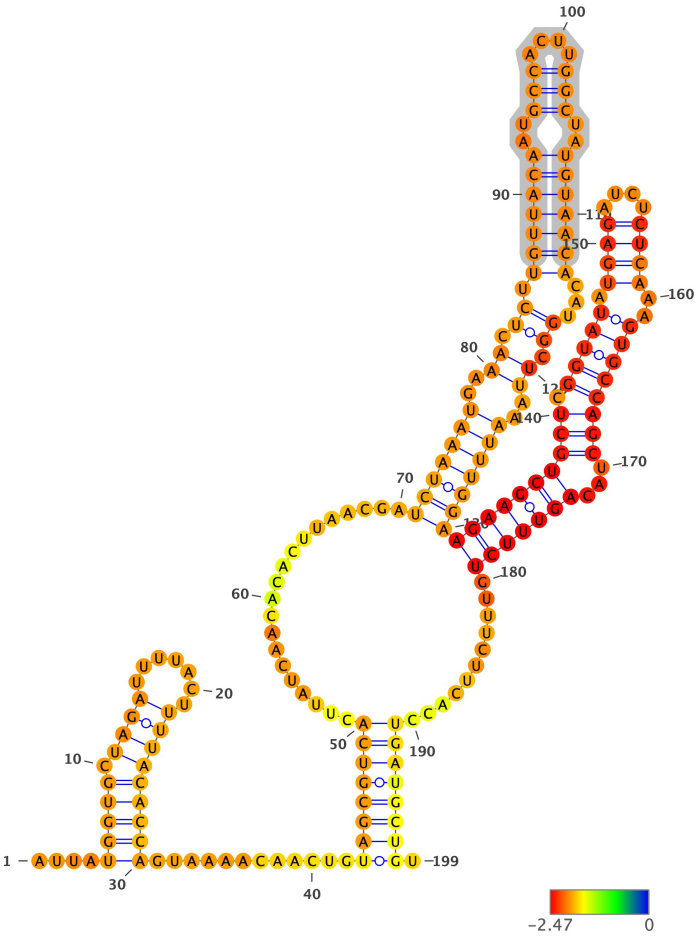
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 81 from nt 4601 to 4626 (nt 87 to 112)

```
5'-GTTACAATGCCACTTGGCTAUGUAAC-3'
5'-((((((..(((....)))..))))))-3'
Motif MFE = -9.5; z-score = -4.42; ED = 0.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4515 to 4713 (motif highlighted in silver):

```
5'-AUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAA
CACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGU-3
5'-....(((((.((((.......)))))))))............((((((((.....................(((((((..((.((.(((((((..(((....)))..)))))
))...)).))..)))))))((((((((((.(((((.((((....))))..)))))))))...)))))))...........)))))))).-3'
MFE = -48.7; z-score = -2.76; ED = 16.93
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

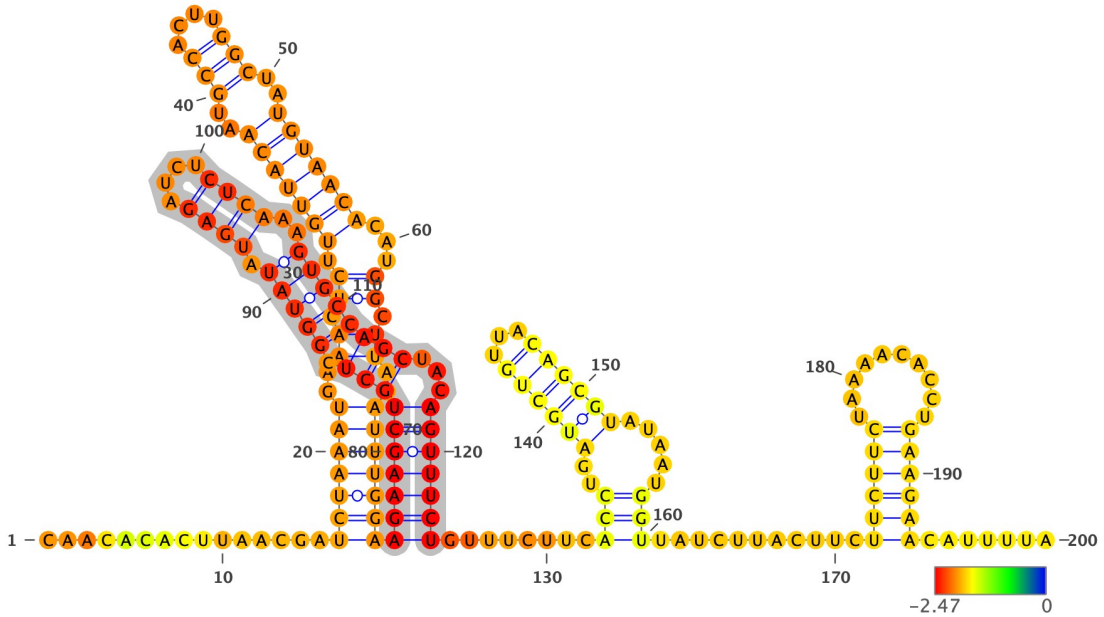
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 82 from nt 4645 to 4693 (nt 76 to 124)

```
5'-AGAAGCTGCTCGGTATATGAGATCTCUCAAAGUGCCAGCTACAGUUUCU-3'
5'-((((((((((.(((((...((....))....))))))))...)))))))-3'
Motif MFE = -17.2; z-score = -3.43; ED = 2.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4570 to 4769 (motif highlighted in silver):

```
5'-CAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCC
AGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUA-3
5'-...............(((((((..((.((.(((((((..(((....)))..)))))))...)).))..)))))))((((((((((.(((((.((((....))))..)))))
)))...)))))))........(((..((((((...))))))).....)))...........((((((..........))))))........-3'
MFE = -44.8; z-score = -2.23; ED = 22.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

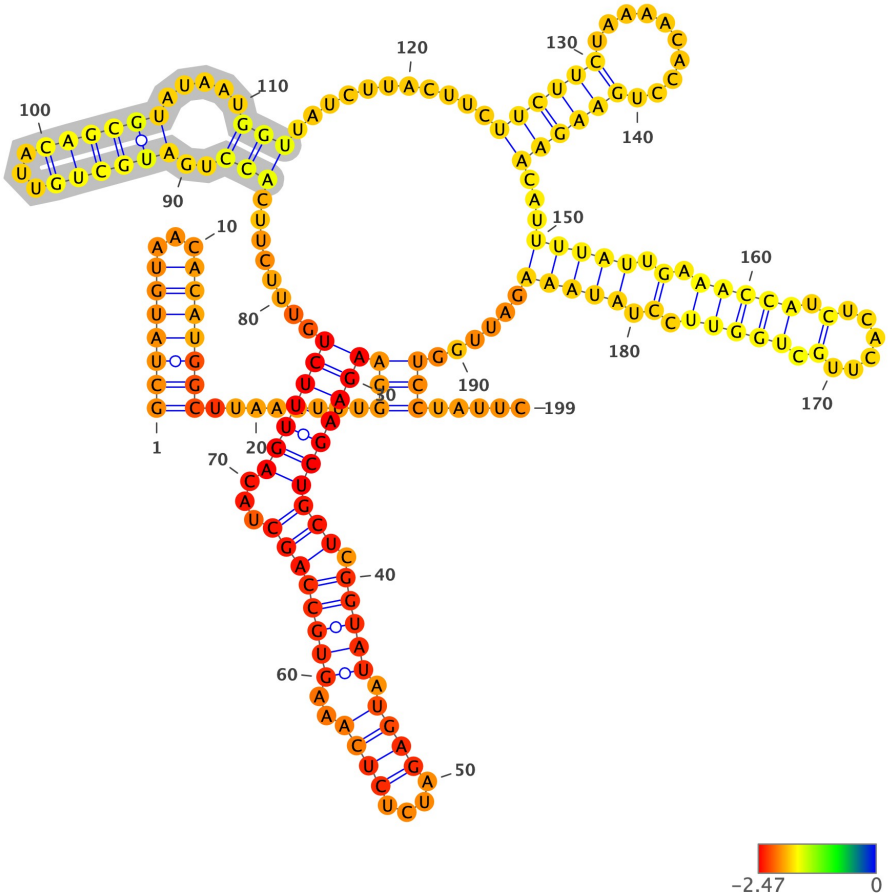
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 83 from nt 4702 to 4729 (nt 86 to 113)

```
5'-ACCTGATGCTGTTACAGCGTATAATGGU-3'
5'-(((...(((((...)))))......)))-3'
Motif MFE = -5.3; z-score = -1.19; ED = 2.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4617 to 4815 (motif highlighted in silver):

```
5'-GCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUG
GUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUC-3
5'-(((((((...)))))))........(((((((((((((.(((((.((((....))))..))))))))...)))))))........(((..((((((...))))))).....)
)).........((((((.........))))))...(((((.(.(((((.(......).))))).).)))))......)))).....-3'
MFE = -44.6; z-score = -2.1; ED = 22.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

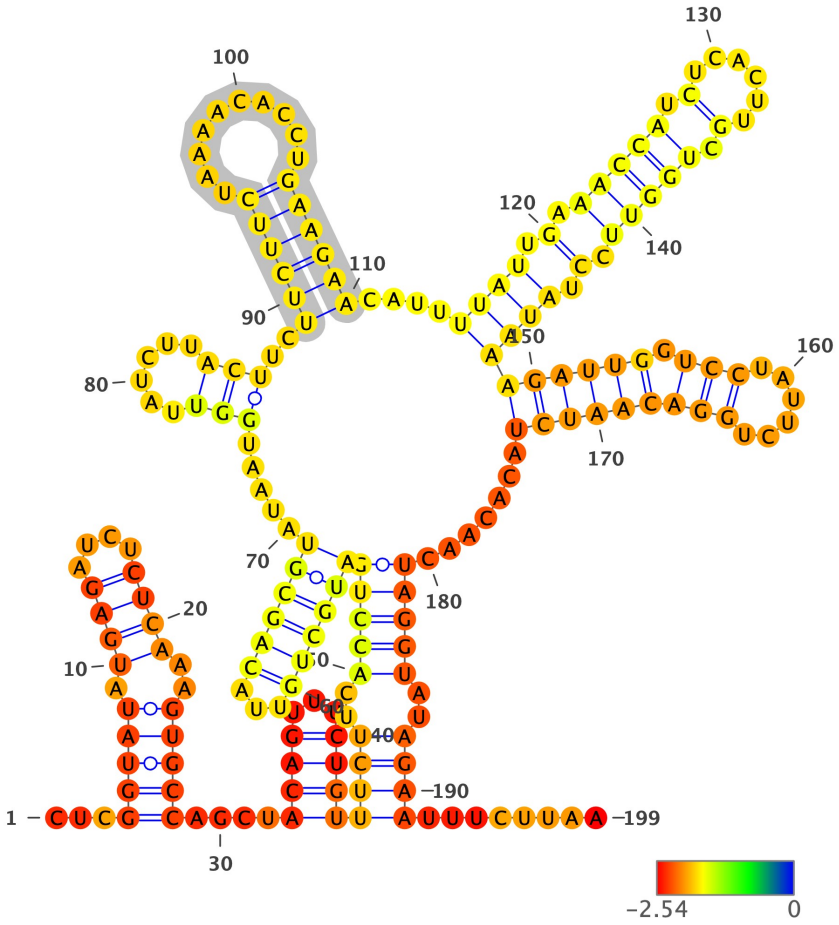
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 84 from nt 4741 to 4762 (nt 89 to 110)

```
5'-TTCTTCTAAAACACCTGAAGAA-3'
5'-((((((..........))))))-3'
Motif MFE = -3.9; z-score = -5.35; ED = 0.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4653 to 4851 (motif highlighted in silver):

```
5'-CUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAAC
AUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAA-3
5'-...(((((.((((....)))).)))))....((((...))))((((..(((((((((((...))))))).....(((......))).((((((..........)))))).
...((((.(.(((((.(......).)))))).).))))((((((.(((......)))))))))).......)))))..))))........-3'
MFE = -42.2; z-score = -2.52; ED = 28.37
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

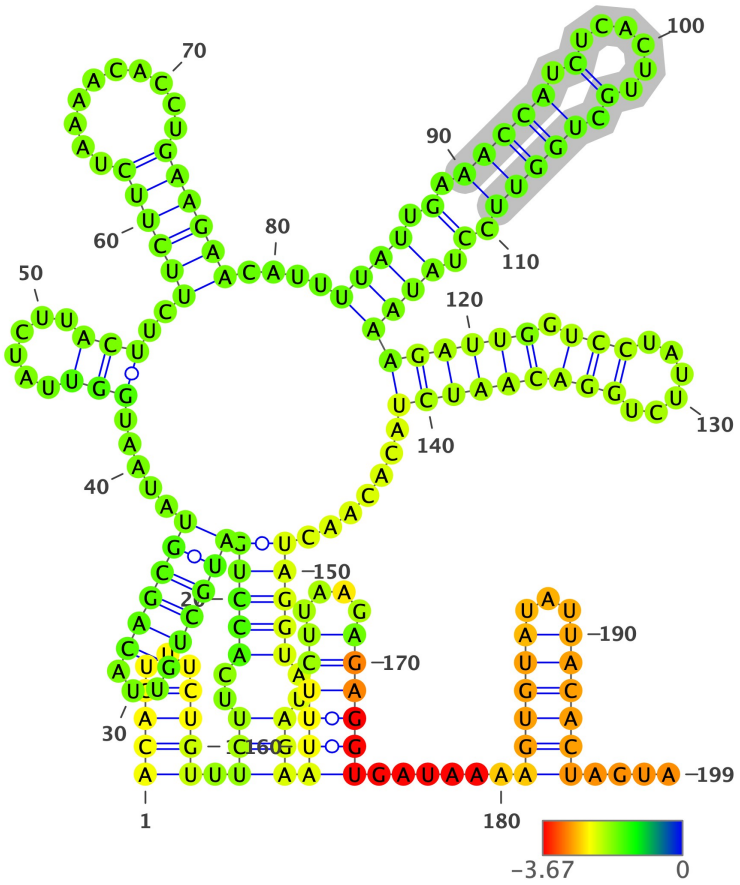
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 85 from nt 4774 to 4793 (nt 90 to 109)

```
5'-AACCATCTCACTTGCUGGUU-3'
5'-(((((.(......).)))))-3'
Motif MFE = -3.5; z-score = -2.46; ED = 0.87
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4685 to 4883 (motif highlighted in silver):

```
5'-ACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCC
UAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUA-3
5'-((((...)))).(((..((((((((((((...))))))).....(((......))).((((((..........))))))....((((.(.(((((.(......).)))))).)
.))))((((((.(((......)))))))))).......)))))..)))((((((....))))))......((((((...))))))....-3'
MFE = -39.3; z-score = -1.77; ED = 38.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

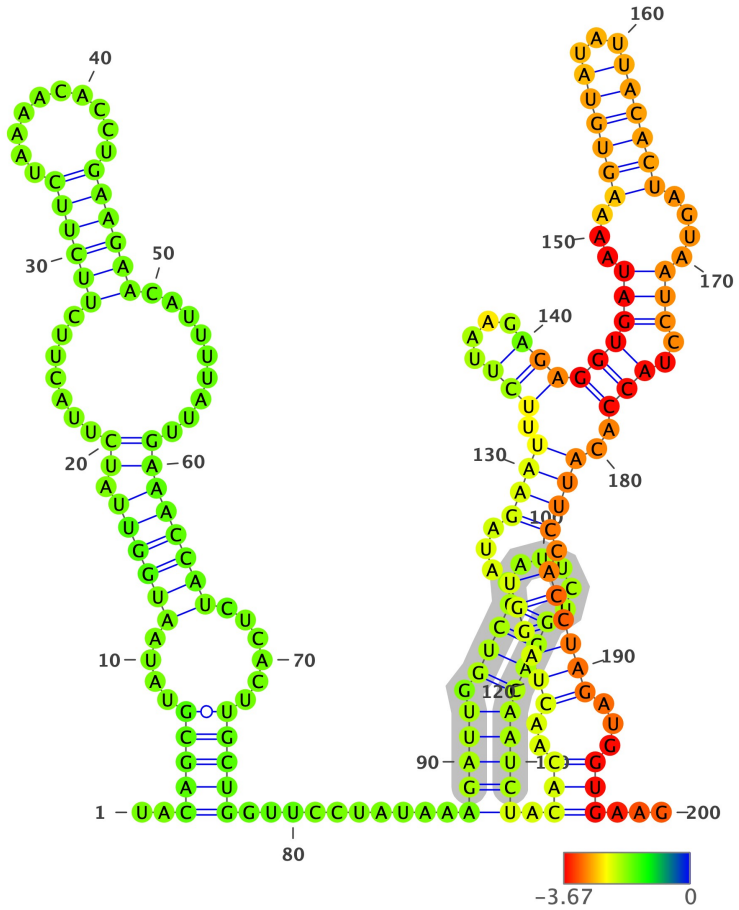
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 86 from nt 4802 to 4824 (nt 89 to 111)

```
5'-GATTGGTCCTATTCTGGACAAUC-3'
5'-((((.((((......))))))))-3'
Motif MFE = -7.3; z-score = -3.57; ED = 1.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4714 to 4913 (motif highlighted in silver):

```
5'-UACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUC
UACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAG-3
5'-..(((((....((((((.((.......((((((..........))))))..........))))))))......)))))..........(((((.((((......))))))))
).(((..((((((...((((.(((....)))((((((...((((((...))))))....)))..)))..)))).))))))...)))...-3'
MFE = -41.0; z-score = -1.97; ED = 37.37
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

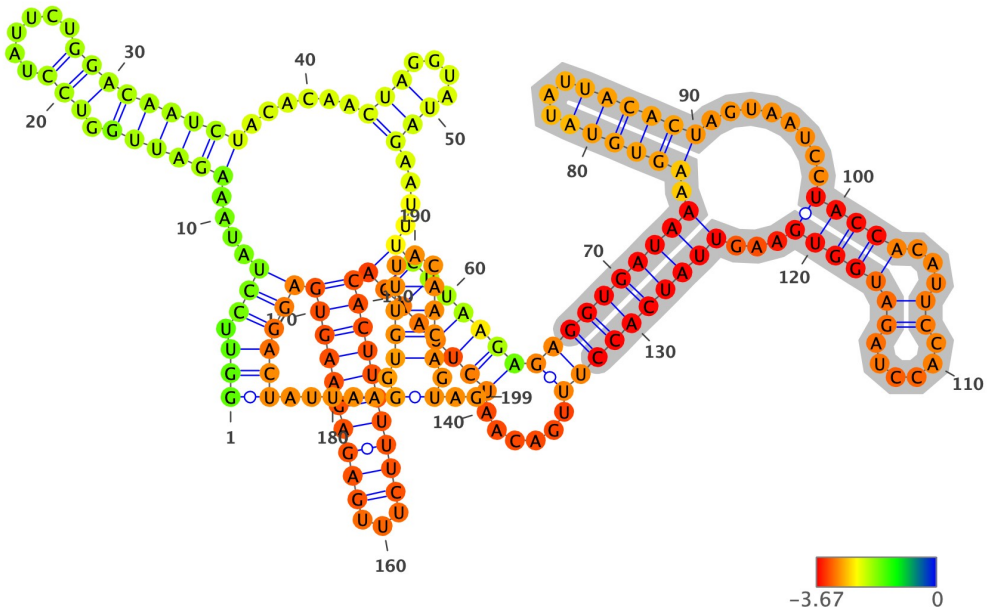
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 87 from nt 4856 to 4921 (nt 67 to 132)

```
5'-GGTGATAAAAGTGTATATTACACTAGTAATCCTACCACATTCCACCTAGATGGUGAAGUUAUCACC-3'
5'-(((((((((..((((.....))))..........((((...............))))...))))))))-3'
Motif MFE = -17.3; z-score = -3.63; ED = 7.97
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4790 to 4988 (motif highlighted in silver):

```
5'-GGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCAC
CUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAG-3
5'-(((.(((....((((((.(((......)))))))))......(((....)))....((((((((((((((((((.((((((...))))))........(((((...((...
...)))))))...))))))))))......))))))))((((((((((...)))))))))))))))))).....(.((((...)))).)..-3'
MFE = -51.3; z-score = -3.92; ED = 19.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

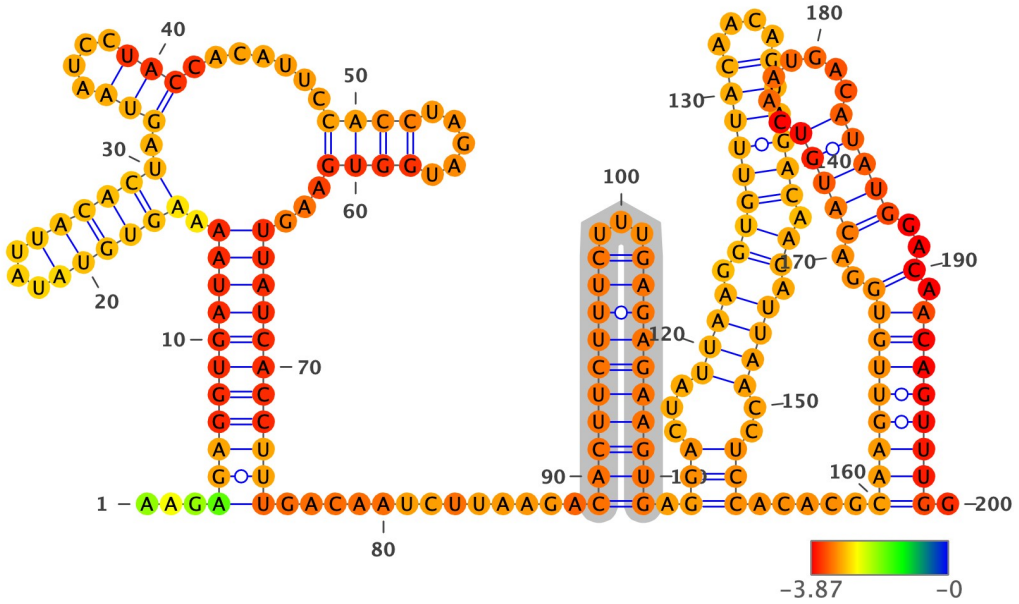
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 88 from nt 4938 to 4960 (nt 89 to 111)

```
5'-CACTTCTTTCTTTGAGAGAAGUG-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -10.7; z-score = -4.99; ED = 0.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4850 to 5049 (motif highlighted in silver):

```
5'-AAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUG
AGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGG-3
5'-...((((((((((.((((((...)))))).(((....))).......(((.....))))...)))))))))).............((((((((((...))))))))))
.(((...((((.(((((((((....)))))))).)).))))..))).....(((((((((..(((((.......)))))..).)))))))).-3'
MFE = -52.1; z-score = -2.94; ED = 36.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

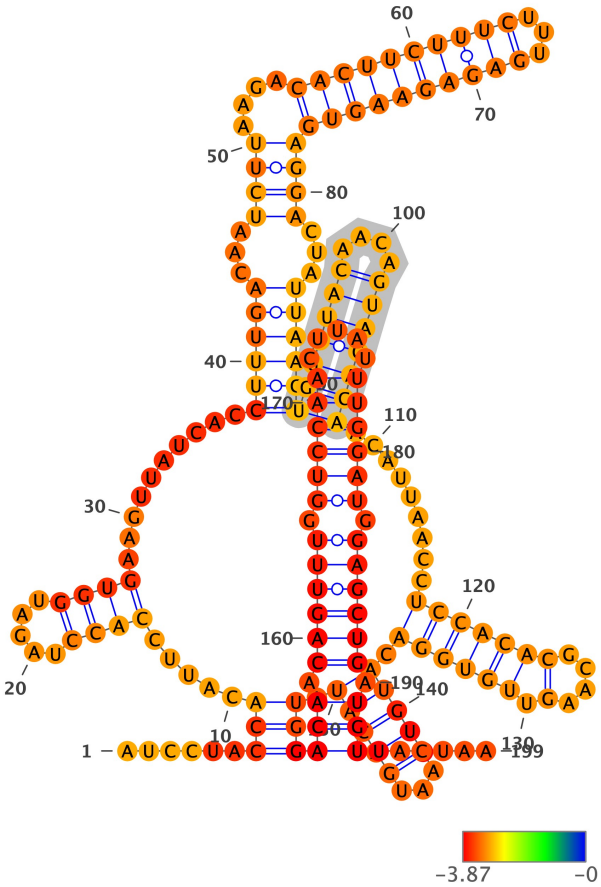
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 89 from nt 4974 to 4991 (nt 91 to 108)

```
5'-TGTTTACAACAGUAGACA-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.1; z-score = -4.8; ED = 0.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4884 to 5082 (motif highlighted in silver):

```
5'-AUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACA
UUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAA-3
5'-......(((.....((((.....))))..........((((((...((((....((((((((((...)))))))))))))...))))))(((((((....)))))))...
......(((((((....).)))))).(((((...))))).)))(((.((((((.((((((.....)))))).)))))).))).....-3'
MFE = -56.6; z-score = -4.13; ED = 31.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

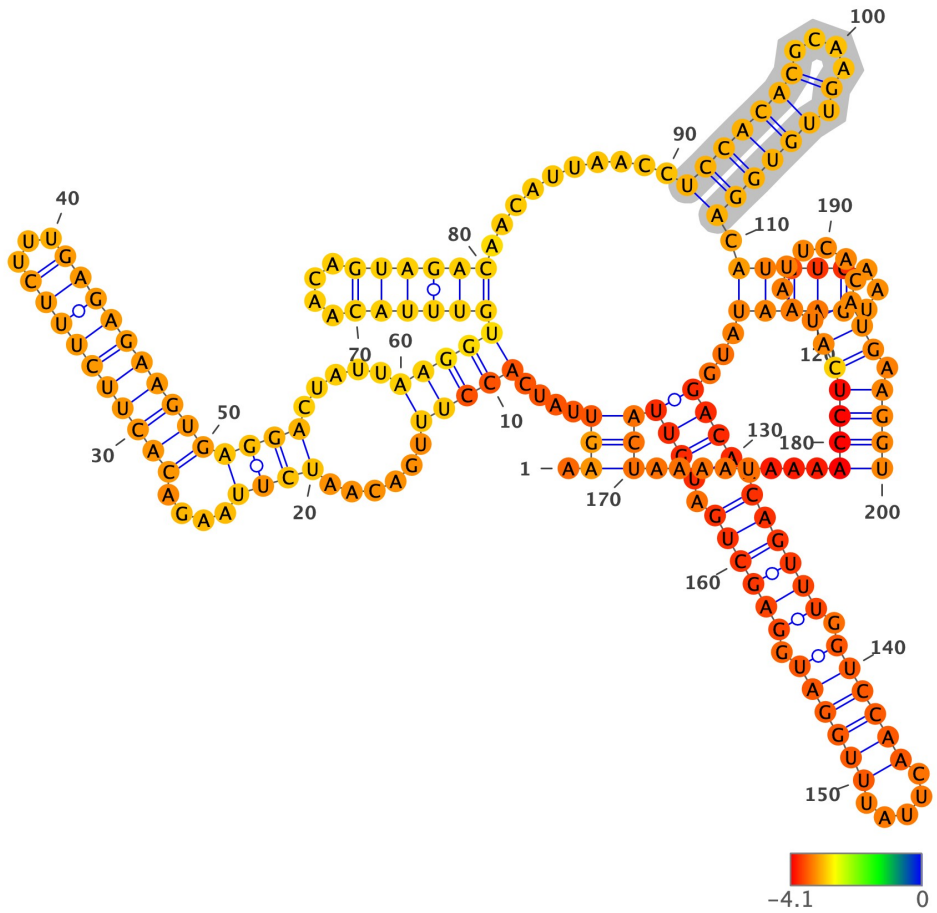
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 90 from nt 5001 to 5019 (nt 91 to 109)

```
5'-TCCACACGCAAGTUGUGGA-3'
5'-(((((((....).)))))))-3'
Motif MFE = -6.7; z-score = -3.23; ED = 1.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4911 to 5110 (motif highlighted in silver):

```
5'-AAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACA
UGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGU-3
5'-.((((....(((((......((((....((((((((((...)))))))))))))).....)))))((((((....)))))).........(((((((....).)))))).(
((((...)))))...(((((.((((((.((((((.....)))))).)))))).)))))).......(((((((.......))).))))-3'
MFE = -54.9; z-score = -4.06; ED = 29.94
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

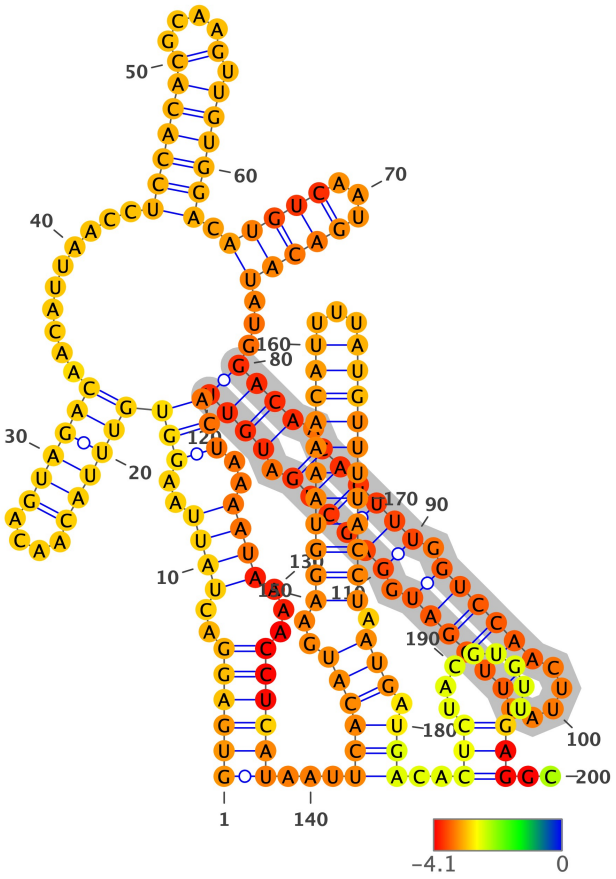
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 91 from nt 5037 to 5077 (nt 80 to 120)

```
5'-GACAACAGTTTGGTCCAACTTATUUGGAUGGAGCUGAUGUU-3'
5'-((((.((((((.((((((.....)))))).)))))).))))-3'
Motif MFE = -17.8; z-score = -4.78; ED = 0.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 4958 to 5157 (motif highlighted in silver):

```
5'-GUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGA
GCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGGC-3
5'-((((((..((((..((((((((((....))))))..........(((((((....).)))))).(((((...)))))...((((.((((((.((((((.....)))))).))
)))).)))))))..))))...))))))...((((((..((((((((((((...)))))))))))).))).))).(((........)))..-3'
MFE = -60.4; z-score = -4.5; ED = 18.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

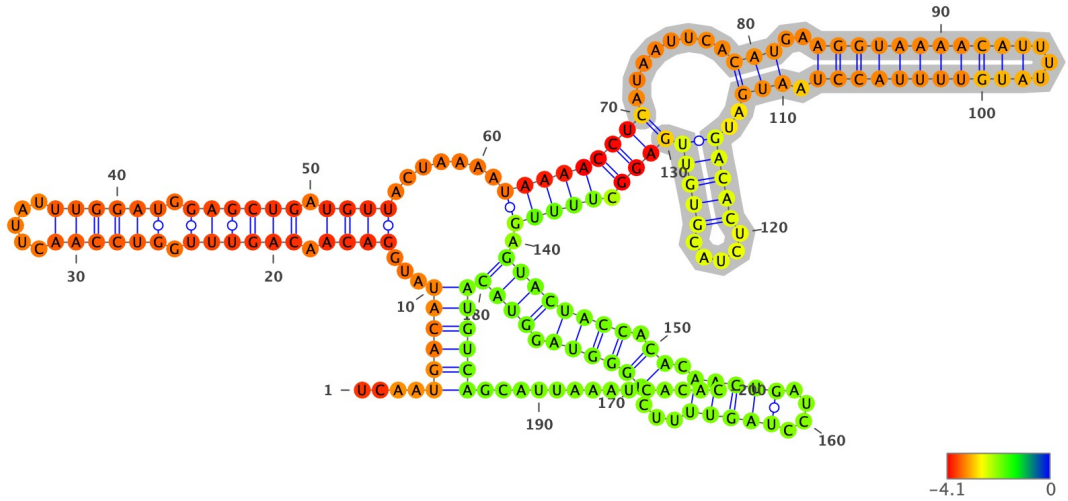
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 92 from nt 5093 to 5153 (nt 70 to 130)

```
5'-CATAATTCACATGAAGGTAAAACATTTTATGUUUUACCUAAUGATGACACTCTACGUGUUG-3'
5'-(........(((..(((((((((.........))))))))).)))..(((((.....))))))-3'
Motif MFE = -16.6; z-score = -4.17; ED = 4.29
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5024 to 5223 (motif highlighted in silver):

```
5'-UCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAU
GAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACAC-3
5'-....((((((...((((.((((((.((((((.....)))))).)))))).))))).......((((((((.........(((..(((((((((((...)))))))))))).))
)..(((((.....))))))))).))))).((((((((.((.(((((....)))))...)))))).))))))))).............-3'
MFE = -56.2; z-score = -4.36; ED = 11.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

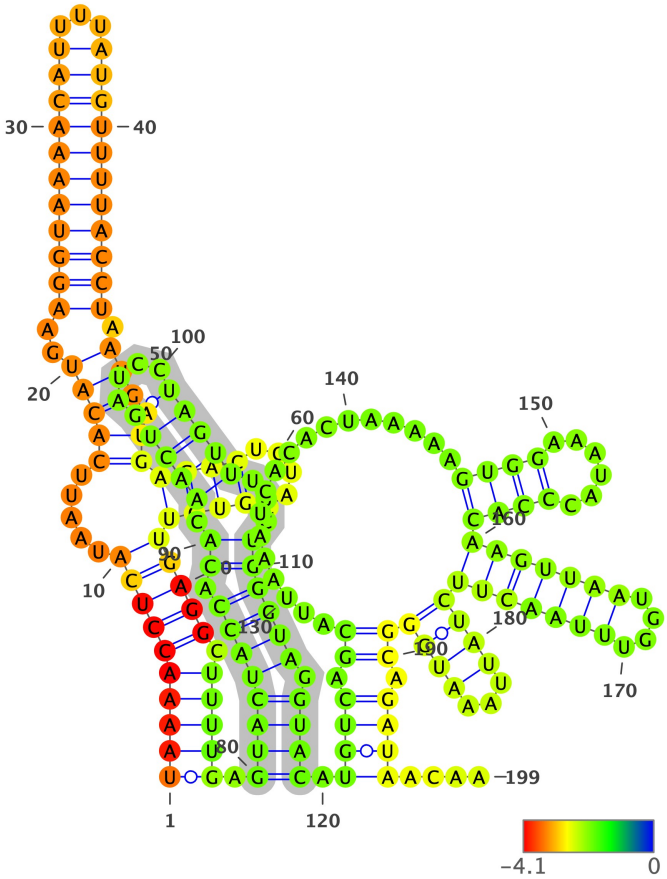
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 93 from nt 5164 to 5203 (nt 80 to 119)

```
5'-GTACTACCACACAACTGATCCTAGUUTTCUGGGUAGGUAC-3'
5'-((((((((.((.((((......))))...)))))).))))-3'
Motif MFE = -9.8; z-score = -2.16; ED = 4.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5085 to 5283 (motif highlighted in silver):

```
5'-UAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGG
GUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAA-3
5'-((((((((((.....(((((..((((((((((((...)))))))))))).))).))((((.....))))))))).))))).((((((((.((.(((((....)))))...)))
))).)))).((((.((.................((((......))))(((((((....)))))))((((...)))))).))))....-3'
MFE = -45.7; z-score = -3.04; ED = 36.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

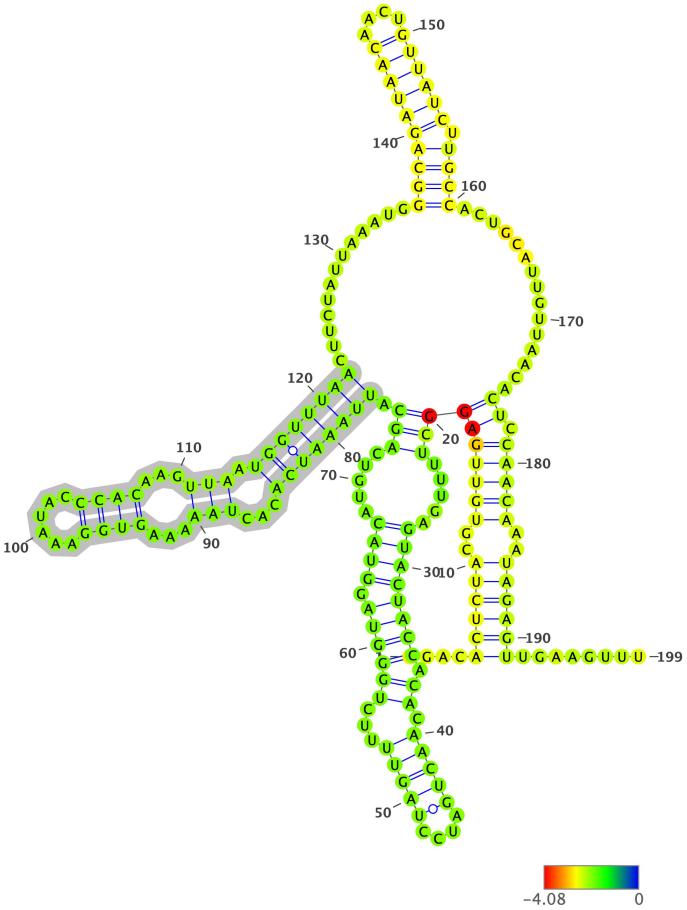
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 94 from nt 5213 to 5258 (nt 77 to 122)

```
5'-TTAAATCACACTAAAAAGTGGAAATACCCACAAGTTAAUGGUUUAA-3'
5'-((((((((.........((((......))))).......))))))))-3'
Motif MFE = -8.9; z-score = -3.38; ED = 2.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5137 to 5335 (motif highlighted in silver):

```
5'-UGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGU
UAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUU-3
5'-....((((((..((((((((((.....((((((((.((.(((((....)))))...)))))).))))).....))).((((((((...(((...((((......))))...)
)).))))))))..............((((((((((....)))))).))))................)).)))))..)))))).........-3'
MFE = -47.3; z-score = -3.03; ED = 19.58
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

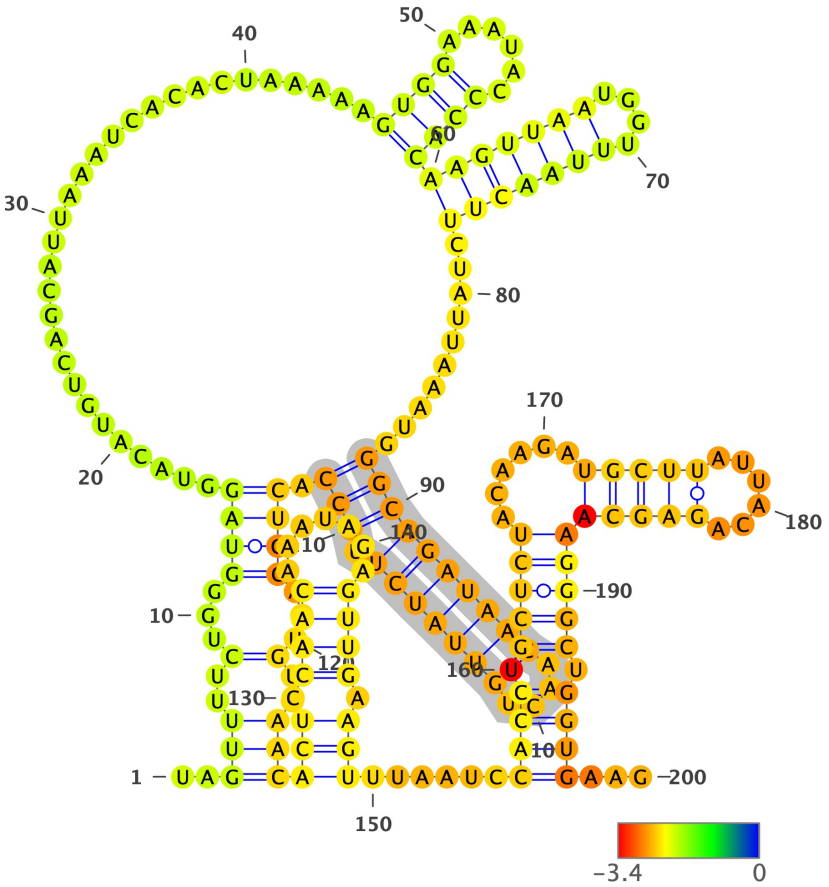
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 95 from nt 5272 to 5296 (nt 88 to 112)

```
5'-GGCAGATAACAACTGUUAUCUTGCC-3'
5'-((((((((((....)))))))).)))-3'
Motif MFE = -10.9; z-score = -4.47; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5185 to 5384 (motif highlighted in silver):

```
5'-UAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGC
CACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAG-3
5'-..(((..(...((((.............................((((......))))(((((((....)))))))..........((((((((((....)))))))).))
).))))...)..)))(((.((((.......)))).))).....((((.(((((......(((((......)))))))))).))))...-3'
MFE = -47.0; z-score = -2.33; ED = 43.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

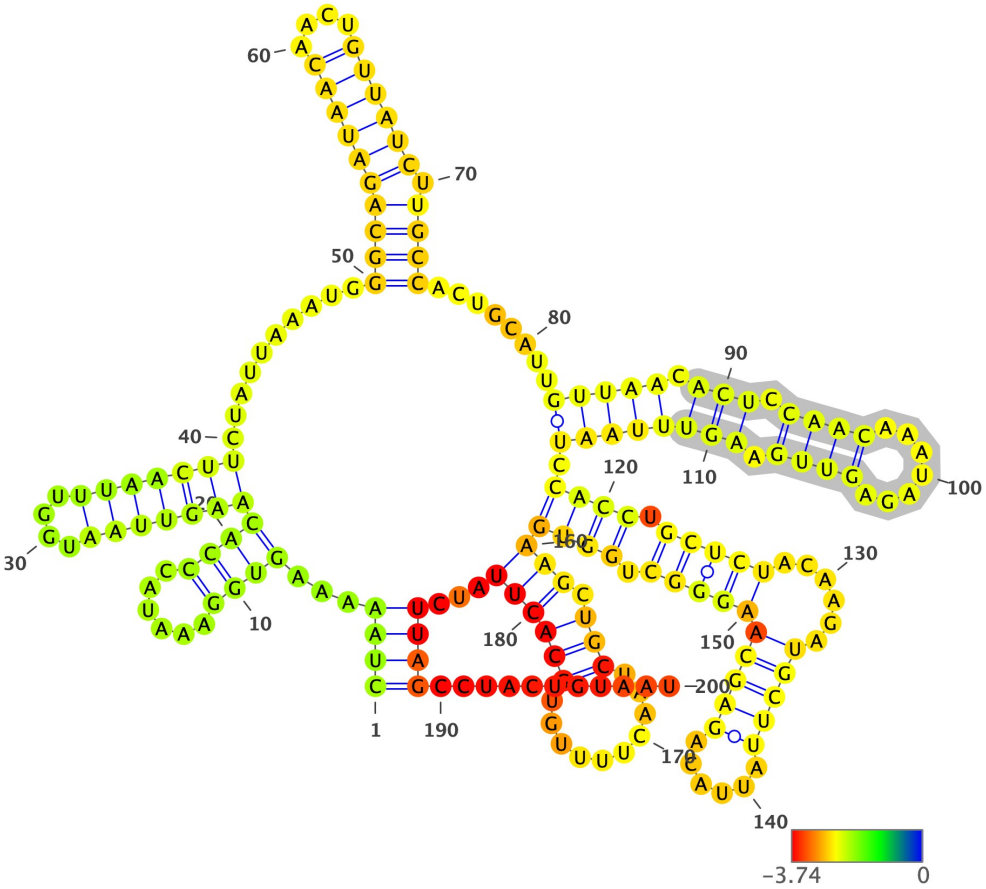
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 96 from nt 5311 to 5333 (nt 89 to 111)

```
5'-ACTCCAACAAATAGAGUUGAAGU-3'
5'-(((.((((.......)))).)))-3'
Motif MFE = -3.3; z-score = -1.82; ED = 1.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5223 to 5422 (motif highlighted in silver):

```
5'-CUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGU
UUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAU-3
5'-(((((...((((......)))))))))))))).....(((((((((((....)))))))).))))........(((((.(((.((((.......)))).)))
)))))).((((.(((((.....((((.....))))))))))).)))))))(.(((.........)))))))...))))...........-3'
MFE = -48.6; z-score = -2.99; ED = 38.6
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

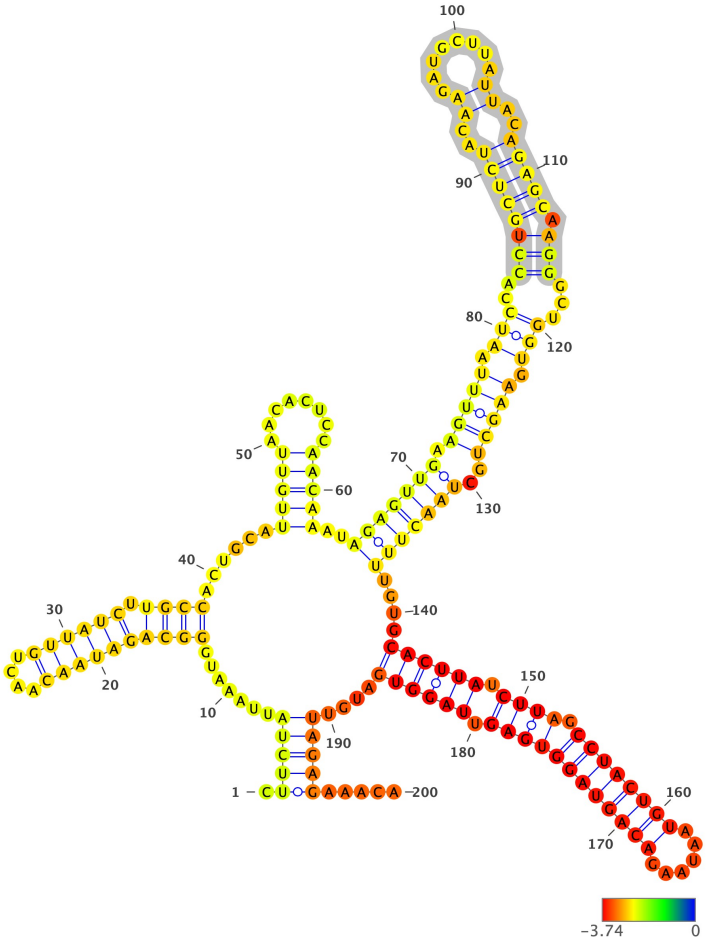
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 97 from nt 5342 to 5374 (nt 84 to 116)

```
5'-CCTGCTCTACAAGATGCTTATTACAGAGCAAGG-3'
5'-((.((((.................))))..))-3'
Motif MFE = -7.5; z-score = -1.89; ED = 3.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5259 to 5458 (motif highlighted in silver):

```
5'-CUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAG
CAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACA-3
5'-.(((((.......((((((((((....)))))).))))......(((((........)))))..(((((((.(((((.(((..((((((((..((........))..))))
).)))...))).)))))..)))))))....((((((.((((.((((((((......)))))))))))).))))))....)))))).....-3'
MFE = -56.6; z-score = -3.8; ED = 30.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

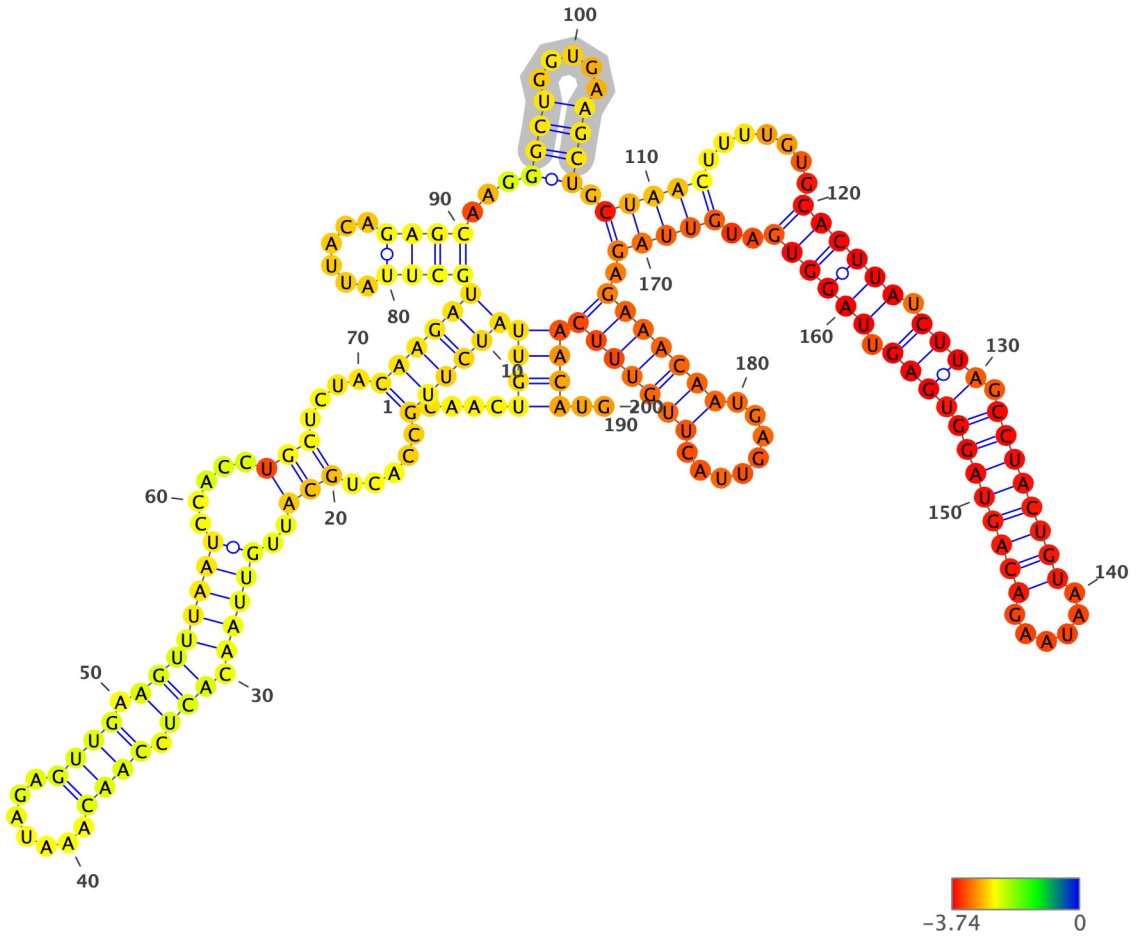
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 98 from nt 5375 to 5385 (nt 95 to 105)

```
5'-GCTGGTGAAGC-3'
5'-(((.....)))-3'
Motif MFE = -1.3; z-score = -2.29; ED = 0.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5281 to 5480 (motif highlighted in silver):

```
5'-CAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAA
CUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUG-3
5'-....((((((((((.....(((..(((((.(((.((((.......)))).))))))))).....)))....))))))((((......))))...((((.....)))).((((
(.......((((((.((((.((((((((.....))))))))))))).))))))..))))).(((((((.......))))))))))..-3'
MFE = -51.3; z-score = -3.78; ED = 39.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

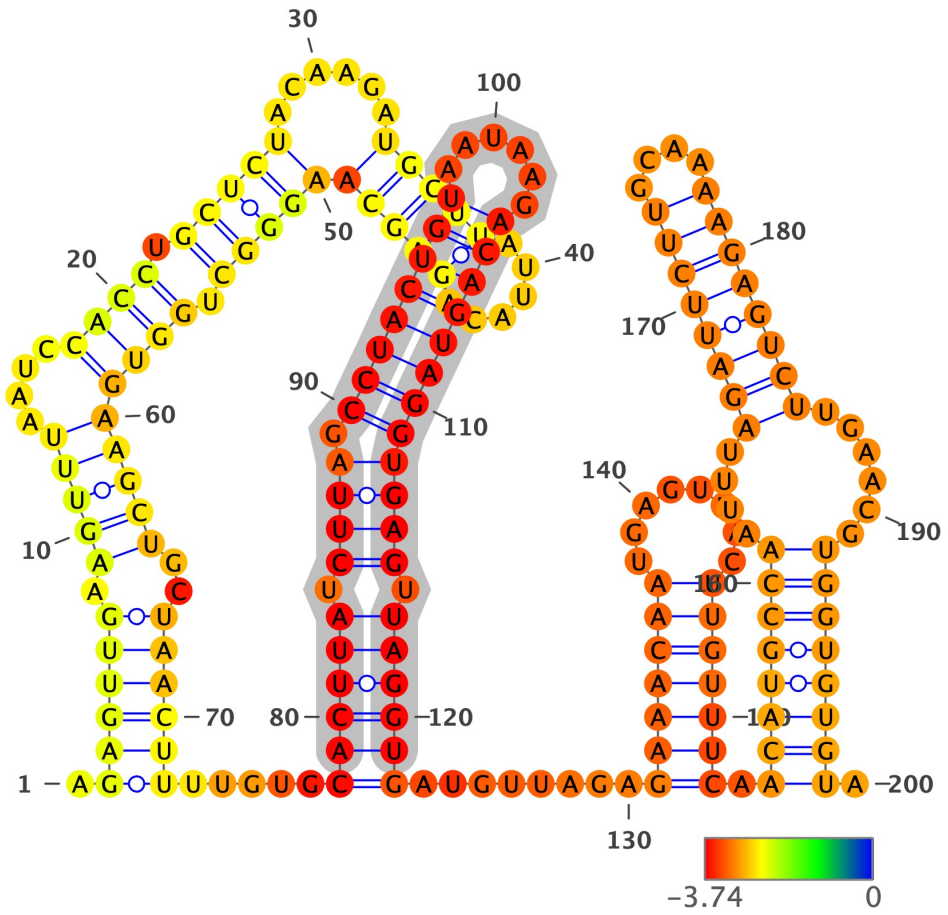
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 99 from nt 5401 to 5443 (nt 79 to 121)

```
5'-ACTTATCTTAGCCTACTGTAATAAGACAGUAGGTGAGTUAGGU-3'
5'-(((((.(((..((((((((......))))))))).))).)))))-3'
Motif MFE = -18.1; z-score = -5.0; ED = 2.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5323 to 5522 (motif highlighted in silver):

```
5'-AGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGG
UGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUA-3
5'-.((((((.(((((....((((.(((((......(((((......)))))))))).))))))))).)))))))..))))))).....((((((.((((.((((((((......))))))))
)))).))))))........(((((((........))))))).((((((((....((((((((....))))))))......))))))))).-3'
MFE = -67.6; z-score = -4.96; ED = 12.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

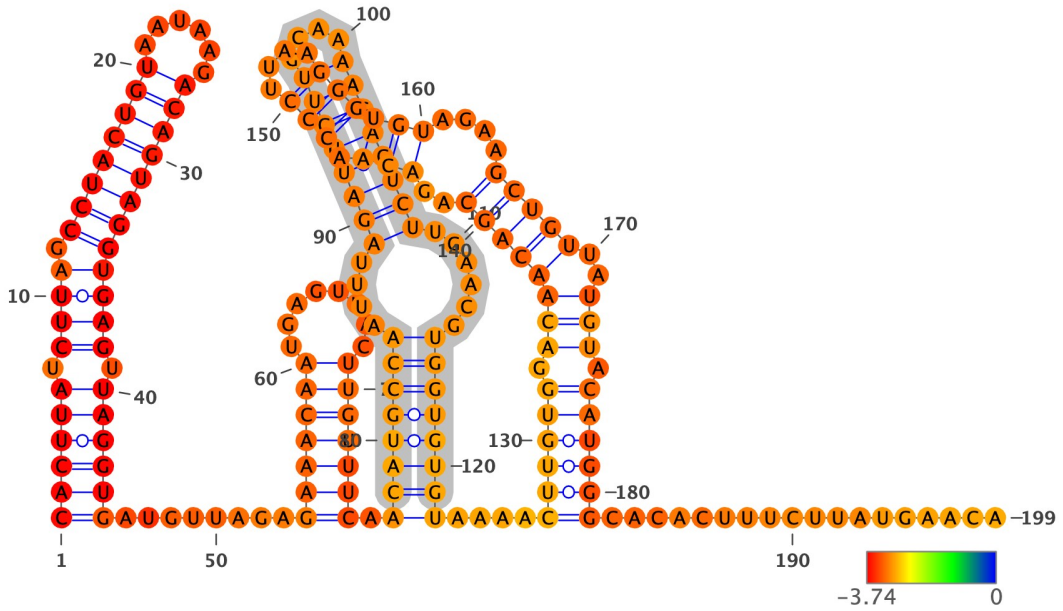
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 100 from nt 5477 to 5520 (nt 78 to 121)

```
5'-CATGCCAATTTAGATTCTTGCAAAAGAGUCUTGAACGUGGUGUG-3'
5'-(((((((....((((((((....))))))))......)))))))-3'
Motif MFE = -15.2; z-score = -3.66; ED = 3.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5400 to 5598 (motif highlighted in silver):

```
5'-CACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGA
ACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACA-3
5'-((((((.((((.((((((((......)))))))))))).))))))........(((((((........)))))))).((((((((....((((((((....))))))))...
...))))))))....((((((.((((((((..(((.(((....))))))....)))))..))).))))))..................-3'
MFE = -63.0; z-score = -4.08; ED = 25.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

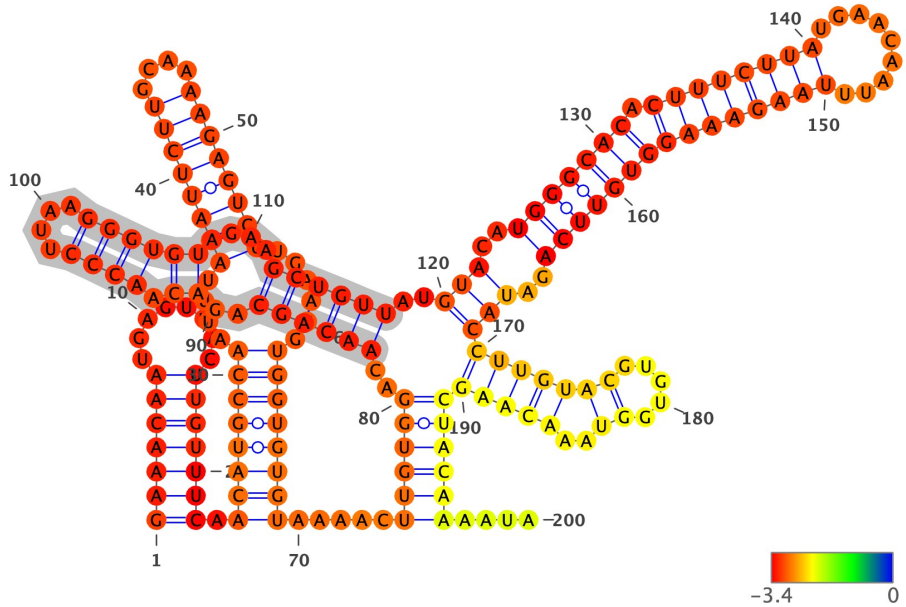
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 101 from nt 5535 to 5569 (nt 83 to 117)

```
5'-AACAGCAGACAACCCTTAAGGGUGTAGAAGCUGUU-3'
5'-((((((.....((((....))))......))))))-3'
Motif MFE = -11.8; z-score = -3.55; ED = 2.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5453 to 5652 (motif highlighted in silver):

```
5'-GAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAA
GCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUA-3
5'-(((((((........)))))))).((((((((....((((((((....))))))))......))))))))).....((((((..((((((..((.((((....))))))....
))))))..(((..(((((((.((((((((.........)))))))))))))))..)))(((((((.....))..)))))))))))....-3'
MFE = -62.7; z-score = -5.04; ED = 25.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

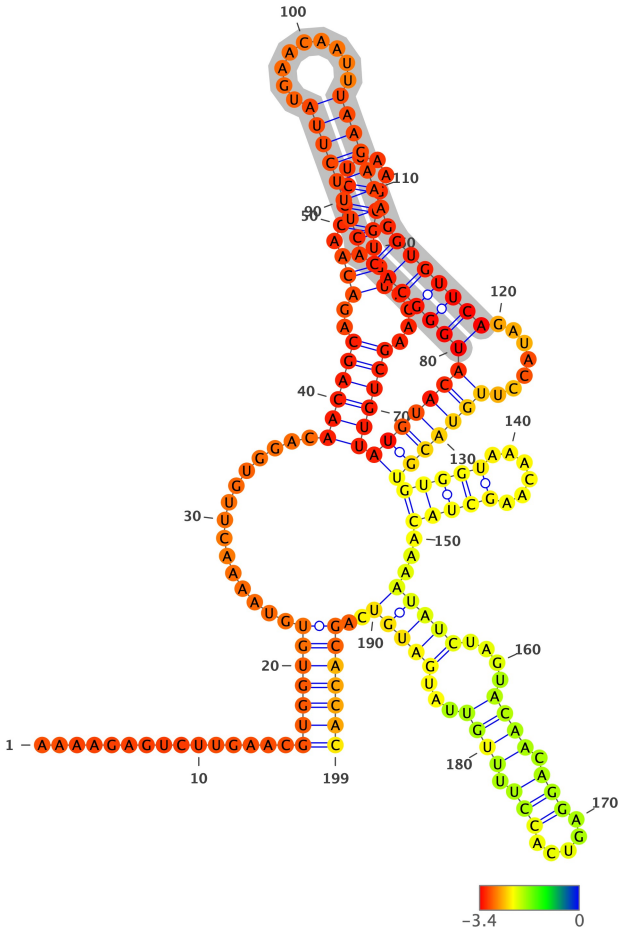
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 102 from nt 5577 to 5616 (nt 80 to 119)

```
5'-TGGGCACACTTTCTTATGAACAATTUAAGAAAGGUGUUCA-3'
5'-(((((((.((((((((.........)))))))))))))))-3'
Motif MFE = -15.3; z-score = -4.71; ED = 1.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5498 to 5696 (motif highlighted in silver):

```
5'-AAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAA
GGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCAC-3
5'-...............(((((((...............((((((..(((.(((....))))))....))))))((((((((((((((.((((((((.........)))))))
))))))))).......)))))))(((((......)))))...(((((....((((.(((.....))).))))...)))))..)))))))-3'
MFE = -56.0; z-score = -3.85; ED = 33.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

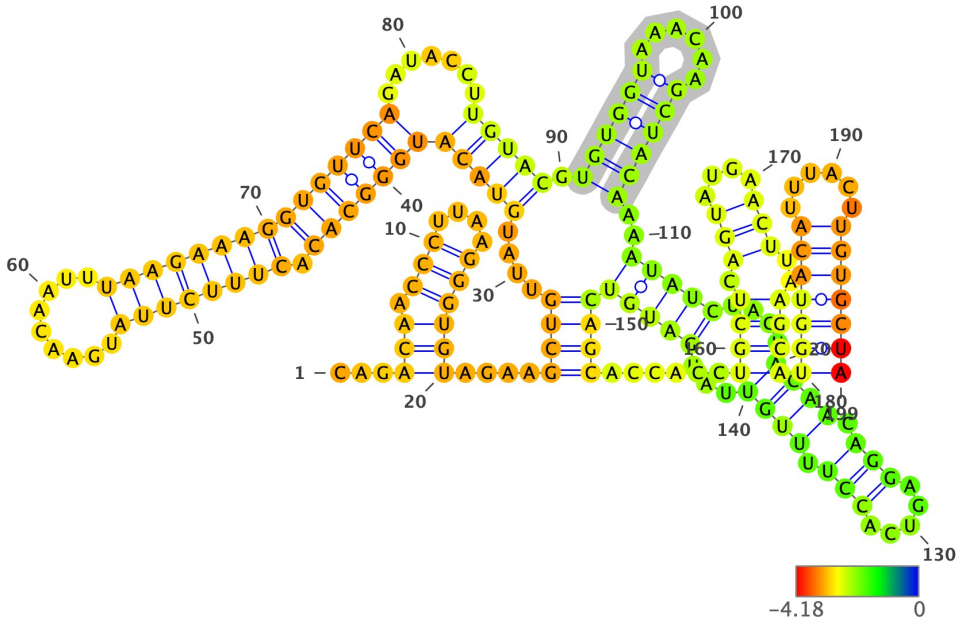
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 103 from nt 5630 to 5647 (nt 91 to 108)

```
5'-TGTGGTAAACAAGCUACA-3'
5'-(((((........)))))-3'
Motif MFE = -4.5; z-score = -3.86; ED = 0.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5540 to 5738 (motif highlighted in silver):

```
5'-CAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAA
UAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUA-3
5'-...(((.(((....))))))....((((....((((((((((((.((((((((.........)))))))))))))).......))))).((((((......))))))..(
((((....((((.(((.....)).))))...)))))))))......((((.(((....)))..))))(((((((......)))))))-3'
MFE = -52.1; z-score = -2.98; ED = 34.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

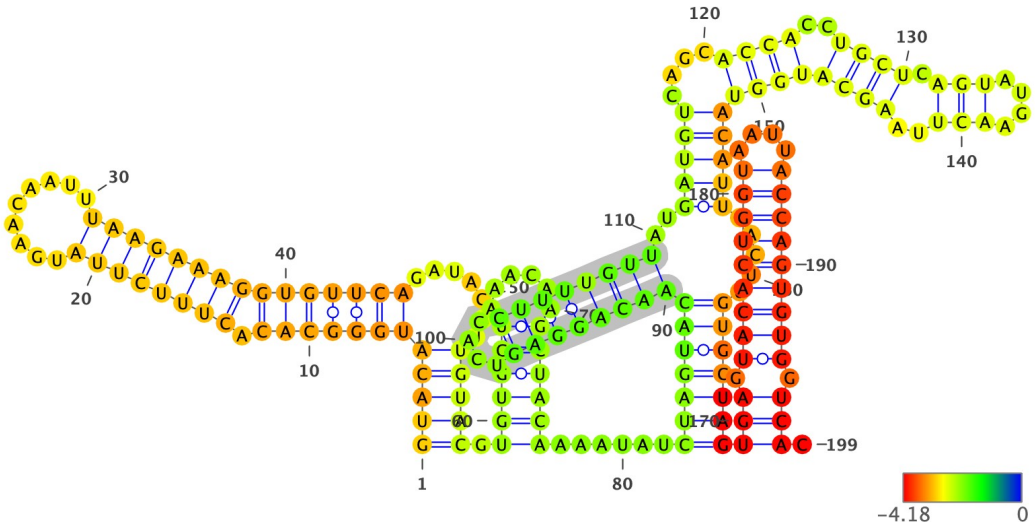
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 104 from nt 5661 to 5680 (nt 90 to 109)

```
5'-AACAGGAGTCACCUUUTGUU-3'
5'-(((.((((....)))).)))-3'
Motif MFE = -4.6; z-score = -3.13; ED = 0.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5572 to 5770 (motif highlighted in silver):

```
5'-GUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAU
GAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCAC-3
5'-(((((((((((.((((((((.........)))))))))))))).......))))).((((((.....)))))).....((((((((((((((....))))))))).
(((((....((((..((((.(((....)))..))))))))))))).....)))))))(((.(((((((((....)))))))))).))).-3'
MFE = -63.4; z-score = -4.85; ED = 33.94
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

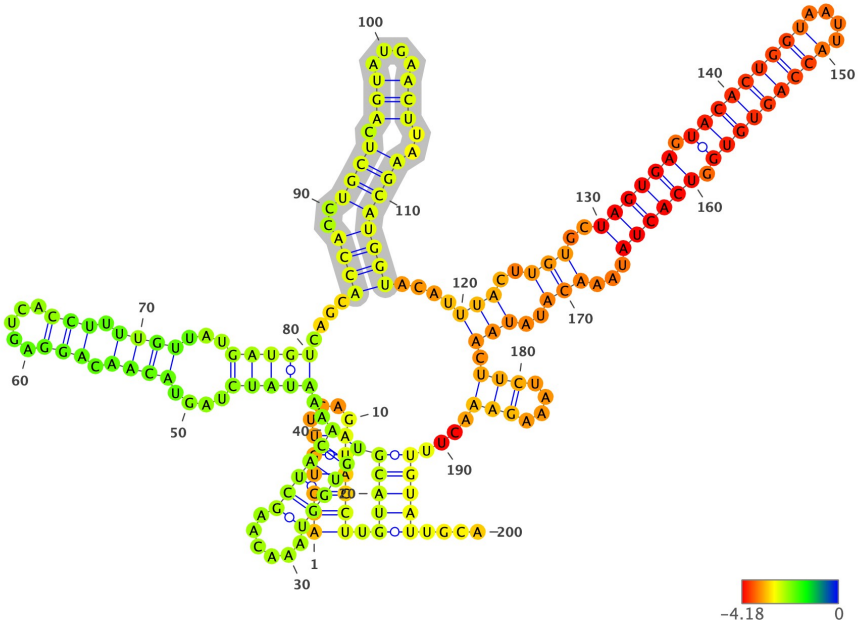
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 105 from nt 5692 to 5722 (nt 85 to 115)

```
5'-ACCACCTGCTCAGTATGAACUTAAGCAUGGU-3'
5'-((((..((((.(((....)))..))))))))-3'
Motif MFE = -6.7; z-score = -2.05; ED = 4.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5608 to 5807 (motif highlighted in silver):

```
5'-AGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCA
UGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCA-3
5'-((((((....)))))).((((((((((.....))))))..(((((....((((.(((.....))).))))...)))))....((((..((((.(((....)))..))))
))))....(((..(((..((((((.((((((((((....)))))))))).))))))...)))..))).(((....)))....)))))....-3'
MFE = -51.5; z-score = -3.08; ED = 39.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

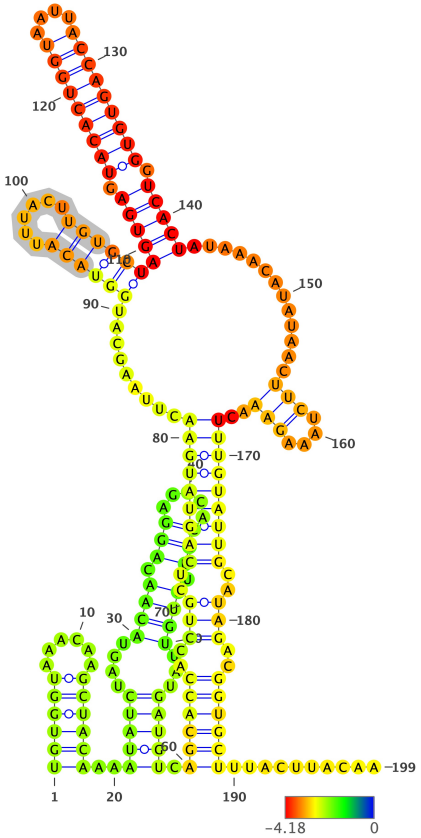
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 106 from nt 5723 to 5734 (nt 94 to 105)

```
5'-ACATTTACTUGU-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5630 to 5828 (motif highlighted in silver):

```
5'-UGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGU
GAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAA-3
5'-((((((......))))))..(((((....((((.(((.....))).))))...))))).((((((..(((..((((((((((.........((((((......))))))(((
((.((((((((((....)))))))))).)))))..............(((....)))..))))))))))..)))..))))))..........-3'
MFE = -57.0; z-score = -4.46; ED = 19.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

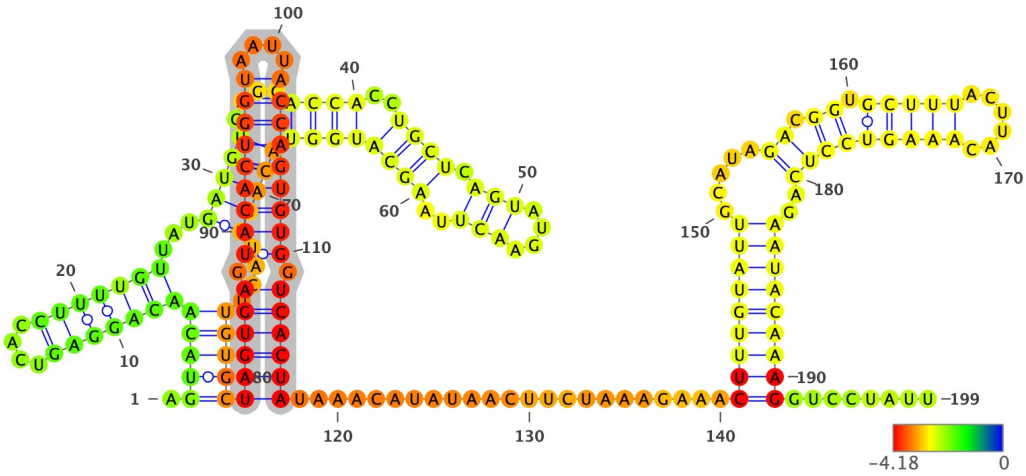
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 107 from nt 5737 to 5772 (nt 82 to 117)

```
5'-TAGTGAGTACACTGGTAATTACCAGUGUGGUCACUA-3'
5'-((((((.(((((((((.....))))))))).))))))-3'
Motif MFE = -22.2; z-score = -6.19; ED = 0.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5656 to 5854 (motif highlighted in silver):

```
5'-AGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGG
UCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUU-3
5'-.(((((((((((((....)))))))...(((((....((((..((((.(((....)))..))))))))))))))....)))))((((((.(((((((((....))))))))).
))))))......................(((((((((.....((.((.(((((.....))))))))).))))))))).........-3'
MFE = -51.6; z-score = -3.4; ED = 62.0
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

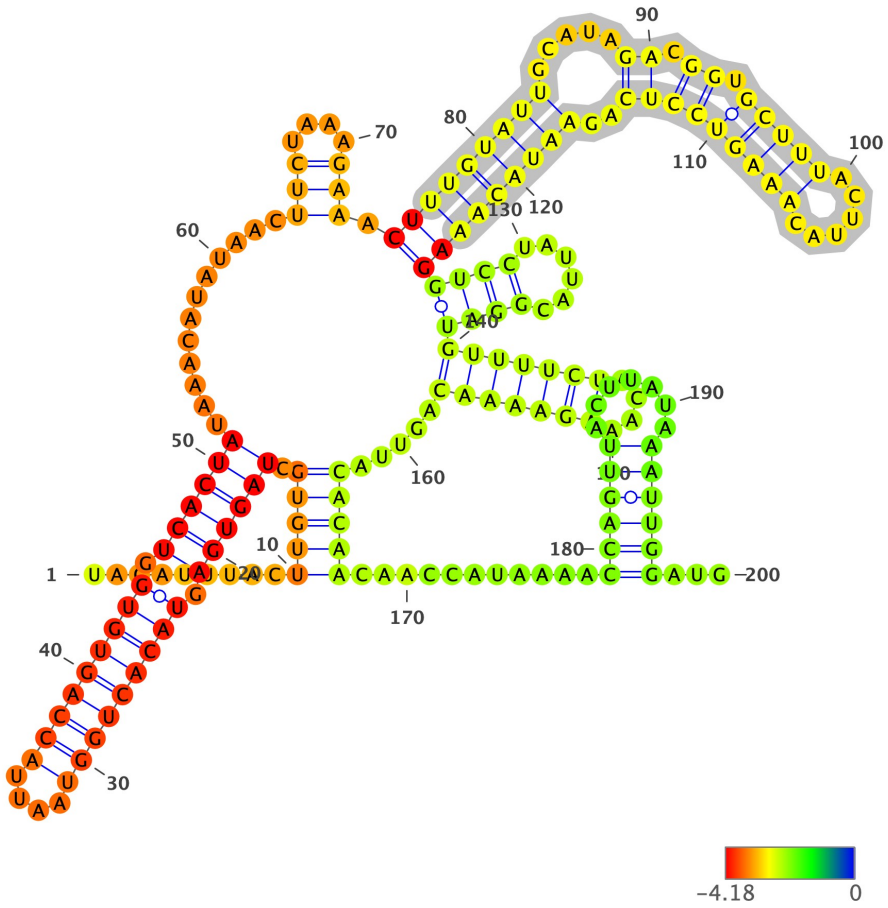
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 108 from nt 5798 to 5844 (nt 77 to 123)

```
5'-TTGTATTGCATAGACGGTGCTTTACTTACAAAGUCCUCAGAAUACAA-3'
5'-(((((((.....((.((.(((((.....)))))))))..)))))))-3'
Motif MFE = -7.5; z-score = -0.97; ED = 7.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5722 to 5921 (motif highlighted in silver):

```
5'-UACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUC
CUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUG-3
5'-.........(((((.(((((((.(((((((((....)))))))))..)))))).............(((....))).(((((((((.....((.((.(((((.....)))))))
)))..)))))))))((((.....))))((((((((....)))))))).....)))))...........((((((.......))))))...-3'
MFE = -52.5; z-score = -4.74; ED = 15.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

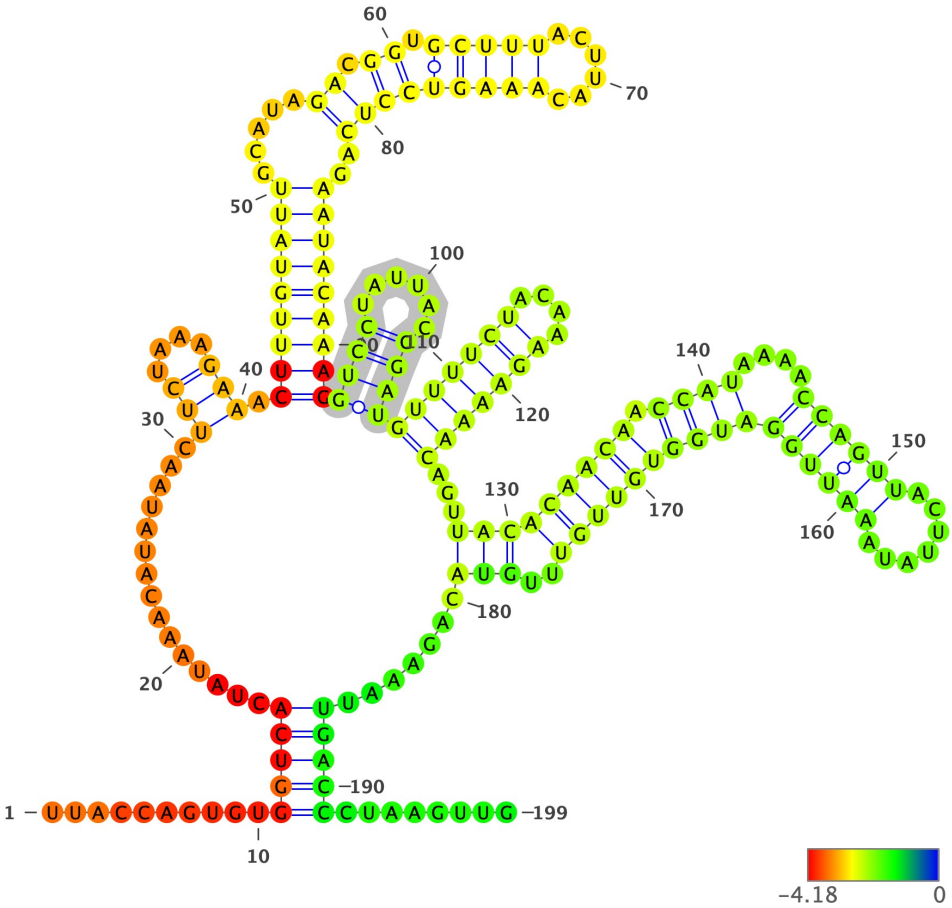
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 109 from nt 5847 to 5860 (nt 93 to 106)

```
5'-GTCCTATTACGGAU-3'
5'-((((......))))-3'
Motif MFE = -2.6; z-score = -4.02; ED = 0.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5755 to 5953 (motif highlighted in silver):

```
5'-UUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUU
CUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUG-3
5'-..........(((((...............(((....))).(((((((((.....((.((.(((((......)))))))))..))))))))))((((......))))(((((
((....)))))))...((((((((((.((((....((((((.......)))))))))))))))))..)))........)))))........-3'
MFE = -41.5; z-score = -2.27; ED = 22.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

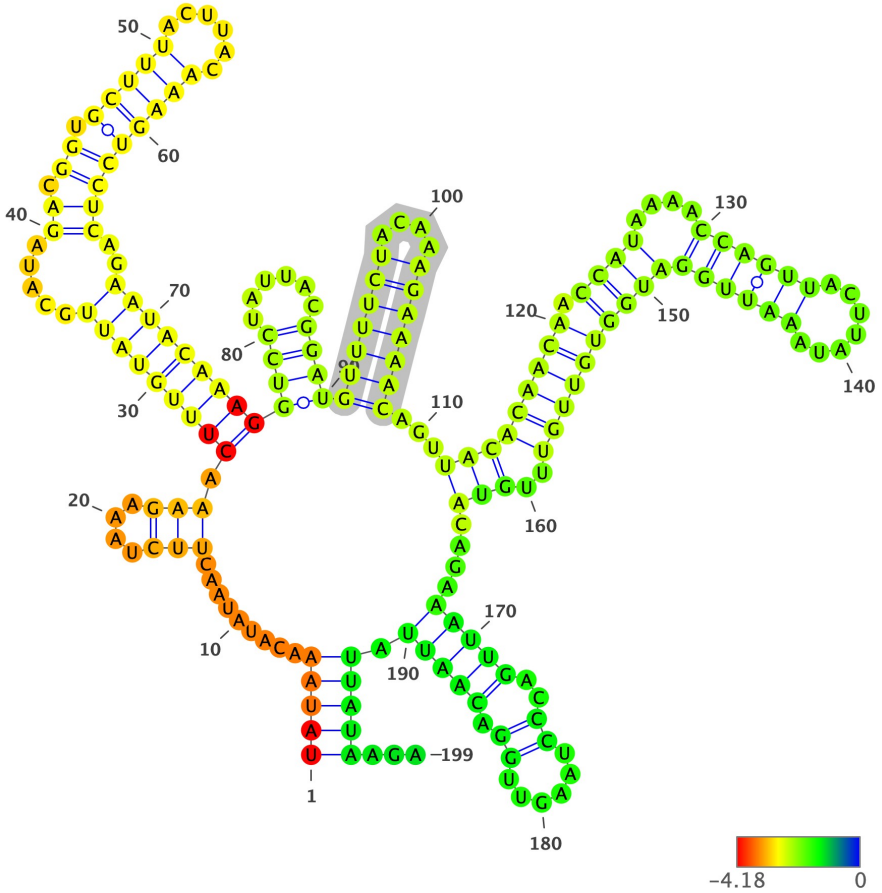
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 110 from nt 5861 to 5878 (nt 91 to 108)

```
5'-GTTTTCTACAAAGAAAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -7.85; ED = 0.35
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5771 to 5969 (motif highlighted in silver):

```
5'-UAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGU
UACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGA-3
5'-(((((.........(((....))).(((((((((.....((.((.(((((......)))))))))..))))))))))((((......))))(((((((....)))))))...
(((((((((.((((....((((((.......)))))))))))))))))..)))....(((((..((......)).)))))).)))))...-3'
MFE = -39.8; z-score = -2.78; ED = 30.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

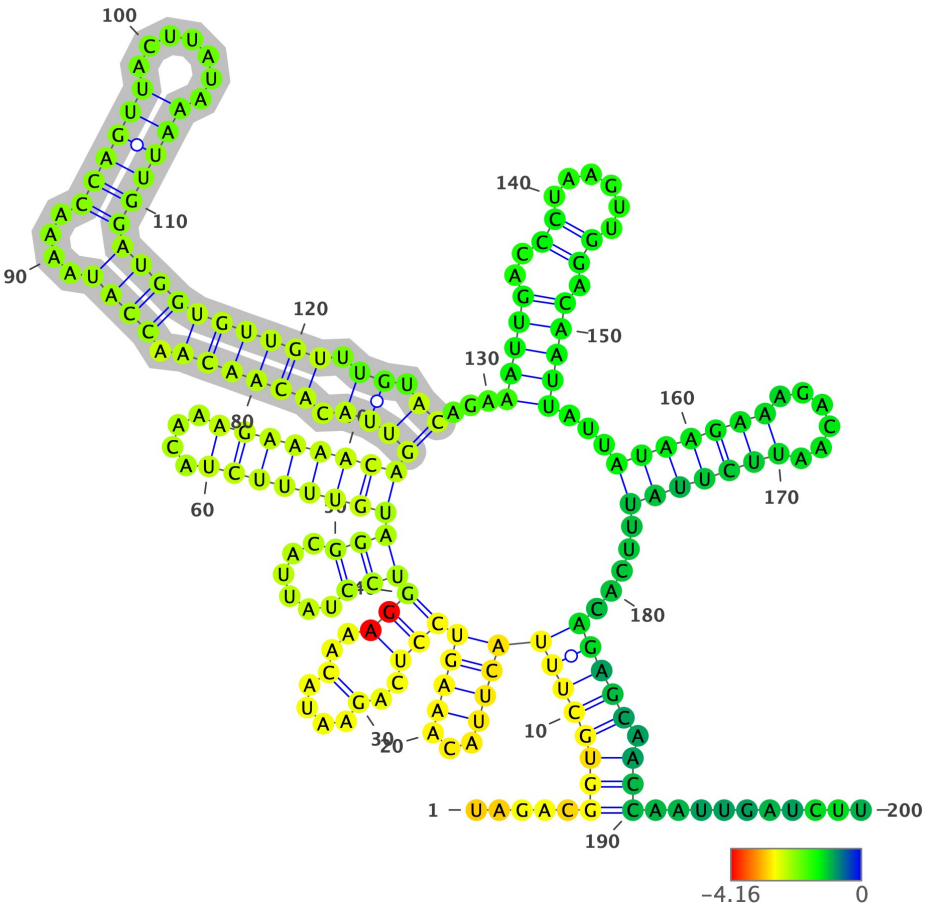
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 111 from nt 5880 to 5934 (nt 73 to 127)

```
5'-GTTACACAACAACCATAAAACCAGTTACTTATAAAUUGGAUGGUGUUGUTTGTAC-3'
5'-((...((((((.((((....((((...........))))))))))))))....))-3'
Motif MFE = -13.5; z-score = -3.28; ED = 5.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5808 to 6007 (motif highlighted in silver):

```
5'-UAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGG
AUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUU-3
5'-.....(((((((((((...))))(((..(....)..)))(((......)))((((((((....))))))))((((.((((((.((((....((((((.......))))))
))))))))))).)).))...(((((..((......)).)))))...(((((((......)))))))).....))))).)))..........-3'
MFE = -39.0; z-score = -2.36; ED = 18.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

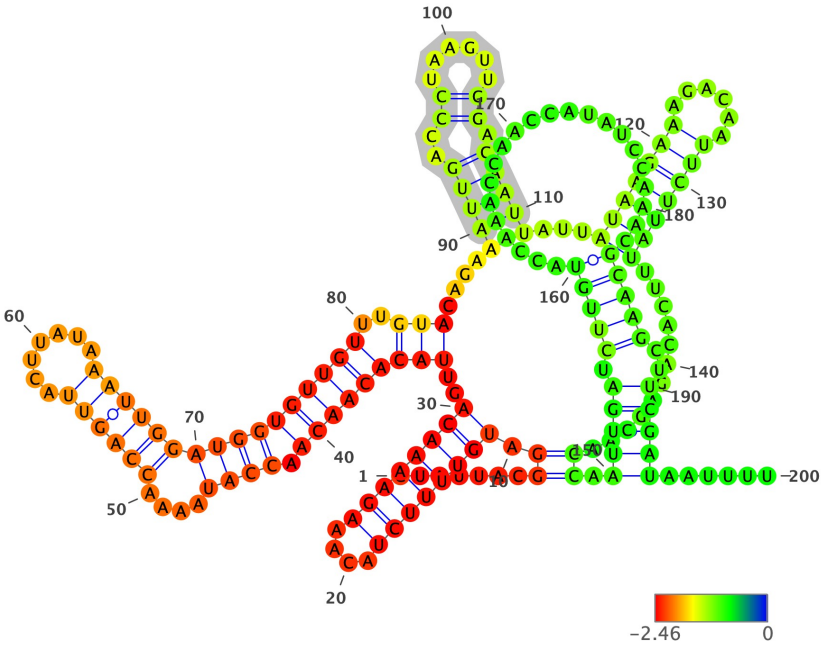
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 112 from nt 5939 to 5959 (nt 90 to 110)

```
5'-ATTGACCCTAAGTTGGACAAU-3'
5'-(((((..((......)).))))-3'
Motif MFE = -1.5; z-score = -0.37; ED = 3.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5850 to 6049 (motif highlighted in silver):

```
5'-CUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUU
AUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUU-3
5'-.......((.(((((((((....)))))))))..(((((((((.((((....((((((.......)))))))))))))))))))..)))....(((((..((......)).)))))
...((((((.....))))))............)).(((((.(((((.....................)))))..)))))......-3'
MFE = -33.2; z-score = -2.32; ED = 34.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

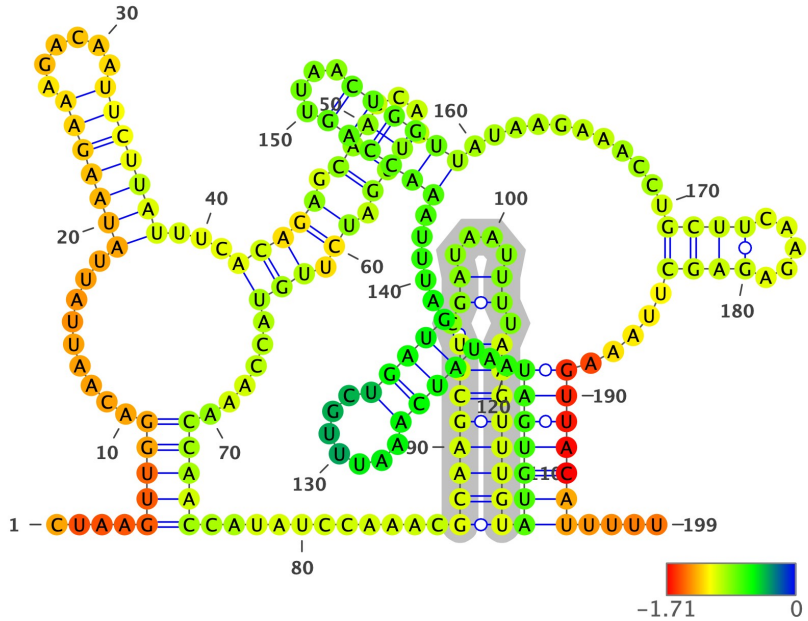
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 113 from nt 6032 to 6057 (nt 87 to 112)

```
5'-GCAAGCTTCGATAATTTTAAGUUUGU-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -6.1; z-score = -2.68; ED = 1.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 5946 to 6144 (motif highlighted in silver):

```
5'-CUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUG
UAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUU-3
5'-....(((((.........(((((((.....)))))))...(((((.(((....)))).)).)))......)))))...........(((((((.((....)).)))))))
)(((((((..(((((.......)))))).....((((((....))))))...........((((.....)))).....)))))))....-3'
MFE = -30.0; z-score = -0.26; ED = 45.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

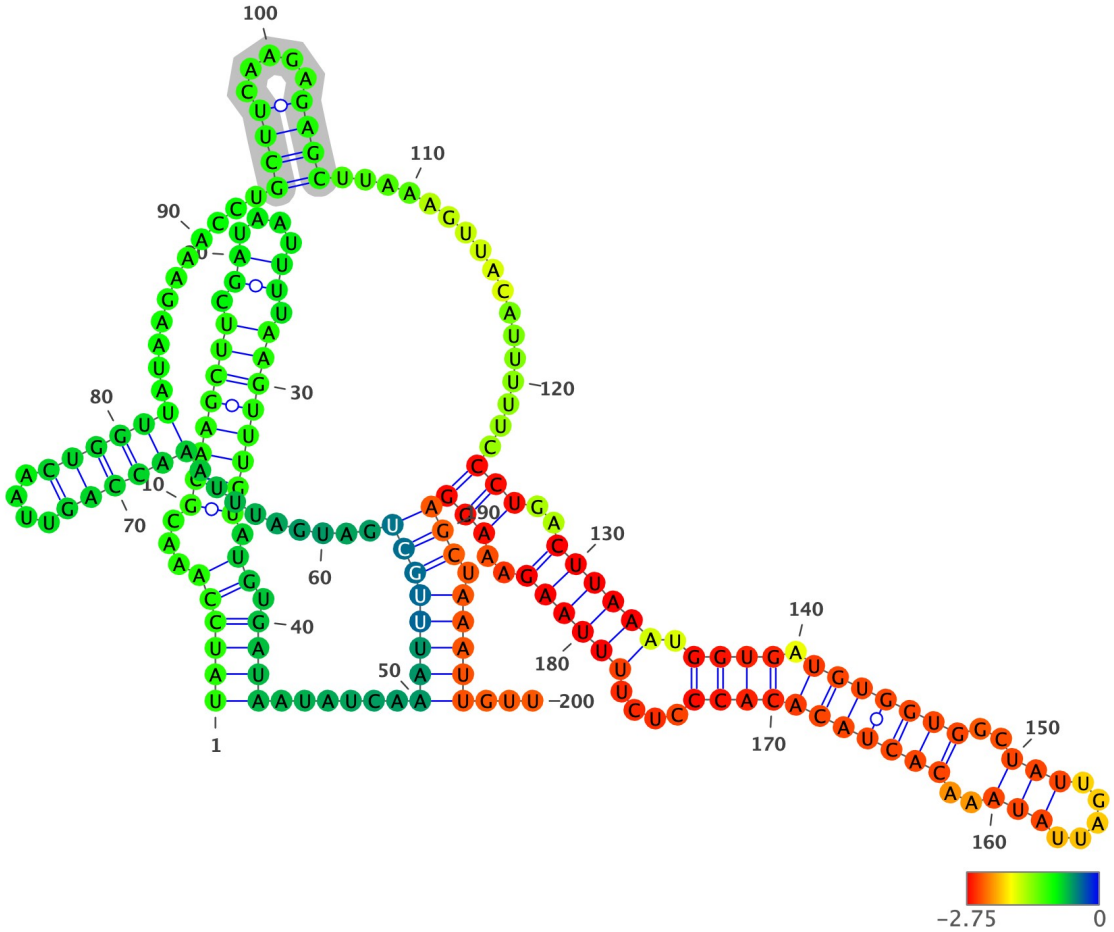
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 114 from nt 6116 to 6128 (nt 94 to 106)

```
5'-GCTTCAAGAGAGC-3'
5'-((((.....))))-3'
Motif MFE = -1.3; z-score = -1.11; ED = 1.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6023 to 6222 (motif highlighted in silver):

```
5'-UAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUGUAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAA
GUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUU-3
5'-((((((...((((((((.((....)).)))))))).)).))))......((((((((.........((((((....))))))...........((((.....))))).....
............(((..((((((.((((.(((((((..(((.....)))..)))))))))))....))))))..))))))).)))))...-3'
MFE = -44.6; z-score = -2.22; ED = 33.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

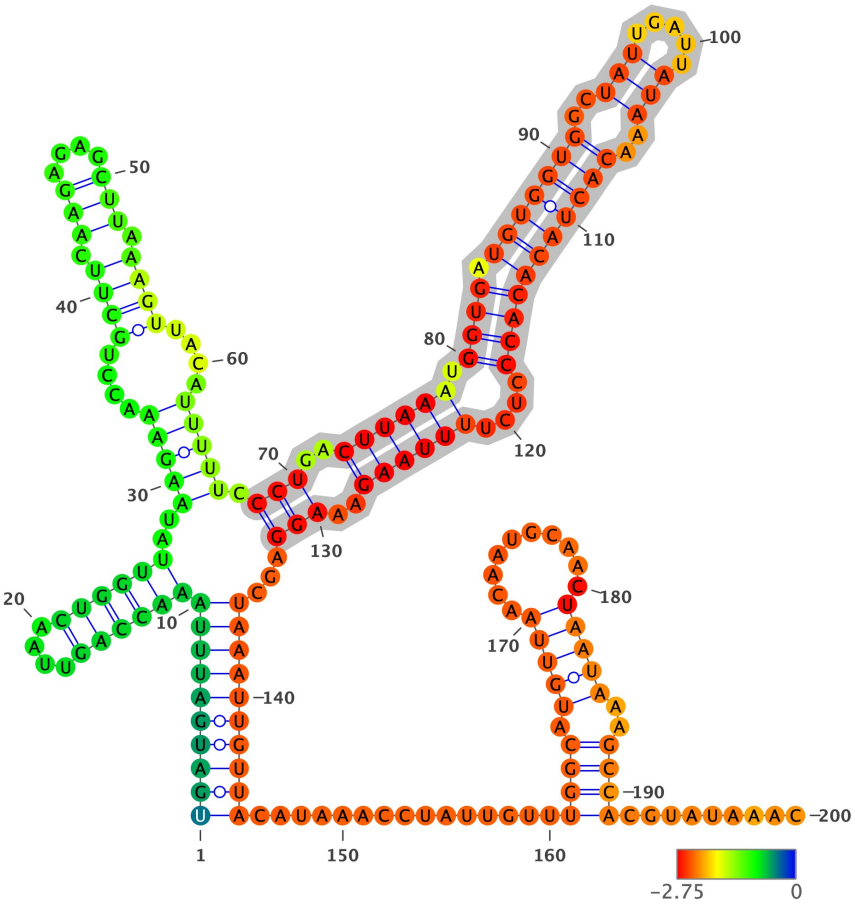
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 115 from nt 6146 to 6210 (nt 68 to 132)

```
5'-CCTGACTTAAATGGTGATGTGGTGGCTATTGATTAUAAACACUACACACCCTCTTUUAAGAAAGG-3'
5'-(((..(((((..((((.(((((((..(((.....)))..)))))))))))).....)))))..)))-3'
Motif MFE = -21.2; z-score = -4.07; ED = 1.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6079 to 6278 (motif highlighted in silver):

```
5'-UGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUA
CACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAAC-3
5'-(((((((((((((((....))))))..(((((....((((.(((....))).))))....))))).(((..((((((.((((.(((((((..(((.....)))..)))))
))))))....))))))..)))...))))))))))..............((((.(((((..........)))))..))))..........-3'
MFE = -40.5; z-score = -1.96; ED = 39.76
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

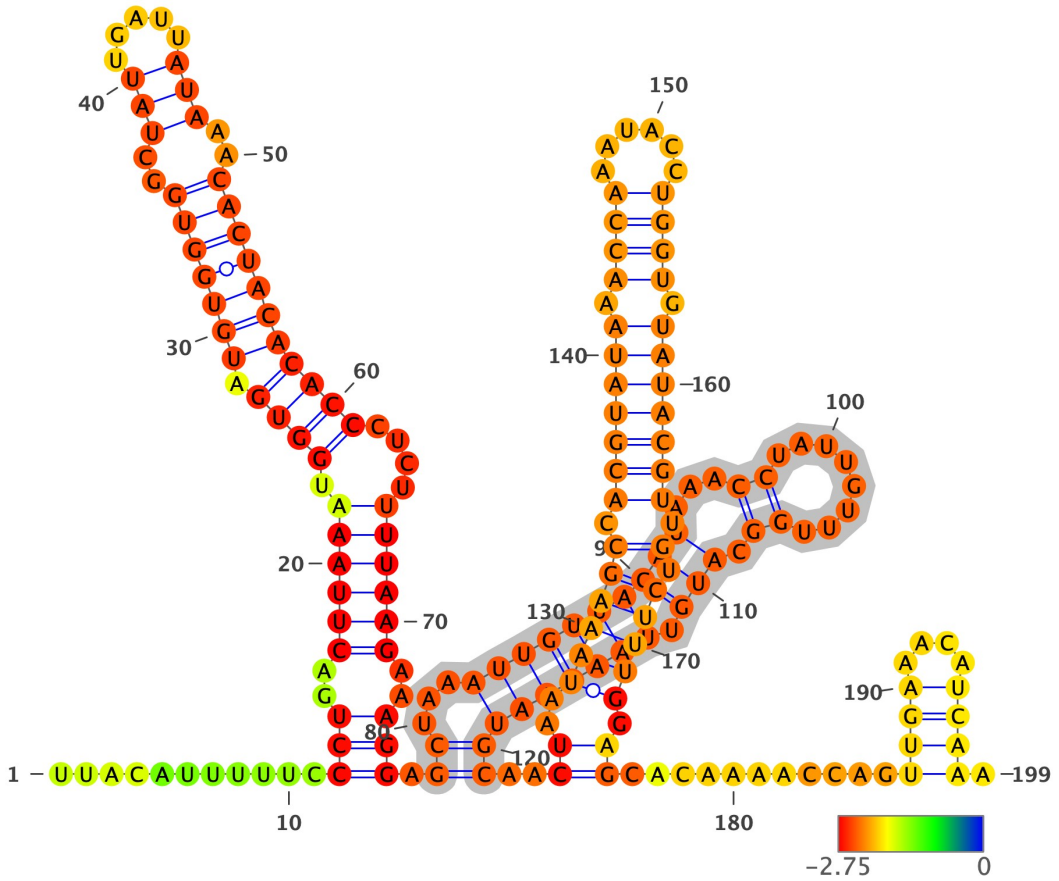
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 116 from nt 6212 to 6255 (nt 78 to 121)

```
5'-GCTAAATTGTTACATAAACCTATTGTTTGGCAUGTUAACAATGC-3'
5'-((....(((((((((....((........))..)).)))))))..))-3'
Motif MFE = -7.6; z-score = -1.18; ED = 4.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6135 to 6333 (motif highlighted in silver):

```
5'-UUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUG
UUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAA-3
5'-...........(((..(((((((.((((.(((((((..(((.....)))..)))))))))))....)))))).)))).((...((((((((((...((........)).)))
.)))))))))..((..(((((((.(((((((.((((......))))).)))))))).).)))))..))...........((((....)))).-3'
MFE = -46.5; z-score = -3.75; ED = 17.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

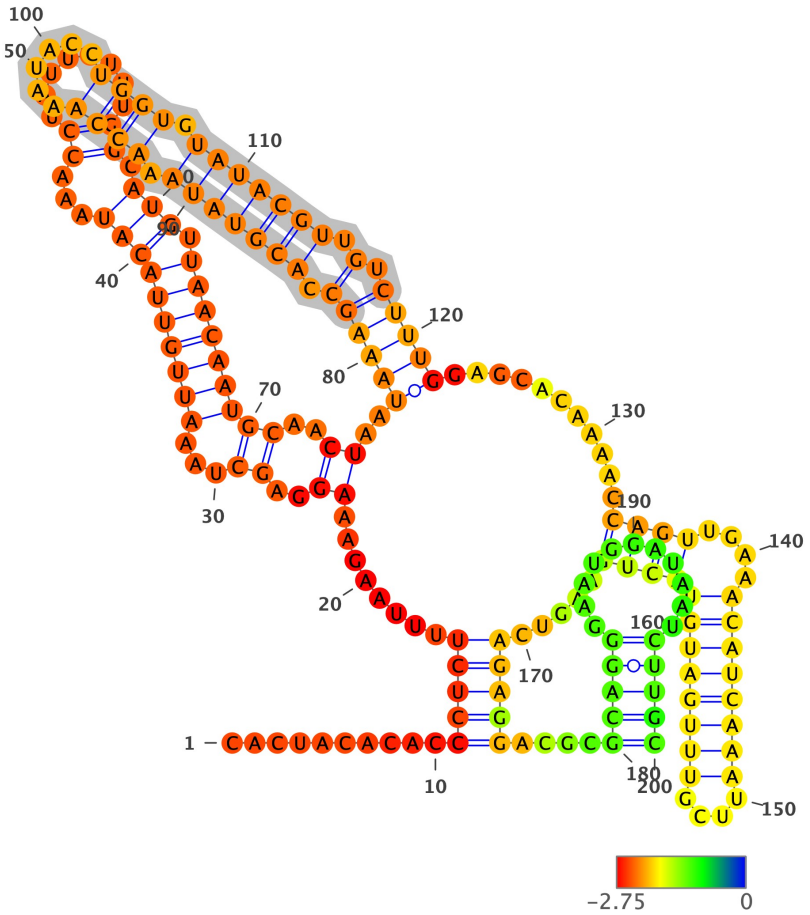
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 117 from nt 6266 to 6302 (nt 82 to 118)

```
5'-GCCACGTATAAACCAAATACCUGGUGUAUACGUTGTC-3'
5'-((.(((((((.((((......)))).))))))).).)-3'
Motif MFE = -12.2; z-score = -4.11; ED = 1.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6185 to 6384 (motif highlighted in silver):

```
5'-CACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUA
CGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGC-3
5'-..........(((((.........((..((...((((((((((...((.........)).))).)))))))))..)).((((((.(((((((.((((......)))).))))
))).).)))))...........((((....((((((((....)))))))))))).....)))))....(((((...........)))))-3'
MFE = -43.0; z-score = -1.84; ED = 31.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

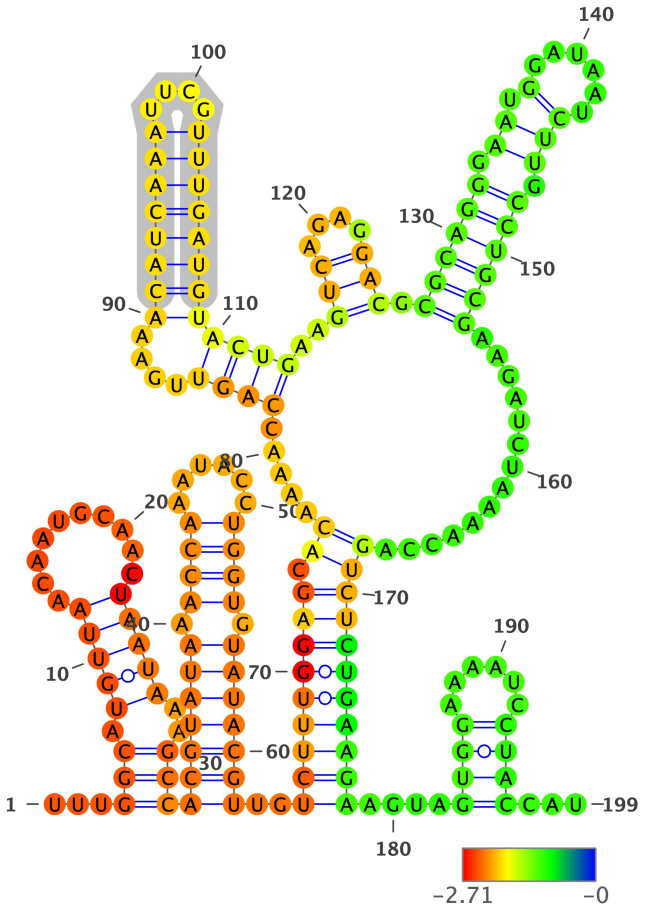
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 118 from nt 6327 to 6344 (nt 91 to 108)

```
5'-CATCAAATTCGUUUGAUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.0; z-score = -4.92; ED = 0.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6237 to 6435 (motif highlighted in silver):

```
5'-UUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUAC
UGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAU-3
5'-...(((.(((((..........)))))..)))(((((((.((((......)))).)))))))..(((((((((.((.....((((....((((((((....))))))))))
))..(((....))).((((((.((.(......))).))))))..............))))))))))....((((......))))...-3'
MFE = -50.1; z-score = -2.13; ED = 32.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

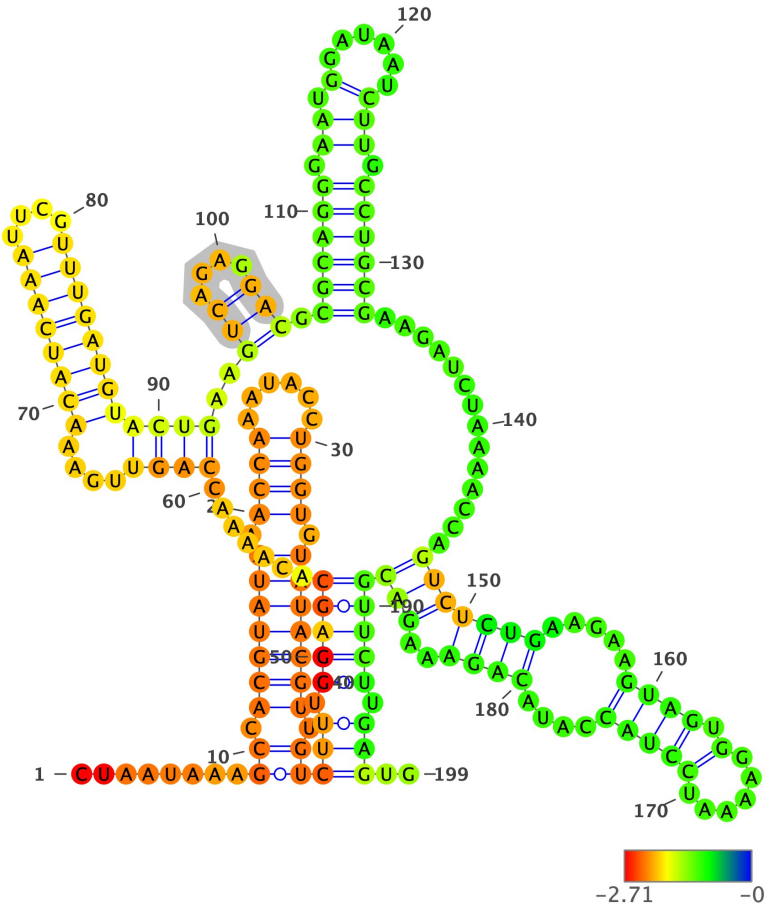
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 119 from nt 6353 to 6360 (nt 96 to 103)

```
5'-TCAGAGGA-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6258 to 6456 (motif highlighted in silver):

```
5'-CUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGG
GAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUG-3
5'-........((.(((((((.((((......)))).)))))))).))(((.(((((.......((((....((((((((....)))))))))))))..(((....))).((((((
.((.(......))).))))))..............(((((((.....((((.(......)))))....))))..)))))))).)))..-3'
MFE = -49.4; z-score = -1.8; ED = 28.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

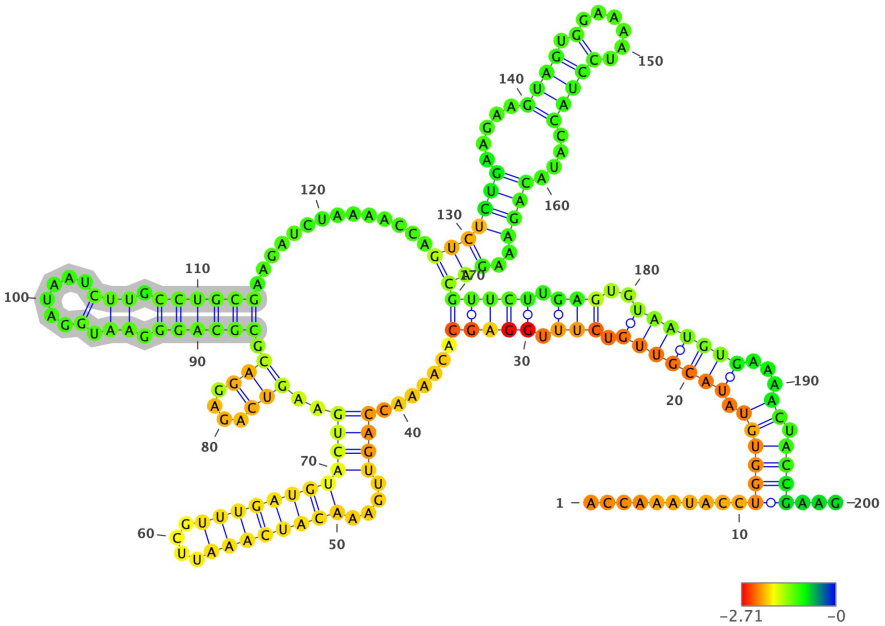
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 120 from nt 6363 to 6389 (nt 87 to 113)

```
5'-CGCAGGGAATGGATAATCUUGCCUGCG-3'
5'-((((((.((.(.....)).)))))))-3'
Motif MFE = -10.0; z-score = -2.6; ED = 3.35
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6277 to 6476 (motif highlighted in silver):

```
5'-ACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUG
CGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAG-3
5'-..........((((((.(((((((.(((.(((((.......(((((....(((((((((....)))))))))))))..(((....))).((((((.((.(.....)).))))
)).............(((((((.....((((.(.....)))))....)))))..)))))))).)))..)))))))...)).)))))...-3'
MFE = -45.8; z-score = -0.99; ED = 32.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

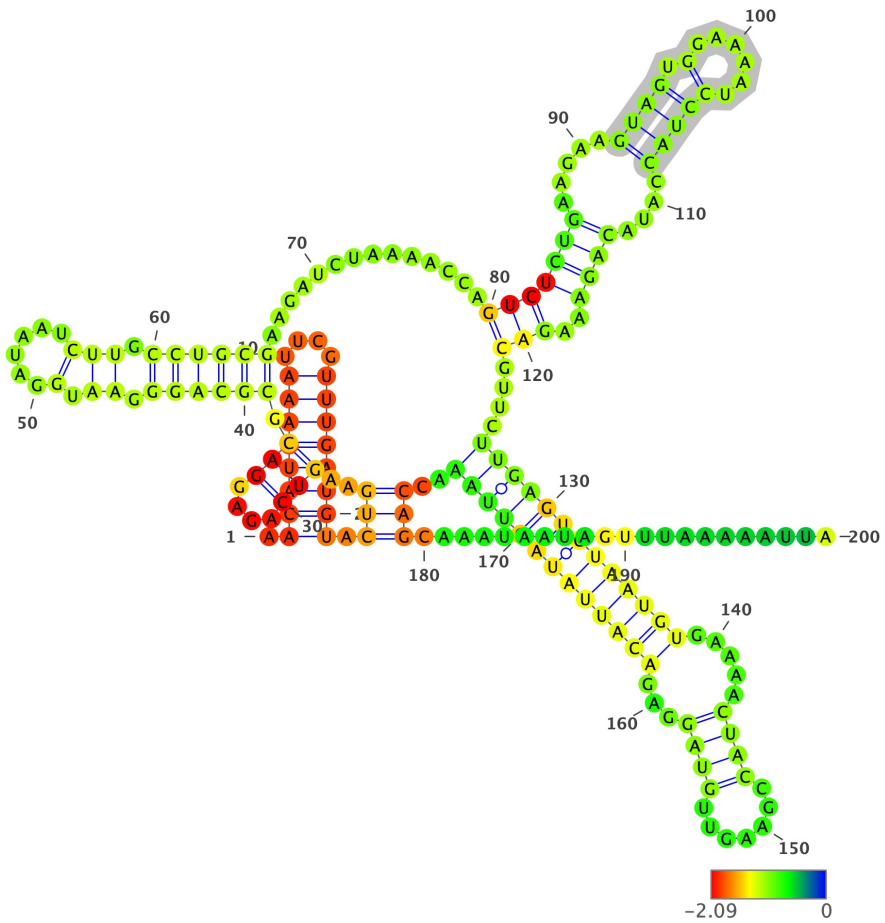
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 121 from nt 6416 to 6432 (nt 92 to 108)

```
5'-GTAGTGGAAAATCCUAC-3'
5'-(((((.........))))-3'
Motif MFE = -1.6; z-score = -1.59; ED = 5.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6325 to 6524 (motif highlighted in silver):

```
5'-AACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAU
ACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUA-3
5'-.(((((((((....)))))))).((((..((((....)))).((((((.((.(......)).)))))).............(((((((.....((((.(......)))))))...
.))))..)))....((((((((((((.....((((.......))))...)))))))))))))..)))....................-3'
MFE = -45.5; z-score = -2.56; ED = 24.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

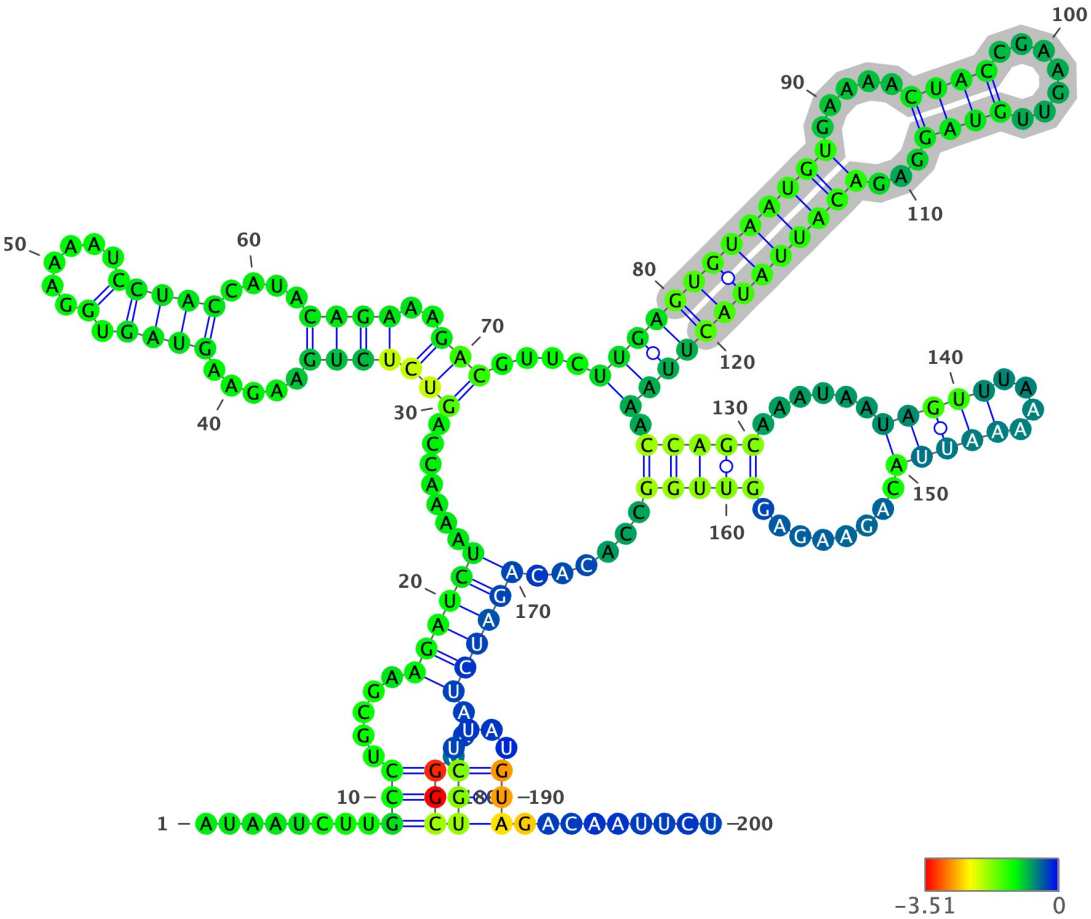
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 122 from nt 6454 to 6494 (nt 80 to 120)

```
5'-GTGTAATGTGAAAACTACCGAAGTTGUAGGAGACAUUAUAC-3'
5'-(((((((((.....((((.......))))...)))))))))-3'
Motif MFE = -10.4; z-score = -2.68; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6375 to 6574 (motif highlighted in silver):

```
5'-AUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAG
ACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCU-3
5'-........(((.....((((((.......(((((((.....((((.(......)))))....))))..)))....((((((((((((.....((((.......))))...
))))))))))))).(((((......(((((....)))))........)))))......))))))...)))(((....)))..........-3'
MFE = -37.6; z-score = -0.98; ED = 42.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

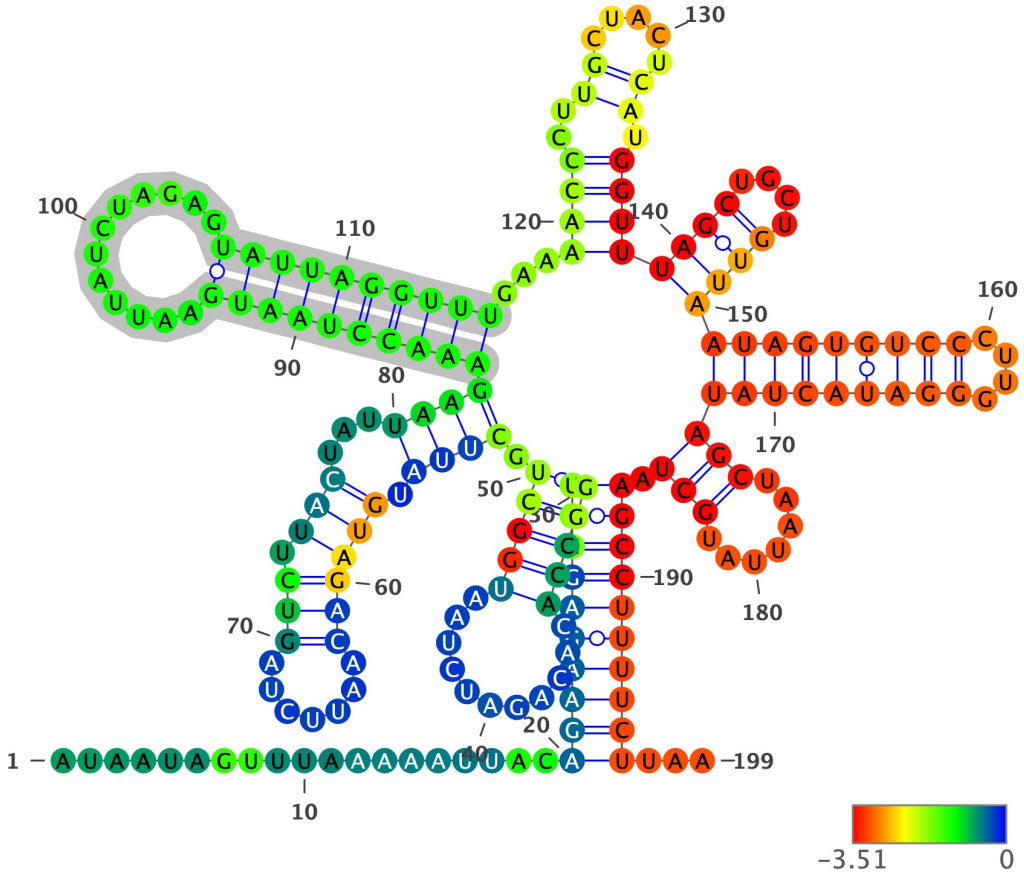
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 123 from nt 6590 to 6621 (nt 84 to 115)

```
5'-AAACCTAATGAATTATCTAGAGUAUUAGGUUU-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -6.8; z-score = -2.79; ED = 2.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6507 to 6705 (motif highlighted in silver):

```
5'-AUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAG
GUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAA-3
5'-...................(((((((((((((((.............))))).((((.((((((.......))).)))...))))((((((((((.............))))))
))))...((((..((.....)).))))((((....))))((((((((((....)))))))))(((.......))).))))))))))...-3'
MFE = -46.9; z-score = -2.34; ED = 33.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

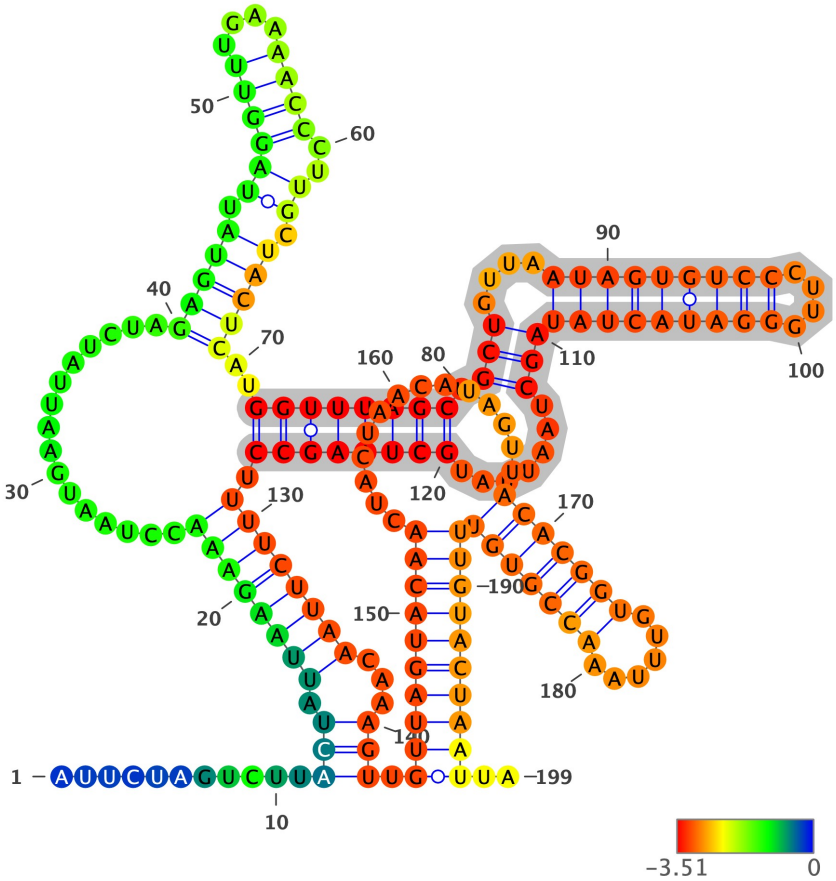
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 124 from nt 6641 to 6696 (nt 72 to 127)

```
5'-GGTTTAGCTGCTGTTAATAGTGTCCCTTGGGAUACUAUAGCTAATTATGCUAAGCC-3'
5'-((((((((.(((....((((((((((....))))))))))))).......))))))))-3'
Motif MFE = -21.7; z-score = -4.56; ED = 4.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6570 to 6768 (motif highlighted in silver):

```
5'-AUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAGGUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAG
CUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUA-3
5'-...........(((.((((((((.................(((((.((((((....))))..)).)))))..((((((((.(((....(((((((((....)))))))))))
).......))))))))).))))))))...))).((((((((((.............(((((((......)))))))))))))))))..-3'
MFE = -49.6; z-score = -4.19; ED = 39.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

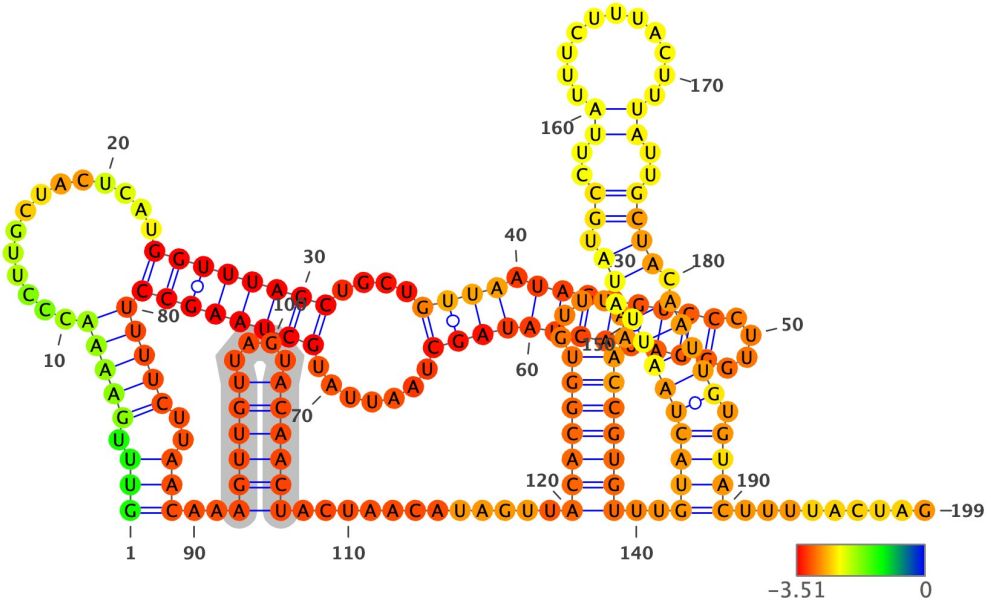
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 125 from nt 6709 to 6724 (nt 92 to 107)

```
5'-AGTTGTTAGTACAACU-3'
5'-((((((....)))))))-3'
Motif MFE = -4.3; z-score = -6.78; ED = 0.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6618 to 6816 (motif highlighted in silver):

```
5'-GUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUA
ACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAG-3
5'-(((.(((((.............(((((((....((((.(((((((((....)))))))))))).......)))))))))))))..)))..((((((....)))))))....
........(((((((......)))))))..(((((((((.((.((..((...........)).)))).)))))).))))).........-3'
MFE = -44.5; z-score = -3.1; ED = 26.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

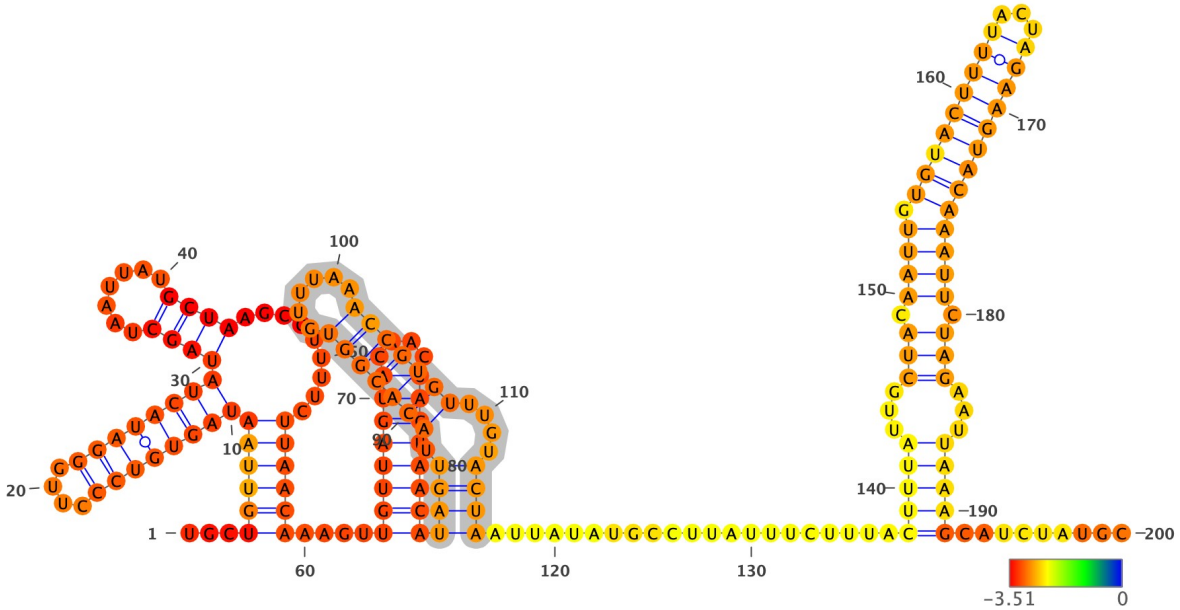
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 126 from nt 6732 to 6764 (nt 84 to 116)

```
5'-TAGTTACACGGTGTTTAAACCGUGUTTGTACUA-3'
5'-((((.(((((..........)))))....))))-3'
Motif MFE = -10.5; z-score = -2.98; ED = 3.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6649 to 6848 (motif highlighted in silver):

```
5'-UGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUG
UACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGC-3
5'-...(((((((((((((....))))))))((((.......))))........))))))....((((((((....))))))))((((.(((((((.....)))))))...
.))))....................(((((...(((.((((.((((((((((...)))))))))))))).)))...)))))).........-3'
MFE = -45.5; z-score = -3.38; ED = 30.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

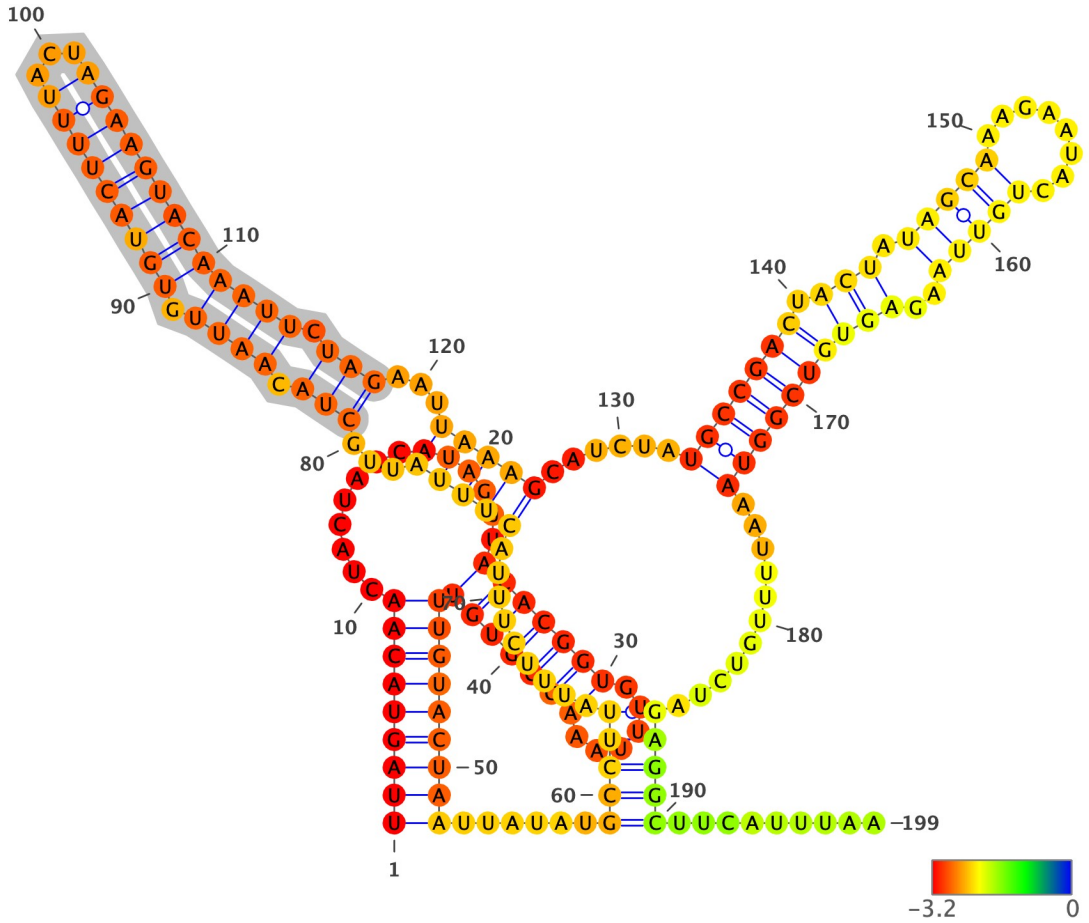
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 127 from nt 6794 to 6831 (nt 81 to 118)

```
5'-CTACAATTGTGTACTTTTACTAGAAGUACAAAUUCUAG-3'
5'-(((.(((((.((.(((((.....))))).))))))).)))-3'
Motif MFE = -8.3; z-score = -2.4; ED = 3.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6714 to 6912 (motif highlighted in silver):

```
5'-UUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAA
AUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAA-3
5'-(((((((((.............(((((((.....)))))))))))))))).....(((((.........(((((...(((.((((.((((((((...)))))))))
)))).)))...)))))).....(((((((.(((.(((((.........)))))..)))))))))).........))))).........-3'
MFE = -51.4; z-score = -5.16; ED = 11.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

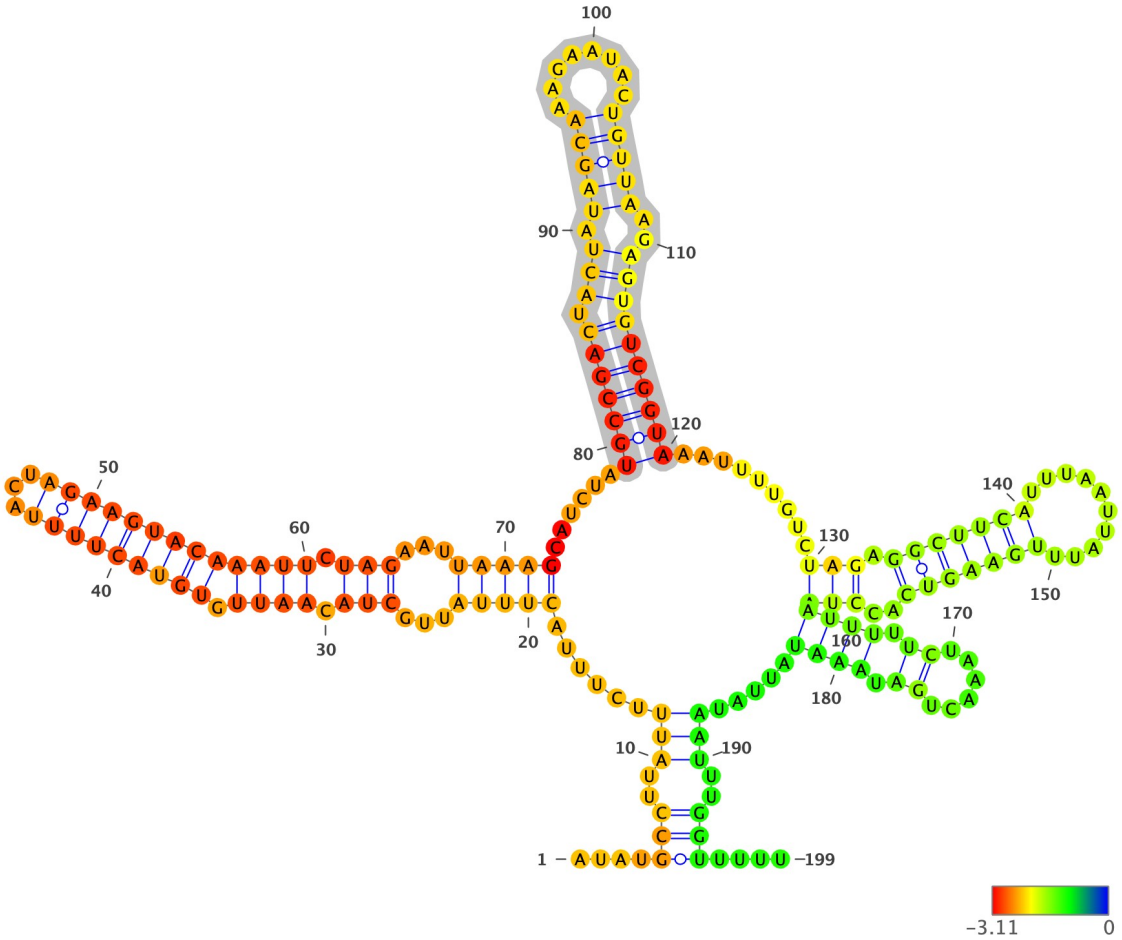
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 128 from nt 6846 to 6887 (nt 79 to 120)

```
5'-TGCCGACTACTATAGCAAAGAATACTGTTAAGAGTGUCGGUA-3'
5'-((((((.............................))))))-3'
Motif MFE = -14.8; z-score = -4.02; ED = 1.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6768 to 6966 (motif highlighted in silver):

```
5'-AUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGA
GUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUU-3
5'-....(((..(((......(((((...(((.((((.((((((((((...)))))))))))))).)))...)))))......(((((((.(((.(((((........)))))..)
))))))))).........(((.(((((((..........)))))))..)))((((.((......)).)))).....)))..)))....-3'
MFE = -40.4; z-score = -2.57; ED = 22.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

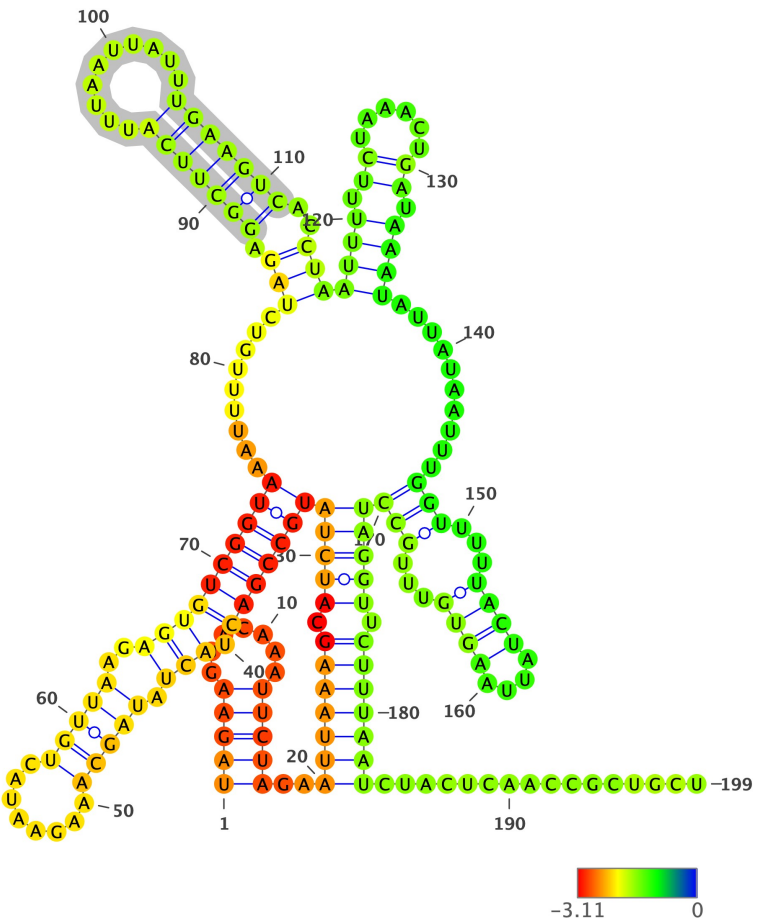
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 129 from nt 6901 to 6924 (nt 88 to 111)

```
5'-GGCTTCATTTAATTATTTGAAGUC-3'
5'-((((((............))))))-3'
Motif MFE = -6.2; z-score = -3.32; ED = 0.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6814 to 7012 (motif highlighted in silver):

```
5'-UAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUC
ACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCU-3
5'-(((((.......)))))..(((((((.(((((((((((((.(((.(((((.........)))))..))))))))))).........(((.(((((((..........)))))))
..)))((((.((......)).))))..........(((...((((....))))...)))))))).)))))))................-3'
MFE = -39.6; z-score = -1.91; ED = 45.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

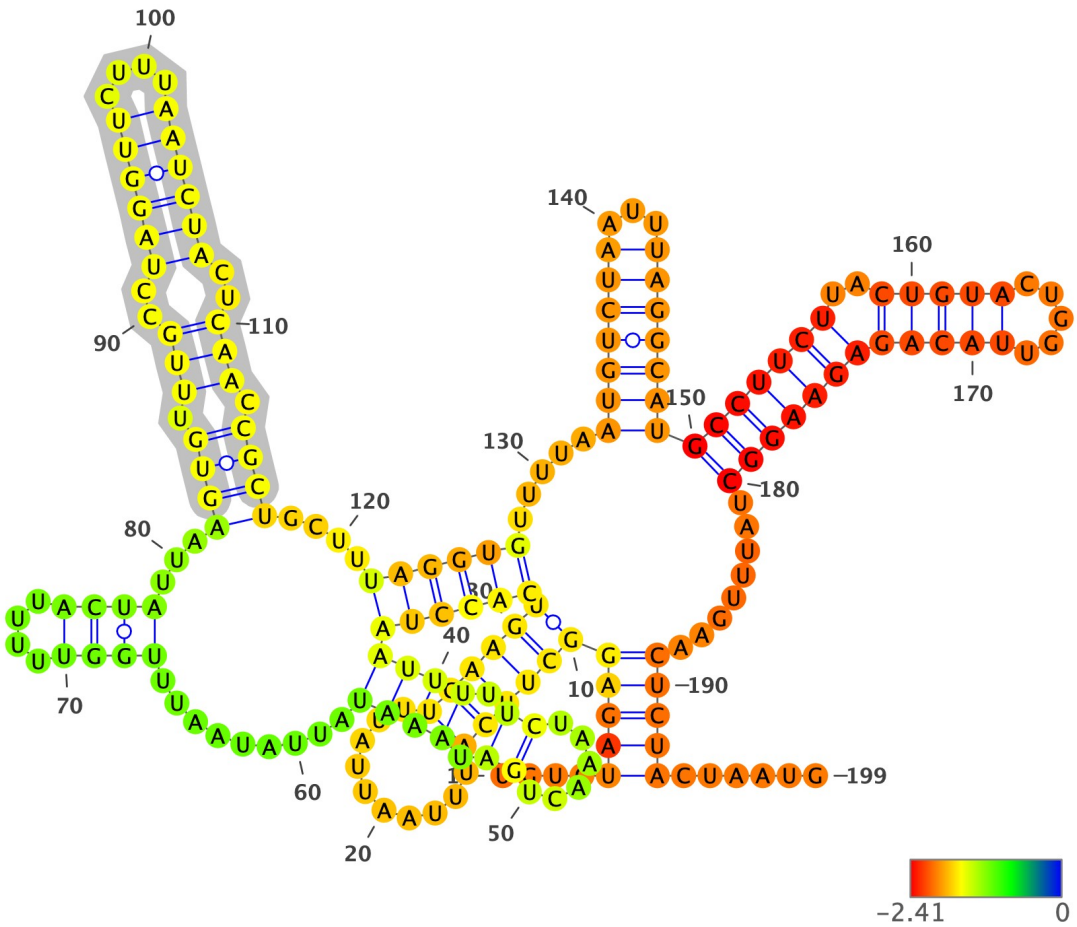
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 130 from nt 6975 to 7008 (nt 83 to 116)

```
5'-GTGTTTGCCTAGGTTCTTTAAUCUACTCAACCGC-3'
5'-(((.(((..((((((....))))))..))).)))-3'
Motif MFE = -5.6; z-score = -1.15; ED = 1.5
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6893 to 7091 (motif highlighted in silver):

```
5'-UGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCA
ACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUG-3
5'-....(((((((((((.........))))))((((((((((.((......)).))))).........((((....))))...((((.(((..((((((....))))))..))
).))))....))))))).....(((((((...)))))))(((((((..(((((.....)))))))))))).........)))))......-3'
MFE = -46.1; z-score = -3.12; ED = 19.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

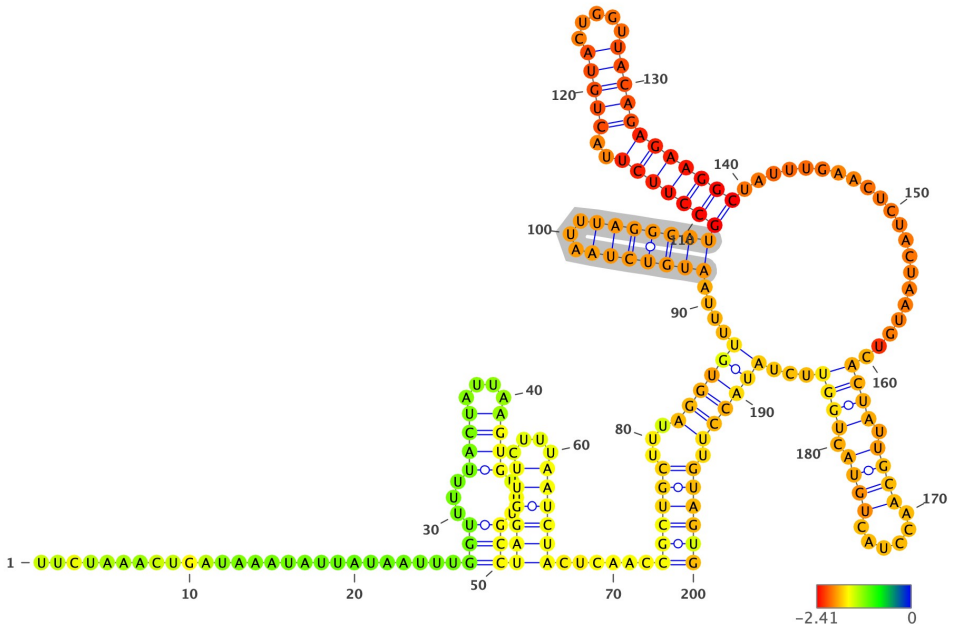
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 131 from nt 7025 to 7041 (nt 92 to 108)

```
5'-ATGTCTAATTTAGGCAU-3'
5'-((((((.....))))))-3'
Motif MFE = -4.2; z-score = -4.37; ED = 1.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6934 to 7133 (motif highlighted in silver):

```
5'-UUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCC
UUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUG-3
5'-.........................(((...((((....))))...)))((((((....))))))......((((((...((((((....(((((((...)))))))(((
((((..(((((.....)))))))))))).....................((((.((((......)))).))))...)))))).))))))-3'
MFE = -41.7; z-score = -1.98; ED = 46.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

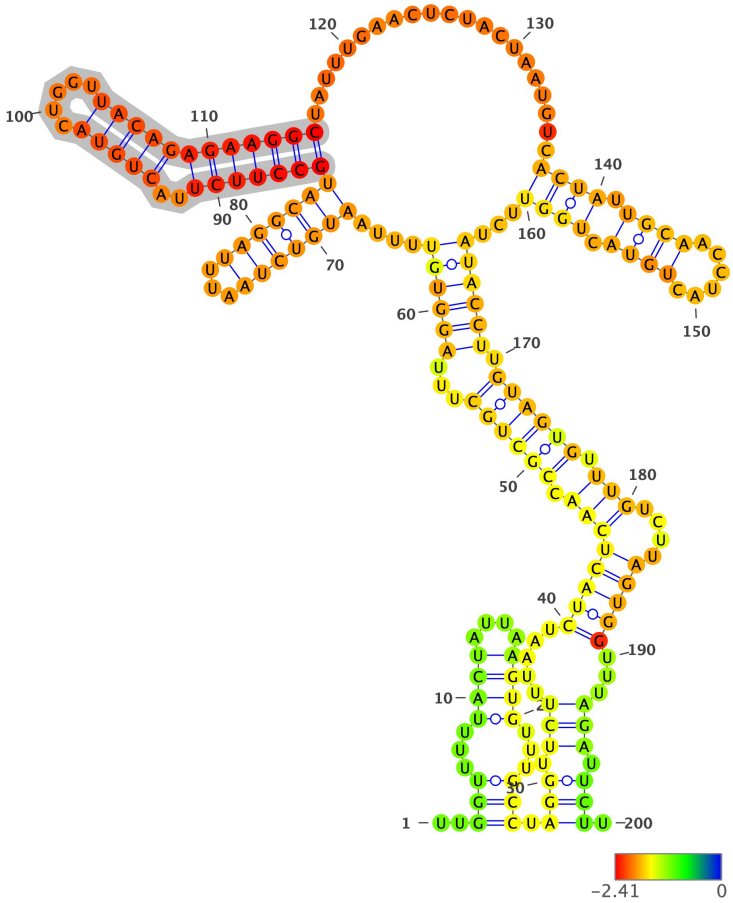
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 132 from nt 7042 to 7072 (nt 85 to 115)

```
5'-GCCTTCTTACTGTACTGGTUACAGAGAAGGC-3'
5'-(((((((..(((((.....)))))))))))-3'
Motif MFE = -13.1; z-score = -3.64; ED = 1.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 6958 to 7157 (motif highlighted in silver):

```
5'-UUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGA
AGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUU-3
5'-..(((...((((....))))...))).(((.(((.....((((((((.((((((...((((((....(((((((...)))))))(((((((..(((((.....))))))))
))))....................((((.((((......)))).))))...)))))).)))))).)))....)))))...))).))).-3'
MFE = -48.6; z-score = -2.82; ED = 48.39
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

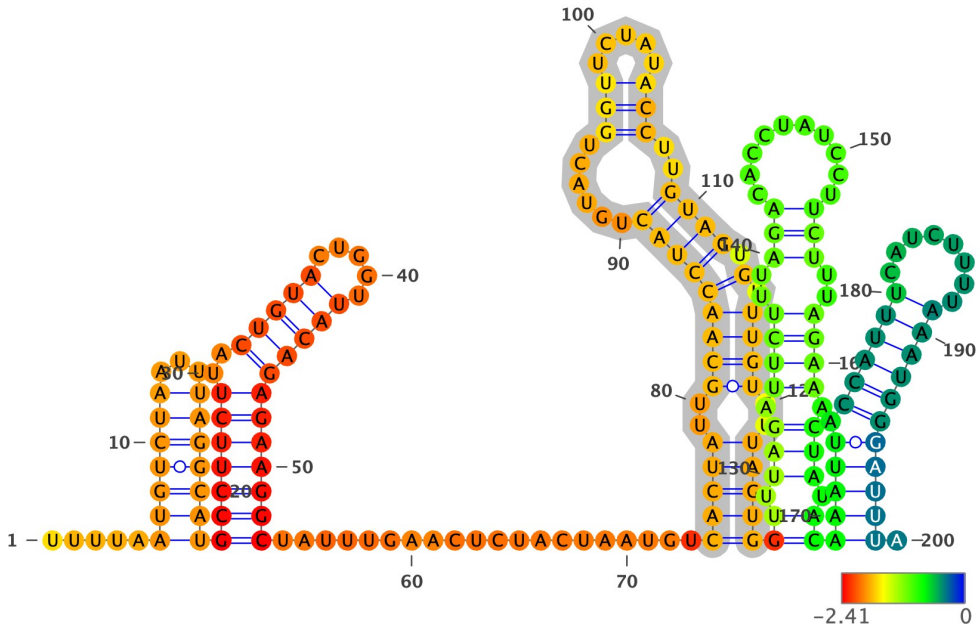
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 133 from nt 7093 to 7145 (nt 74 to 126)

```
5'-CACTATTGCAACCTACTGTACTGGTTCTATACCTTGUAGTGTUUGUCTUAGUG-3'
5'-(((((..(((((((((.................)))).).))))..)))))-3'
Motif MFE = -12.3; z-score = -2.12; ED = 8.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7020 to 7219 (motif highlighted in silver):

```
5'-UUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUA
GUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAGAAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUA-3
5'-.....(((((((...)))))))(((((((..(((((.....)))))))))))).....................(((((..(((((((((......(((.....)))..)))
).).))))..)))))((.(((.((((..(((..........)))..)))).))).))(((((.((((((........)))))))))).-3'
MFE = -45.1; z-score = -3.28; ED = 16.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

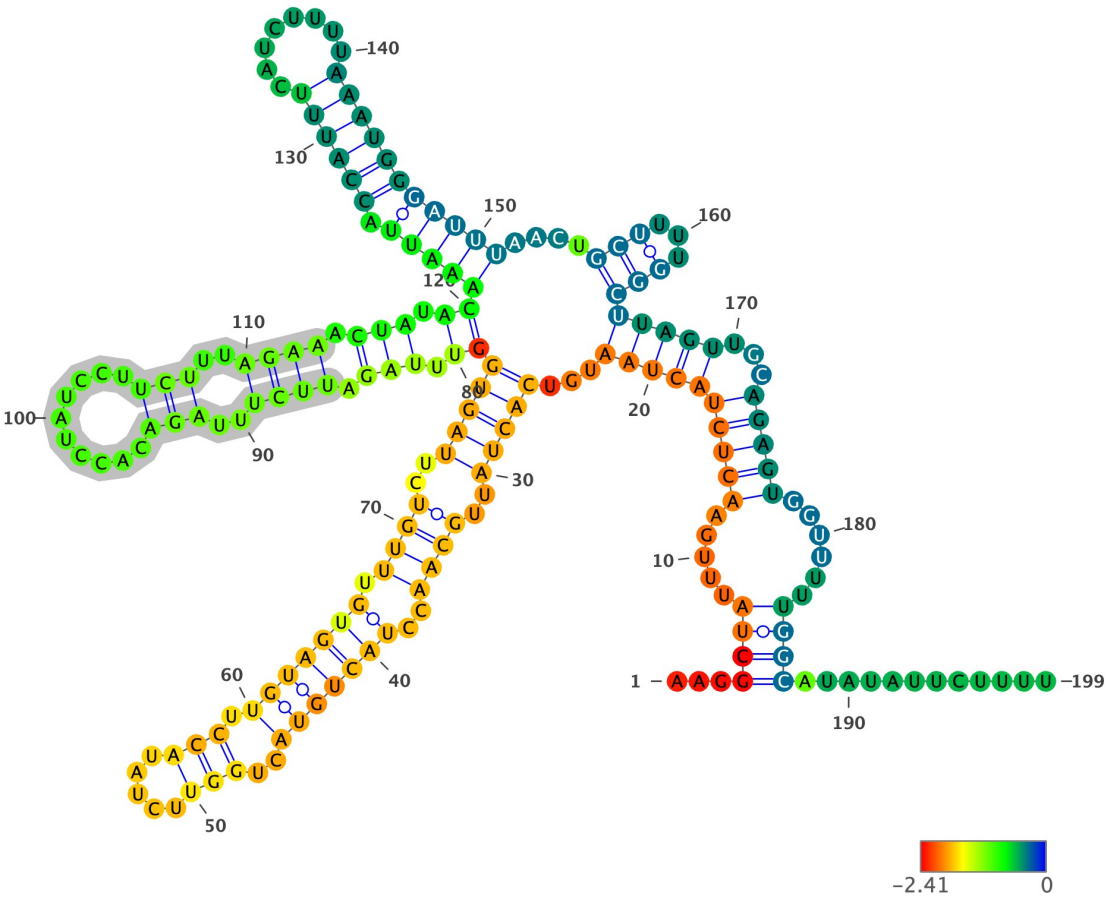
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 134 from nt 7153 to 7180 (nt 86 to 113)

```
5'-TTCTTTAGACACCTATCCTTCUTTAGAA-3'
5'-((((..((............))..))))-3'
Motif MFE = -2.1; z-score = -2.19; ED = 2.06
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7068 to 7266 (motif highlighted in silver):

```
5'-AAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAG
AAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUU-3
5'-...((((.....((((((((((...(((((..((((..(((((((..(((.....))).)))))))).))))..)))))((.(((.((((..(((..........)))..))
)).))).))(((((.((((((........)))))))))))....(((...)))))))))...)))))......))))............-3'
MFE = -37.9; z-score = -1.33; ED = 34.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

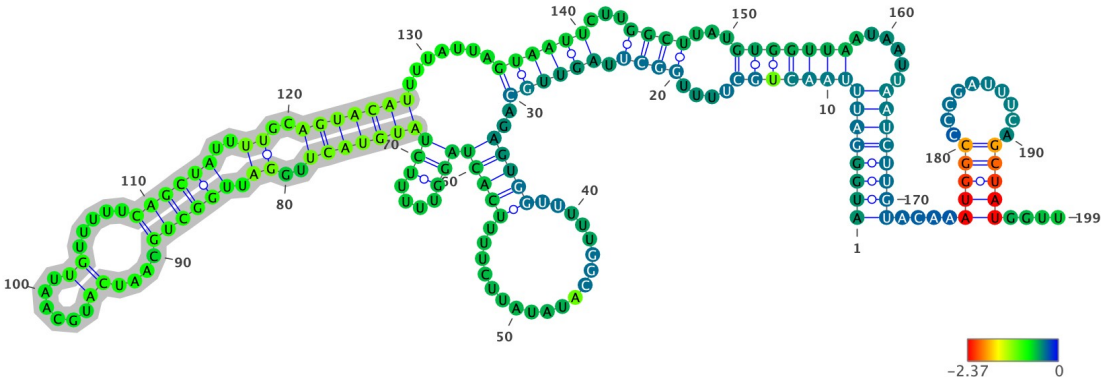
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 135 from nt 7281 to 7336 (nt 72 to 127)

```
5'-ATGTACTTGGATTGGCTGCAATCATGCAATUGTTTTTCAGCUATTUUGCAGUACAU-3'
5'-(((((((..((.................................))..)))))))-3'
Motif MFE = -14.5; z-score = -2.82; ED = 8.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7210 to 7408 (motif highlighted in silver):

```
5'-AUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUUCACUAGGUUUUUCUAUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAG
CUAUUUUGCAGUACAUUUUAUUAGUAAUUCUUGGCUUAUGUGGUUAAUAAUUAAUCUUGUACAAAUGGCCCCGAUUUCAGCUAUGGUU-3
5'-(((((((((((((((....((((.((((((..(((((.................)))))(((....)))(((((((..((.((((((....((......)).....)))
)))..))..)))))))).......))))))...))))...)))))))......))))))))....(((((..........)))))....-3'
MFE = -33.8; z-score = 0.31; ED = 64.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

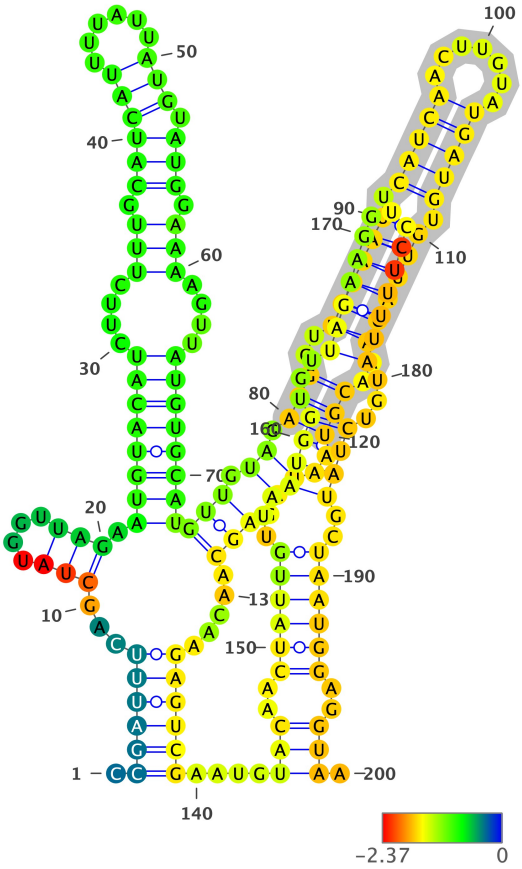
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 136 from nt 7470 to 7510 (nt 80 to 120)

```
5'-ACGGTTGTAATTCATCAACTTGTAUGAUGTGUUACAAACGU-3'
5'-(((..(((((((.(((((.......)))))).)))))))..)))-3'
Motif MFE = -13.3; z-score = -3.36; ED = 1.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7391 to 7590 (motif highlighted in silver):

```
5'-CCGAUUUCAGCUAUGGUUAGAAUGUACAUCUUCUUUGCAUCAUUUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGU
UACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAA-3
5'-.(((((((...(((....))).(((((((.....((((.(((((((.......))))))).)))).))).....)))))))))((((.((.((((..(((((((.(((((.......)))))).))
))))).))))..)).))).....)))))).....(((..(((((((...((((...(((((((...)))))))...)))))..)))))))..))).-3'
MFE = -45.4; z-score = -1.7; ED = 60.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

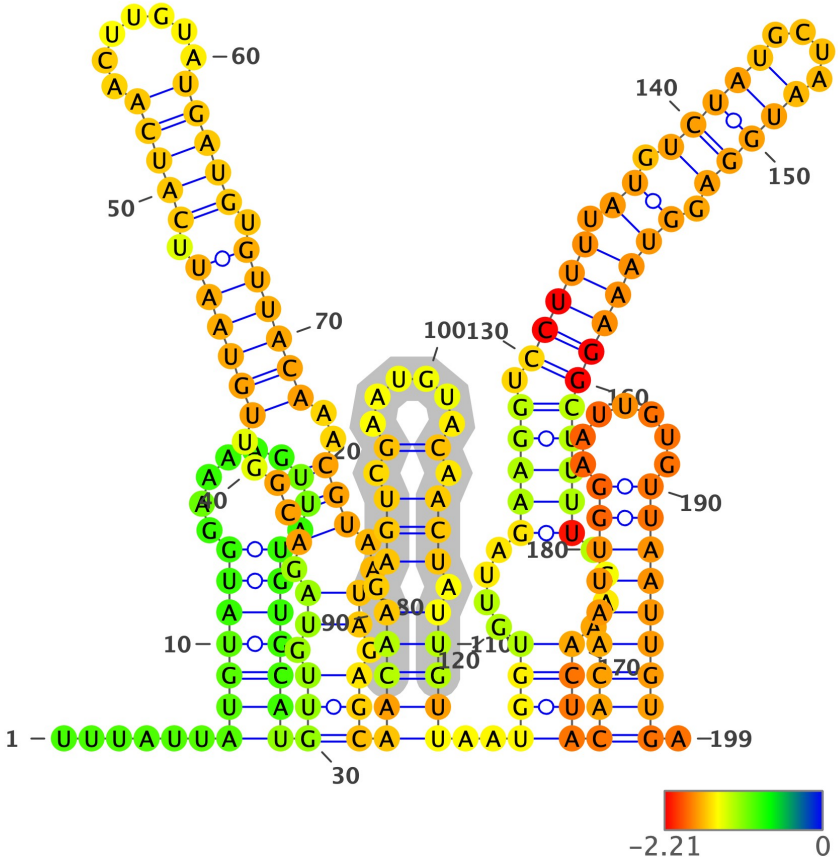
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 137 from nt 7521 to 7544 (nt 88 to 111)

```
5'-CAAGAGTCGAATGTACAACTATUG-3'
5'-((....................))-3'
Motif MFE = 0.0; z-score = 0.83; ED = 4.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7434 to 7632 (motif highlighted in silver):

```
5'-UUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUG
UUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGA-3
5'-......(((((((.........)))))))(((.((.(((..((((((.(((((.......))))).))))))..)))..)).)))(((((.(((.(......).))).)))
))..((((....(((((.(((((.((.(((((....))))).))))))))))))....))))((((((((.......)))))))).-3'
MFE = -47.5; z-score = -2.09; ED = 24.45
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

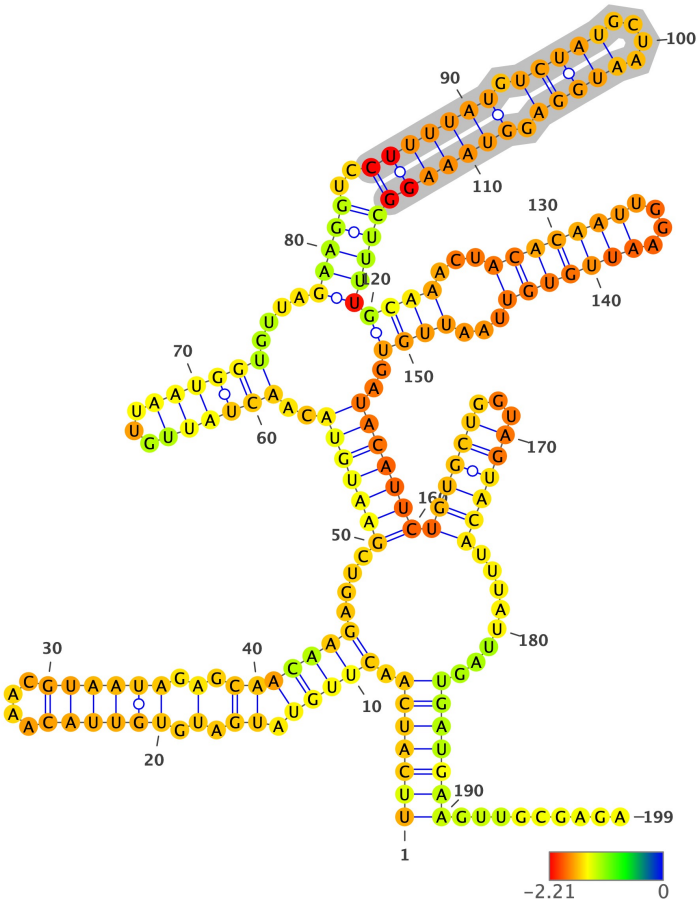
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 138 from nt 7564 to 7593 (nt 85 to 114)

```
5'-CTTTTATGTCTATGCTAAUGGAGGUAAAGG-3'
5'-(((((((.((((.....)))).)))))))-3'
Motif MFE = -10.4; z-score = -3.93; ED = 0.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7480 to 7678 (motif highlighted in silver):

```
5'-UUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAA
AGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGA-3
5'-(((((((.(((((.((.(.((((((....)))))).).)))))))....(((((((..((((((...)))))).....(((((..(((((((.(((((....))))).))))
))))))))((((...(((((((....)))))))...))))..)))))))((((((...)))))).....))))))).........-3'
MFE = -48.5; z-score = -2.51; ED = 48.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

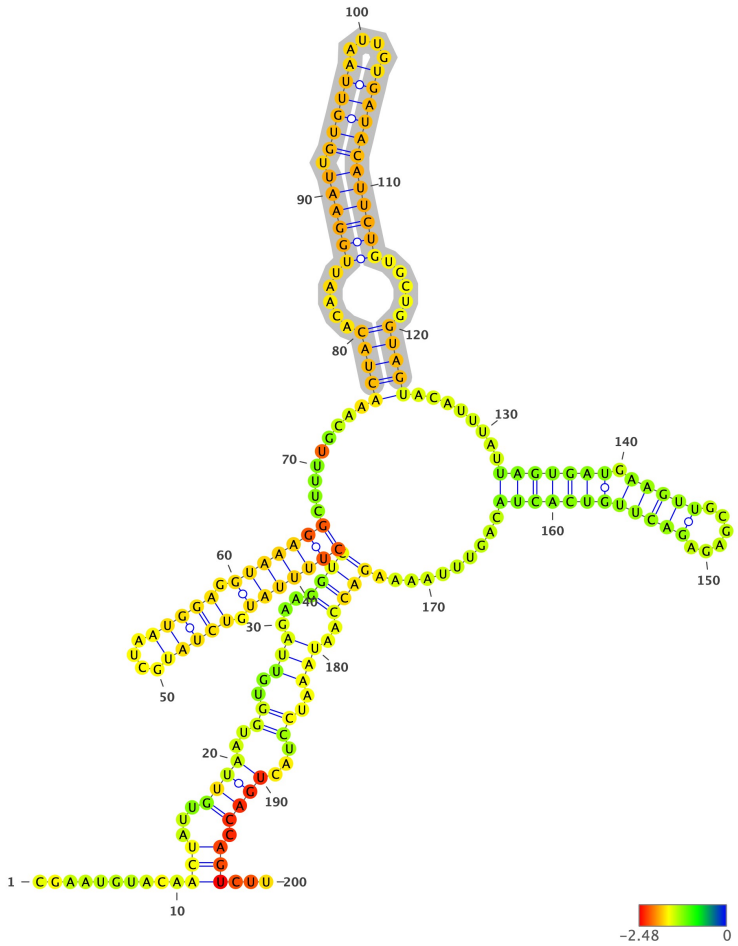
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 139 from nt 7604 to 7650 (nt 77 to 123)

```
5'-CTACACAATTGGAATTGTGTTAATTGTGAUACAUUCUGTGCTGGUAG-3'
5'-((((......(((((.(((((......)))))))))).....))))-3'
Motif MFE = -9.9; z-score = -1.58; ED = 5.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7528 to 7727 (motif highlighted in silver):

```
5'-CGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUU
CUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUU-3
5'-..........(((...((((..((..(((...(((((((((((.(((((....))))).)))))))).........(((((.....((((((.((((((....)))))))))
)))).....)))))........(((((((.(((((......))))))))))))..........))))..)))..))...)))).)))...-3'
MFE = -43.5; z-score = -2.67; ED = 49.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

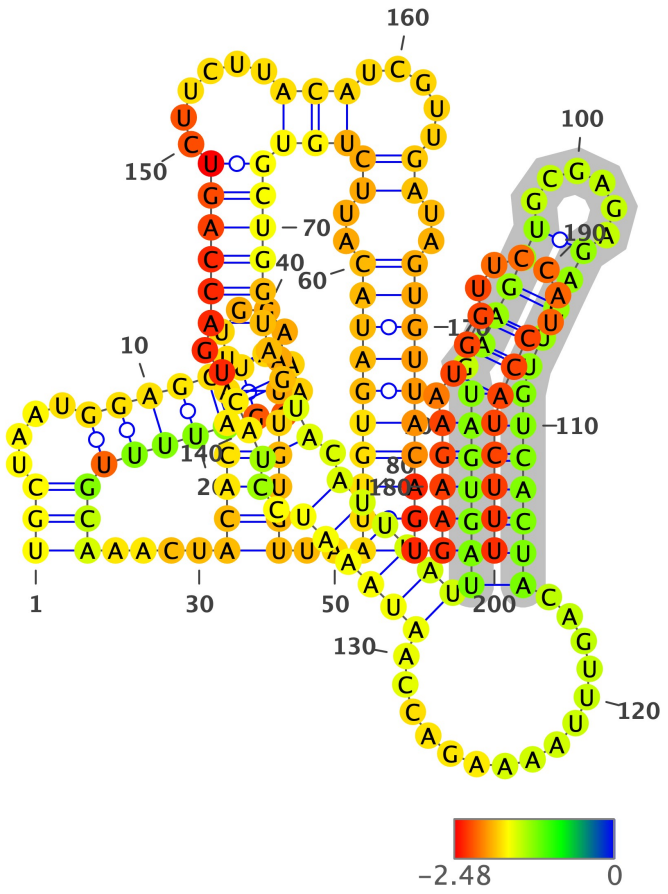
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 140 from nt 7660 to 7690 (nt 85 to 115)

```
5'-TAGTGATGAAGTTGCGAGAGACUUGUCACUA-3'
5'-(((((((.(((((.....))))))))))))-3'
Motif MFE = -10.2; z-score = -3.54; ED = 2.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7576 to 7775 (motif highlighted in silver):

```
5'-UGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUC
ACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUU-3
5'-(((....((((((....)))))))))....(((((((....)))))))..((((((((((..((((((((((((((((.((((((((((((((.(((((.....))))))))
))))...............))))))..)))).))))))......)))).....))..))))))))))(((((.(((.....))))))))-3'
MFE = -44.5; z-score = -1.6; ED = 55.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

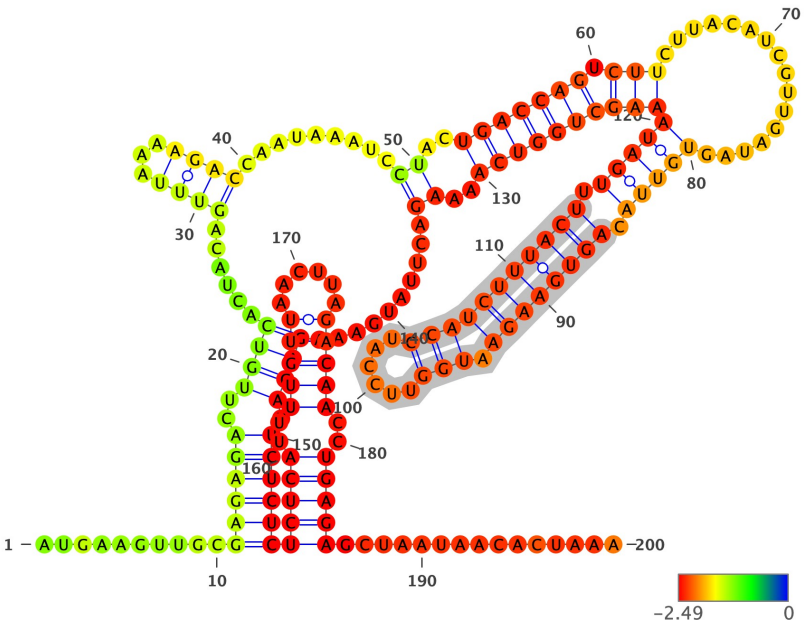
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 141 from nt 7750 to 7778 (nt 86 to 114)

```
5'-AGTGAAGAATGGTTCCATCCAUCUUUACU-3'
5'-((((((((.(((......)))))))))))-3'
Motif MFE = -10.4; z-score = -4.09; ED = 1.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7665 to 7864 (motif highlighted in silver):

```
5'-AUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUU
ACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAA-3
5'-..........((((((..((((......((((...))))..........((..(((((((.(((................(((((.((((((((.(((......))))))))
))).))))))))))))))..)).........))))).))))))(((((..(((((......)))))..)))))................-3'
MFE = -44.4; z-score = -2.65; ED = 44.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

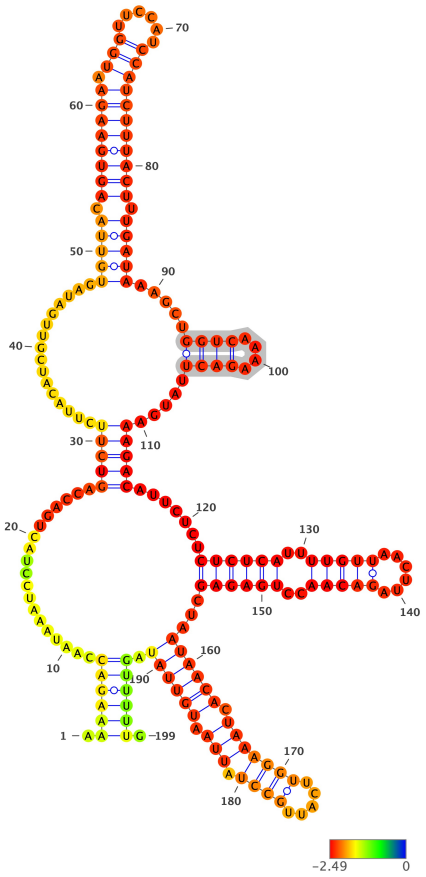
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 142 from nt 7790 to 7801 (nt 94 to 105)

```
5'-GGTCAAAAGACU-3'
5'-((((....))))-3'
Motif MFE = -2.1; z-score = -5.74; ED = 0.57
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7697 to 7895 (motif highlighted in silver):

```
5'-AAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAA
AGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUG-3
5'-.((((((.....................(((((.................(((((.((((((((.(((.......)))))))))))).)))))).....((((....)))).....)
))))).......((((((..(((((......)))))..))))))...((((((.(((((((.....)))).))).)))))).)))))).-3'
MFE = -40.5; z-score = -3.15; ED = 26.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

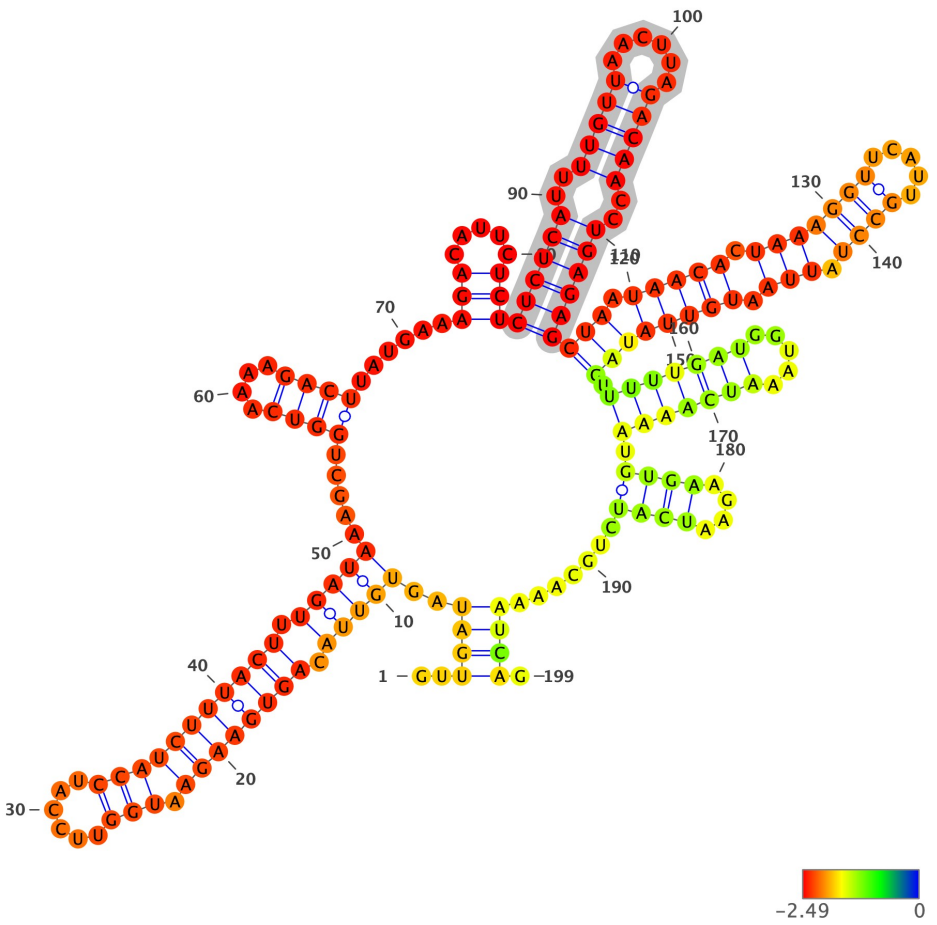
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 143 from nt 7819 to 7850 (nt 84 to 115)

```
5'-CTCTCATTTTGTTAACTTAGACAACCUGAGAG-3'
5'-((((((..(((..........)))..))))))-3'
Motif MFE = -10.3; z-score = -3.56; ED = 0.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7736 to 7934 (motif highlighted in silver):

```
5'-GUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUG
AGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAG-3
5'-..((((..(((((.((((((((.(((......)))))))))))).))))).....((((....))))......(((.....)))((((((..(((((......)))))..))
))))(((.(((((.(((((((.....)))).))).)))))))).(((((((.....)))))))).((((....))))........)))).-3'
MFE = -44.9; z-score = -2.67; ED = 30.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

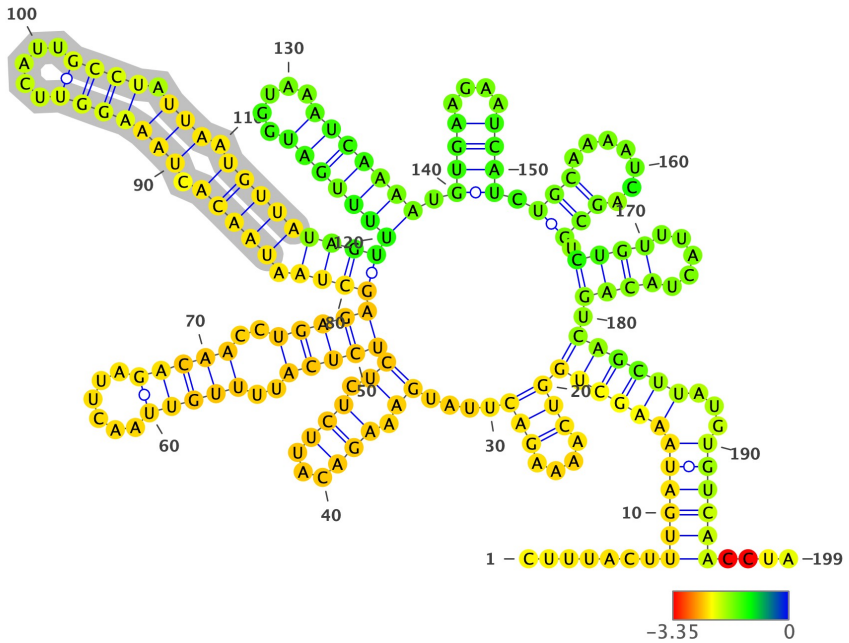
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 144 from nt 7855 to 7886 (nt 84 to 115)

```
5'-TAACACTAAAGGTTCATTGCCUAUUAAUGUUA-3'
5'-(((((.(((((((.....)))).))).)))))-3'
Motif MFE = -6.5; z-score = -2.79; ED = 1.37
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7772 to 7970 (motif highlighted in silver):

```
5'-CUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAU
GUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUA-3
5'-.......((((((((((((((....)))....((.(((...))).))(((((..(((((......)))))..)))))((((.(((((.(((((((.....)))).))).)
))))))))(((((((.....))))))).((((....)))).(((.......))).((((.....)))).))))))...))))))....-3'
MFE = -43.5; z-score = -2.43; ED = 28.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

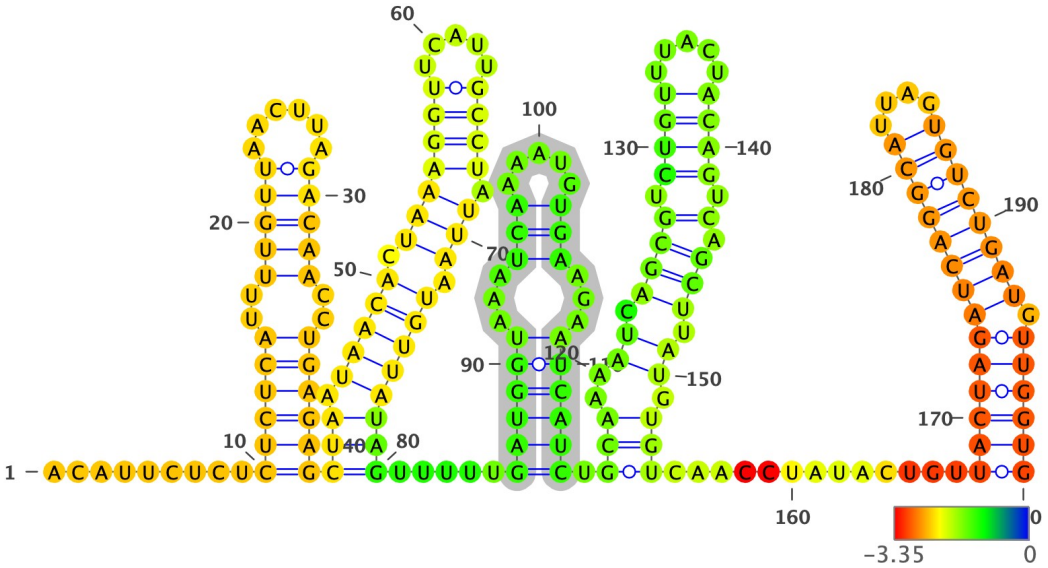
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 145 from nt 7895 to 7923 (nt 86 to 114)

```
5'-GATGGTAAATCAAAATGUGAAGAAUCAUC-3'
5'-(((((....(((.....)))....)))))-3'
Motif MFE = -4.2; z-score = -2.14; ED = 1.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7810 to 8009 (motif highlighted in silver):

```
5'-ACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUC
AUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUG-3
5'-.........((((((..(((((......)))))..)))))))(((.(((((.(((((((.....)))).))).)).)))))))).....((((((...(((.....)))...)))
))).(((..((.((((.((((.....)))).).))).)).))).............((((((((((((....)))))))).)))))-3'
MFE = -44.9; z-score = -2.25; ED = 19.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

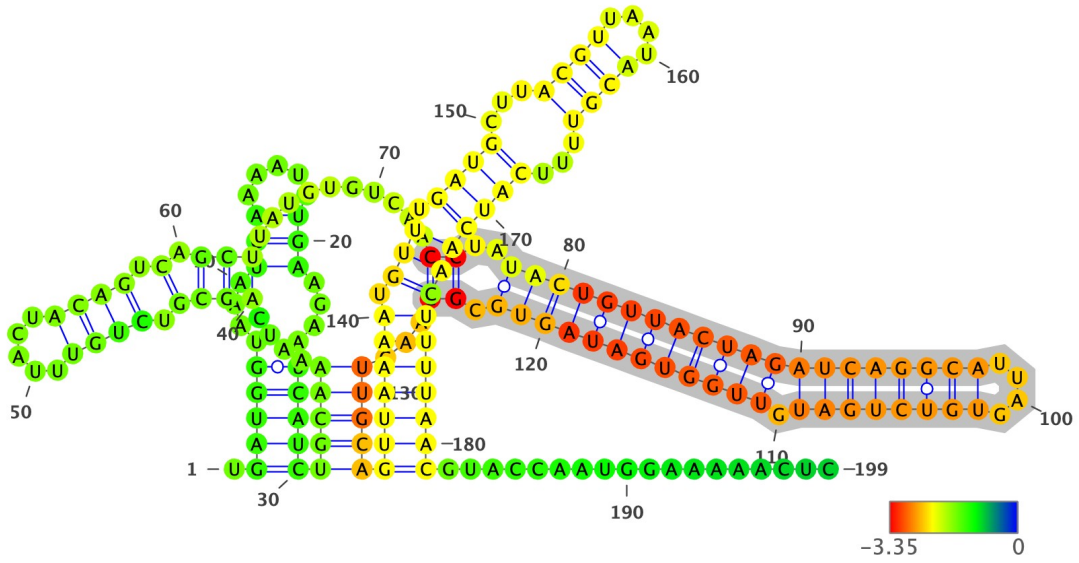
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 146 from nt 7967 to 8018 (nt 74 to 125)

```
5'-CCTATACTGTTACTAGATCAGGCATTAGUGUCUGAUGUUGGUGAUAGTGCGG-3'
5'-((.....(((((((((((((((((....)))))))).))))))))....))-3'
Motif MFE = -22.2; z-score = -4.27; ED = 3.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7894 to 8092 (motif highlighted in silver):

```
5'-UGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGU
UGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUC-3
5'-.((((((...(((.....)))...))))))(((((....((((.((((.....)))).).))).........((..((((((((((((((((((....)))))))).)
))))))))))).))...)))))(((((((.(((.((((...((((....))))...))))))))))))))).................-3'
MFE = -51.4; z-score = -2.86; ED = 23.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

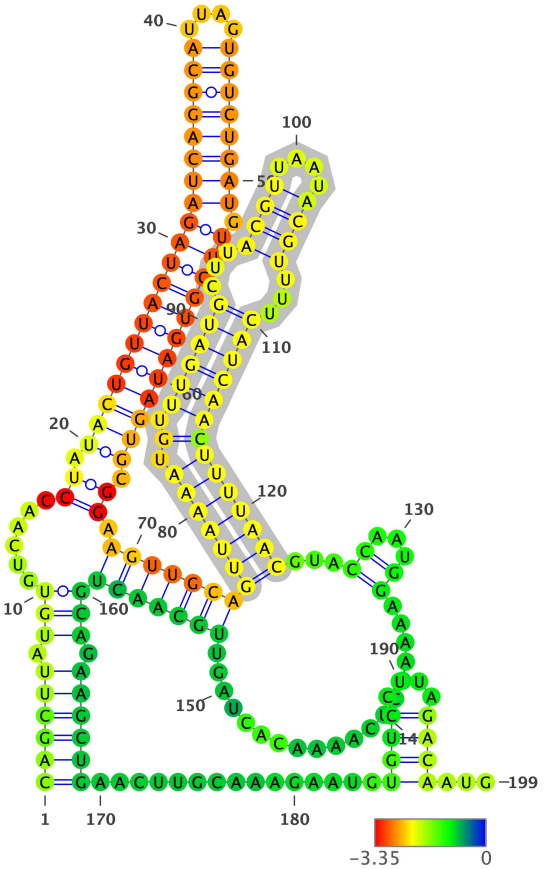
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 147 from nt 8027 to 8074 (nt 76 to 123)

```
5'-GTTAAAATGTTTGATGCTTACGTTAATACGUTTTCAUCAACUUUUAAC-3'
5'-(((((((...((((((...(((......)))...)))))).)))))))-3'
Motif MFE = -12.4; z-score = -3.98; ED = 2.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7952 to 8150 (motif highlighted in silver):

```
5'-CAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCA
UCAACUUUUAACGUACCAAUGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUG-3
5'-((((((.(((......((.((((((((((((((((((((....))))))))).))))))))))))).)).((((((((((((((.(.((((((...((((....))))...))
))))))))))))...((...))...................))))))))))).))))))...............((((....))))...-3'
MFE = -54.0; z-score = -3.17; ED = 17.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

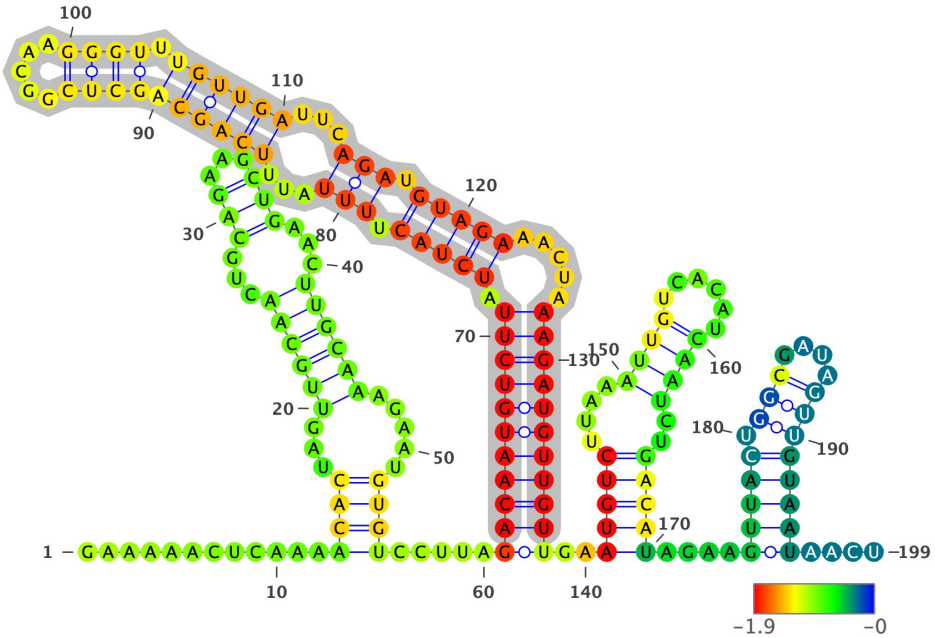
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 148 from nt 8145 to 8220 (nt 62 to 137)

```
5'-ACAATGTCTTATCTACTTTTATTTCAGCAGCTCGGCAAGGGUTTGUUGATTCAGATGUAGAAACTAAAGAUGUUGU-3'
5'-((((((((((.(((((.(((...(((((.((((.....))))..)))))...))).)))))).....))))))))))-3'
Motif MFE = -22.3; z-score = -3.35; ED = 5.97
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8084 to 8282 (motif highlighted in silver):

```
5'-GAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAU
UCAGAUGUAGAAACUAAAGAUGUUGUUGAAUGUCUUAAAUUGUCACAUCAAUCUGACAUAGAAGUUACUGGCGAUAGUUGUAAUAACU-3
5'-............((((...((((((...(((...)))...))))))).....)))).....((((((((((.(((((.(((...((((((((((.....)))).)))))).
..))).)))))).....))))))))))..(((((....((((......)))).))))).....(((((.(((....))))))))....-3'
MFE = -43.2; z-score = -2.0; ED = 39.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

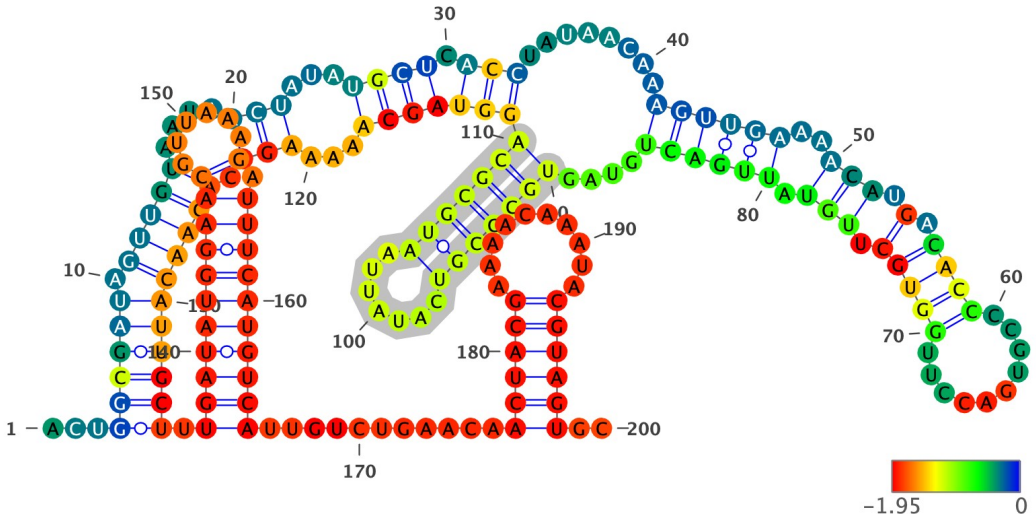
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 149 from nt 8350 to 8370 (nt 90 to 110)

```
5'-TGCGCGTCATATTAAUGCGCA-3'
5'-(((((((.......)))))))-3'
Motif MFE = -7.8; z-score = -3.37; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8261 to 8460 (motif highlighted in silver):

```
5'-ACUGGCGAUAGUUGUAAUAACUAUAUGCUCACCUAUAACAAAGUUGAAAACAUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAG
GUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGC-3
5'-...((((((.(((((....(((...((((.(((........((((((..(((.(.((((..........))))).))).))))))....(((((((.......))))))))
))))))...))).))))))))))).((((((((((.......).))))))))))...........((((((..........))))))..-3'
MFE = -47.6; z-score = -2.34; ED = 11.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

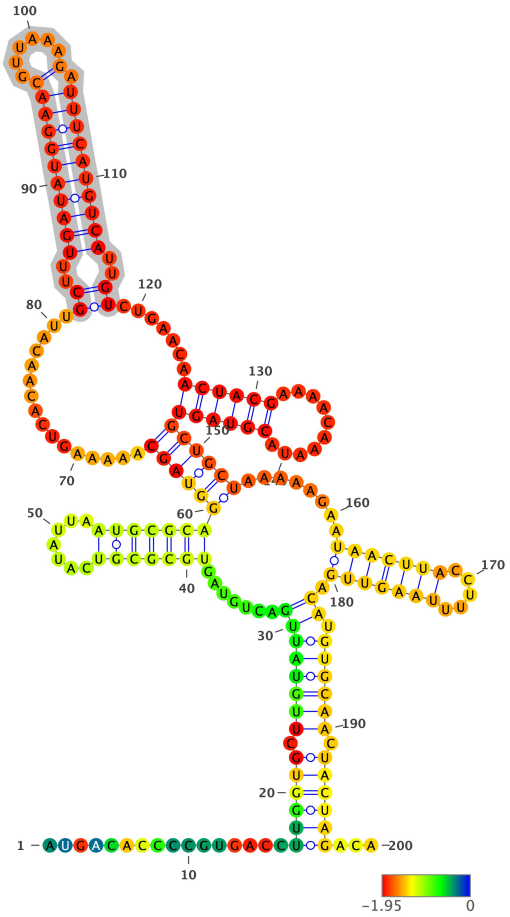
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 150 from nt 8393 to 8429 (nt 82 to 118)

```
5'-GCTTTGATATGGAACGTTAAAGAUUUCAUGUCATTGU-3'
5'-((..((((((((((.........))))))))))..))-3'
Motif MFE = -11.0; z-score = -3.54; ED = 1.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8312 to 8511 (motif highlighted in silver):

```
5'-AUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUG
UCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACA-3
5'-................((((((.((((((((.......(((((((.......)))))))((((((.................((..((((((((((.....).)))))))
)))..))).......((((((..........))))))))))))........(((((((.....)))))))).)).)))))).))))))...-3'
MFE = -42.4; z-score = -0.72; ED = 44.0
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

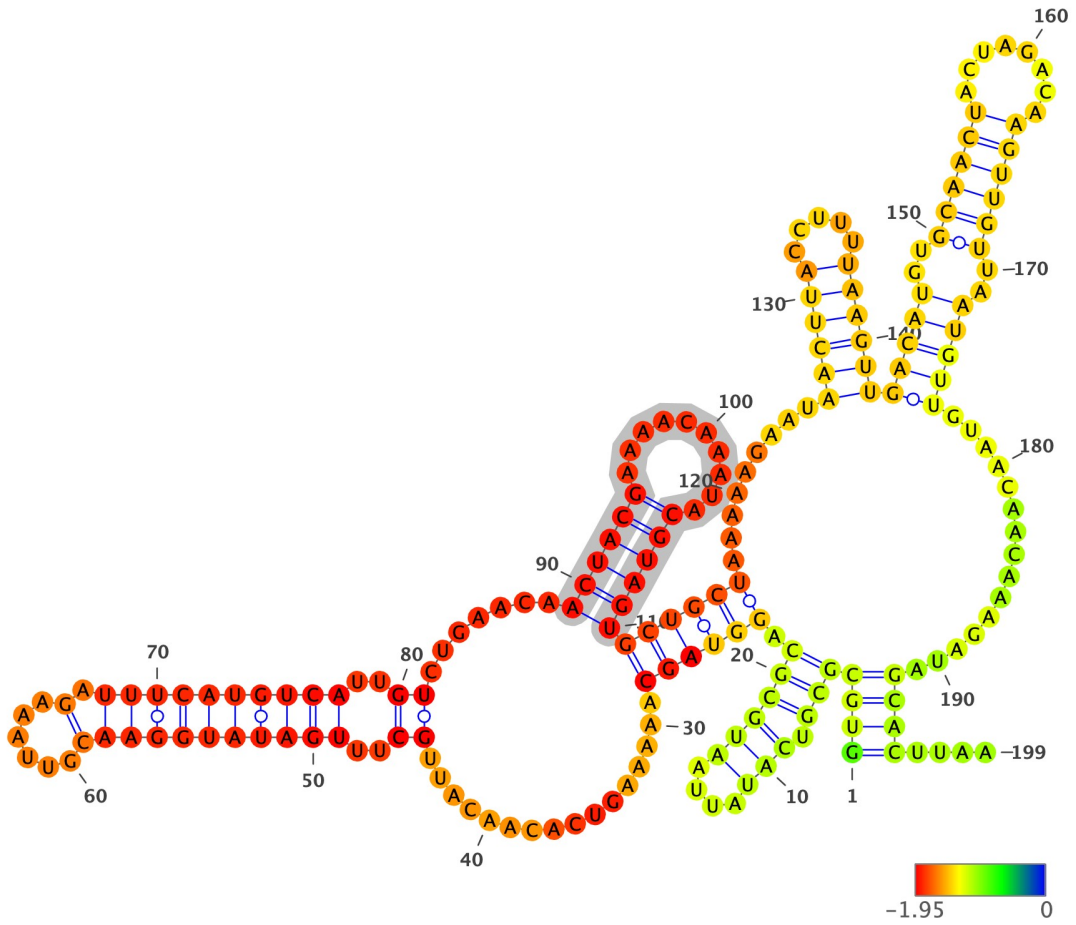
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 151 from nt 8437 to 8458 (nt 89 to 110)

```
5'-ACTACGAAAACAAATACGUAGU-3'
5'-((((((..........))))))-3'
Motif MFE = -4.3; z-score = -5.92; ED = 0.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8349 to 8547 (motif highlighted in silver):

```
5'-GUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUG
CUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAA-3
5'-(((((((.(((....)))))).((((((................((..((((((((((.......).))))))))))..)).......((((((..........)))))))
)))))).........((((((.....))))))(((((..((((((........))))))..)))))...............))))....-3'
MFE = -46.2; z-score = -3.34; ED = 37.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

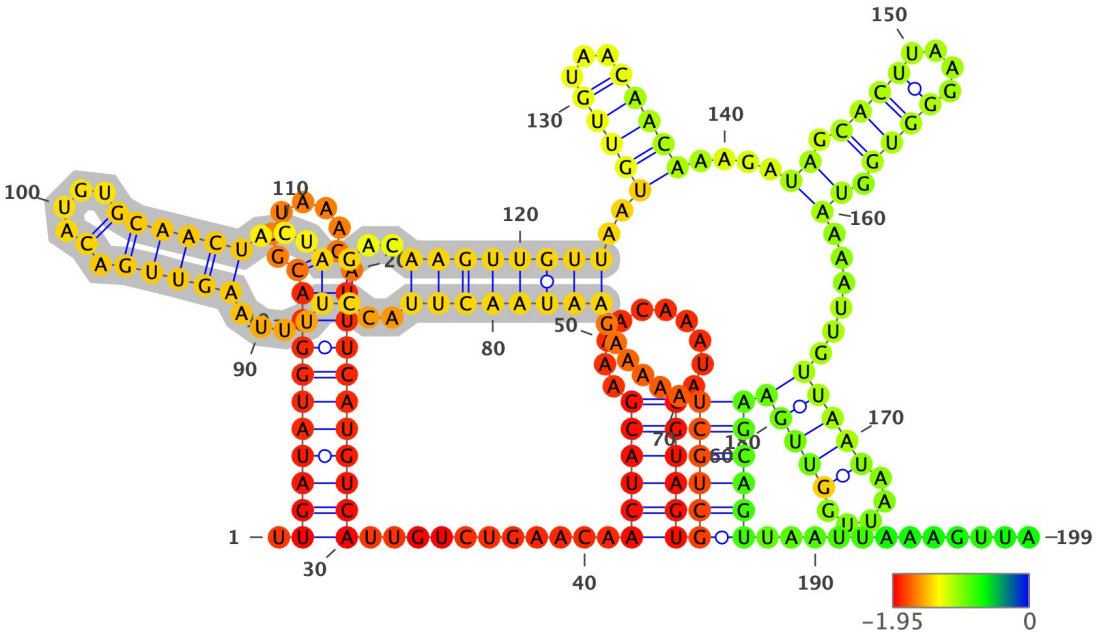
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 152 from nt 8471 to 8518 (nt 76 to 123)

```
5'-AATAACTTACCTTTTAAGTTGACATGTGCAACUACTAGACAAGUUGUU-3'
5'-((((((((..((....(((((.......)))))...))..))))))))-3'
Motif MFE = -8.5; z-score = -1.72; ED = 5.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8396 to 8594 (motif highlighted in silver):

```
5'-UUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACU
AGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAAUUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUA-3
5'-.(((((((((((......).))))))))))...........((((((..........))))))((((((......((((((((..((....(((((.(....))))))...
))..))))))))..(((((...)))))....((.((((....)))).))......(((((.....)))))))))))).............-3'
MFE = -38.3; z-score = -1.99; ED = 25.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

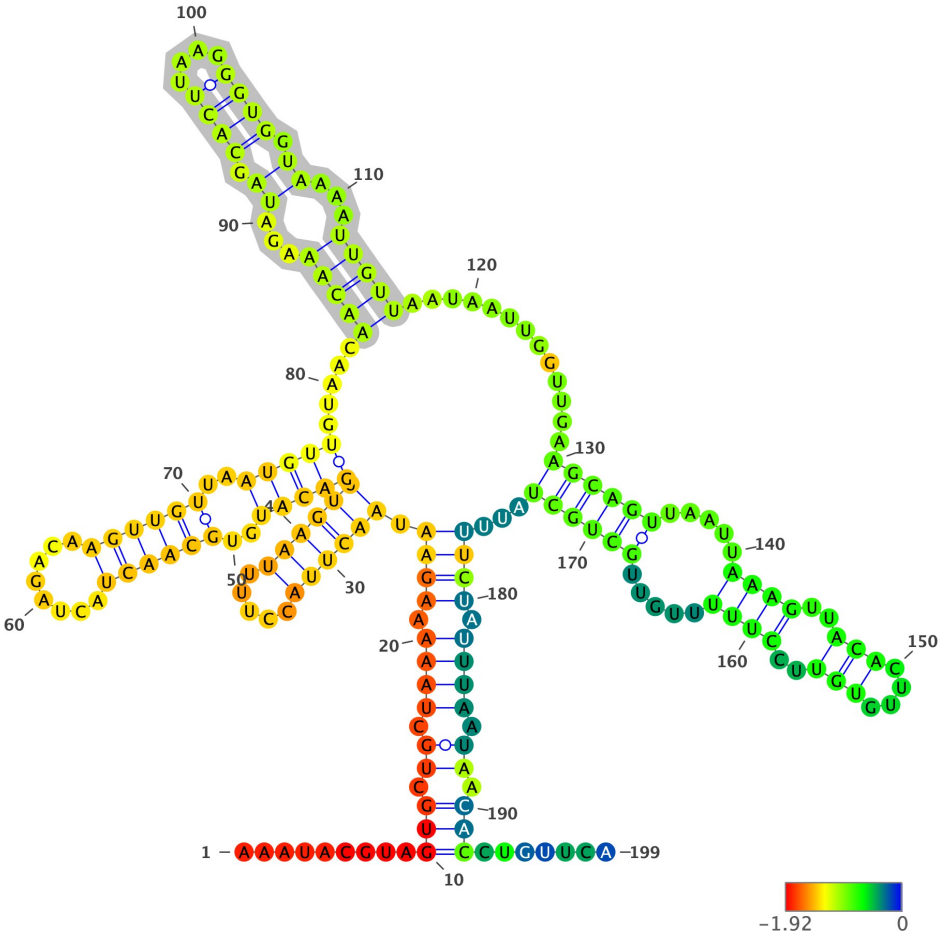
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 153 from nt 8530 to 8563 (nt 83 to 116)

```
5'-AACAAAGATAGCACTTAAGGGUGGUAAAAUUGUU-3'
5'-(((((...((.((((....)))).))...)))))-3'
Motif MFE = -5.9; z-score = -2.48; ED = 1.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8448 to 8646 (motif highlighted in silver):

```
5'-AAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAA
UUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUACACUUGUGUUCCUUUUUGUUGCUGCUAUUUUCUAUUUAAUAACACCUGUUCA-3
5'-.........(((.((.((((.((((.((((((.....))))))(((((..((((((.........))))))..)))))).....(((((...((.((((....)))).))...
)))))..............((((((.....((((..(((....)))..)))).....))))))...)))).)))).)).))).......-3'
MFE = -36.0; z-score = -0.77; ED = 39.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

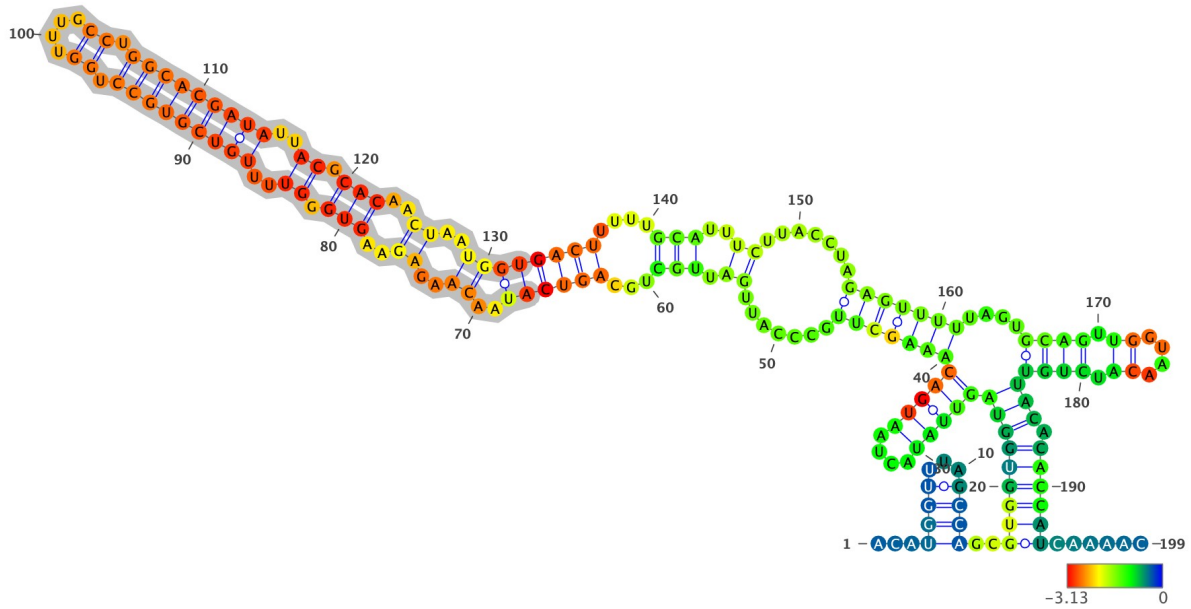
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 154 from nt 8837 to 8902 (nt 67 to 132)

```
5'-ATAACAAGAGAAGTGGGTTTTGTCGTGCCTGGTTTGCCTGGCACGAUATTACGCACAACTAATGGU-3'
5'-(...........(((.((..(((((((((.((....)).))))))))..)).))).........)-3'
Motif MFE = -27.2; z-score = -4.03; ED = 1.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8771 to 8969 (motif highlighted in silver):

```
5'-ACAUGGUUUAGCCAGCGUGGUGGUAGUUAUACUAAUGACAAAGCUUGCCCAUUGAUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACG
AUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGUGCAGUUGGUAACAUCUGUUACACACCAUCAAAAC-3
5'-...((((...)))).((((((((((((((....)))))))))))))).....((.(((...(((((((..((..((..((..((((.((..(((((((((.((....)).)))))))
)))..)).)))..)).)).))))))))....)))..)).....)))))))....((((.((....)).)))))))).))))))......-3'
MFE = -59.2; z-score = -2.67; ED = 35.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

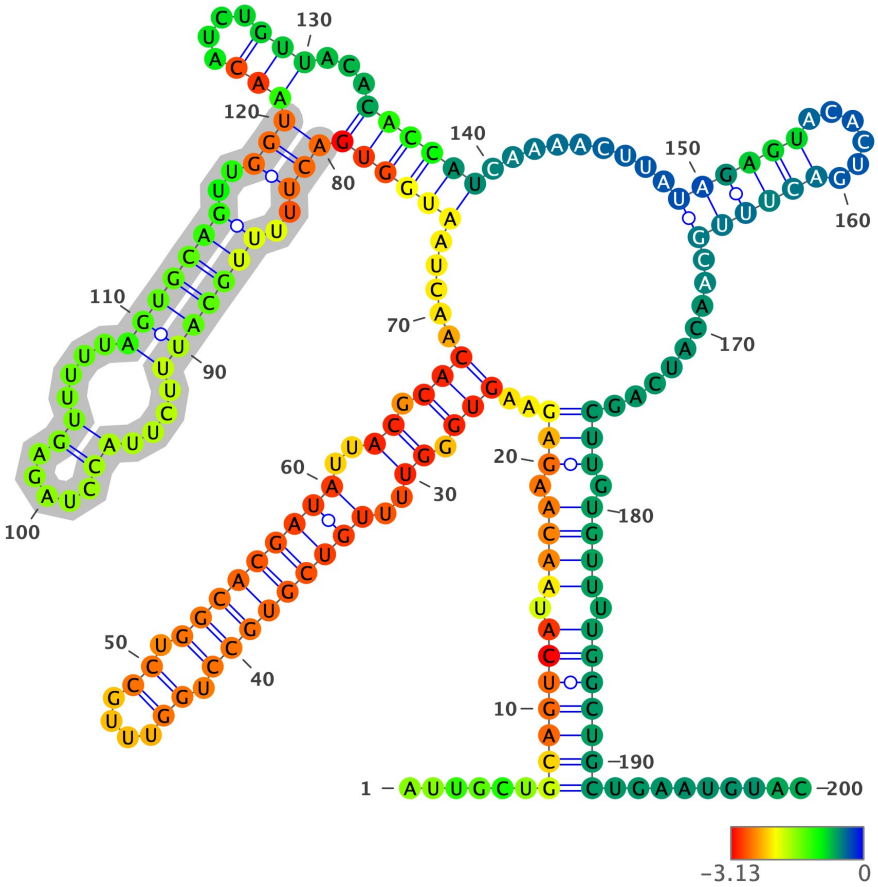
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 155 from nt 8904 to 8944 (nt 80 to 120)

```
5'-ACTTTTTGCATTTCTTACCTAGAGTTTTTAGUGCAGTTGGU-3'
5'-(((....(((.....................))).....)))-3'
Motif MFE = -5.9; z-score = -1.18; ED = 5.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8825 to 9024 (motif highlighted in silver):

```
5'-AUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGU
GCAGUUGGUAACAUCUGUUACACACCAUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUAC-3
5'-......(((((((.((((.(((..(((.((..(((((((((.((....)).))))))))).)).))).....((((((((..(((((((....((.....)).....)))
))))..)))(((....)))...))))))).........((((((......))))))).........))).)))).)))))))..........-3'
MFE = -55.9; z-score = -3.21; ED = 25.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

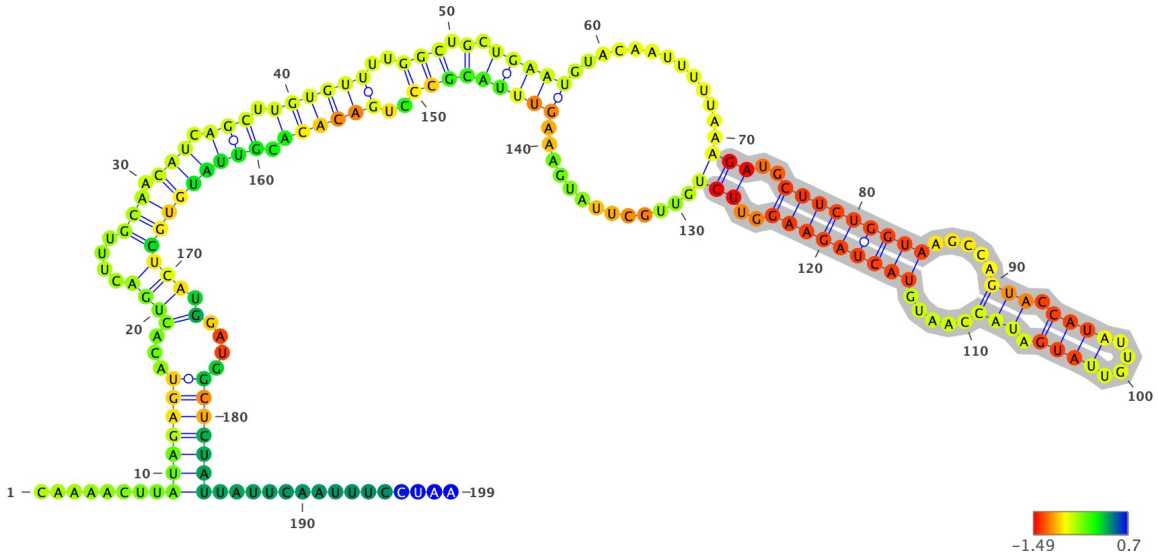
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 156 from nt 9035 to 9090 (nt 72 to 127)

```
5'-GATGCTTCTGGTAAGCCAGTACCATATTGTTAUGATACCAATGUACUAGAAGGTUC-3'
5'-((..((((((((((.........(((......)))........))))))))))..))-3'
Motif MFE = -15.8; z-score = -3.05; ED = 1.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8964 to 9162 (motif highlighted in silver):

```
5'-CAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCA
AUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGCCCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAA-3
5'-........(((((((...((((....(((.(((.(((((((..(((.(.(((((.............(((..((((((((((.....(((.((((....)))).)))..
...))))))))))..)))............))))))))..)))))).))))))))))))).)....)))))))................-3'
MFE = -46.2; z-score = -1.48; ED = 18.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

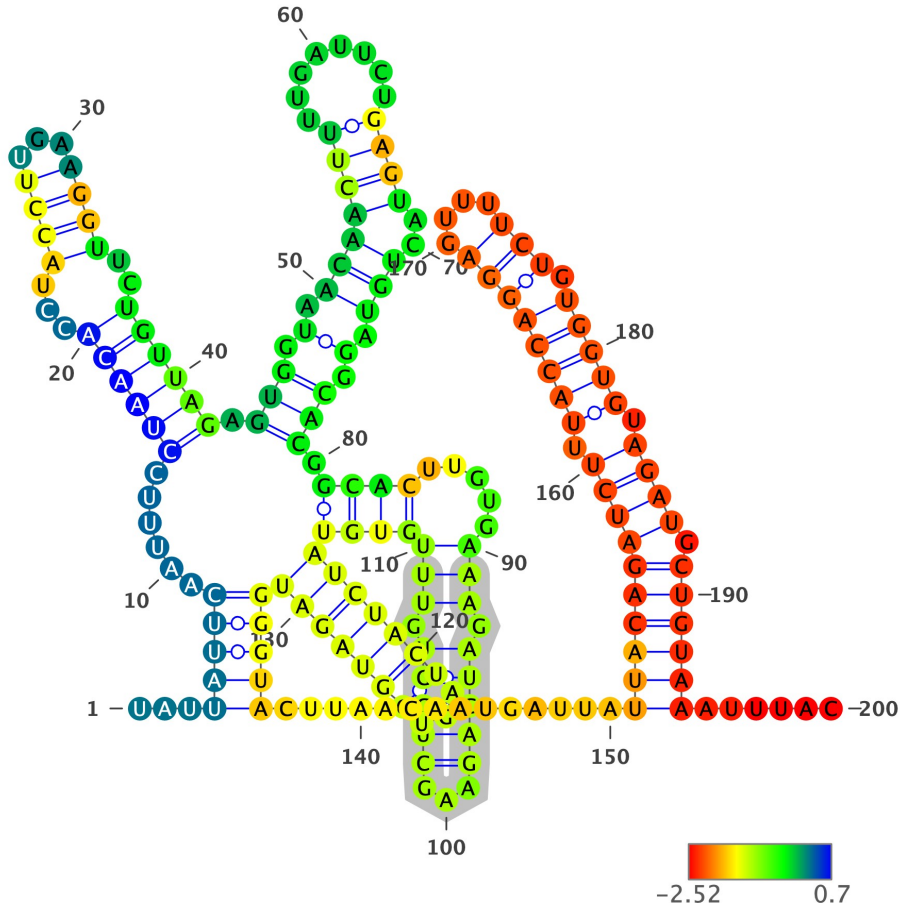
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 157 from nt 9235 to 9253 (nt 91 to 109)

```
5'-AAGATCAGAAGCUGGUGUU-3'
5'-((.(((((...))))).))-3'
Motif MFE = -2.8; z-score = -1.95; ED = 1.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9145 to 9344 (motif highlighted in silver):

```
5'-UAUUAUUCAAUUUCCUAACACCUACCUUGAAGGUUCUGUUAGAGUGGUAACAACUUUUGAUUCUGAGUACUGUAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUG
UGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUAC-3
5'-...(((((......((((((...((((...))))..)))))).(((.(.(((((((.........))))..))).).))).((((.....(((.(((((...))))).))))
)))(((((((...))))))))))))..............((((((((((.((((((((....))).))))).)))).))))))......-3'
MFE = -45.4; z-score = -1.33; ED = 37.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

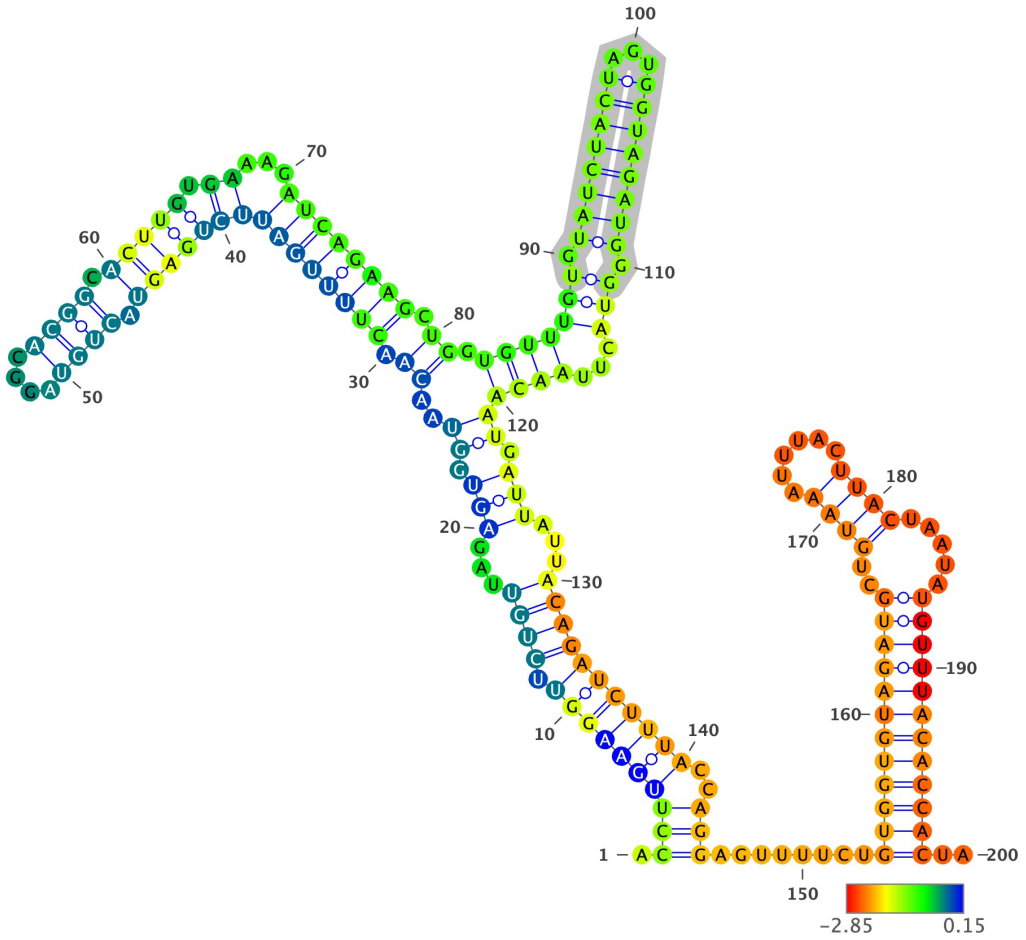
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 158 from nt 9256 to 9278 (nt 89 to 111)

```
5'-TGTATCTACTAGTGGUAGAUGGG-3'
5'-(.(((((((.....)))))))).)-3'
Motif MFE = -6.6; z-score = -3.49; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9168 to 9367 (motif highlighted in silver):

```
5'-ACCUUGAAGGUUCUGUUAGAGUGGUAACAACUUUUGAUUCUGAGUACUGUAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGG
UACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUA-3
5'-.(((((((((.((((...((((.((...((.((((((((((((((.((((....)))).)))))).))...)))))))).)).(((((((.((((((((...)))))))).)
))...)))))).)))...))))))))))..)))........((((((((((..((((......)))).....)))))))))))..-3'
MFE = -49.0; z-score = -2.01; ED = 35.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

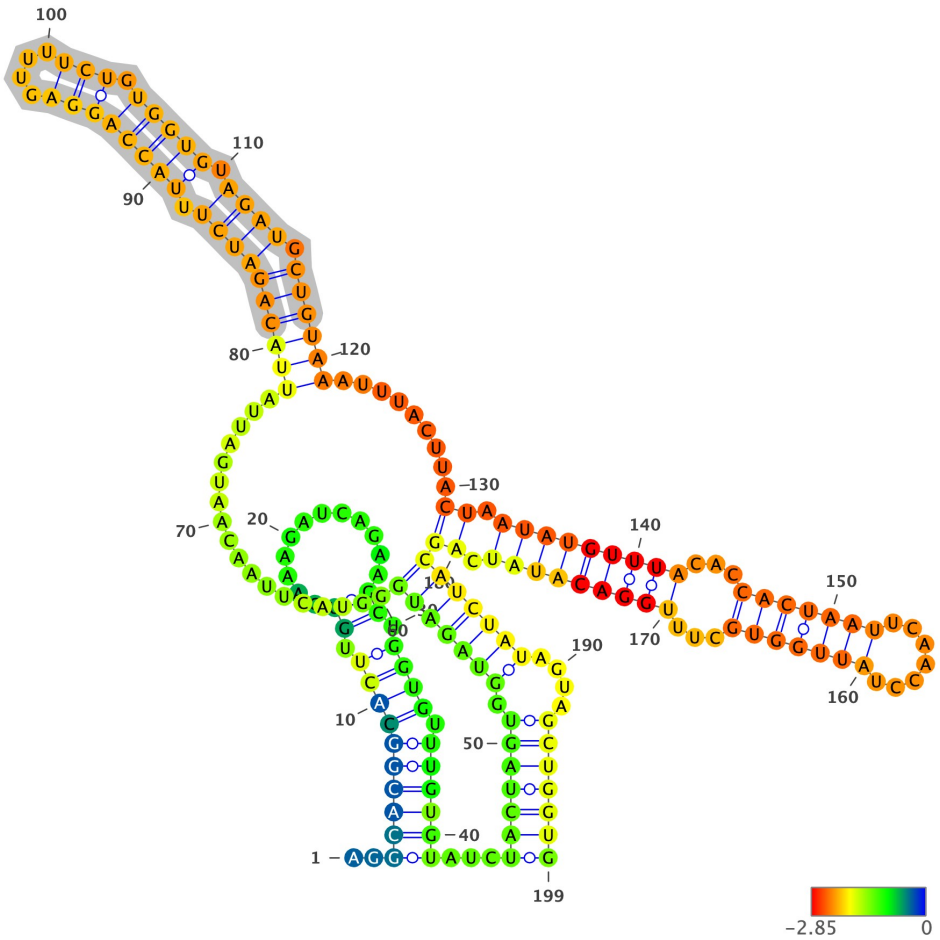
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 159 from nt 9298 to 9335 (nt 81 to 118)

```
5'-CAGATCTTTACCAGGAGTTTTCTGUGGUGTAGAUGCUG-3'
5'-(((((((.(((((...........))))).)))).)))-3'
Motif MFE = -11.6; z-score = -2.76; ED = 3.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9218 to 9416 (motif highlighted in silver):

```
5'-AGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUA
GAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG-3
5'-..(((((((((((.((.............)).)))).))))))...(((((((.(((((((.................(((((((((.((((((((....))).))))).)
))).))))))).........((.(((((((((...(((((((.......)))))))...))))))))).))))))))).....)))))))-3'
MFE = -50.3; z-score = -2.15; ED = 53.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

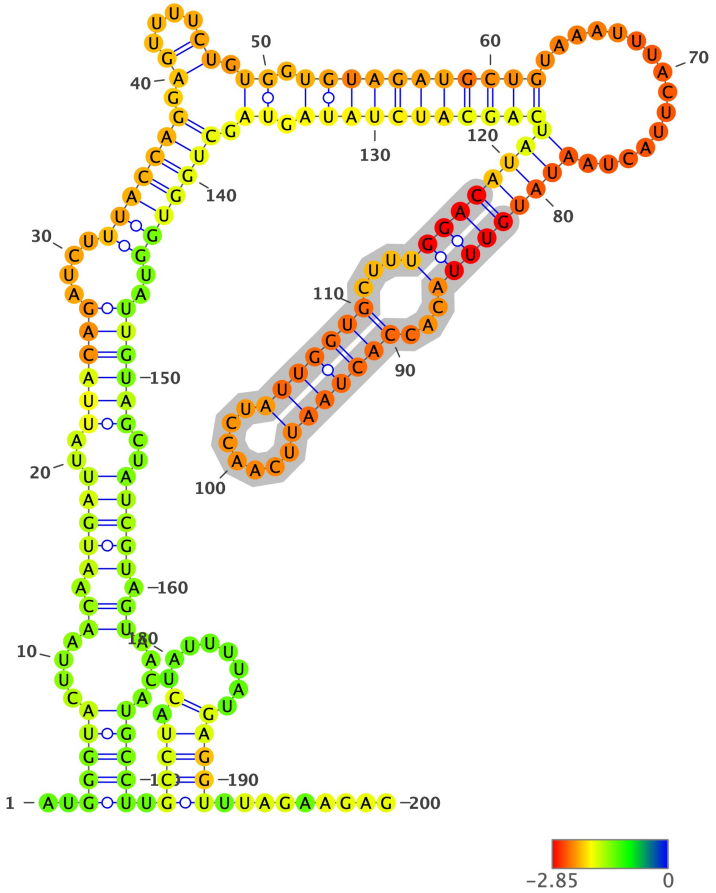
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 160 from nt 9355 to 9391 (nt 82 to 118)

```
5'-GTTTACACCACTAATTCAACCTAUUGGUGCTTTGGAC-3'
5'-((((....((((((.........))))))....))))-3'
Motif MFE = -6.6; z-score = -1.6; ED = 6.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9274 to 9473 (motif highlighted in silver):

```
5'-AUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGC
UUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAG-3
5'-..((((((....((.((((((..(((((((....(((((((.((....)).((.(((((((((((.............(((((((((...(((((((.......)))))))).
..))))))))))))))))))).)).)))))))..)))))).)))))).)).....)))))).((((.(........)))))).........-3'
MFE = -48.3; z-score = -2.08; ED = 57.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

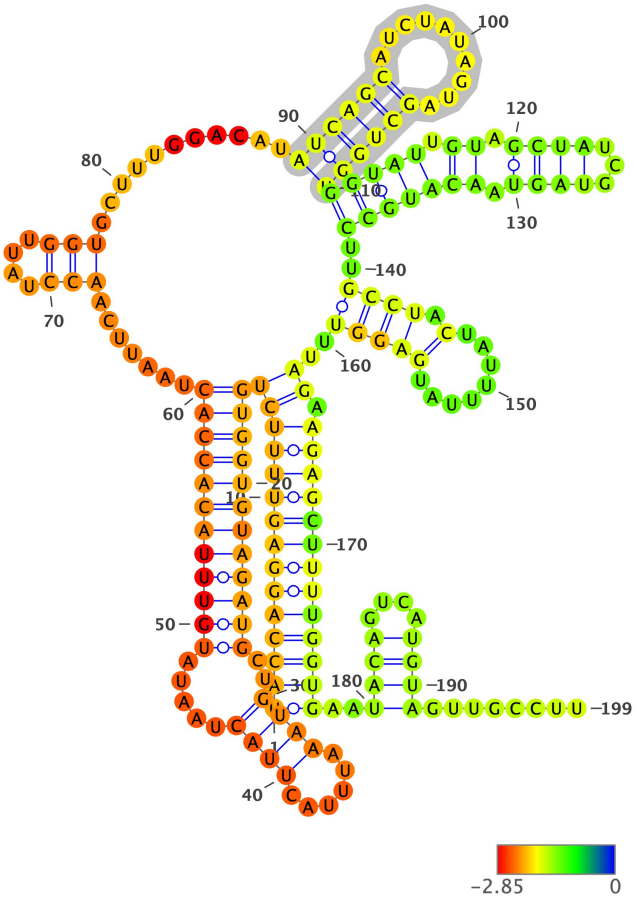
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 161 from nt 9394 to 9415 (nt 89 to 110)

```
5'-ATCAGCATCTATAGTAGCUGGU-3'
5'-((((((..........))))))-3'
Motif MFE = -5.0; z-score = -2.13; ED = 1.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9306 to 9504 (motif highlighted in silver):

```
5'-UACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG
GUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUU-3
5'-(((((((((((((((((((((((((((..((((......))))).....))))))))))))).......(((....)))...........((((((..........))))))(
((((.((.((((...)))).)))))))..((((.(........)))))..)).)))))))))))))..((((....))))........-3'
MFE = -51.3; z-score = -2.84; ED = 19.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

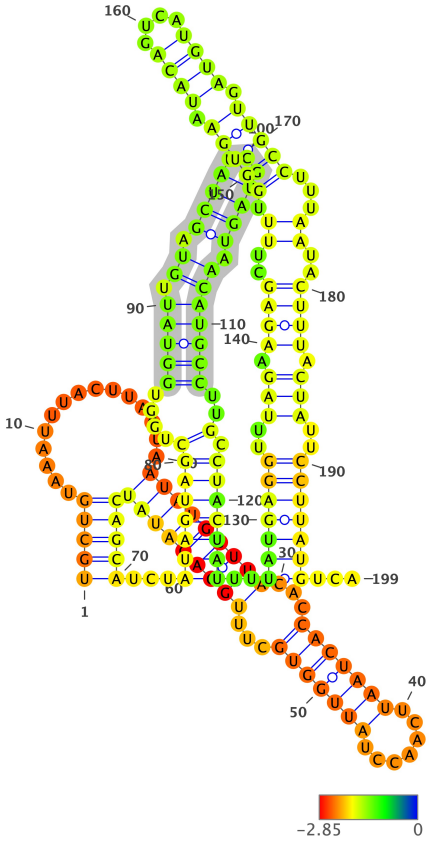
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 162 from nt 9416 to 9443 (nt 86 to 113)

```
5'-GGTATTGTAGCTATCGTAGUAACAUGCC-3'
5'-(((((.((.(((.....))).)))))))-3'
Motif MFE = -6.5; z-score = -1.94; ED = 1.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9331 to 9529 (motif highlighted in silver):

```
5'-UGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUG
CCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCA-3
5'-(((((...............(((((((((...(((((((.......)))))))...))))))))))))))...((((((((....(((((.((.((((...)))).)))))
))..).)))))))..(((((((..(((.((((..((.(((((.((((....)))).)))))...))..)))).)))..)))))))...-3'
MFE = -49.6; z-score = -3.15; ED = 16.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

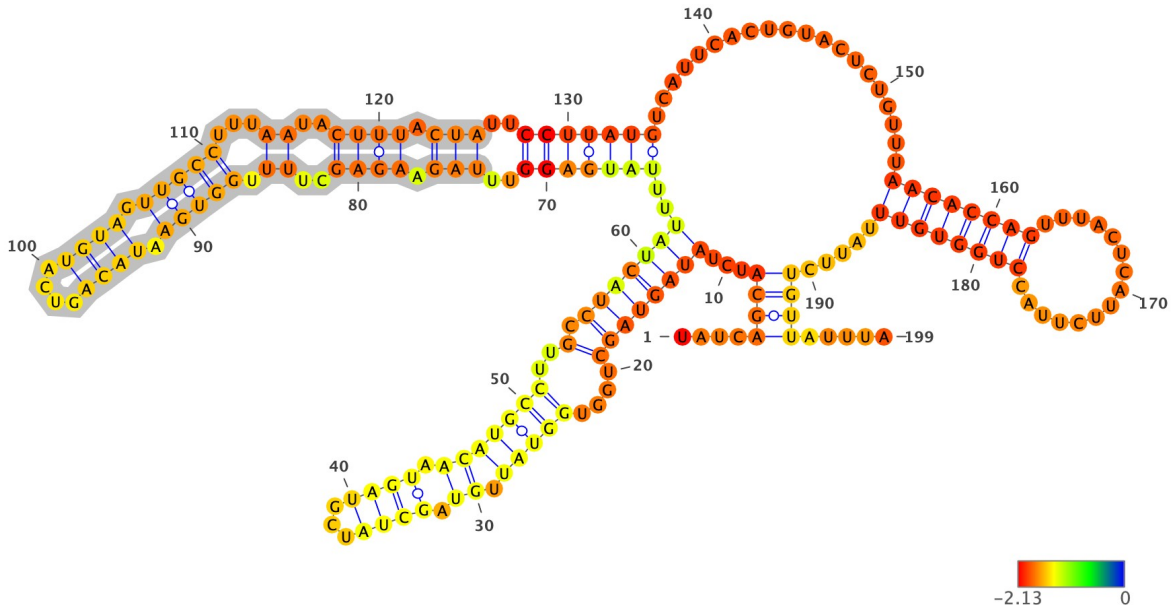
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 163 from nt 9466 to 9517 (nt 74 to 125)

```
5'-TAGAAGAGCTTTTGGTGAATACAGTCAUGUAGUUGCCTTTAATACUUUACUA-3'
5'-(((.((((..((.(((((.((((....)))).)))))...))..)))).)))-3'
Motif MFE = -8.9; z-score = -0.99; ED = 6.48
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9393 to 9591 (motif highlighted in silver):

```
5'-UAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCU
UUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUA-3
5'-....((((...((((((((....(((((.((.((((...)))).)))))))..).)))))))..(((((((..(((.((((..((.(((((.((((....)))).)))))).
..))..)))).)))..)))))))....................((((((((...............))))))))).....))))).....-3'
MFE = -42.6; z-score = -1.92; ED = 22.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

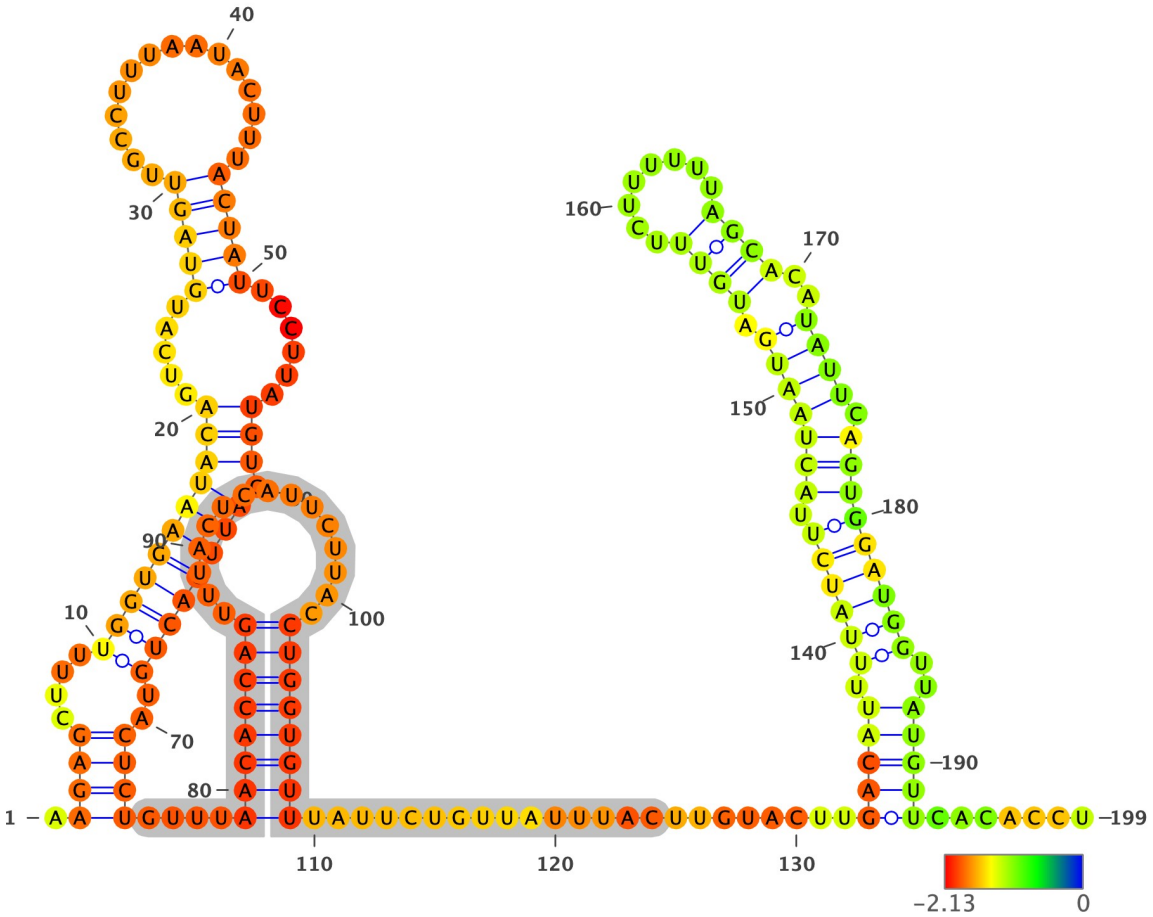
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 164 from nt 9543 to 9592 (nt 75 to 124)

```
5'-GTTTAACACCAGTTTACTCATTCTTACCUGGUGUUTATTCTGTTATTTAC-3'
5'-(...((((((((.............))))))))..............)-3'
Motif MFE = -9.0; z-score = -3.02; ED = 3.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9469 to 9667 (motif highlighted in silver):

```
5'-AAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUA
UUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCU-3
5'-.((((....(((((((((((.....(((((.............)))))......))).))))))))..))))....((((((((.............))))))))..
.....................(((((.((((((.(((((((.((((........))))..)))).))))))))..)))))........-3'
MFE = -32.9; z-score = -1.38; ED = 23.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

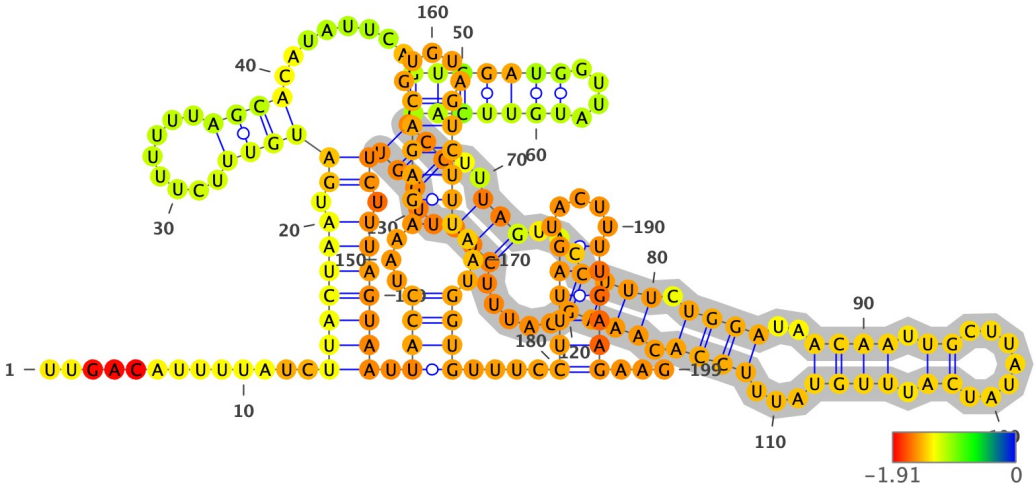
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 165 from nt 9664 to 9731 (nt 66 to 133)

```
5'-ACCTTTAGTACCTTTCTGGATAACAATTGCTTATATCATUUGUATTUCCACAAAGCATTTCTATTGGU-3'
5'-(((........((((.((((..((((.((.......)).))))...)))).)))).........)))-3'
Motif MFE = -12.1; z-score = -2.37; ED = 2.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9599 to 9797 (motif highlighted in silver):

```
5'-UUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUU
UCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAG-3
5'-.............(((((((.((((((........))))........(((((((....)))))))(((..(((...((((.((((..((((.((.......)).))))...
)))).)))).....)))..))))).))))))).((((...((((((.....))))))...)))).....((((((.....))))))...-3'
MFE = -36.1; z-score = -1.39; ED = 51.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

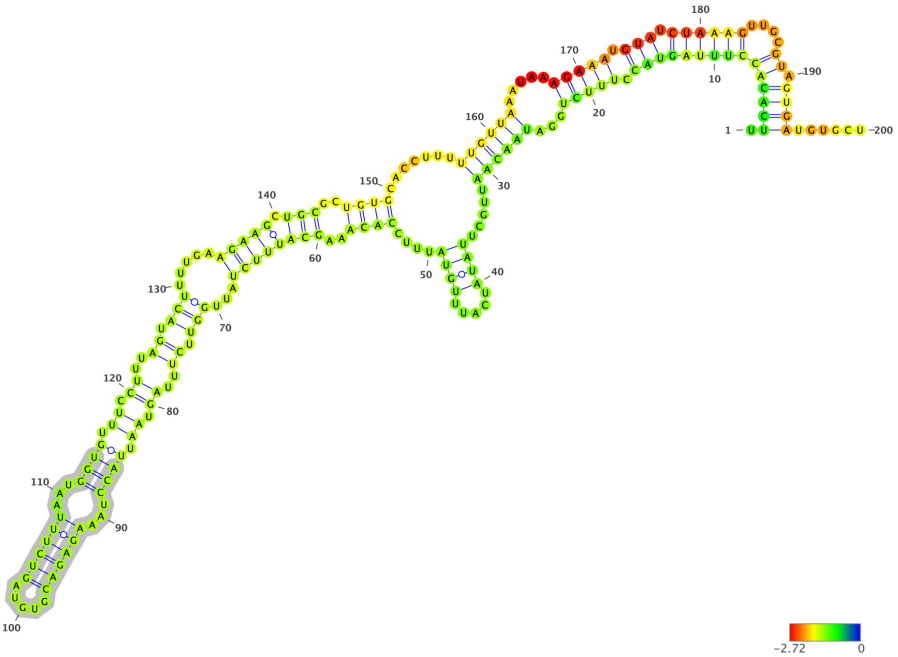
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 166 from nt 9744 to 9772 (nt 86 to 114)

```
5'-ACCTAAAGAGACGTGTAGUCUUTAATGGU-3'
5'-(((....(((((.....)))))....)))-3'
Motif MFE = -8.1; z-score = -2.97; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9659 to 9858 (motif highlighted in silver):

```
5'-UUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAU
GGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCU-3
5'-.(((((((((((((((.(((((...((((((.....((((.....))))....((((..((((((((...(((.((..((.((.((((...((((((.....))))))...
)))).)).))..)).))).....))))).)))..))))).......))))))).....))))).))).))))))....)).))))......-3'
MFE = -40.2; z-score = -1.51; ED = 57.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

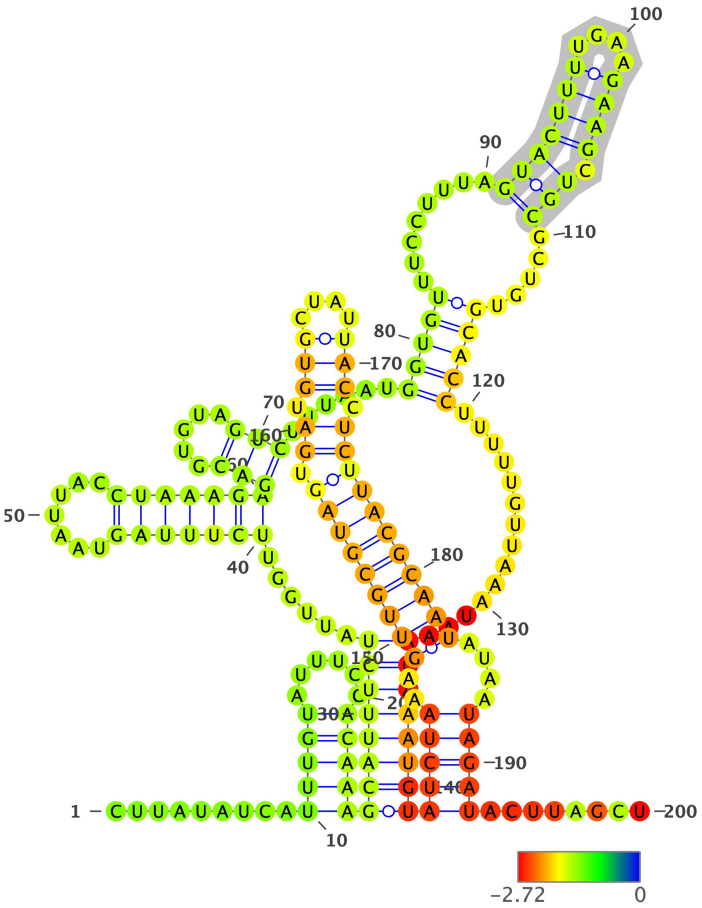
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 167 from nt 9783 to 9801 (nt 91 to 109)

```
5'-GTACTTTTGAAGAAGCUGC-3'
5'-(((((((....)))).)))-3'
Motif MFE = -0.8; z-score = 0.27; ED = 3.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9693 to 9892 (motif highlighted in silver):

```
5'-CUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGC
UGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCU-3
5'-.........(((((......)))))((((((((......(((((((.......)))))))(((.....)))......(((((........(((((((....)))).)))..
...)))))..............))))))))(((((..((((((((((.((.(((....))).))))))))))....)))))........-3'
MFE = -38.6; z-score = -2.03; ED = 33.21
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

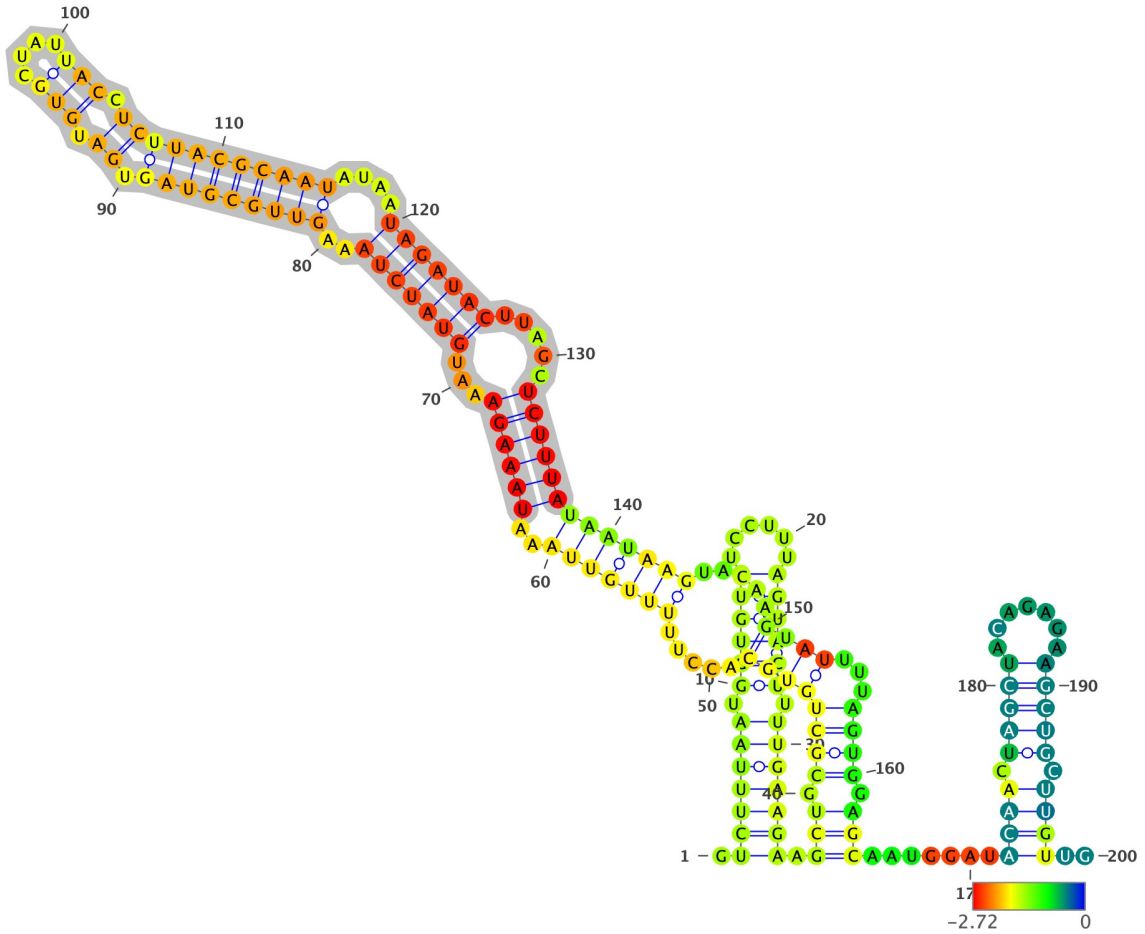
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 168 from nt 9823 to 9897 (nt 63 to 137)

```
5'-TAAAGAAATGTATCTAAAGTTGCGTAGTGATGTGCTATTACCUCTUACGCAAUATAAUAGAUACTTAGCUCUUUA-3'
5'-((((((...(((((((..((((((((..((.((......)).)).))))))))....)))))))).....))))))-3'
Motif MFE = -20.9; z-score = -4.69; ED = 5.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9761 to 9960 (motif highlighted in silver):

```
5'-GUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACG
CAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAGUGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUUG-3
5'-.(((((((.((((((......))))))).)))))))).(((.(((((((((.....(((((((..((((((...(((((((..(((((((((.((.(((....))).)))))))
))))....)))))))).....))))))))))))).....))))...)))).))).......((((.(((((.......))))).))))..-3'
MFE = -50.0; z-score = -2.22; ED = 19.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

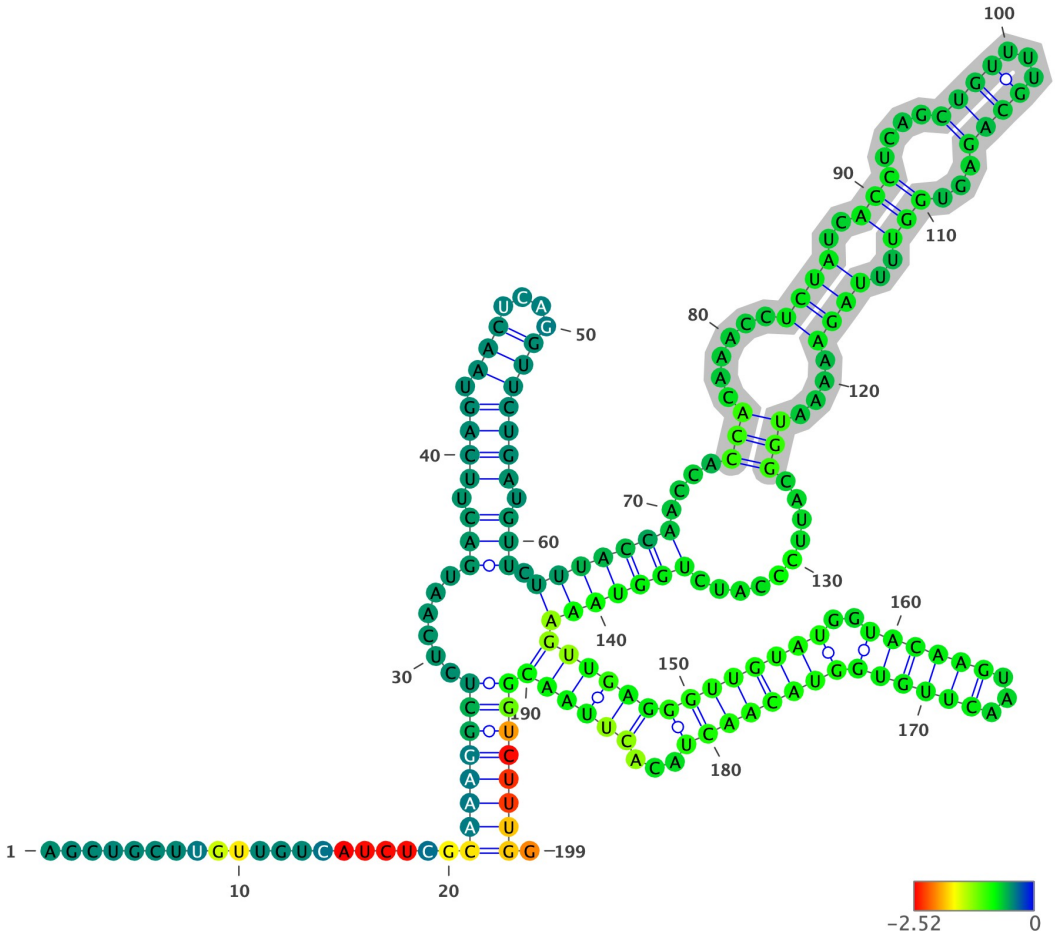
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 169 from nt 10022 to 10073 (nt 74 to 125)

```
5'-CCACAAACCTCTATCACCTCAGCTGTTTTGCAGAGTGGUTTUAGAAAAAUGG-3'
5'-(((.............................................)))-3'
Motif MFE = -9.6; z-score = -0.94; ED = 9.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9949 to 10147 (motif highlighted in silver):

```
5'-AGCUGCUUGUUGUCAUCUCGCAAAGGCUCUCAAUGACUUCAGUAACUCAGGUUCUGAUGUUCUUUACCAACCACCACAAACCUCUAUCACCUCAGCUGUUUUGCAGAGUGG
UUUUAGAAAAAUGGCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGG-3
5'-....................((((((((......(((.((((.(((....)))))))).))).(((((((....(((......((((..(((....((((...))))...))
)..))))....)))..........)))))))((((((((((((((..((((((...)))))))))))))))...))))))))))))))).-3'
MFE = -45.7; z-score = -1.09; ED = 35.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

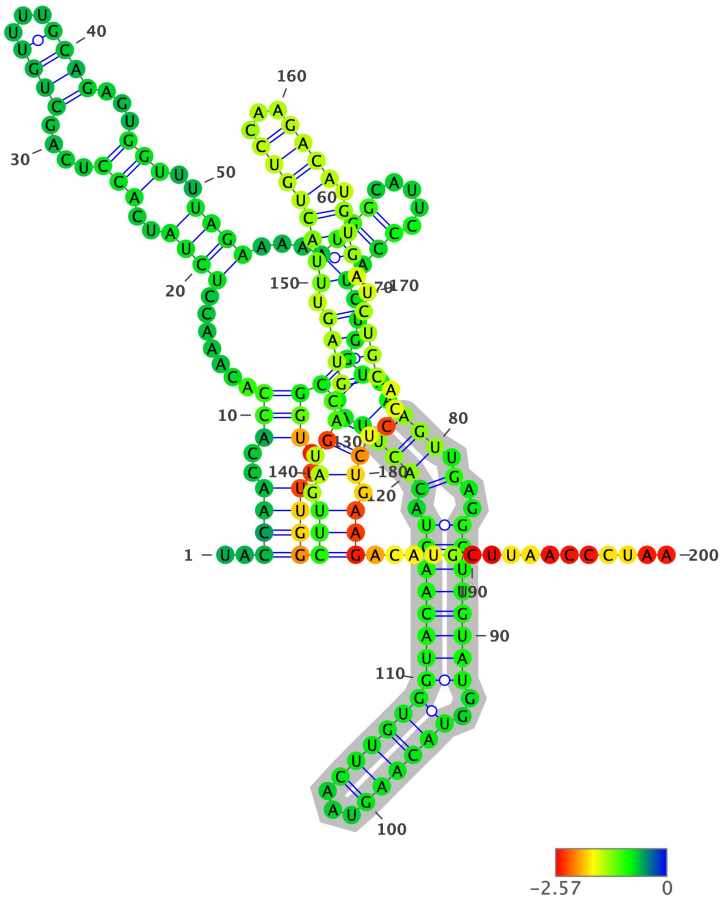
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 170 from nt 10090 to 10134 (nt 78 to 122)

```
5'-AGTTGAGGGTTGTATGGTACAAGTAACUUGUGGUACAACUACACU-3'
5'-(((.....................................)))-3'
Motif MFE = -11.9; z-score = -2.13; ED = 3.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10013 to 10212 (motif highlighted in silver):

```
5'-UACCAACCACCACAAACCUCUAUCACCUCAGCUGUUUUGCAGAGUGGUUUUAGAAAAAUGGCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGU
ACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACAUGCUUAACCCUAA-3
5'-..((((..(((.......((((..(((....((((...))))...)))..))))...((((.....))))...((.((((.(..(((((((((..((((((...))))))))
)))))).))))).))))).))))(((.(.((.((((.(((((((((...)))).)))).))))...))).))).................-3'
MFE = -43.8; z-score = -0.88; ED = 42.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

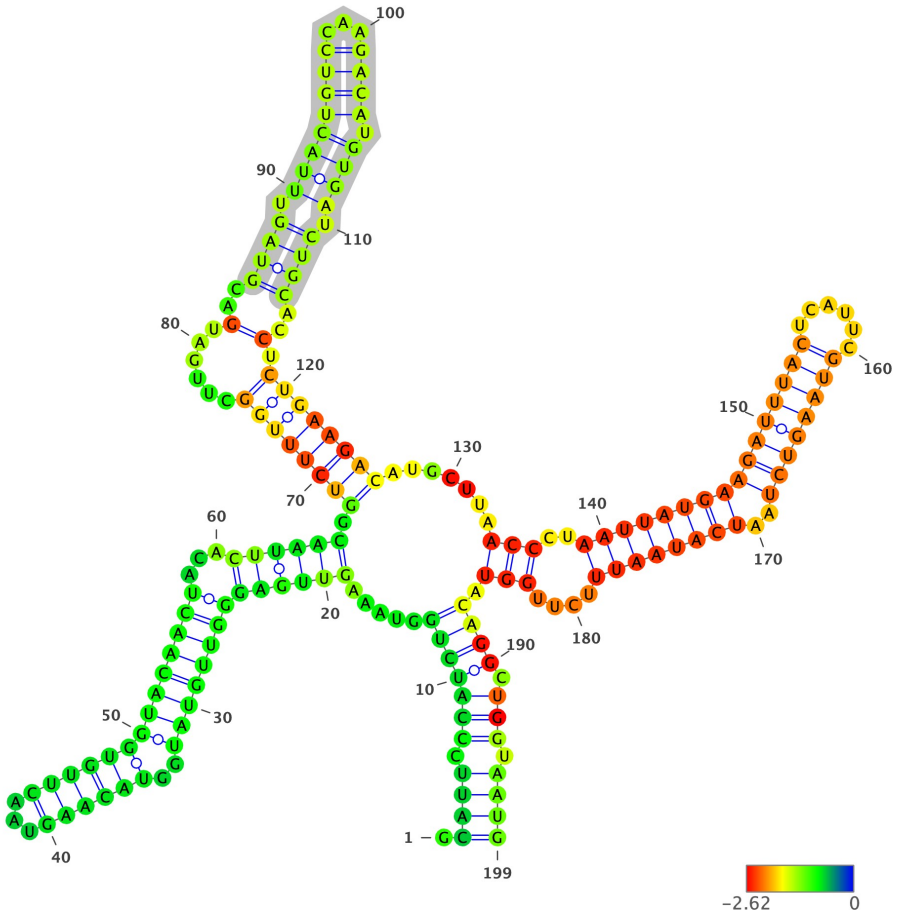
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 171 from nt 10157 to 10186 (nt 85 to 114)

```
5'-GTAGTTTACTGTCCAAGACATGTGATCUGC-3'
5'-((((.....((((...))))......))))-3'
Motif MFE = -8.9; z-score = -2.73; ED = 0.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10073 to 10271 (motif highlighted in silver):

```
5'-GCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUC
UGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUG-3
5'-.((((.(((((((.....(((((((((((((..((((((...)))))))))))))...)))))).((((((((......(..((((.((((((((...)))).)))).)
)))..).))))))))).......(((..((((((((((((((((.....))))))))..))))))))....))).)))).))).))))-3'
MFE = -55.2; z-score = -2.67; ED = 15.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

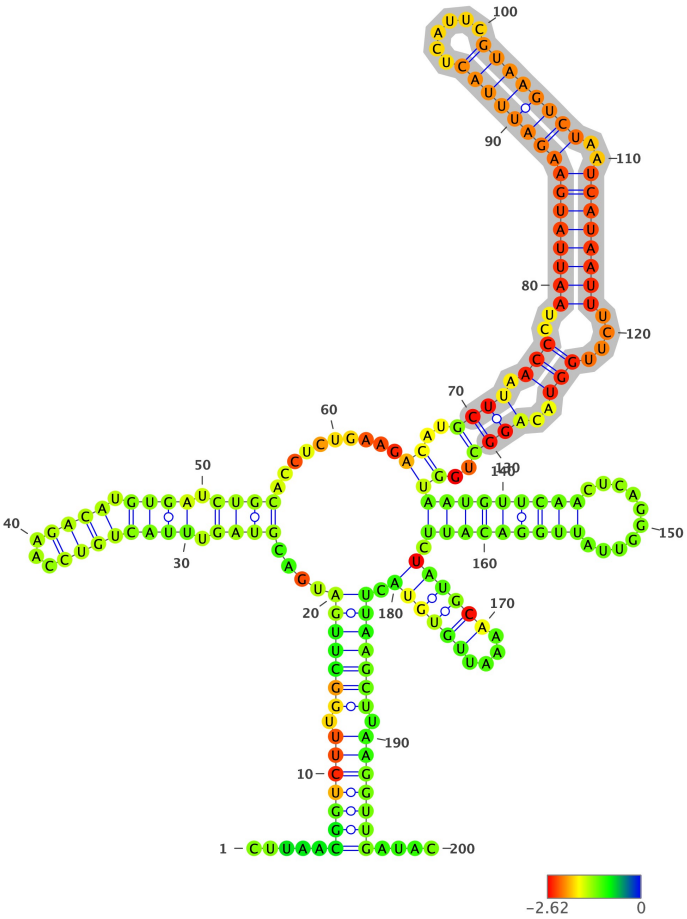
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 172 from nt 10202 to 10262 (nt 70 to 130)

```
5'-CTTAACCCTAATTATGAAGATTTACTCATTCGUAAGUCUAAUCAUAAUUTCTTGGUACAGG-3'
5'-((..(((..((((((((((((((((.....))))))))..))))))))....)))...))-3'
Motif MFE = -15.7; z-score = -3.49; ED = 2.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10133 to 10332 (motif highlighted in silver):

```
5'-CUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAU
CAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUAC-3
5'-.....(((((((.(((((((....((((.((((((((...)))).)))).))))..........((..((((.(((..((((((((((((((((.....))))))))..)
)))))))....)))..))))..))((((((((.........))))))))).((((((....)))))).))))))).))))))....-3'
MFE = -49.6; z-score = -2.69; ED = 25.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

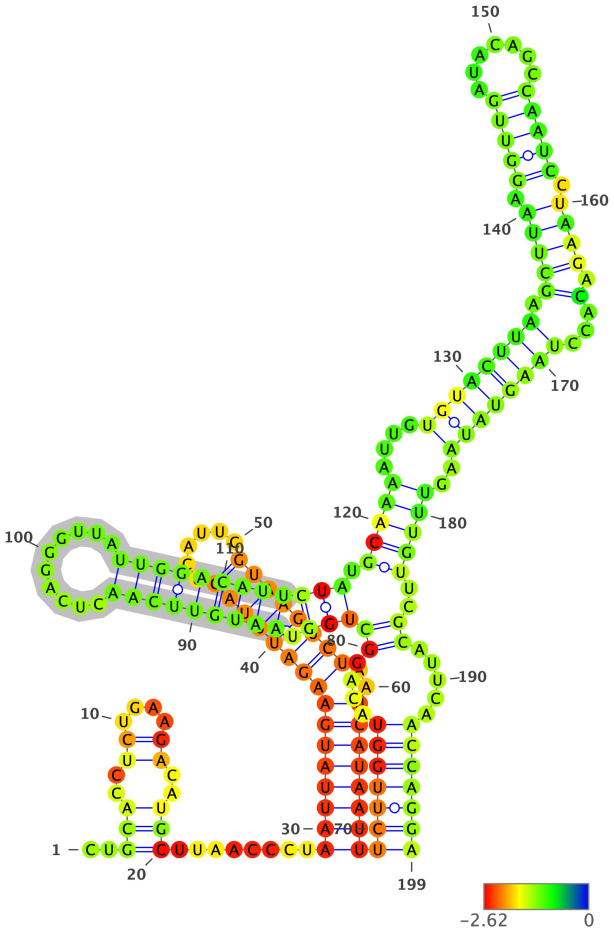
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 173 from nt 10268 to 10295 (nt 86 to 113)

```
5'-AATGTTCAACTCAGGGTTAUUGGACAUU-3'
5'-((((((((((.........))))))))))-3'
Motif MFE = -5.2; z-score = -1.47; ED = 3.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10183 to 10381 (motif highlighted in silver):

```
5'-CUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACA
UUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGA-3
5'-..(((..((....))..))).........(((((((((((((((.....))))))))..))))))))(((((((....(((((.((((((((.........)))))))
))))).(((((....((((((((.(((((.(((((.......))))).)))).)...))))))))..)))))..))).....)))))))-3'
MFE = -45.2; z-score = -1.84; ED = 39.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

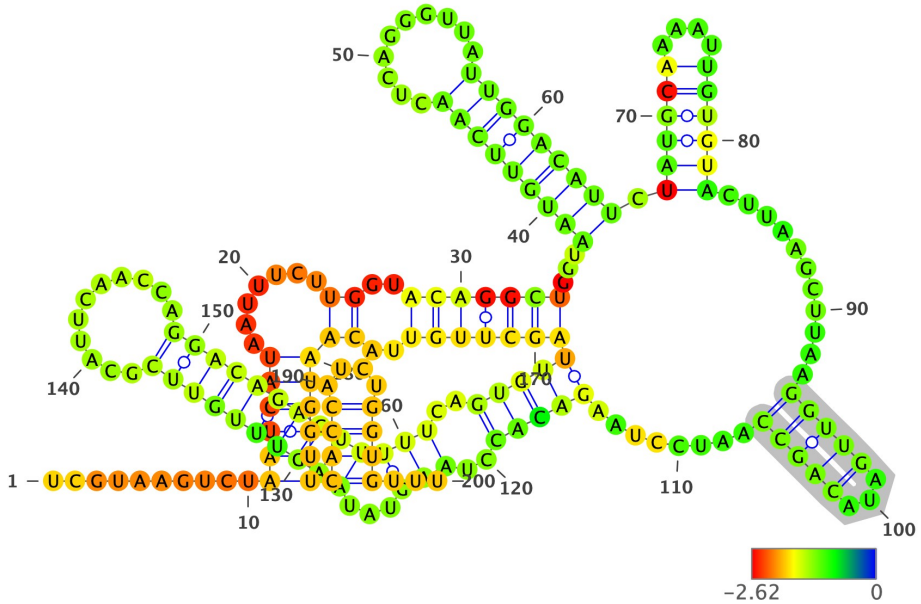
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 174 from nt 10324 to 10336 (nt 94 to 106)

```
5'-GGTTGATACAGCC-3'
5'-(((((...)))))-3'
Motif MFE = -3.1; z-score = -3.07; ED = 0.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10231 to 10430 (motif highlighted in silver):

```
5'-UCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCC
UAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUU-3
5'-..........((((((.......((..(((((((...((((((((((..........))))))))).((((((....)))))).........(((((...)))))..... ...(((((..(((...((((((((((.........))))))))))))..))))))))))))..))))))))((((....))))...-3'
MFE = -42.7; z-score = -0.96; ED = 30.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

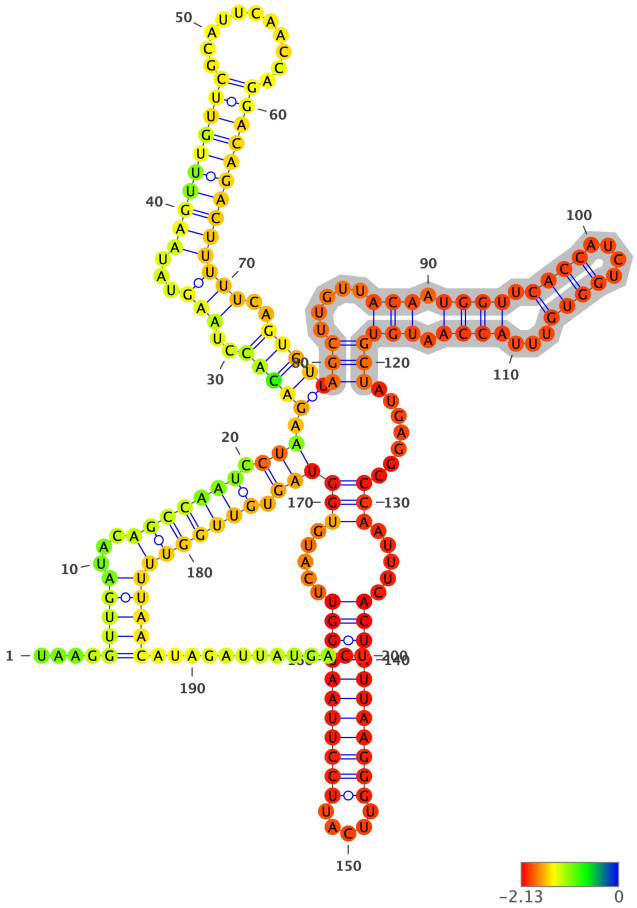
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 175 from nt 10399 to 10441 (nt 79 to 121)

```
5'-AGCTTGTTACAATGGTTCACCATCTGGUGTTTACCAAUGUGCU-3'
5'-(((.....(((.((((.((((....))))...)))).))))))-3'
Motif MFE = -11.7; z-score = -2.32; ED = 2.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10321 to 10520 (motif highlighted in silver):

```
5'-UAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUA
CCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACU-3
5'-....(((((...(((((((.(((.(((((..(((...(((((((((((.....)))))))))))))..)))))(((.....(((.((((.((((....))))...)
))).))))))).....(((.....((((((((((((.....)))))))))))).....))))))).))))))))))))).............-3'
MFE = -50.9; z-score = -2.73; ED = 24.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

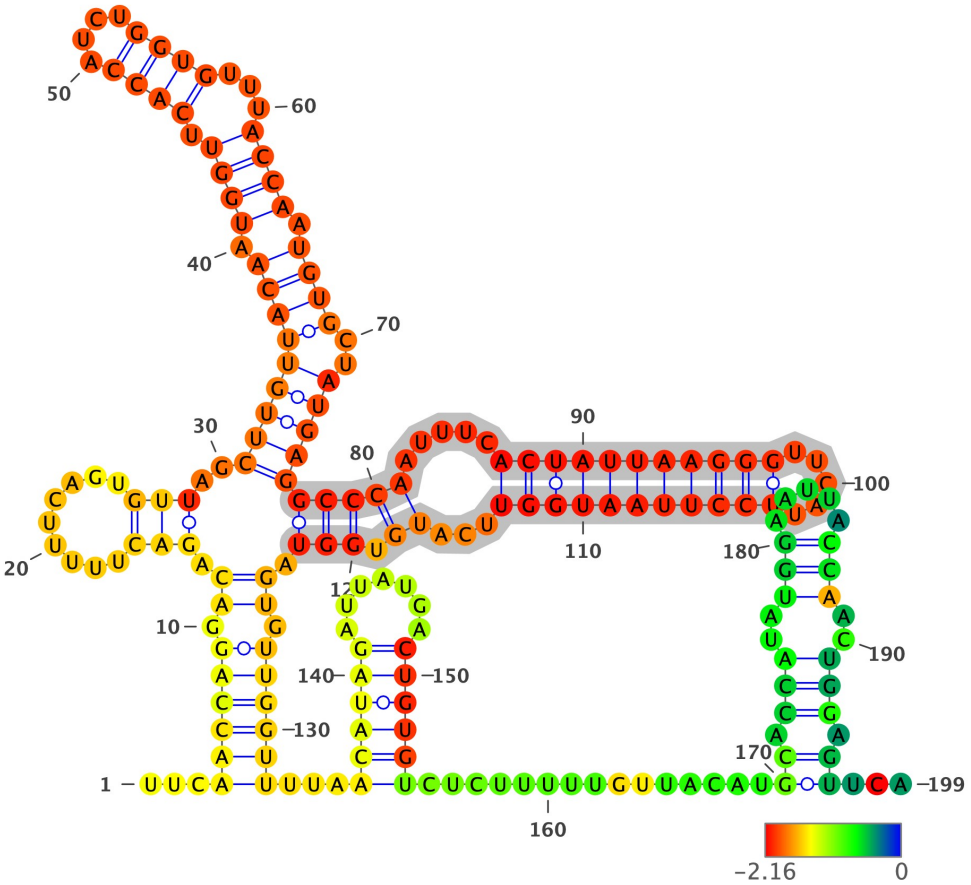
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 176 from nt 10447 to 10492 (nt 77 to 122)

```
5'-GCCCAATTTCACTATTAAGGGTTCATUCCUUAAUGGUTCATGTGGU-3'
5'-(((.......((((((((((.....)))))))))).....)))-3'
Motif MFE = -15.0; z-score = -3.75; ED = 2.97
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10371 to 10569 (motif highlighted in silver):

```
5'-UUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUG
GUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCA-3
5'-...((((((.((.(((.........)))..((((((((((.((((.((((....))))...)))).))))..)))))(((((.....((((((((((.....))))))))))
))...)).))).)).))))))...((((((.......))))))...............((.(((..(((.....)))..))).))...-3'
MFE = -45.3; z-score = -1.55; ED = 49.93
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

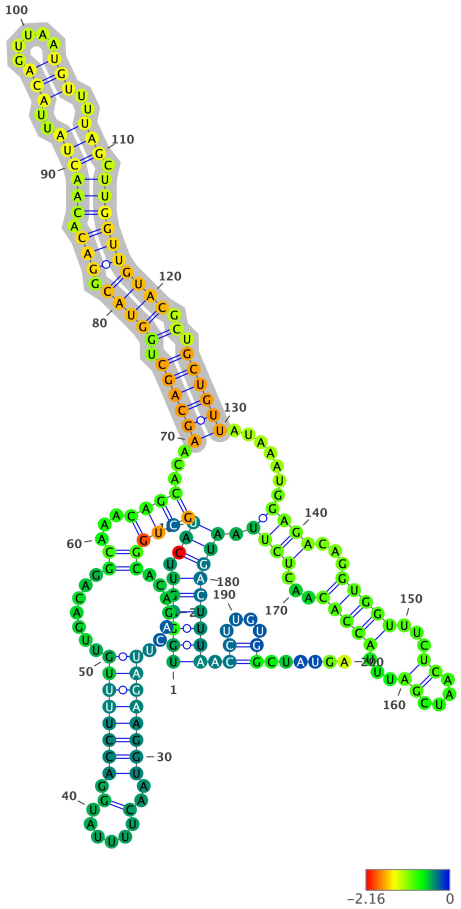
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 177 from nt 10630 to 10690 (nt 70 to 130)

```
5'-AGCAGCTGGTACGGACACAACTATTACAGTTAAUGUTTUAGCTTGGUUGUACGCTGCUGUU-3'
5'-((((((..(((((.(((....(((..(((.....)))..)))....)))))))).....)))))))-3'
Motif MFE = -20.6; z-score = -2.96; ED = 7.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10561 to 10760 (motif highlighted in silver):

```
5'-UGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGC
UUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCACAACUCUUAAUGACUUUAACCUUGUGGCUAUGA-3
5'-((((((.(((((((((.......(((((((..(......).)))))))).......))...)))))...((((((.(((((.(((.((((((..(((.....)))).)).))).
)))))))))).).))))))).......((((...((((((...((....))...)))))...)))).)))))))))).((....)).....-3'
MFE = -48.5; z-score = -0.95; ED = 20.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

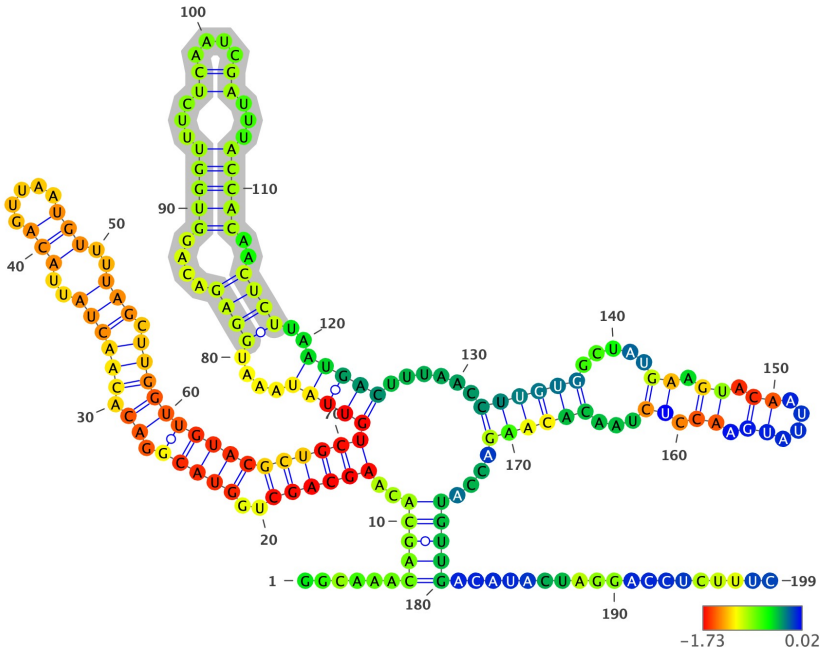
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 178 from nt 10697 to 10734 (nt 81 to 118)

```
5'-GGAGACAGGTGGTTTCTCAATCGATTTACCACAACUCU-3'
5'-((((.............................))))-3'
Motif MFE = -9.0; z-score = -1.95; ED = 3.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10617 to 10815 (motif highlighted in silver):

```
5'-GGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCA
CAACUCUUAAUGACUUUAACCUUGUGGCUAUGAAGUACAAUUAUGAACCUCUAACACAAGACCAUGUUGACAUACUAGGACCUCUUUC-3
5'-......(((((..((((((..(((((.((.((((((..(((.....)))..))).)))))))))))))))((((.....((((....(((((...((....))...))))
)..))))..)))))......((((((.....((.((.((....)).)).))...))))))....)))))...................-3'
MFE = -44.1; z-score = -1.41; ED = 16.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

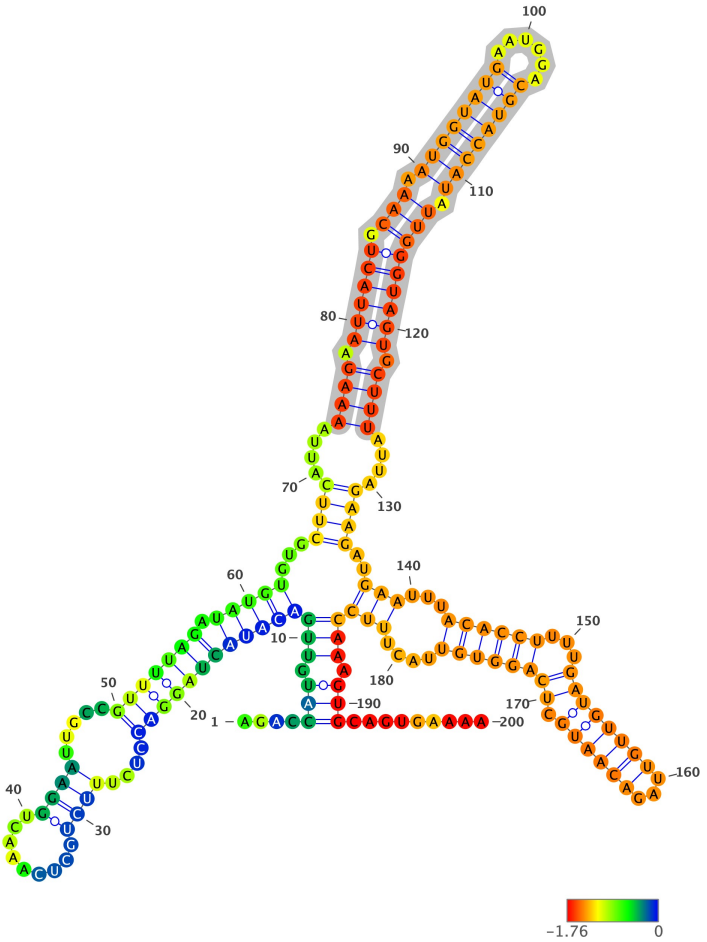
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 179 from nt 10859 to 10911 (nt 74 to 126)

```
5'-AAAGAATTACTGCAAAATGGTATGAATGGACGUACCAUAUUGGGUAGUGCUUU-3'
5'-((((.((((((.(((.((((((((.....)))))))).))))))))).))))-3'
Motif MFE = -17.1; z-score = -3.74; ED = 2.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10786 to 10985 (motif highlighted in silver):

```
5'-AGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUAUGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAU
AUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAA-3
5'-....(((.(((((((((((((((....((((.........))))).....)))))))).)))))...((((....((((.((((((.(((.((((((((.....))))))))
.))))))))).))))....))))..(((...((((((...((((((((...)))))).))))))))....)))))).)))........-3'
MFE = -42.2; z-score = -0.47; ED = 30.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

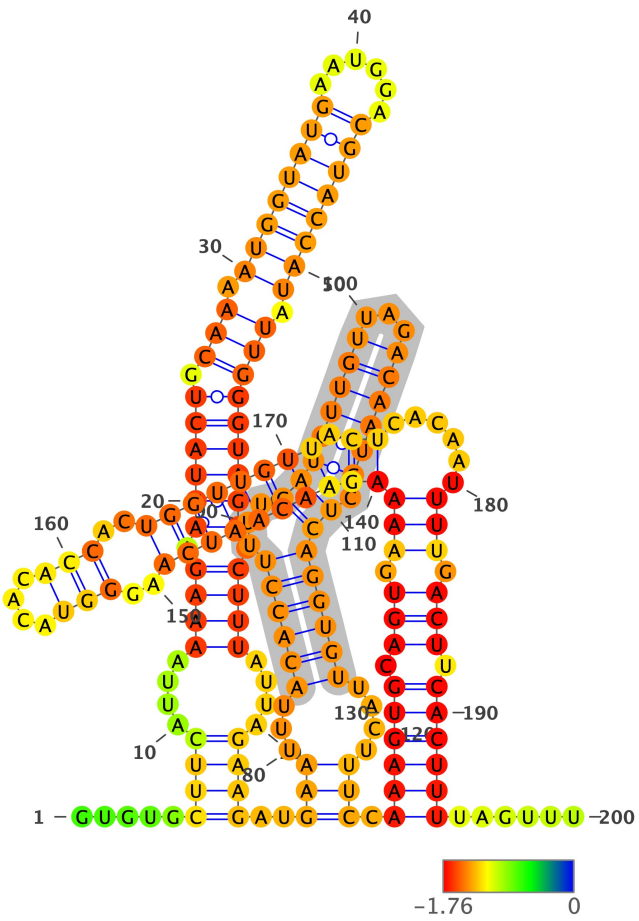
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 180 from nt 10928 to 10962 (nt 83 to 117)

```
5'-ACACCTTTTGATGTTGTTAGACAAUGCTCAGGUGU-3'
5'-((((((......((((.....)))).....))))))-3'
Motif MFE = -8.1; z-score = -2.19; ED = 6.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10846 to 11045 (motif highlighted in silver):

```
5'-GUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUC
AGGUGUUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUU-3
5'-.....((((....((((.((((((.(((.((((((((......)))))))).))))))))).))))....))))..(((...((((((...((((((((...))))))).))
))))))....))).((((((.(((.(((((((((((((..(((....)))..)))))))).))......))).))).))))))......-3'
MFE = -50.7; z-score = -2.13; ED = 27.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

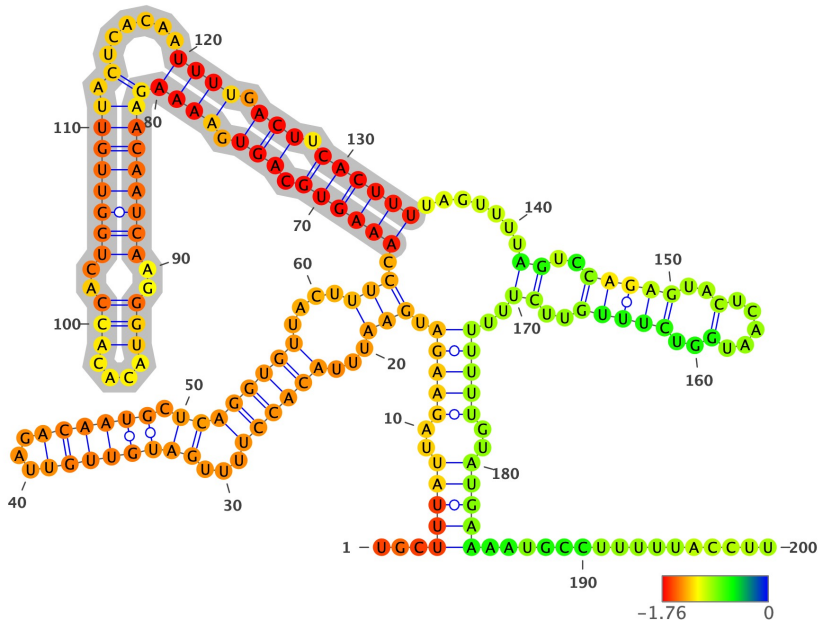
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 181 from nt 10971 to 11039 (nt 66 to 134)

```
5'-AAAGTGCAGTGAAAAGAACAATCAAGGGTACACACCACUGGUUGUTACTCACAAUUUTGACUTCACUUU-3'
5'-((((((.(((..(((..(((((((..(........)..)))))))).........)))..))).))))))-3'
Motif MFE = -19.0; z-score = -3.63; ED = 4.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10906 to 11105 (motif highlighted in silver):

```
5'-UGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUU
ACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUU-3
5'-...(((((..(((((.(((...((((((...((((((((...)))))).))))))))....))).((((((.(((.((((((((((((..(((....)))..)))))))))
.).....)))).))).))))))).......((..(((((..(.....)..)))))..))..)))))..)))))................-3'
MFE = -37.5; z-score = -1.1; ED = 37.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

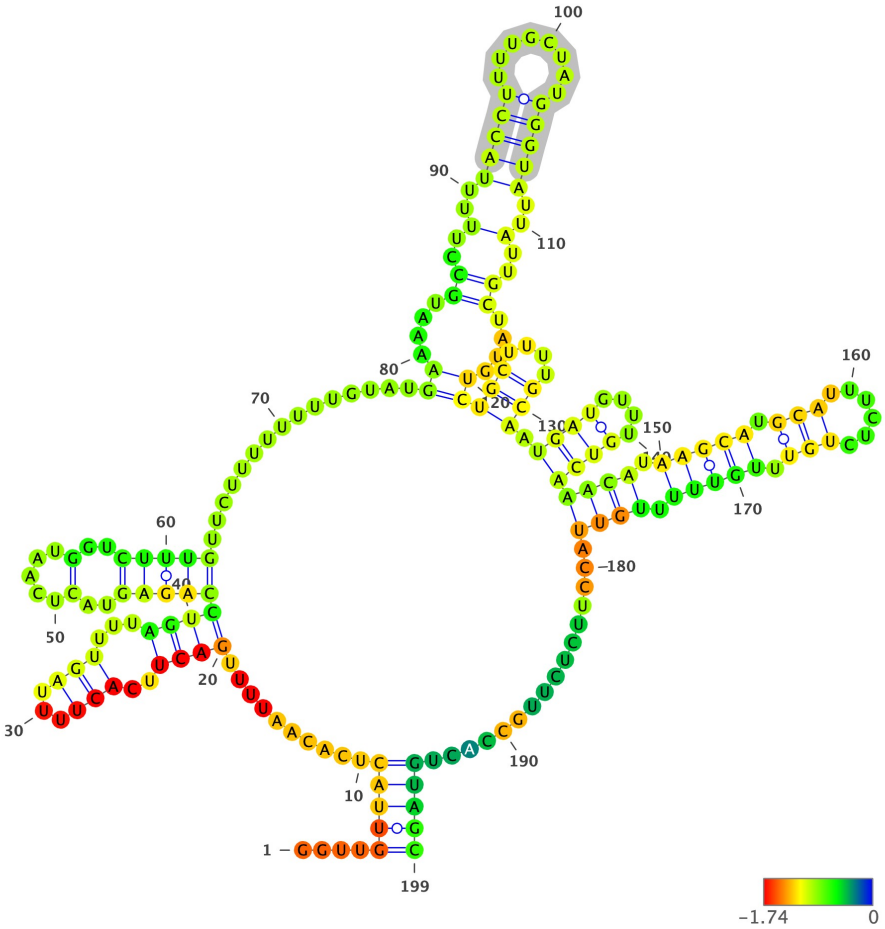
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 182 from nt 11101 to 11116 (nt 92 to 107)

```
5'-ACCTTTTGCTATGGGU-3'
5'-((((........))))-3'
Motif MFE = -2.5; z-score = -2.43; ED = 1.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11010 to 11208 (motif highlighted in silver):

```
5'-GGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUA
UUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGC-3
5'-....(((((..........((((..(((...)))...))))(((((..(.....)..)))))...............((....((..(..(((((........)))))..)
..))....))(((....))).((((....))))((((.(((((.(((......))).)))))).))))................)))))-3'
MFE = -31.5; z-score = -0.76; ED = 44.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

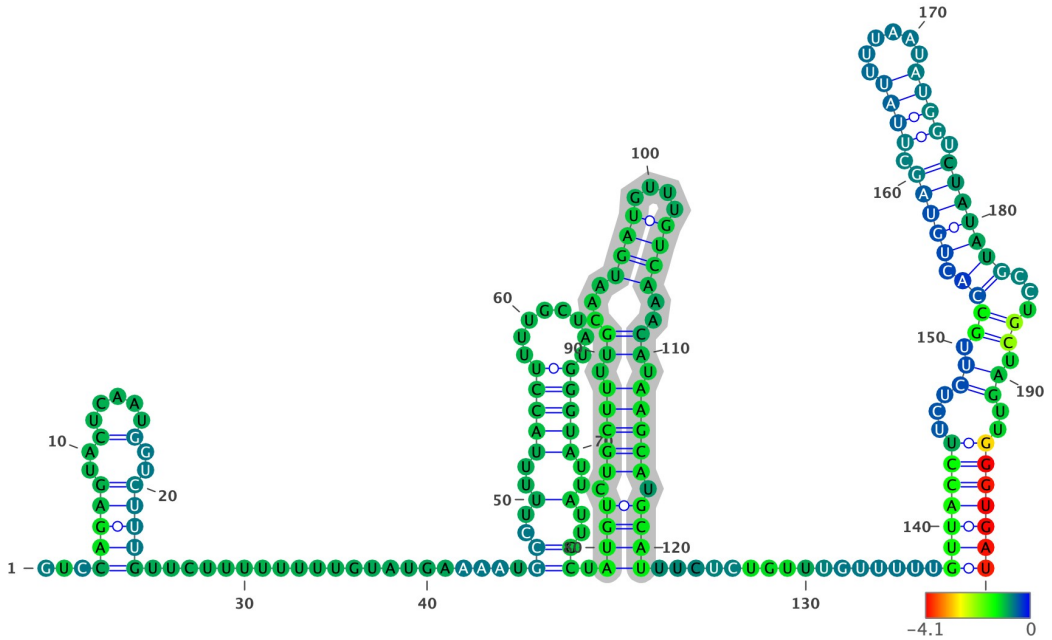
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 183 from nt 11126 to 11168 (nt 79 to 121)

```
5'-ATGTCTGCTTTTGCAATGATGTTTGUCAAACATAAGCATGCAU-3'
5'-((((.(((((.......(((....)))......))))).))))-3'
Motif MFE = -9.7; z-score = -2.21; ED = 7.49
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11048 to 11247 (motif highlighted in silver):

```
5'-GUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAU
AAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAU-3
5'-...(((((..(.....)..)))))......................((..(..(((((........)))))..)..)).((((.(((((.((...((((....))))..)).
))))).))))................(((((((...((.((((.(((((.((((......)))).)))))))...)).))..)))))))-3'
MFE = -33.8; z-score = -2.16; ED = 35.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

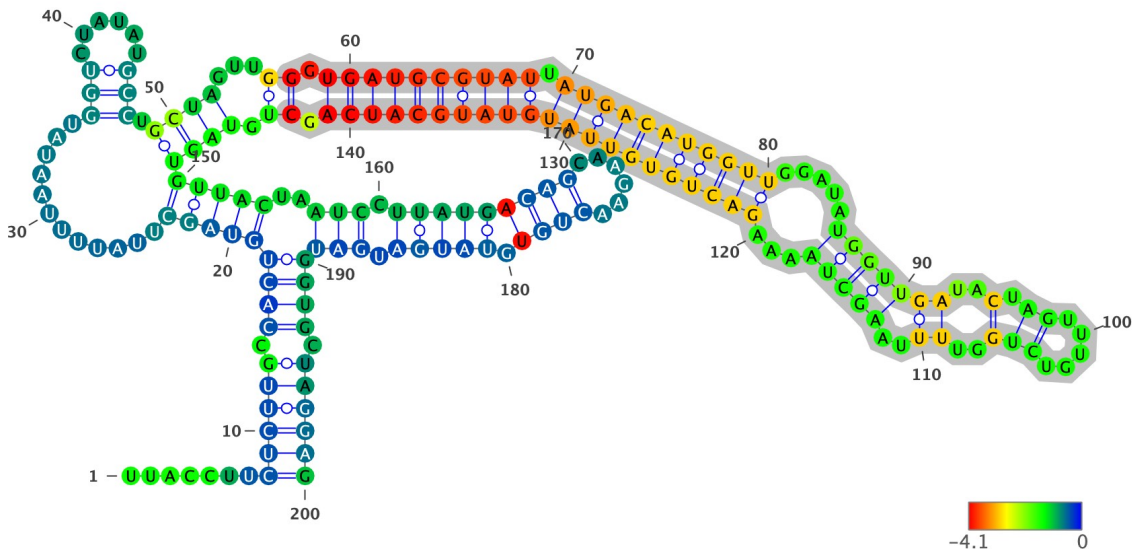
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 184 from nt 11242 to 11328 (nt 57 to 143)

```
5'-GGTGATGCGTATTATGACATGGTTGGATATGGTTGATACTAGTTTGTCTGGTUUTAAGCTAAAAGACUGUGUUAUGUAUGCAUCAGC-3'
5'-(.(((((((((.(((((((((((.........((..(..........)..)).........)))))))))))))))))))).)-3'
Motif MFE = -33.7; z-score = -5.89; ED = 5.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11186 to 11385 (motif highlighted in silver):

```
5'-UUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUU
AAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAG-3
5'-.......((((((.(((((((((.............((......))).((((...((.((((((((((.(((((((((((.....(((((((..(.((.....)))..)).
.)))))...))))))))))))))))))))).)).)))))))))..(((.((((((((((......)))).)))))).)))))))).))))))-3'
MFE = -49.4; z-score = -2.67; ED = 31.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

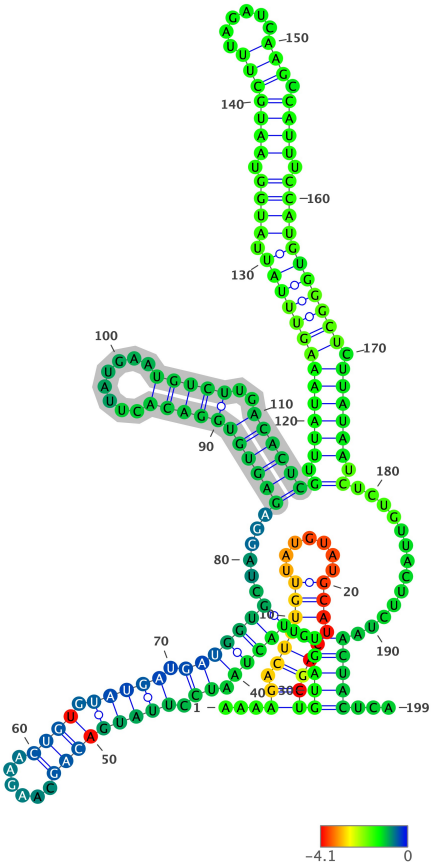
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 185 from nt 11385 to 11416 (nt 84 to 115)

```
5'-GAGTGTGGACACTTATGAAUGUCUTGACACUC-3'
5'-(((((((((((........)))))..))))))-3'
Motif MFE = -10.6; z-score = -2.95; ED = 3.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11302 to 11500 (motif highlighted in silver):

```
5'-AAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAGAGUGUGGACACUUAUGAAUGUCUUGAC
ACUCGUUUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUUCCAUGUGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCA-3
5'-...((.((((((.......))).)))))(((((..(((((.((.(((((((((.....)))).)))))).)))))))......((((((((((.........)))))..))
))))(.((((((((((((.((((.(((((((.....))).)))).))))))))))).)))))).).............)))))...-3'
MFE = -44.4; z-score = -0.84; ED = 20.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

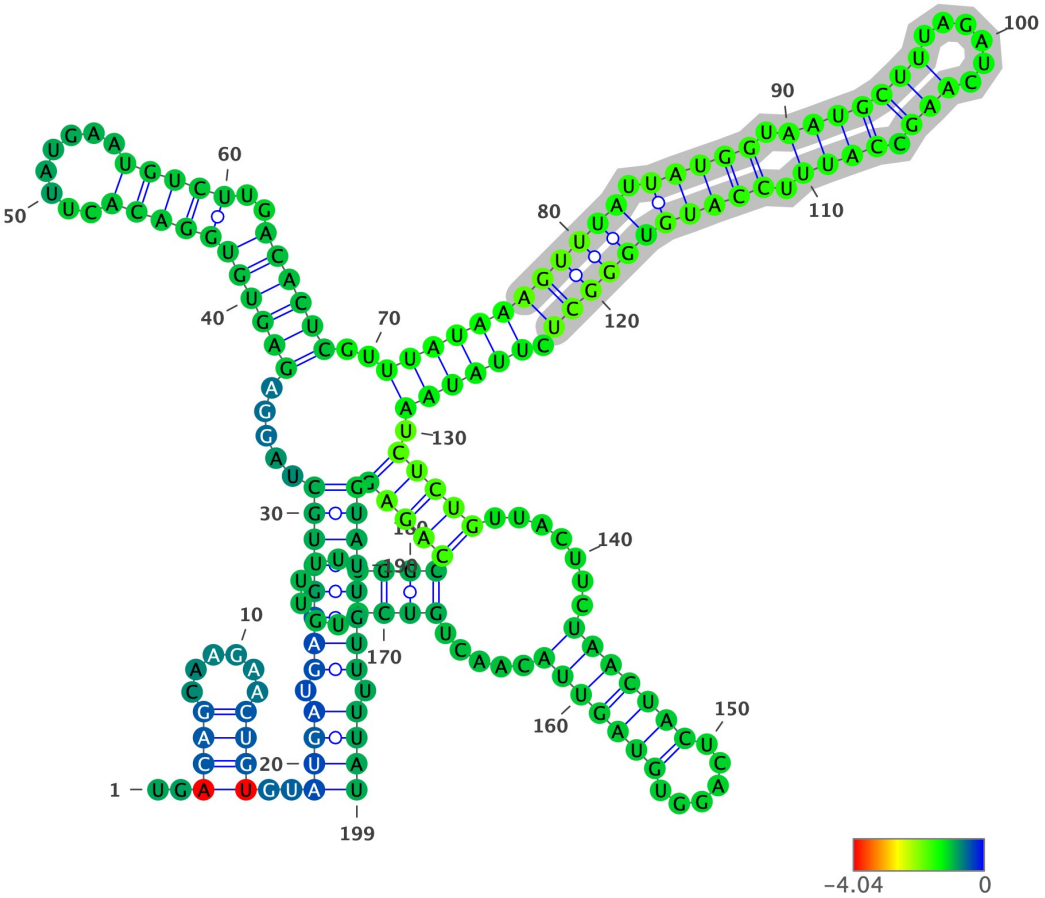
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 186 from nt 11425 to 11470 (nt 77 to 122)

```
5'-AGTTTATTATGGTAATGCTTTAGATCAAGCCAUUTCCAUGTGGGCU-3'
5'-((((...(((((.(((((((......))).)))).)))))..))))-3'
Motif MFE = -11.4; z-score = -2.3; ED = 3.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11349 to 11547 (motif highlighted in silver):

```
5'-UGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAGAGUGUGGACACUUAUGAAUGUCUUGACACUCGUUUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUU
CCAUGUGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAU-3
5'-..((((......))))..((((.((((((((.....((((((((((.........)))))..))))))..((((((((((((.(((((.(((((((......))).)))).
)))))))))))).)))))).(((((.......(((((((......)))))))).....((((......)))))))))))))))))).))))-3'
MFE = -48.4; z-score = -1.31; ED = 33.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

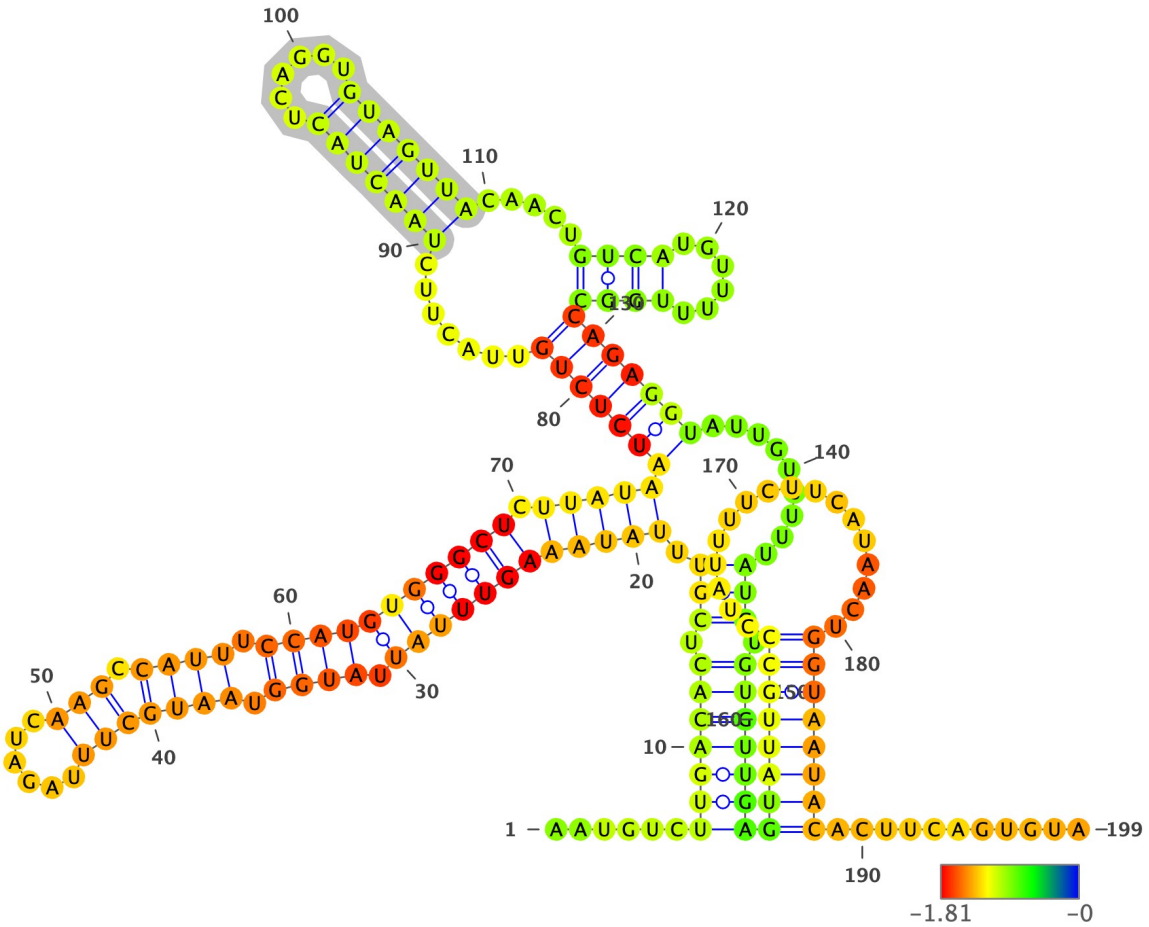
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 187 from nt 11491 to 11510 (nt 90 to 109)

```
5'-TAACTACTCAGGTGUAGUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.2; z-score = -3.91; ED = 0.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11402 to 11600 (motif highlighted in silver):

```
5'-AAUGUCUUGACACUCGUUUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUUCCAUGUGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACA
ACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUA-3
5'-......(((((((.(((.(((((((((((.((((.(((((((.....))).)))).)))))))))))).)))))(((((((.......(((((((.....)))))))..
...((((.....)))))))))).........))).)))))))((((((((.................)))))))).........-3'
MFE = -43.3; z-score = -1.91; ED = 20.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

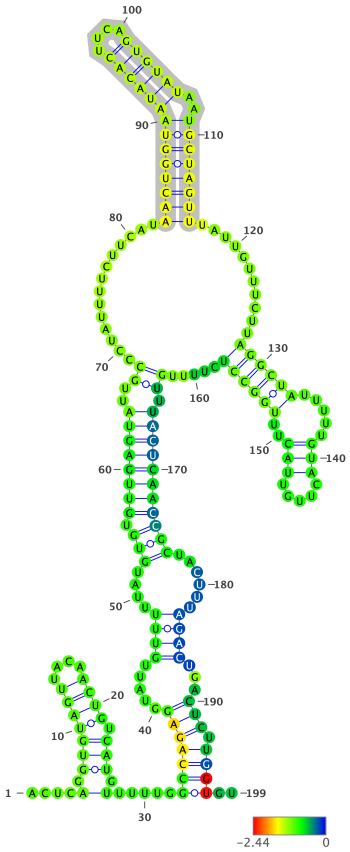
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 188 from nt 11578 to 11611 (nt 83 to 116)

```
5'-AACTGGTAATACACTTCAGUGUAUAATGCUAGUU-3'
5'-(((((((.((((((....))))))...)))))))-3'
Motif MFE = -11.8; z-score = -3.98; ED = 1.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11496 to 11694 (motif highlighted in silver):

```
5'-ACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGC
UAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGU-3
5'-....(.(((((((....)))).))).).....(((((((.....((((....(((.((((((((..((..............((((((((((((((....))))))..)))
)))))..........((((((.....(((.....)))..))))))).....)).)))))))))))).....))))...))).))))..-3'
MFE = -42.0; z-score = -1.51; ED = 31.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

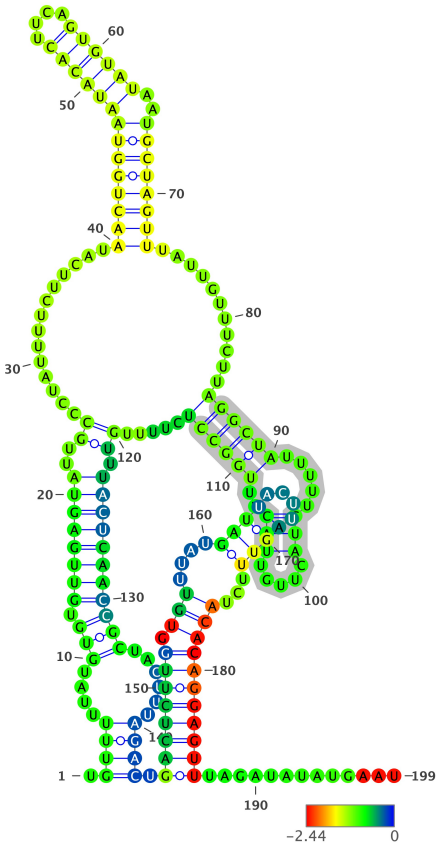
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 189 from nt 11624 to 11651 (nt 86 to 113)

```
5'-GGCTATTTTTGTACTTGTTACTTTGGCC-3'
5'-((((.....................))))-3'
Motif MFE = -4.4; z-score = -1.58; ED = 1.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11539 to 11737 (motif highlighted in silver):

```
5'-UGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGCUAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGG
CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAU-3
5'-.((((....(((.(((((((((..((..............((((((((((((((....))))))..))))))))...........((((((.....(((.....)))..)))
)))).....)).))))))))))).....)))).((((((((.(((....((((....))))...)))))))))))..............-3'
MFE = -41.8; z-score = -2.58; ED = 23.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

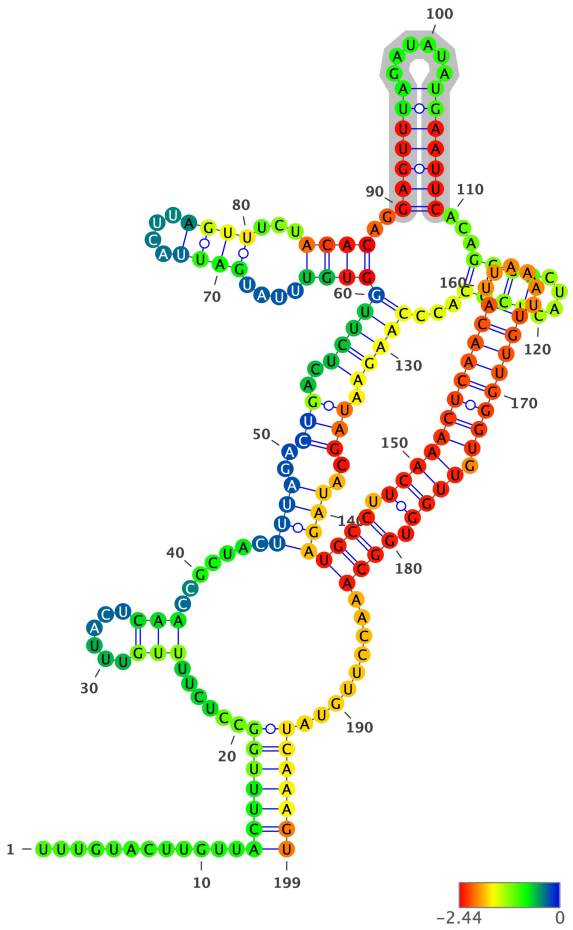
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 190 from nt 11720 to 11739 (nt 90 to 109)

```
5'-GAGTTTAGATATATGAAUUC-3'
5'-(((((..........)))))-3'
Motif MFE = -3.4; z-score = -3.52; ED = 0.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11631 to 11829 (motif highlighted in silver):

```
5'-UUUGUACUUGUUACUUUGGCCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCAC
AGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGU-3
5'-............(((((((......(((......)))........((((..(((..((((((((((....((((....))))...))))..(((((((......)))))))..
.((((....))))...)))))).)))..))))((((.((((((((((((......))))))))).)))).)))).........)))))))-3'
MFE = -40.2; z-score = -0.6; ED = 40.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

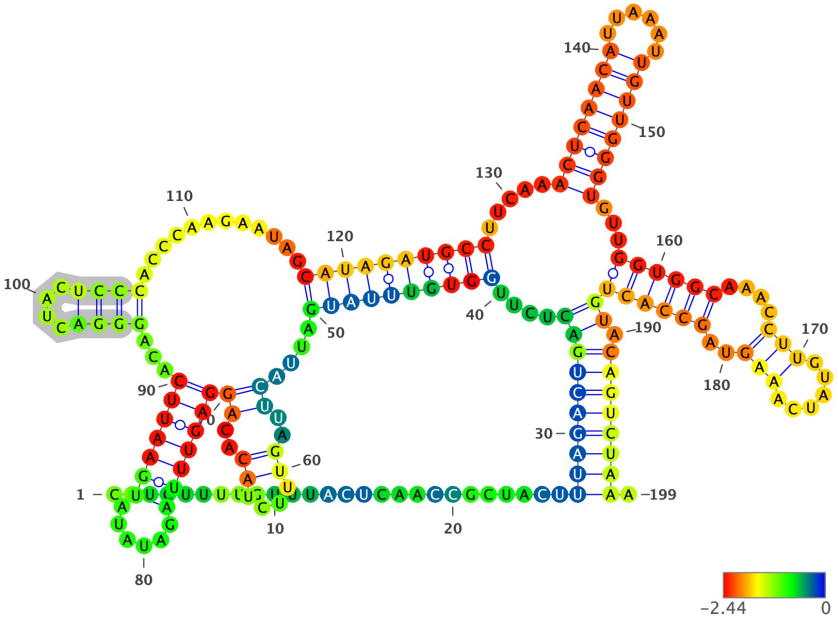
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 191 from nt 11744 to 11753 (nt 95 to 104)

```
5'-GGACTACTCC-3'
5'-((......))-3'
Motif MFE = -0.3; z-score = -3.36; ED = 1.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11650 to 11848 (motif highlighted in silver):

```
5'-CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAA
GAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAA-3
5'-.........................((((((((((....((((((((((....((..((....))..))(((((((......)))))))...((((....))))......
......))))))))))).....((((((((......))))))))...((((((....(((......)))..)))))))).)))))))).-3'
MFE = -47.9; z-score = -2.13; ED = 38.33
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

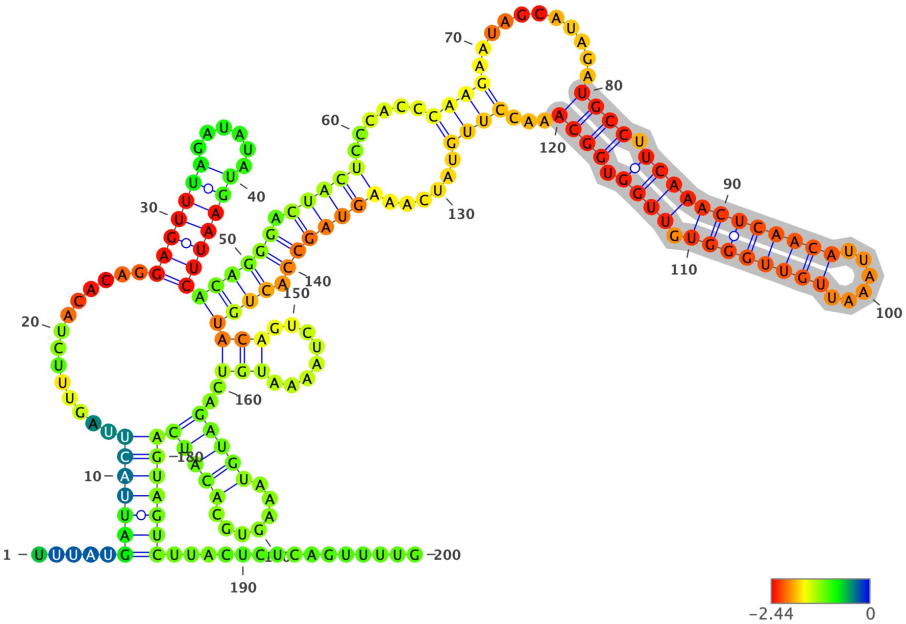
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 192 from nt 11773 to 11813 (nt 80 to 120)

```
5'-TGCCTTCAAACTCAACATTAAATUGUUGGGUGUUGGTGGCA-3'
5'-((((.(((((((((((((.....)))))))).)))).))))-3'
Motif MFE = -17.7; z-score = -4.3; ED = 1.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11694 to 11893 (motif highlighted in silver):

```
5'-UUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUG
UUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUG-3
5'-.....(((((((..............(((((((.....)))))))((((((.(((((.....((((...........((((.(((((((((((((.....)))))))).
)))).))))...))))......)))))))).))))(((........)))..(((((.......)))))))))))).................-3'
MFE = -45.0; z-score = -1.71; ED = 28.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

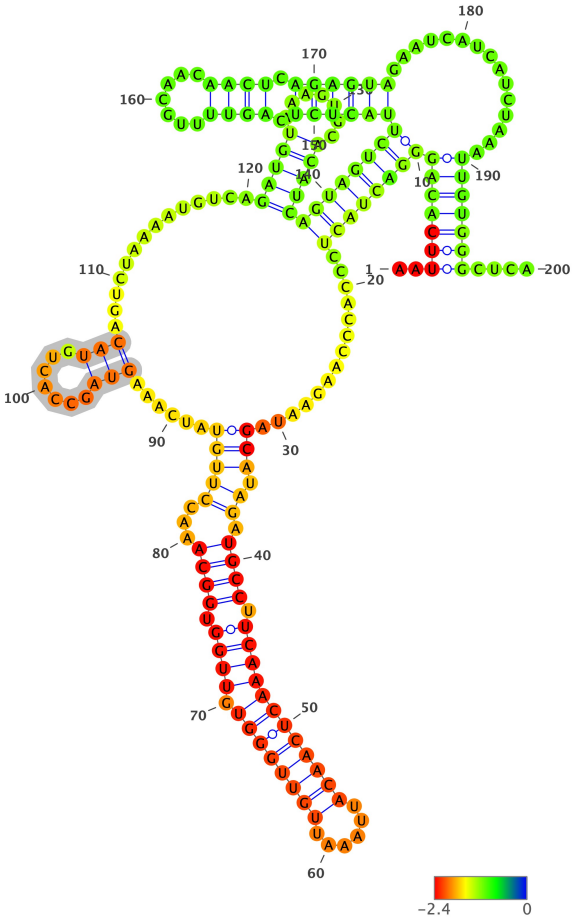
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 193 from nt 11828 to 11840 (nt 94 to 106)

```
5'-GTAGCCACTGUAC-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.4; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11735 to 11934 (motif highlighted in silver):

```
5'-AAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCU
AAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCA-3
5'-..(((((((((((((((.............(((.((.((((.((((((((((((.....))))))))).))))).))))...)))))......(((.......)))..... .........(((((.......)))))))))))))((((((.((((.......)))).))))))...............)))))))....-3'
MFE = -42.8; z-score = -2.8; ED = 34.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

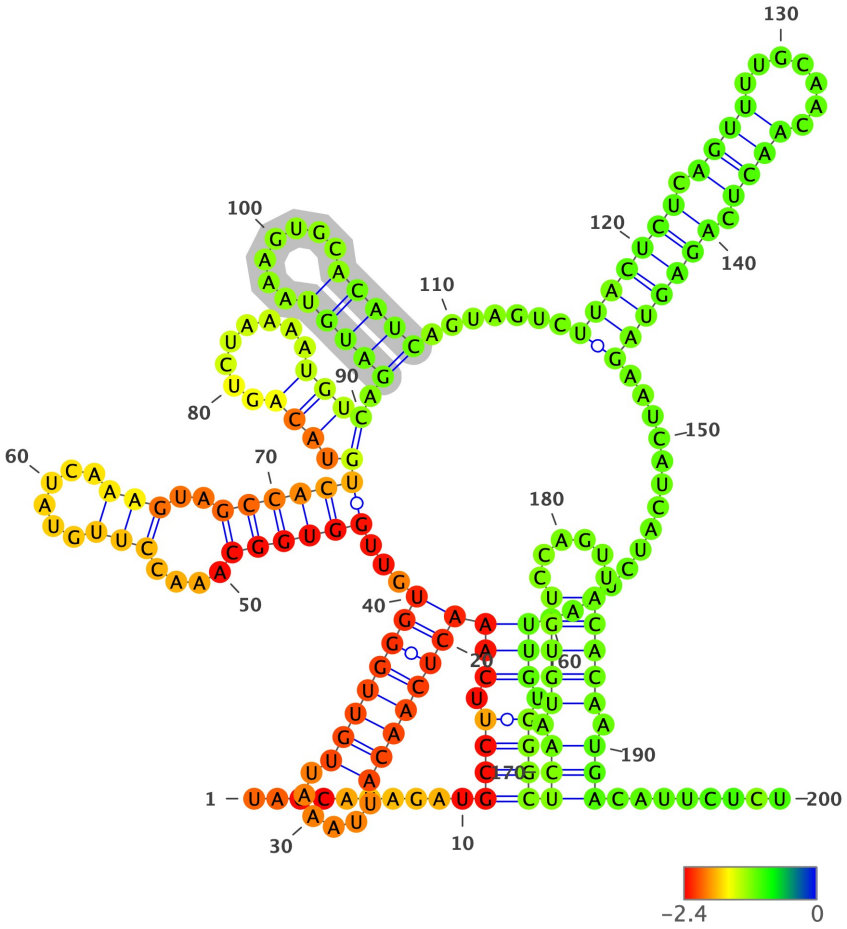
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 194 from nt 11855 to 11871 (nt 92 to 108)

```
5'-GATGTAAAGTGCACAUC-3'
5'-((((.........))))-3'
Motif MFE = -2.1; z-score = -1.64; ED = 1.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11764 to 11963 (motif highlighted in silver):

```
5'-UAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGU
AGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCU-3
5'-..........((((.(((((((((((......))))))))...((((((....(((......)))..))))))(.(((........)))).(((((.......)))))...
....(((((((.((((.......)))).)))))))..............))).))))(((.(((((......))))).))).........-3'
MFE = -45.8; z-score = -2.49; ED = 42.42
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

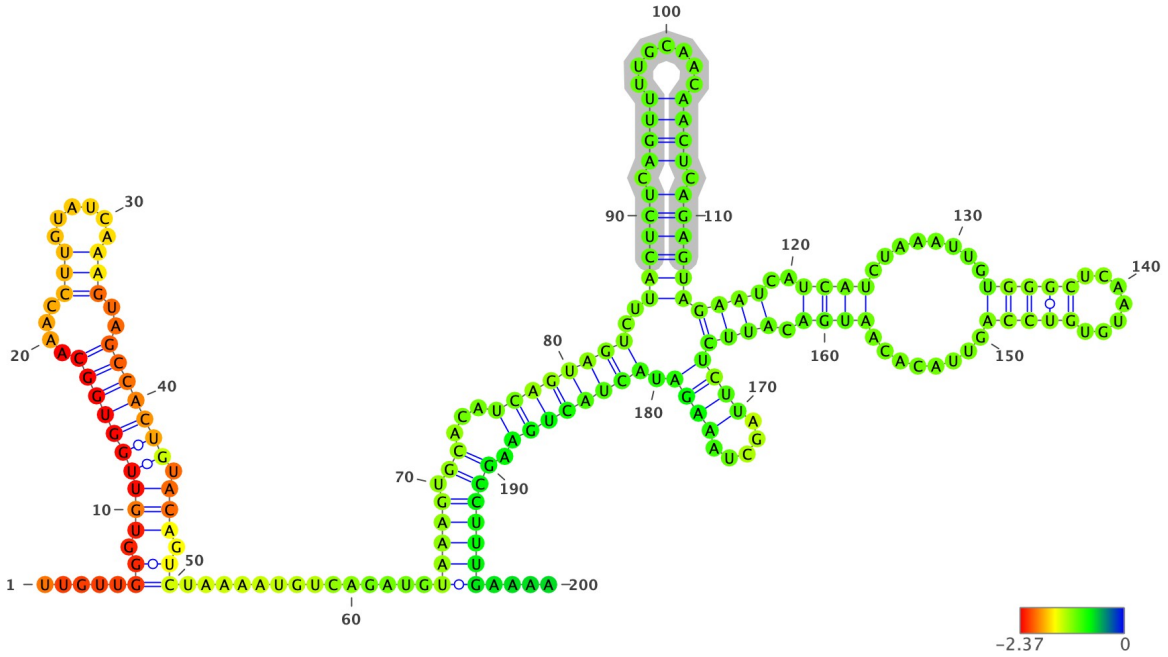
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 195 from nt 11882 to 11906 (nt 88 to 112)

```
5'-CTCTCAGTTTTGCAACAACUCAGAG-3'
5'-((((.((((.......)))).)))).))))-3'
Motif MFE = -4.0; z-score = -1.59; ED = 1.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11795 to 11994 (motif highlighted in silver):

```
5'-UUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGA
GUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAA-3
5'-.....((.((((((((((....(((.....)))..)))))))).))).)).............(((((.((...((((((((..((((((.((((.......)))).)))
)))(((((..((((.......(((((.......)))))).......)))).)))))((((.....)))).)))))))).)))))))....-3'
MFE = -45.6; z-score = -1.14; ED = 33.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

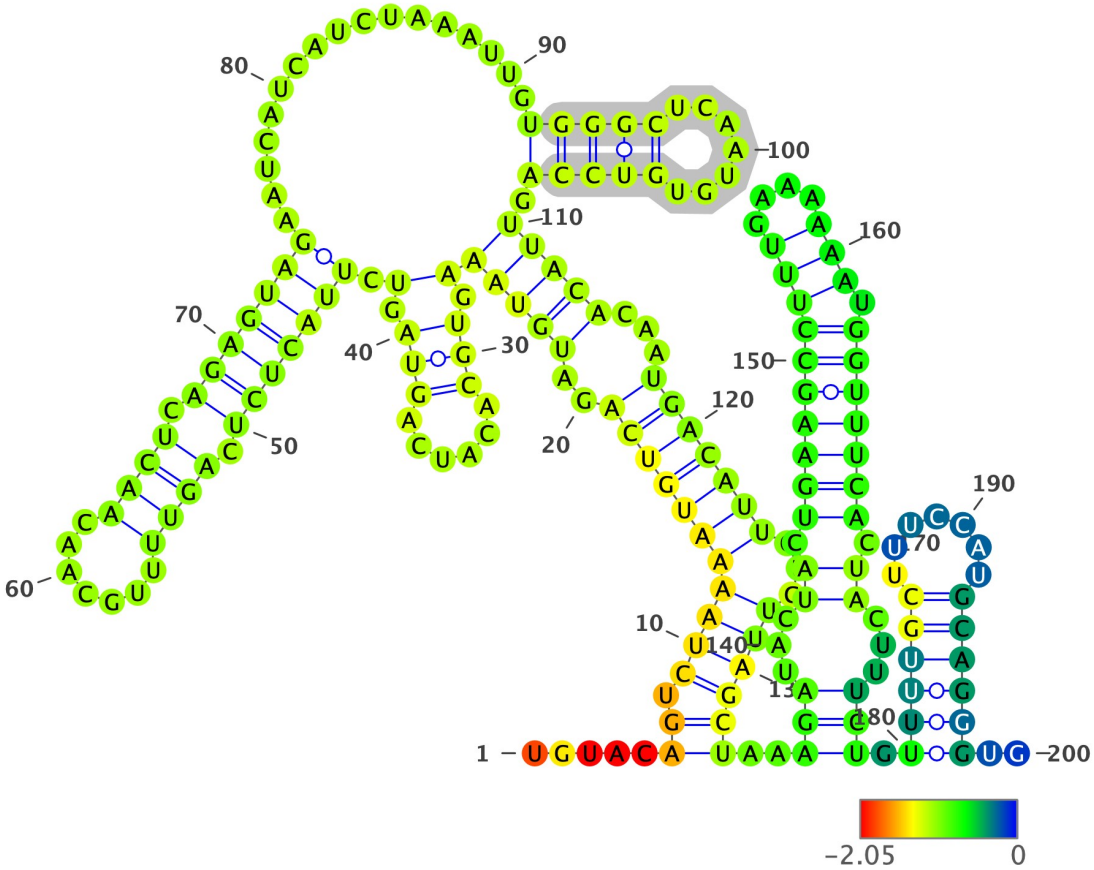
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 196 from nt 11928 to 11942 (nt 93 to 107)

```
5'-GGGCTCAATGTGUCC-3'
5'-((((.......))))-3'
Motif MFE = -3.4; z-score = -1.73; ED = 0.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11836 to 12035 (motif highlighted in silver):

```
5'-UGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUU
ACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAAAAUGGUUUCACUACUUUCUGUUUUGCUUUCCAUGCAGGGUG-3
5'-.....((.(((((((((((..((((((.(((......))).).(((((((.((((.......)))).)))))))).................(((((.......))))).))
)))...)))))))...))))))..(((...((.((((((((((....))).)))))))).))...))).((((((.......))))))..-3'
MFE = -38.8; z-score = -0.63; ED = 43.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

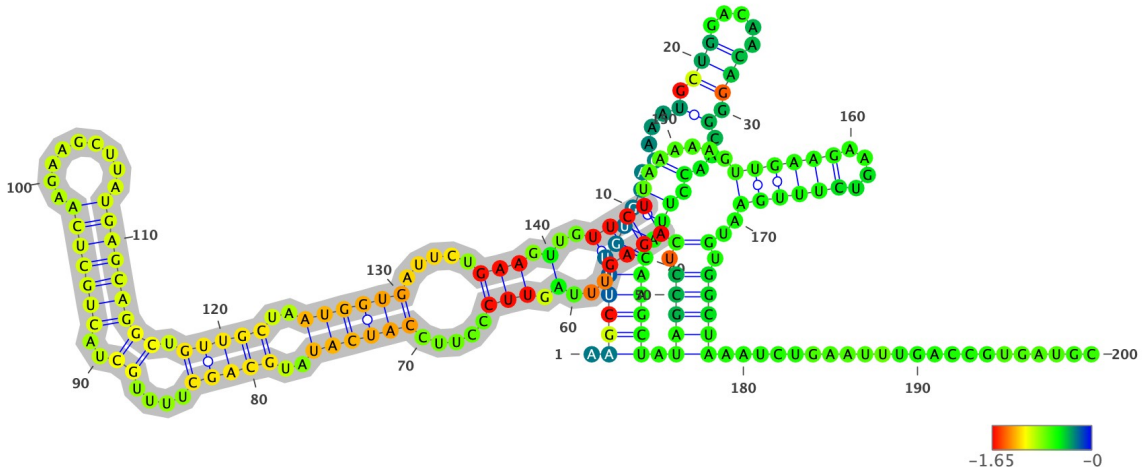
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 197 from nt 12103 to 12195 (nt 54 to 146)

```
5'-AGAGTTTAGTTCCCTTCCATCATATGCAGCTTTTGCTACTGCTCAAGAAGCTTATGAGCAGGCTGUUGCTAAUGGUGATTCTGAAGTTGUUCU-3'

5'-((((.....(((.....((((((..((((((....((..((((((...........)))))))).)))))..)))))).....)))....))))-3'
Motif MFE = -22.3; z-score = -1.24; ED = 17.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12050 to 12249 (motif highlighted in silver):

```
5'-AAGCUUUGUGAAGAAAUGCUGGACAACAGGGCAACCUUACAAGCUAUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUUAUGAG
CAGGCUGUUGCUAAUGGUGAUUCUGAAGUUGUUCUUAAAAAGUUGAAGAAGUCUUUGAAUGUGGCUAAAUCUGAAUUUGACCGUGAUGC-3
5'-.(((((.((((.(...(.(((.....))).)...).)))))))).(((((.((((((...(.(((.....((((((..(((((.....((..(((((((.........))))
)))))).)))))..)))))).....))).)..)))).......((((((....)))))).)..)))).....................-3'
MFE = -40.1; z-score = 0.04; ED = 20.58
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

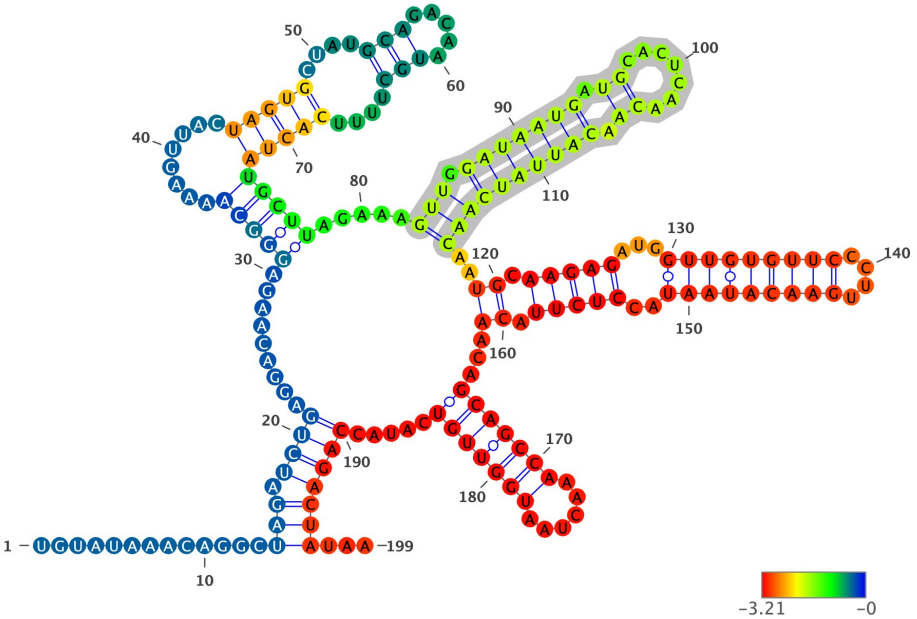
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 198 from nt 12382 to 12415 (nt 83 to 116)

```
5'-GTTGGATAATGATGCACTCAACAACAUUAUCAAC-3'
5'-(((.(((((((.((.......)).)))))))))-3'
Motif MFE = -6.3; z-score = -2.01; ED = 3.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12300 to 12498 (motif highlighted in silver):

```
5'-UGUAUAAACAGGCUAGAUCUGAGGACAAGAGGGCAAAAGUUACUAGUGCUAUGCAGACAAUGCUUUUCACUAUGCUUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUA
UCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAA-3
5'-............(((.((((.........(((((........(((((....(((.....)))....)))))))))).....(((.(((((((.((.......)).)))))
)))))..((.(((((...(((((((((....)))))))))..)))))).))...(((((((......)))))))....)))))))...-3'
MFE = -44.7; z-score = -2.03; ED = 27.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

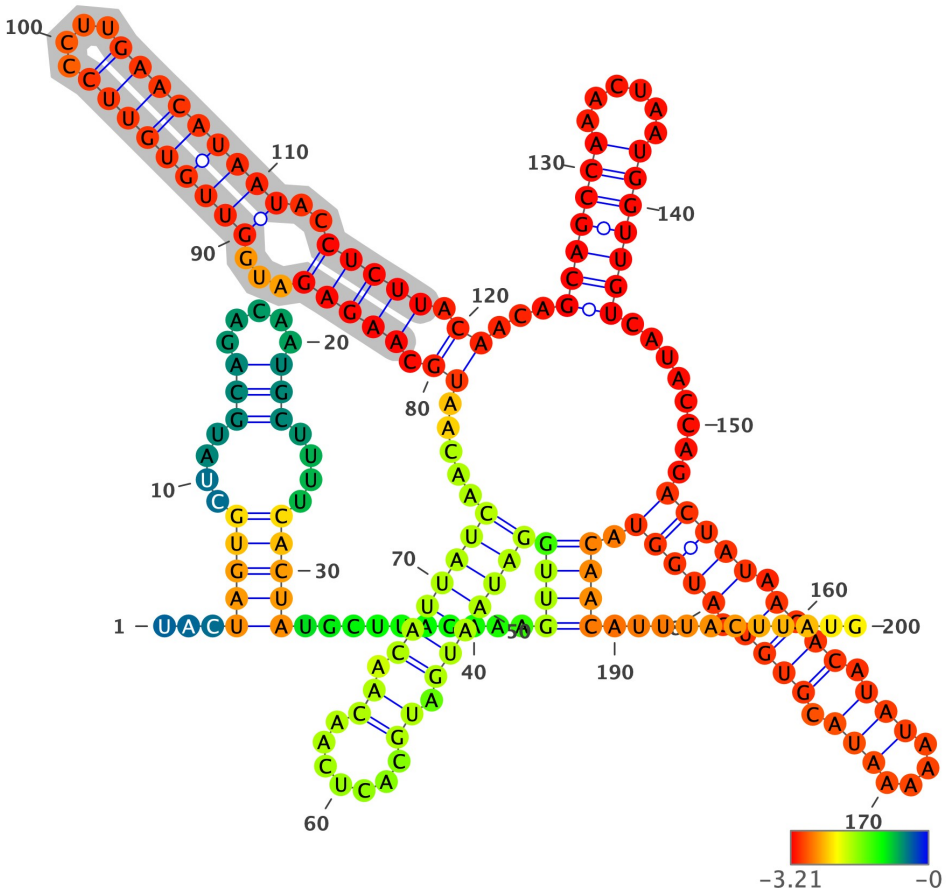
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 199 from nt 12421 to 12457 (nt 82 to 118)

```
5'-AAGAGATGGTTGTGTTCCCTTGAACAUAAUACCUCUU-3'
5'-(((((...(((((((((....)))))))))..)))))-3'
Motif MFE = -11.7; z-score = -3.47; ED = 5.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12340 to 12539 (motif highlighted in silver):

```
5'-UACUAGUGCUAUGCAGACAAUGCUUUUCACUAUGCUUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAU
ACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUG-3
5'-...(((((....((((.....)))....)))))..........((((((((((.((.......)).)))))))).....((.((((((...(((((((((....)))))))))
..)))))).))...(((((((.....)))))))........(((((.((((.(((....))).)))).)))))..)))).....-3'
MFE = -46.4; z-score = -3.68; ED = 16.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

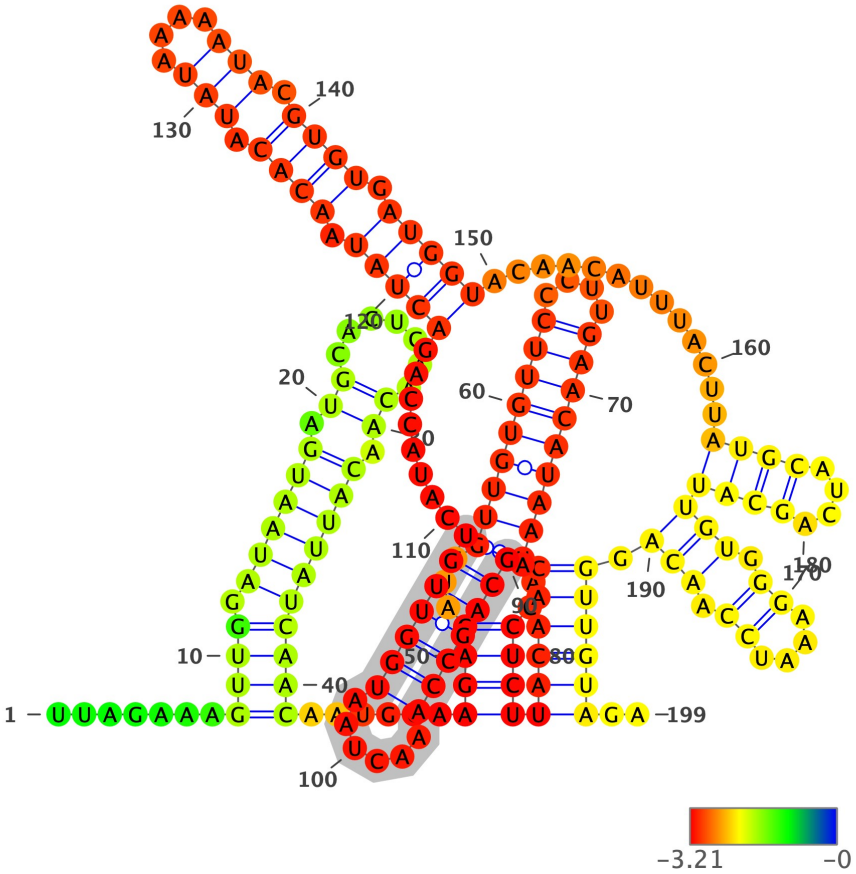
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 200 from nt 12464 to 12483 (nt 90 to 109)

```
5'-GCAGCCAAACTAAUGGUUGU-3'
5'-(((((((......)))))))-3'
Motif MFE = -7.5; z-score = -3.57; ED = 0.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12375 to 12573 (motif highlighted in silver):

```
5'-UUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCA
UACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGA-3
5'-.......((((.((((((.((.......)).))))))))))......((((...((((((((((....)))))))))..))))((((((.(((((((......)))))))..
......(((((.((((.(((....))).)))).)))))..............((((....))))(((.((....)).))).))))))..-3'
MFE = -46.3; z-score = -3.43; ED = 39.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

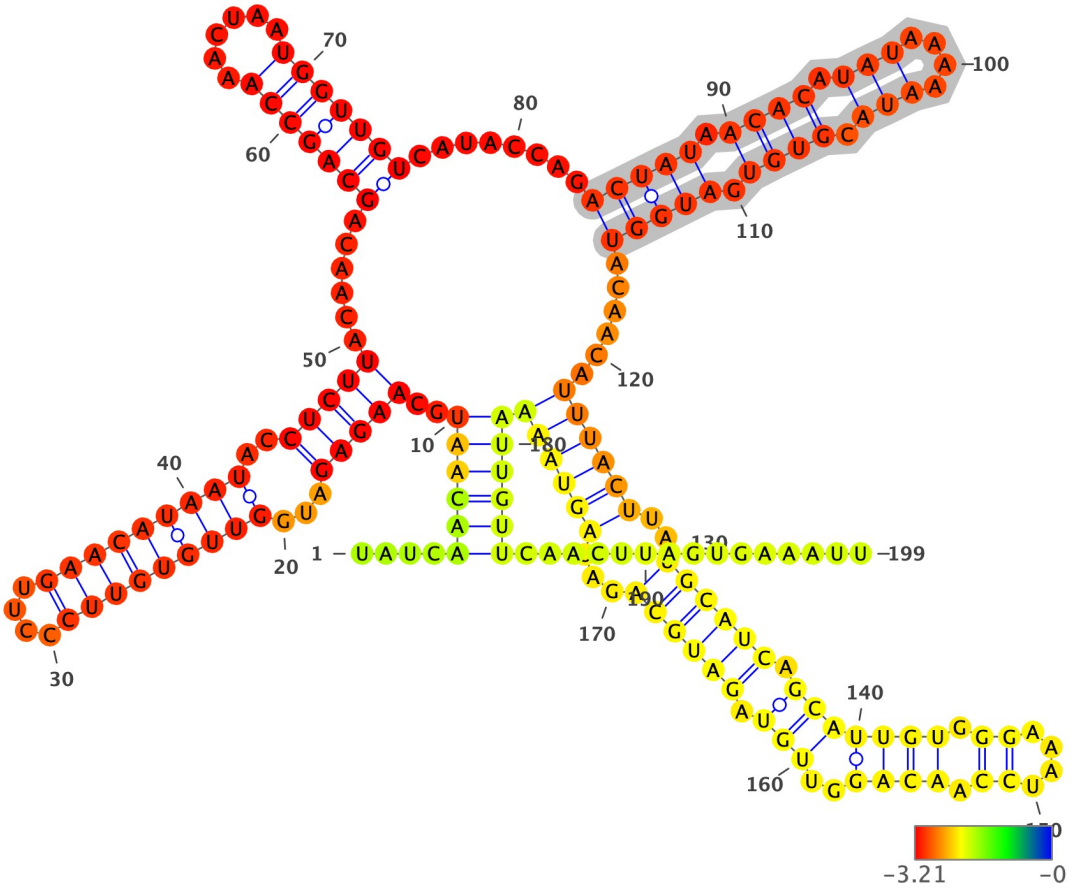
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 201 from nt 12492 to 12523 (nt 84 to 115)

```
5'-ACTATAACACATATAAAAATACGUGUGAUGGU-3'
5'-(((((.((((............)))).)))))-3'
Motif MFE = -6.6; z-score = -2.55; ED = 2.88
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12409 to 12607 (motif highlighted in silver):

```
5'-UAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGA
UGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUU-3
5'-....((((((..(((((...(((((((((....)))))))))..)))))......(((((((......)))))))........(((((.((((.(((....))).)))).)
))))......((((((..((((((.(((((((.((....)).)))))..))).))))))...))))))))))))).................-3'
MFE = -49.2; z-score = -3.54; ED = 23.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 202 from nt 12538 to 12577 (nt 80 to 119)

```
5'-TGCATCAGCATTGTGGGAAATCCAACAGGTUGUAGAUGCA-3'
5'-((((((.(((((((.((....)).)))).)))).))))))-3'
Motif MFE = -12.1; z-score = -2.24; ED = 7.45
```

Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12459 to 12657 (motif highlighted in silver):

```
5'-CAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUG
UAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUU-3
5'-....((..((((..((((((((.....)))).(((((.((((.(((....))).)))).)))))).......(((((..((((((.(((((((.((....)).)))).)))
).))))))...)))))((((((((((((.........))).))))))))).........))))..))))..)).................-3'
MFE = -44.0; z-score = -2.45; ED = 25.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

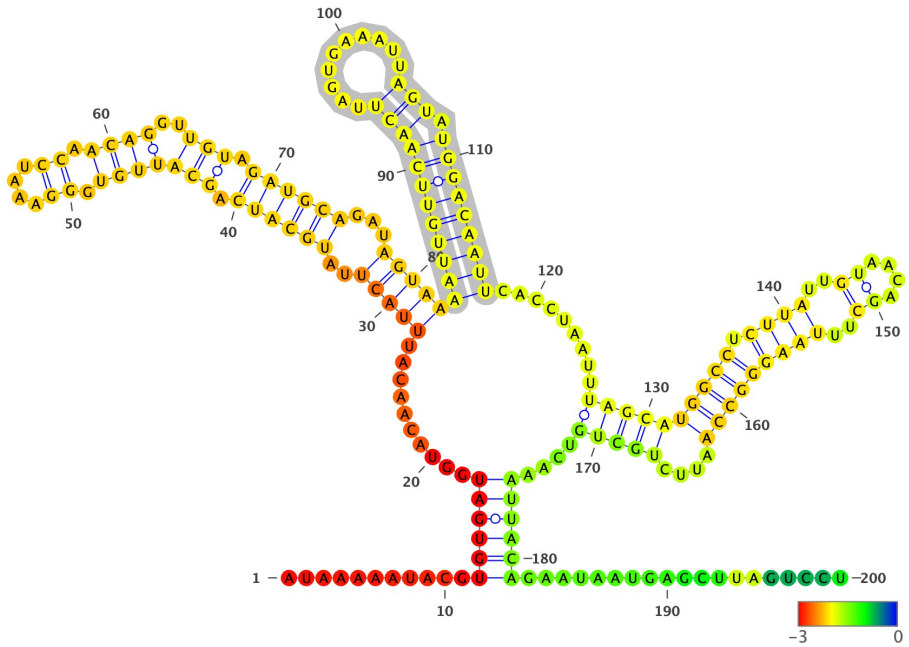
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 203 from nt 12586 to 12620 (nt 83 to 117)

```
5'-AATTGTTCAACTTAGTGAAATTAGUAUGGACAAUU-3'
5'-(((((((((((((.........))).)))))))))-3'
Motif MFE = -7.4; z-score = -2.59; ED = 4.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12504 to 12703 (motif highlighted in silver):

```
5'-AUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGG
ACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGCCAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCU-3
5'-...........((((((..........(((((..((((((.(((((((.((....)).))))..))).))))))...)))))((((((((((((.........))).)))
))))))........((((((((((.((((..((....))..)))))))))....)))))....))))))...................-3'
MFE = -45.3; z-score = -2.26; ED = 33.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

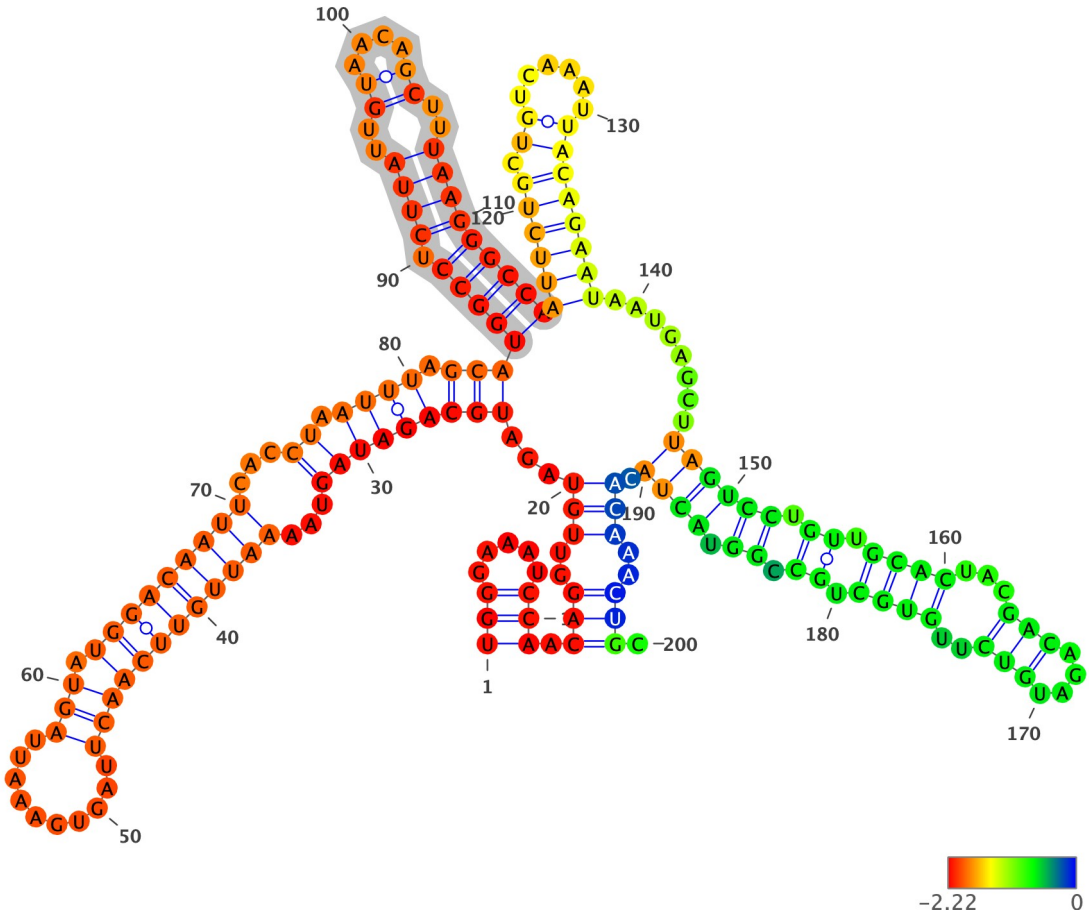
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 204 from nt 12635 to 12665 (nt 85 to 115)

```
5'-TGGCCTCTTATTGTAACAGCTTUAAGGGCCA-3'
5'-(((((.((((..(......)..)))))))))-3'
Motif MFE = -12.7; z-score = -3.84; ED = 0.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12551 to 12750 (motif highlighted in silver):

```
5'-UGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGG
GCCAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCUGUUGCACUACGACAGAUGUCUUGUGCUGCCGGUACUACACAAACUGC-3
5'-(((.....))).(((..(((...((((((((((...((((((((((((.........))).))))))))))...)).)))).)))(((((.((((..((....))..)))))
))))((((((.((......))))))).......((((((.((.((((...(((....)))..)))).)).)).)))).)))..))).-3'
MFE = -50.4; z-score = -2.15; ED = 21.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

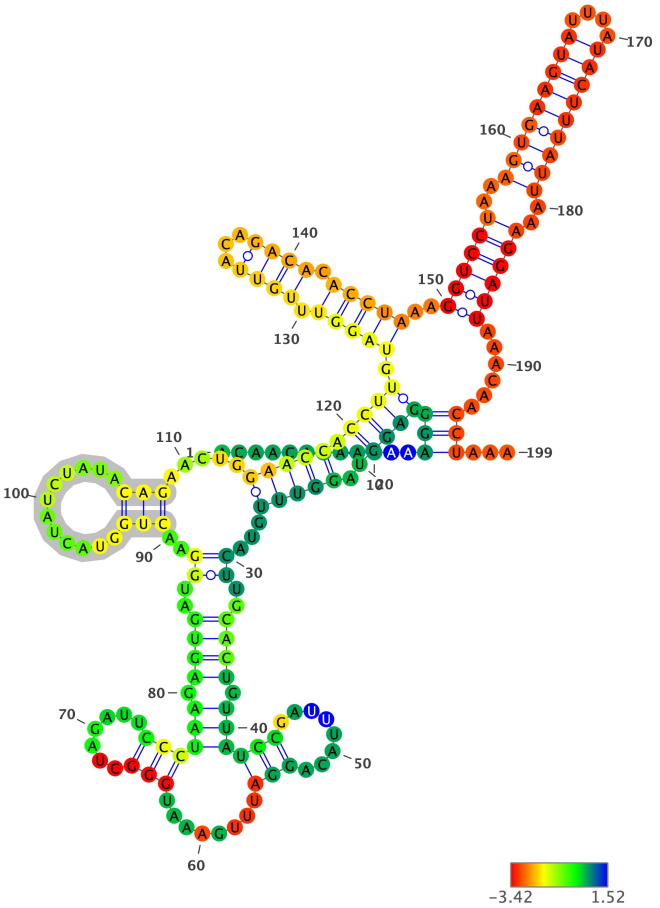
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 205 from nt 12870 to 12887 (nt 91 to 108)

```
5'-CTGGTACTATCTATACAG-3'
5'-(((............)))-3'
Motif MFE = 0.0; z-score = 0.48; ED = 3.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12780 to 12978 (motif highlighted in silver):

```
5'-ACAACACAACAAAGGGAGGUAGGUUUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAAC
UGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAA-3
5'-............((((((((.(((((...((..((((.((((((........)))........(((.......)))))).))))..))..(((............)))...
..)))))))))).(((((.((((...)))).)))))..((((((..((((((((((....)))))))))..))))))......)))...-3'
MFE = -41.9; z-score = -1.49; ED = 45.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

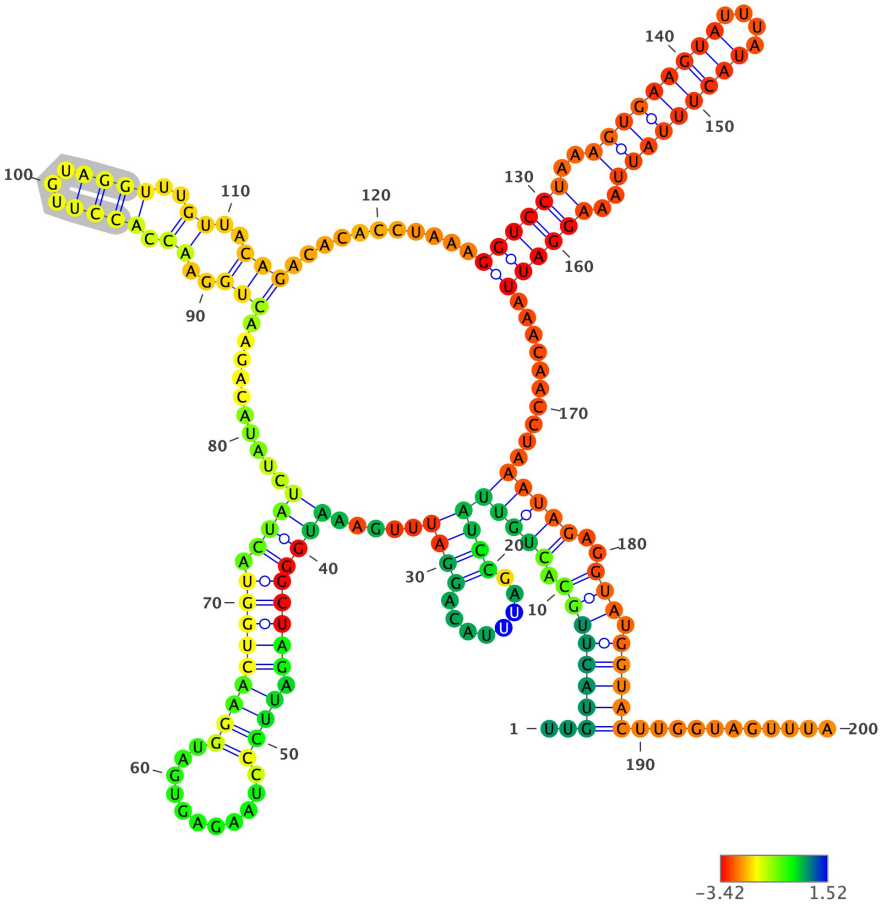
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 206 from nt 12899 to 12907 (nt 96 to 104)

```
5'-CCTTGTAGG-3'
5'-(((...)))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 1.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12804 to 13003 (motif highlighted in silver):

```
5'-UUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUA
CAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUA-3
5'-..((((((((.(((((((((........))))).....((((((((((.((((...........))))))))).))))..........(((..((.((((...))))..))..
)))...........((((((..((((((((((....)))))))))..))))))..........)))))..))).)))))...........-3'
MFE = -41.1; z-score = -0.99; ED = 39.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

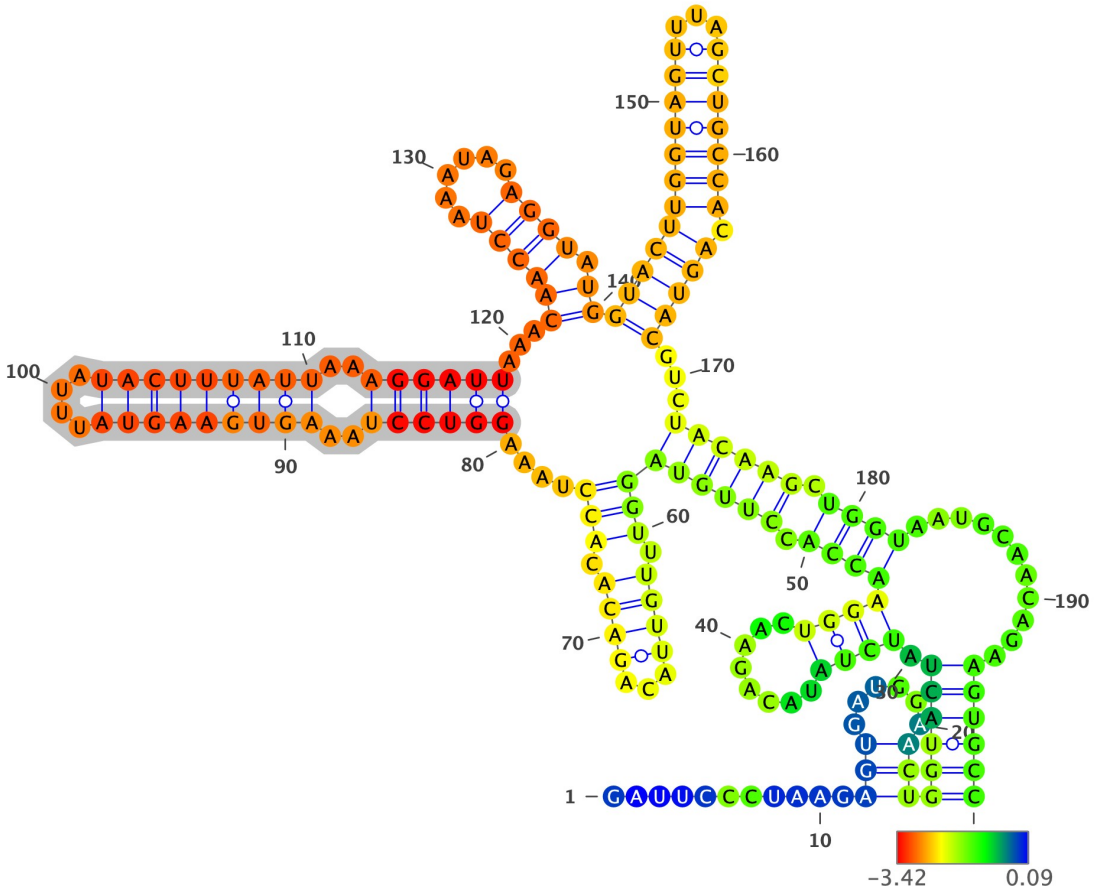
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 207 from nt 12929 to 12966 (nt 81 to 118)

```
5'-GGTCCTAAAGTGAAGTATTTAUACUUTATTAAAGGAUU-3'
5'-(((((.......(((((....)))))).......)))))-3'
Motif MFE = -11.9; z-score = -4.56; ED = 1.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12849 to 13047 (motif highlighted in silver):

```
5'-GAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUA
AAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCC-3
5'-...........(((......)))((((((.((((........))))((((.(((((((((.((((...)))).))).....((((((..(((((((((....))))))))).
.))))))...((((((......)))).))((((((((((((...)))))))).)))))...)))))).)))).........))))))-3'
MFE = -52.5; z-score = -2.94; ED = 24.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

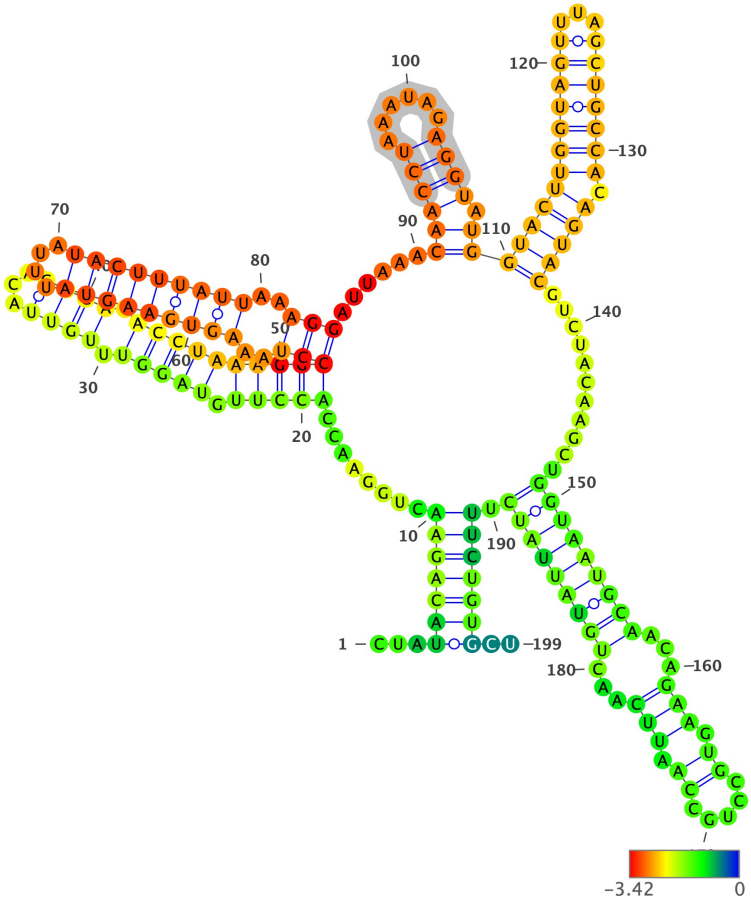
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 208 from nt 12973 to 12984 (nt 94 to 105)

```
5'-CCTAAATAGAGG-3'
5'-(((......)))-3'
Motif MFE = -0.5; z-score = -1.38; ED = 1.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12880 to 13078 (motif highlighted in silver):

```
5'-CUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGU
ACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCU-3
5'-...(((((((.........(((((.(((((.((((...)))).))))))))))(((..((((((((((....)))))))))..)))......((((((......)))).))((
((((((((((...)))))))).)))))...........((((((((...(((.((.....)).)))...))))))))).)))))))..-3'
MFE = -55.3; z-score = -3.34; ED = 29.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

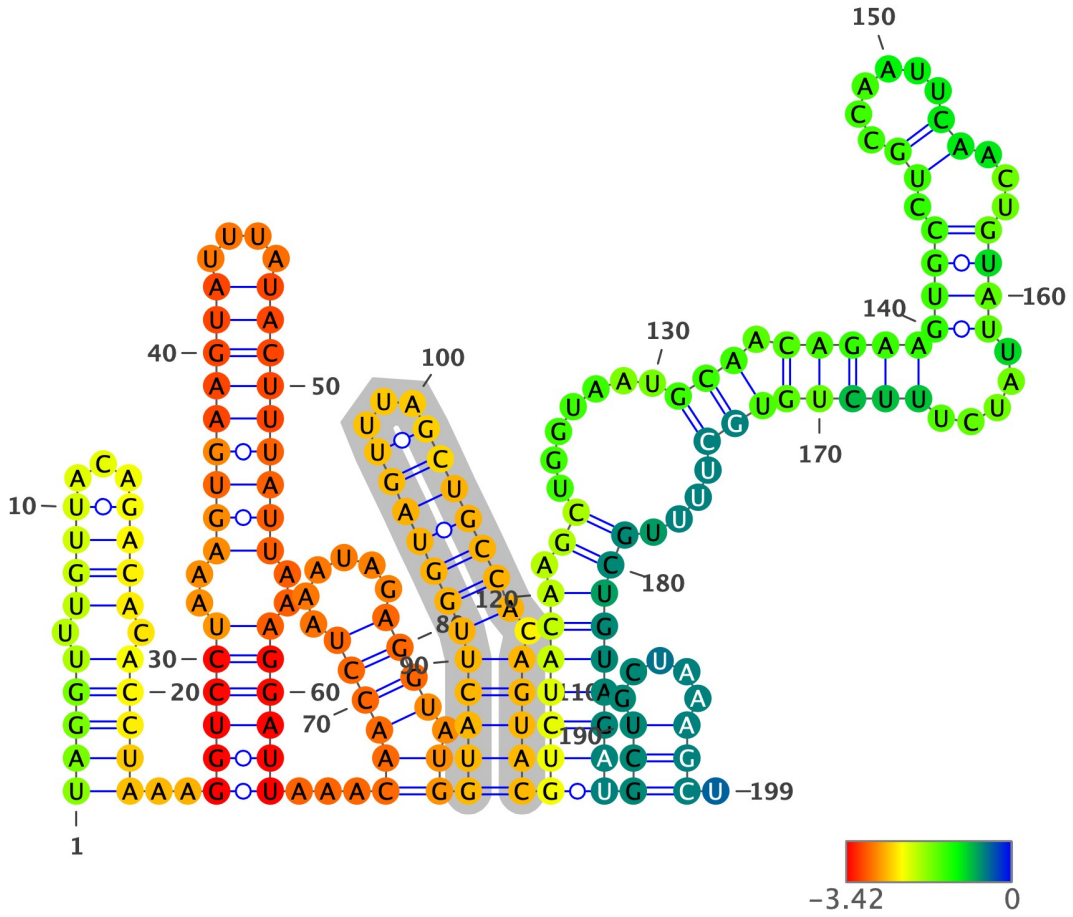
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 209 from nt 12989 to 13016 (nt 86 to 113)

```
5'-GTACTTGGTAGTTTAGCUGCCACAGUAC-3'
5'-((((((((((.......))))).)))))-3'
Motif MFE = -12.5; z-score = -4.01; ED = 0.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12904 to 13102 (motif highlighted in silver):

```
5'-UAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGU
ACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCU-3
5'-(((((.((((...)))).)))))..((((((..(((((((((....)))))))))..))))))...((((((......)))).))(((((((((((...)))))))).)))
))(((((((.((.......(((.(((((((((.((......))...))))).....)))))))).....)))))))))(((.....))).-3'
MFE = -55.6; z-score = -3.62; ED = 21.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

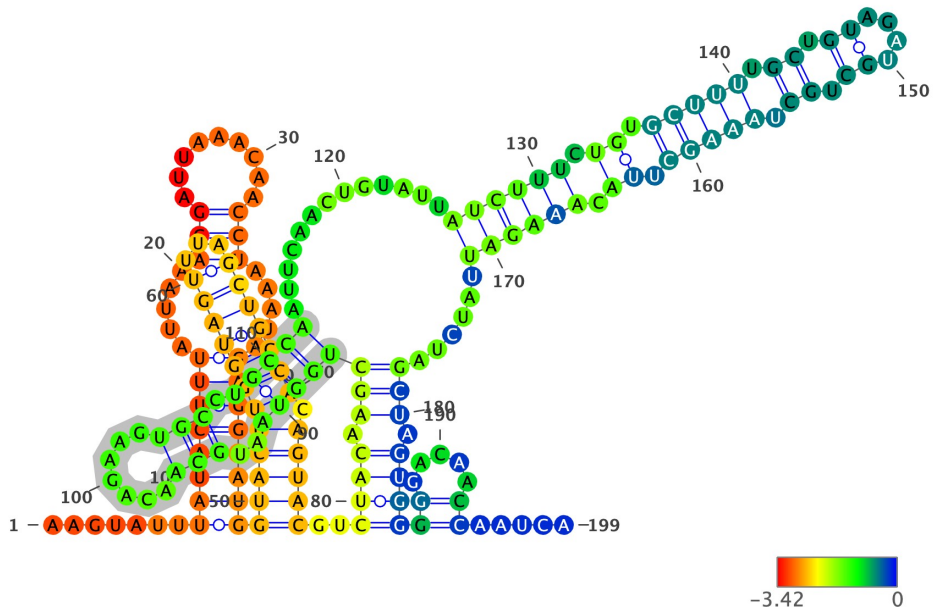
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 210 from nt 13027 to 13052 (nt 87 to 112)

```
5'-TGGTAATGCAACAGAAGUGCCUGCCA-3'
5'-(((((..(((.......))).)))))-3'
Motif MFE = -5.2; z-score = -1.31; ED = 2.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12941 to 13139 (motif highlighted in silver):

```
5'-AAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCC
AAUUCAACUGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCA-3
5'-.......(((((((.....(((.........)))).....)))))))((((((((((((...)))))))).)))))..((((.(((((((..(((.......))).))))
).............((((((.((.(((((.((.((....)).)).)))))).)).)))))).....))).)))))((.....)).....-3'
MFE = -45.3; z-score = -2.44; ED = 33.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

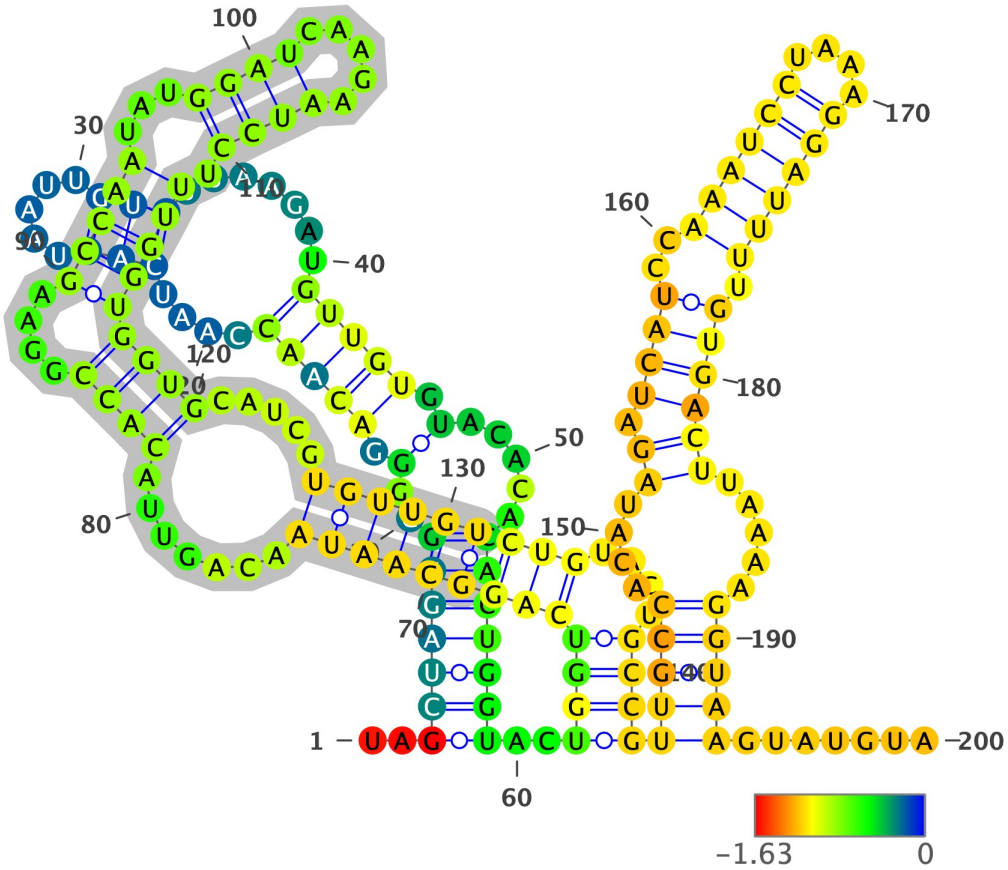
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 211 from nt 13184 to 13246 (nt 69 to 131)

```
5'-GCAATAACAGTTACACCGGAAGCCAATATGGATCAAGAAUCCTUUGGUGGUGCATCGUGUUGU-3'
5'-((((((.....................................................))))))-3'
Motif MFE = -15.3; z-score = -1.51; ED = 9.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13116 to 13315 (motif highlighted in silver):

```
5'-UAGCUAGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAUGUUGUGUACACACACUGGUACUGGUCAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCU
UUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUA-3
5'-..(((((((..(.(((((....(((.....)))).......)))))).)....)))))))..((((((((((((.......((((....(((((...((((.....)))).
))))))))).....))))))))).....))))(((((....((.((((..((((((....)))))).))))))).....)))))).......-3'
MFE = -50.1; z-score = -0.85; ED = 37.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

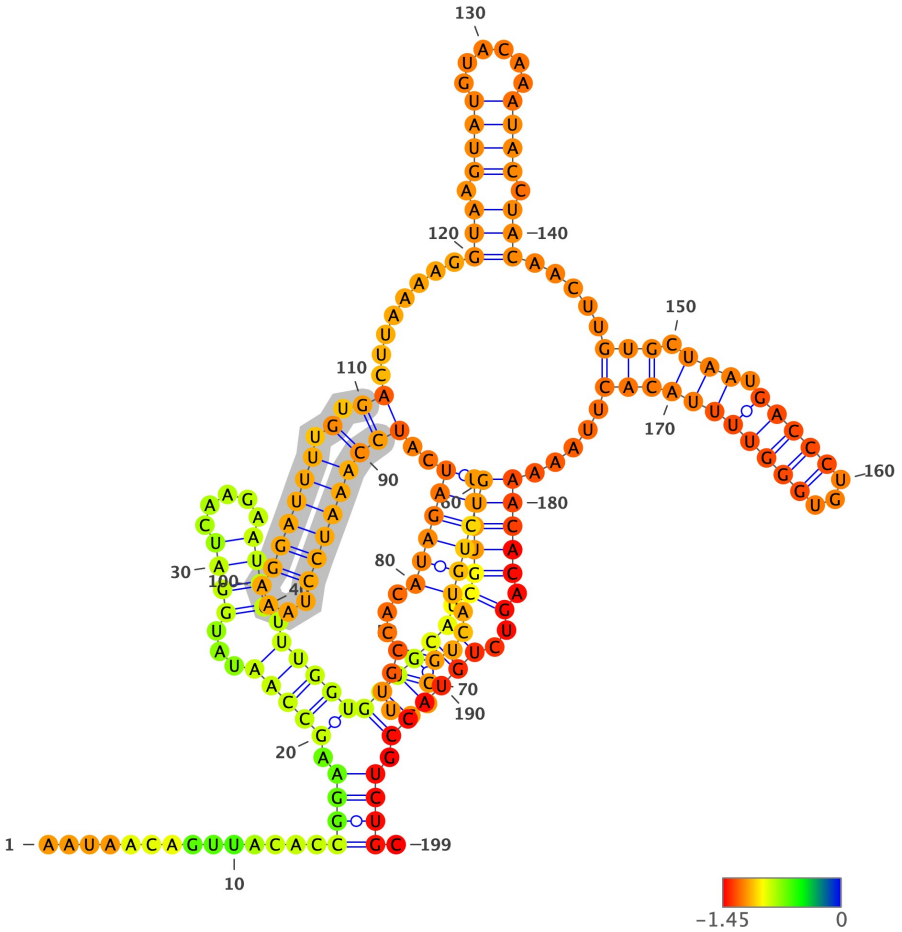
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 212 from nt 13274 to 13295 (nt 89 to 110)

```
5'-CCAAATCCTAAAGGAUUUTGTG-3'
5'-(.((((((....))))))...)-3'
Motif MFE = -4.1; z-score = -1.72; ED = 2.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13186 to 13384 (motif highlighted in silver):

```
5'-AAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGA
CUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGC-3
5'-..............((((.(((((...((((.....)))).)))))((((((.((((((((((((...((....))...))))))..((((((((((....)))))).).))
........(((.((((......)))).)))).....(((.(((.(((((...)))))))))))).....))))).)..)))))).)))).-3'
MFE = -40.1; z-score = -0.71; ED = 50.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

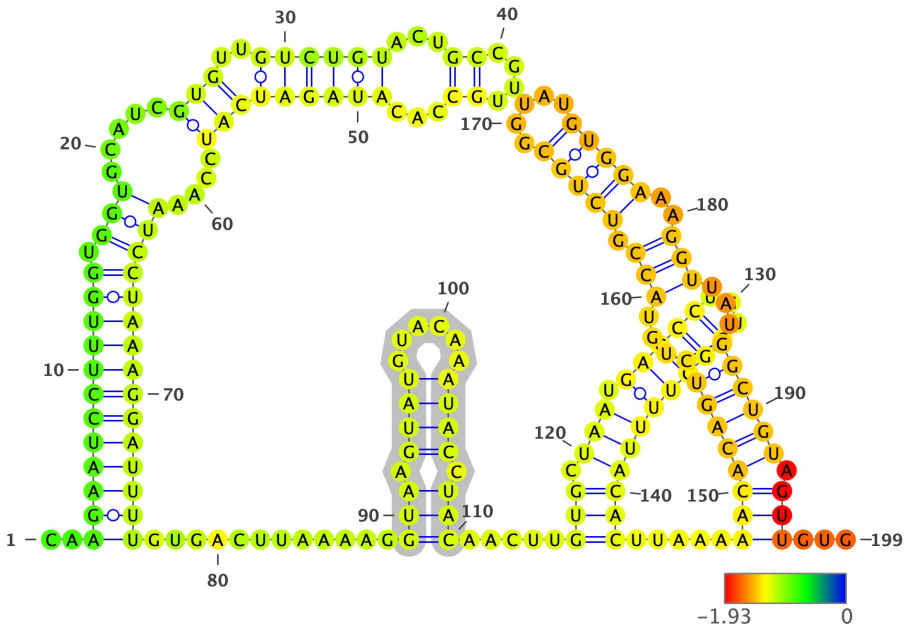
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 213 from nt 13305 to 13326 (nt 89 to 110)

```
5'-GTAAGTATGTACAAAUACCUAC-3'
5'-(((.(((........))).)))-3'
Motif MFE = -3.0; z-score = -2.13; ED = 1.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13217 to 13415 (motif highlighted in silver):

```
5'-CAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACA
ACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUG-3
5'-..(((((((((((.(((.....(((..((((((...((....))...)))))))))....))))))))))))))).............(((.((((......)))).))).
....(((.(((.(((((...)))))))))))).....(((((((((...(((.(((((.....)))))..)))...)))))).)))...-3'
MFE = -49.6; z-score = -1.51; ED = 57.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

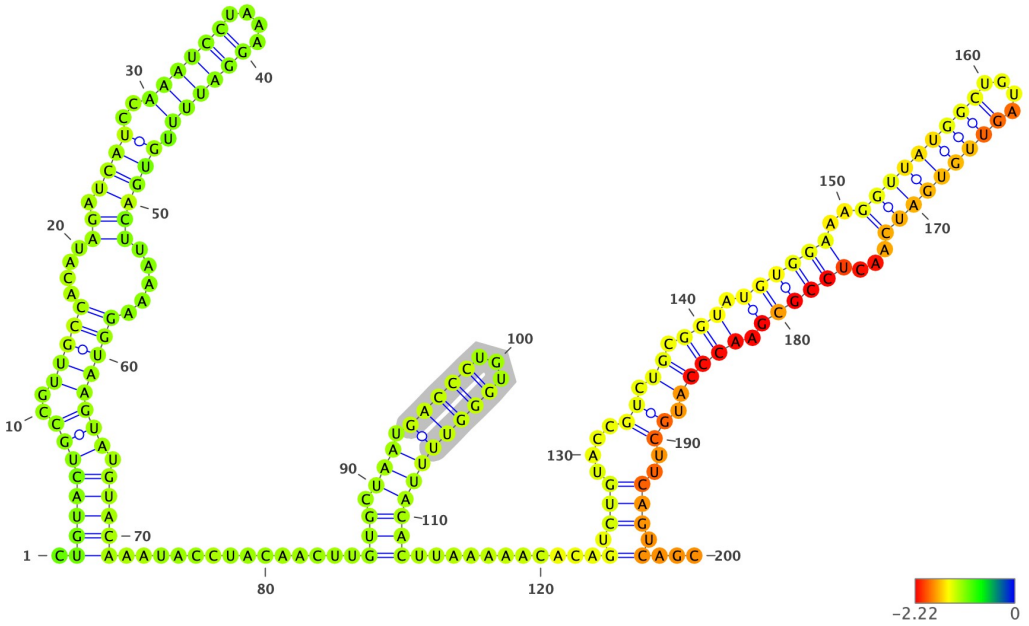
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 214 from nt 13340 to 13352 (nt 94 to 106)

```
5'-GACCCTGTGGGUU-3'
5'-(((((...)))))-3'
Motif MFE = -4.2; z-score = -3.65; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13247 to 13446 (motif highlighted in silver):

```
5'-CUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACA
CUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGC-3
5'-.((((((((..(((((....((.((((..((((((....)))))).))))))).....)))))))).))))).............(((.(((.(((((...)))))))))
)...........(.(((....((.((.(((.((((((..(((((((((....)))))))))...)))))).))))).))..))).)...-3'
MFE = -47.6; z-score = -0.83; ED = 55.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

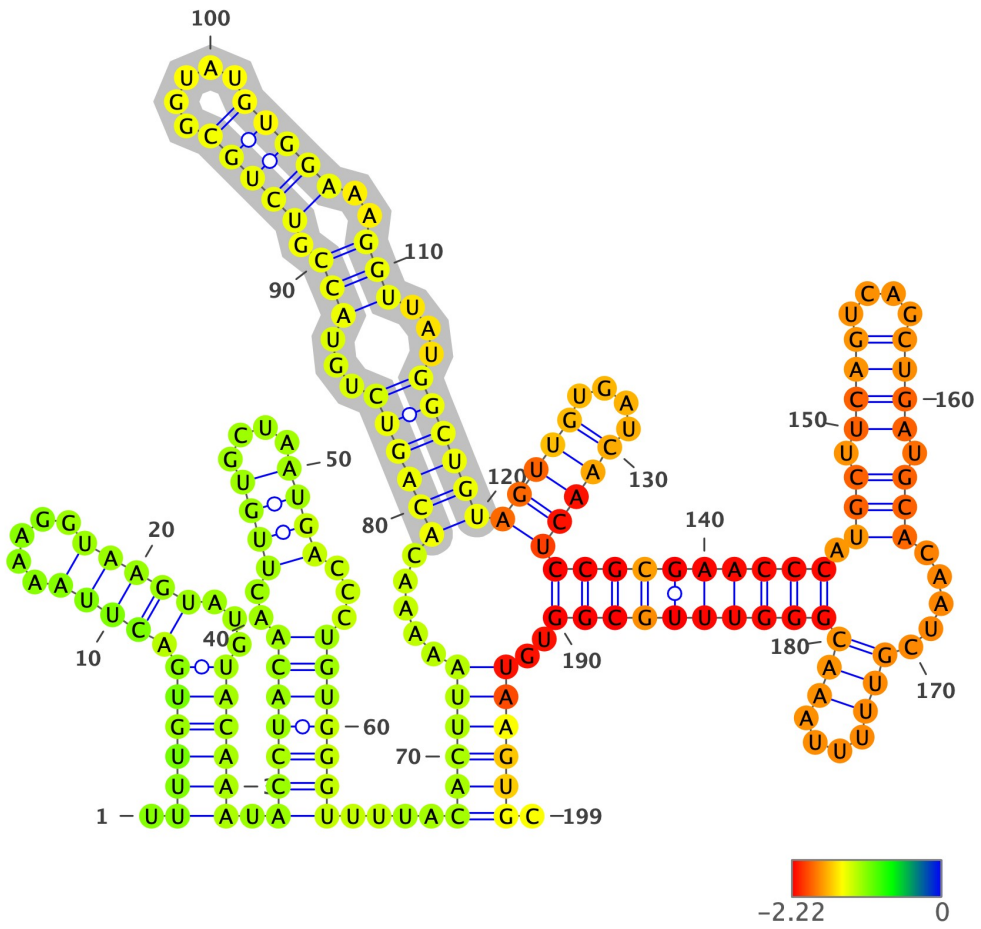
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 215 from nt 13367 to 13408 (nt 79 to 120)

```
5'-ACAGTCTGTACCGTCTGCGGTATGTGGAAAGGUTATGGCUGU-3'
5'-(((((....(((.(((.........)))..)))....)))))-3'
Motif MFE = -14.5; z-score = -2.5; ED = 2.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13289 to 13487 (motif highlighted in silver):

```
5'-UUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGU
UAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGC-3
5'-.(((((((((((.....)))))...)))))).(((((((..((((....))))...)))))))....((((((.....((((((...(((.(((((.....)))))..)))
...))))))(((((....)))))((((((((((.(((.((((....)))).)))).....(((....)))))))))))))..)))))).-3'
MFE = -57.6; z-score = -2.25; ED = 40.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 180--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 180 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

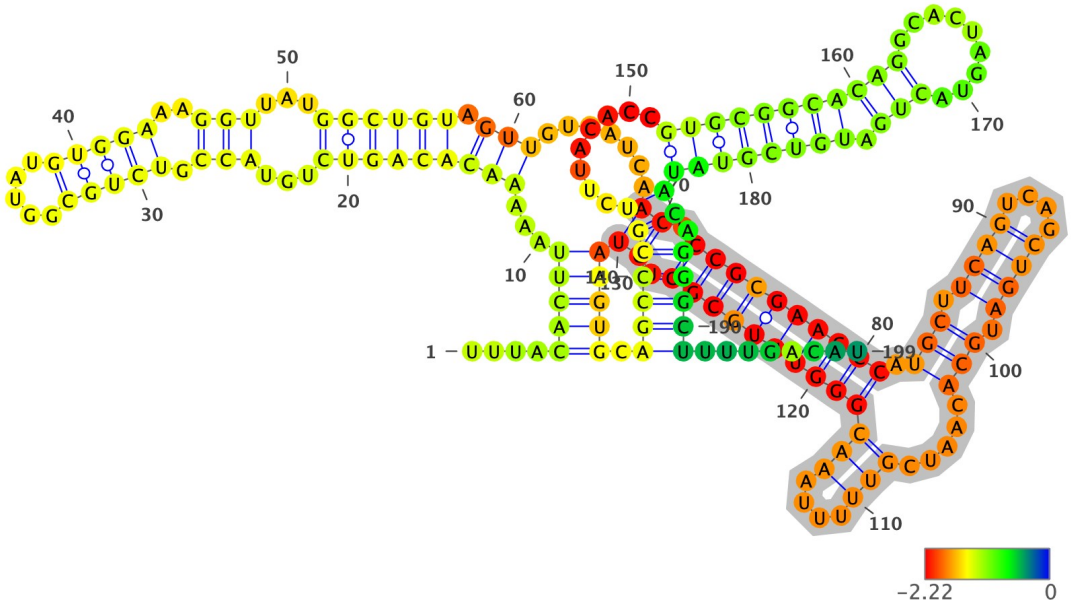
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 195--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 216 from nt 13420 to 13481 (nt 69 to 130)

```
5'-ACTCCGCGAACCCATGCTTCAGTCAGCTGATGCACAATCGTTTTTAAACGGGUUUGCGGTGU-3'
5'-((.(((.((((((..((.((........)).))................))))))).))).))-3'
Motif MFE = -24.3; z-score = -3.95; ED = 3.08
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13352 to 13550 (motif highlighted in silver):

```
5'-UUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUU
UUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAU-3
5'-....(((((...(((((((((...(((.(((((.....))))).)))...)))))).))).......((.((((((((((.(((.((((....)))).))).....(((.
...))))))))))))).))))))).(((((((........((((((((((.........))).))))))))))).))))).........-3'
MFE = -63.8; z-score = -2.49; ED = 27.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 117--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 117 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

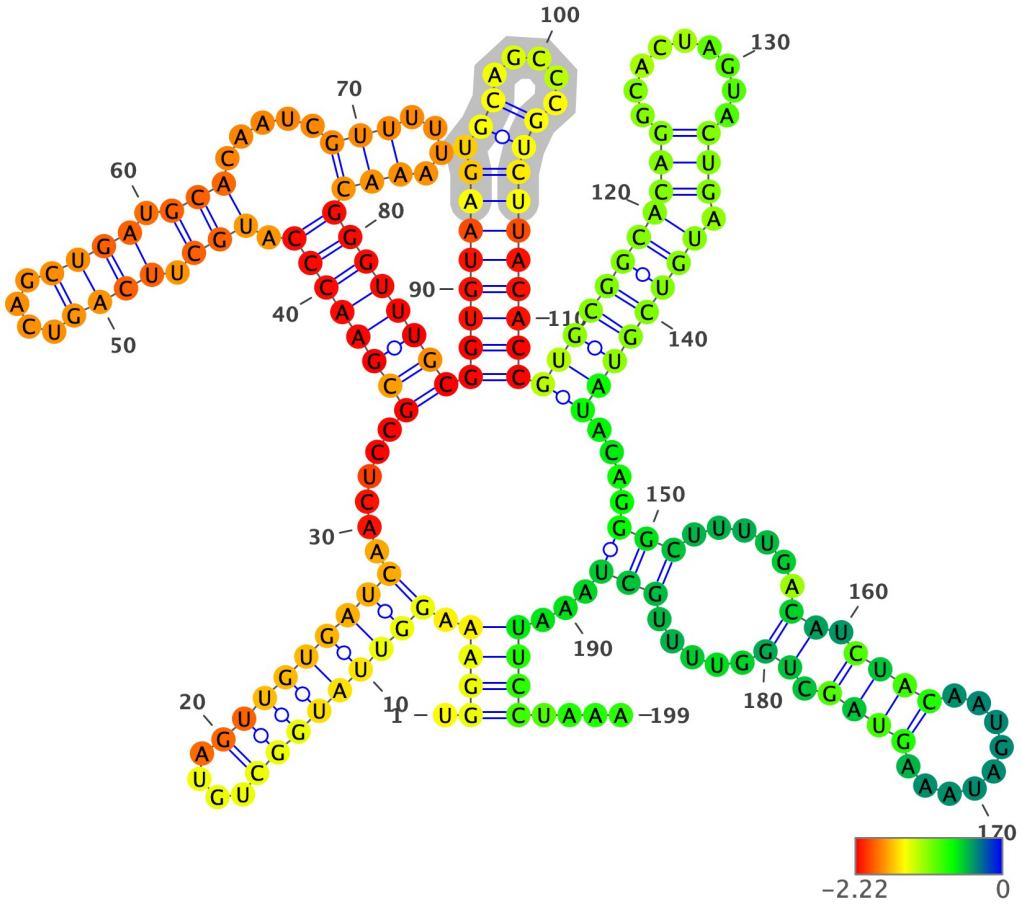
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 132--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 217 from nt 13483 to 13496 (nt 93 to 106)

```
5'-AGTGCAGCCCGUCU-3'
5'-(..((.....)).)-3'
Motif MFE = 0.0; z-score = 0.8; ED = 0.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13391 to 13589 (motif highlighted in silver):

```
5'-UGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACAC
CGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAA-3
5'-.((((.(((((((((....)))))))))......((((((((.(((.((((....)))).)))).....(((....)))))))))))((((((((.((.....)))))))))
)((((((((((.........))).))))))))....(((......((.((((.........)))).))).....)))...))))....-3'
MFE = -58.8; z-score = -1.94; ED = 38.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 78--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 78 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

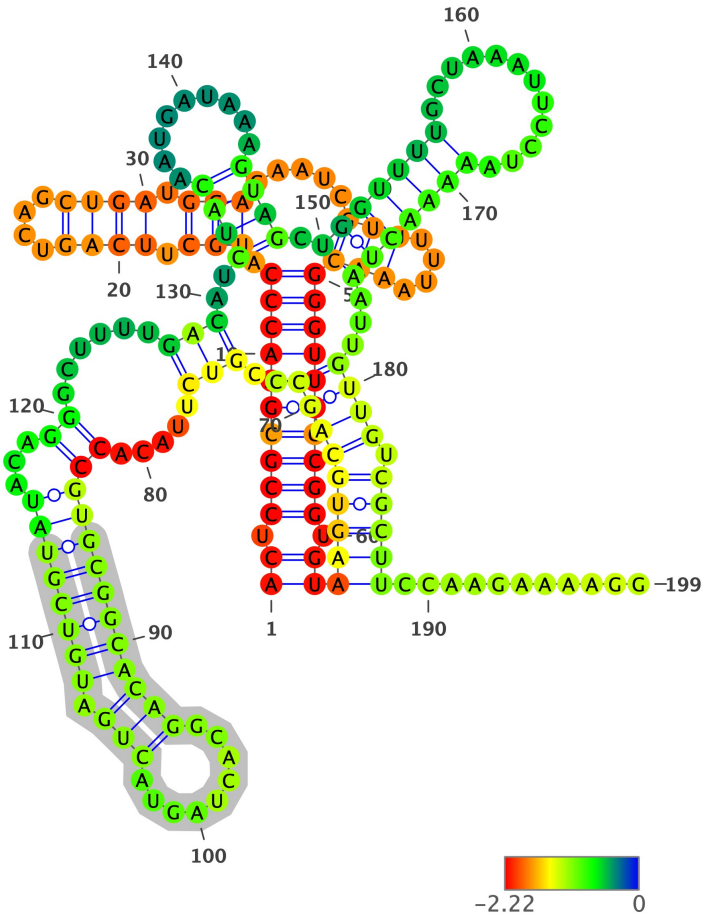
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 93--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 218 from nt 13505 to 13532 (nt 86 to 113)

```
5'-GCGGCACAGGCACTAGTACUGAUGUCGU-3'
5'-((((((((((.........))).))))))-3'
Motif MFE = -9.2; z-score = -2.42; ED = 1.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13420 to 13618 (motif highlighted in silver):

```
5'-ACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUC
GUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGG-3
5'-((.((((((((((.(((.((((....)))).))).....(((....)))))))))))))).))((((((((((..(((.....((((((((((((((.........))).))))
))))...))......))).((((.........)))).(((((((.............)))))))...)))).)))))...........-3'
MFE = -52.5; z-score = -0.93; ED = 45.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 49--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 49 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

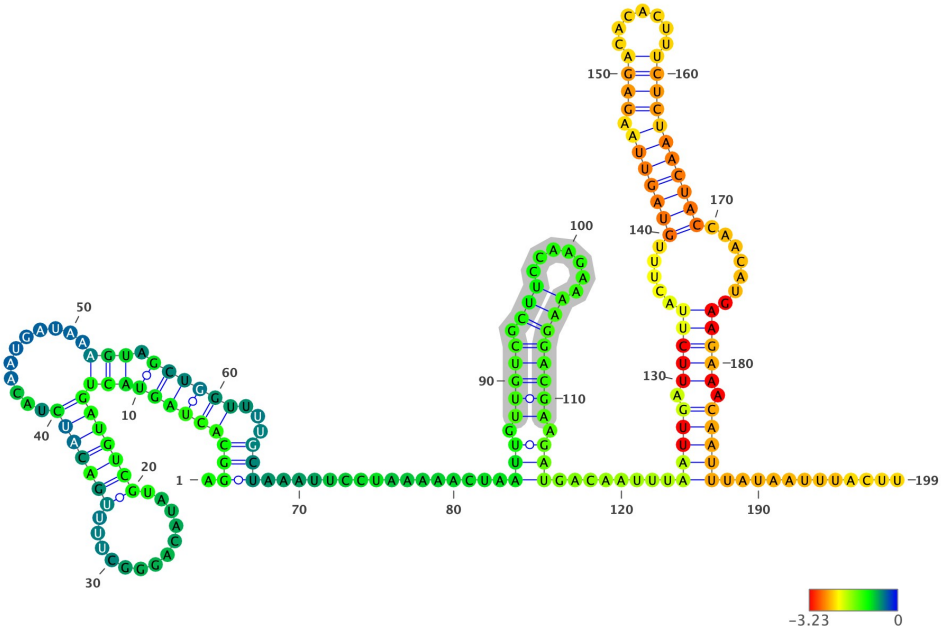
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 64--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 219 from nt 13599 to 13622 (nt 88 to 111)

```
5'-TTGTCGCTTCCAAGAAAAGGACGA-3'
5'-(((((.............)))))-3'
Motif MFE = -3.5; z-score = -0.73; ED = 4.97
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13512 to 13710 (motif highlighted in silver):

```
5'-AGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGA
AGAUGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUU-3
5'-.(((((((((((((((((((.............)))))))).............))).)))))))...))).................(((.(((((.(((.......)))))))))
.))).........(((((.(((((.....(((((((.((((.......)))))))))))).......)))))).)))))............-3'
MFE = -34.8; z-score = -1.85; ED = 29.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

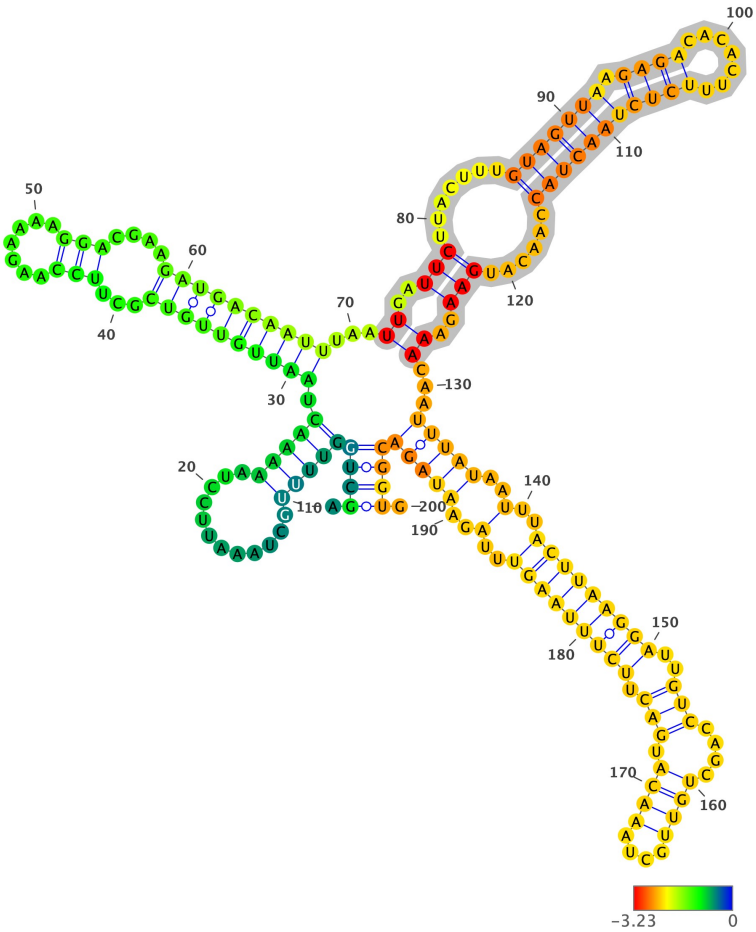
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 220 from nt 13637 to 13693 (nt 72 to 128)

```
5'-TTGATTCTTACTTTGTAGTTAAGAGACACACTTTCUCTAACUACCAACATGAAGAAA-3'
5'-((..(((.......((((((..(((.........))).))))))......)))..))-3'
Motif MFE = -12.2; z-score = -3.07; ED = 6.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13566 to 13765 (motif highlighted in silver):

```
5'-AGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAUGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAA
CUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUG-3
5'-.(((((((((.............))))).((((((((((...(((.......)))....)))))))))))...((..(((.......(((((((.((((.......)))))))
))))......)))..))...(((((..(..(((((((((..(((....((((....)))).))).))))))))..)..))))))))).-3'
MFE = -38.0; z-score = -2.12; ED = 32.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

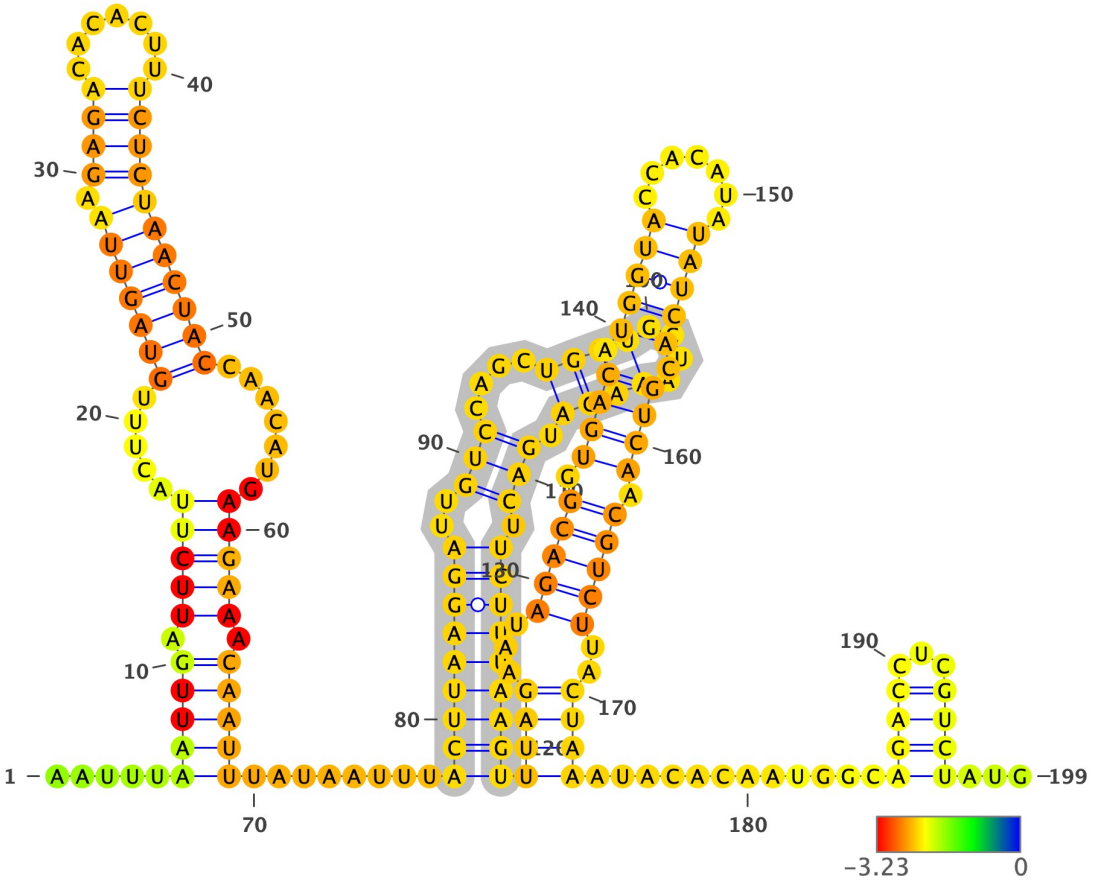
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 221 from nt 13707 to 13750 (nt 78 to 121)

```
5'-ACTTAAGGATTGTCCAGCTGTTGCTAAACATGACTUCUUUAAGU-3'
5'-(((((((((..(((....(((......))).))).)))))))))-3'
Motif MFE = -11.0; z-score = -2.94; ED = 6.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13630 to 13828 (motif highlighted in silver):

```
5'-AAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGAC
UUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUG-3
5'-.....(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))........(((((((((..(((....((((....)))).)))
.)))))))))((((...(((((.((((.(((((.......))))).)))).)))))..))))............((((...))))...-3'
MFE = -44.4; z-score = -3.13; ED = 22.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

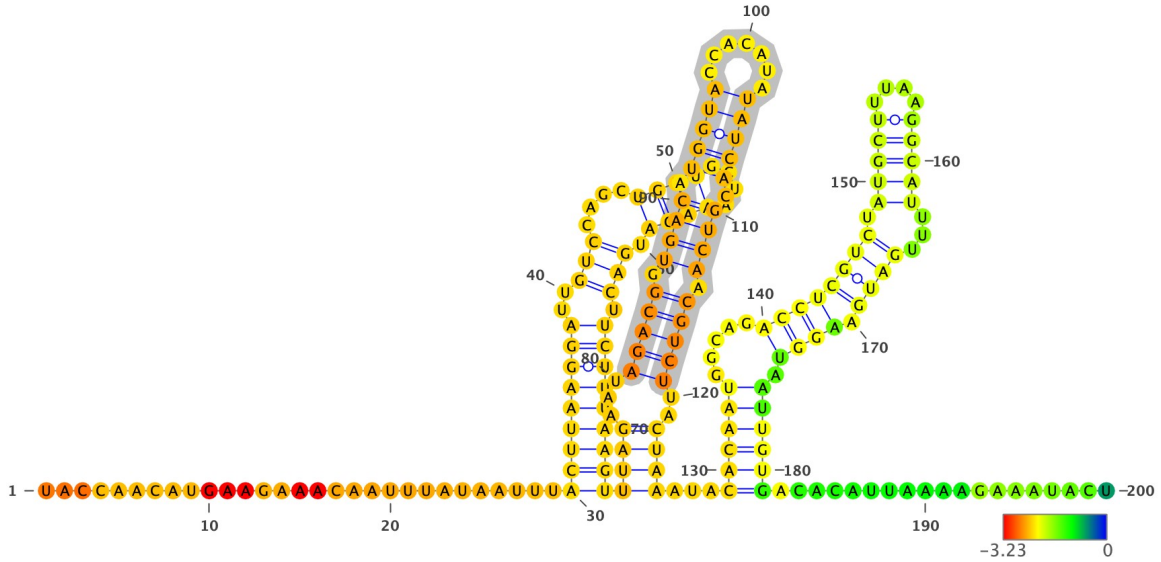
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 222 from nt 13758 to 13796 (nt 81 to 119)

```
5'-AGACGGTGACATGGTACCACATAUAUCACGUCAACGUCU-3'
5'-(((((.((((.(((((.......))))).)))).)))))-3'
Motif MFE = -13.3; z-score = -3.49; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13678 to 13877 (motif highlighted in silver):

```
5'-UACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGU
CAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUGAAGGUAAUUGUGACACAUUAAAAGAAAUACU-3
5'-...............................(((((((((..(((....((((....)))).))).)))))))))((((...(((((.((((.(((((.......)))))).))
)).)))))..)))))...((((((.....((((((((.(((((....)))))...)))))).)))).)))))).....................-3'
MFE = -42.5; z-score = -2.28; ED = 32.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

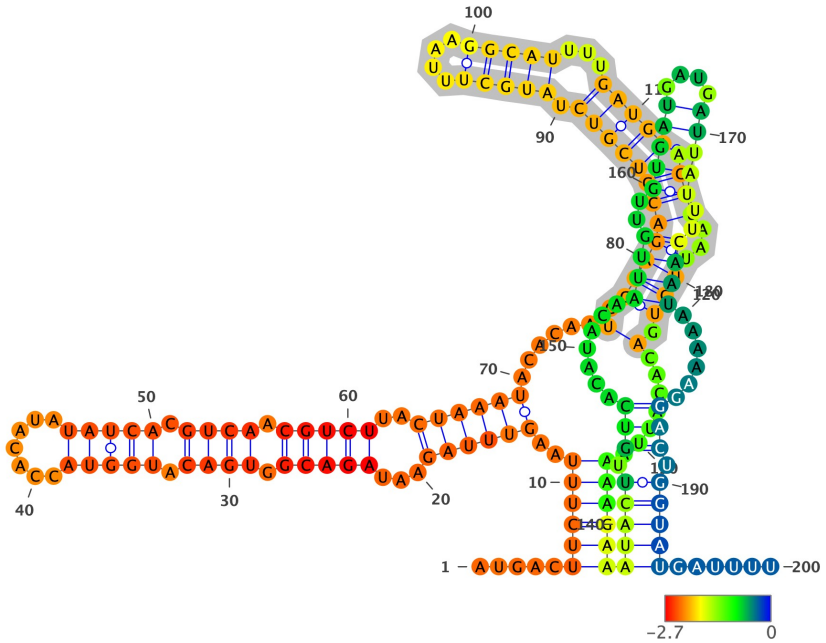
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 223 from nt 13811 to 13859 (nt 76 to 124)

```
5'-TGGCAGACCTCGTCTATGCTTTAAGGCAUTTTGAUGAAGGTAATUGUGA-3'
5'-(.(((..(((((((.((((......))))...)))))).))....))).)-3'
Motif MFE = -13.4; z-score = -1.97; ED = 3.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13736 to 13935 (motif highlighted in silver):

```
5'-AUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUG
AAGGUAAUUGUGACACAUUAAAAGAAAUACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAUUUU-3
5'-.....((((((..((((((...(((((.((((.(((((.......)))))).)))).)))))..))))))......(.((((((((((((.(((((....)))))...))))
).)))..)))).).......))))))(((((.(((.......((((..(((((....)))))..))))......))).)))))......-3'
MFE = -44.6; z-score = -2.9; ED = 34.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

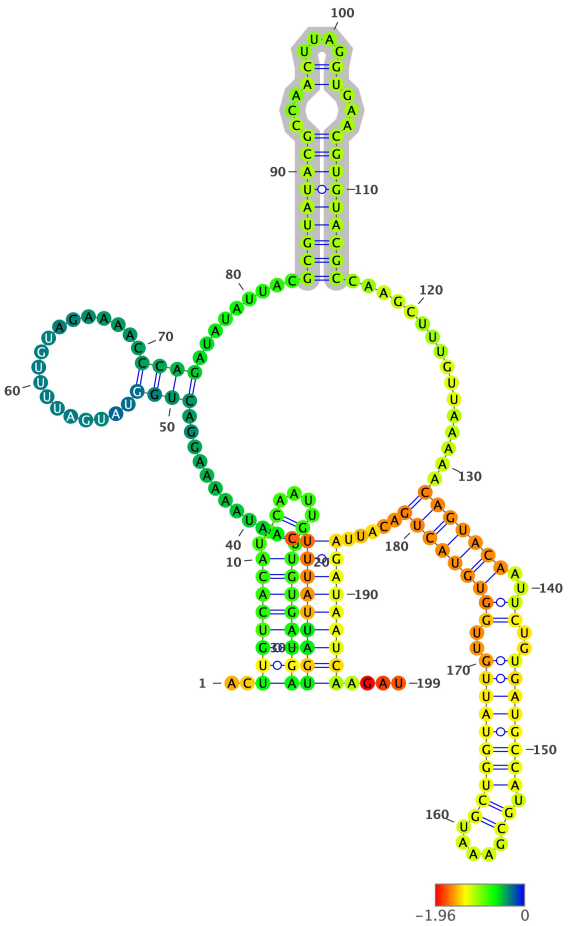
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 224 from nt 13958 to 13989 (nt 84 to 115)

```
5'-GCGTATACGCCAACTTAGGUGAACGUGUACGC-3'
5'-((((((((((...((....))...)))))))))-3'
Motif MFE = -13.3; z-score = -3.1; ED = 1.82
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13875 to 14073 (motif highlighted in silver):

```
5'-ACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAUUUUGUAGAAAACCCAGAUAUAUUACGCGUAUACGCCAACUUAGGUGAACGUGU
ACGCCAAGCUUUGUUAAAAACAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUGACAUUAGAUAAUCAAGAU-3
5'-..((((((((.((....)))))))))((((((((.............((((.................))))..........((((((((...((....))...)))))
))))................(((((((..((..((((((((.((.....)))))))))..)))))))))).....)))))))))....-3'
MFE = -46.8; z-score = -2.23; ED = 22.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

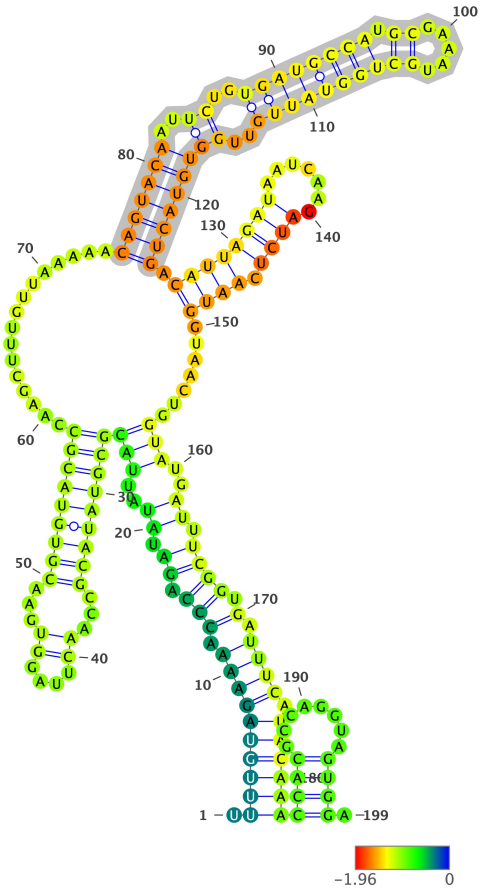
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 225 from nt 14006 to 14055 (nt 75 to 124)

```
5'-CAGTACAATTCTGTGATGCCATGCGAAATGCUGGUAUUGTTGGUGUACUG-3'
5'-(((((((.......(((((((.((.....)))))))))).....)))))))-3'
Motif MFE = -16.7; z-score = -3.13; ED = 3.57
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13932 to 14130 (motif highlighted in silver):

```
5'-UUUUGUAGAAAACCCAGAUAUAUUACGCGUAUACGCCAACUUAGGUGAACGUGUACGCCAAGCUUUGUUAAAAACAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAU
UGUUGGUGUACUGACAUUAGAUAAUCAAGAUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCCAGGUAGUGGA-3
5'-.((((((((((.(((.((.((..(((((((((((((...((....))...)))))))))).................(((((((..((..((((((((.((.....))))))))
))..))))))))).((((((((.......)))).))))).......)))..)).)))).).)))).))))))((((........)))).-3'
MFE = -52.0; z-score = -2.52; ED = 24.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

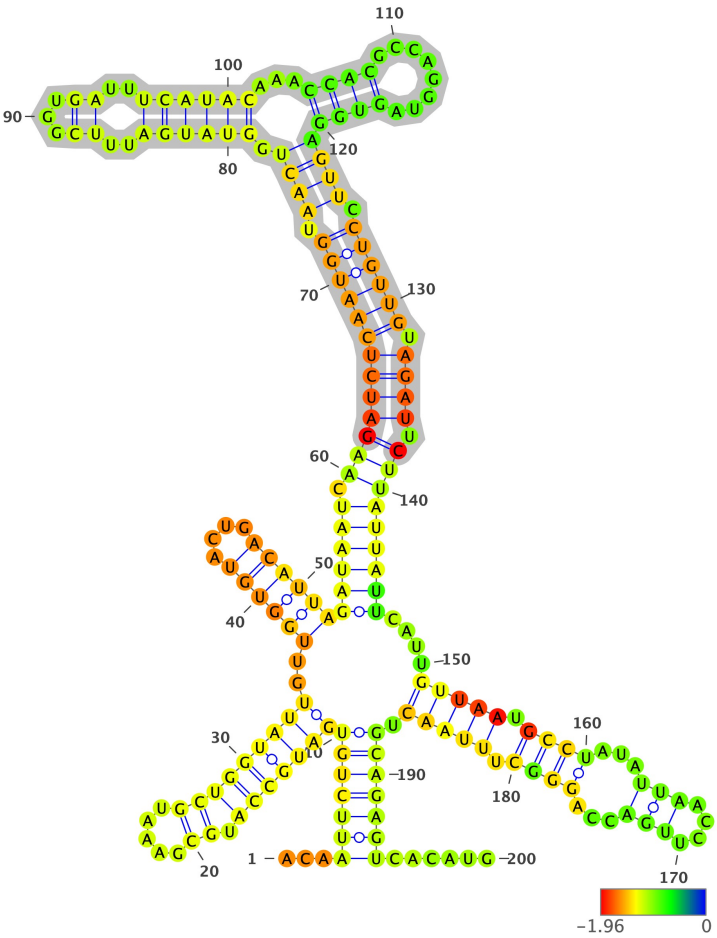
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 226 from nt 14071 to 14147 (nt 62 to 138)

```
5'-GATCTCAATGGTAACTGGTATGATTTCGGTGATTUCAUACAAACCACGCCAGGTAGUGGAGUUCCUGUUGTAGAUTC-3'
5'-(((((((((((.(((..((((((..((...))..))))))...................))).)))))).)))).)-3'
Motif MFE = -21.8; z-score = -1.99; ED = 2.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14010 to 14209 (motif highlighted in silver):

```
5'-ACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUGACAUUAGAUAAUCAAGAUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCC
AGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUG-3
5'-...((((((((((((((.((.....)))))))))..((((((....))))))((((((.((((((((((((((.((((.((((((..((...))..))))))...((((...
.....))))))))).))))))).)))).))))))))).....(((((.((((...(((....)))...)))).))))).)))))))......-3'
MFE = -52.7; z-score = -2.12; ED = 36.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

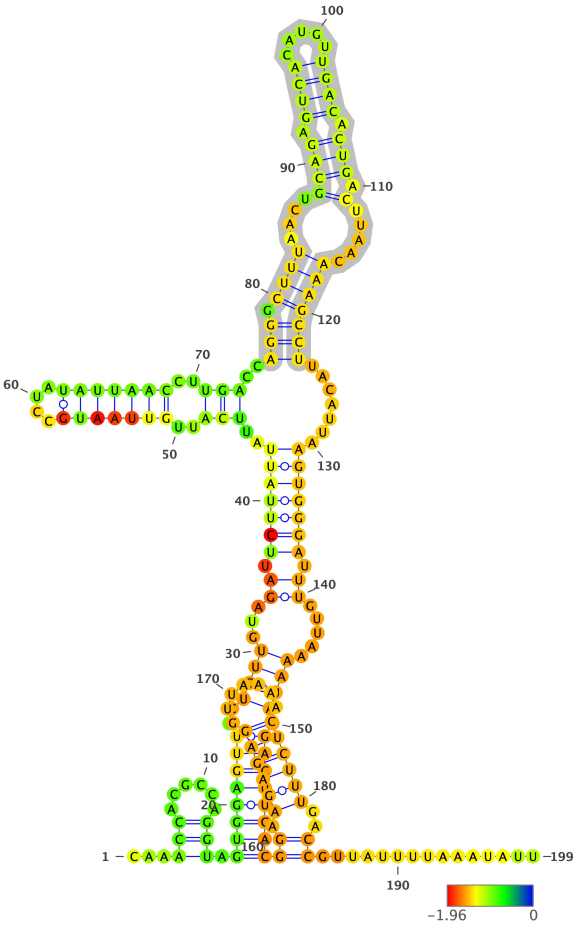
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 227 from nt 14185 to 14232 (nt 76 to 123)

```
5'-AGGGCTTTAACTGCAGAGTCACATGTUGACACUGACTTAACAAAGCCU-3'
5'-(((.((((.....(((.((((.....)))).))).......)))))))-3'
Motif MFE = -13.5; z-score = -2.65; ED = 3.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14110 to 14308 (motif highlighted in silver):

```
5'-CAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGAC
UUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUU-3
5'-...(((......))).(((((((((..((((...((.(((((((..(((..(((((((....)))))))..)))..(((.((((....((((.((((.....)))).))).)
.....)))))))).......)))))))..))).....)))).))))))))((.((((((.......))))))..)).................-3'
MFE = -38.4; z-score = -1.15; ED = 41.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

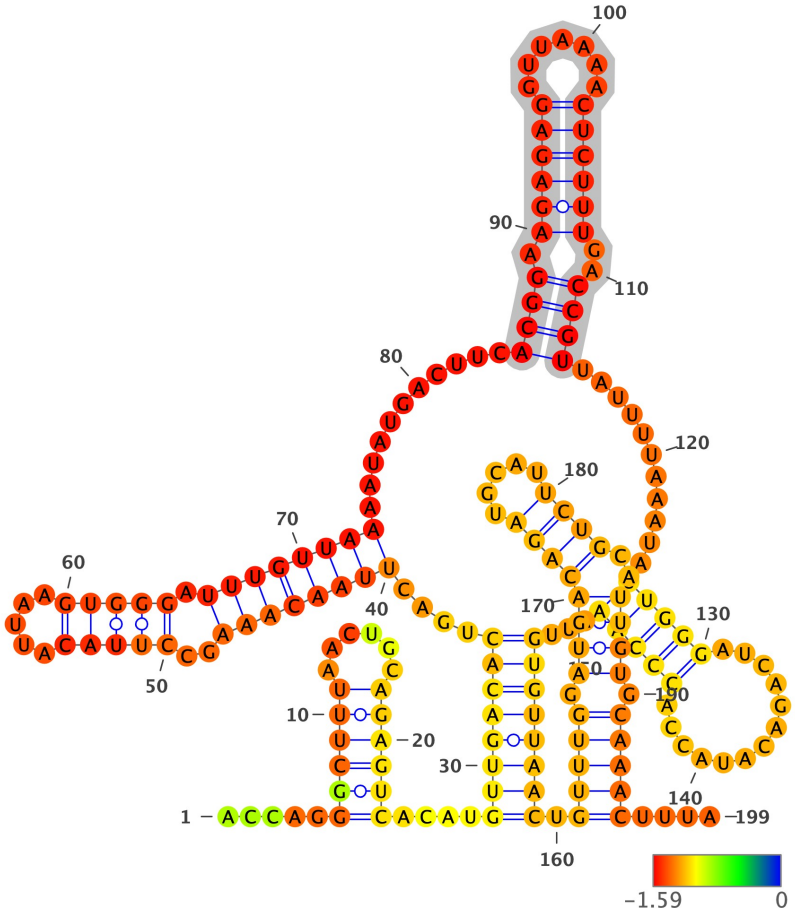
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 228 from nt 14266 to 14295 (nt 85 to 114)

```
5'-ACGGAAGAGAGGTTAAAACUCUUUGACCGU-3'
5'-((((.((((((.......))))))..))))-3'
Motif MFE = -10.5; z-score = -3.4; ED = 0.72
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14182 to 14380 (motif highlighted in silver):

```
5'-ACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGAC
CGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUA-3
5'-.....((((((......))))))....((((((((....((((((((..(((((.....))))).))))))))...........((((.((((((.......))))))..)
)))...........(((((.............)))))...)))))))).(((((.((((((((.....))))..)))).)))))....-3'
MFE = -47.5; z-score = -1.79; ED = 39.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

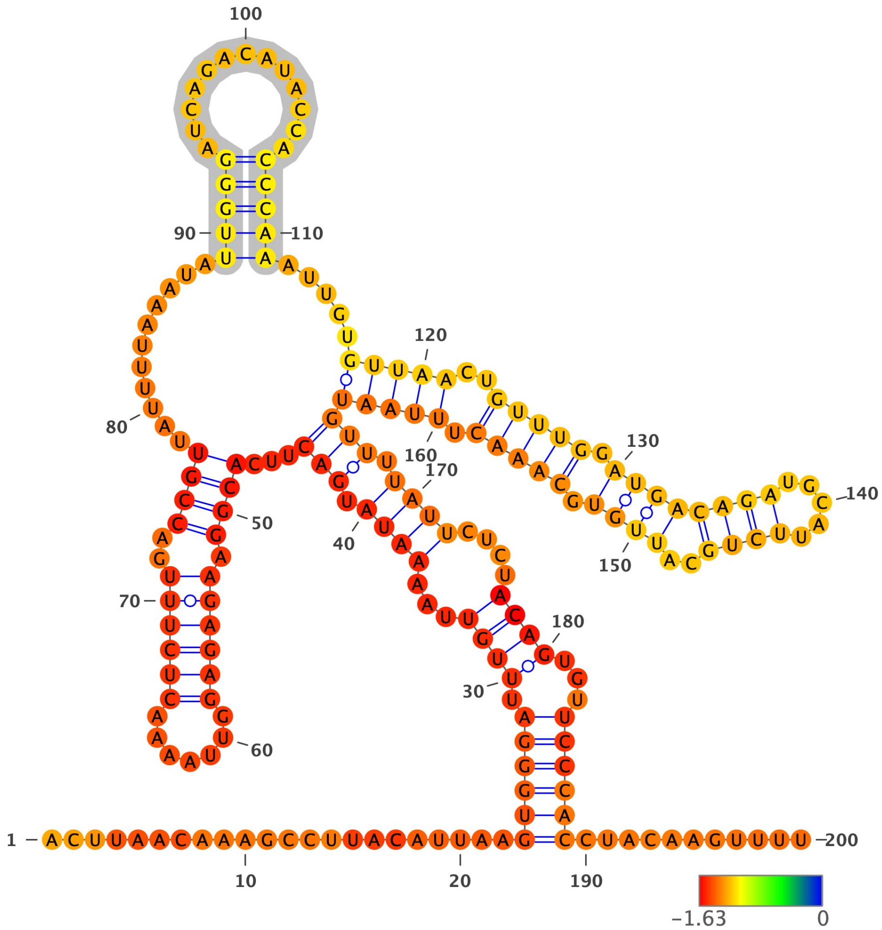
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 229 from nt 14307 to 14329 (nt 89 to 111)

5'-TTGGGATCAGACATACCACCCAA-3'
5'-(((((.............)))))-3'
Motif MFE = -3.5; z-score = -1.74; ED = 1.33



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14219 to 14418 (motif highlighted in silver):

5'-ACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAA
AUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUU-3
5'-.......................((((((.((((...((((.(((...((((.((((((.......))))))..))))...........(((((............)))))
.....(((((..(((((.((((((((.....))))..)))).))))).)))))))).))))....))))...))))))...........-3'
MFE = -39.3; z-score = -1.45; ED = 60.59

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

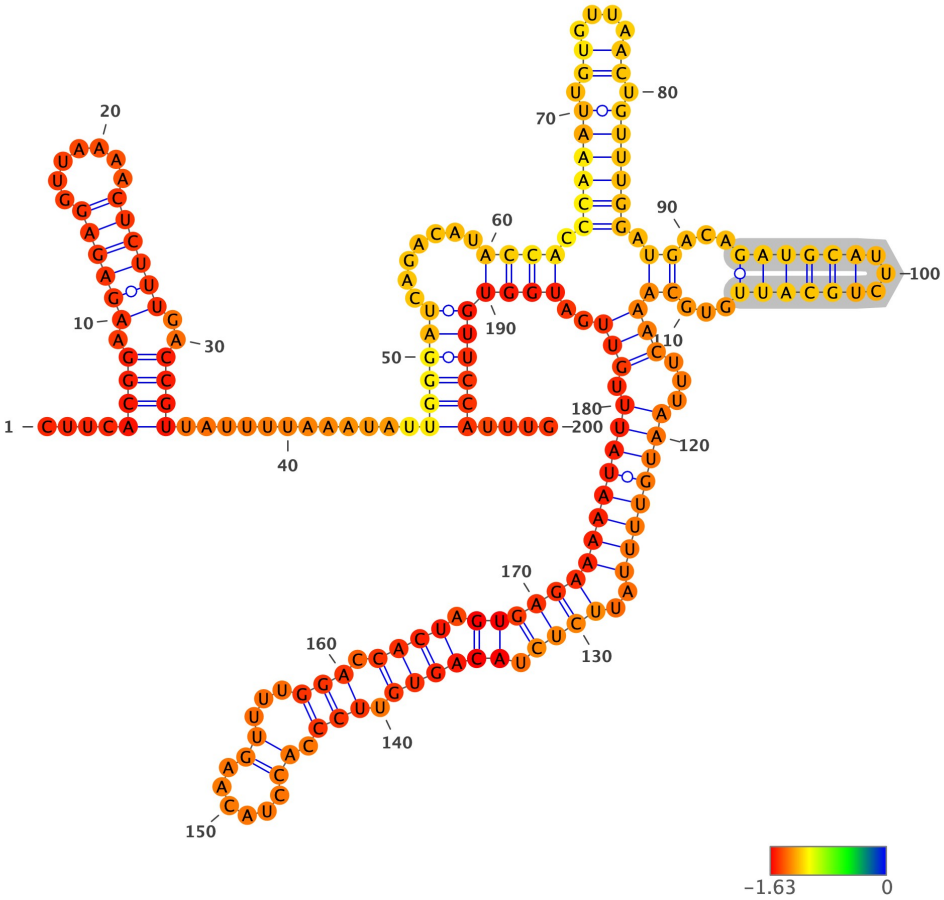
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 230 from nt 14354 to 14368 (nt 93 to 107)

```
5'-GATGCATTCTGCAUU-3'
5'-(((((.....)))))-3'
Motif MFE = -3.6; z-score = -3.97; ED = 1.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14262 to 14461 (motif highlighted in silver):

```
5'-CUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGC
AAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUG-3
5'-....((((.((((((.......))))))..))))............((((((.......((((.((((((.((....)).)))))).((...((((((...))))))...)
)(((...((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))).)))..)))))))))).....-3'
MFE = -45.5; z-score = -1.43; ED = 31.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

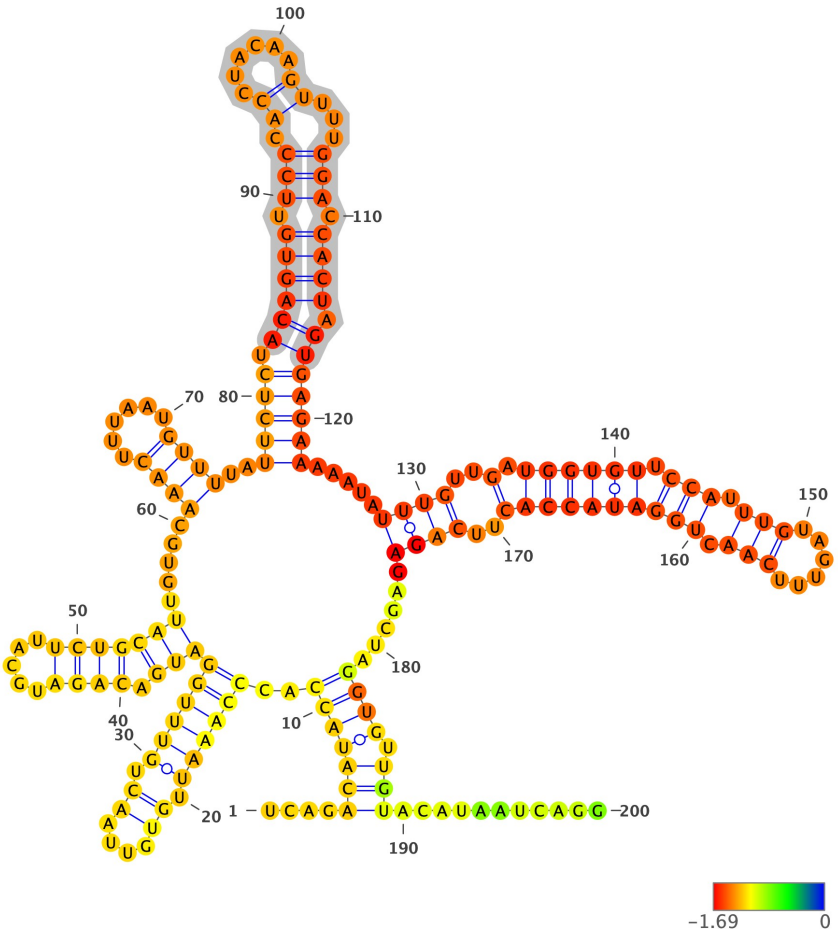
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 231 from nt 14395 to 14429 (nt 83 to 117)

```
5'-ACAGTGTTCCCACCTACAAGTTTTGGACCACUAGU-3'
5'-((((((.(((..............))).)))).))-3'
Motif MFE = -6.0; z-score = -1.53; ED = 3.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14313 to 14512 (motif highlighted in silver):

```
5'-UCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACC
ACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGG-3
5'-....(((((((..((((((.((....)).))))))(((.((((.....)))))))).....((((......))))..(((((.((((((.(((.((......))...))).)
))).)))))))).....((((..(.((((((.(((.(((......))).))))))))))..))))......)))).))).........-3'
MFE = -46.8; z-score = -1.71; ED = 39.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

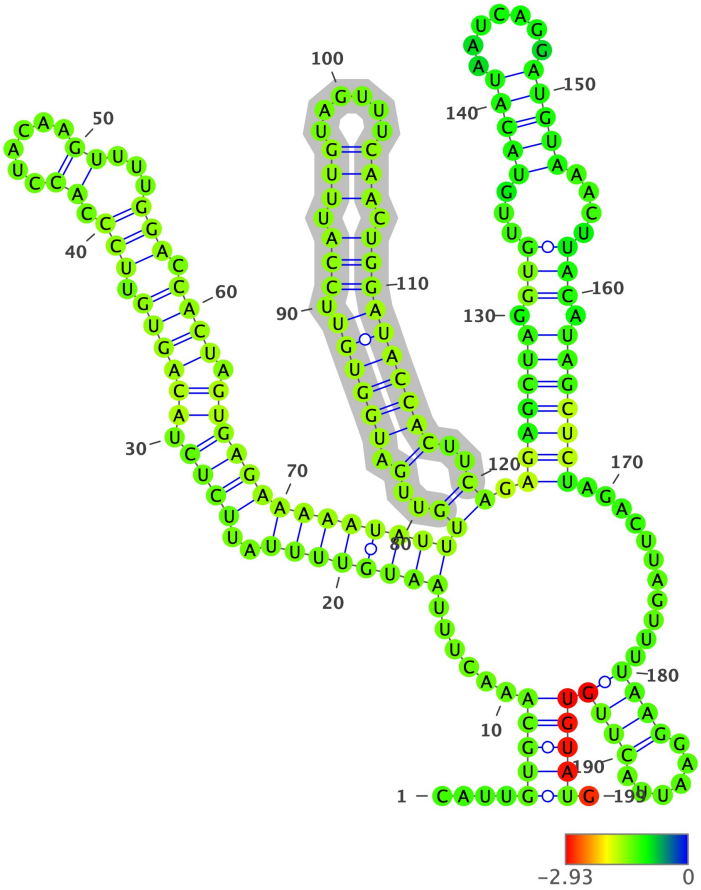
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 232 from nt 14443 to 14484 (nt 79 to 120)

```
5'-GTTGATGGTGTTCCATTTGTAGTTTCAACUGGAUACCACTTC-3'
5'-(..(.(((((((.(((.(((......))).))))))))))..)-3'
Motif MFE = -11.4; z-score = -2.61; ED = 2.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14365 to 14563 (motif highlighted in silver):

```
5'-CAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGA
UACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUG-3
5'-....(((((......((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))((..(.((((((.(((.(((......))).))))
))))))..)).(((((((.(((...(((((.......)))))....))).)))))))...........((((......)))))))).-3'
MFE = -46.1; z-score = -1.73; ED = 22.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

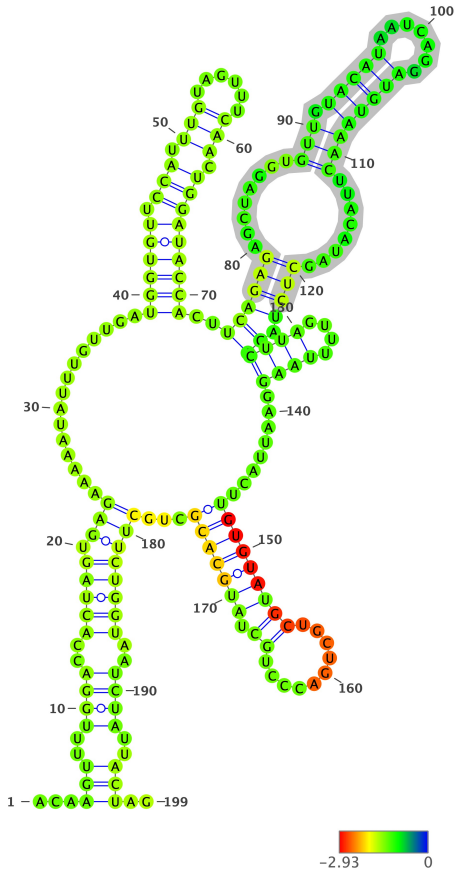
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 233 from nt 14486 to 14531 (nt 77 to 122)

```
5'-GAGAGCTAGGTGTTGTACATAATCAGGAUGUAAACTTACATAGCUC-3'
5'-(((........(((.(((((.......))))))))........)))-3'
Motif MFE = -12.0; z-score = -2.79; ED = 2.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14410 to 14608 (motif highlighted in silver):

```
5'-ACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAAC
UUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAG-3
5'-...(((..((((..(((((.(((...............((((((.(((.(((......))).)))))))))..((((((........(((.(((((.......))))))))
........)))).))((((....))))........(((((((((..........)).)))))))...)))))))))..))))..)))..-3'
MFE = -39.3; z-score = -1.42; ED = 28.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

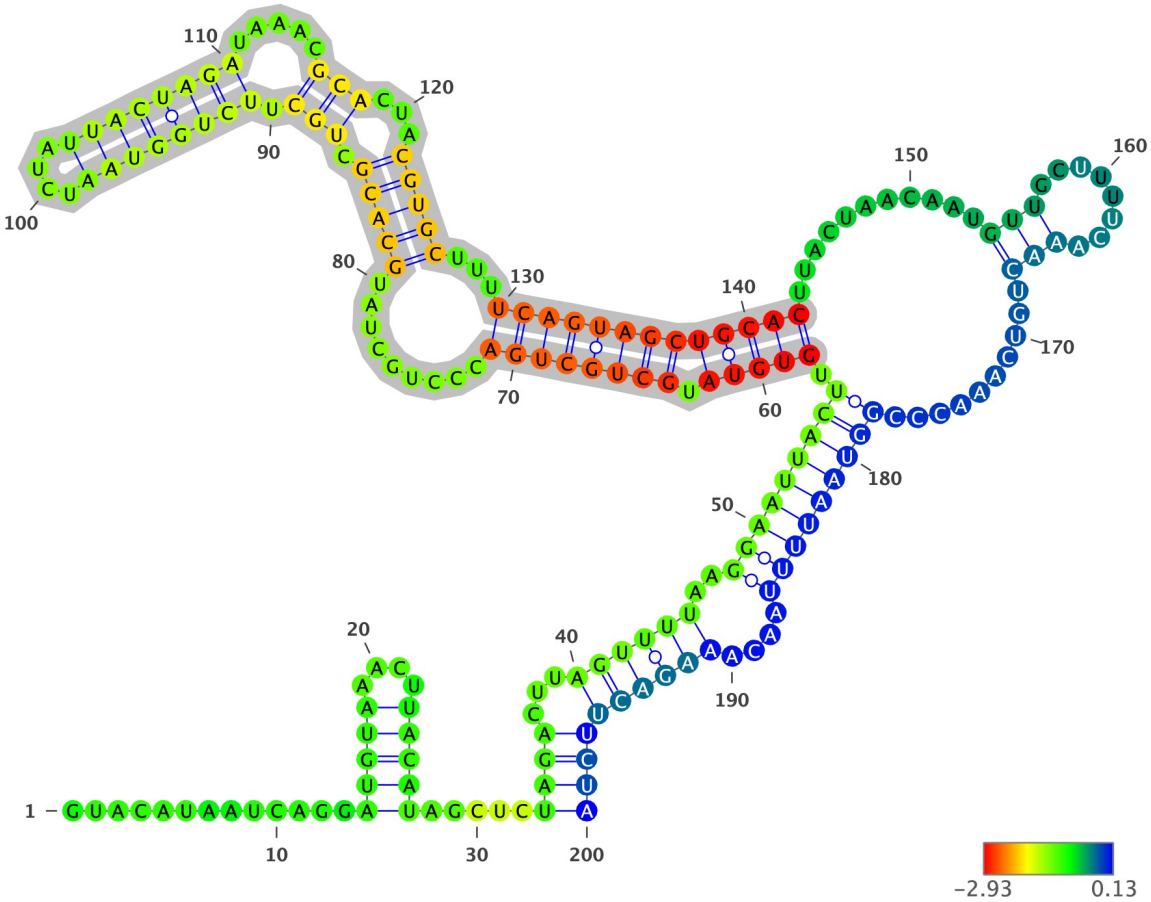
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 234 from nt 14557 to 14641 (nt 58 to 142)

```
5'-GTGTATGCTGCTGACCCTGCTATGCACGCTGCTTCTGGTAATCTATUACUAGATAAACGCACTACGUGCTTTUCAGUAGCUGCAC-3'
5'-(((((.(((((((((.........(((((.(((.(((((((.......)))))))).....)))...)))))...))))))))))))-3'
Motif MFE = -29.9; z-score = -3.67; ED = 4.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14500 to 14699 (motif highlighted in silver):

```
5'-GUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAU
AAACGCACUACGUGCUUUUCAGUAGCUGCACUUACUAACAAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUA-3
5'-.............(((((....)))))).....((((...((((((..(((((((((.(((((.((((((((.........(((((.(((.((((((((....)))))))).
....)))...)))))...))))))))))))).........(((........)))..........)))))))))....)))))))))-3'
MFE = -41.1; z-score = -1.59; ED = 20.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

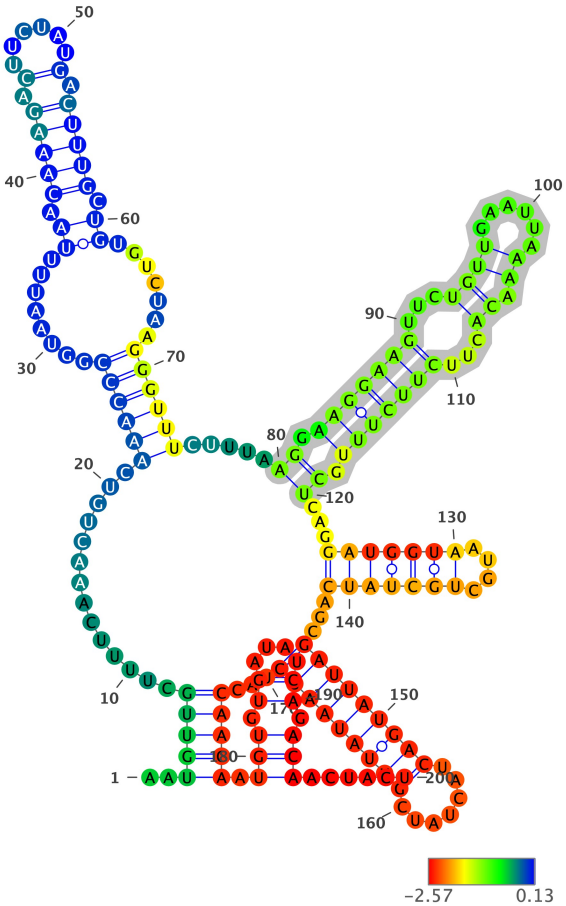
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 235 from nt 14729 to 14769 (nt 80 to 120)

```
5'-AGGAAGGAAGTTCTGTTGAATTAAAACACTTCUUCUUTGCU-3'
5'-((..((((((...((((......)).))...))))))..))-3'
Motif MFE = -10.6; z-score = -2.76; ED = 1.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14650 to 14849 (motif highlighted in silver):

```
5'-AAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUC
UUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACU-3
5'-..(((((..............((((((........((.(((((.(......).))))).))........))))))).....((.(((((((...((((......)).))...)
))))))).))...(((((((....)))))))...((((((((.......)))))))))...))))).(((.((....)).)))......-3'
MFE = -39.2; z-score = -1.33; ED = 35.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

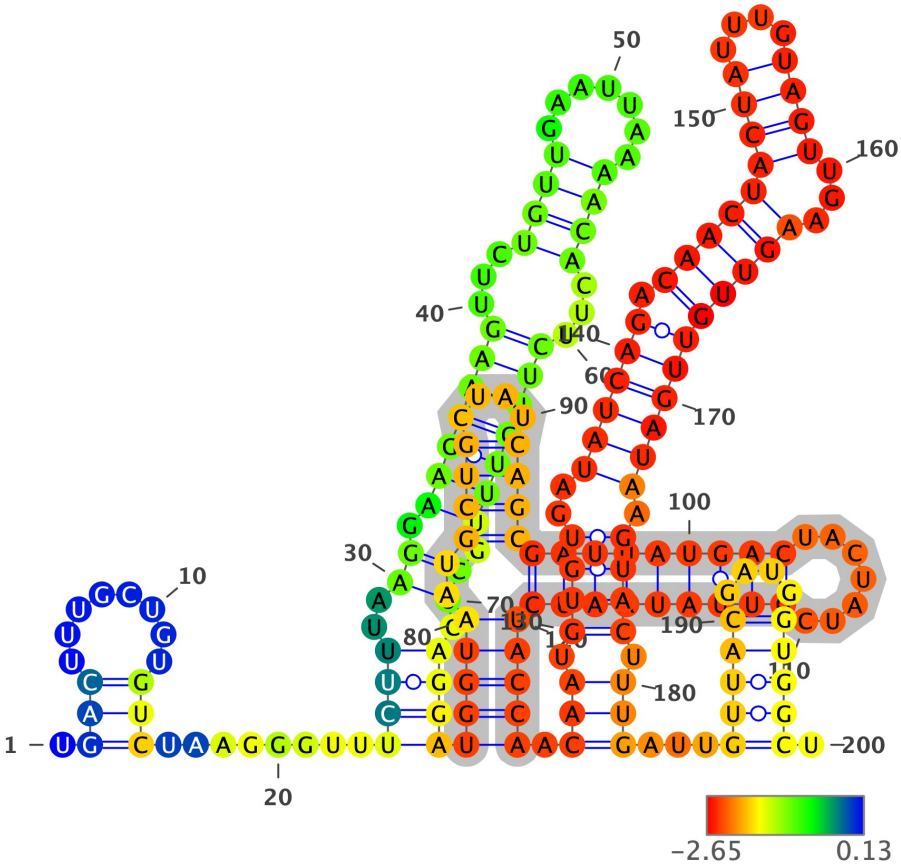
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 236 from nt 14775 to 14823 (nt 76 to 124)

```
5'-TGGTAATGCTGCTATCAGCGATTATGACTACTATCGUUAUAAUCTACCA-3'
5'-((((...((((....))))((((((((.......)))))))).))))-3'
Motif MFE = -14.4; z-score = -3.64; ED = 1.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14700 to 14899 (motif highlighted in silver):

```
5'-UGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCG
UUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCU-3
5'-.(((........)))........((((..((.(((((((...((((.......))))...)))))))).)).))))(((((..((((....))))((((((((.......)
))))))))))))).(((.((((..((((((.((((((((....))))...)))))))))))).)))).)))...(((((....))))).-3'
MFE = -46.6; z-score = -2.76; ED = 53.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

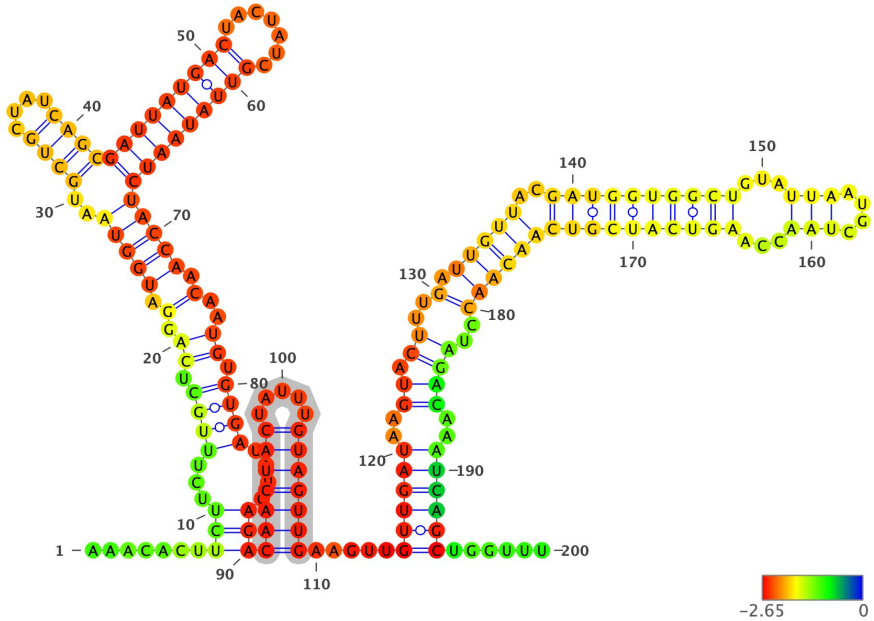
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 237 from nt 14842 to 14860 (nt 91 to 109)

```
5'-CAACTACTATTTGUAGUUG-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.2; z-score = -4.93; ED = 0.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14752 to 14951 (motif highlighted in silver):

```
5'-AAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAA
GUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGCUGGUUU-3
5'-.......(((...((((.((.(.(((((..((((....))))((((((((.......)))))))))))))).)..)).))))....)))(((((((.....)))))))..
...((((((..((.((..(.(((((..((((((((((...(((....)))...)))))))))))))))..))))..))))))......-3'
MFE = -48.8; z-score = -2.92; ED = 41.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

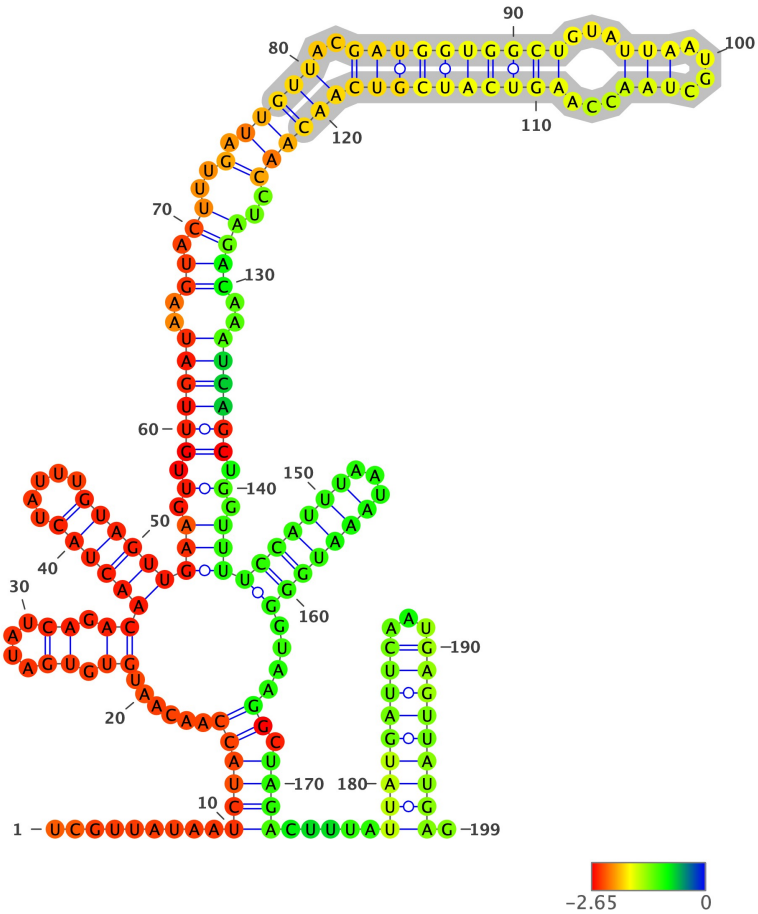
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 238 from nt 14885 to 14928 (nt 78 to 121)

```
5'-GTTACGATGGTGGCTGTATTAATGCTAACCAAGUCAUCGUCAAC-3'
5'-(((..((((((((((.................))))))))))))-3'
Motif MFE = -12.5; z-score = -1.98; ED = 3.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14808 to 15006 (motif highlighted in silver):

```
5'-UCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGU
CAUCGUCAACAACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAG-3
5'-.........((((((......((.((....)).))((((((.....))))))(((.(.((((((..((.((..(.(((((..((((((((((...(((....)))...)))
))))))))))))..))))..))))))).).)))(((((((...)))))))....)).)))).....((((((((...)))))))))).-3'
MFE = -43.9; z-score = -1.4; ED = 39.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

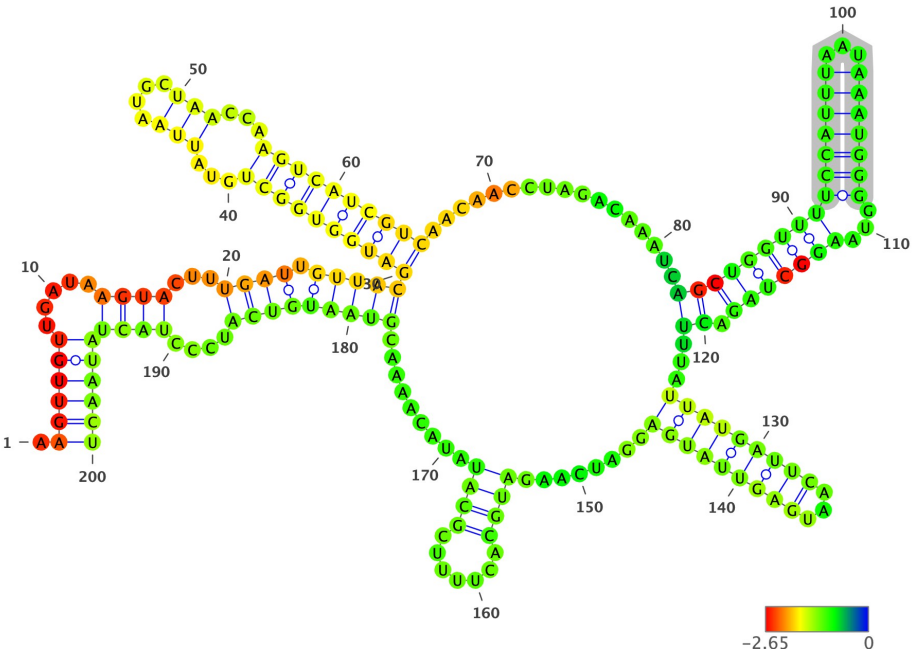
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 239 from nt 14952 to 14968 (nt 92 to 108)

```
5'-TCCATTTAATAAAUGGG-3'
5'-((((.........))))-3'
Motif MFE = -3.9; z-score = -6.64; ED = 1.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14861 to 15060 (motif highlighted in silver):

```
5'-AAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUA
AGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACU-3
5'-.((((((.....((((...((((.((((((((((((((...(((....)))...))))))))))).................((((((((((((((...)))))))...
)))))))).))...((((((((...)))))))))........((((.......))))........))))))))....))))))))))-3'
MFE = -39.3; z-score = -0.42; ED = 54.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

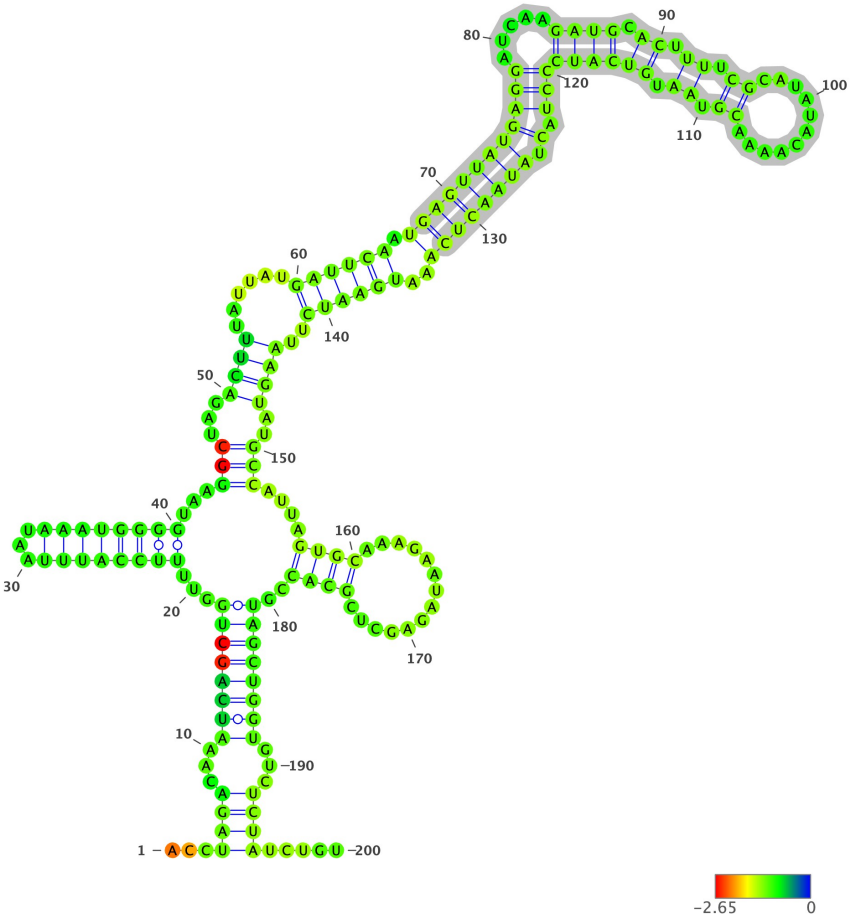
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 240 from nt 14997 to 15061 (nt 68 to 132)

```
5'-GAGTTATGAGGATCAAGATGCACTTTTCGCATATACAAAACGTAATGUCAUCCCUACTAUAACUC-3'
5'-((...((((((.....((((.((.((.((...........)).)).)))))))))).).))...))-3'
Motif MFE = -11.1; z-score = -1.62; ED = 11.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14930 to 15129 (motif highlighted in silver):

```
5'-ACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUA
AUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGU-3
5'-...((((...((((((((...((((((((...))))))))...(((...((((......((((((.(((((((((((((.....((((.((.((.((...........)).)
).)))))))))).).)))))))))..))))))..))))..)))....((((..............))))..))))))))...))))).....-3'
MFE = -44.2; z-score = -1.54; ED = 36.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

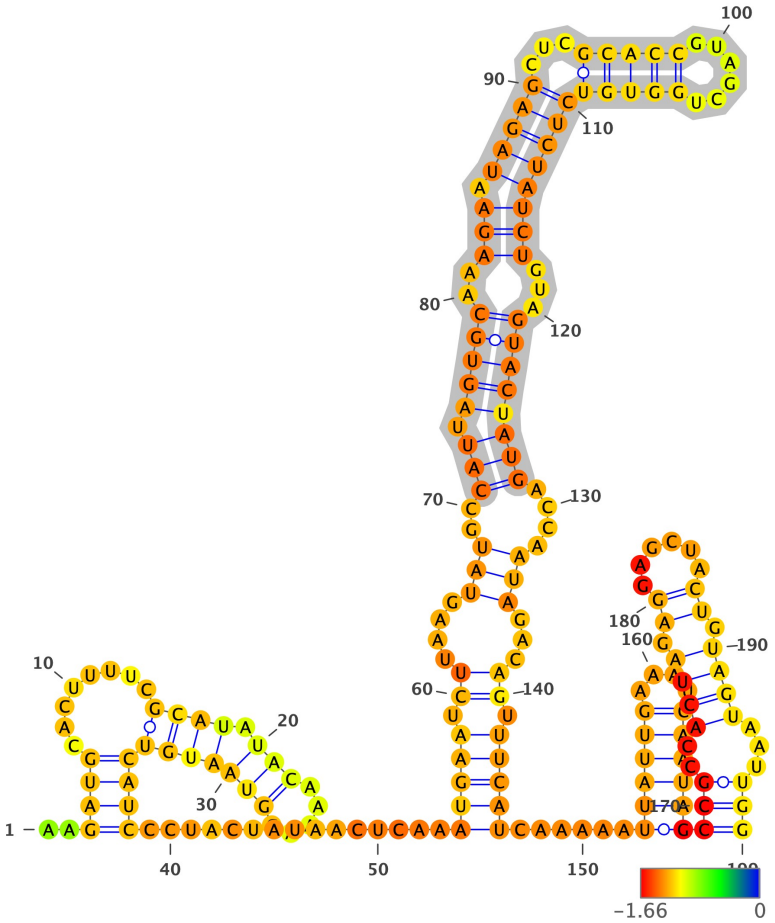
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 241 from nt 15081 to 15138 (nt 71 to 128)

```
5'-CATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGUGUCUCUAUCUGTAGUACTAUG-3'
5'-(((..((((..(((.(((((...(((((......))))))))))))...)))).)))-3'
Motif MFE = -19.4; z-score = -3.68; ED = 3.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15011 to 15209 (motif highlighted in silver):

```
5'-AAGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCU
CUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGG-3
5'-..((((........((((.(((.....)))))))))).................(((((.((....(((..(((.(((((..(((.(((((...(((((......)))))))
))))))...))))))))....)))...)).)))))......((((((....))))))(((..((((.((......)).))))...)))-3'
MFE = -34.8; z-score = -0.49; ED = 42.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

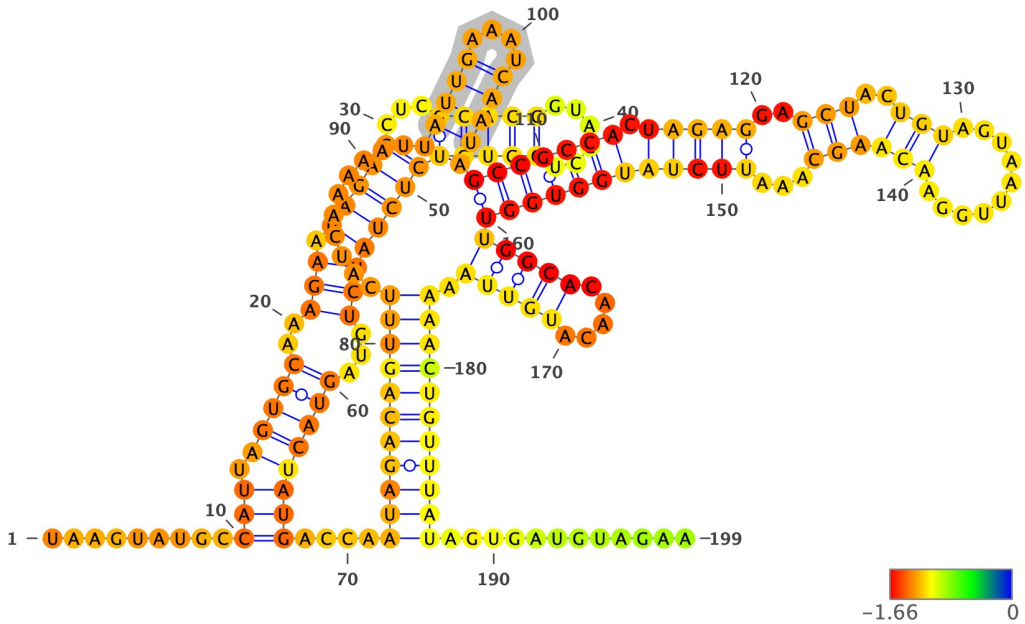
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 242 from nt 15165 to 15176 (nt 94 to 105)

```
5'-ATTGAAATCAAU-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15072 to 15270 (motif highlighted in silver):

```
5'-UAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGC
CACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAA-3
5'-.........(((.(((((..(((.(((((...(((((......)))))))))))))...))))))))....((((((((((.........(((((....)))))(((((
((.(((((..(((..(((.........))))))...))))))))))))(((((.....))))).))))))))))).............-3'
MFE = -49.3; z-score = -2.68; ED = 31.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

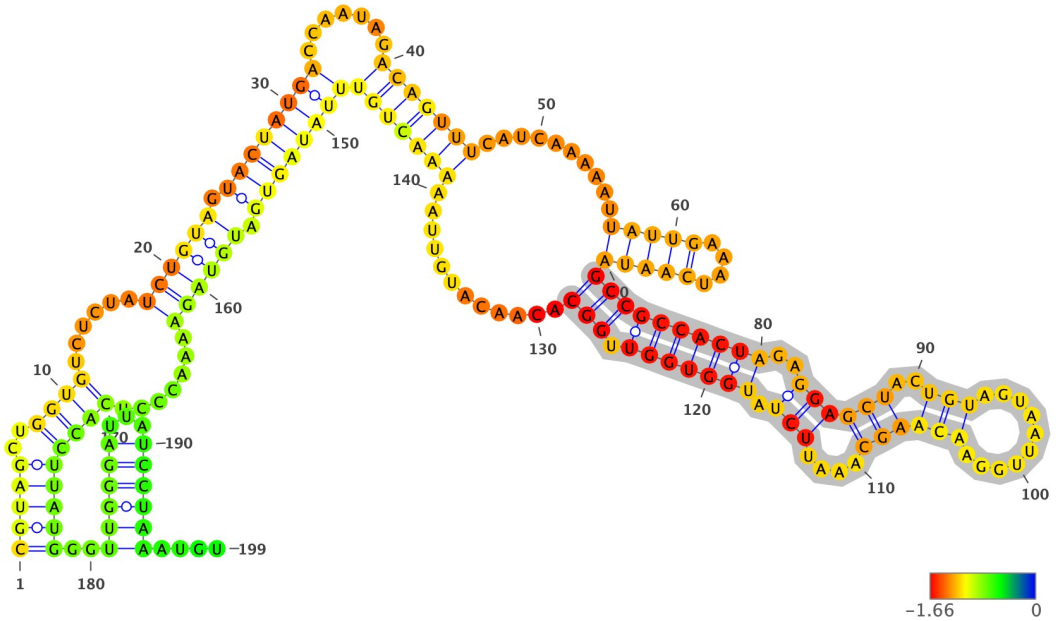
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 243 from nt 15178 to 15235 (nt 71 to 128)

```
5'-GCCGCCACTAGAGGAGCTACTGTAGTAATTGGAACAAGCAAATUCTATGGUGGUTGGC-3'
5'-(((((((((....(((((.................)))....))...)))))).)))-3'
Motif MFE = -16.8; z-score = -1.94; ED = 13.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15108 to 15306 (motif highlighted in silver):

```
5'-CGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAA
AUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAUGU-3
5'-(((((..((((......((((((.((((((((.......((((((.........(((((....)))))((((((((((..((((((..(((.........))))))..
..))).)))))))).)))............))))))))))))))).))))))).......)))))))))..((((((...))))))....-3'
MFE = -41.2; z-score = -1.19; ED = 36.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

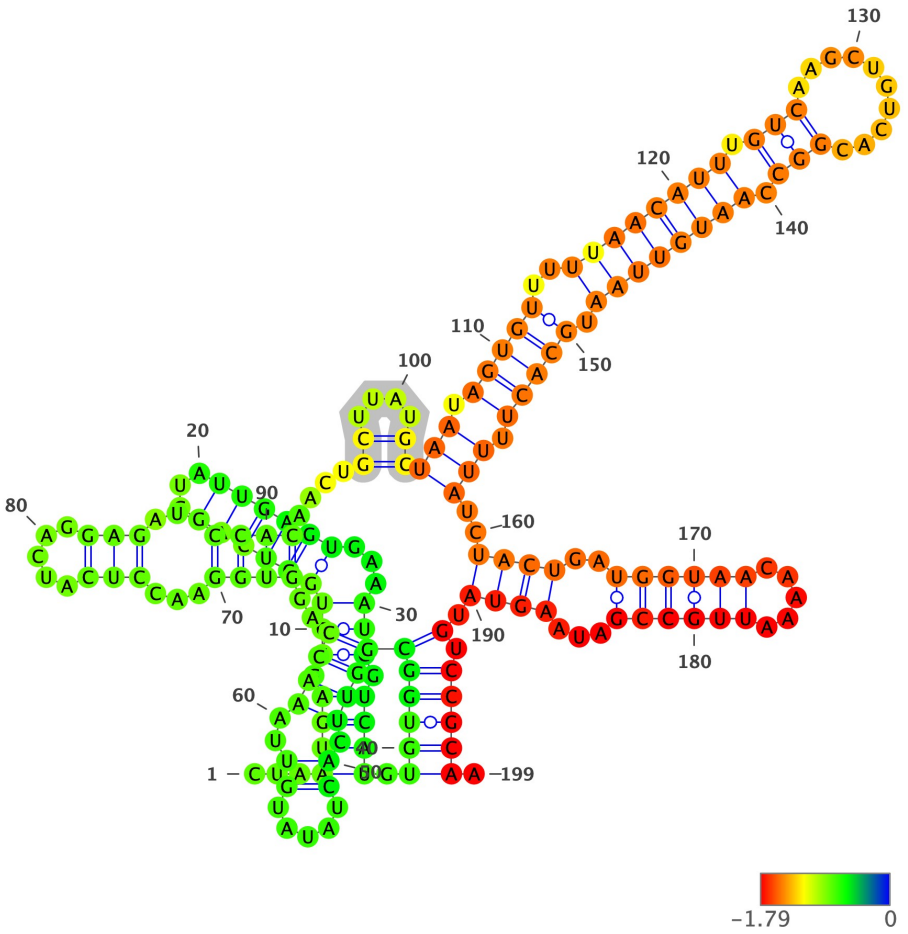
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 244 from nt 15502 to 15509 (nt 96 to 103)

```
5'-GCTTATGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15407 to 15605 (motif highlighted in silver):

```
5'-CUAAUGAGUGUGCUCAAGUAUUGAGUGAAAUGGUCAUGUGUGGCGGUUCACUAUAUGUUAAACCAGGUGGAACCUCAUCAGGAGAUGCCACAACUGCUUAUGCUAAUAGUG
UUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAA-3
5'-...((((.(((((((((...))))))...))).)))).((((((((((.((.....)).)))).((((...(((.....)))...)))).....((....))(((.((((
(..((((((((.(((.........))).)))))))).))))).))).((((..((((((.....))))))...)))).).))))).-3'
MFE = -47.2; z-score = -0.83; ED = 58.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

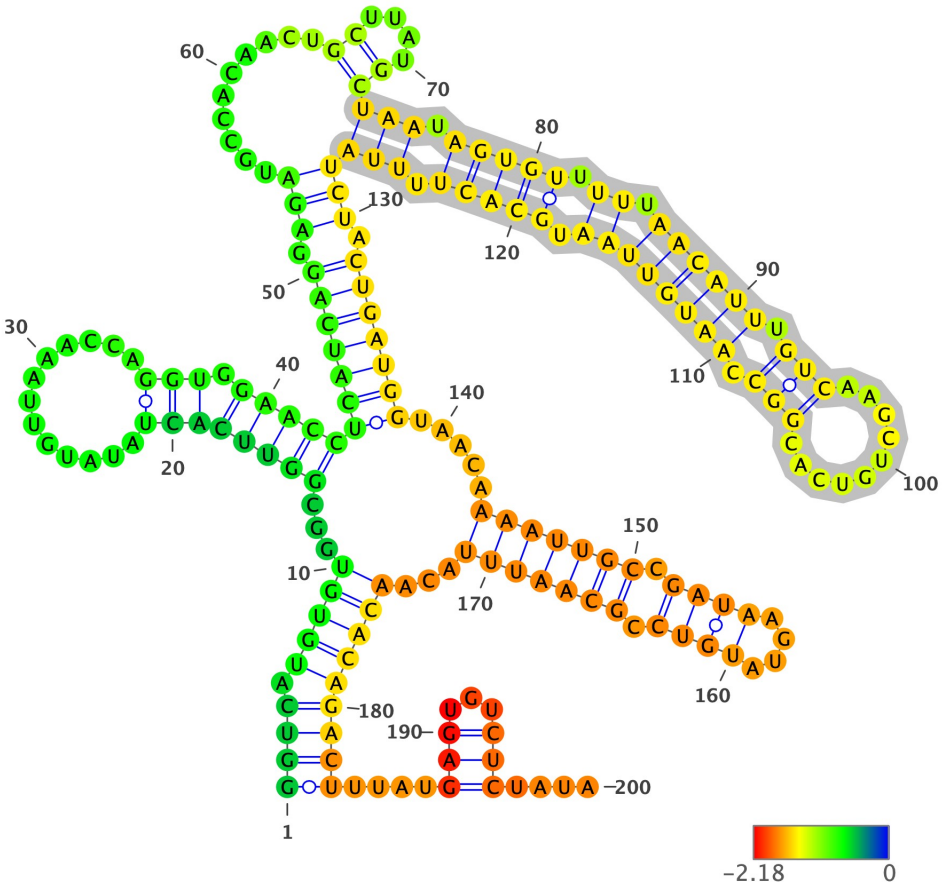
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 245 from nt 15510 to 15564 (nt 73 to 127)

```
5'-TAATAGTGTTTTTAACATTTGTCAAGCTGTCACGGCCAAUGUUAATGCACUTUUA-3'
5'-(((.(((((.((.(((((((.(((.........))).)))))))).)))))).)))-3'
Motif MFE = -13.3; z-score = -2.6; ED = 5.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15438 to 15637 (motif highlighted in silver):

```
5'-GGUCAUGUGUGGCGGUUCACUAUAUGUUAAACCAGGUGGAACCUCAUCAGGAGAUGCCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAA
UGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUA-3
5'-((((.(((((...(((((((((.............))).)))))(((((((.(((..........((....))(((.(((((.((.(((((((.(((..........))).))
))))))).)))))).)))))).)))))))).....(((((((.((((....)))).)))))))...)))))))))....(((...)))....-3'
MFE = -44.9; z-score = -1.71; ED = 20.7
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

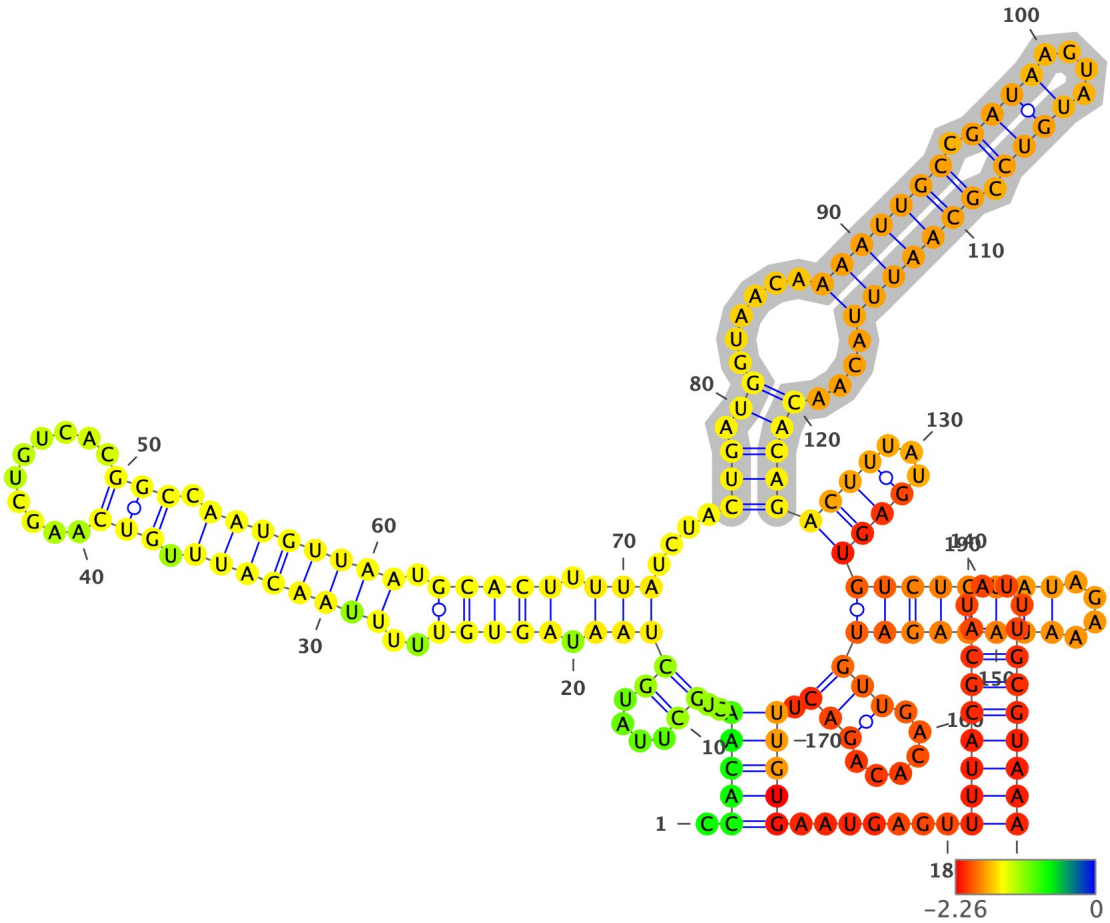
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 246 from nt 15569 to 15617 (nt 76 to 124)

```
5'-CTGATGGTAACAAAATTGCCGATAAGTATGUCCGCAAUUUACAACACAG-3'
5'-(((.((......(((((((.(((......))).)))))))....)))))-3'
Motif MFE = -9.6; z-score = -2.02; ED = 6.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15494 to 15693 (motif highlighted in silver):

```
5'-CCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCA
AUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAA-3
5'-.(((((..((....))(((.(((((..((((((((.(((..........))).)))))))).))))).)))....(((.((......(((((((.((((....)))).)))
)))).....)))))((((...))))((((((((....))))))))(((......))).)))))........((((((((....))))))))-3'
MFE = -49.0; z-score = -2.9; ED = 24.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

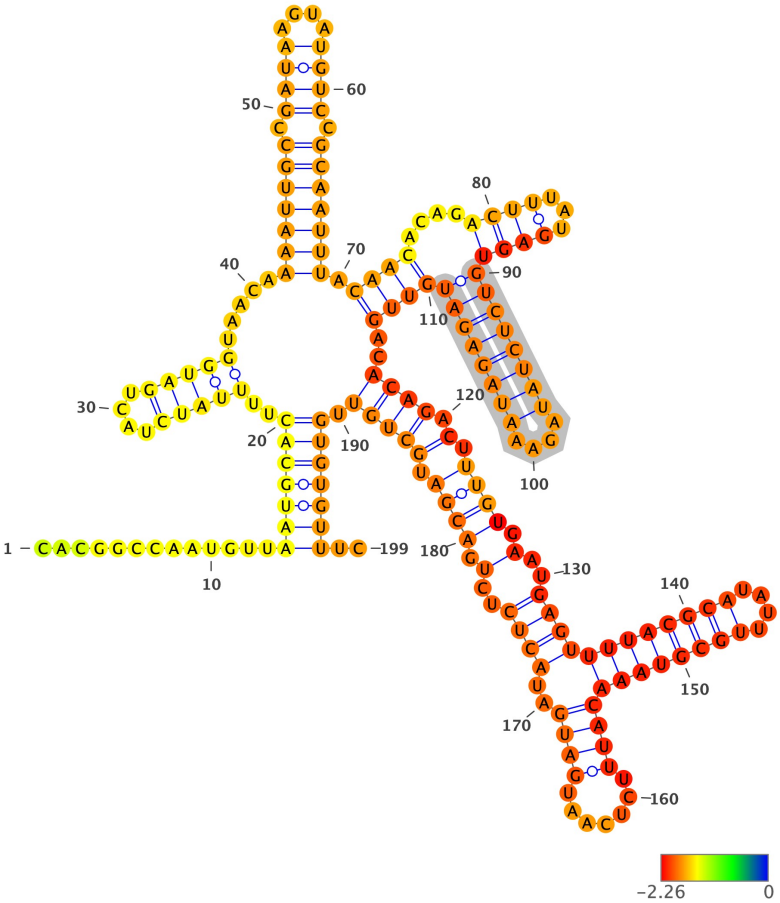
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 247 from nt 15629 to 15648 (nt 90 to 109)

```
5'-GTCTCTATAGAAATAGAGAU-3'
5'-((((((........))))))-3'
Motif MFE = -7.2; z-score = -5.5; ED = 0.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15540 to 15738 (motif highlighted in silver):

```
5'-CACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGU
UGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUC-3
5'-.............(((((((..(((((....))))).....(((((((.((((....)))).)))))))).((((....((((...))))((((((((....))))))))))
))..((((.(.((((.(..((((((((((((....))))))))((((.......))))..))))..).)))).))))).)))))))..-3'
MFE = -44.7; z-score = -1.27; ED = 54.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

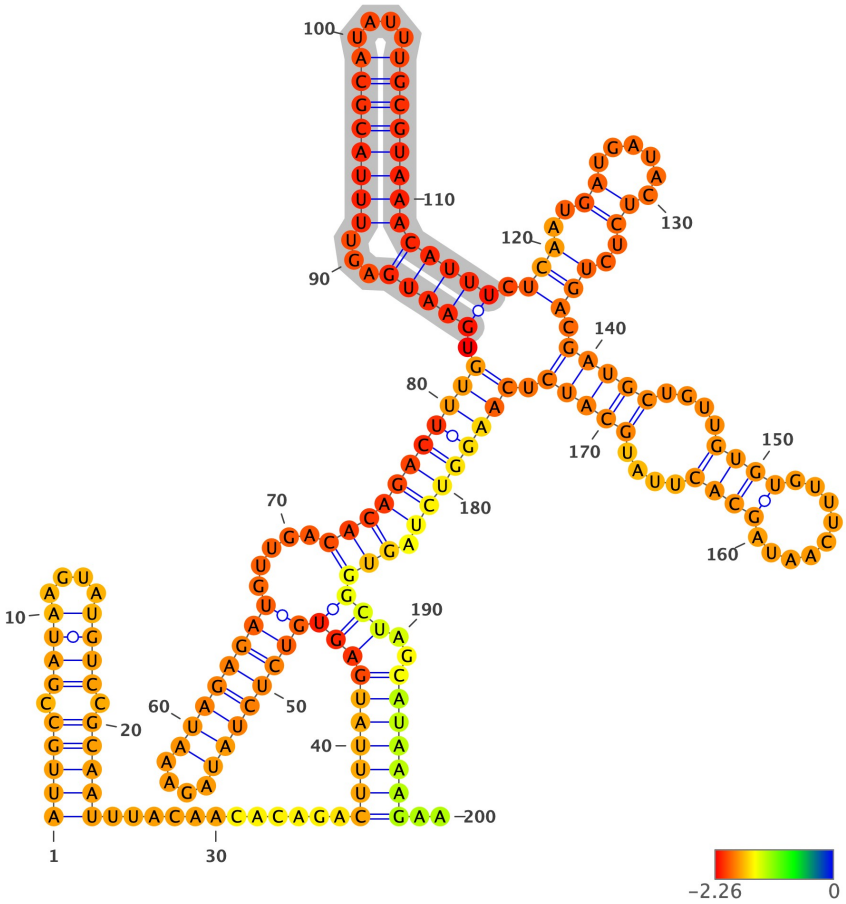
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 248 from nt 15666 to 15698 (nt 84 to 116)

```
5'-GAATGAGTTTTACGCATATTTGCGUAAACAUUU-3'
5'-(((((...(((((((......))))))))))))-3'
Motif MFE = -10.0; z-score = -3.54; ED = 4.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15583 to 15782 (motif highlighted in silver):

```
5'-AUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAA
CAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAA-3
5'-(((((.((((....)))).)))))............((((((((((((((((((....))))))))).....((((((((((.(((((...((((((((....))))))))
))))).(((..((......))..))).(((((....((((.........))))....))))).))))))))).))))))..)))))))..-3'
MFE = -52.3; z-score = -3.65; ED = 24.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

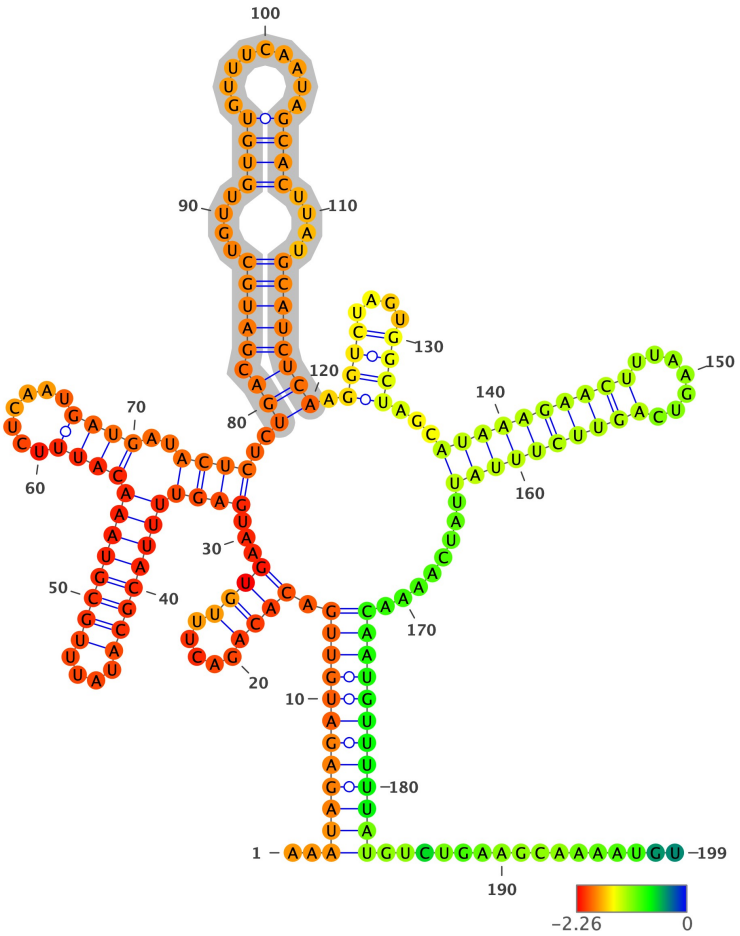
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 249 from nt 15717 to 15758 (nt 79 to 120)

```
5'-TGACGATGCTGTTGTGTGTTTCAATAGCACTTATGCAUCUCA-3'
5'-(((.(((((....((((.........))))....)))))))-3'
Motif MFE = -11.5; z-score = -2.41; ED = 7.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15639 to 15837 (motif highlighted in silver):

```
5'-AAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUA
UGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGU-3
5'-..(((((((((((.((((.....)))).....((((((((((....)))))))))((((.......)))).)))).)))).((((.(((((....((((.........)))))....
.)))))))).((((....)))).....((((((((((.......))))))))))).........))))))))))).................-3'
MFE = -46.3; z-score = -2.93; ED = 38.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

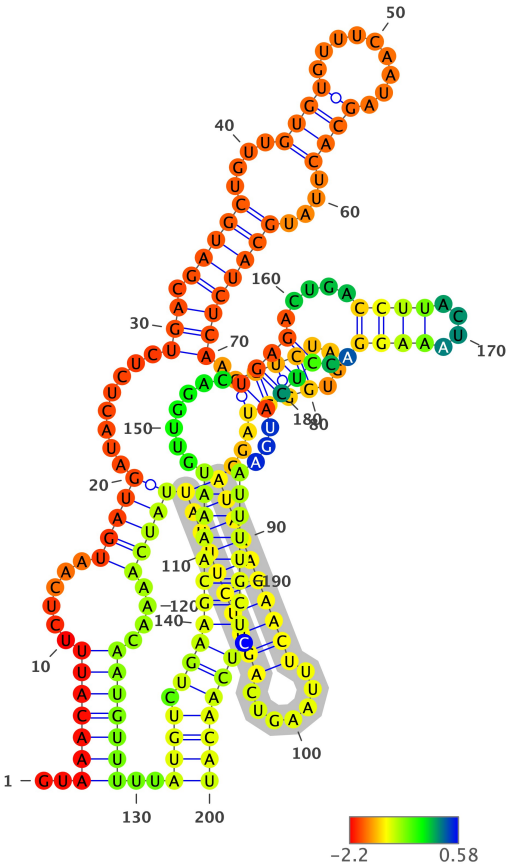
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 250 from nt 15775 to 15801 (nt 87 to 113)

```
5'-ATAAAGAACTTTAAGTCAGUUCUUUAU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -7.5; z-score = -4.19; ED = 0.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15689 to 15888 (motif highlighted in silver):

```
5'-GUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUU
AUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGUUGGACUGAGACUGACCUUACUAAAGGACCUCAUGAAUUUUGCUCUCAACAU-3
5'-..(((((((.....(((((.........(((.(((((....((((.........))))....)))))))).((((....))))...((((((((((.......))))))))
)))))))....)))))))..(((((.((((((((((.......((((.....((((....))))..))))...)))))))).)))))))-3'
MFE = -41.9; z-score = -1.38; ED = 26.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

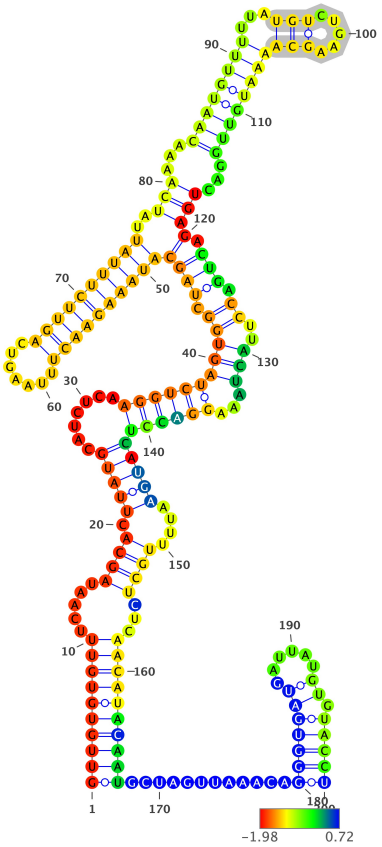
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 251 from nt 15821 to 15831 (nt 95 to 105)

```
5'-TGTCTGAAGCA-3'
5'-(((.....)))-3'
Motif MFE = 0.0; z-score = 0.18; ED = 0.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15727 to 15926 (motif highlighted in silver):

```
5'-GUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGU
UGGACUGAGACUGACCUUACUAAAGGACCUCAUGAAUUUUGCUCUCAACAUACAAUGCUAGUUAAACAGGGUGAUGAUUAUGUGUACCU-3
5'-((((((((((.....((((.(((((.......((((((((((.((((((((((((((.......))))))))))..(((...((((((((...(((.....)))))))))
))...)))).))).))..)))...))))))))))).....))))...))))))))))............(((((((.....)).)))))-3'
MFE = -36.5; z-score = -1.01; ED = 60.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

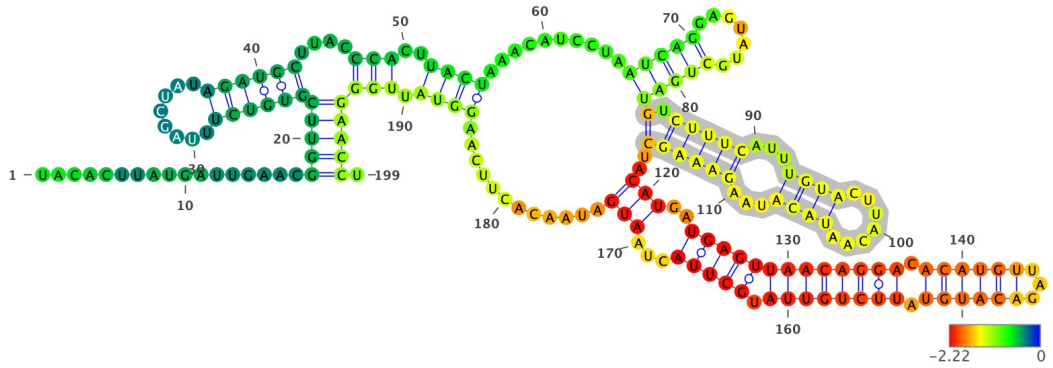
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 252 from nt 16078 to 16111 (nt 83 to 116)

```
5'-GTCTTTCATTTGTACTTACAAUACATAAGAAAGC-3'
5'-(.(((((....(((.......)))....))))))-3'
Motif MFE = -4.4; z-score = -1.26; ED = 2.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15996 to 16194 (motif highlighted in silver):

```
5'-UACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAG
AAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCU-3
5'-.................(((((((((((.........))))))....(((..((((..........(((((.......)))))(.(((((...((((.......))))...)
)))))..(((..((((((((((((((.((((((...)))))).)))))))).)))))...))).............)))).)))))))).-3'
MFE = -42.0; z-score = -2.11; ED = 28.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

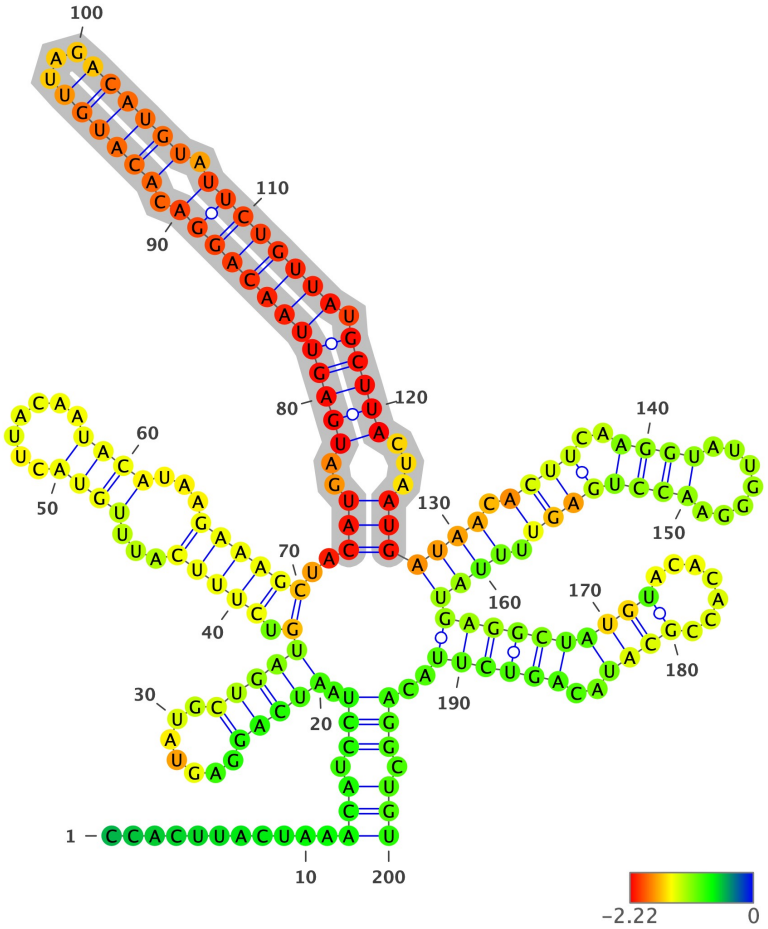
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 253 from nt 16114 to 16168 (nt 73 to 127)

```
5'-CATGATGAGTTAACAGGACACATGTTAGACAUGUAUUCUGUUATGCUUACTAAUG-3'
5'-(((..(((((((((((((.(((((.....))))).))))))))).)))))...)))-3'
Motif MFE = -17.3; z-score = -3.69; ED = 3.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16042 to 16241 (motif highlighted in silver):

```
5'-CCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCU
GUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGU-3
5'-...........(((.(((.(((((.......)))))(.(((((...((((.......))))...))))))..(((..((((((((((((.((((((...)))))).))))
)))).)))))...)))((((.((((..((((.......))))))))).))))((((((((((.......))))..))))))..))).)))-3'
MFE = -44.3; z-score = -1.55; ED = 41.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

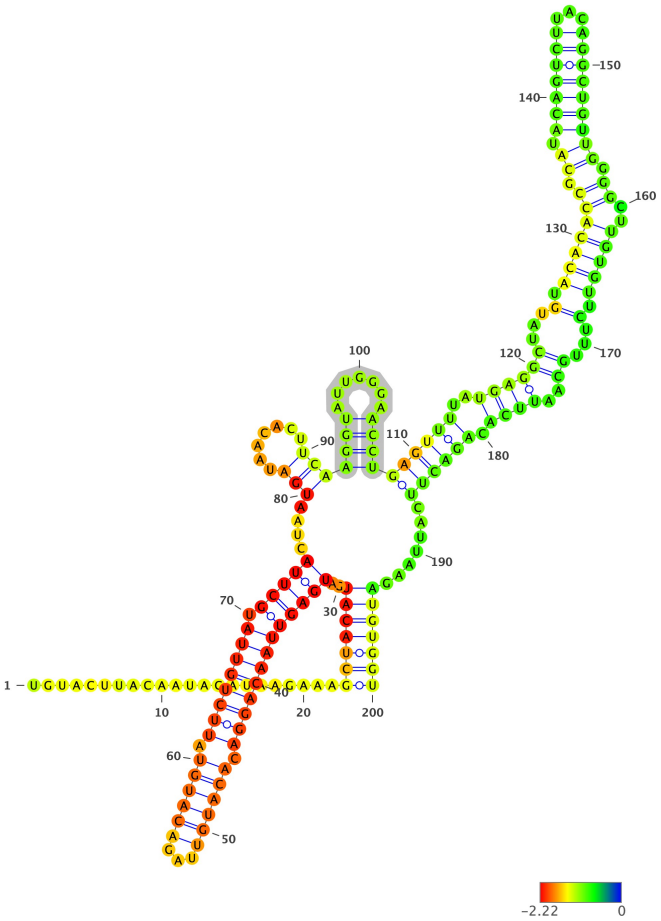
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 254 from nt 16180 to 16194 (nt 93 to 107)

```
5'-AGGTATTGGGAACCU-3'
5'-((((.......))))-3'
Motif MFE = -1.6; z-score = -1.59; ED = 0.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16088 to 16287 (motif highlighted in silver):

```
5'-UGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGU
UUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUUCACAGACUUCAUUAAGAUGUGGU-3
5'-.......................(((((((..(((((((((((((.((((((...)))))).)))))))).)))))....(((.......)))((((.......))))((((
((..((((((...(.(((((((.((.(((((((...)))))))))).))..)))))).)...))..)))).))))))).......)))))))-3'
MFE = -50.1; z-score = -1.75; ED = 32.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

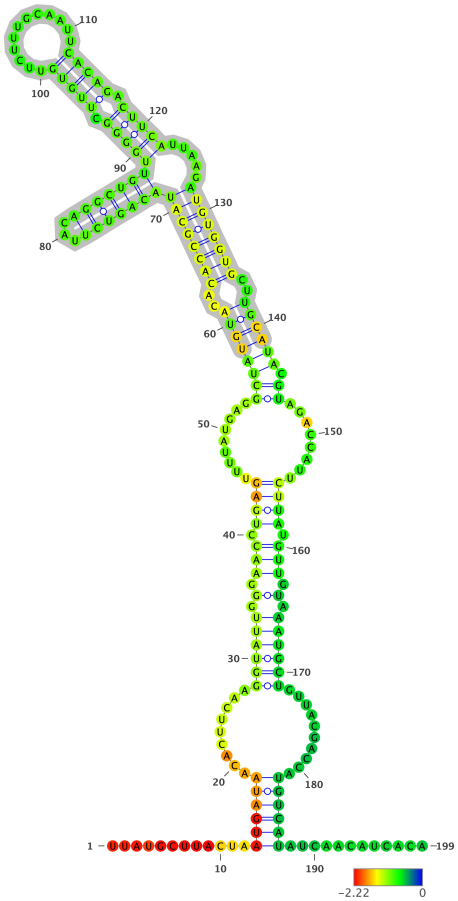
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 255 from nt 16211 to 16294 (nt 58 to 141)

```
5'-TGTACACACCGCATACAGTCTTACAGGCUGTTGGGGCTTGTGTTCTTTGCAATTCACAGACUUCATTAAGAUGUGGUGCTTGCA-3'
5'-((....(((((((.................(((((.(...................).)))))......)))))))....))-3'
Motif MFE = -25.9; z-score = -2.36; ED = 19.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16154 to 16352 (motif highlighted in silver):

```
5'-UUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUU
CACAGACUUCAUUAAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACA-3
5'-............((((((.........((((((.(.(((.((((.........((((((((..((((((((((((((((...)))))))(((((.(((((.............
)))))).)))))).....))))))))..)))))).))........)))).))).).))))))..........))))))............-3'
MFE = -43.6; z-score = -0.53; ED = 35.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

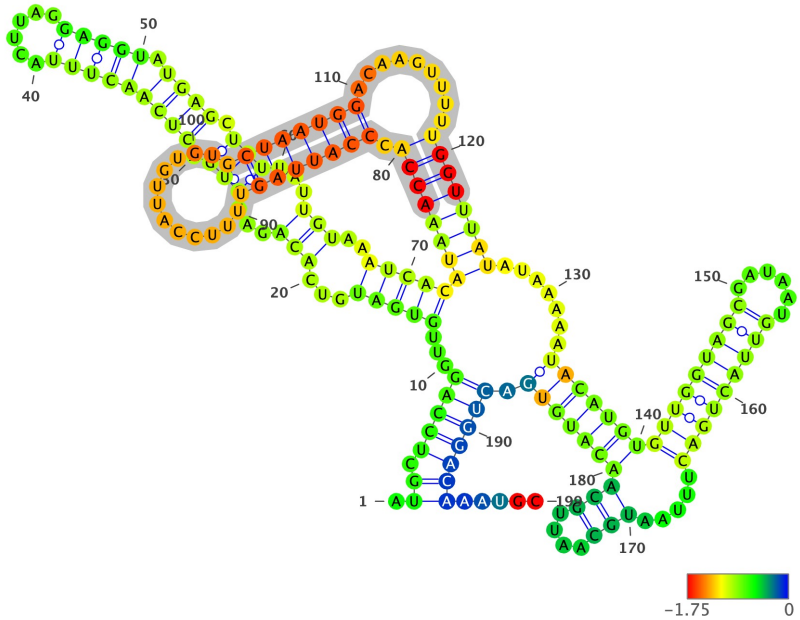
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 256 from nt 16464 to 16509 (nt 77 to 122)

```
5'-ACCACCCATTAGTTTTCCATTGTGTGCUAAUGGACAAGTTTTTGGU-3'
5'-(((..(((((((.............)))))))..........)))-3'
Motif MFE = -9.0; z-score = -1.15; ED = 14.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16388 to 16586 (motif highlighted in silver):

```
5'-AUGCUCCAGGUUGUGAUGUCACAGAUGUGACUCAACUUUACUUAGGAGGUAUGAGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGAC
AAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGACUUUAAUGCAAUUGCAACAUGUGACUGGACAAAUGC-3
5'-.((.(((((...(((((...(((...(((.((((((((.......))))).)))).)))...)))..)))))((((((((.((((((((.............))))))))..
.......))))))))).......((((((((((((((((.......)))))))))).....(((....)))))))))).)))))))).....-3'
MFE = -49.6; z-score = -2.55; ED = 19.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

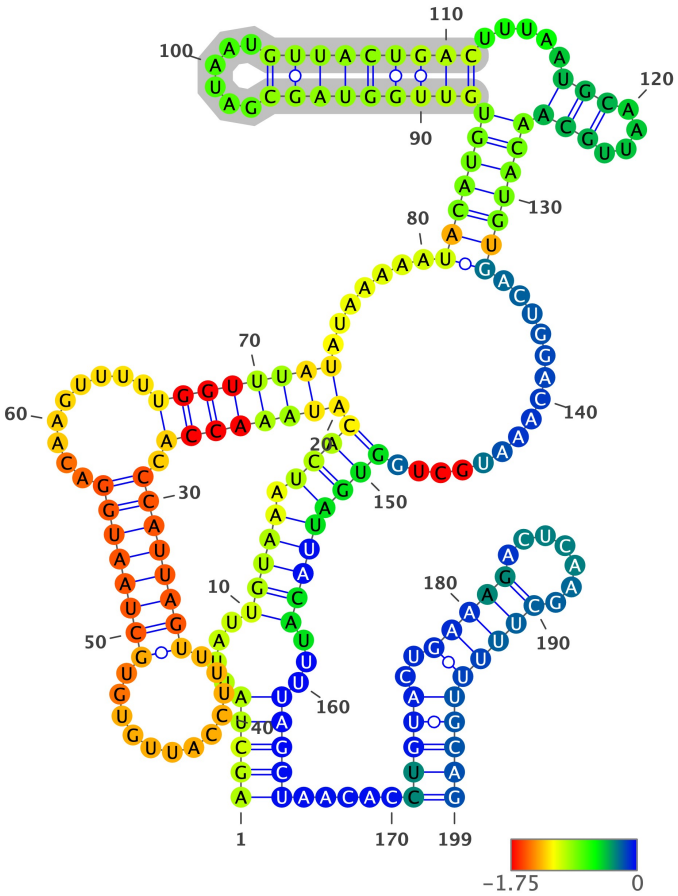
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 257 from nt 16528 to 16551 (nt 88 to 111)

```
5'-GTTGGTAGCGATAATGUUACUGAC-3'
5'-(......................)-3'
Motif MFE = -8.0; z-score = -3.05; ED = 0.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16441 to 16639 (motif highlighted in silver):

```
5'-AGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGAC
UUUAAUGCAAUUGCAACAUGUGACUGGACAAAUGCUGGUGAUUACAUUUUAGCUAACACCUGUACUGAAAGACUCAAGCUUUUUGCAG-3
5'-(((((....(((((.(((((((((((((.((((((((.............)))))))).........)))))))).......(((((((((((((((((......)))))))))
.....(((....))))))))))).................))))))))...)))))).....(((((..(((((.......))))))))))-3'
MFE = -45.0; z-score = -1.97; ED = 22.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

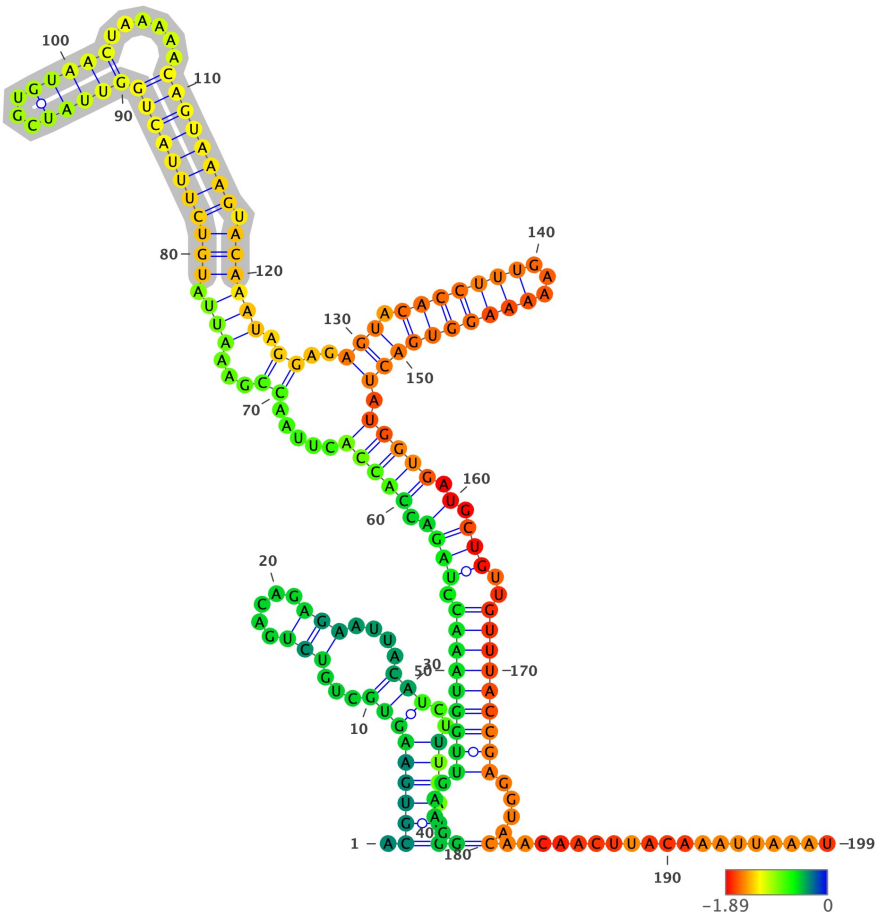
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 258 from nt 16776 to 16817 (nt 79 to 120)

```
5'-TGTCTTTACTGGTTATCGTGTAACTAAAAACAGUAAAGTACA-3'
5'-((((((((((((.....................))))))))).)))-3'
Motif MFE = -9.5; z-score = -2.31; ED = 4.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16698 to 16896 (motif highlighted in silver):

```
5'-ACGUGAAGUGCUGUCUGACAGAGAAUUACAUCUUUCAUGGGAAGUUGGUAAACCUAGACCACCACUUAACCGAAAUUAUGUCUUUACUGGUUAUCGUGUAACUAAAAACAG
UAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAU-3
5'-.(((((((((...(((.....)))....)))..))))))(....(((((((((.((((.(((((.....((...(((.((((((((((((((((...)))))).....)))
))))).)))))).))..(((.(((((((...)))))))))).))))).).)))..)))))))))....).....................-3'
MFE = -41.4; z-score = -0.95; ED = 49.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

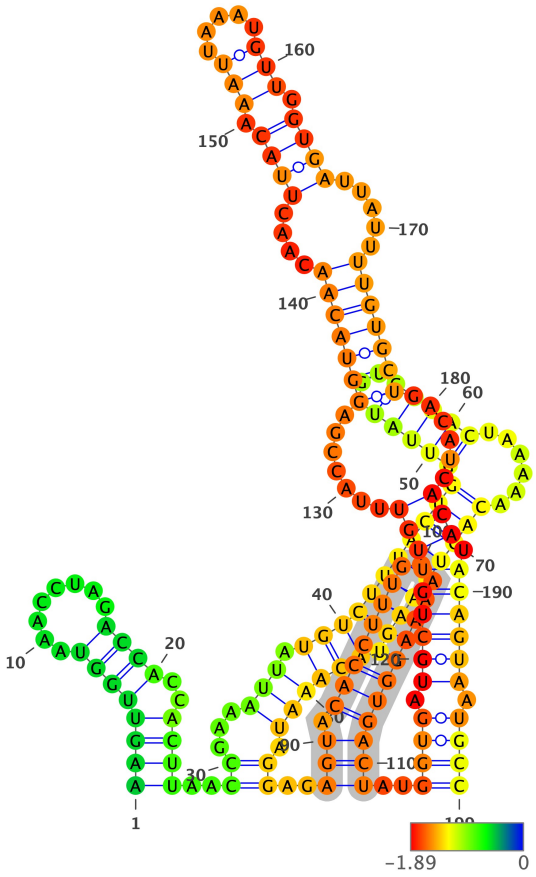
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 259 from nt 16826 to 16849 (nt 88 to 111)

```
5'-AGTACACCTTTGAAAAAGGUGACU-3'
5'-(((.((((.........)))))))-3'
Motif MFE = -8.0; z-score = -4.55; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16739 to 16937 (motif highlighted in silver):

```
5'-AAGUUGGUAAACCUAGACCACCACUUAACCGAAAUUAUGUCUUUACUGGUUAUCGUGUAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACU
AUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCC-3
5'-((((((((........))))..))))..((...(((.((((((((((((((((...)))))).....)))))))).)))))).))..(((.(((((((...)))))))))
..((((.(((((((((.......(((((((....((((.(((.....))).))))).....)))))))).....))).)))))).))))-3'
MFE = -42.1; z-score = -1.33; ED = 47.68
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

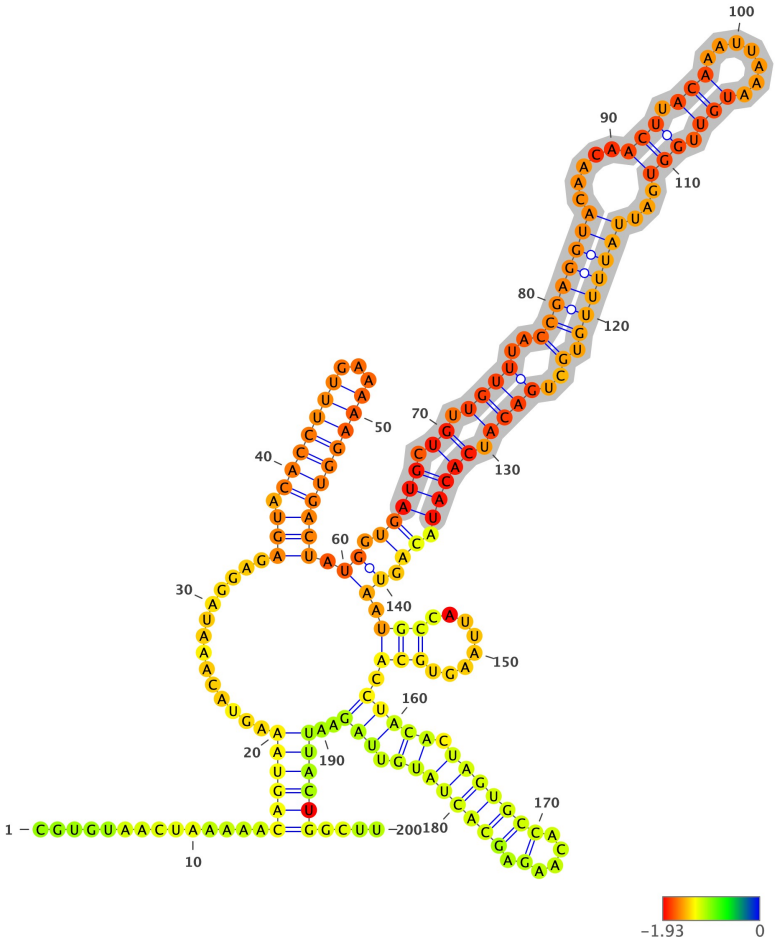
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 260 from nt 16856 to 16926 (nt 65 to 135)

```
5'-ATGCTGTTGTTTACCGAGGTACAACAACTTACAAATTAAAUGUTGGUGATTATTTTGTGCTGACATCACAU-3'
5'-(((.((.((((...............(((.(((.......))).))).............)))).)))))-3'
Motif MFE = -11.9; z-score = -0.52; ED = 18.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16792 to 16991 (motif highlighted in silver):

```
5'-CGUGUAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGU
GAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUU-3
5'-..............((((((..............(((.(((((((...)))))))))).((.(((((.((.((((..((((((((.....(((.(((.......))).)))
...)))))))).)..)))).)))))).)).)).(((........))).(((((.(((((((....).)))))))).)))..))))))....-3'
MFE = -37.3; z-score = -2.09; ED = 35.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

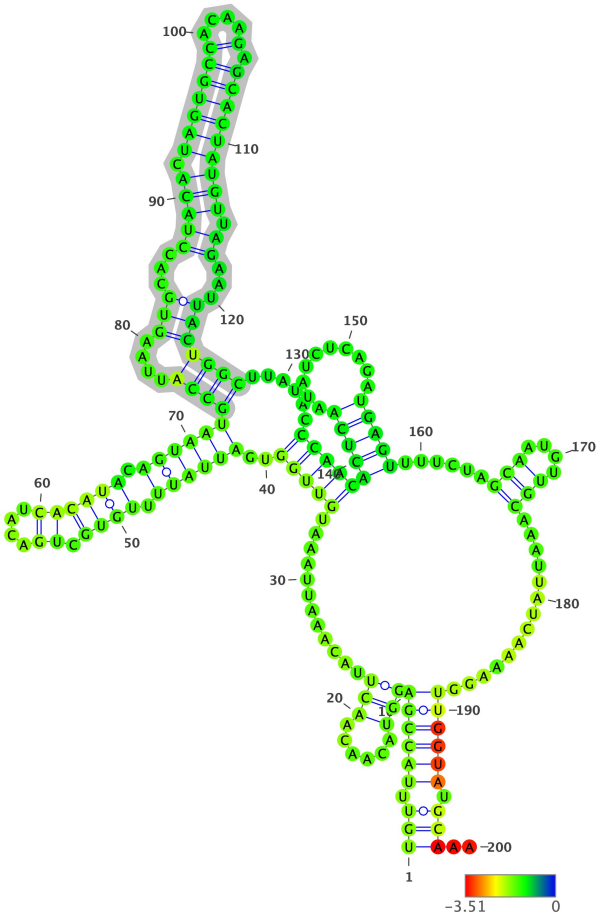
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 261 from nt 16935 to 16989 (nt 73 to 127)

```
5'-GCCATTAAGTGCACCTACACTAGTGCCACAAGAGCACUAUGUTAGAATTACTGGC-3'
5'-(((.............(((.(((((.........))))))))..........)))-3'
Motif MFE = -12.9; z-score = -2.0; ED = 8.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16863 to 17062 (motif highlighted in silver):

```
5'-UGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUA
UGUUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAA-3
5'-(((.(((((((((......)))............(((((..((((((.((((.((....)))))).))))))((((....(((...(((((.(((((((....).))))))
))).))...)))))))......)))))(((((..........)))))......(((....)))..............))))))).)))..-3'
MFE = -36.0; z-score = -0.68; ED = 47.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

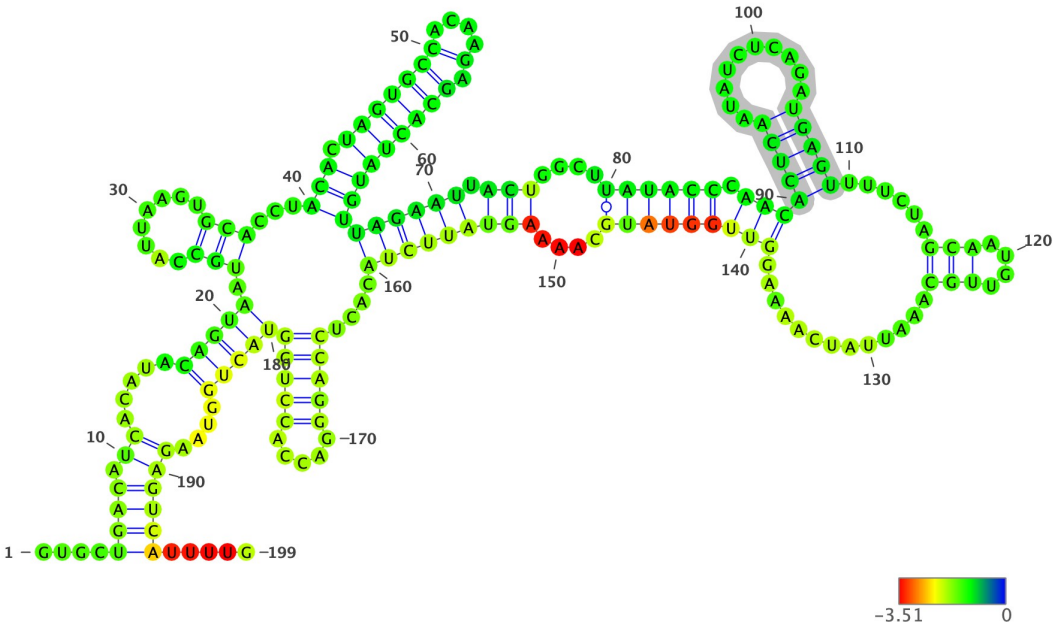
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 262 from nt 17001 to 17020 (nt 90 to 109)

```
5'-ACTCAATATCTCAGATGAGU-3'
5'-(((((.............))))-3'
Motif MFE = -2.1; z-score = -1.41; ED = 2.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16912 to 17110 (motif highlighted in silver):

```
5'-GUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUU
UCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUG-3
5'-....(((((.(((.....(((((.(((........))).....((((.(((((((.....).))))))))))))))(((((.((((....((((((.(((((((((.........)))))))..
....(((....))).............)))))))))....))))))))....(((((.....)))))))))).....))))))).....-3'
MFE = -43.0; z-score = -1.06; ED = 45.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

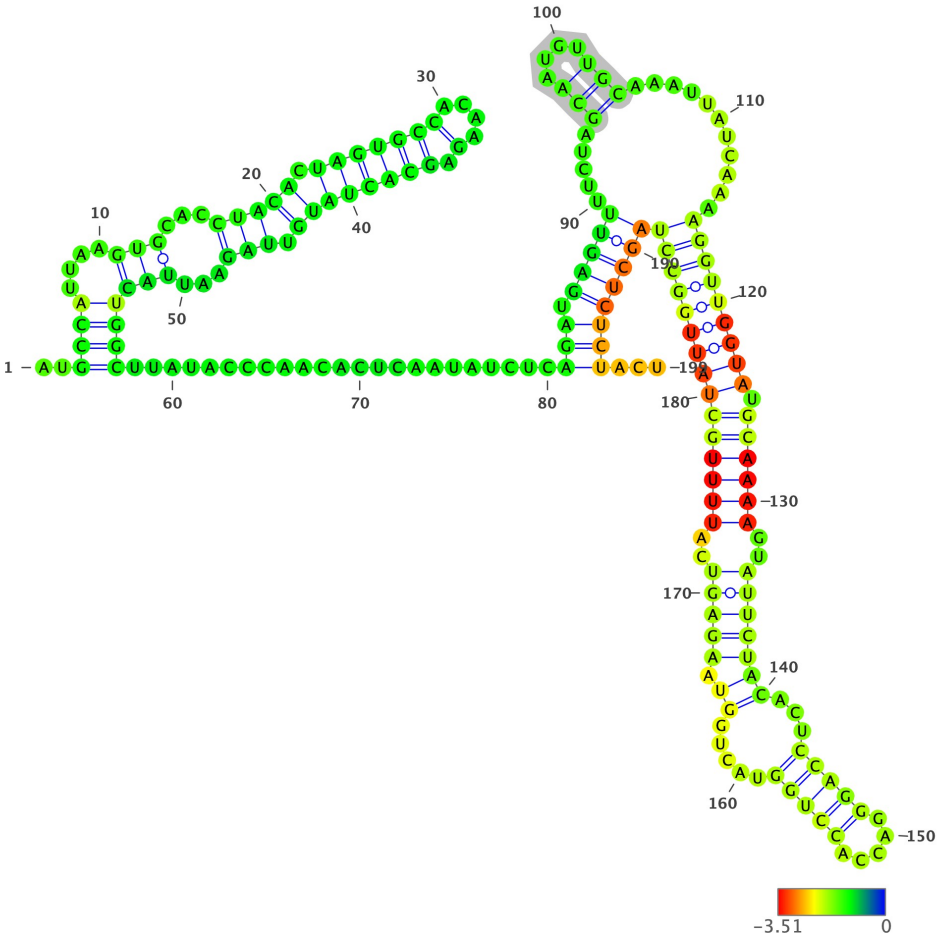
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 263 from nt 17027 to 17036 (nt 95 to 104)

```
5'-GCAATGTTGC-3'
5'-((......))-3'
Motif MFE = -0.4; z-score = -4.62; ED = 1.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16933 to 17131 (motif highlighted in silver):

```
5'-AUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAU
CAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACU-3
5'-..((((....(((...(((((.(((((((....).))))))))).)))...)))))))........................(((.(((((.....(((....)))........
....(((((((((.((((((..(((((((...(((((.....)))))).....)).)))))..))))))))))))))))))))))...-3'
MFE = -48.3; z-score = -2.08; ED = 34.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

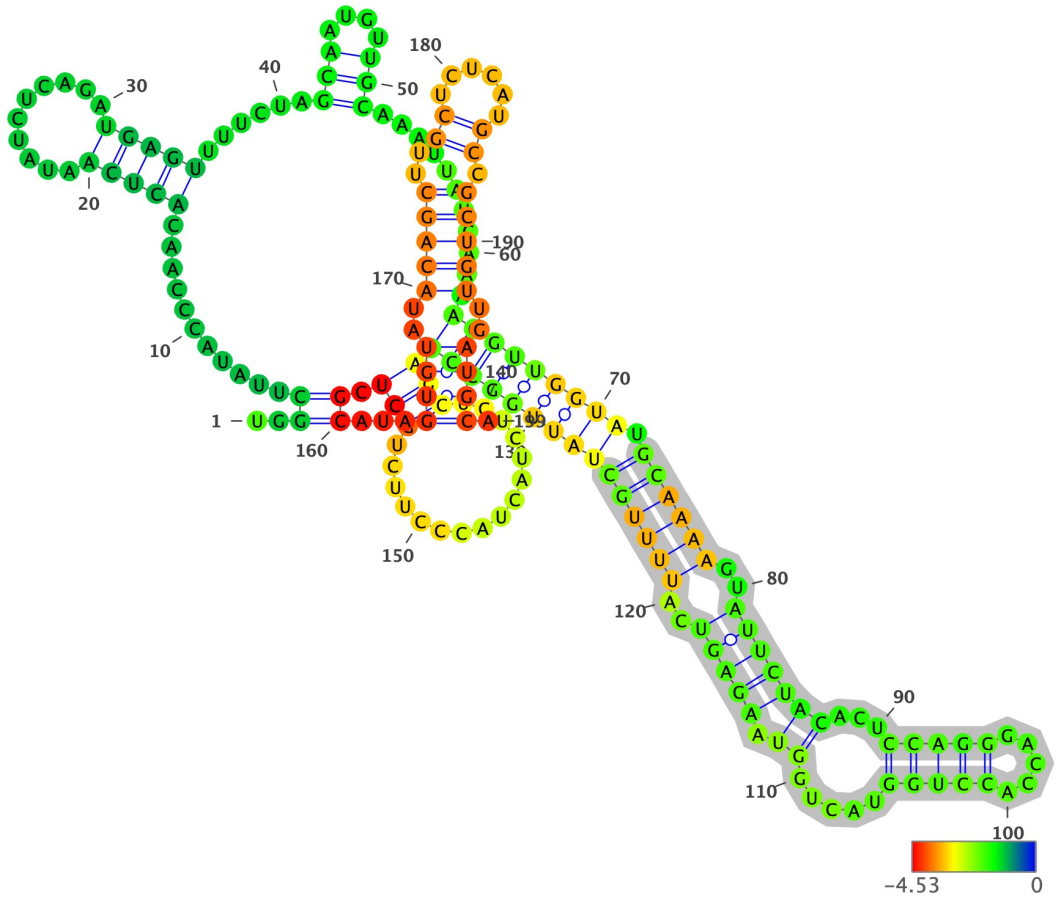
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 264 from nt 17058 to 17111 (nt 73 to 126)

```
5'-GCAAAAGTATTCTACACTCCAGGGACCACCUGGTACTGGTAAGAGUCATTTTGC-3'
5'-((......(((((.....(((.(.....).))).......))))).....))-3'
Motif MFE = -18.1; z-score = -3.16; ED = 3.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16986 to 17184 (motif highlighted in silver):

```
5'-UGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGG
UAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCA-3
5'-..((...........(((((..........))))).....(((....))).........(((((((((.((((((..(((((((...(((((.....))))).....)
).)))))..))))))))))))))(((................))).))...((((..(((((..((......)).)))))..)))).-3'
MFE = -46.5; z-score = -1.22; ED = 31.58
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

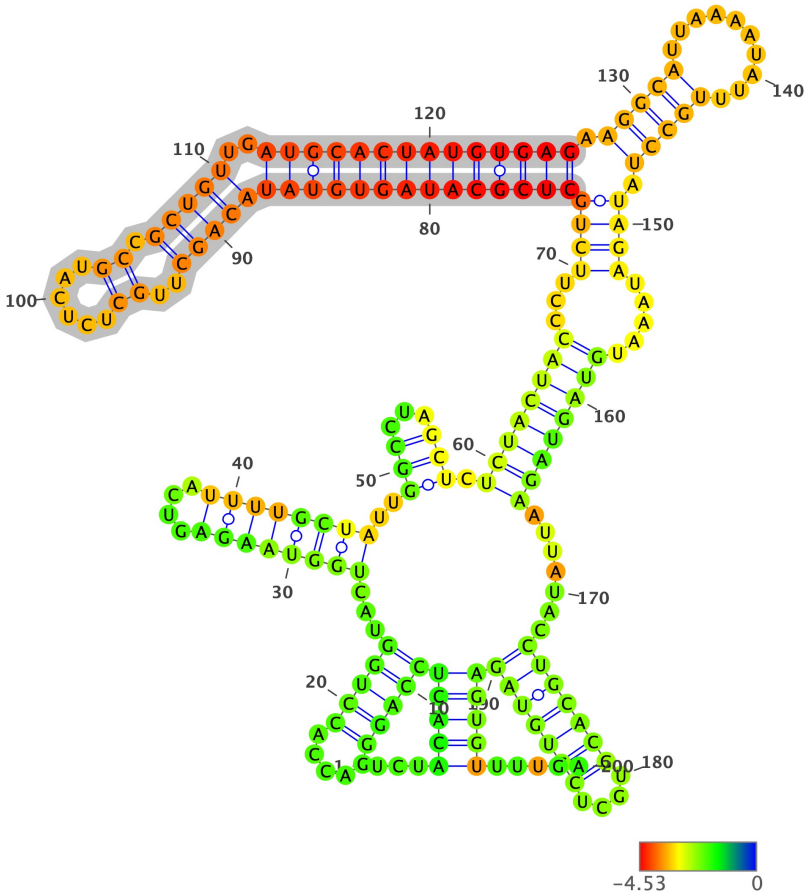
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 265 from nt 17141 to 17193 (nt 74 to 126)

```
5'-CTCGCATAGTGTATACAGCTTGCTCTCATGCCGCUGUTGAUGCACUAUGUGAG-3'
5'-(((((((((((((((((((..((......)).)))))..))))))))))))))-3'
Motif MFE = -27.7; z-score = -5.28; ED = 1.26
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17068 to 17267 (motif highlighted in silver):

```
5'-UCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUU
GAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGA-3
5'-...(((((((((((.....)))))...((((((((....))))))))..(((...))).((((((((...((((((((((((((((((((((((..((......)).)))))).
.))))))))))))))).(((((..........)))))).))))).....))))))))).......(((((((....)))))))))))))).....-3'
MFE = -73.0; z-score = -5.33; ED = 14.79
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

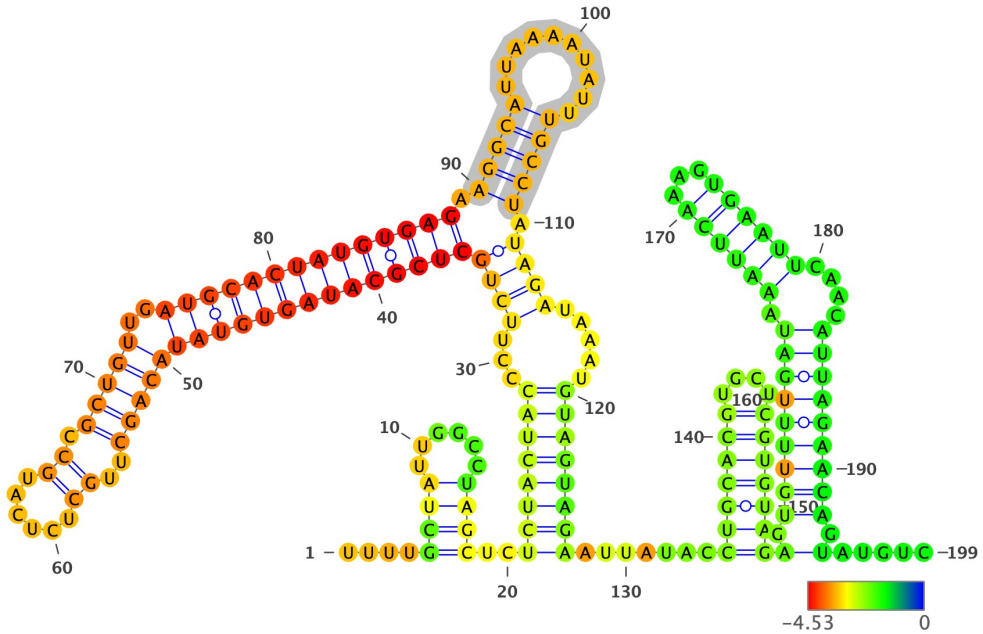
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 266 from nt 17195 to 17214 (nt 90 to 109)

```
5'-AGGCATTAAAATATTUGCCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.1; z-score = -4.14; ED = 0.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17106 to 17304 (motif highlighted in silver):

```
5'-UUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAU
AGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUC-3
5'-....((((......))))..((((((((...((((((((((((((((((((((..((......)).)))))..))))))))))))))).(((((..........)))))).)
)))).....))))))))).......(((((((....)))))))(.((((((((.((((((...)))))).....)))))))))).).....-3'
MFE = -65.4; z-score = -5.32; ED = 24.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

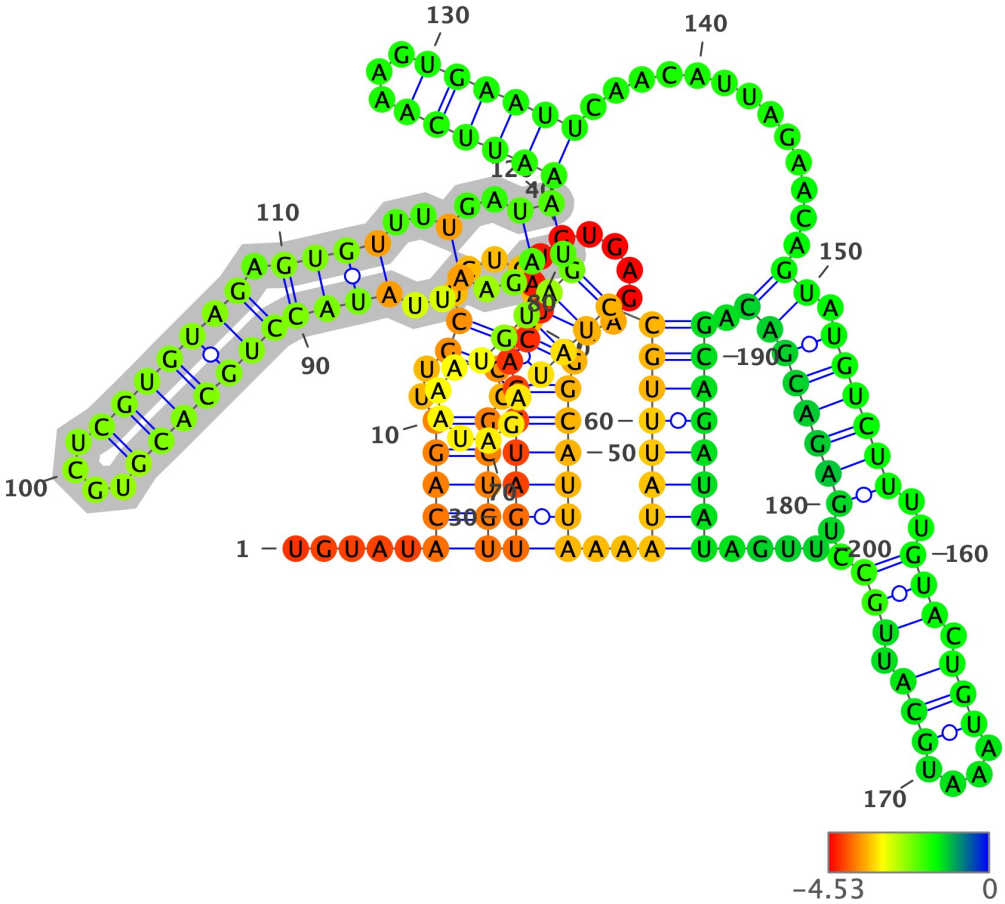
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 267 from nt 17229 to 17269 (nt 80 to 120)

```
5'-TAGAATTATACCTGCACGTGCTCGUGUAGAGUGTTTTGAUA-3'
5'-((......(((((((((......)))))).)))......))-3'
Motif MFE = -12.4; z-score = -3.16; ED = 3.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17150 to 17349 (motif highlighted in silver):

```
5'-UGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGU
GUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUU-3
5'-.....(((((..((......)).)))))((((((.((........))))))))..((((((((((((.....)))))((..(..((((((((((....)))))))).))
))..)..))((((((...))))))..............((.((((((..(((.(((....))).)))..)))))))).))))))))....-3'
MFE = -47.6; z-score = -2.28; ED = 56.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

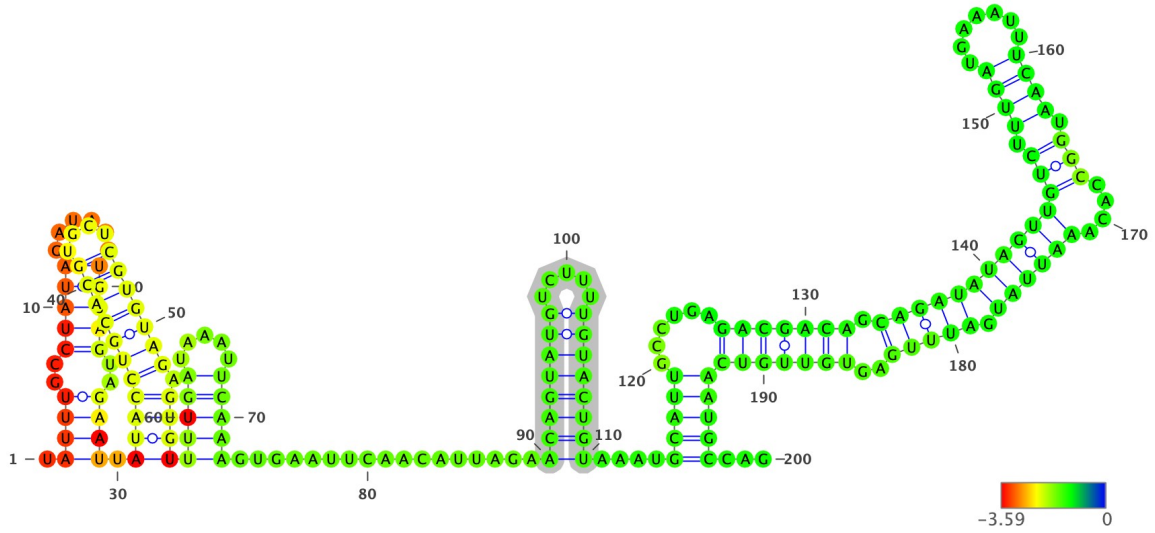
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 268 from nt 17295 to 17315 (nt 90 to 110)

```
5'-ACAGTATGTCTTTTGUACUGU-3'
5'-(((((((.......)))))))-3'
Motif MFE = -5.8; z-score = -3.95; ED = 0.85
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17206 to 17405 (motif highlighted in silver):

```
5'-UAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUA
AAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAG-3
5'-.((((..(((((......)))))..)))).((((((((((....)))))))).))))(((((.....)))))..................((((((((.....)))))))).
...(((((......(((((((.((((((((((((((.((((.......)))).)))....)))))).)))))..))))))))))))...-3'
MFE = -46.0; z-score = -1.62; ED = 31.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

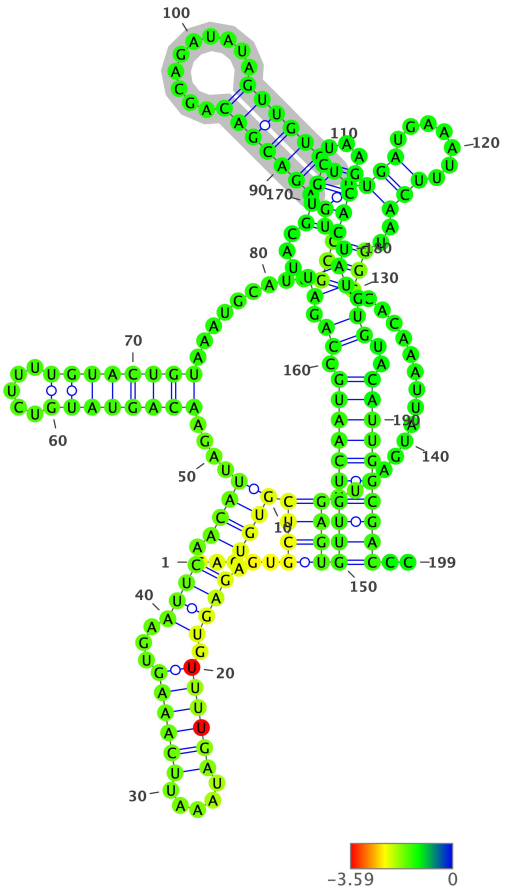
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 269 from nt 17330 to 17353 (nt 88 to 111)

```
5'-AGACGACAGCAGATATAGUUGUCU-3'
5'-(((((((..........)))))))-3'
Motif MFE = -6.7; z-score = -3.2; ED = 6.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17243 to 17441 (motif highlighted in silver):

```
5'-CACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCU
UUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCC-3
5'-.....((((((((.((((.((((((.....))))))...)))).))))....((((((((.....))))))))..........(((.((((((((..........)))))))
)(((.......)))..)))...............))))((((((((((.((.((...((((...)))).)).))..)))))))))..-3'
MFE = -44.6; z-score = -0.76; ED = 40.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

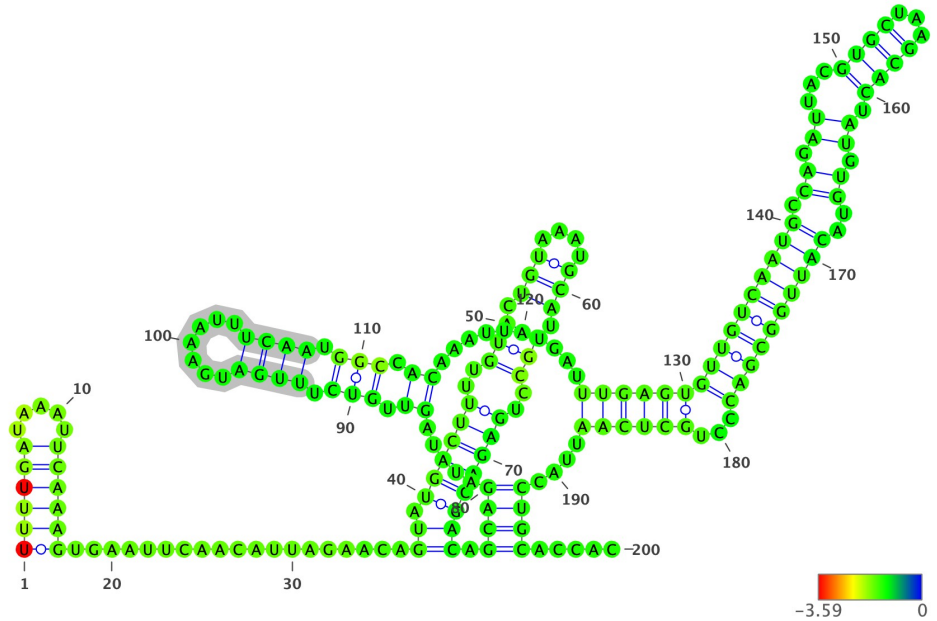
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 270 from nt 17354 to 17368 (nt 93 to 107)

```
5'-TTGATGAAATTUCAA-3'
5'-((((.......))))-3'
Motif MFE = -0.2; z-score = -1.14; ED = 2.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17262 to 17461 (motif highlighted in silver):

```
5'-UUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGC
CACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCAC-3
5'-((((((.....))))))...................((.((((((..(((.(((....))).)))..)))))))).((((.....((.(((.((((.......)))).)))
.)).........((((((((((((((((.((.((...((((...)))).)).)).)))))))))))...))))))....))))).....-3'
MFE = -44.8; z-score = -1.46; ED = 42.21
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

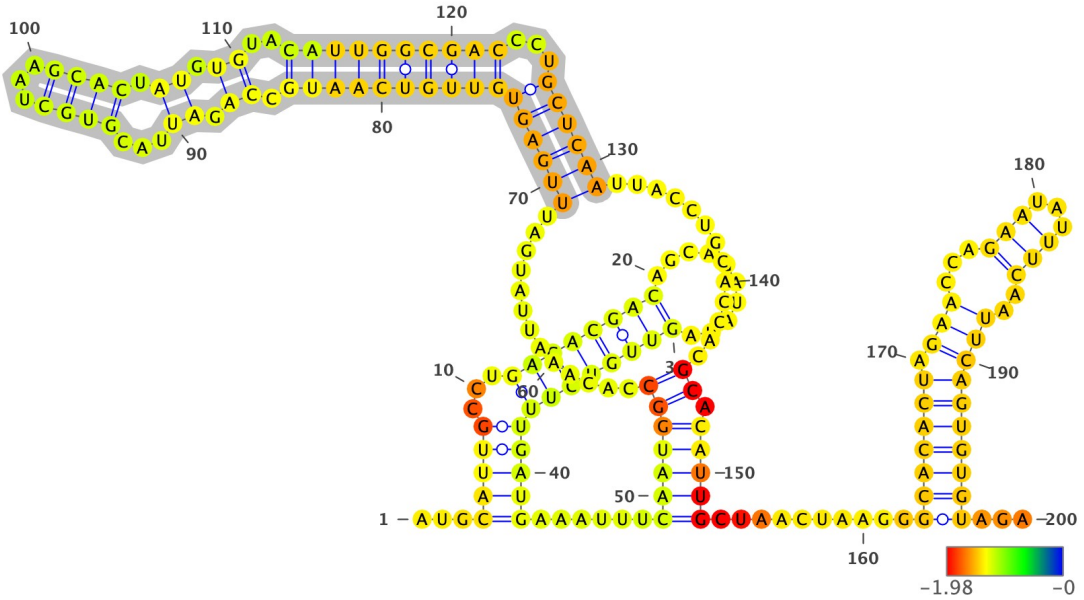
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 271 from nt 17386 to 17448 (nt 69 to 131)

```
5'-TTGAGTGTTGTCAATGCCAGATTACGTGCTAAGCACTAUGUGTACAUUGGCGACCCTGCUCAA-3'
5'-(((((((((((((...((.((...((((...)))).)).))....))))))))...))))))-3'
Motif MFE = -21.9; z-score = -3.55; ED = 3.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17318 to 17517 (motif highlighted in silver):

```
5'-AUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGU
ACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGA-3
5'-...(((((...((((((((..........))))))))))))).....(((((((.............(((((((((((((((.((.((...((((...)))).)).)).
.))))))))))...))))))..............)).)))))..........(((((((.(((...(((...)))..)))))))))))...-3'
MFE = -47.0; z-score = -1.08; ED = 34.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

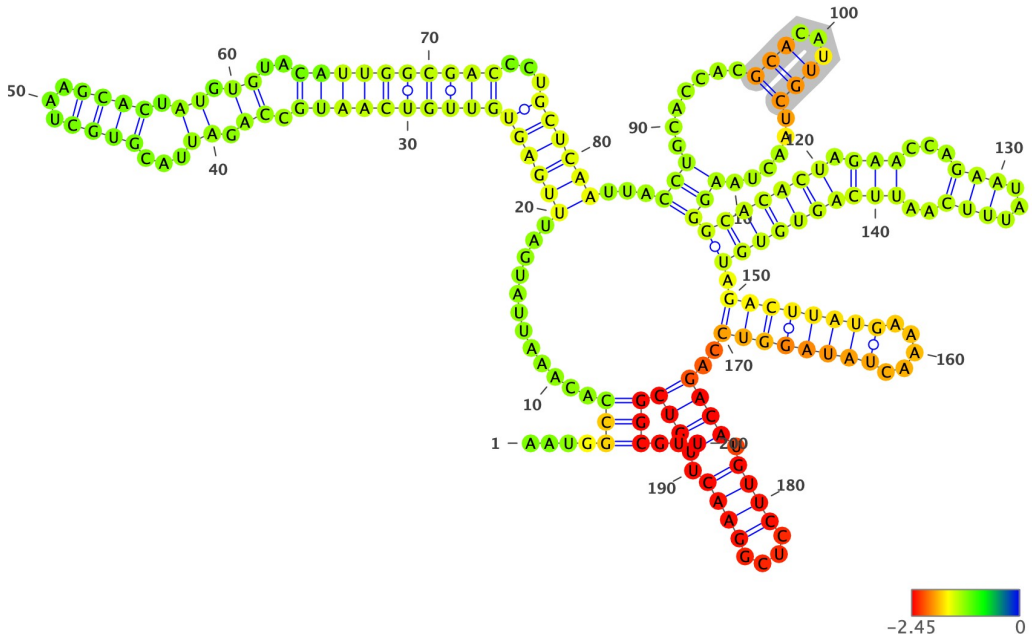
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 272 from nt 17462 to 17470 (nt 96 to 104)

```
5'-GCACATUGC-3'
5'-(((...)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17367 to 17566 (motif highlighted in silver):

```
5'-AAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAA
GGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUU-3
5'-....(((............((((((((((((((((.((.((...((((...)))).)).))..))))))))))...))))))...(((.......(((...)))......)
))(((((((.(((...(((...)))..)))))))))).((((((((.....))))))))..((((.((((....)))).)))))))...-3'
MFE = -58.3; z-score = -3.8; ED = 11.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

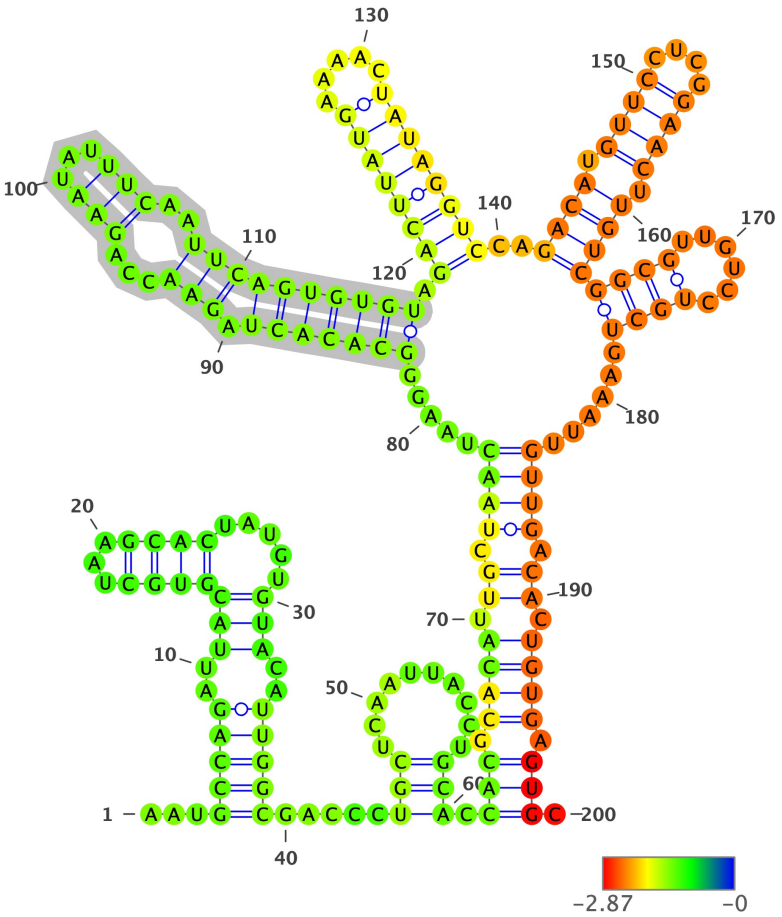
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 273 from nt 17480 to 17514 (nt 83 to 117)

```
5'-GCACACTAGAACCAGAATATTTCAATTCAGUGUGU-3'
5'-(((((((.....................)))))))-3'
Motif MFE = -8.4; z-score = -3.25; ED = 3.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17398 to 17597 (motif highlighted in silver):

```
5'-AAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCA
GUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGC-3
5'-...(((((..(((((((...))))).....)))..)))))).....(((..........))).(((.((((.((.((((.....(((((((.(((...(((...)))..))))
)))))).((((((((.....))))))))..((((.((((....)))).))))((((......))))......)))).)).)))).))).-3'
MFE = -50.2; z-score = -1.04; ED = 42.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

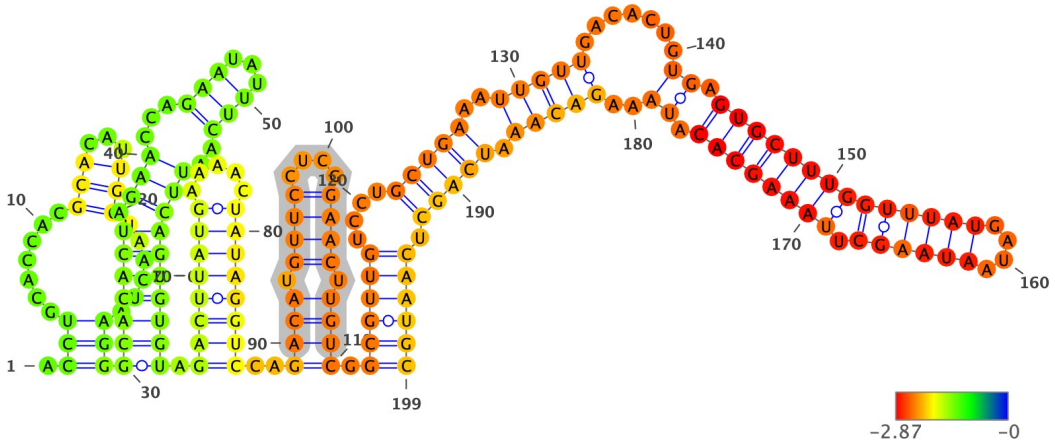
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 274 from nt 17540 to 17559 (nt 90 to 109)

```
5'-ACATGTTCCTCGGAACTUGU-3'
5'-(((.((((....)))).)))-3'
Motif MFE = -6.0; z-score = -3.15; ED = 0.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17451 to 17649 (motif highlighted in silver):

```
5'-ACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCG
GCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGC-3
5'-.(((.......(((...)))......)))(((((((.(((...(((...)))..)))))))))).((((((((.....))))))))..((((.((((....)))).)))).
((((((....(((((..(((((.......((.((((((((((((((....)))))).))))))))).))..))))).)))))).))))))-3'
MFE = -56.6; z-score = -3.43; ED = 16.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

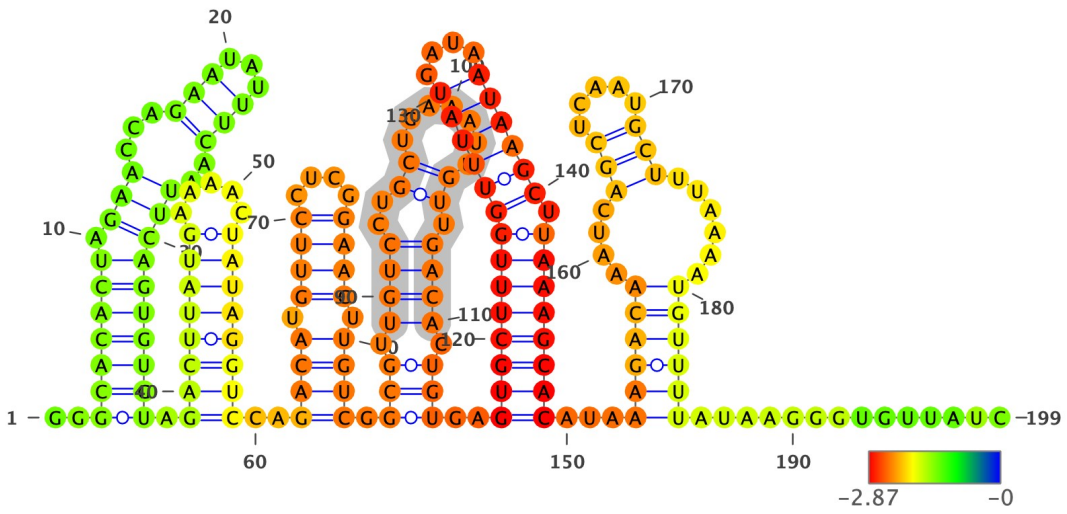
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 275 from nt 17566 to 17587 (nt 89 to 110)

```
5'-TGTCCTGCTGAAATTGUTGACA-3'
5'-((((..((.......)).))))-3'
Motif MFE = -2.6; z-score = -0.66; ED = 0.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17478 to 17676 (motif highlighted in silver):

```
5'-GGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACAC
UGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUC-3
5'-..(((((((.(((...(((...))).))))))))))).((((((((.....))))))))..((((.((((....)))).)))).(((.((((..((.......)).)))).
)))..((((((((((((((....)))))).))))))))...((((((....(((.....)))......))))))..............-3'
MFE = -50.8; z-score = -3.37; ED = 31.44
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

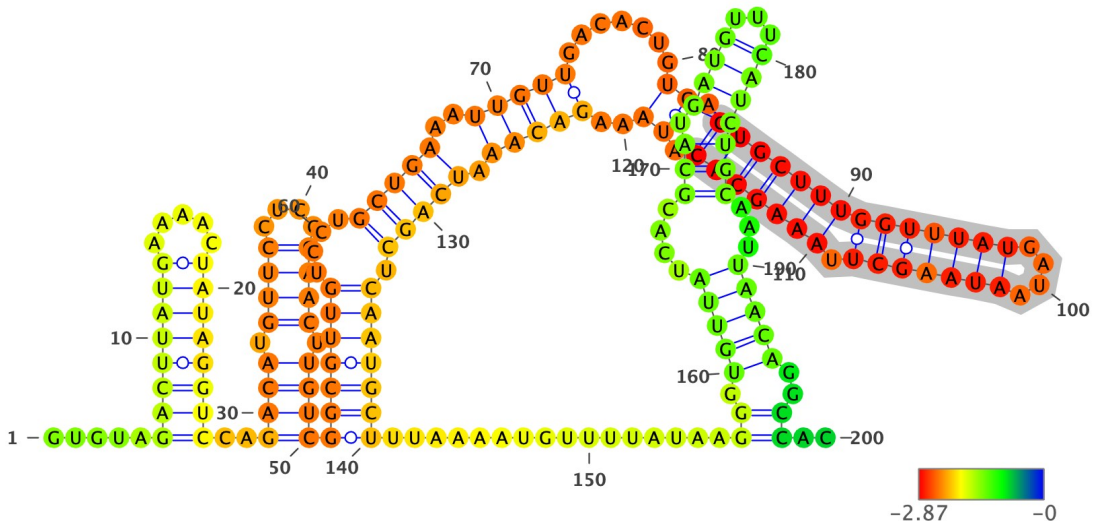
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 276 from nt 17594 to 17626 (nt 84 to 116)

```
5'-GTGCTTTGGTTTATGATAAUAAGCUTAAAGCAC-3'
5'-((((((((((.(((....))).))).)))))))-3'
Motif MFE = -13.2; z-score = -5.19; ED = 1.37
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17511 to 17710 (motif highlighted in silver):

```
5'-GUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAA
AGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAGGCCAC-3
5'-.....((((((((.....))))))))..((((.((((....)))).))))(((((((....(((((..(((((.......((.((((((((((((((....)))))))).))
))))).))..))))).))))).)))))))................((.(((((....(((.((((...)))))))...))))).))..-3'
MFE = -56.4; z-score = -3.1; ED = 24.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

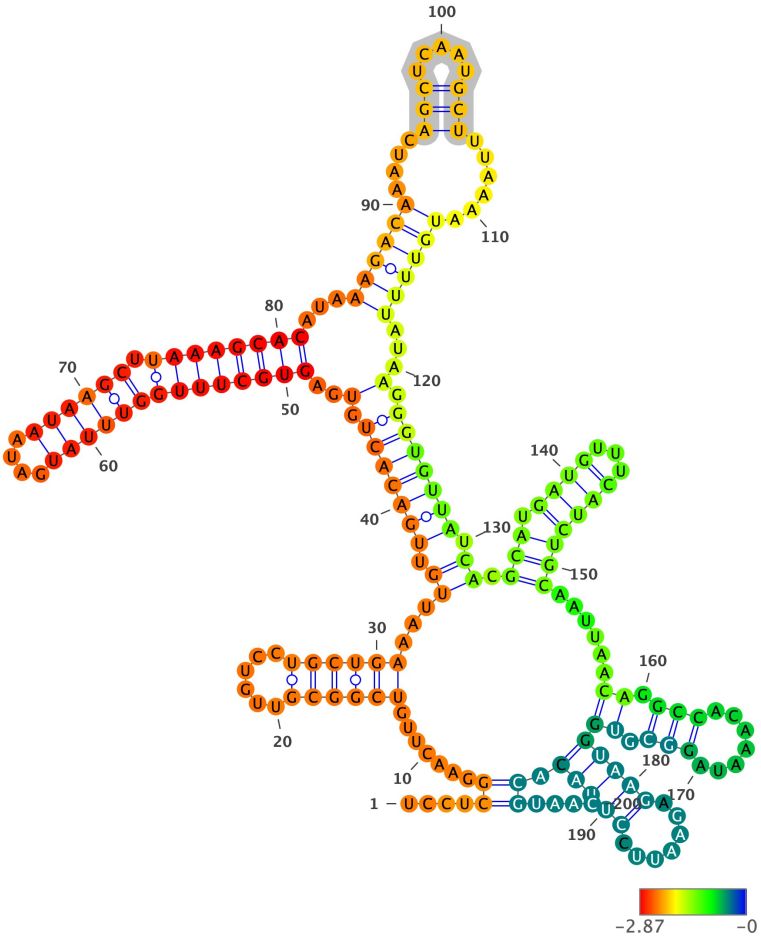
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 277 from nt 17640 to 17650 (nt 95 to 105)

```
5'-AGCTCAATGCU-3'
5'-(((.....)))-3'
Motif MFE = -1.4; z-score = -6.67; ED = 0.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17546 to 17745 (motif highlighted in silver):

```
5'-UCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAA
UGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAAC-3
5'-....((.......((((((.....))))))...((.(((((((.(..(((((((((((((((....)))))))).))))))))...((((((....(((.....)))).....
))))))...).)))))))..)).(((.((((...)))))))......((.(((.......))).))(((((.......))))).)).....-3'
MFE = -49.1; z-score = -2.13; ED = 41.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

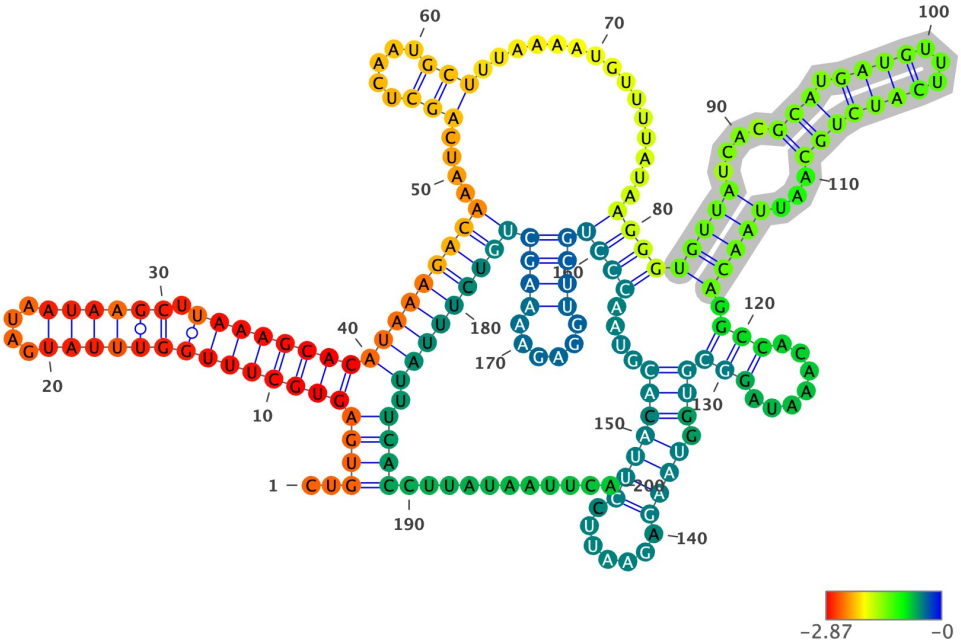
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 278 from nt 17670 to 17704 (nt 83 to 117)

```
5'-TGTTATCACGCATGATGTTTCAUCUGCAATUAACA-3'
5'-(((((....(((.(((.....)))))))...)))))-3'
Motif MFE = -7.2; z-score = -2.51; ED = 1.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17588 to 17787 (motif highlighted in silver):

```
5'-CUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAA
UUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCA-3
5'-..(((((((((((((((((....)))))))).)))))))))(((((((((....(((.....)))).............(((((((((....(((.((((...)))))))).
.)))))).(((.......)))(((.((((.......)))))))....)))))((((.....)))))))))))))).))))...........-3'
MFE = -50.2; z-score = -3.26; ED = 17.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

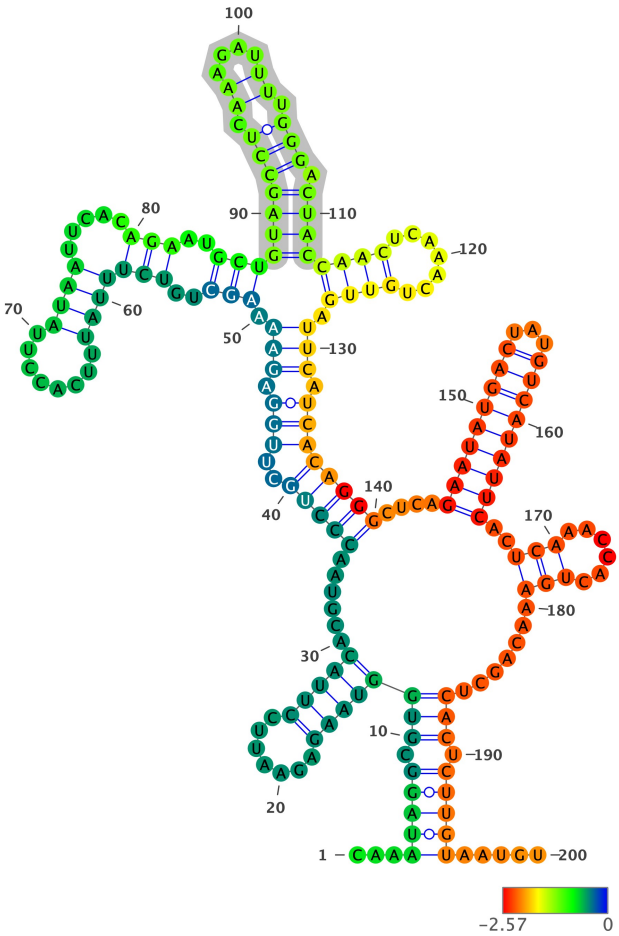
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 279 from nt 17797 to 17821 (nt 88 to 112)

```
5'-GTAGCCTCAAAGATUUTGGGACUAC-3'
5'-(((((((.((....)).))).))))-3'
Motif MFE = -6.7; z-score = -1.72; ED = 2.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17710 to 17909 (motif highlighted in silver):

```
5'-CAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUA
CCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGU-3
5'-...(((((.((((((((.......)))))......(((((..(((.(((.(((..(((((((.........))))).....))).)))(((((((.((....)).))).)))
)((((.......)))).))).)))))))).....((((((((...)))))))))..(((......)))........))).)))))).....-3'
MFE = -41.0; z-score = -1.72; ED = 44.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

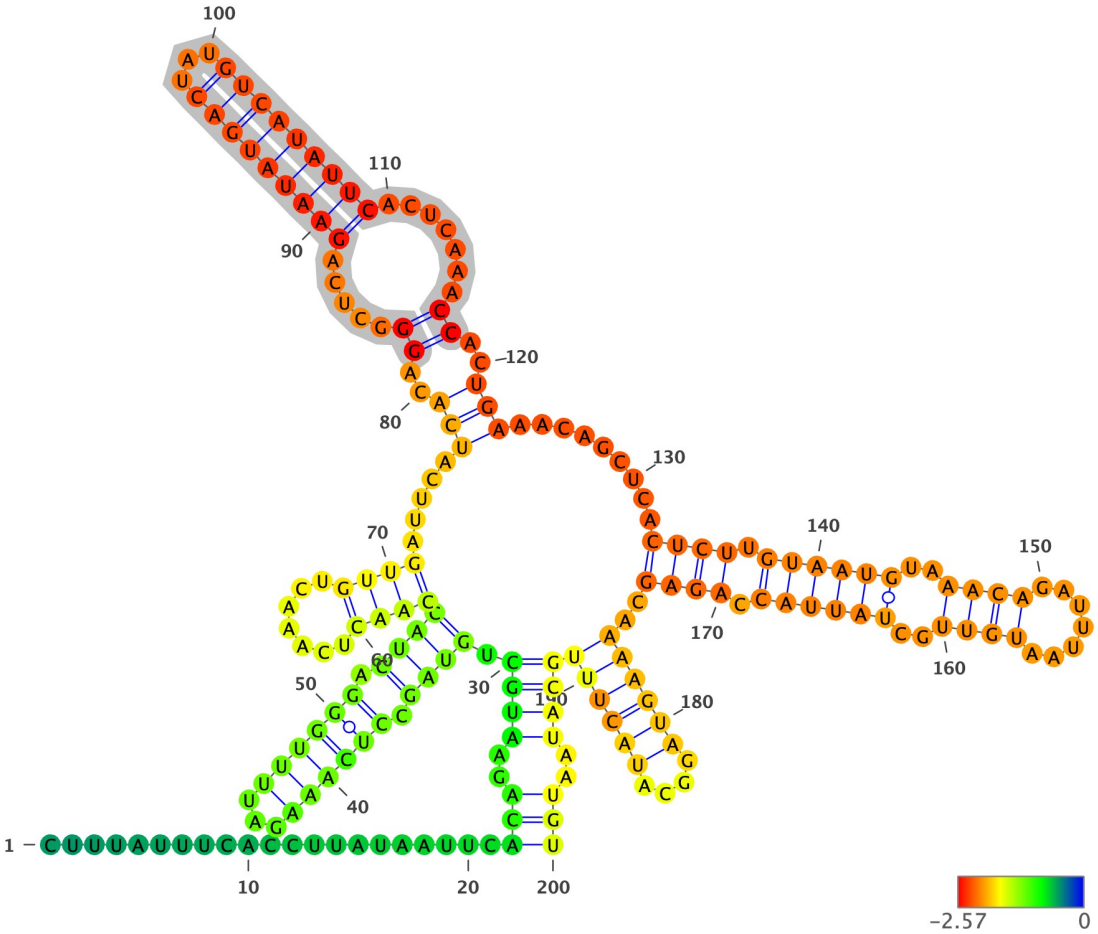
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 280 from nt 17847 to 17883 (nt 82 to 118)

```
5'-GGGCTCAGAATATGACTATGUCAUAUUCACTCAAACC-3'
5'-((.....((((((((((...)))))))))).......))-3'
Motif MFE = -9.6; z-score = -3.04; ED = 2.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17766 to 17965 (motif highlighted in silver):

```
5'-CUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCAC
UCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGU-3
5'-.....................(((..((((.((((.((((((...)))))).))))((((.......))))).....(((..((.....((((((((...)))))))))..
.....))..))).........((((.((((((..((((.......))))..)))))).))))..((((((....)))))))))..)))-3'
MFE = -42.7; z-score = -2.73; ED = 23.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

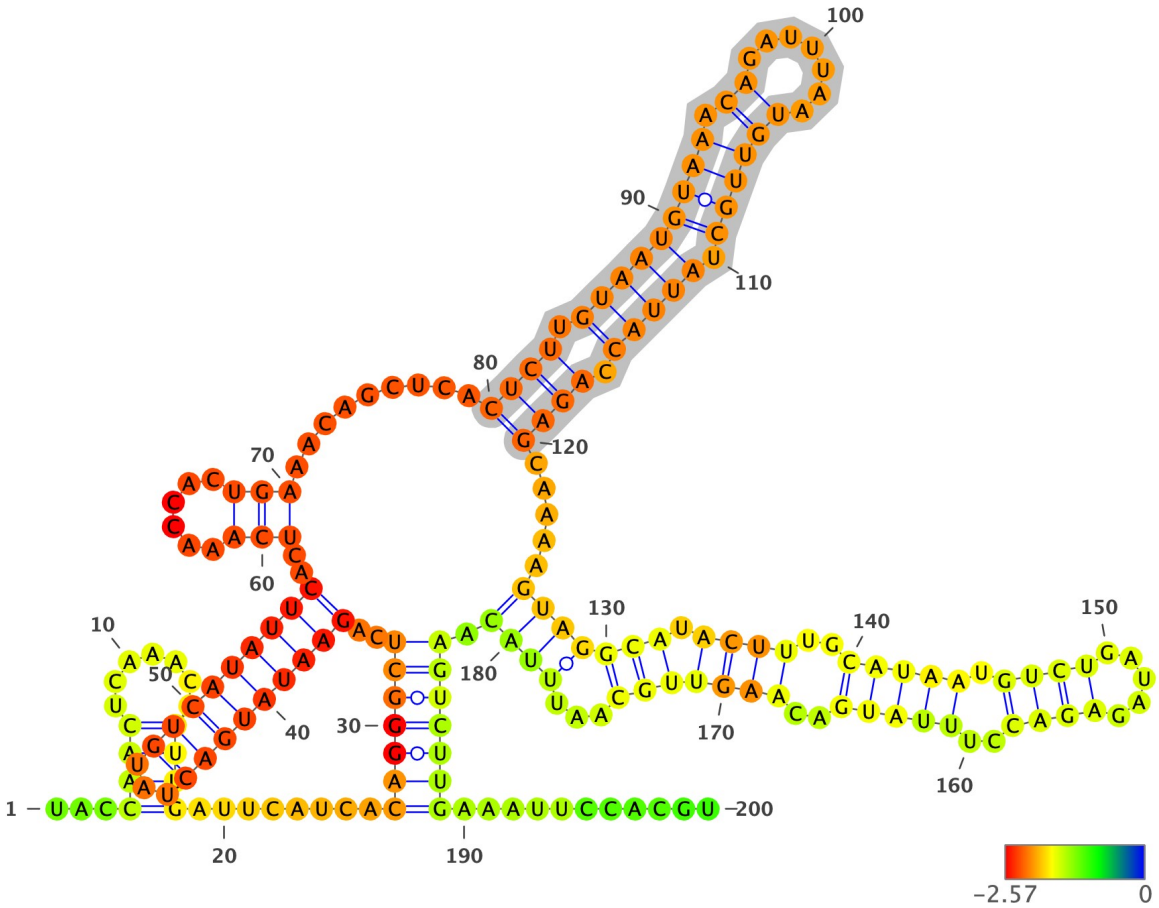
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 281 from nt 17898 to 17938 (nt 80 to 120)

```
5'-CTCTTGTAATGTAAACAGATTTAAUGUUGCTAUUACCAGAG-3'
5'-((((.(((((((((.((.......)))))))).)))))).))))-3'
Motif MFE = -9.7; z-score = -2.67; ED = 3.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17819 to 18018 (motif highlighted in silver):

```
5'-UACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUA
UUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGU-3
5'-...((((.......)))).......(((((((..(((((((((...)))))))))..(((.......))).........((((.(((((((((.(((.......)))))))).)
)))).)))).....(((((((.((((..(((((.((((.....)))).)).)))))..)))))))...)))).)))))))...........-3'
MFE = -44.4; z-score = -2.88; ED = 19.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

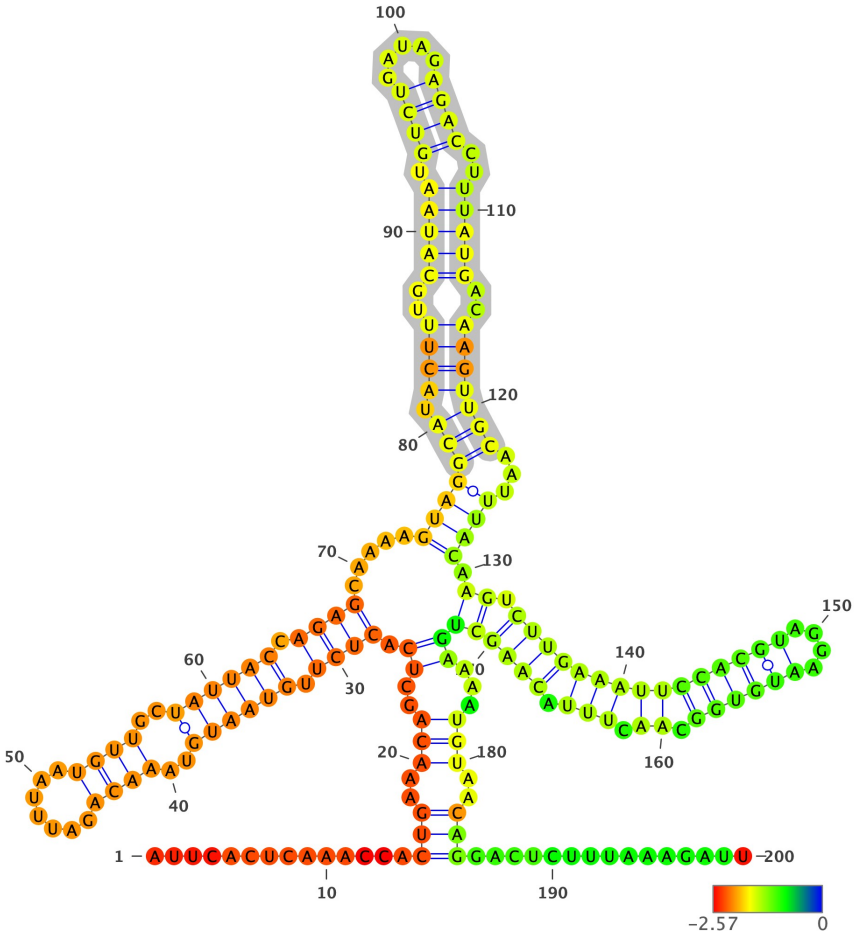
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 282 from nt 17948 to 17992 (nt 78 to 122)

```
5'-GCATACTTTGCATAATGTCTGATAGAGACCTTTAUGACAAGTUGC-3'
5'-(((....(..(((...((((.....))))....)))..)...)))-3'
Motif MFE = -12.2; z-score = -2.61; ED = 3.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17871 to 18070 (motif highlighted in silver):

```
5'-AUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUA
UGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUU-3
5'-..............(((..(((..((.((((.((((((..((((.......))))..)))))).))))).....(((((((.((((..(((((.((((.....))))..)))
))..)))))))...)))).((.((((((((((((((....)))))).)).))).))))))))...)))..))).................-3'
MFE = -38.1; z-score = -1.59; ED = 39.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

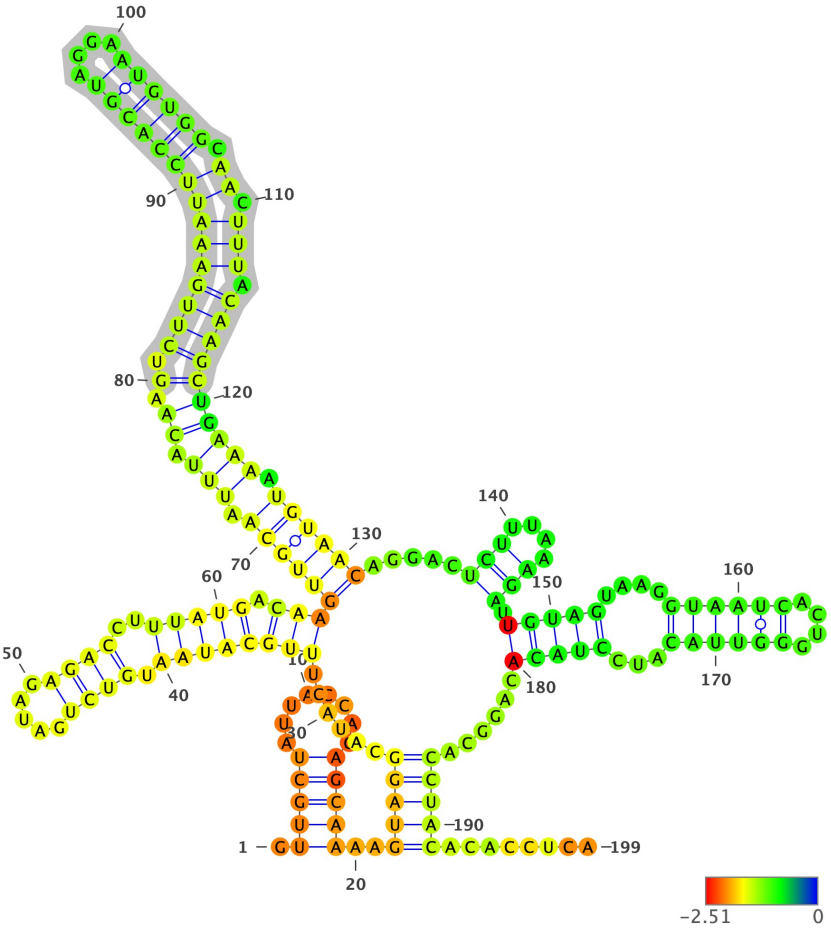
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 283 from nt 18002 to 18041 (nt 80 to 119)

```
5'-GTCTTGAAATTCCACGTAGGAATGUGGCAACUUUACAAGC-3'
5'-(.(((((((((((((.........)))).)).))).)))))-3'
Motif MFE = -8.1; z-score = -1.16; ED = 5.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17923 to 18121 (motif highlighted in silver):

```
5'-GUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACU
UUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCA-3
5'-.(((((........)))))..(((((......((((((((.((((.....)))).)))))).)))((((((.(((.((.(.(((((((((((((((....)))))).)).)
)).)))))))))).))))))).....(((....))).(((((....((((((....))))))...)))))......)))))........-3'
MFE = -44.1; z-score = -1.69; ED = 41.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

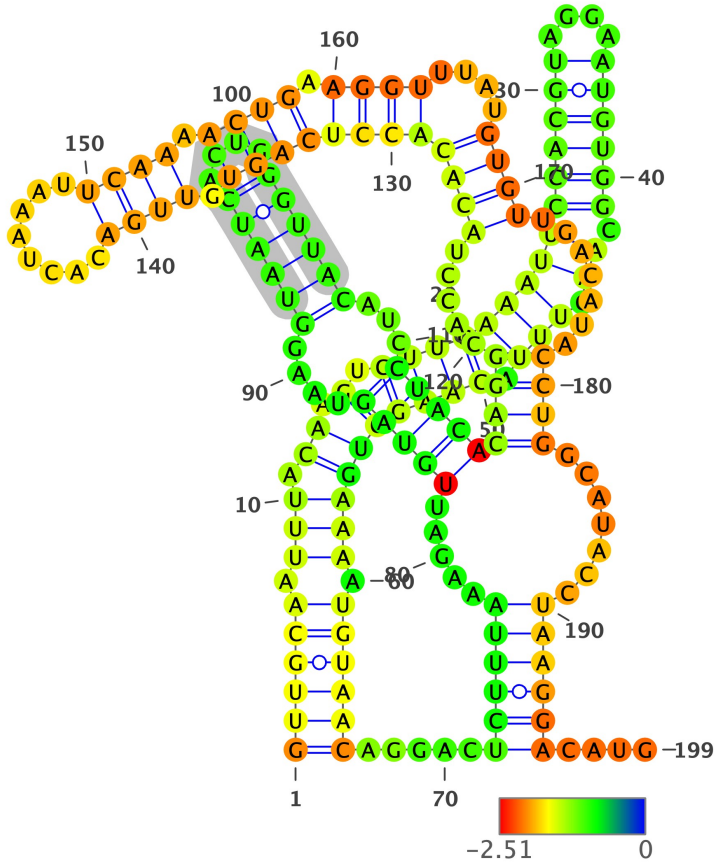
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 284 from nt 18080 to 18093 (nt 93 to 106)

```
5'-TAATCACTGGGUUA-3'
5'-(((((....)))))-3'
Motif MFE = -0.4; z-score = -0.38; ED = 2.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17988 to 18186 (motif highlighted in silver):

```
5'-GUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCC
UACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUG-3
5'-((((((.(((.((.(.((((((((((((((((....)))))).)).))).))))))))).))))))).....((((((.....(((((....((((((....))))))...)
))))((((.....((((((((((((.((((.........)))).)))).)))).....)))).....))))).....))))).....-3'
MFE = -45.3; z-score = -1.64; ED = 23.37
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

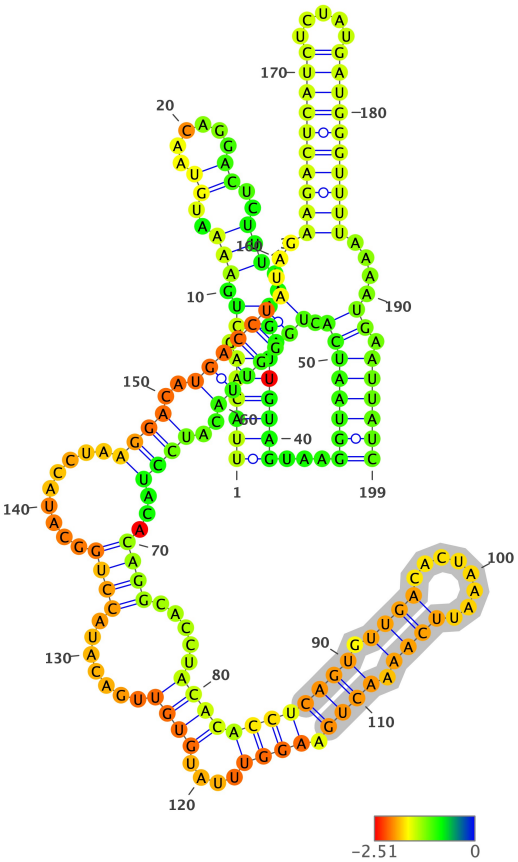
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 285 from nt 18120 to 18145 (nt 87 to 112)

```
5'-CAGTGTTGACACTAAATUCAAAACUG-3'
5'-((((.((((........)))).))))-3'
Motif MFE = -4.6; z-score = -2.3; ED = 1.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18034 to 18232 (motif highlighted in silver):

```
5'-UUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACU
GAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUC-3
5'-((((((.((.(((..((......))..)))..)).))))))...((((((((.(((((((..((((...((((.....(((((((((((.((((........)))).)))
).))))....))))).......))))..........))))..)))))))...((((((((((.....))))))))))....)).))))))-3'
MFE = -43.4; z-score = -1.81; ED = 40.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

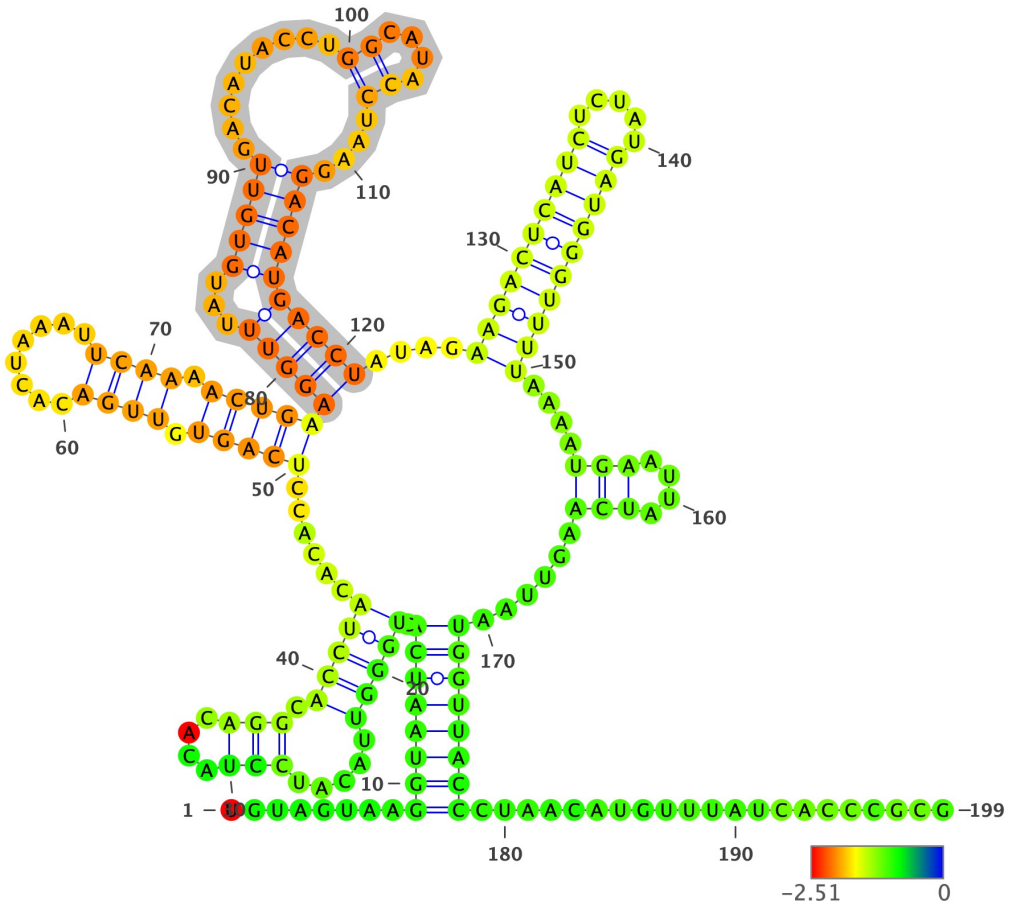
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 286 from nt 18147 to 18190 (nt 78 to 121)

```
5'-AGGTTTATGTGTTGACATACCTGGCATACCTAAGGACAUGACCU-3'
5'-(((((...(((((.....................))))))))))-3'
Motif MFE = -7.5; z-score = -0.38; ED = 16.48
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18070 to 18268 (motif highlighted in silver):

```
5'-UGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAG
GACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCG-3
5'-........((((((((.(((((.....(((....))).)))))......(((((.((((........)))).)))))(((((...(((((.........((....)).....
))))))))))....((((((((((.....)))))))))....(((....)))......))))))))......................-3'
MFE = -38.0; z-score = -2.16; ED = 32.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

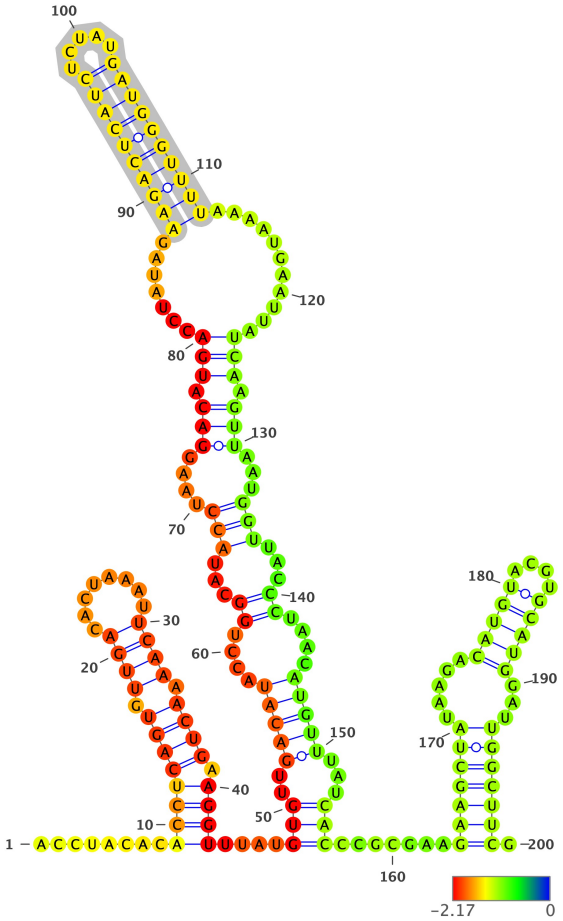
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 287 from nt 18195 to 18219 (nt 88 to 112)

```
5'-AAGACTCATCTCTATGAUGGGUUUU-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -10.1; z-score = -5.04; ED = 0.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18108 to 18307 (motif highlighted in silver):

```
5'-ACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUU
UAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCG-3
5'-........((((((((.((((........)))).)))).))))....(((..(((((....((...(((....(((.(((.......((((((((((.....)))))))))
).........))).)))...)))...))....)))))...)))......(((((((.....(((((....)))))...)))))))).-3'
MFE = -46.8; z-score = -1.67; ED = 35.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

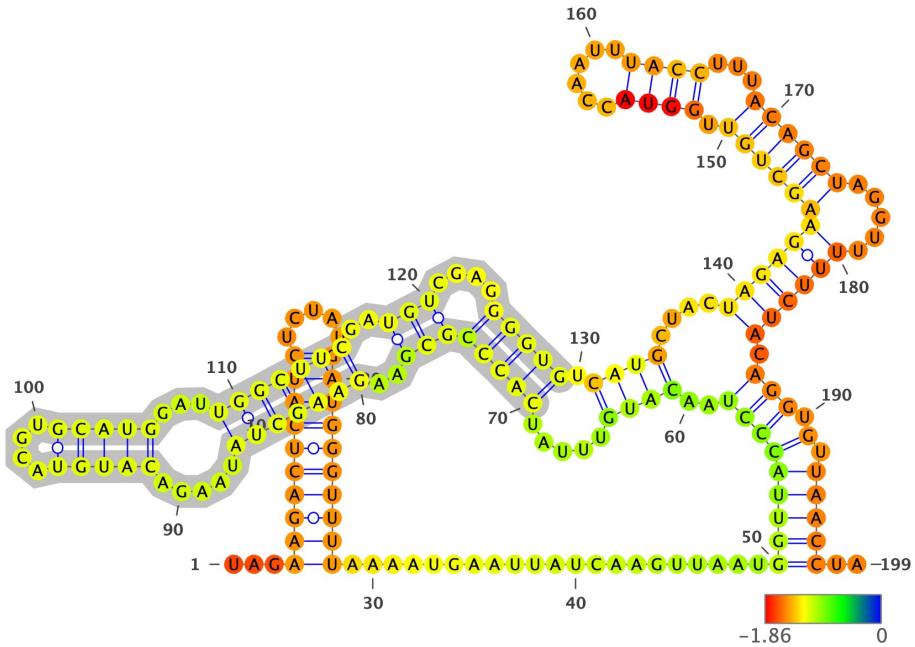
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 288 from nt 18261 to 18320 (nt 70 to 129)

```
5'-CACCCGCGAAGAAGCTATAAGACATGTACGTGCAUGGATUGGCUUCGATGUCGAGGGGUG-3'
5'-((((.((...(((((((.....(((((....)))))...)))))))...)).....))))-3'
Motif MFE = -22.2; z-score = -2.52; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18192 to 18390 (motif highlighted in silver):

```
5'-UAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGG
CUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUA-3
5'-...((((((((((.....))))))))))....................(((((((((..((((.....((((((((..(((((((.....(((((....)))))...)))
))))..)))....))))).))))....((((((((((((.((((......))))...))))))).....)))))).))).).)))))..-3'
MFE = -53.3; z-score = -2.33; ED = 26.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

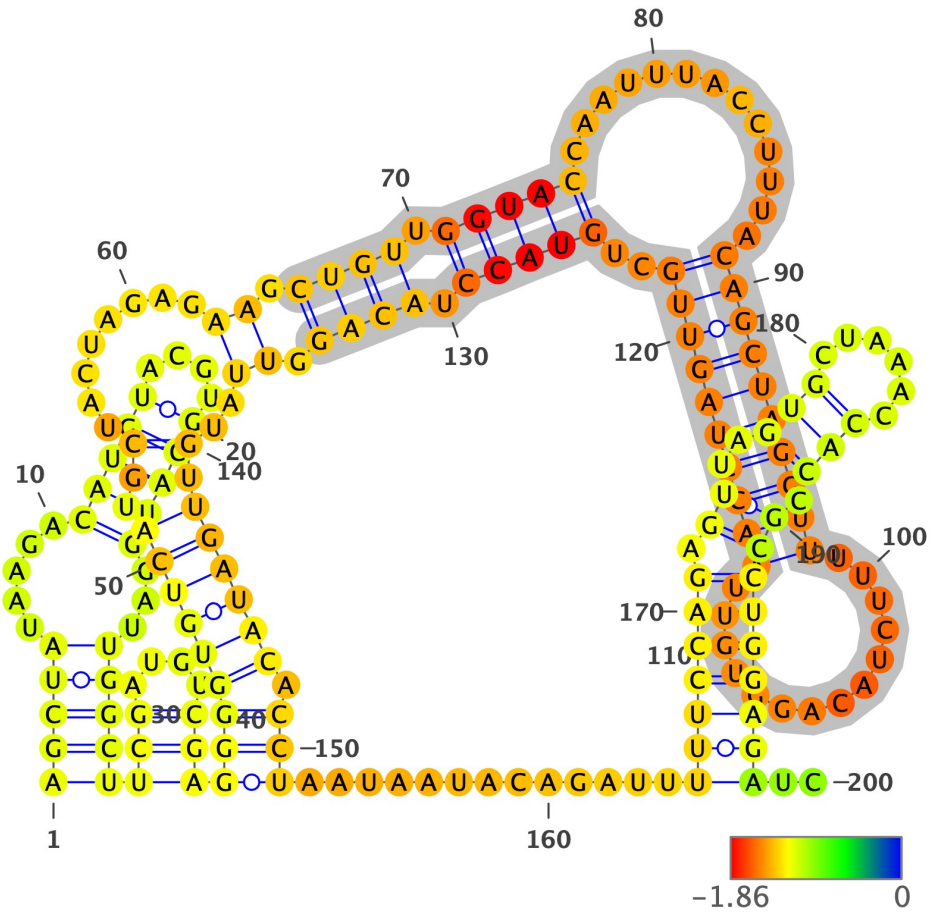
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 289 from nt 18338 to 18406 (nt 66 to 134)

```
5'-CTGTTGGTACCAATTTACCTTTACAGCTAGGTTTTTCTACAGGTGTTAACCUAGUUGCTGTACCTACAG-3'
5'-((((...................((((((((((..............))))))))))........))))-3'
Motif MFE = -19.4; z-score = -2.69; ED = 4.06
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18273 to 18472 (motif highlighted in silver):

```
5'-AGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGU
UAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUC-3
5'-(((((.....(((((....)))))...)))))(((....)))(((((((((.((.........((.((((.(((((.............((((((((((.............
.))))))))))..)))))).))))..))))))))).)))............(((((((.((..(((......))).)))))))))..-3'
MFE = -50.7; z-score = -1.59; ED = 39.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

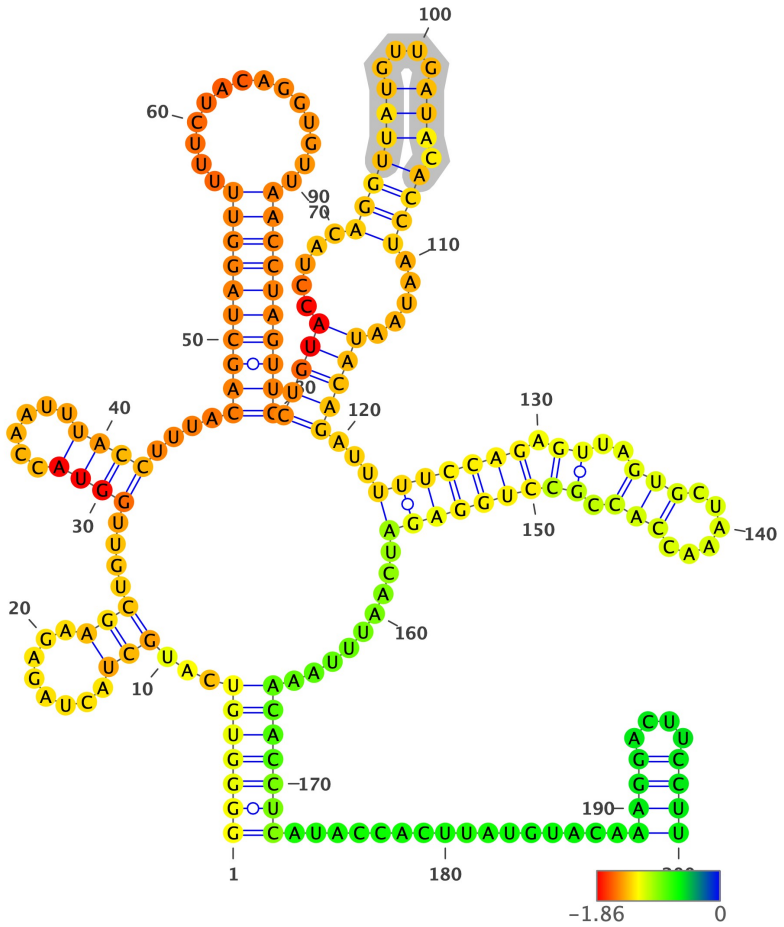
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 290 from nt 18408 to 18420 (nt 94 to 106)

```
5'-TTATGTTGATACA-3'
5'-(...........)-3'
Motif MFE = 0.0; z-score = 0.23; ED = 1.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18315 to 18514 (motif highlighted in silver):

```
5'-GGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAA
UAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUU-3
5'-(((((((...(((........)))....((((......))))....((((((((((.............)))))))))))((((.....(((((((....))).)))))..
...)))))...(((((((.((..((((......)))).)))))))).........)))))).................((((....))))-3'
MFE = -48.9; z-score = -2.41; ED = 21.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

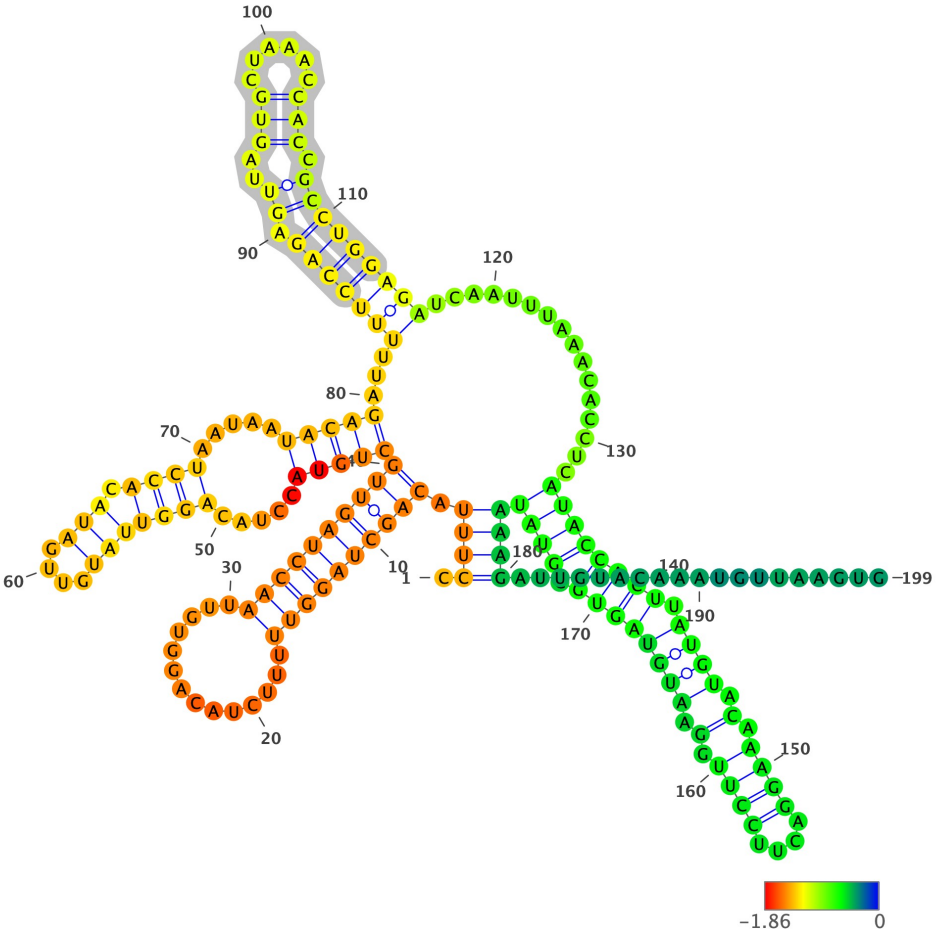
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 291 from nt 18440 to 18467 (nt 86 to 113)

```
5'-CCAGAGTTAGTGCTAAACCACCGCCUGG-3'
5'-((((....................))))-3'
Motif MFE = -6.1; z-score = -0.73; ED = 0.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18355 to 18553 (motif highlighted in silver):

```
5'-CCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCU
GGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUUGGAAUGUAGUGCGUAUAAAGAUUGUACAAAUGUUAAGUG-3
5'-.((((.(((((((((((.............))))))))))(((((.....(((((((....))).))))).....)))))...(((((((.((..(((......))).))))
)))))................(((((((.((((.(.((((....)))).).)))))))).))))))))....................-3'
MFE = -42.5; z-score = -1.26; ED = 28.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

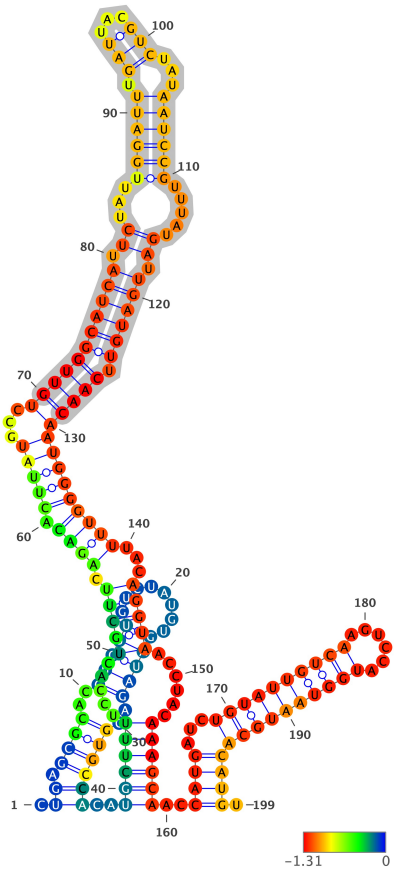
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 292 from nt 18716 to 18775 (nt 70 to 129)

```
5'-GTTGGCATCATTCTATTGGATTTGATTACGUCTATAAUCCGTTTATGATUGAUGUTCAAC-3'
5'-((((((((((.((.................................)).)))))).))))-3'
Motif MFE = -15.3; z-score = -3.14; ED = 5.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18647 to 18845 (motif highlighted in silver):

```
5'-CUGAGCGCACCUGUUGUCUAUGUGAUAGACGUGCCACAUGCUUUUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGU
UUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGU-3
5'-.((.((((..(((((........)))))..))))))..((((((.....(((((.((((.(((((...((((((((((((.((...((((((.(((...)))...)))))).
....)).))))))).))))))))))))))...)))))......))))))..((((...((((((((((......)))))))))))))).-3'
MFE = -46.7; z-score = -0.93; ED = 52.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

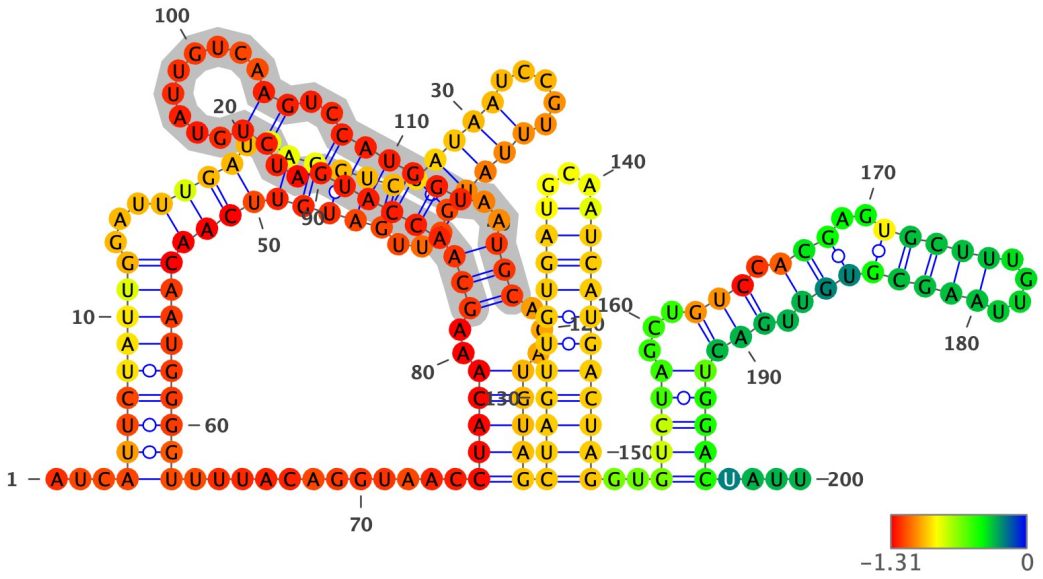
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 293 from nt 18803 to 18839 (nt 82 to 118)

```
5'-GCAACCATGATCTGTATTGTCAAGTCCAUGGUAAUGC-3'
5'-(((((((((..((.........))..))))))..)))-3'
Motif MFE = -9.5; z-score = -1.7; ED = 4.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18722 to 18921 (motif highlighted in silver):

```
5'-AUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUG
GUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUU-3
5'-...(((((((((...((((..((((((((((.....)))))...))))))))))))))))).............(((((..(((((((((..((.........))..))))
))..)))...)))))((((((((((...))))))))))..(((((...(((.(((..(((((....)))))))).))))))))....-3'
MFE = -49.4; z-score = -1.25; ED = 44.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

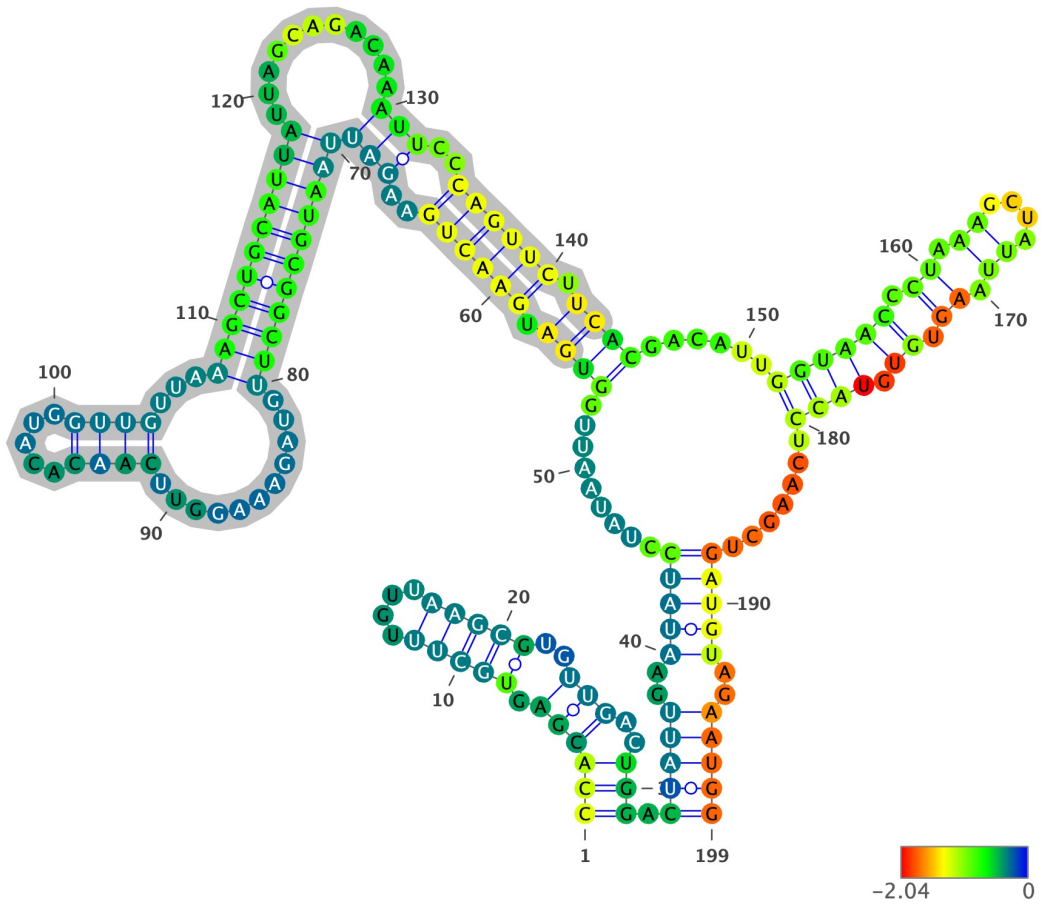
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 294 from nt 18940 to 19027 (nt 56 to 143)

```
5'-GATGAACTGAAGATTAATGCGGCTTGTAGAAAGGTTCAACACATGGTTGTTAAAGCUGCAUTATTAGCAGACAAATTCCCAGUUCTUC-3'
5'-((.(((((((.....))))))).))-3'
Motif MFE = -20.5; z-score = -1.9; ED = 12.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18885 to 19083 (motif highlighted in silver):

```
5'-CCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGAACUGAAGAUUAAUGCGGCUUGUAGAAAGGUUCAACACAUGGUUGUUAAAGC
UGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGG-3
5'-((((((.(((((....)))))..)))..)))..(((((..(((((.........((((.(((((((..(((((((((((((.....))))))))...))))
)))))))).....)))..)))))).)))).....((((((.((.((....)).)).)).)))).....))))))..))))))-3'
MFE = -40.7; z-score = 0.6; ED = 35.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

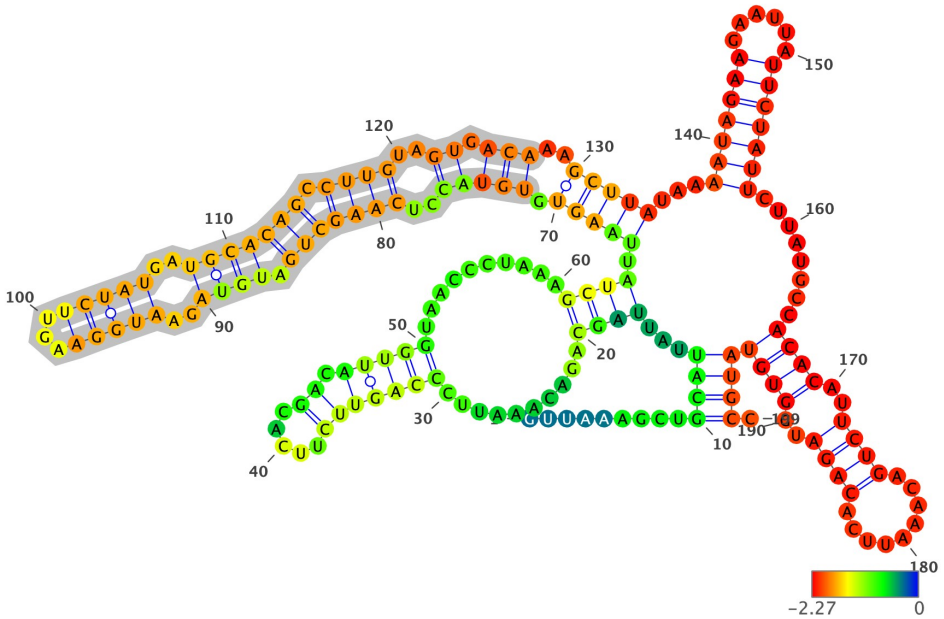
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 295 from nt 19059 to 19114 (nt 72 to 127)

```
5'-TGTACCTCAAGCTGATGTAGAATGGAAGTTCTAUGATGCACAGCCUUGTAGTGACA-3'
5'-((.....(((((((.......((((.....)))).....))).)))).....))-3'
Motif MFE = -16.8; z-score = -2.69; ED = 4.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18988 to 19186 (motif highlighted in silver):

```
5'-GUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCA
CAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCC-3
5'-.........((((...((((..........(((((((.....)).)))))..........)))).(((((.(((((..(((((((.((((..(((((...)))))..))))
)))).))))..)).)))..)))))...(((((((.....)))))))........((((..((((.........))))..)))))))).-3'
MFE = -43.6; z-score = -1.73; ED = 29.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

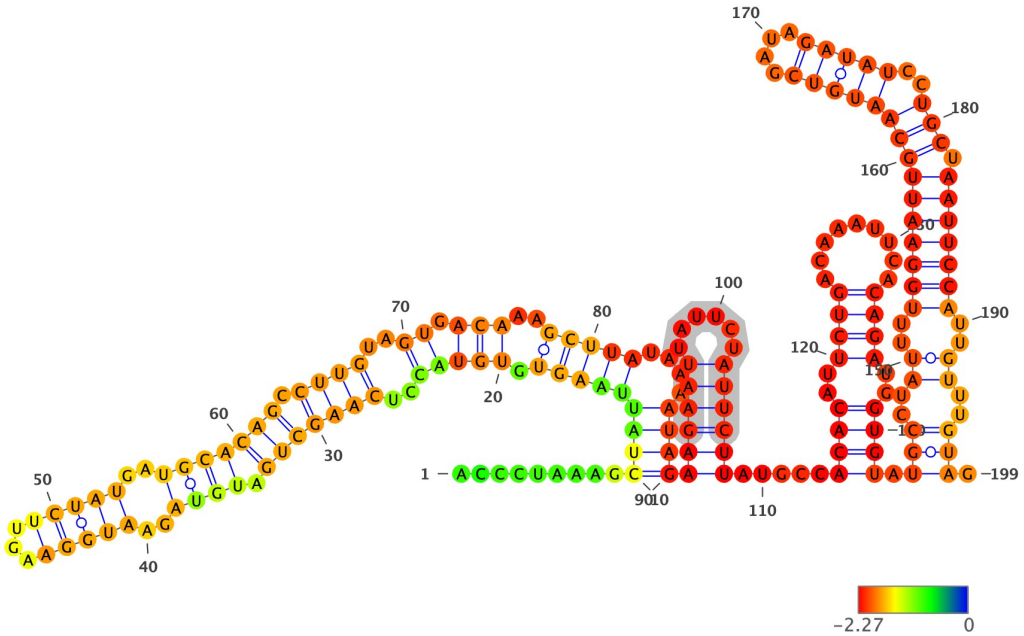
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 296 from nt 19132 to 19145 (nt 93 to 106)

```
5'-GAATTATTCTAUUC-3'
5'-((((......))))-3'
Motif MFE = 0.0; z-score = 0.14; ED = 2.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19040 to 19238 (motif highlighted in silver):

```
5'-ACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUG
CCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAG-3
5'-.........(((((((((.(((((..(((((((.((((..(((((...)))))..)))))))).))))..)).)))..)))))....))))((((((......))))))...
..((((..((((.........))))..)))).(((..((..((((((((((((((....)))))..))).)))))))..))..))).-3'
MFE = -49.9; z-score = -2.59; ED = 21.5
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

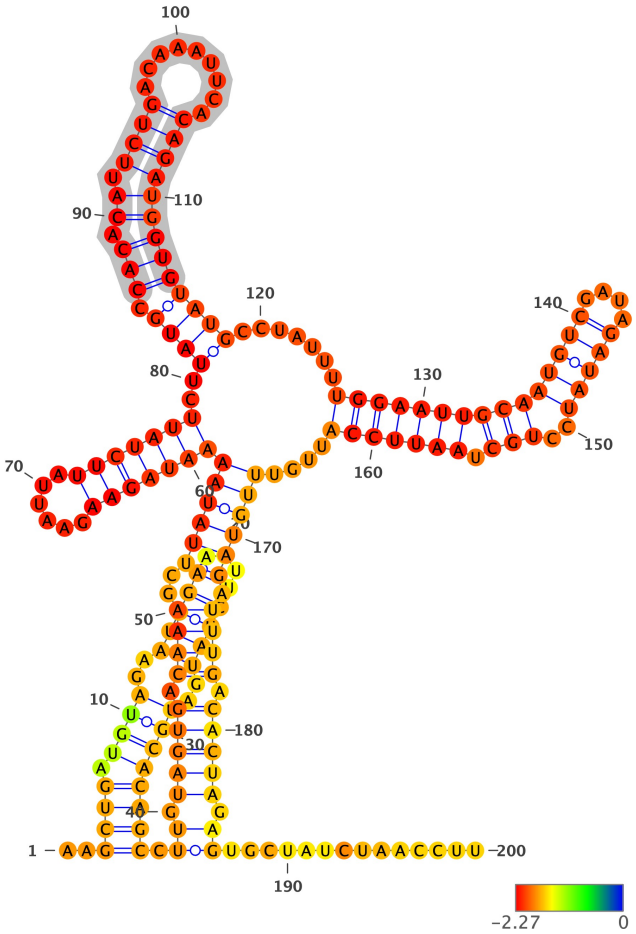
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 297 from nt 19152 to 19180 (nt 86 to 114)

```
5'-CACACATTCTGACAAATTCACAGATGGUG-3'
5'-(((....((((.........))))..)))-3'
Motif MFE = -6.1; z-score = -2.03; ED = 2.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19067 to 19266 (motif highlighted in silver):

```
5'-AAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUG
GUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUU-3
5'-..((((.((((..(((((...)))))..))))))))).((.(((((.((((..((((((((((((((.....)))))))..((((.(((.((.((((.........))))))
)))))))).......((((((((((((((((....)))))..))).)))))))....)))))).)))).)))))).)).............-3'
MFE = -47.4; z-score = -2.93; ED = 25.54
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

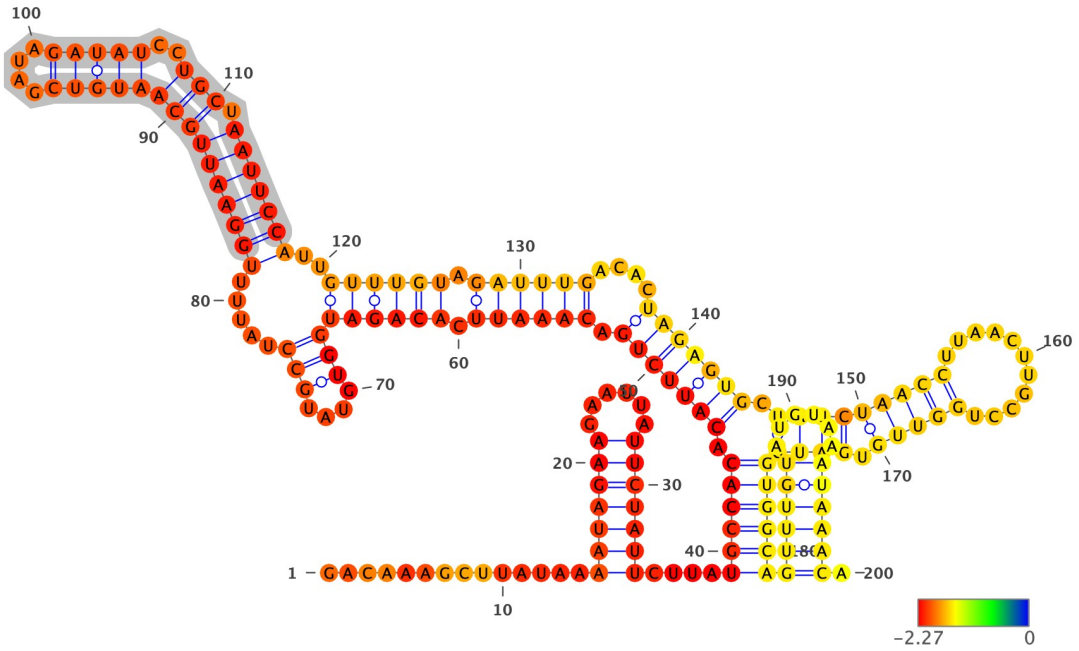
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 298 from nt 19193 to 19227 (nt 83 to 117)

```
5'-GGAATTGCAATGTCGATAGAUAUCCUGCTAAUUCC-3'
5'-(((((((((((((....)))))..))).))))))-3'
Motif MFE = -11.2; z-score = -3.6; ED = 0.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19111 to 19310 (motif highlighted in silver):

```
5'-GACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCU
AAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACA-3
5'-..............(((((((......)))))))....((((((.(((((((.((((((.(((((((((....)))).....((((((((((((((....)))))..))).
)))))))..)))))).)))))).....))))))).(((((((((...........))))).))))))))))((((((......)))))).-3'
MFE = -49.3; z-score = -2.41; ED = 27.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

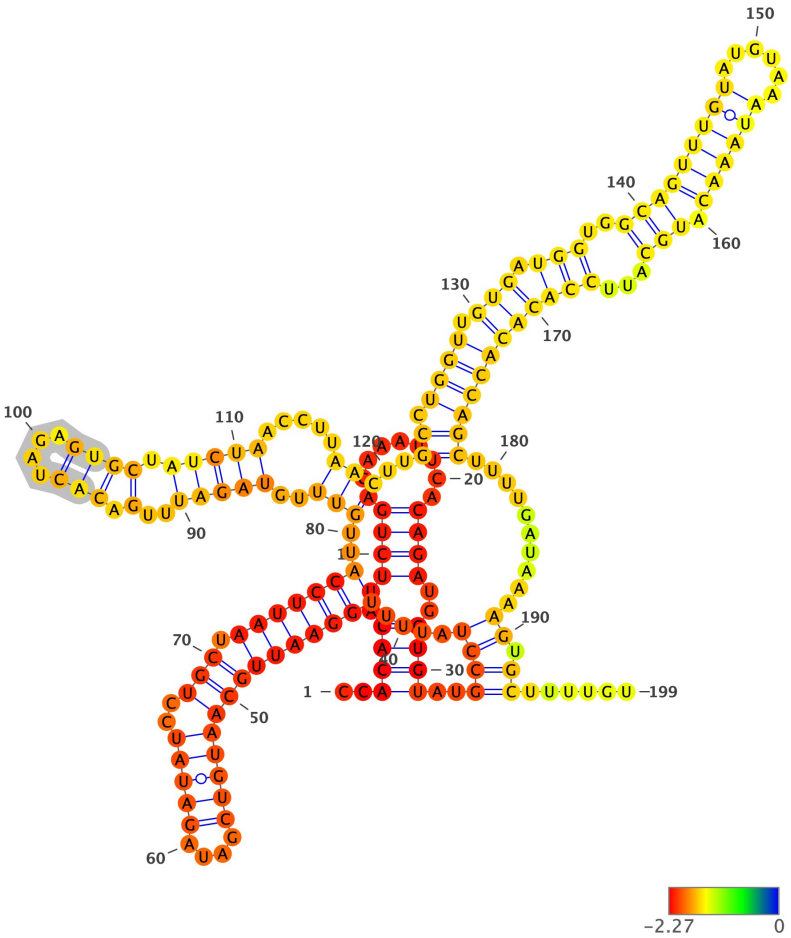
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 299 from nt 19246 to 19253 (nt 96 to 103)

```
5'-ACTAGAGU-3'
5'-(......)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19151 to 19349 (motif highlighted in silver):

```
5'-CCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUA
ACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGU-3
5'-..((((..((((.........))))..))))..((((....(((((((((((((((....)))))..))).)))))))..(((..(((((..(.(((....)))).)))))
.....)))..((.((((.(((.(((..(((((((((.....)))))).)))...)))))))))))).........)).)).....-3'
MFE = -47.5; z-score = -2.26; ED = 32.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

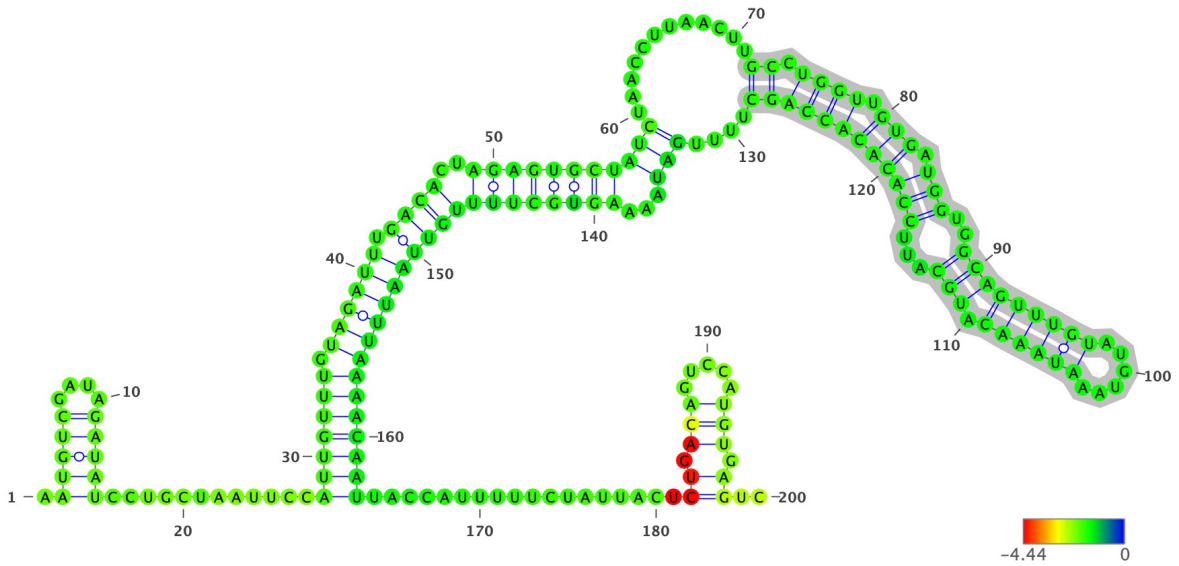
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 300 from nt 19272 to 19328 (nt 72 to 128)

```
5'-GCCTGGTTGTGATGGTGGCAGTTTGTATGTAAATAAACAUGCATTCCACACACCAGC-3'
5'-((.((((.(((.(((..(((((((.........)))).)))...)))))))))))-3'
Motif MFE = -20.3; z-score = -3.54; ED = 3.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19201 to 19400 (motif highlighted in silver):

```
5'-AAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAU
GCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUC-3
5'-.(((((....)))))............(((((((.((((((.((((..(((((((((((.............((.((((.(((.(((..(((((((((......))))))).)
))...))))))))))))....)))...))))))))))))))))))))))))))))).................((.(((.....))).))..-3'
MFE = -40.1; z-score = -1.15; ED = 27.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

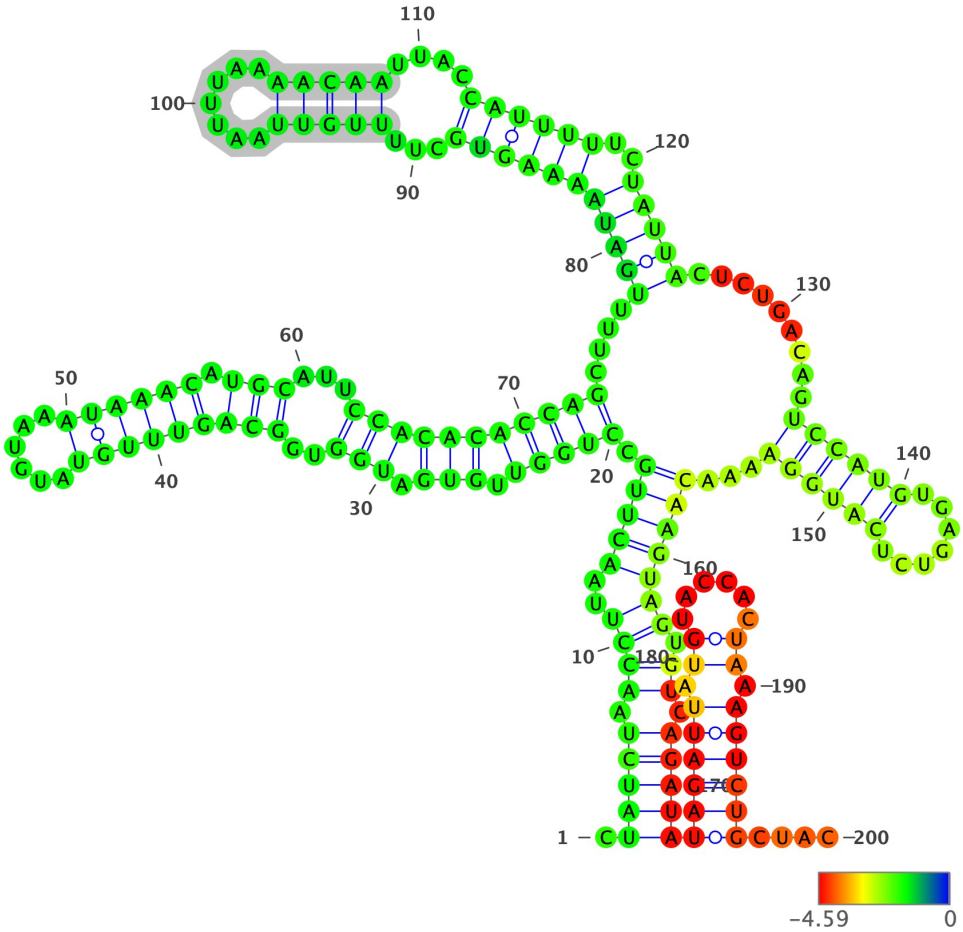
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 301 from nt 19346 to 19362 (nt 92 to 108)

```
5'-TTGTTAATTTAAAACAA-3'
5'-(((((.......)))))-3'
Motif MFE = -0.2; z-score = -1.05; ED = 2.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19255 to 19454 (motif highlighted in silver):

```
5'-CUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUA
CCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUAC-3
5'-.(((((.((((..(((((.(((((.(((.(((..(((((((((.......))))))).)))...)))))))))))....((((((((((...(((((.......)))))...
.))))))..)))))).........((((((.......))))))...)))))))).)).)))))((((((.((......)).))))))....-3'
MFE = -41.6; z-score = -1.95; ED = 63.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

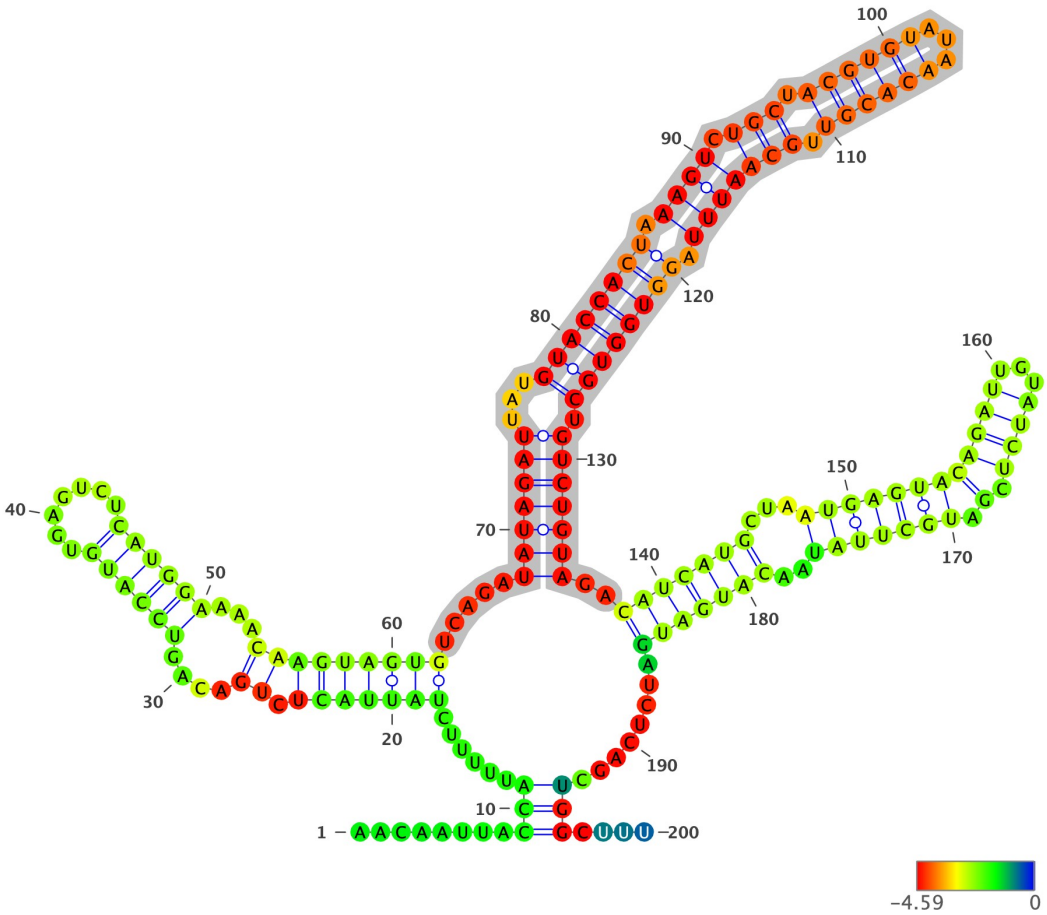
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 302 from nt 19420 to 19494 (nt 63 to 137)

```
5'-TCAGATATAGATTATGTACCACTAAAGTCTGCTACGTGTATAACACGUTGCAAUUUAGGUGGUGCTGUCUGUAGA-3'
5'-((...(((((((...((((((...((((.(((.(((((.....))))).)))))))...)))))).)))))))))-3'
Motif MFE = -29.9; z-score = -5.06; ED = 3.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19358 to 19557 (motif highlighted in silver):

```
5'-AACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUU
GCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUGAUCUCAGCUGGCUUU-3
5'-........(((......(((((((.((....((((((.......))))))...)))))))))).....(((((((...((((((((.((((.(((.((((((...)))))).
)))))))).))))))))).)))))))..(((((((...((((((((((((...)))).).)))))))..)))))))........)))....-3'
MFE = -57.2; z-score = -4.34; ED = 33.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

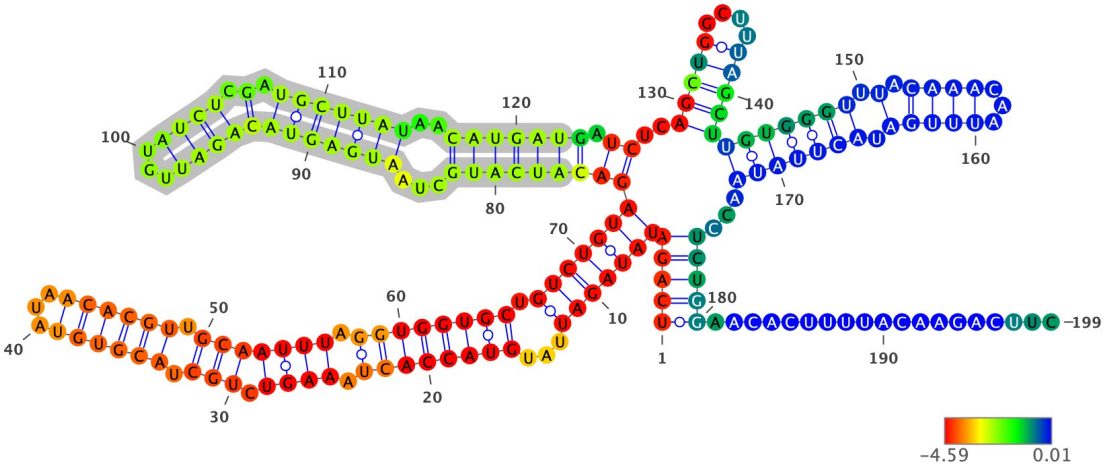
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 303 from nt 19496 to 19541 (nt 77 to 122)

```
5'-ATCATGCTAATGAGTACAGATTGTAUCUCGAUGCUUATAACAUGAU-3'
5'-((((((....((((((.(((.....)))...))))))...))))))-3'
Motif MFE = -10.4; z-score = -2.61; ED = 5.06
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19420 to 19618 (motif highlighted in silver):

```
5'-UCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCU
UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUC-3
5'-(((((((((((...((((((((.((((.(((.((((((...)))))).)))))))).))))))))).)))))))(((((((((...((((((((((((...)))).).))))
)))..)))))))).))..(((((....)))))(((((((.(.((((...)))))).)))))))...)))))).....................-3'
MFE = -56.0; z-score = -4.0; ED = 13.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

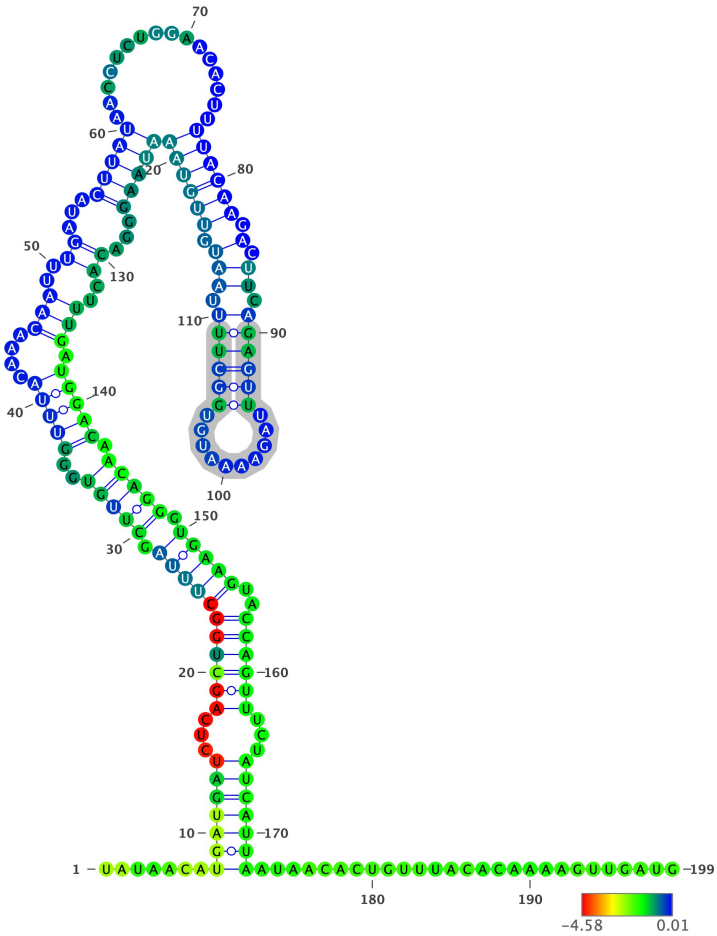
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 304 from nt 19620 to 19639 (nt 90 to 109)

```
5'-GAGTTTAGAAAATGTGGCUU-3'
5'-((..(..........)..))-3'
Motif MFE = -0.3; z-score = 0.08; ED = 3.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19531 to 19729 (motif highlighted in silver):

```
5'-UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUU
AAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUG-3
5'-.......(((((((...(((((((((((.(((((..(((((....(((..((...(((((.................((((((.(.((.((((((..........)))))).
))).))))))))))...))..))).))))).))))).))))))..))))))...)))))))..........................-3'
MFE = -33.4; z-score = -0.12; ED = 48.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

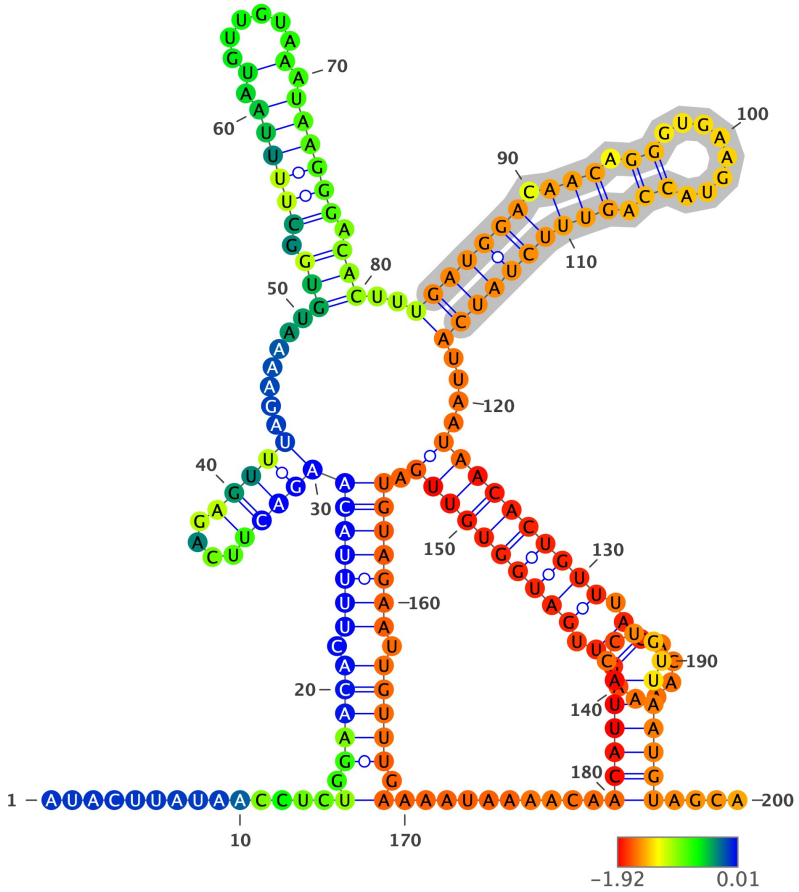
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 305 from nt 19666 to 19698 (nt 84 to 116)

```
5'-GATGGACAACAGGGTGAAGTACCAGUUUCUAUC-3'
5'-((((((.(((.((........)).)))))))))-3'
Motif MFE = -8.7; z-score = -2.24; ED = 3.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19583 to 19782 (motif highlighted in silver):

```
5'-AUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUU
CUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCA-3
5'-..............(.(((((.(((((((((((((....)))))).......(((.((((((.(......).)))))).)))..(((((((.(((.((........)).))))
))))))....((((((((((.((......)).))))))))))).))))))).)))))).)..........((((((.....))))))....-3'
MFE = -38.3; z-score = -1.21; ED = 47.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

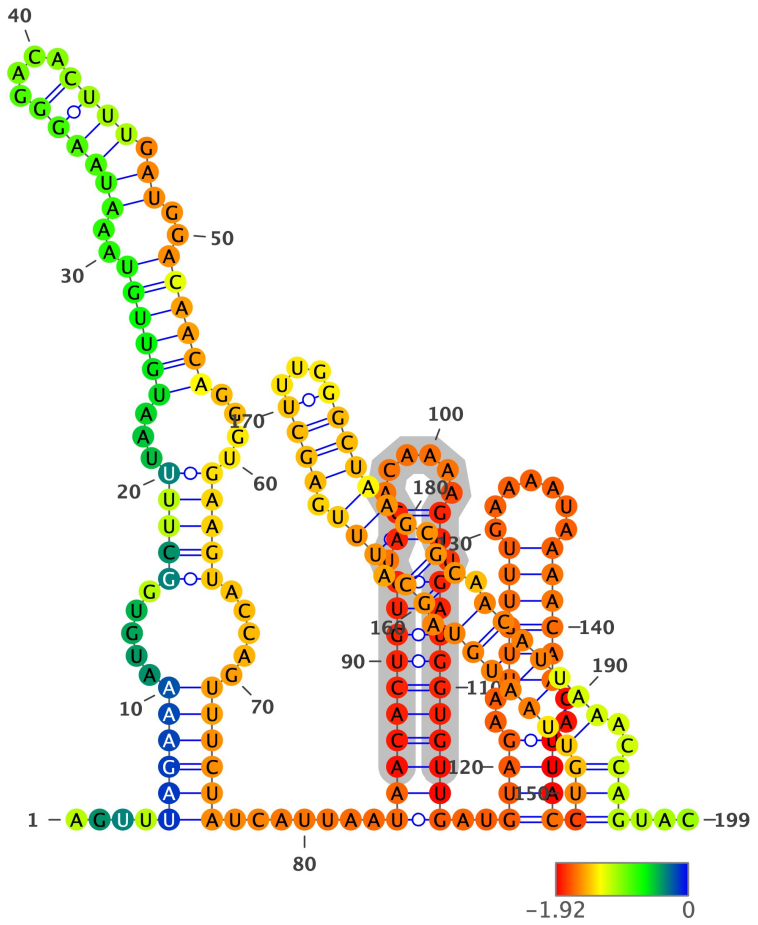
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 306 from nt 19706 to 19733 (nt 86 to 113)

```
5'-ACACTGTTTACACAAAAGUTGAUGGUGU-3'
5'-((((((((.((......)).))))))))-3'
Motif MFE = -6.9; z-score = -2.57; ED = 1.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19621 to 19819 (motif highlighted in silver):

```
5'-AGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGU
GUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUAC-3
5'-....((((((.....(((((...((((((..((((((....)))).))..))))))....)))))).....)))))).......((((((((((.((......)).))))))
))))..((((..((((((.......))))))..))))((((((((((.((.(((.((((...)))))))).)).)))))))..)))...-3'
MFE = -43.8; z-score = -1.87; ED = 49.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

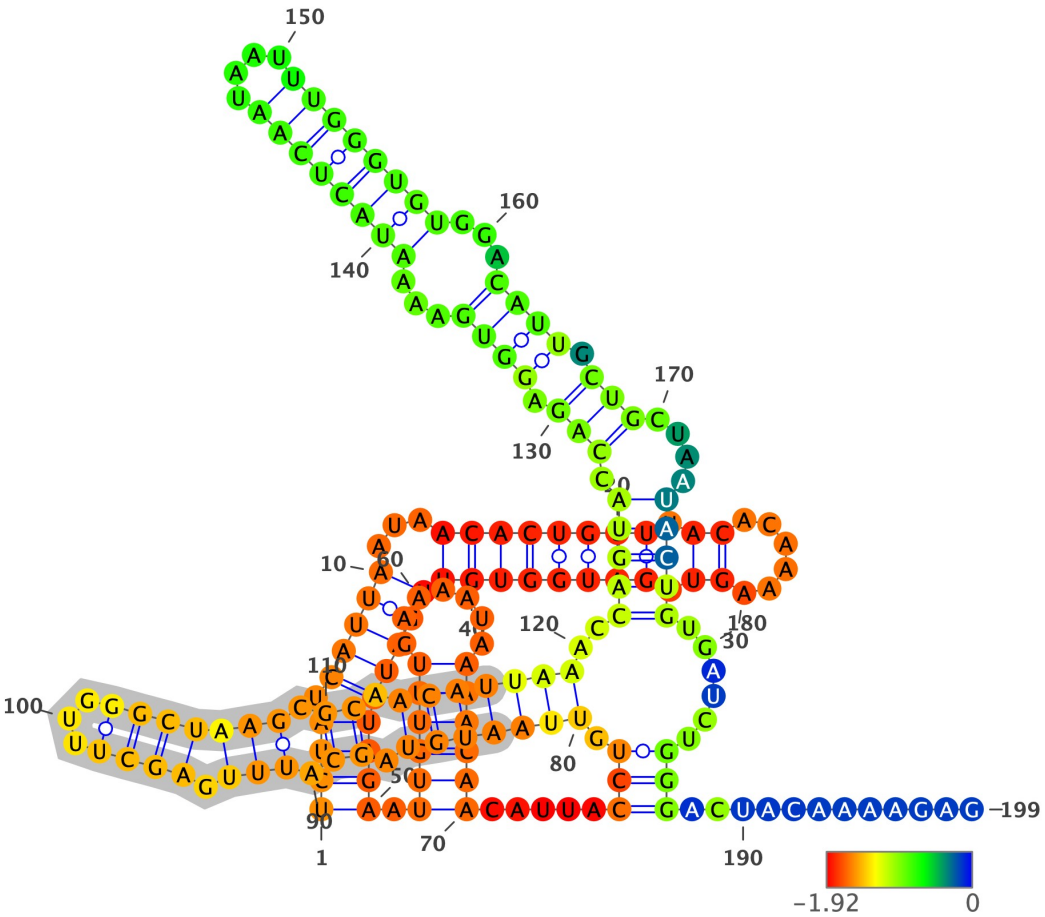
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 307 from nt 19775 to 19808 (nt 83 to 116)

```
5'-ATGTAGCATTTGAGCTTTGGGCUAAGCGCAACAU-3'
5'-((((.((.((..(((.....))).)).)).))))-3'
Motif MFE = -7.3; z-score = -0.97; ED = 3.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19693 to 19891 (motif highlighted in silver):

```
5'-UCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGC
AACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAG-3
5'-((((.(((((...((((((((.((......)).)))))))))))))))).((((((.......))))))).....(((.(((((((.((.(((.((((...)))))))).))
.)))))))..(((((.(((.((((...((((((((....))))))))...)))).)))....)))))......)))............-3'
MFE = -43.7; z-score = -1.51; ED = 26.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

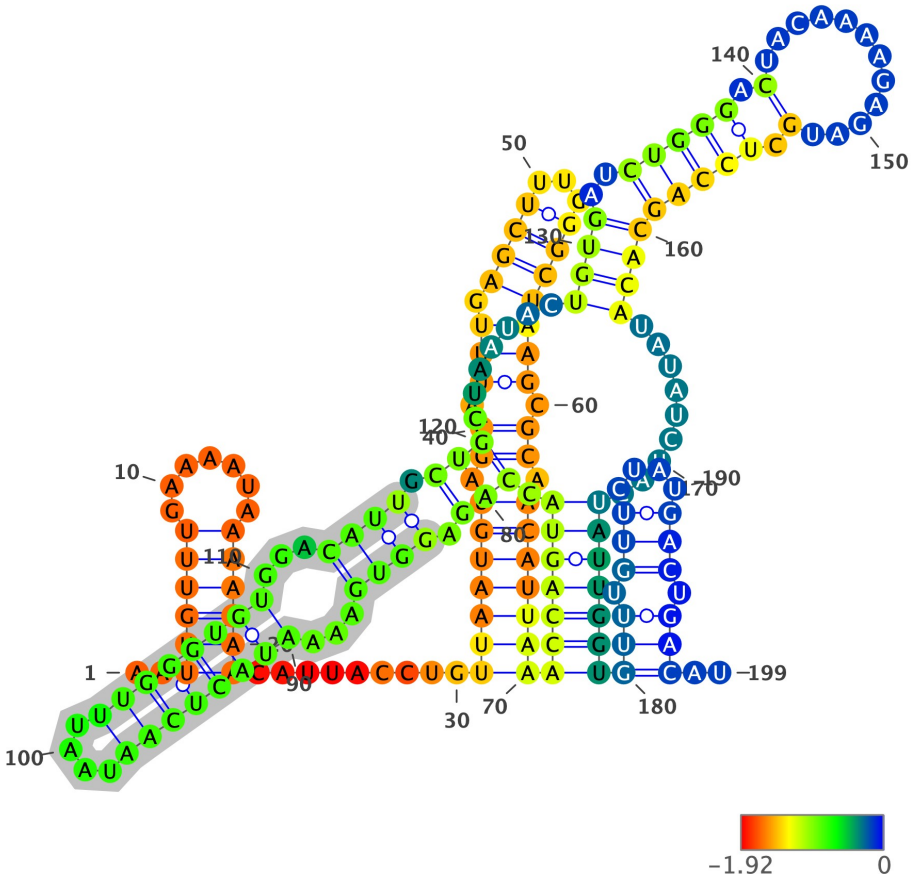
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 308 from nt 19824 to 19857 (nt 83 to 116)

```
5'-GGTGAAAATACTCAATAATTUGGGUGUGGACAUU-3'
5'-(................................)-3'
Motif MFE = -8.8; z-score = -3.1; ED = 1.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19742 to 19940 (motif highlighted in silver):

```
5'-AAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGG
ACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAGAUGCUCCAGCACAUAUAUCUACUAUUGGUGUUUGUUCUAUGACUGACAU-3
5'-..((((((.......))))))........(((((((.((.(((.((((...)))))))).)).)))))))(((((((.(((.((((...((((((((....))))))))..
.)))).)))......((((..(((((.(............).)))))))))........)))))))(((.(((....))).)))..-3'
MFE = -40.8; z-score = -0.63; ED = 34.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

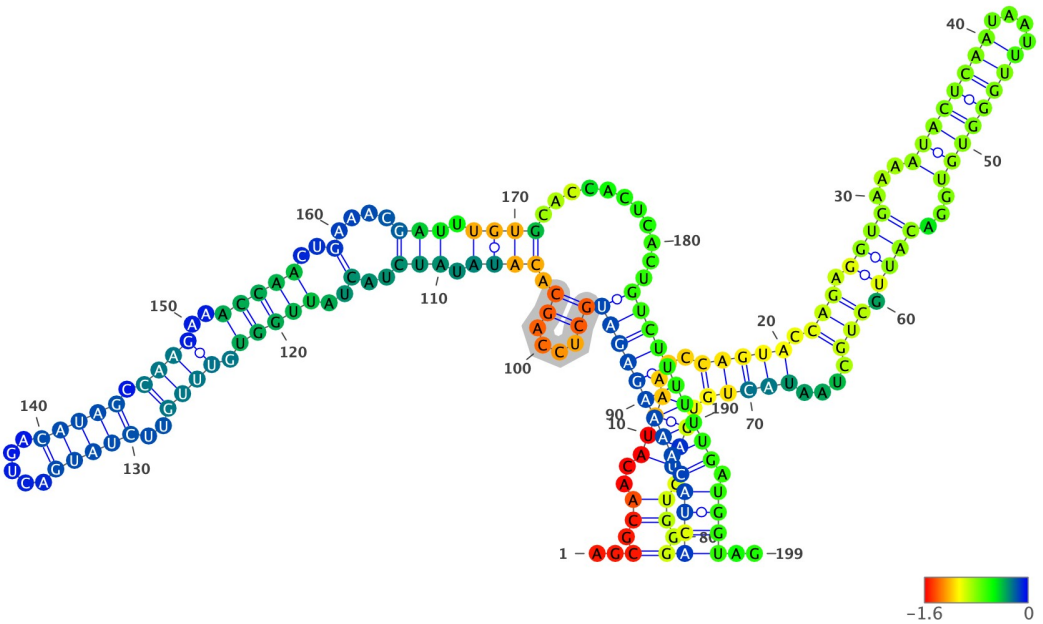
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 309 from nt 19894 to 19901 (nt 96 to 103)

```
5'-GCTCCAGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19799 to 19997 (motif highlighted in silver):

```
5'-AGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAGAUGCUCCAGCACAUAUAU
CUACUAUUGGUGUUUGUUCUAUGACUGACAUAGCCAAGAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAG-3
5'-..(.((..((((...(((((.(((.((((...((((((((....))))))))...)))).)))....)))))))))).)).)((((((((((((((((....)).((((.((
(..(..(((((.((((..(((((.....))))).))))..)))))..)....))).)))).....)))))))))).))))..-3'
MFE = -40.7; z-score = -0.37; ED = 43.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

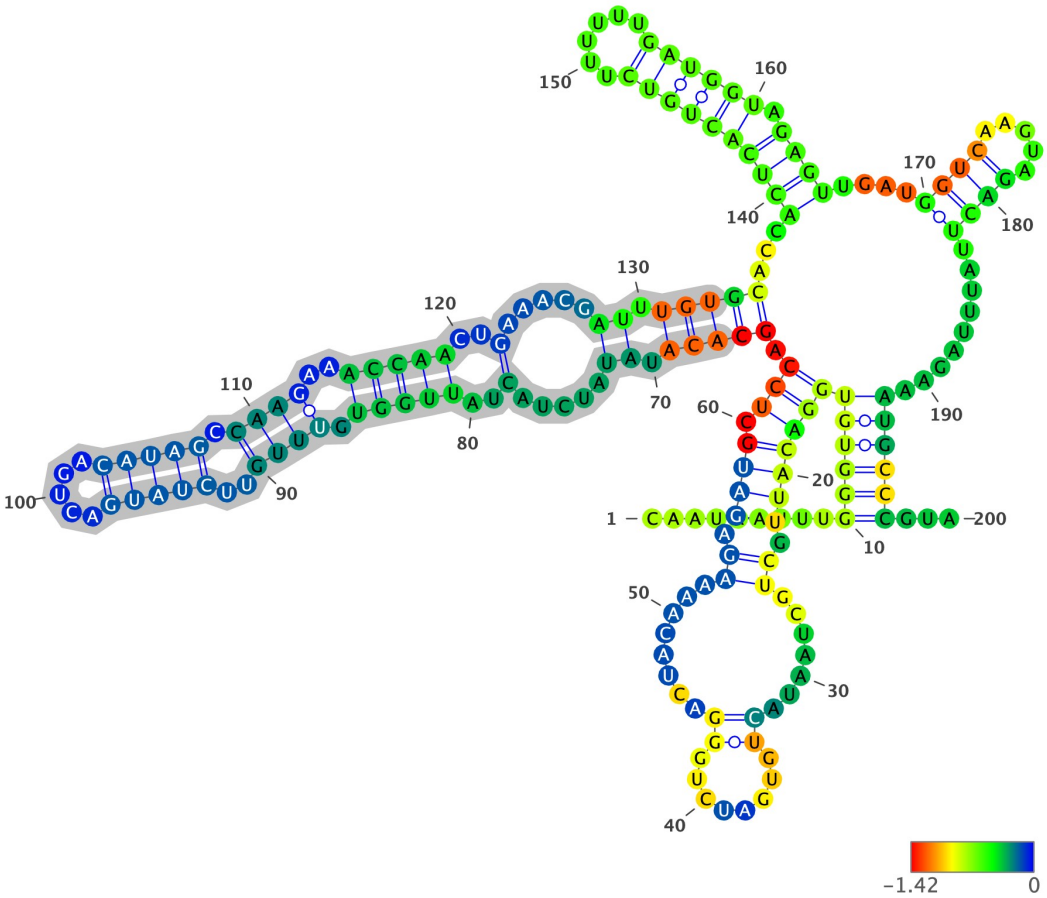
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 310 from nt 19902 to 19968 (nt 67 to 133)

```
5'-ACATATATCTACTATTGGTGTTTGTTCTATGACTGACAUAGCCAAGAAACCAACTGAAACGATTUGU-3'
5'-(((.............................................................)))-3'
Motif MFE = -9.4; z-score = -0.51; ED = 9.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19836 to 20035 (motif highlighted in silver):

```
5'-CAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAGAUGCUCCAGCACAUAUAUCUACUAUUGGUGUUUGUUCUAUGACUGACAUAGCCAA
GAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAGAGUUGAUGGUCAAGUAGACUUAUUUAGAAAUGCCCGUA-3
5'-.........((((((((((((.((.......((........)).......)).)))).))).(((((.((.....(..(((((.((((..(((((.....)))))).)))
)..)))))..).....)).)))))...((((((((((.....)))))).)))).....((((.....)))).........)))))).....-3'
MFE = -42.1; z-score = 0.09; ED = 29.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

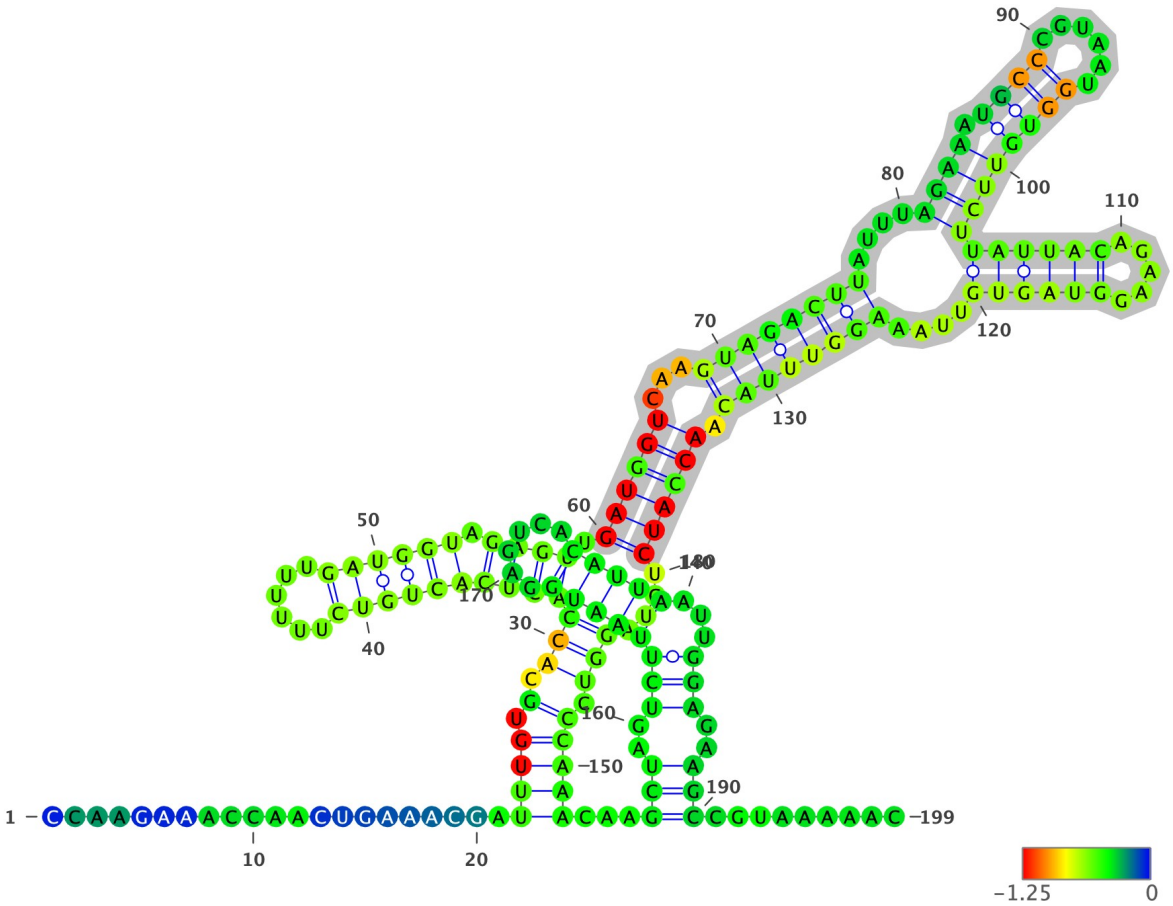
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 311 from nt 20002 to 20081 (nt 60 to 139)

```
5'-GATGGTCAAGTAGACTTATTTAGAAATGCCCGTAATGGTGTTCTTATTACAGAAGGTAGTGTTAAAGGTTTACAACCAUC-3'
5'-(((.((.....................((......)).....................................)).)))-3'
Motif MFE = -20.7; z-score = -2.37; ED = 6.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19943 to 20141 (motif highlighted in silver):

```
5'-CCAAGAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAGAGUUGAUGGUCAAGUAGACUUAUUUAGAAAUGCCCGUAAUGGUGUUCUUAUUACAG
AAGGUAGUGUUAAAGGUUUACAACCAUCUGUAGGUCCCAAACAAGCUAGUCUUAAUGGAGUCACAUUAAUUGGAGAAGCCGUAAAAAC-3
5'-.....................((((.(.(((((((((((((.......)))))).)))).((((((...((((((((....((((.((((.......))))))))((((((..
...))))))....))))))))).))))))....))).)))))...(((..((((((((.......)))))...)))..)))..........-3'
MFE = -40.3; z-score = -0.33; ED = 20.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

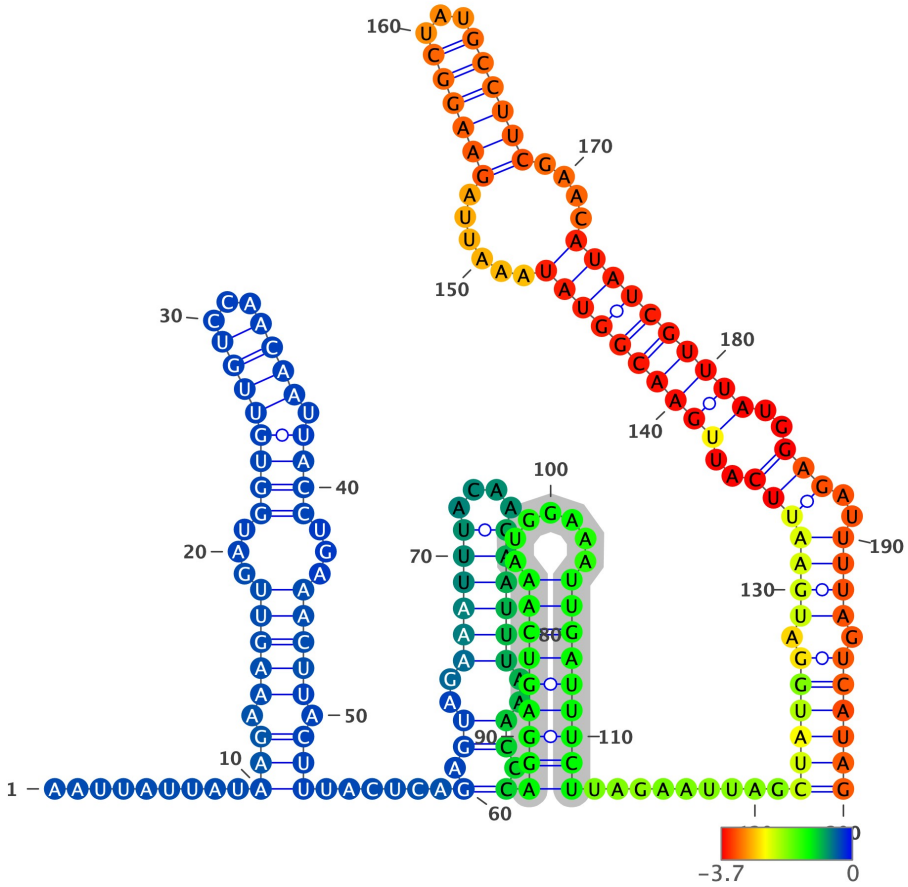
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 312 from nt 20236 to 20260 (nt 88 to 112)

```
5'-AGGAGTCAAATGGAAAUUGAUUUCU-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.1; z-score = -3.69; ED = 2.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20149 to 20348 (motif highlighted in silver):

```
5'-AAUUAUUAUAAGAAAGUUGAUGGUGUUGUCCAACAAUUACCUGAAACUUACUUUACUCAGAGUAGAAAUUUACAAGAAUUUAAACCCAGGAGUCAAAUGGAAAUUGAUUUC
UUAGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAG-3
5'-.........(((.(((((...((((((((...)))).))))...))))).))).....(.((..((((((....))))))..)).)((((((((.......))))))))
).........((((((.(((((((..((((((((((.....((((((...))))))....)))))))))).))))..)))).))))))-3'
MFE = -43.7; z-score = -2.6; ED = 26.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

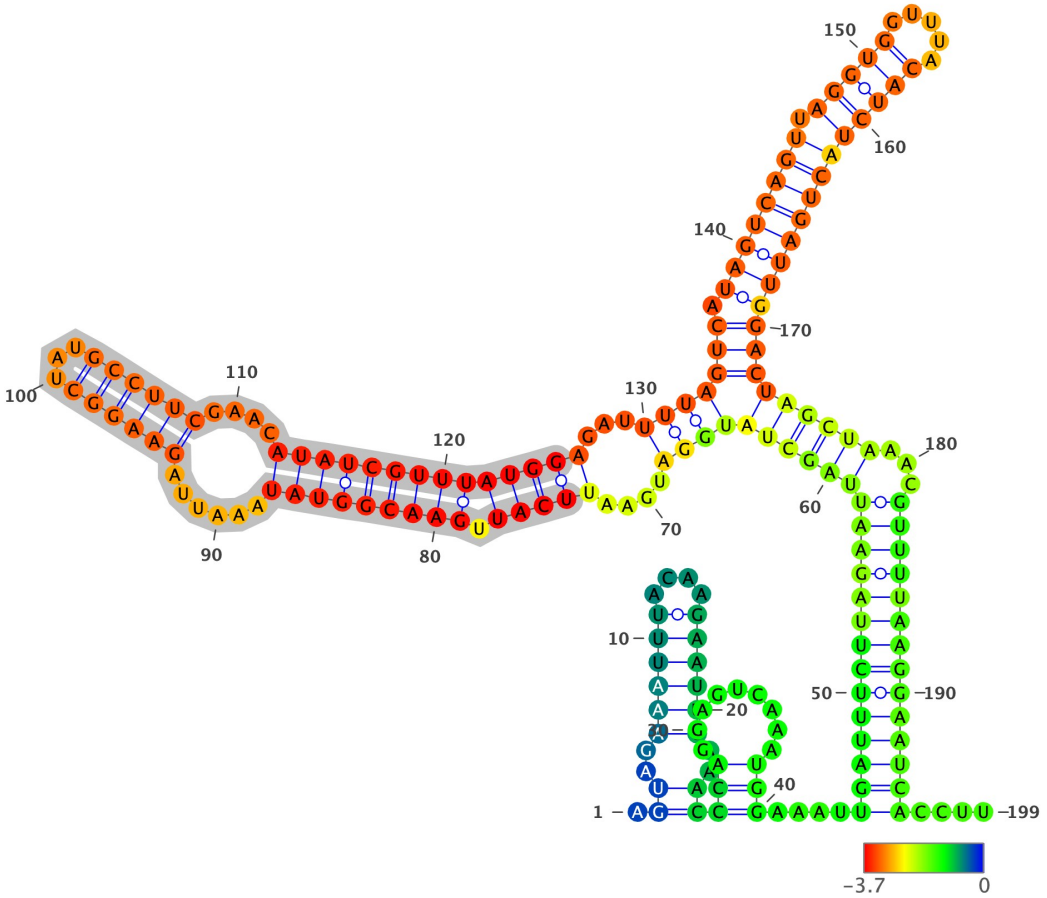
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 313 from nt 20282 to 20333 (nt 74 to 125)

```
5'-TCATTGAACGGTATAAATTAGAAGGCTATGCCUUCGAACAUAUCGUUUAUGG-3'
5'-((((.(((((((((.....((((((...)))))).....)))))))))))))-3'
Motif MFE = -17.3; z-score = -3.46; ED = 3.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20209 to 20407 (motif highlighted in silver):

```
5'-AGUAGAAAUUUACAAGAAUUUAAACCCAGGAGUCAAAUGGAAAUUGAUUUCUUAGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAA
CAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUU-3
5'-.((..((((((....))))))..))(((.........))).....(((((((((((((((((((((((....(((((.(((((((((.....((((((...))))))...
.)))))))))))))...))))(((.((((((((.(((((.....)))))))))))))))))))))))...)))))))))))))....-3'
MFE = -57.1; z-score = -4.34; ED = 16.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

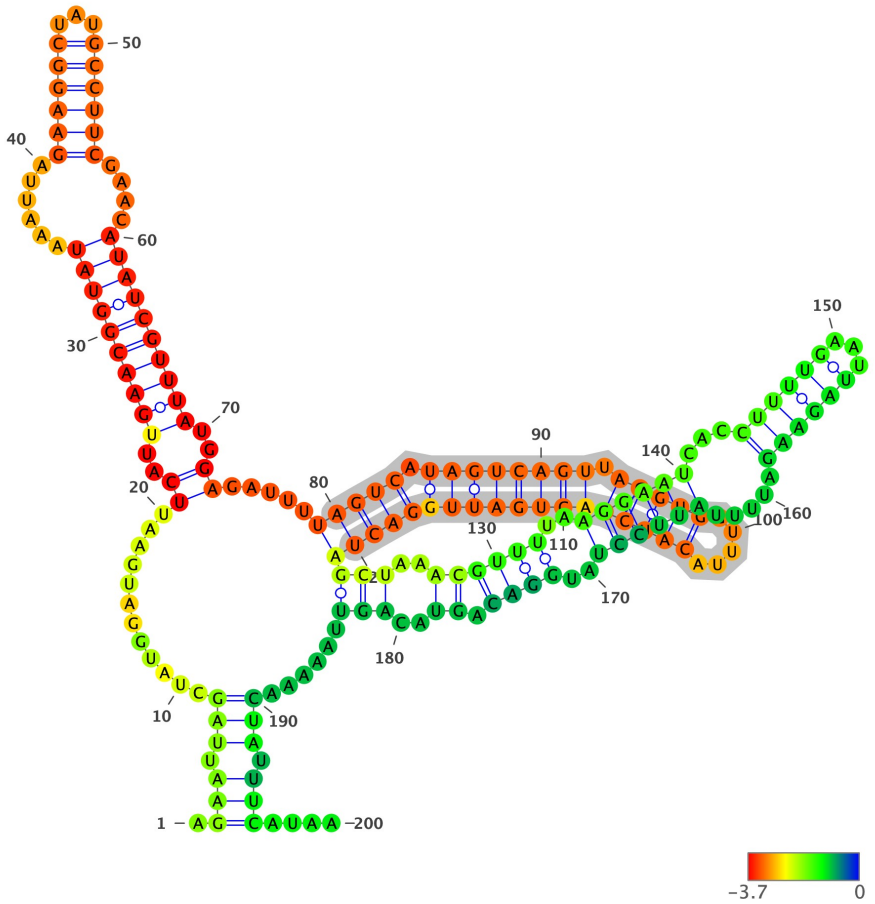
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 314 from nt 20341 to 20381 (nt 80 to 120)

```
5'-AGTCATAGTCAGTTAGGTGGTTTACAUCUACUGAUUGGACU-3'
5'-((((..(((((((..(((((.....))))).))))))).))))-3'
Motif MFE = -17.7; z-score = -4.98; ED = 1.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20262 to 20461 (motif highlighted in silver):

```
5'-AGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACU
GAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAA-3
5'-.(((.(((............((..(((((((((((......((((((...))))))....))))))))))..)).....(((((.((((((((.(((((.....))))))))
))))))))))(((..(((((((..((((((...((((((...))))))).....))))))..)))).))..)))......))).)))....-3'
MFE = -50.7; z-score = -3.06; ED = 32.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

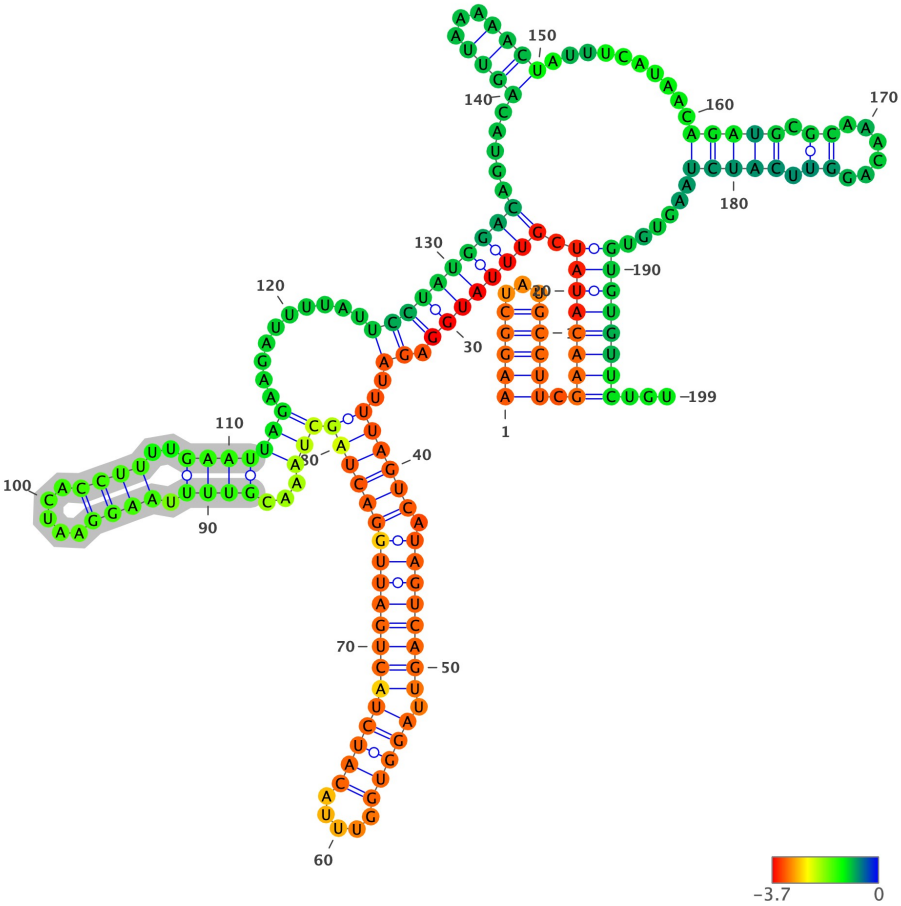
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 315 from nt 20390 to 20413 (nt 88 to 111)

```
5'-GTTTTAAGGAATCACCUUTTGAAU-3'
5'-((((.((((.....))))..))))-3'
Motif MFE = -1.8; z-score = -0.69; ED = 5.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20303 to 20501 (motif highlighted in silver):

```
5'-AAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAU
UAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGU-3
5'-(((((...))))).((((((((.((((((((.((..((((((.((((((((.(((((.....)))))))))))))))))))(((...((((.((((.....))))..))))
))).........))))))))))).....((((...)))).........(((((.((......)).)))))......))))))))...-3'
MFE = -45.3; z-score = -1.68; ED = 34.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

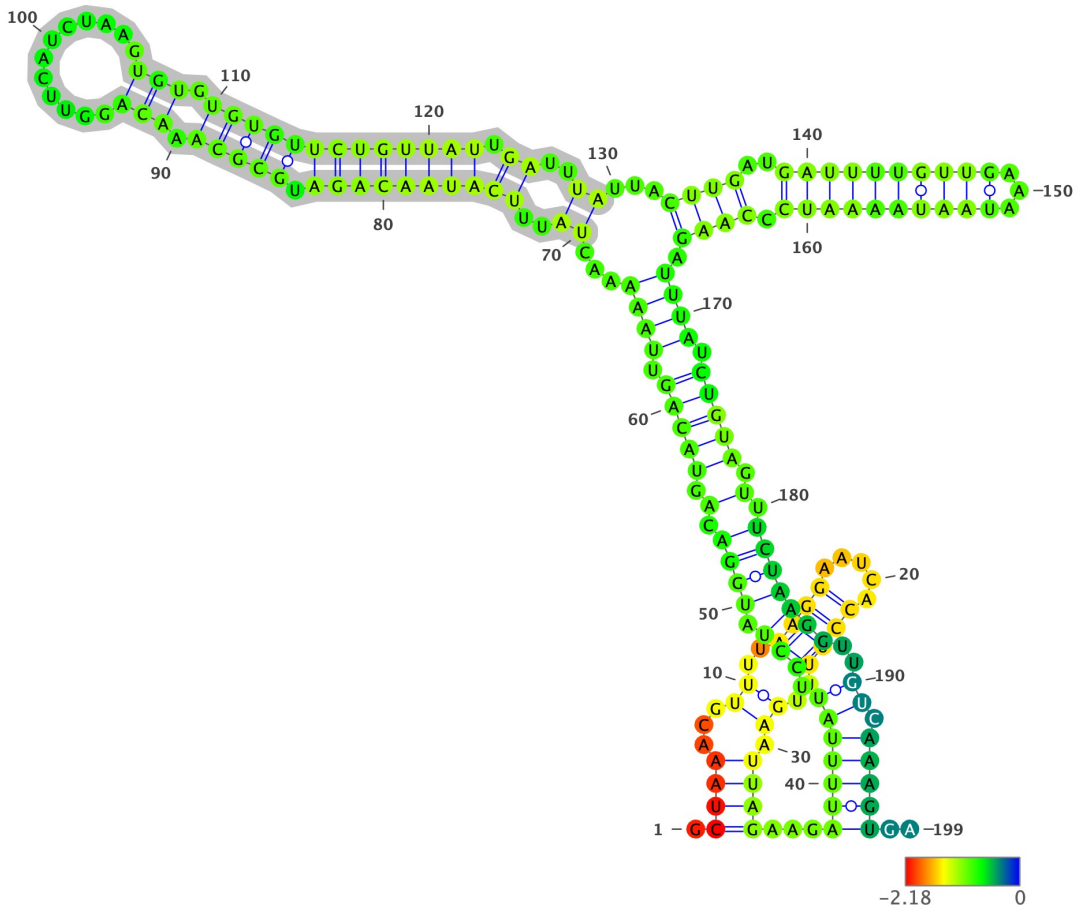
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 316 from nt 20452 to 20511 (nt 70 to 129)

```
5'-TATTTCATAACAGATGCGCAAACAGGTTCATCTAAGUGUGUGUGTUCUGUUAUTGATTUA-3'
5'-((..((((((((((.............................))))))))).))..))-3'
Motif MFE = -15.2; z-score = -2.96; ED = 13.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20383 to 20581 (motif highlighted in silver):

```
5'-GCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUG
UGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGA-3
5'-.((((...((..((((.....))))..)).))))...(((((((.(((.((((.(.(((((.((((...((..((((((((((.(((((.(((.............))).))
))))))))))).))..))...((((..((((((((((...)))))))))).)))).)))).)))))).).)))))))..)).)))))..-3'
MFE = -39.1; z-score = -1.07; ED = 57.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

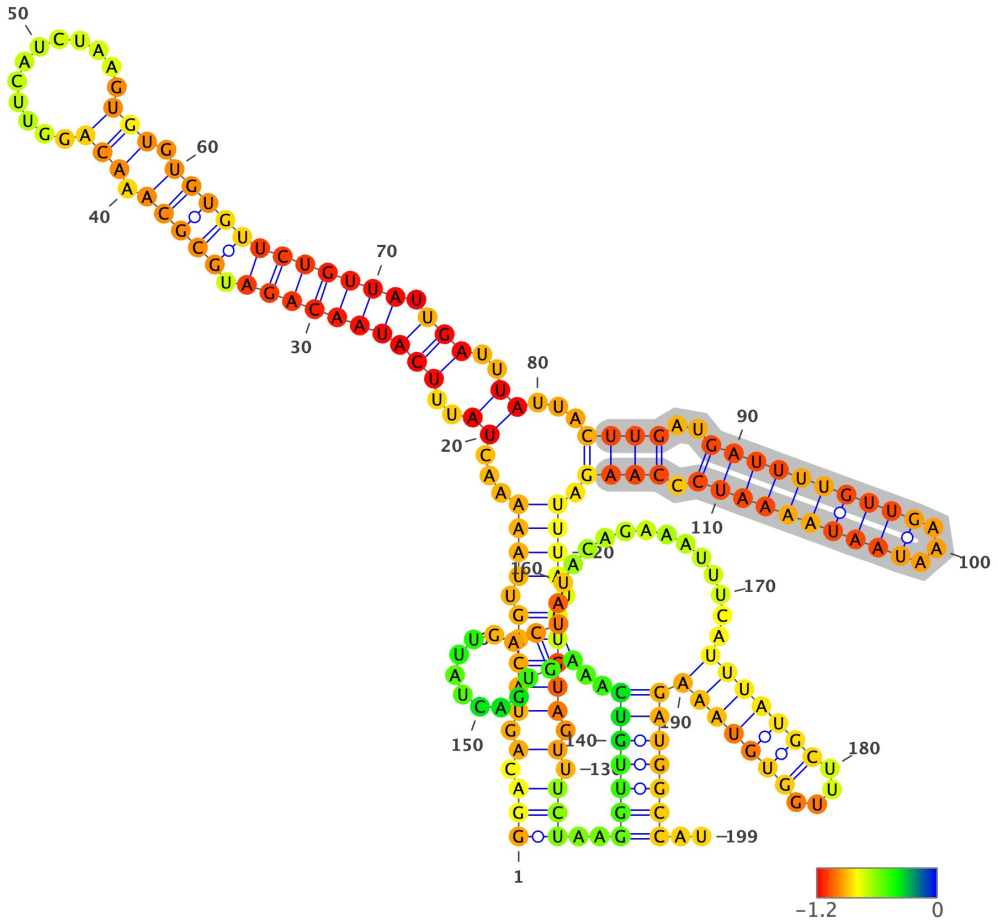
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 317 from nt 20516 to 20547 (nt 84 to 115)

```
5'-TTGATGATTTTGTTGAAATAAUAAAAUCCCAA-3'
5'-(((..((((..(((.....)))..)))).)))-3'
Motif MFE = -5.4; z-score = -2.8; ED = 1.94
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20433 to 20631 (motif highlighted in silver):

```
5'-GGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUC
CCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAU-3
5'-(((.(.(((((.((((...((..((((((((((.(((((.(((............))).))))))))))))).)))..))...((((..((((((((((...))))))))))
.)))).)))).)))))).).)))..(((((((..(((........)))..............(((((((....)))))))))))))..-3'
MFE = -41.9; z-score = -1.43; ED = 46.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

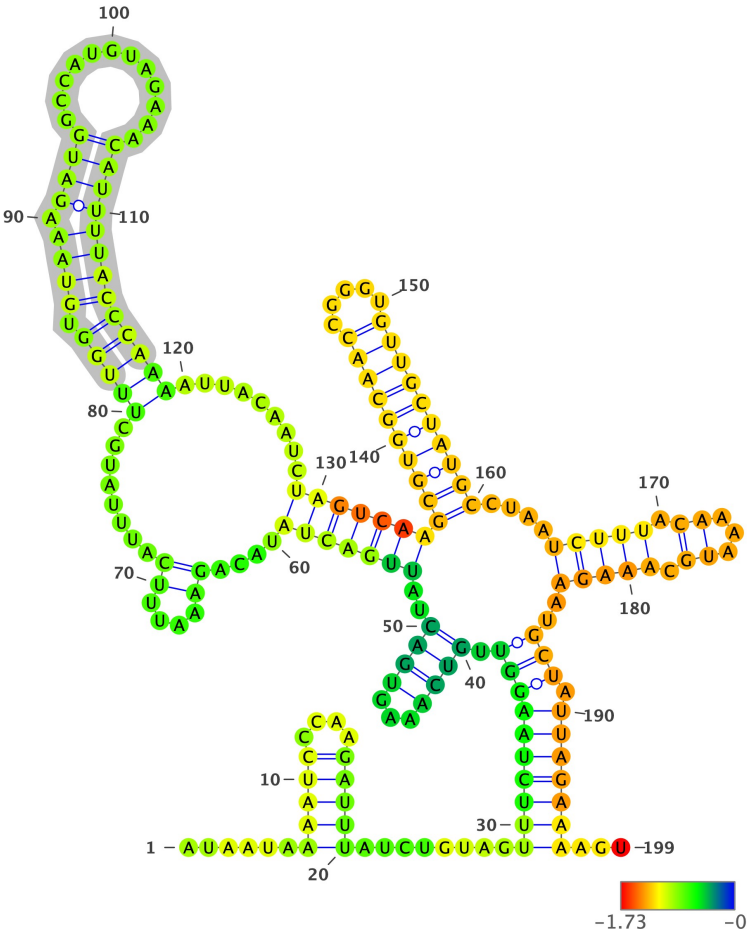
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 318 from nt 20614 to 20649 (nt 82 to 117)

```
5'-TGGTGTAAAGATGGCCATGTAGAAACAUUUTACCCA-3'
5'-((..((.........................)).))-3'
Motif MFE = -5.9; z-score = -1.43; ED = 4.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20533 to 20731 (motif highlighted in silver):

```
5'-AUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUU
UACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGU-3
5'-......(((((....)))))........((((((((((.((((...)))).((((((((....((....))........(((((.((((.((((.............)))))
))))))))).........)))))))((((((((((.....)))))))))....(((((.((...)).)))))..))).)))))))...-3'
MFE = -36.7; z-score = -0.91; ED = 55.82
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

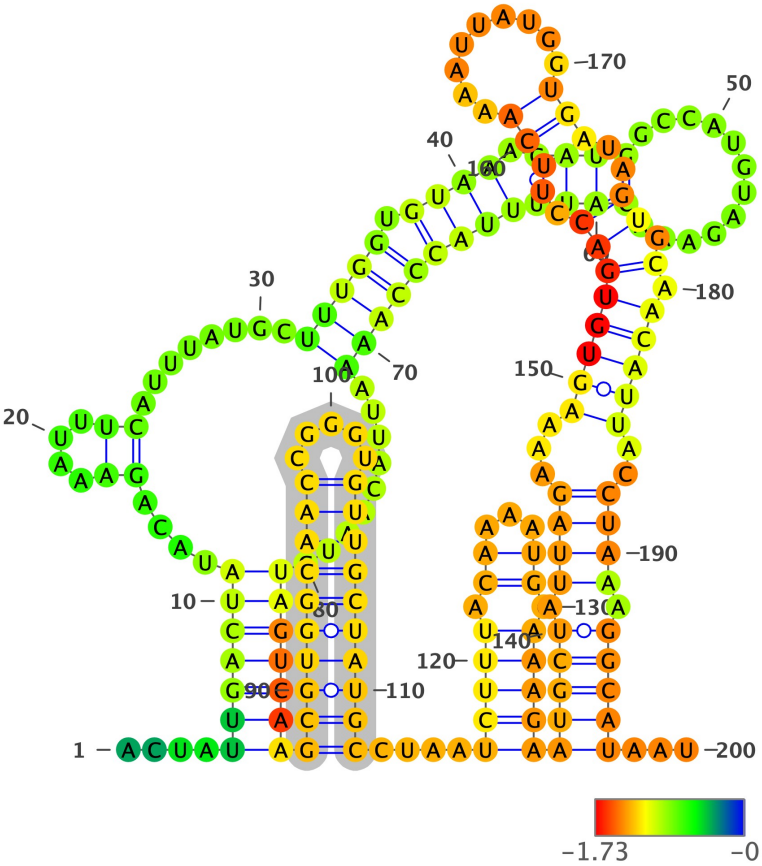
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 319 from nt 20668 to 20692 (nt 88 to 112)

```
5'-GCGTGGCAACCGGGTGUUGCUAUGC-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -13.0; z-score = -3.42; ED = 0.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20581 to 20780 (motif highlighted in silver):

```
5'-ACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUG
CCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAU-3
5'-....(((((((....((....)).........(((((.((((.((((.............)))))))))))))).........)))))))((((((((((.....)))))))))
)....(((((.((...)).)))))(((((.((((...((((((((..(((.........)))..)).).)))))..)))).)))))...-3'
MFE = -39.4; z-score = -0.75; ED = 42.59
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

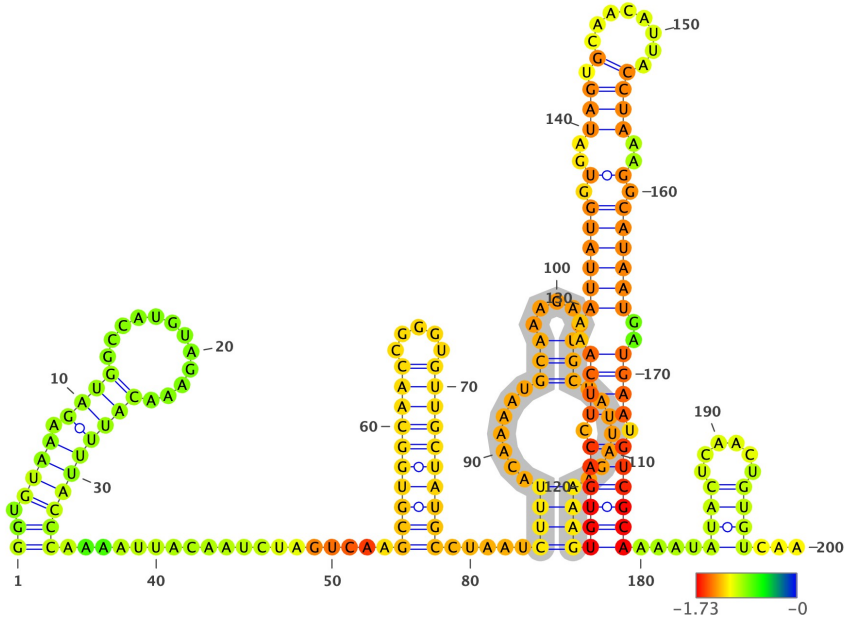
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 320 from nt 20698 to 20730 (nt 84 to 116)

```
5'-CTTTACAAAATGCAAAGAAUGCTATTAGAAAAG-3'
5'-((((.......(((.....)))......))))-3'
Motif MFE = -1.3; z-score = -0.11; ED = 5.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20615 to 20814 (motif highlighted in silver):

```
5'-GGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAG
AAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAA-3
5'-((.((((.((((............))))))))).....................((((((((((.....)))))))))).....((((.......(((.....)))......
.))))((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))....((((......))))...-3'
MFE = -41.4; z-score = -1.85; ED = 29.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

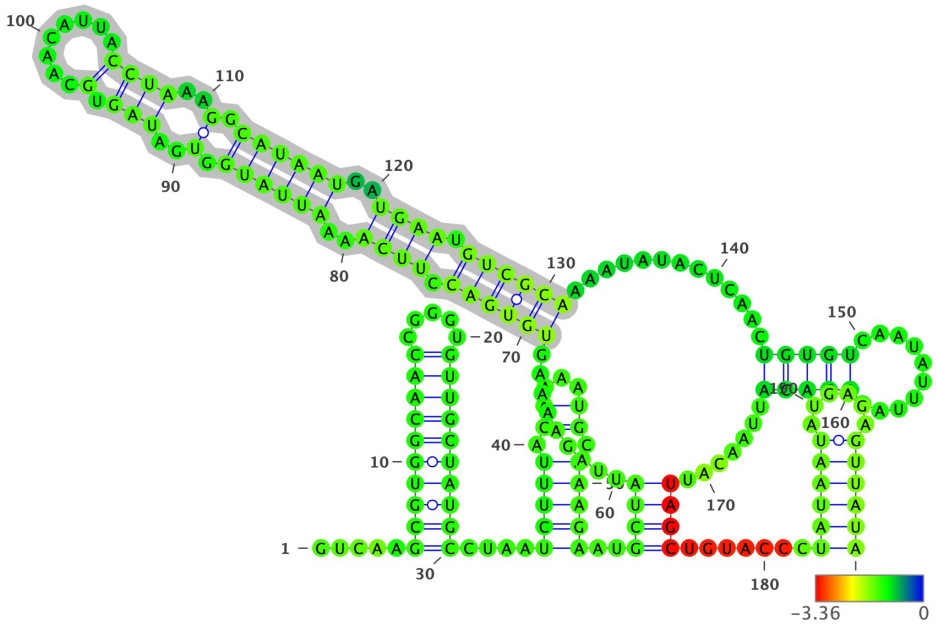
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 321 from nt 20731 to 20793 (nt 69 to 131)

```
5'-TGTGACCTTCAAAATTATGGTGATAGTGCAACATTACCUAAAGGCAUAAUGAUGAATGUCGCA-3'
5'-((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))-3'
Motif MFE = -17.6; z-score = -3.16; ED = 4.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20663 to 20862 (motif highlighted in silver):

```
5'-GUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAG
GCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUUAACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUA-3
5'-.....((((((((((.....)))))))))....(((((.((...)).)))))..((((.........((((((.((((..((((((.(..(((.(........))))..)
.))))))..)))).))))))..............(((((..........)))))........))))........((((((......))))))-3'
MFE = -39.0; z-score = -1.21; ED = 33.44
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

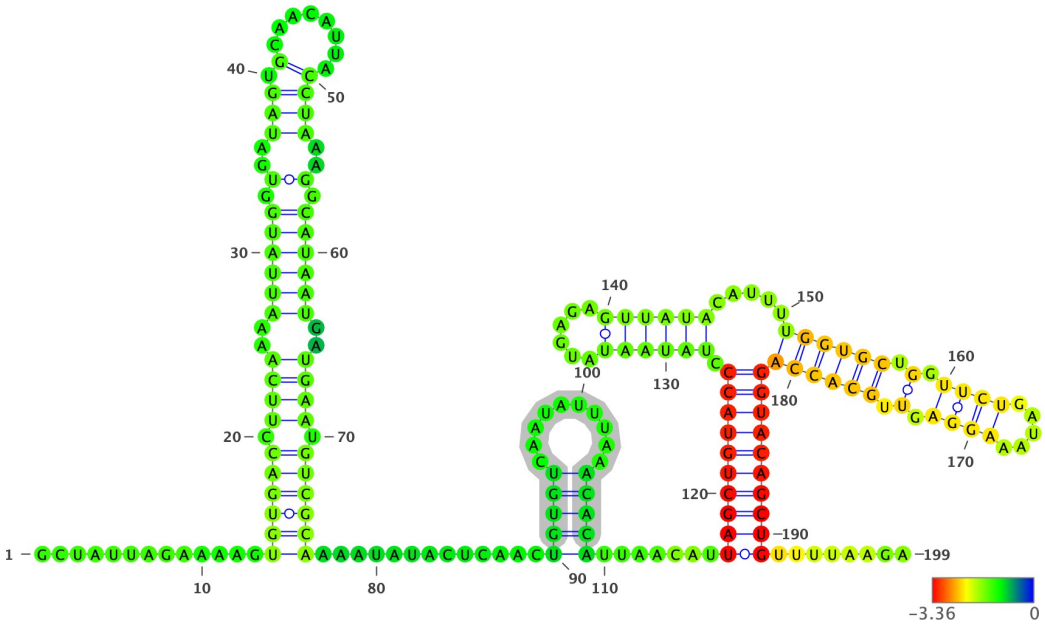
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 322 from nt 20808 to 20825 (nt 91 to 108)

```
5'-GTGTCAATATTTAAACAC-3'
5'-((((..........))))-3'
Motif MFE = -0.2; z-score = -0.04; ED = 2.42
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20718 to 20916 (motif highlighted in silver):

```
5'-GCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUU
AACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGA-3
5'-.............((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))............(((((..........)))))..
.....((((((((((.((((((......))))))).....((((((.(.((((.....)))).).))))))))))))))))........-3'
MFE = -50.4; z-score = -3.41; ED = 15.54
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

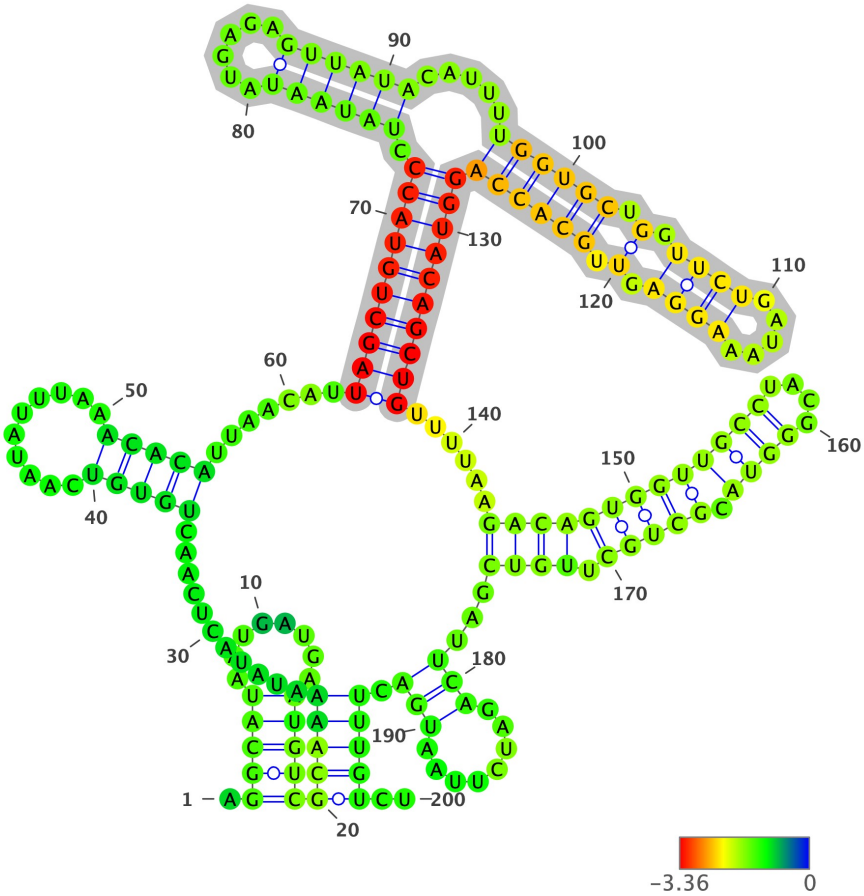
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 323 from nt 20834 to 20908 (nt 63 to 137)

```
5'-TAGCTGTACCCTATAATATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGUTGCACCAGGUACAGCUG-3'
5'-((((((((((.........................(((((.(.((((.....)))).).))))).))))))))))-3'
Motif MFE = -28.8; z-score = -4.12; ED = 3.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20772 to 20971 (motif highlighted in silver):

```
5'-AGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUUAACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGA
UAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCU-3
5'-.(((((........)))))(((((...........(((((..........)))))).......((((((((((.((((((......))))))).....((((((.(.((((..
...)))).).))))))))))))))))).....((((((((((((....)))).))))).))))...(((........))).)))))..-3'
MFE = -52.2; z-score = -2.24; ED = 38.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

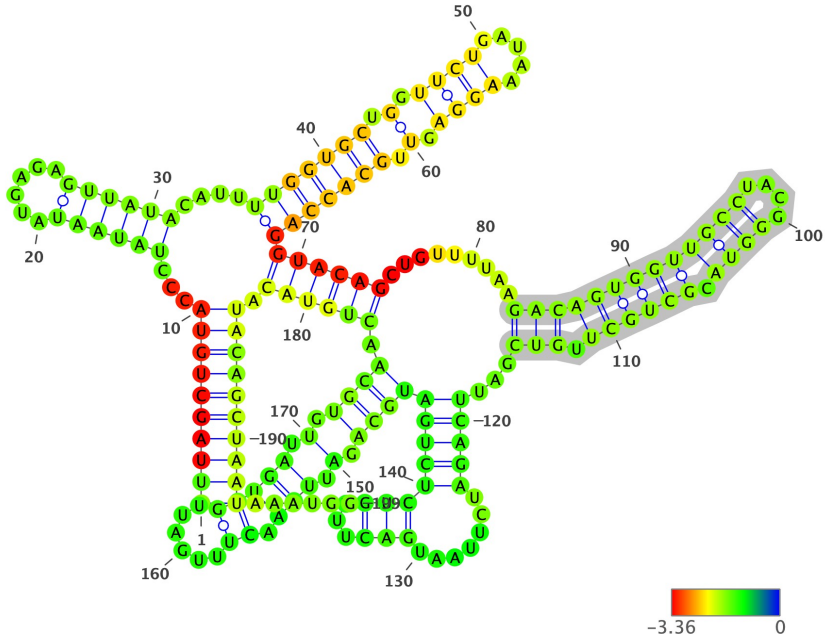
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 324 from nt 20915 to 20946 (nt 84 to 115)

```
5'-GACAGTGGTTGCCTACGGGUACGCUGCUTGUC-3'
5'-(((((((((((((....)))))).)))))))..)))-3'
Motif MFE = -12.6; z-score = -2.33; ED = 1.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20832 to 21030 (motif highlighted in silver):

```
5'-AUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCU
UGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGG-3
5'-((((((((((...((((((.....))))))....(((((((.(.((((.....)))).).)))))))((((((.........((((((((((((....)))).))))))
.)))...(((((.......(((...)))))))))((((.(.((((.((.....)))))).).)))).)))))).)))))))))).....-3'
MFE = -58.9; z-score = -3.1; ED = 32.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

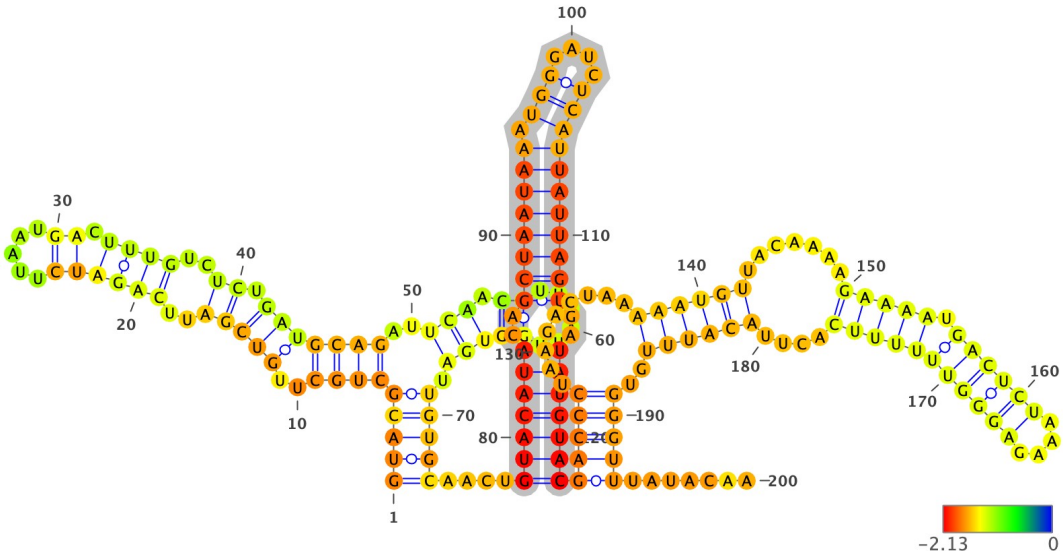
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 325 from nt 21010 to 21054 (nt 78 to 122)

```
5'-GTACATACAGCTAATAAATGGGATCTCATUAUUAGUGAUAUGUAC-3'
5'-(((((((..(((((((.............)))))))..)))))))-3'
Motif MFE = -14.9; z-score = -5.29; ED = 2.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20933 to 21132 (motif highlighted in silver):

```
5'-GUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUA
GUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAA-3
5'-(((((((((..(((((..((((((.....)).))))..)).)))))))..(((.((.....))))).)))))....(((((((..((((((((.(((....)))))))))
))..)))))))(((((.........((((((.......(((((.((((((....)))))))))))....))))))..)))))........-3'
MFE = -43.4; z-score = -1.47; ED = 44.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

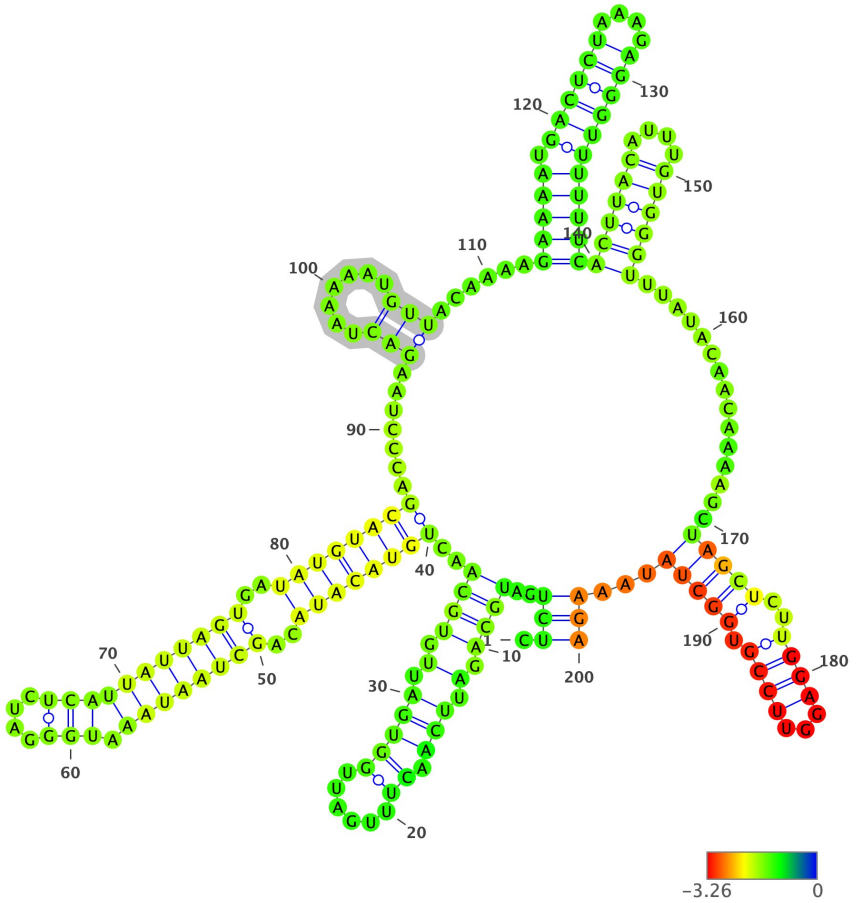
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 326 from nt 21063 to 21075 (nt 94 to 106)

```
5'-GACTAAAAATGUU-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.14; ED = 1.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20970 to 21169 (motif highlighted in silver):

```
5'-CUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAA
AGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGA-3
5'-.(((..((((.(.(((.((......))))).).))))..((((((((..((((((((.(((....)))))))))))..))))))))).......(((.......))).....
.(((((.((((((....)))))))))))((((((....))))))...............(((((..((((...)))).)))))...)))-3'
MFE = -45.4; z-score = -2.27; ED = 21.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

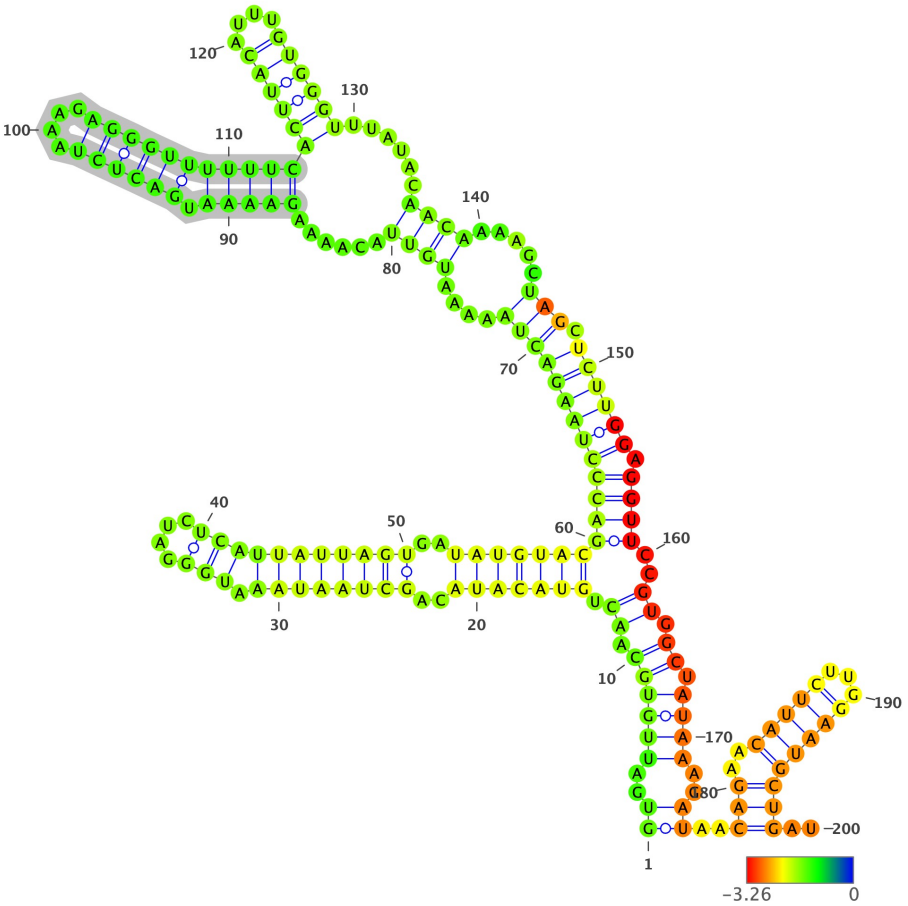
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 327 from nt 21082 to 21108 (nt 87 to 113)

```
5'-GAAAATGACTCTAAAGAGGGUUUUUUC-3'
5'-(((((.((((((....)))))))))))-3'
Motif MFE = -6.0; z-score = -2.27; ED = 2.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20996 to 21195 (motif highlighted in silver):

```
5'-GUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUU
UCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU-3
5'-((..((((((.((.(((((((..((((((((.(((....)))))))))))..)))))))((((((((((((....((((......(((((.((((((....)))))))))
))((((((....))))))......))))).....))).)))))).))))..)).)).))))..))..(((..(((((...))))))))..-3'
MFE = -43.9; z-score = -1.68; ED = 49.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

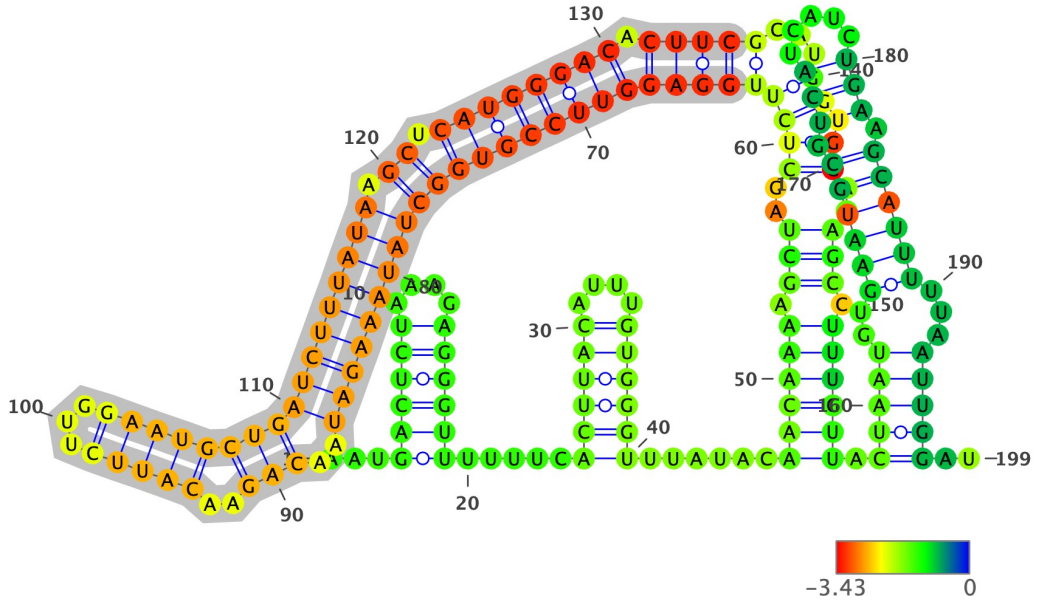
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 328 from nt 21148 to 21219 (nt 64 to 135)

```
5'-GGAGGTTCCGTGGCTATAAAGATAACAGAACATTCTTGGAAUGCUGAUCUUUAUAAGCTCAUGGGACACUUC-3'
5'-(((((((((((((((((((((((..(((..((((.....))))))))))))))).)).))))))).))))-3'
Motif MFE = -29.1; z-score = -4.85; ED = 2.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21085 to 21283 (motif highlighted in silver):

```
5'-AAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU
CUUUAUAAGCUCAUGGGACACUUCGCAUGGUGGACAGCCUUUGUUACUAAUGUGAAUGCGUCAUCAUCUGAAGCAUUUUUAAUUGGAU-3
5'-...((((((....))))))).....((((((....))))))......((((((.(((..((((((((((((((((((((((((((((..(((..(((((...)))))))))))
))))))).)).)))))))).)))))...)).)).)).))).)))))).(((((..((((((.(((.....))).))))))...)))))..-3'
MFE = -57.5; z-score = -3.7; ED = 15.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

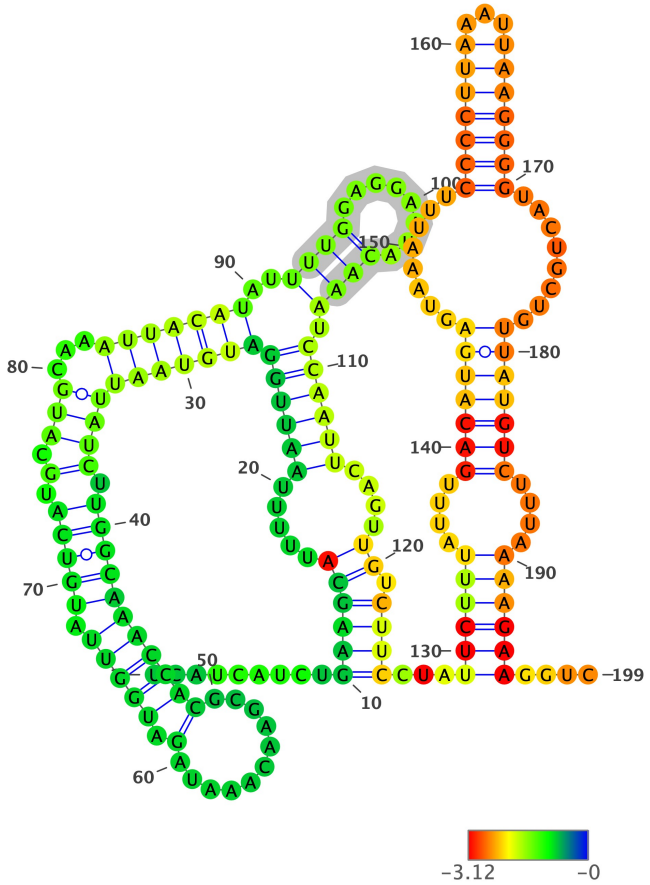
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 329 from nt 21348 to 21361 (nt 93 to 106)

```
5'-TTGGAGGAATACAA-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.16; ED = 1.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21256 to 21454 (motif highlighted in silver):

```
5'-UCAUCAUCUGAAGCAUUUUUAAUUGGAUGUAAUUAUCUUGGCAAACCACGCGAACAAAUAGAUGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCA
AUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUC-3
5'-.........((((((.....(((((((((((((((((.((((((((((((...........).)))))).)))))).).)))...)))))))..((((........)))).)))
)))....)).))))...((((((....(((((((........(((((((...)))))))........)))))))....))))))....-3'
MFE = -42.8; z-score = -1.68; ED = 19.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

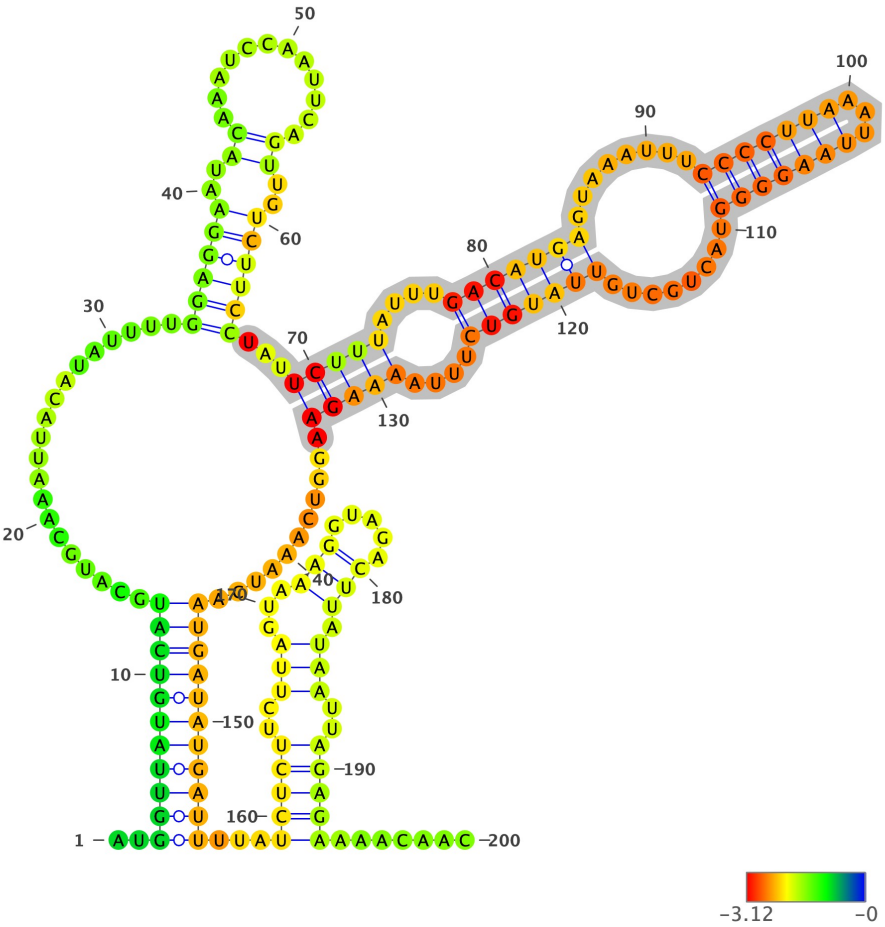
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 330 from nt 21382 to 21450 (nt 66 to 134)

```
5'-TATTCTTTATTTGACATGAGTAAATTTCCCCTTAAATTAAGGGGTACTGCTGTTATGUCTTTAAAAGAA-3'
5'-(..((........((............((((.........))))............))........)))-3'
Motif MFE = -20.9; z-score = -4.81; ED = 4.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21317 to 21516 (motif highlighted in silver):

```
5'-AUGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUA
CUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAAC-3
5'-..(((((((((((.....................((((((..((............))..))))))...(((((....(((((((.........(((((((...)))))))..
......)))))))....)))))...........))))))))))...(((((..(((...(((.....))).)))..)))))........-3'
MFE = -41.5; z-score = -2.52; ED = 28.84
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

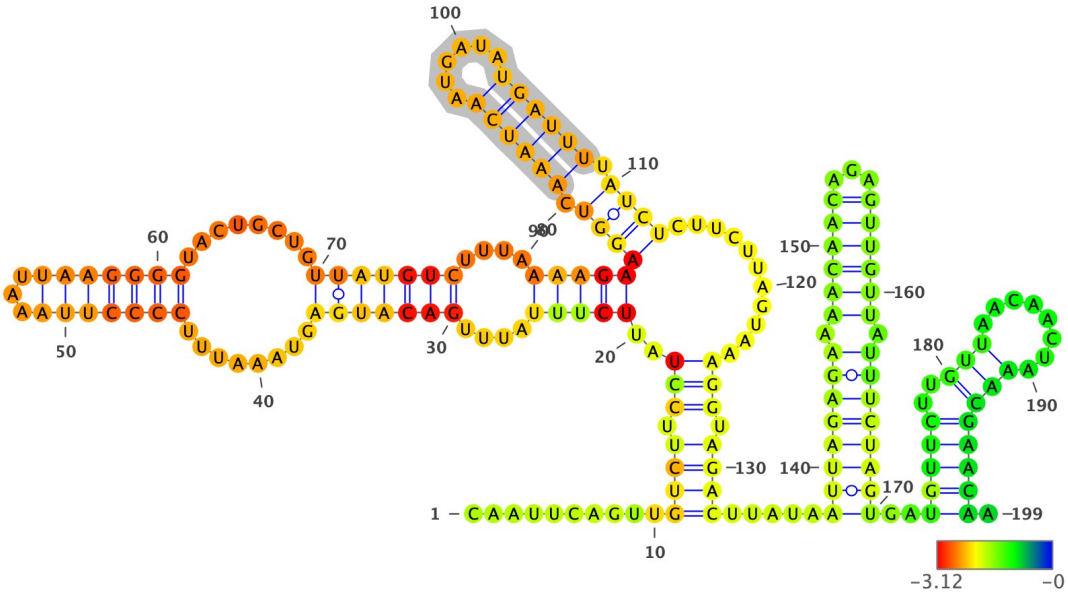
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 331 from nt 21455 to 21472 (nt 91 to 108)

```
5'-AAATCAATGATATGAUUU-3'
5'-(((((........)))))-3'
Motif MFE = -1.8; z-score = -2.93; ED = 1.28
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21365 to 21563 (motif highlighted in silver):

```
5'-CAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAU
CUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAA-3
5'-..........((((.(((..(((((....(((((((........(((((((...)))))))........)))))))....)))))((((.((((((......))))))..))
))...........))).))))).....((((((((.((((((...)))))).))))))))..(((((..(((........))))))))).-3'
MFE = -46.8; z-score = -3.44; ED = 32.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 191--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 191--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 199 to 199--gene, gene-GU280_gp02, 21563-25384(+)

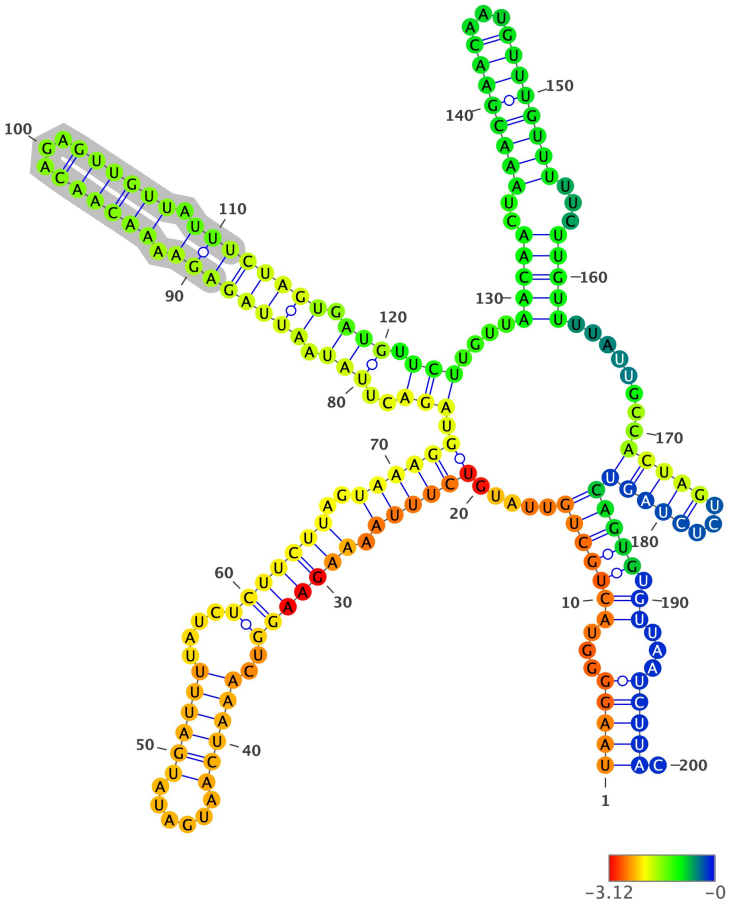
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 199 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 332 from nt 21507 to 21529 (nt 89 to 111)

```
5'-AGAAAACAACAGAGUUGUUATTU-3'
5'-(...((((((...))))))...)-3'
Motif MFE = -3.4; z-score = -2.58; ED = 2.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21419 to 21618 (motif highlighted in silver):

```
5'-UAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUU
CUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUCUUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUAC-3
5'-(((((...(((((((.....((((((.(((((((..((((((......))))))....)))))))..)))))).(((..(((.(((((((((.((((((...))))))).)))
))))).))).)))....(((((..(((((((((...)))))))))...)))))........(((((...)))))))))).))...))))).-3'
MFE = -39.1; z-score = -0.64; ED = 42.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 137--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 137--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 145 to 200--gene, gene-GU280_gp02, 21563-25384(+)

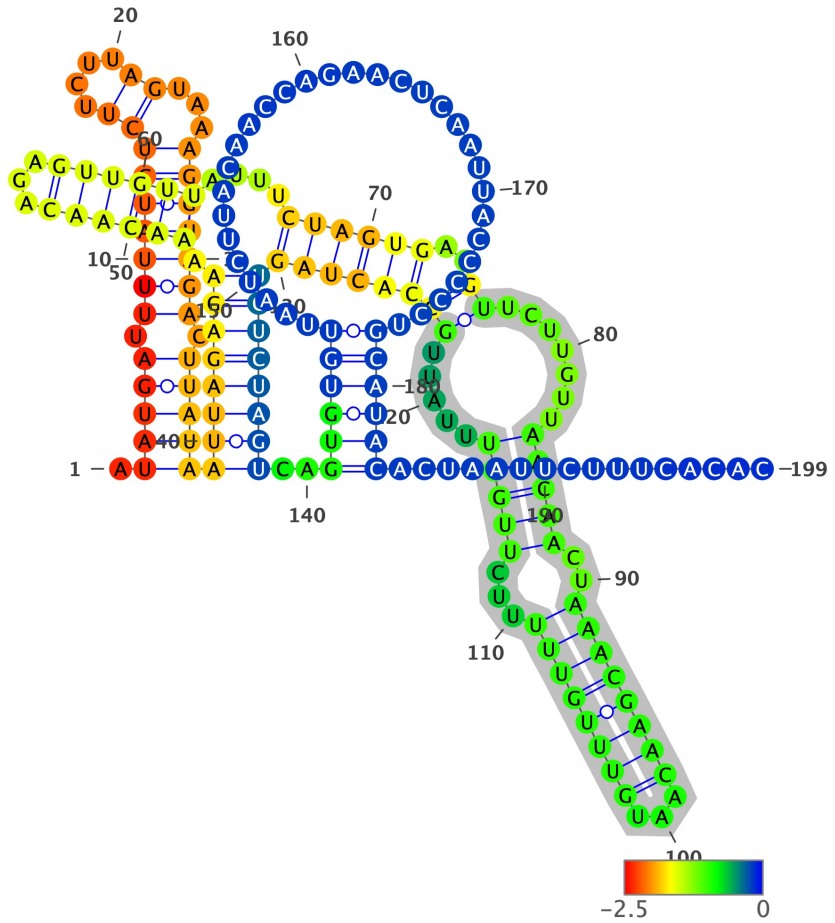
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 145 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 333 from nt 21539 to 21586 (nt 76 to 123)

```
5'-TTCTTGTTAACAACTAAACGAACAATGUUUGUUUTTCUUGUUTTATTG-3'
5'-(.......(((((.......................)))))).....)-3'
Motif MFE = -6.8; z-score = -1.77; ED = 2.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21464 to 21662 (motif highlighted in silver):

```
5'-AUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUU
CUUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACAC-3
5'-.(((((.(((((((((....))...)))))))).)))))((((((((.((((((...))))))....((((((..((.......(((((..((((((((...))))))))..
.)))))).....))))))))))))))))..((((((.................................))))))................-3'
MFE = -31.37; z-score = -1.19; ED = 29.82
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 92--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 92--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 100 to 199--gene, gene-GU280_gp02, 21563-25384(+)

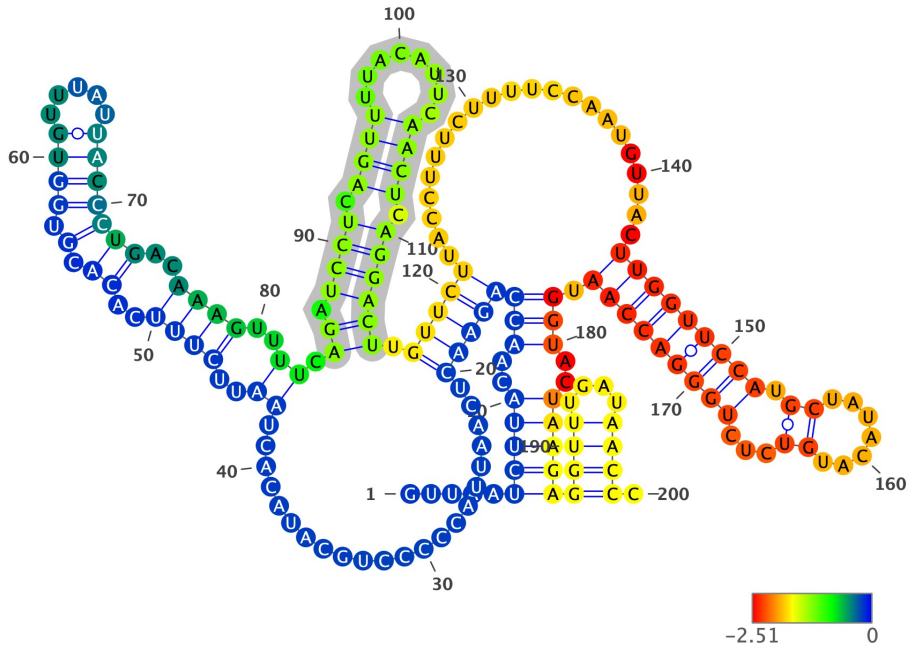
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 100 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 334 from nt 21692 to 21722 (nt 85 to 115)

```
5'-AGATCCTCAGTTTTACATTCAACUCAGGACU-3'
5'-((.((((.((((........)))).))))))-3'
Motif MFE = -5.8; z-score = -2.23; ED = 1.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21608 to 21807 (motif highlighted in silver):

```
5'-GUUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACGUGGUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAG
GACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCC-3
5'-.....(((((..((((((((.......................((..((((..((.(.((((.....)))))))..))))..)).((.((((.((((........)))).))
)))).)))))......................(((((((((.((.......))...)))))))))).)))..)))))((((....)))).-3'
MFE = -32.4; z-score = -1.18; ED = 37.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

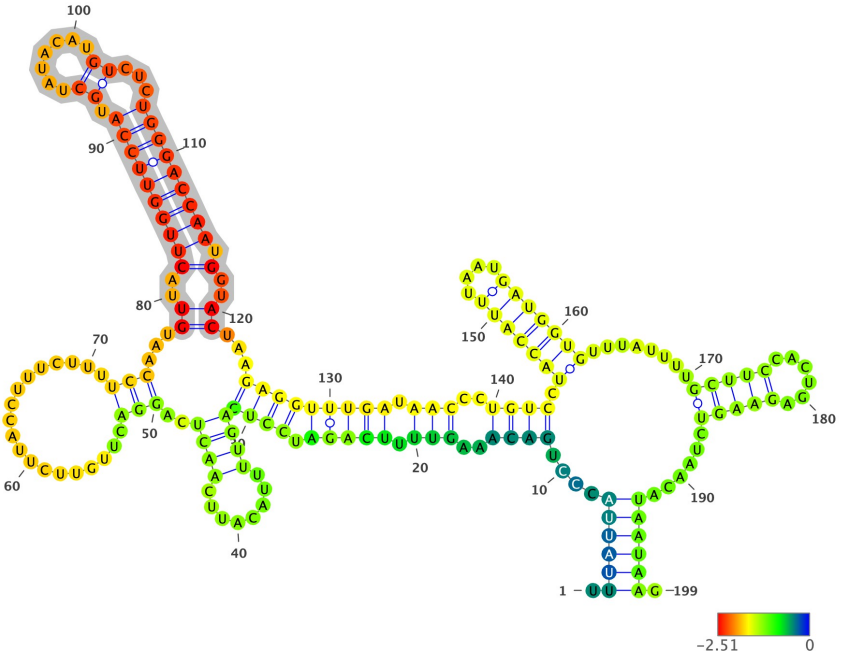
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 335 from nt 21746 to 21789 (nt 78 to 121)

```
5'-GTTACTTGGTTCCATGCTATACATGUCTCUGGGACCAATGGTAC-3'
5'-((..((((((((((.((.......))...)))))))))).)..))-3'
Motif MFE = -12.8; z-score = -2.4; ED = 5.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21669 to 21867 (motif highlighted in silver):

```
5'-UUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGGACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGA
CCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAG-3
5'-.(((((.....((((..((((.(((((.(((((((.......))))).(((.................))).....((..((((((((((.((.......)).....))))))
))))).)..)).....))))))))).))).)).))))).(((((((....)))))))........((((.....)))))).....)))))).-3'
MFE = -40.3; z-score = -2.4; ED = 35.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

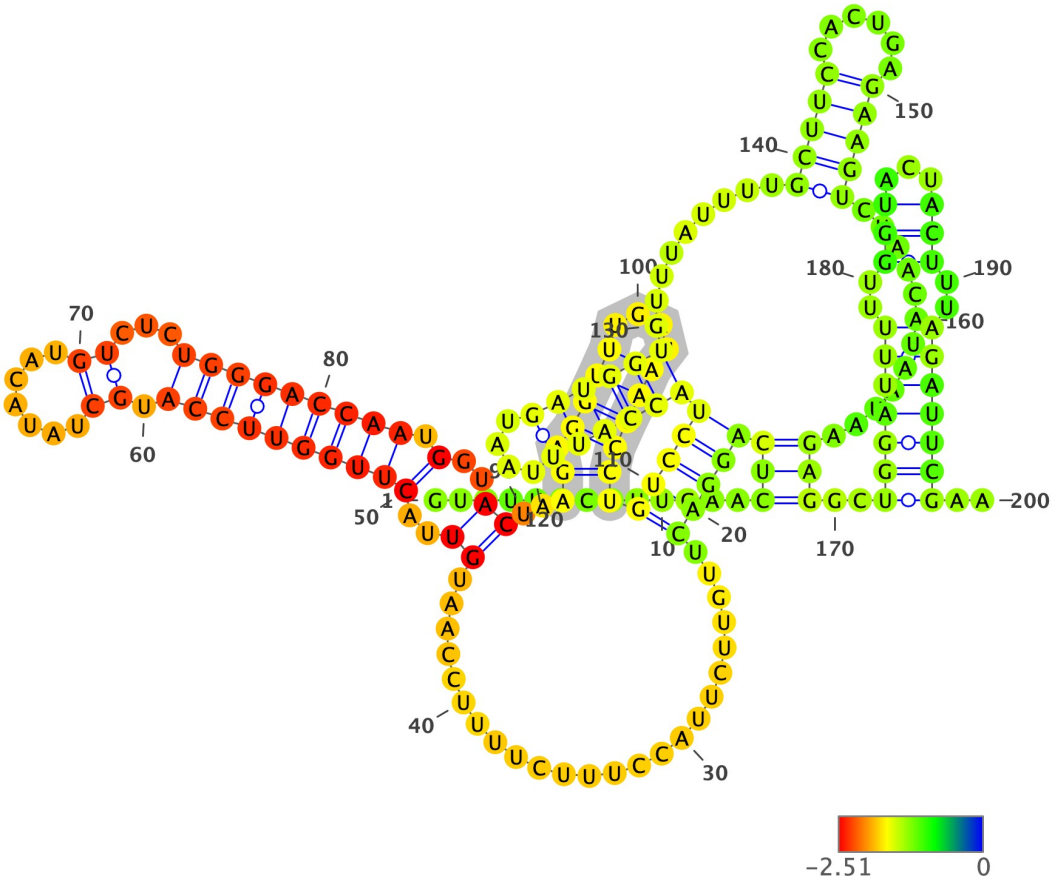
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 336 from nt 21792 to 21808 (nt 92 to 108)

```
5'-AGAGGTTTGATAACCCU-3'
5'-((.((((....))))))-3'
Motif MFE = -2.8; z-score = -2.02; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21701 to 21900 (motif highlighted in silver):

```
5'-GUUUUACAUUCAACUCAGGACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUC
CUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAA-3
5'-.............((((((((.......................((..(((((((((((.((.......))...))))))))).)..))..((.((((....)))))))))
))((((((....))))))).........(((((......)))))............)))..(((((((..(((...)))..)))))))..-3'
MFE = -38.0; z-score = -1.08; ED = 37.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

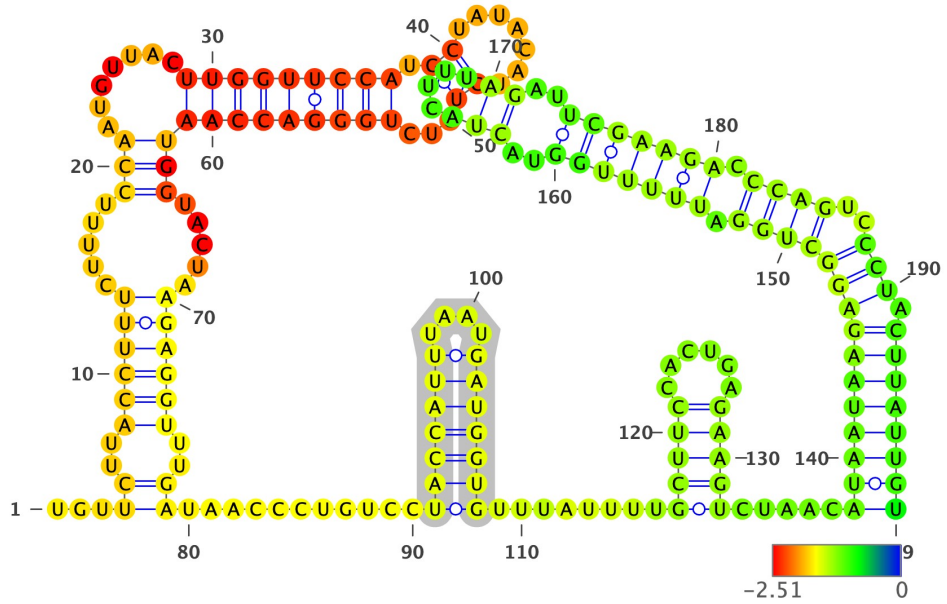
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 337 from nt 21813 to 21830 (nt 91 to 108)

```
5'-TACCATTTAATGAUGGUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.8; z-score = -4.98; ED = 0.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21723 to 21921 (motif highlighted in silver):

```
5'-UGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUU
AUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGACCCAGUCCCUACUUAUUGU-3
5'-...((..((((((.....(((.......(((((((((.((.......))...))))))))))))).....))))))..)).........((((((.....)))))))...
.....(((((......))))).....((((((((((((((.(((((((..(((...)))..)))))))).))))..))).))))))))-3'
MFE = -48.3; z-score = -2.81; ED = 19.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

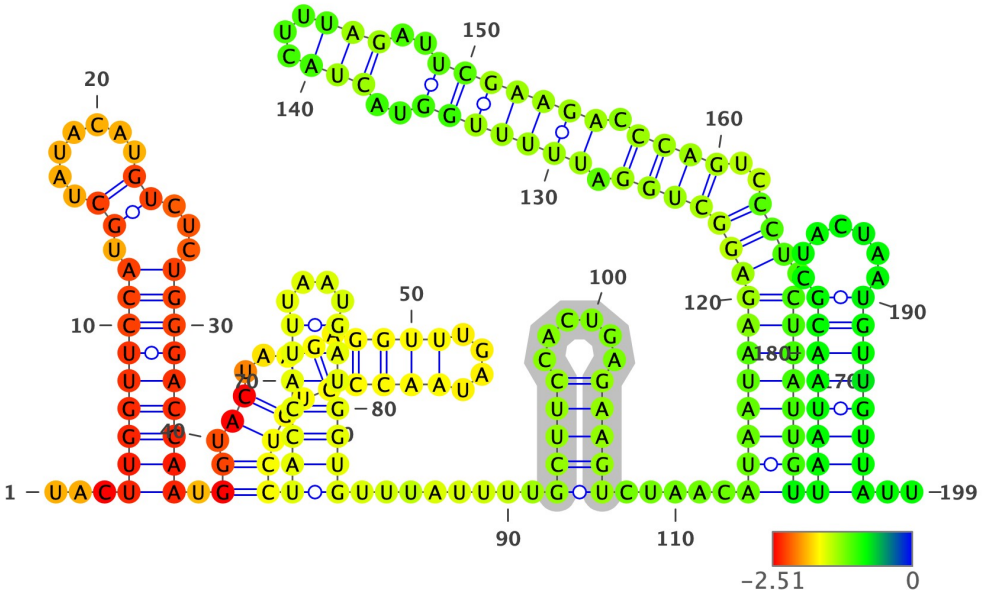
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 338 from nt 21839 to 21854 (nt 92 to 107)

```
5'-GCTTCCACTGAGAAGU-3'
5'-(((((......)))))-3'
Motif MFE = -3.0; z-score = -2.65; ED = 0.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21748 to 21946 (motif highlighted in silver):

```
5'-UACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAA
CAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUU-3
5'-...(((((((((.((.......))...))))))))).((.((..((.((((....)))))))))))(((((((....)))))))........(((((......)))))....
.((((((((((((((.(((((((..(((...)))..)))))))).))))..))).))))))))((((((((.......))))))))..-3'
MFE = -48.6; z-score = -2.14; ED = 33.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

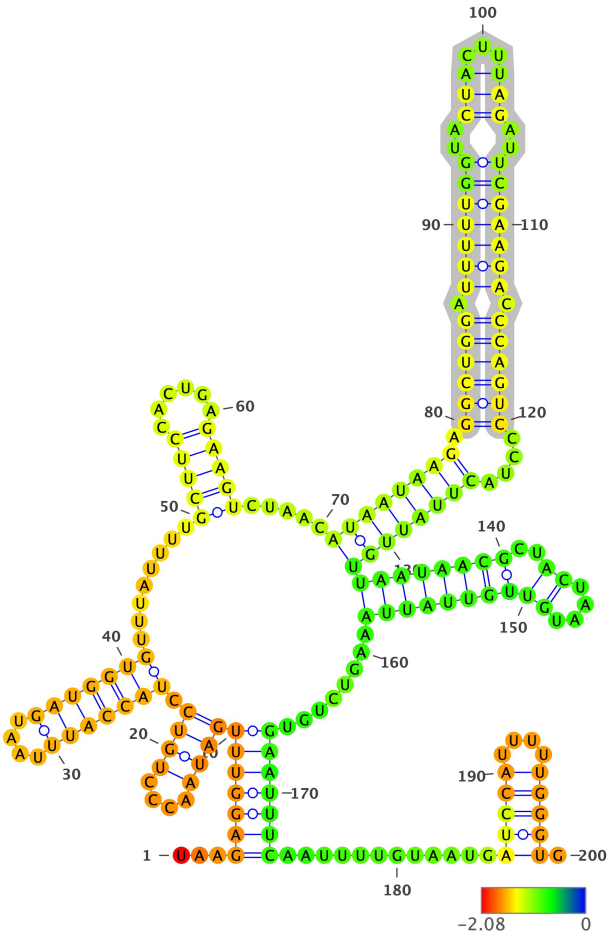
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 339 from nt 21869 to 21909 (nt 80 to 120)

```
5'-GGCTGGATTTTTGGTACTACTTTAGATTCGAAGACCCAGUC-3'
5'-((((((.(((((....((.....)).....))))).))))))-3'
Motif MFE = -11.8; z-score = -1.85; ED = 2.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21790 to 21989 (motif highlighted in silver):

```
5'-UAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAA
GACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUG-3
5'-...(((((((((((....)))).(((((((....)))))))........(((((......)))))).....((((((((.((((((.(((((((..(((...)))..)))))
)).))))))....))))))))((((((((..((....)))))))))).........)))))))............(((((....))))).-3'
MFE = -41.5; z-score = -1.14; ED = 38.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

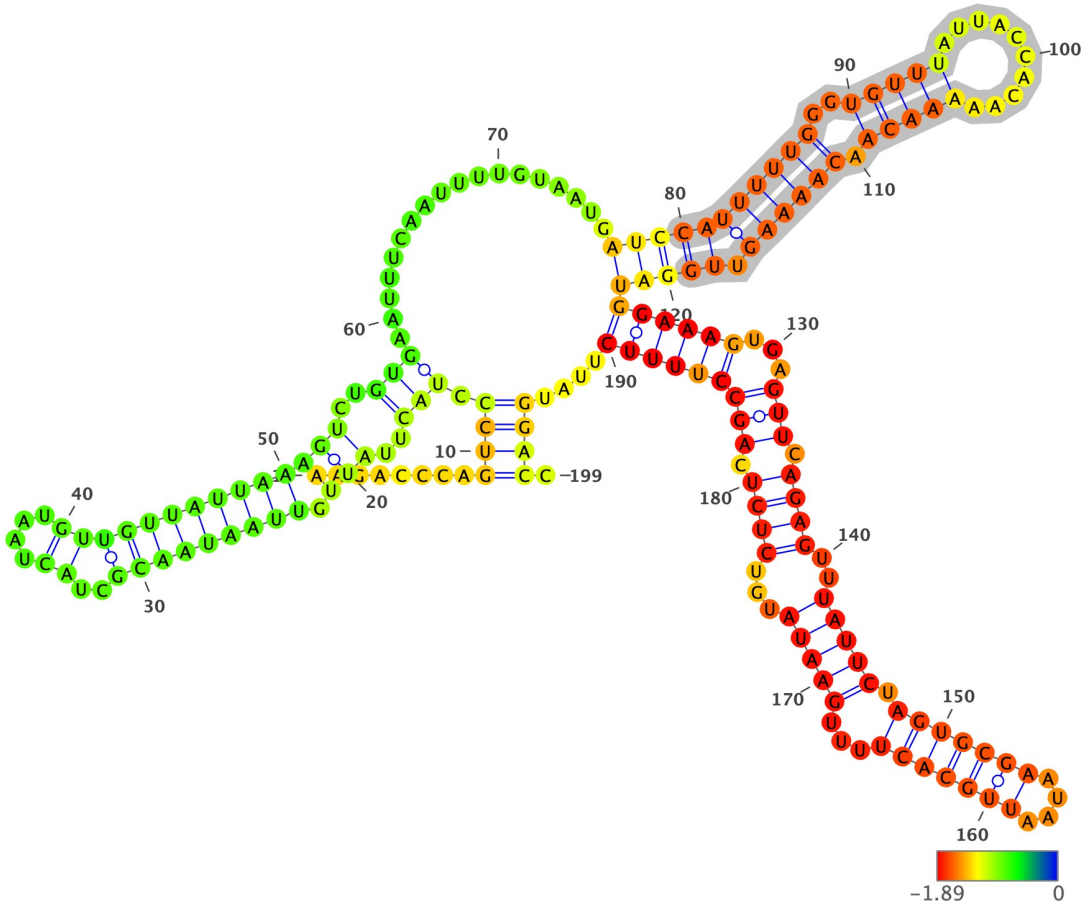
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 340 from nt 21978 to 22017 (nt 80 to 119)

```
5'-CATTTTTGGGTGTTTATTACCACAAAAACAACAAAAGTUG-3'
5'-((((((((..((((.............)))).)))))).))-3'
Motif MFE = -8.7; z-score = -2.88; ED = 1.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21899 to 22097 (motif highlighted in silver):

```
5'-AAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAAC
AAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACC-3
5'-........((((.(((..(((.(((((((((..((....))))))))))))))..))).................((((((((((..(((((..........))))).)
))))).)))))((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))....)))).-3'
MFE = -41.3; z-score = -1.74; ED = 32.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

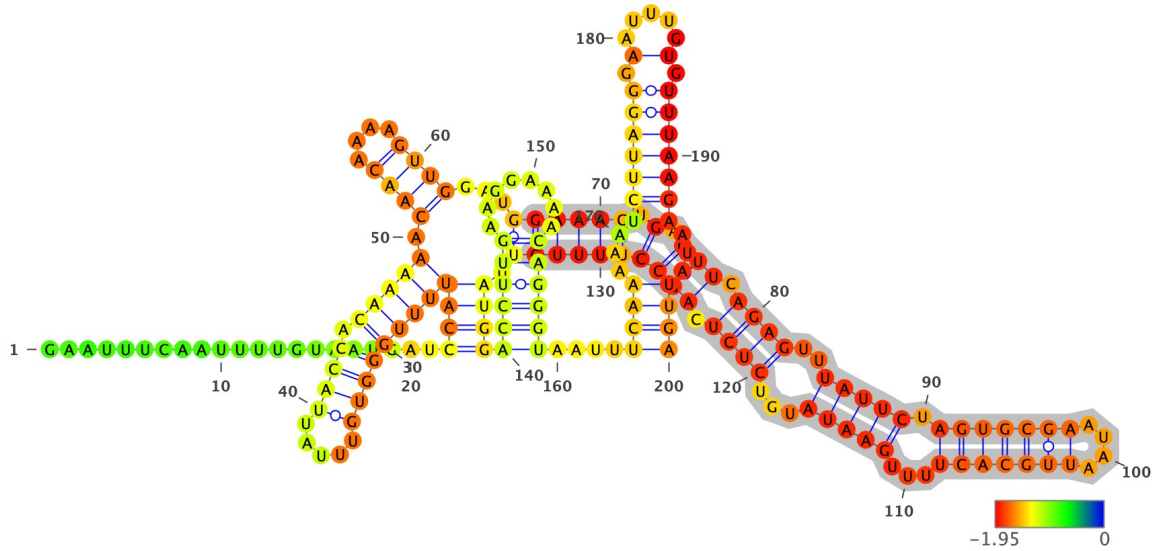
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 341 from nt 22022 to 22088 (nt 67 to 133)

```
5'-GAAAGTGAGTTCAGAGTTTATTCTAGTGCGAATAAUUGCACUTTTGAAUATGTCUCUCAGCCTUUUC-3'
5'-((((..(.(((.((((..(((((.(((((((....)))))))...)))))...)))).)))).))))-3'
Motif MFE = -17.6; z-score = -2.45; ED = 7.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21956 to 22155 (motif highlighted in silver):

```
5'-GAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUU
GAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGA-3
5'-.....................(((((((((((((.....)))).))))).((((....))))...((((((.(.(((.((((..(((((.(((((((....)))))))...
)))))...)))).))))))))))).))))((((((........))))))....((((...(((((((.(.....).)))))))...))))-3'
MFE = -42.6; z-score = -1.62; ED = 36.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

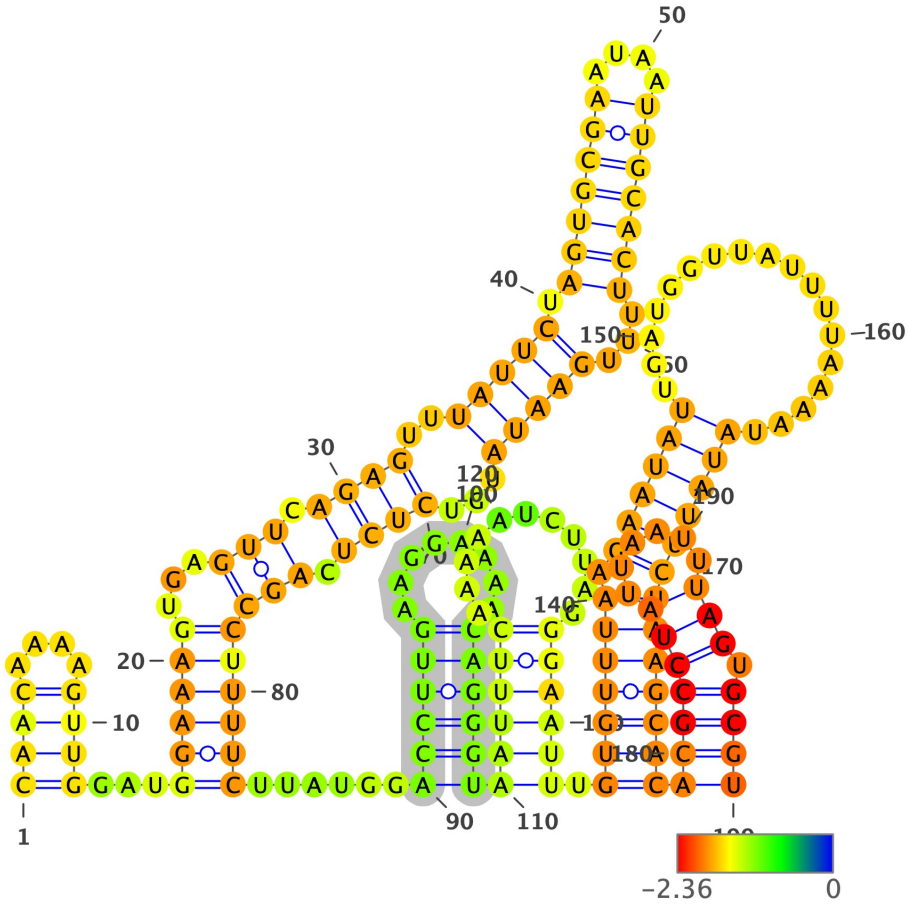
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 342 from nt 22095 to 22114 (nt 90 to 109)

```
5'-ACCTTGAAGGAAAACAGGGU-3'
5'-((((((........))))))-3'
Motif MFE = -5.4; z-score = -3.46; ED = 0.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22006 to 22204 (motif highlighted in silver):

```
5'-CAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAA
UUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGU-3
5'-((((....))))...((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))).....((((((........))))))((
((((...........)))))).(((((((.((((((.................))))))))))))))(((((((......))).))))-3'
MFE = -45.6; z-score = -1.95; ED = 25.05
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

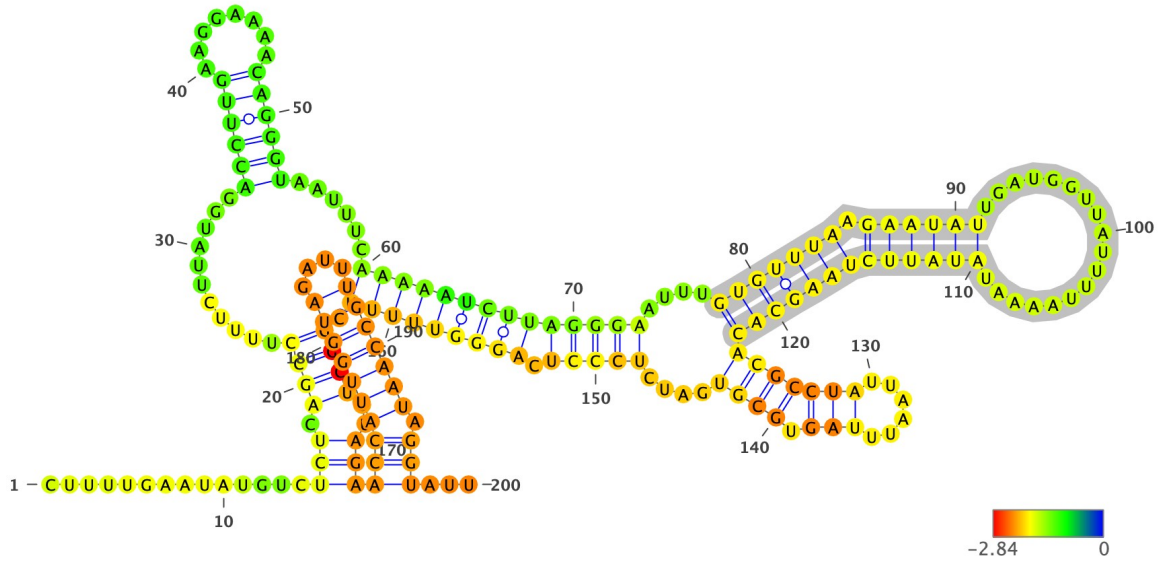
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 343 from nt 22139 to 22183 (nt 78 to 122)

```
5'-GTGTTTAAGAATATTGATGGTTATTTTAAAATAUAUUCUAAGCAC-3'
5'-(((((((.((((((.................)))))))))))))-3'
Motif MFE = -8.5; z-score = -2.4; ED = 5.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22062 to 22261 (motif highlighted in silver):

```
5'-CUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAU
AUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUU-3
5'-..............(((.((((...........((((((........))))))......((((((((((((((....(((((((.((((((.................))
))))))))))))(((((((......))).))))....))))).))))))))).))))..)))((((((((((....)))))))).)))...-3'
MFE = -50.3; z-score = -2.69; ED = 13.45
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

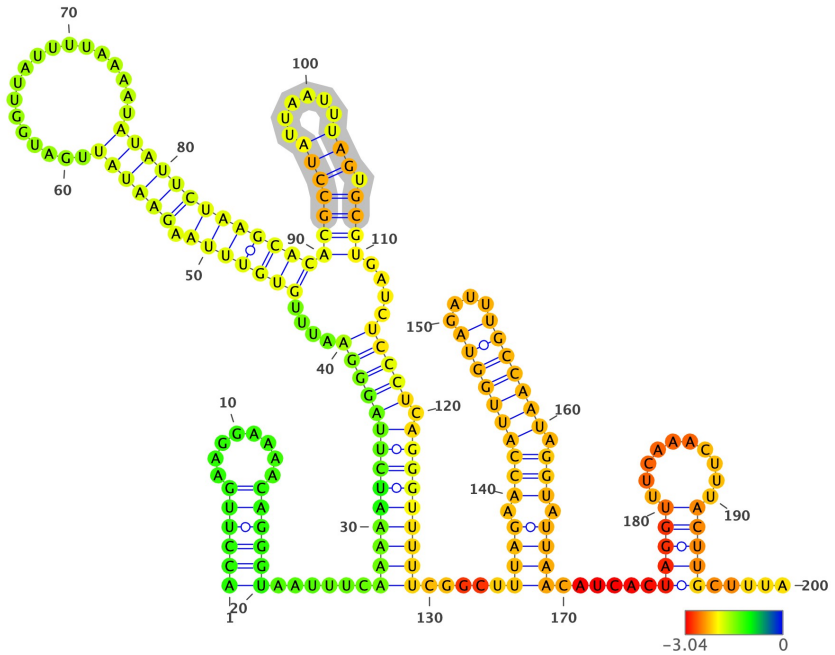
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 344 from nt 22186 to 22202 (nt 92 to 108)

```
5'-GCCTATTAATTTAGTGC-3'
5'-((((........)).))-3'
Motif MFE = -2.1; z-score = -2.1; ED = 0.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22095 to 22294 (motif highlighted in silver):

```
5'-ACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUG
AUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUA-3
5'-((((((........)))))).....(((((((((((((....(((((((.((((((.................)))))))))))))((((((.......)).)))).
...)))))).)))))))))).....((((.((((((((((....)))))))).))).)))).....(((((..........)))))).....-3'
MFE = -46.1; z-score = -2.24; ED = 22.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

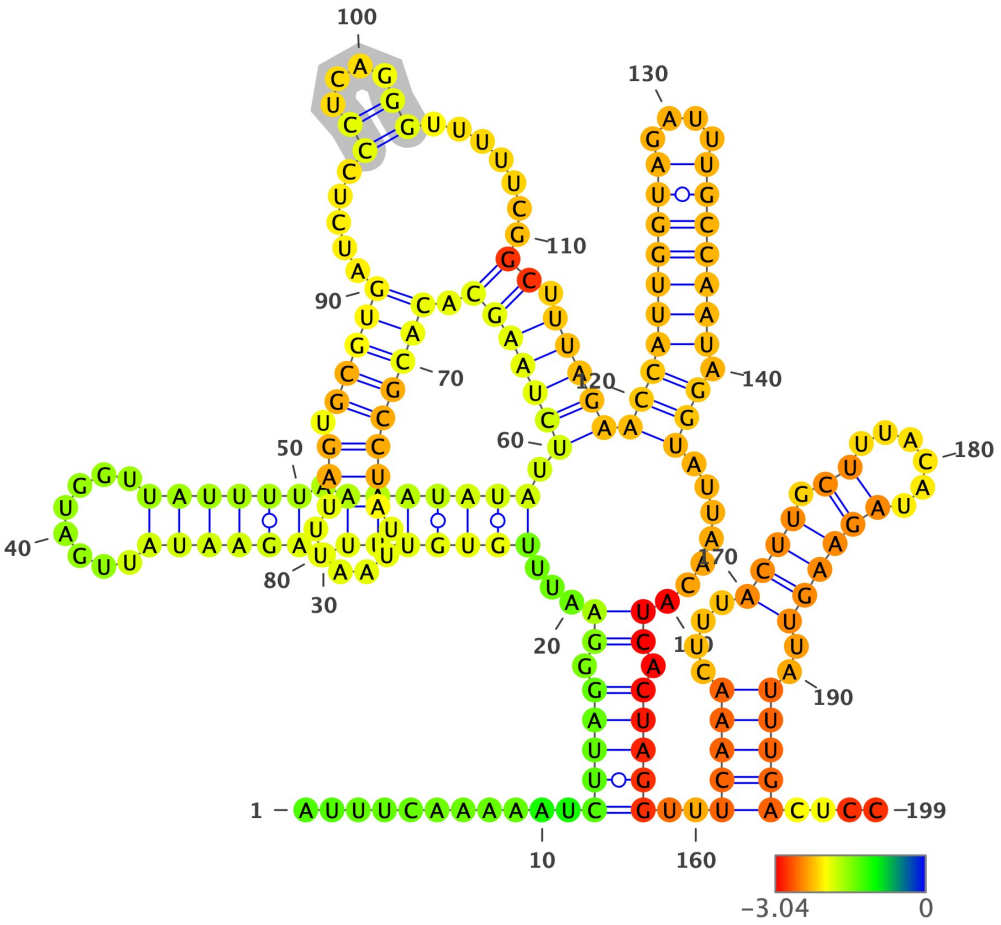
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 345 from nt 22211 to 22218 (nt 96 to 103)

```
5'-CCTCAGGG-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 1.35
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22116 to 22314 (motif highlighted in silver):

```
5'-AUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGG
CUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCC-3
5'-...........(((((.((...(((((((.((((((........)))))).)))))))).(((((((.((((((((......))).)))))).....((....)).......)
).)))))((((((((((....)))))))).))).......)).)))))..(((((....((((.((......))))))..)))))....-3'
MFE = -37.4; z-score = -2.57; ED = 49.42
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

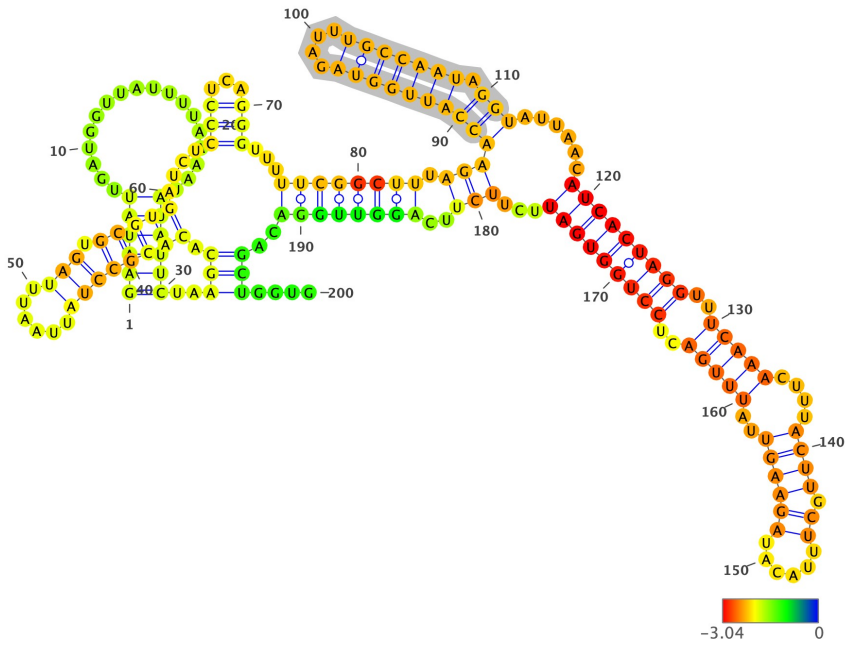
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 346 from nt 22235 to 22257 (nt 89 to 111)

```
5'-CCATTGGTAGATTTGCCAAUAGG-3'
5'-((((((((......))))))).))-3'
Motif MFE = -7.4; z-score = -2.99; ED = 1.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22147 to 22346 (motif highlighted in silver):

```
5'-GAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGG
UAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUG-3
5'-((((((.................))))))..(((.((((((((......))).)))))....(((...)))...((((((((.((((((((((((....)))))))).))
).....((((((((..(((((....((((.((......))))))..)))))..)))))))))...)))..)))))))))..)))....-3'
MFE = -50.3; z-score = -2.34; ED = 26.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

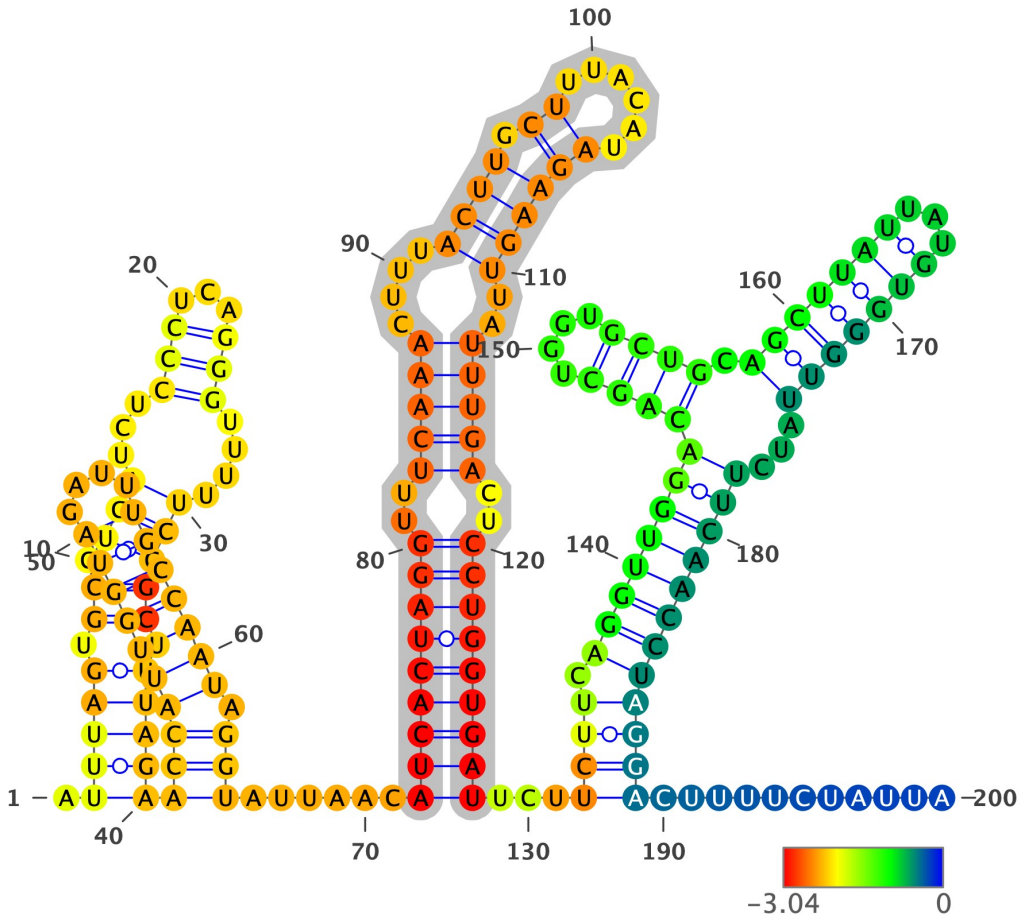
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 347 from nt 22265 to 22321 (nt 72 to 128)

```
5'-ATCACTAGGTTTCAAACTTTACTTGCTTTACATAGAAGUTAUUUGACTCCUGGUGAU-3'
5'-(((((((((..(((((....((((.((......)))))))..)))))..)))))))))-3'
Motif MFE = -18.6; z-score = -4.43; ED = 4.51
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22194 to 22393 (motif highlighted in silver):

```
5'-AUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUU
AUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUGCUGCAGCUUAUUAUGUGGGUUAUCUUCAACCUAGGACUUUUCUAUUA-3
5'-.(((((.((.(((...(((...)))....)))))).)))))((((((((((....)))))))).))).....(((((((((..(((((....((((.((......)))))).
.)))))..)))))))))...((((.((((((((((((....)))).(((((((...)))))))...)))))))))))).....-3'
MFE = -54.3; z-score = -3.2; ED = 21.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

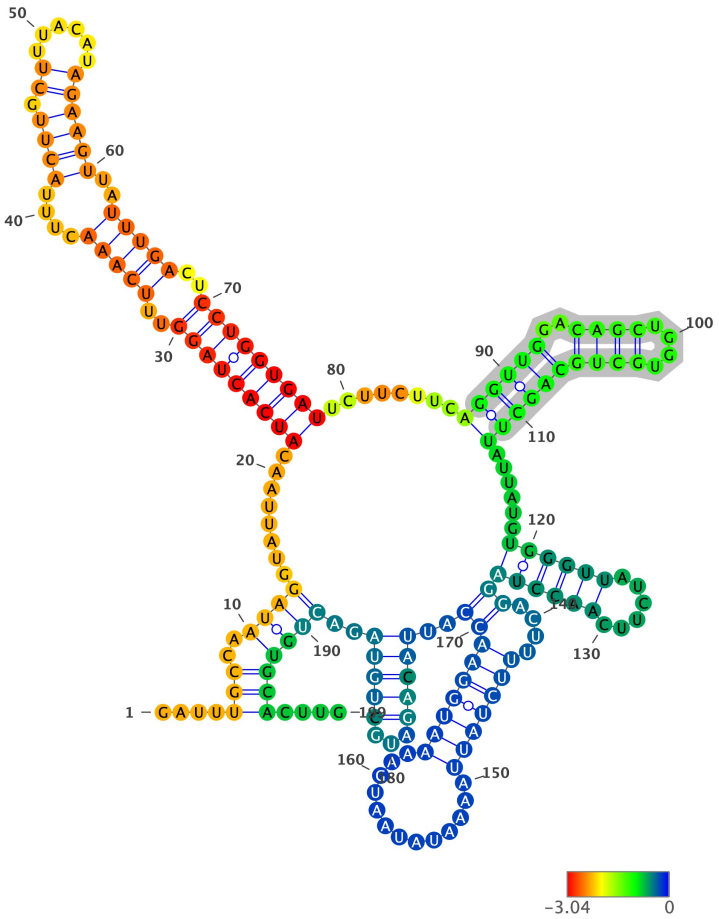
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 348 from nt 22331 to 22354 (nt 88 to 111)

```
5'-GGTTGGACAGCTGGTGCUGCAGCU-3'
5'-(((((..((((....)))))))))-3'
Motif MFE = -8.1; z-score = -1.58; ED = 2.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22244 to 22442 (motif highlighted in silver):

```
5'-GAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUGCUGCAGCU
UAUUAUGUGGGUUAUCUUCAACCUAGGACUUUUCUAUUAAAAUAUAAUGAAAAUGGAACCAUUACAGAUGCUGUAGACUGUGCACUUG-3
5'-....(((..((((.........(((((((((..(((((....((((.((......))))))..)))))..)))))))))........((((((..((((....)))))))))
)......((((((......))))))((....(((((((.............)))))))))..(((((...)))))..)))))))....-3'
MFE = -43.6; z-score = -1.38; ED = 28.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

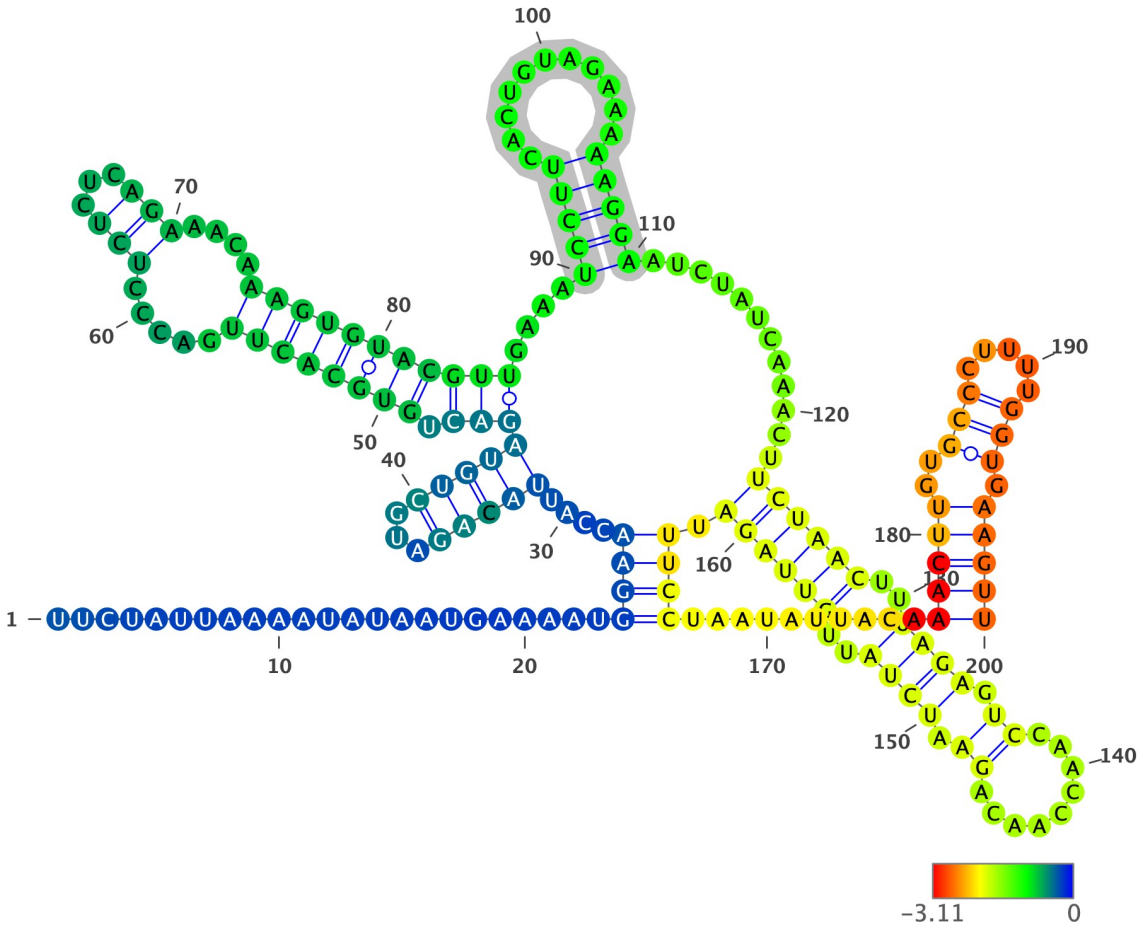
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 349 from nt 22475 to 22495 (nt 90 to 110)

```
5'-TCCTTCACTGTAGAAAAAGGA-3'
5'-(((((..........)))))-3'
Motif MFE = -1.8; z-score = -0.62; ED = 2.94
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22386 to 22585 (motif highlighted in silver):

```
5'-UUCUAUUAAAAUAUAAUGAAAAUGGAACCAUUACAGAUGCUGUAGACUGUGCACUUGACCCUCUCUCAGAAACAAAGUGUACGUUGAAAUCCUUCACUGUAGAAAAAGGAA
UCUAUCAAACUUCUAACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUU-3
5'-......................((((....(((((...)))))))((.(((((((((.....(((...))).....)))))))))))....(((((...........))))).
...........((((((..((((.(((........)).)))))..)))))).))))..........(((((..(((.....))).)))))-3'
MFE = -33.1; z-score = -1.38; ED = 29.84
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

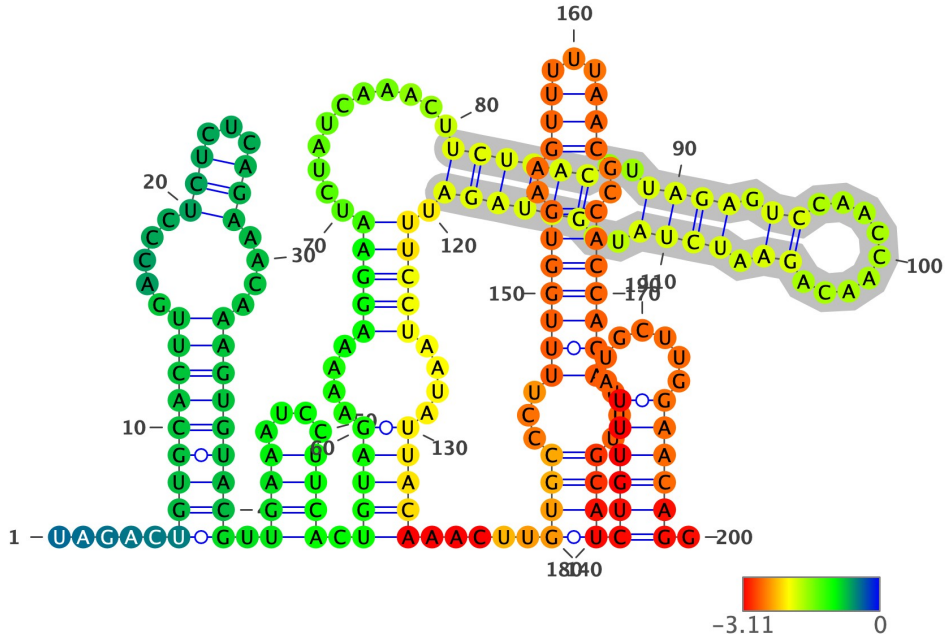
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 350 from nt 22508 to 22546 (nt 81 to 119)

```
5'-TCTAACTTTAGAGTCCAACCAACAGAAUCUATTGUUAGA-3'
5'-((((((..(((((.((.........)).)))))..)))))))-3'
Motif MFE = -9.2; z-score = -3.44; ED = 1.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22428 to 22627 (motif highlighted in silver):

```
5'-UAGACUGUGCACUUGACCCUCUCUCAGAAACAAAGUGUACGUUGAAAUCCUUCACUGUAGAAAAAGGAAUCUAUCAAACUUCUAACUUUAGAGUCCAACCAACAGAAUCUA
UUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGG-3
5'-.....(((((((((.....(((...)))....)))))))))).((((....)))).(((((....(((((..........((((((..((((.(((.........)).))))
..)))))).)))))....)))))).....((((...(((((((..(((...)))).)))))))...))))((((((.......)))))).-3'
MFE = -42.3; z-score = -1.82; ED = 33.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

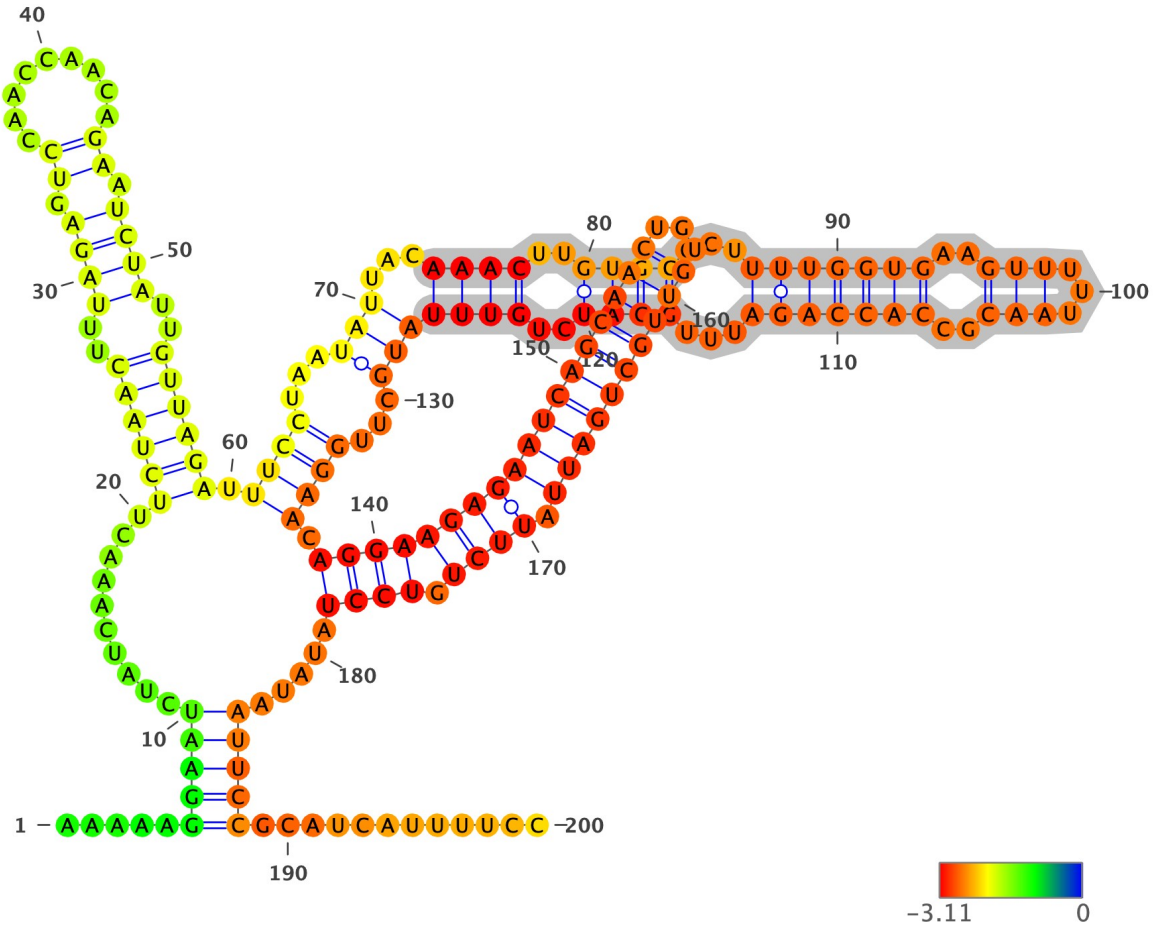
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 351 from nt 22561 to 22613 (nt 74 to 126)

```
5'-AAACTTGTGCCCTTTTGGTGAAGTTTTTAACGCCACCAGATTTGCATCTGUUU-3'
5'-((((.........(((((((..(((...)))..)))))))).........))))-3'
Motif MFE = -15.2; z-score = -3.48; ED = 1.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22488 to 22687 (motif highlighted in silver):

```
5'-AAAAAGGAAUCUAUCAAACUUCUAACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCA
GAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCC-3
5'-.....(((((..........((((((..((((.((.........)).))))..)))))).((((...(((...((((..((((...(((((((..(((...)))..)))))
))...))))..)))))))...)))).((((((((((((((((((...)))))))))).)))).))))).....)))))............-3'
MFE = -51.5; z-score = -3.99; ED = 20.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

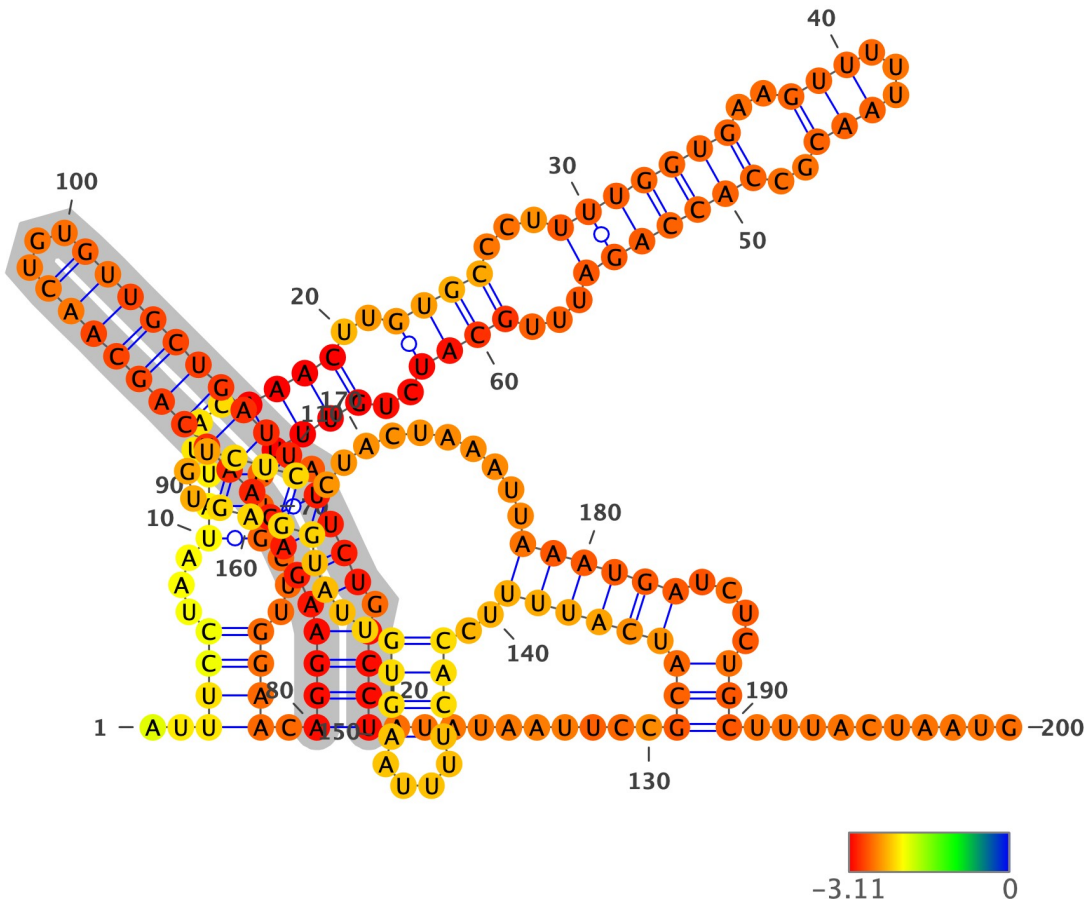
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 352 from nt 22625 to 22665 (nt 80 to 120)

```
5'-AGGAAGAGAATCAGCAACTGTGTUGCUGAUUAUUCUGUCCU-3'
5'-(((((((((((((((.......)))))))).)))).))))-3'
Motif MFE = -18.8; z-score = -4.14; ED = 1.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22546 to 22745 (motif highlighted in silver):

```
5'-AUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUA
UUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUG-3
5'-..((((...(((...((((..((((...(((((((..(((...)))..)))))))...))))..)))))))...)))).((((((((((((((((...)))))))))).
)))).))))..........(((((((((..((((....))))....((((...))))........))))))....)))..........-3'
MFE = -46.6; z-score = -2.48; ED = 23.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

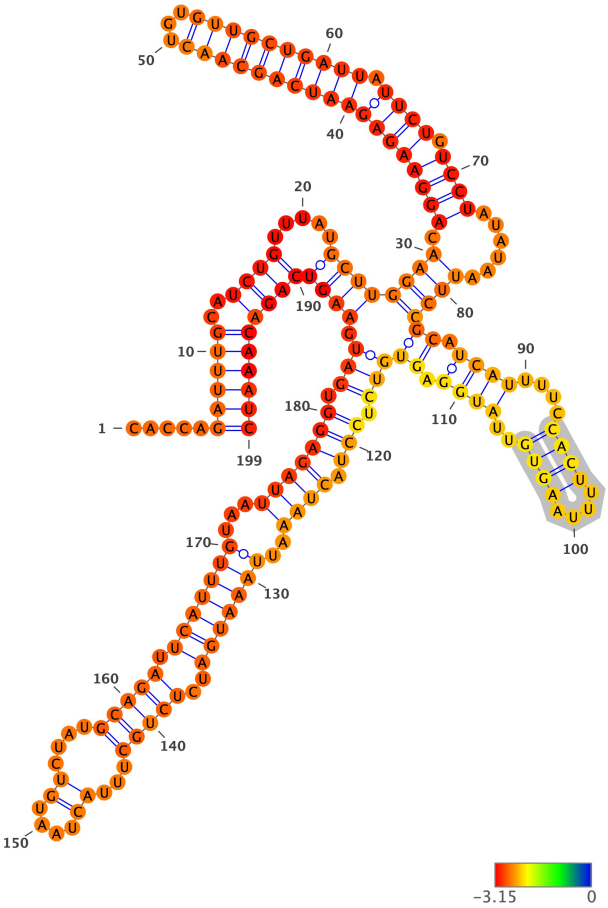
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 353 from nt 22687 to 22698 (nt 94 to 105)

```
5'-CACTTTTAAGUG-3'
5'-(((......)))-3'
Motif MFE = -1.0; z-score = -3.58; ED = 1.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22594 to 22792 (motif highlighted in silver):

```
5'-CACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGG
AGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUC-3
5'-.....((((((..((((.....((((((((.((((((((((((((((((...)))))))))).)))).))))......))))((.((((....((((....))))..))))
.))(((.(((.((((..(((((((..(((((...((....))....))))).)))))))...)))))))).))).))))))))))))))-3'
MFE = -52.5; z-score = -4.03; ED = 30.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

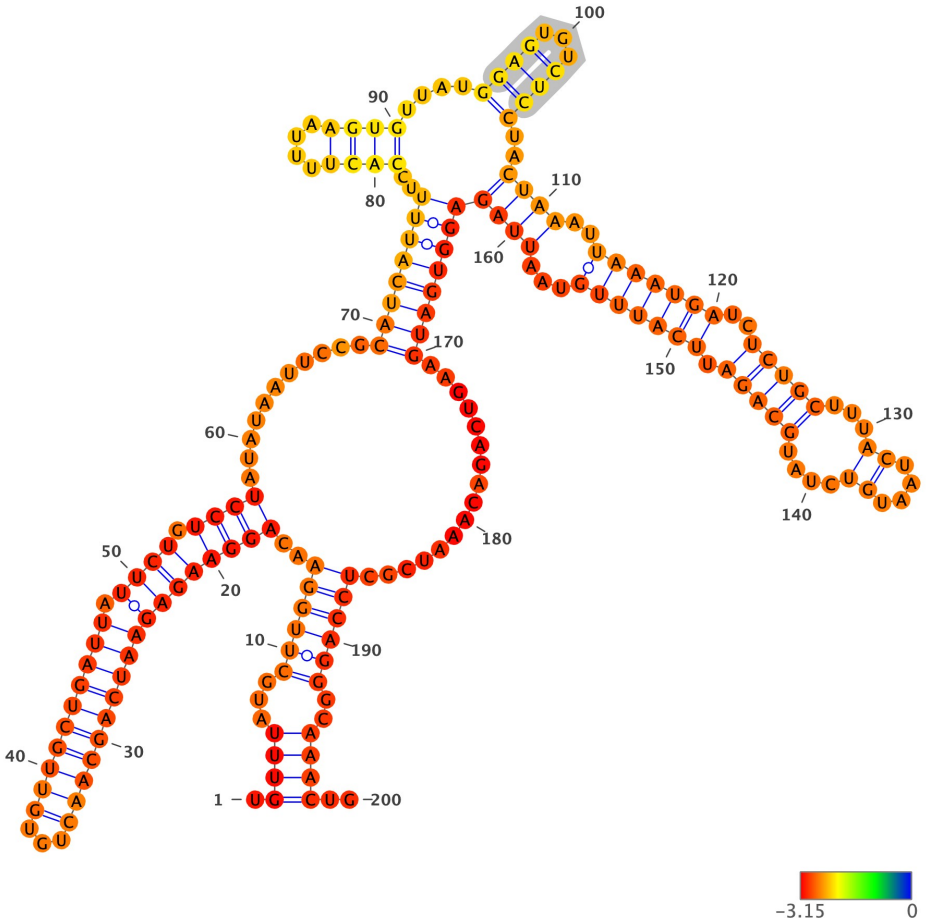
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 354 from nt 22704 to 22712 (nt 96 to 104)

```
5'-GAGTGTCUC-3'
5'-(((...)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22609 to 22808 (motif highlighted in silver):

```
5'-UGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAA
AUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUG-3
5'-.((((...((((((..((((((((((((((((((...)))))))))).)))).))))...........((((((((..((((....))))....((((...))))..((((
..(((((((..(((((...((....))....)))))).)))))))...))))))))))))...............))))))..))))..-3'
MFE = -51.2; z-score = -3.19; ED = 31.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

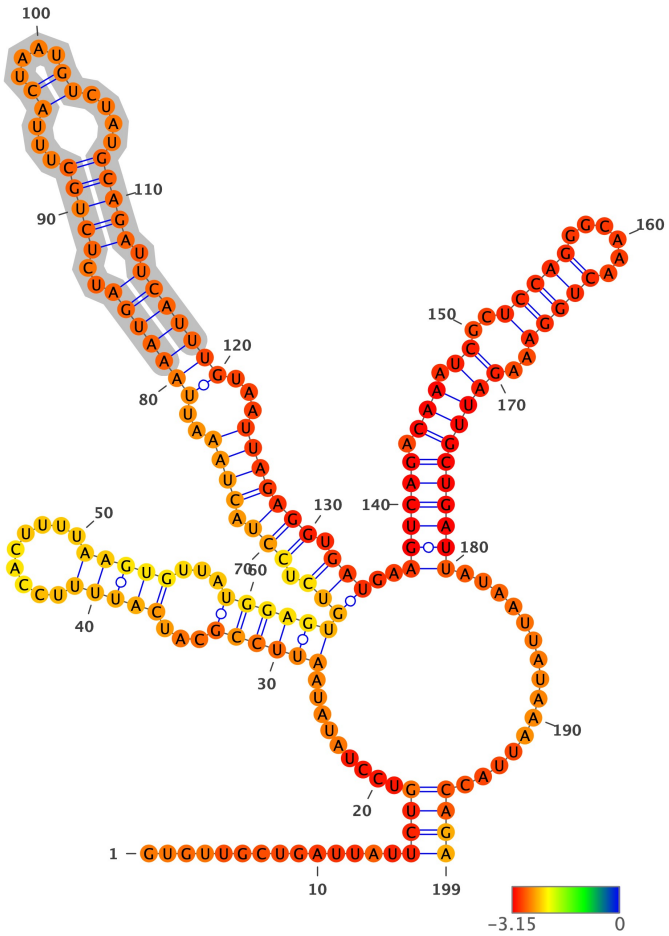
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 355 from nt 22724 to 22761 (nt 81 to 118)

```
5'-AATGATCTCTGCTTTACTAATGTCTATGCAGATUCAUU-3'
5'-(((((..((.((...............)).)).)))))-3'
Motif MFE = -8.9; z-score = -3.77; ED = 2.08
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22644 to 22842 (motif highlighted in silver):

```
5'-GUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAG
AUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGA-3
5'-..............((((.........((((((...(((((.........)))))...))))))(((.(((.((((..(((((((..(((((...((....)).....))))
).)))))))...)))))))).)))..((((((.(((.((..(((((......)))))..))))))))))).................))))-3'
MFE = -46.3; z-score = -2.28; ED = 33.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

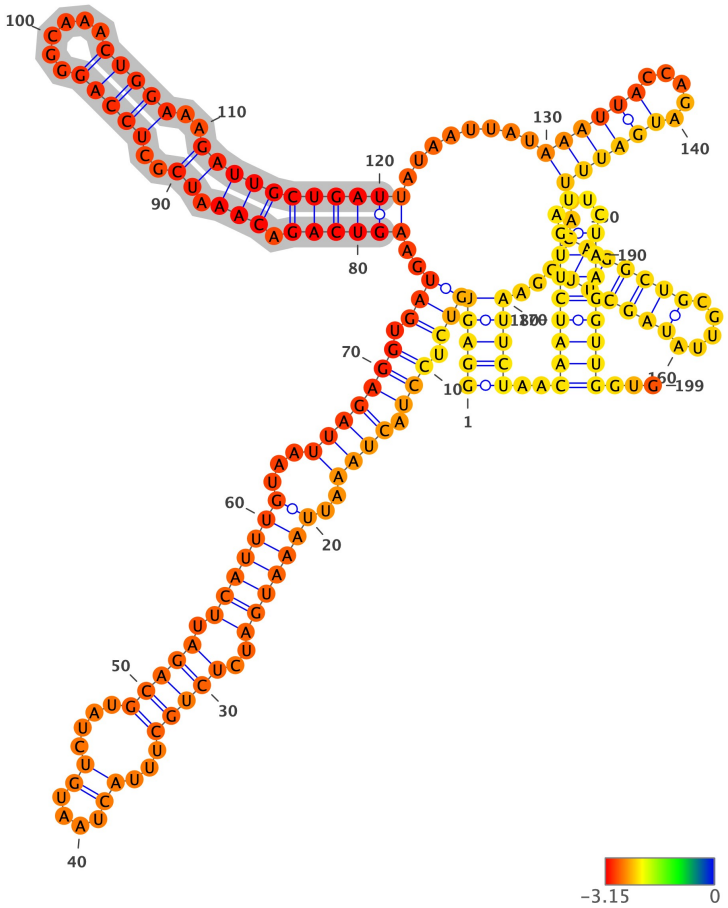
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 356 from nt 22781 to 22822 (nt 79 to 120)

```
5'-GTCAGACAAATCGCTCCAGGGCAAACUGGAAAGAUUGCUGAU-3'
5'-(((((.(((.((..(((((.....)))))..)))))))))-3'
Motif MFE = -15.9; z-score = -3.67; ED = 2.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22703 to 22901 (motif highlighted in silver):

```
5'-GGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAG
AUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUG-3
5'-(((((((((.(((.(((((..(((((((..((((((...((....))....)))))).)))))))...)))))))).)))..((((((.(((.((..(((((.....)))))..)
)))))))))).......((((((.....)))))).((((((.....)))))))..)))))..(((((((((....)))))))))...-3'
MFE = -53.4; z-score = -3.51; ED = 20.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

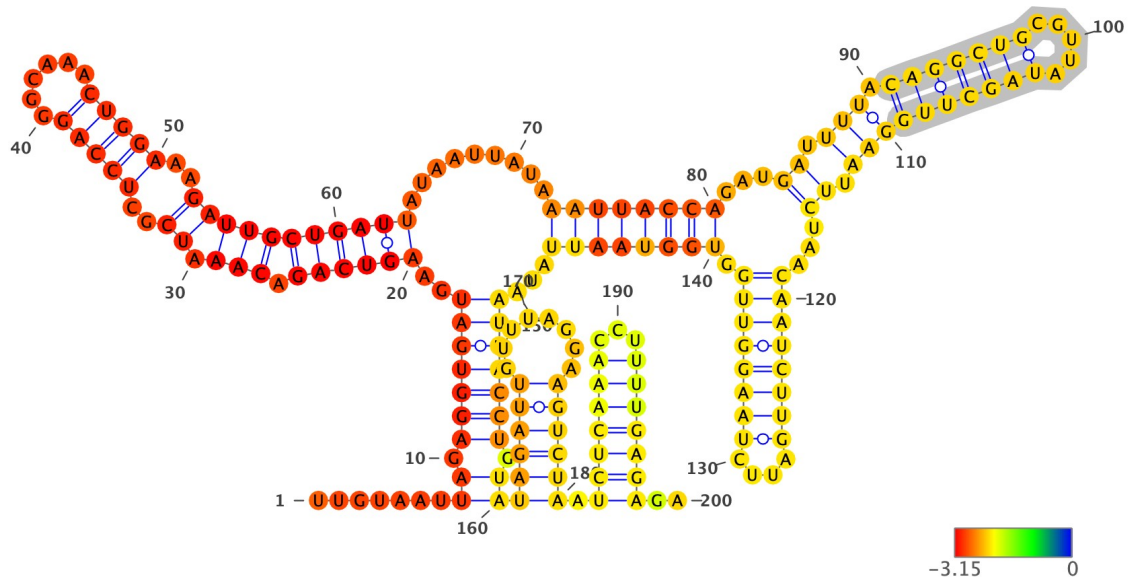
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 357 from nt 22851 to 22869 (nt 91 to 109)

```
5'-CAGGCTGCGTTATAGCUUG-3'
5'-(((((.........)))))-3'
Motif MFE = -5.7; z-score = -2.28; ED = 0.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22761 to 22960 (motif highlighted in silver):

```
5'-UUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGA
AUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGA-3
5'-.......((.(((((((..((((((.(((.((..(((((.....)))))..))))))))))).........((((((((...((.(((.(((((((.....)))))))))
).))...((((((((....)))))))).))))))))...))))))).))((((((.........)))))).(((((((...)))))))..-3'
MFE = -54.5; z-score = -3.63; ED = 17.05
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

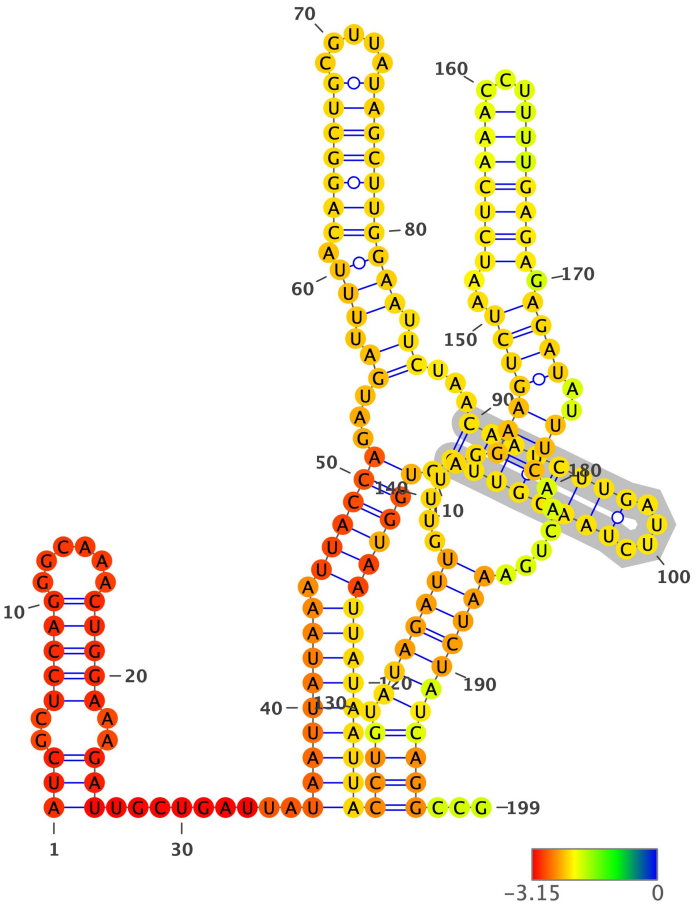
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 358 from nt 22879 to 22898 (nt 90 to 109)

```
5'-CAATCTTGATTCTAAGGUUG-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.8; z-score = -3.98; ED = 0.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22790 to 22988 (motif highlighted in silver):

```
5'-AUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGU
GGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCG-3
5'-(((..(((((......)))))..)))..........(((((((((.((((((...((.(((.(((((((.....)))))))))).))...((((((((....)))))))).)
))))))))))))))((((.(((((((......(((((((..(((((((...)))))))).))))..)))......)))))))))))...-3'
MFE = -55.5; z-score = -3.29; ED = 20.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

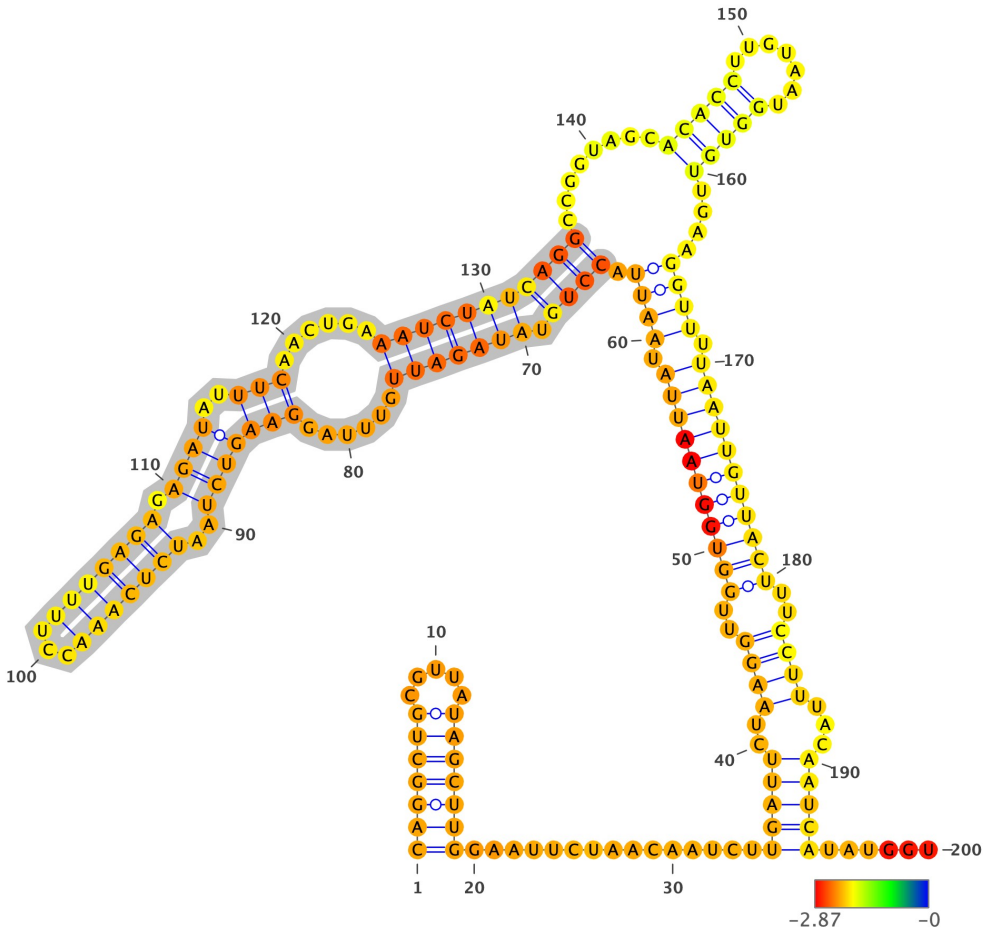
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 359 from nt 22915 to 22985 (nt 65 to 135)

```
5'-CCTGTATAGATTGTTTAGGAAGTCTAATCTCAAACCTTTTGAGAGAGAUATUUCAACTGAAAUCUATCAGG-3'
5'-(((....(((((......(((((((..((((.........)))).))))..)))......)))))...)))-3'
Motif MFE = -21.1; z-score = -3.6; ED = 8.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22851 to 23050 (motif highlighted in silver):

```
5'-CAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAG
AUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGU-3
5'-(((((((.....)))))))...............(((((..((((..(((((((((((.((((.((((.(((((((......(((((((..(((((((...)))))))).))
))..)))......))))))))))).........(((((.......)))))....)))).))))))))))..))))...)))))......-3'
MFE = -48.4; z-score = -3.39; ED = 32.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

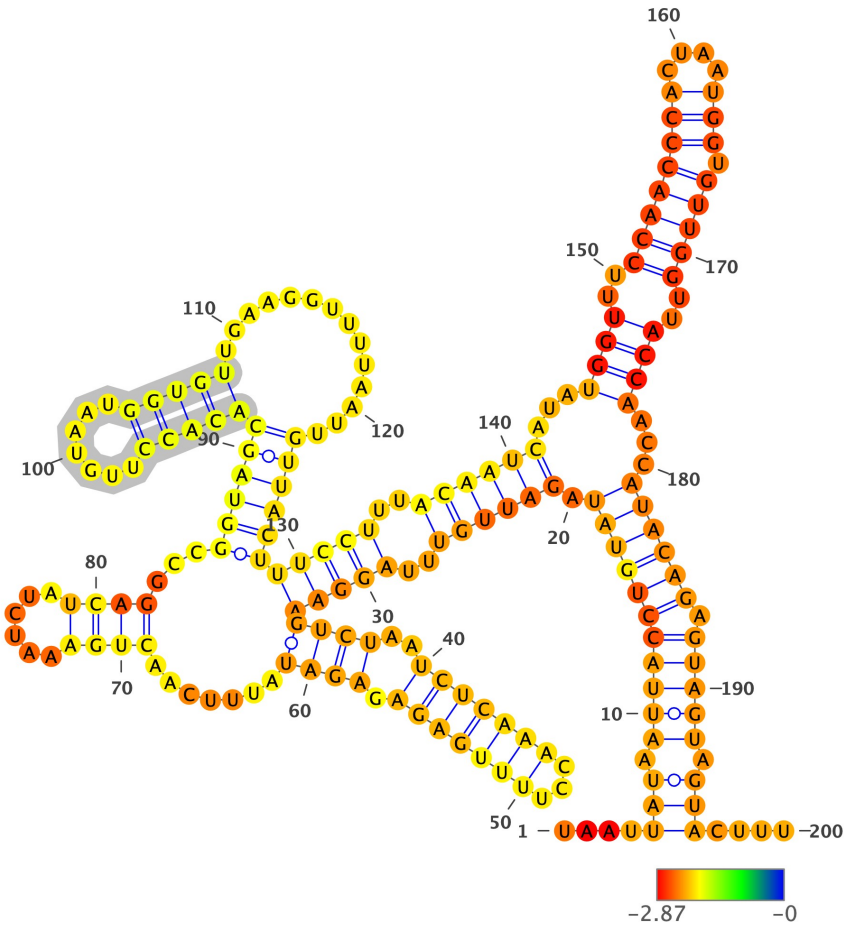
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 360 from nt 22994 to 23010 (nt 92 to 108)

```
5'-ACACCTTGTAATGGUGU-3'
5'-(((((.......)))))-3'
Motif MFE = -5.4; z-score = -4.62; ED = 0.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22903 to 23102 (motif highlighted in silver):

```
5'-UAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGA
AGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUU-3
5'-....(((.(((((((((((.((((((..((((((((((..(((((((...)))))))).))))).......((((......))))...(((((((((((.......)))))...
...........))))))))))))..))))))...((((..((((((((....))).)))))..))))...))))))).)))))).)))....-3'
MFE = -57.3; z-score = -5.04; ED = 32.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

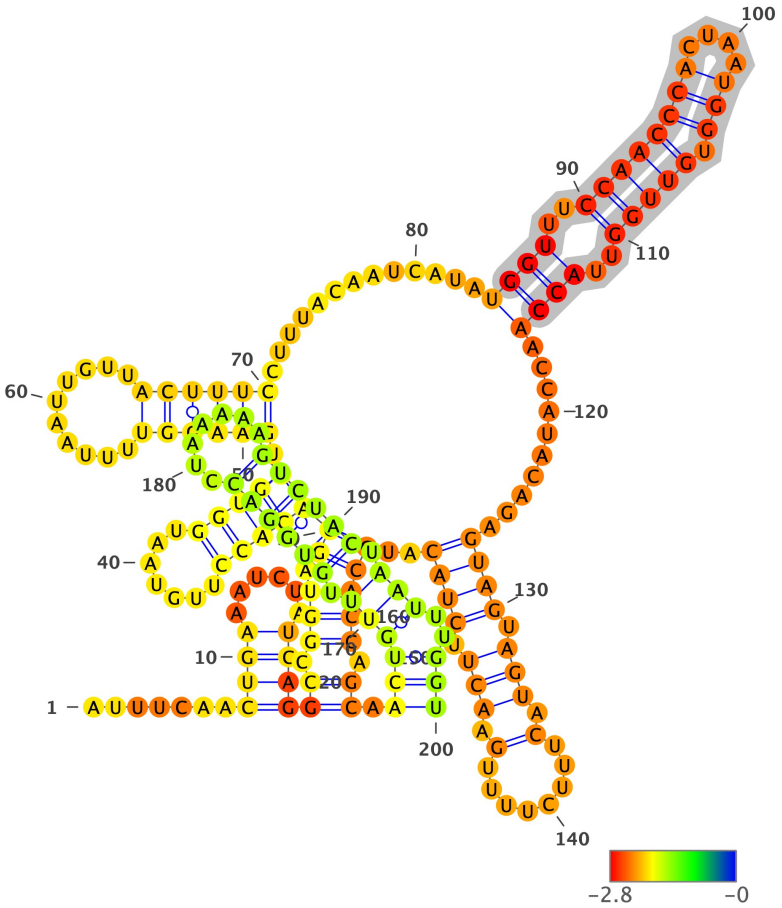
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 361 from nt 23048 to 23078 (nt 85 to 115)

```
5'-GGTTTCCAACCCACTAATGGTGUUGGTTACC-3'
5'-(((..(((((((......)).)))))..)))-3'
Motif MFE = -13.1; z-score = -4.2; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22964 to 23163 (motif highlighted in silver):

```
5'-AUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGU
UACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGU-3
5'-.......((((......))))((.(((.(((((((.......))))).((((((..........))))))..............((((..((((((((....))).)))))).
.))))..........((((.(((.(........).))).))))..)))))).)).((((((.((((((.......)))))).)))..)))-3'
MFE = -48.1; z-score = -2.59; ED = 55.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

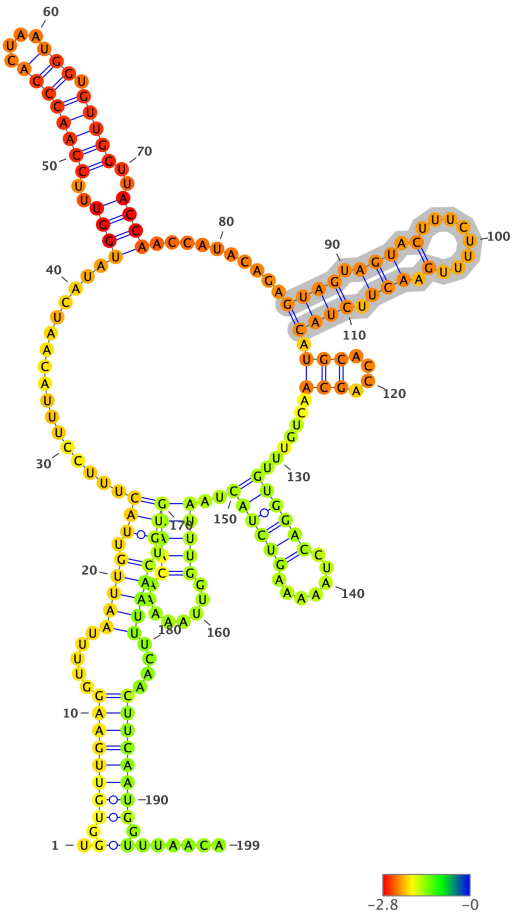
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 362 from nt 23090 to 23117 (nt 86 to 113)

```
5'-GTAGTAGTACTTTCTTTTGAACUTCUAC-3'
5'-((((.(((.(........).))).))))-3'
Motif MFE = -4.1; z-score = -1.91; ED = 3.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23005 to 23203 (motif highlighted in silver):

```
5'-UGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCU
ACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACA-3
5'-.(.((((((((.....(((((.(((.................((((..((((((((....))).)))))..))))..........((((.(((.(........).))).))
)).(((....)))......((((((.......))))))..(((((........))))))))).)))))....)))))))).)......-3'
MFE = -43.6; z-score = -2.51; ED = 29.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

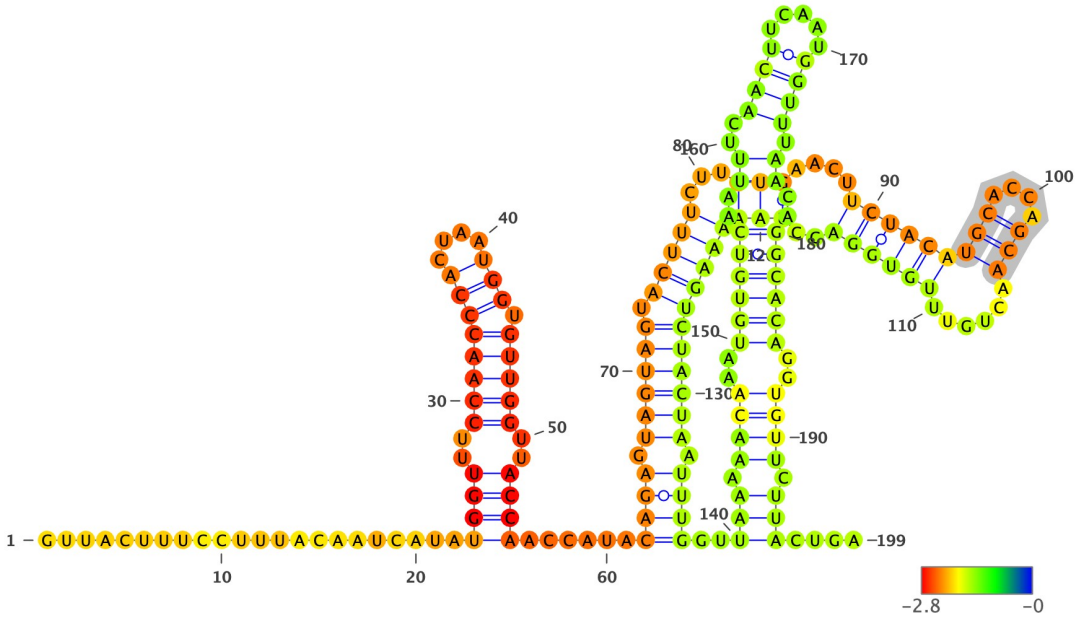
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 363 from nt 23119 to 23128 (nt 95 to 104)

```
5'-TGCACCAGCA-3'
5'-(((....)))-3'
Motif MFE = -0.9; z-score = -6.33; ED = 0.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23025 to 23223 (motif highlighted in silver):

```
5'-GUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUU
GUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGA-3
5'-.......................((((..((((((((....))).)))))..))))......((((.((((((.(((((...(((....(((((((((....)))......)
)))))..))))))))))))))).))))..(((.((((..((((((..((..((((.....)))).))..))))))..)))).)))....-3'
MFE = -43.5; z-score = -2.79; ED = 35.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

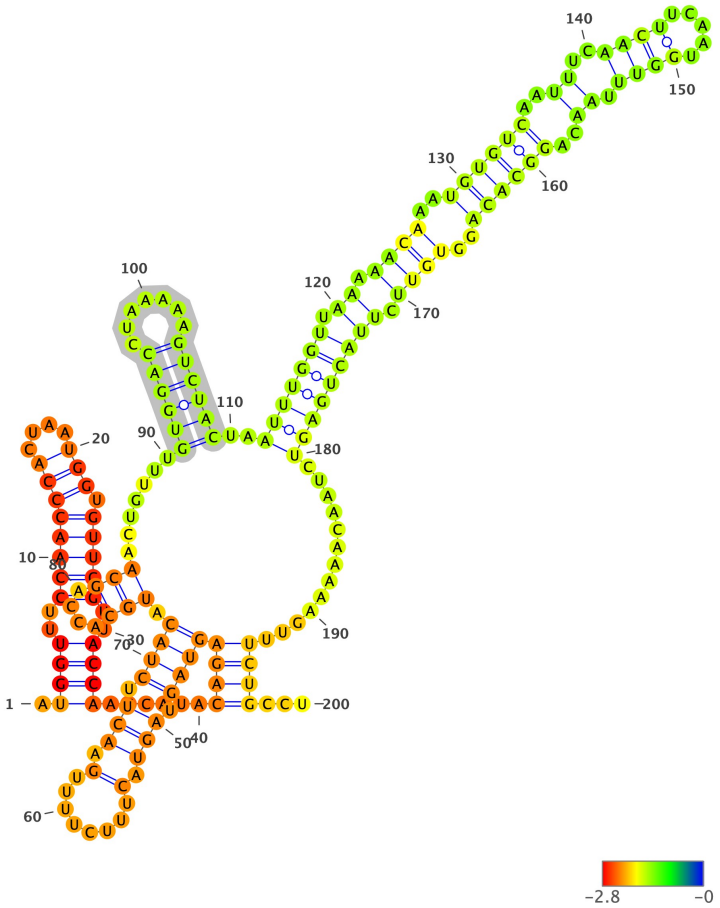
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 364 from nt 23136 to 23154 (nt 91 to 109)

```
5'-GTGGACCTAAAAAGUCUAC-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -2.99; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23046 to 23245 (motif highlighted in silver):

```
5'-AUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUA
AUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCU-3
5'-.((((..((((((((....))).)))))..))))......((((((((.(((.(........).))).)))).(((....)))).......((((((.......))))))..
(((((((.((.((((..((((((..((..((((.....)))).))..))))))..)))).))))))))).............))))...-3'
MFE = -47.5; z-score = -3.32; ED = 25.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

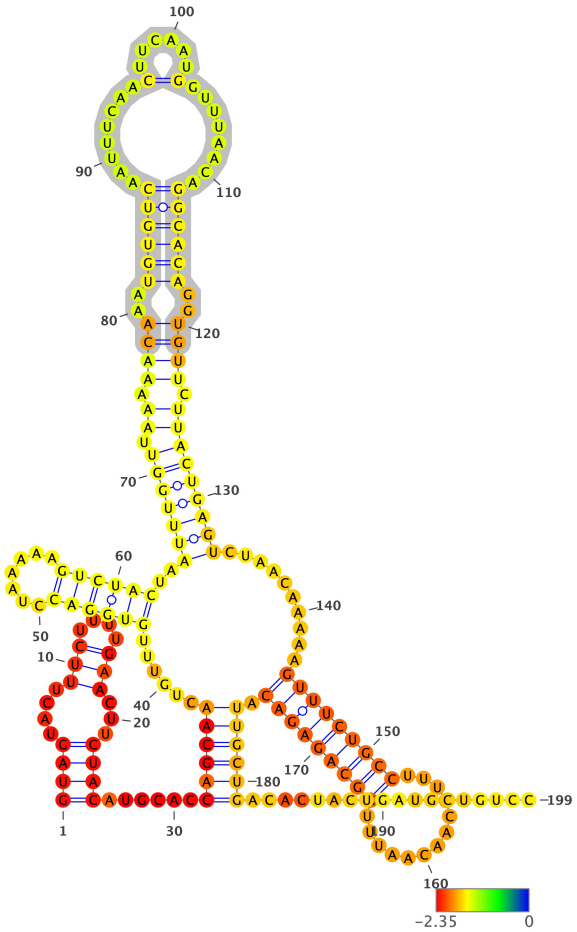
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 365 from nt 23170 to 23213 (nt 78 to 121)

```
5'-CAAATGTGTCAATTTCAACTTCAATGGTTTAACAGGCACAGGUG-3'
5'-((..((((((........(......)........))))))..))-3'
Motif MFE = -8.1; z-score = -1.4; ED = 3.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23093 to 23291 (motif highlighted in silver):

```
5'-GUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACA
GGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCC-3
5'-((((....(((....)))...)))).....((((((......((((((.......))))))..(((((((.((.((((..((((((........(......).......
))))))..)))).))))))))).........(((((((((.............)))))))))).))))))..................-3'
MFE = -44.4; z-score = -2.37; ED = 25.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

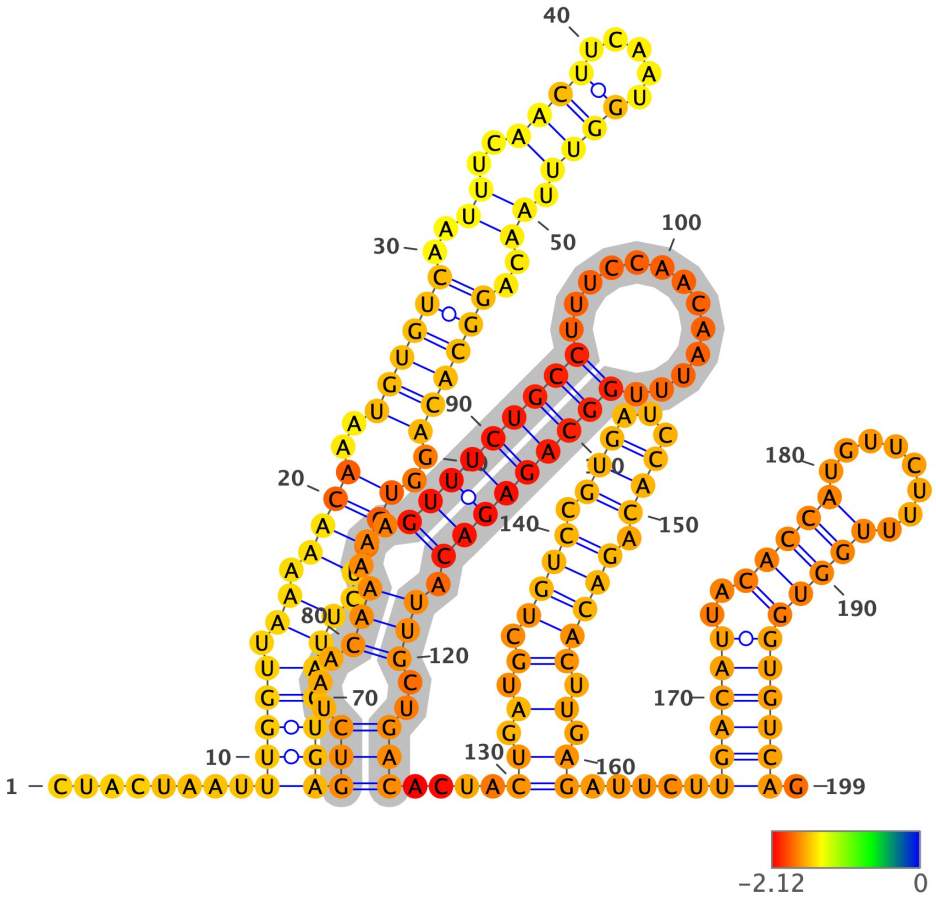
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 366 from nt 23224 to 23275 (nt 74 to 125)

```
5'-GTCTAACAAAAAGTTTCTGCCTTTCCAACAATTTGGCAGAGACAUUGCTGAC-3'
5'-(((...(((...(((((((((.............)))))))))..)))..)))-3'
Motif MFE = -15.0; z-score = -3.29; ED = 3.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23151 to 23349 (motif highlighted in silver):

```
5'-CUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCA
GAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAG-3
5'-........(((((.((.(((((..(((((((..((..((((.....)))).))..))))))..)))).)))))))(((...(((...(((((((((.............))))
)))))).)))..)))....((.(.(.(((((.(((...))).)))))).).)).....((((((..(((((........)))))))))))).-3'
MFE = -49.4; z-score = -2.74; ED = 38.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

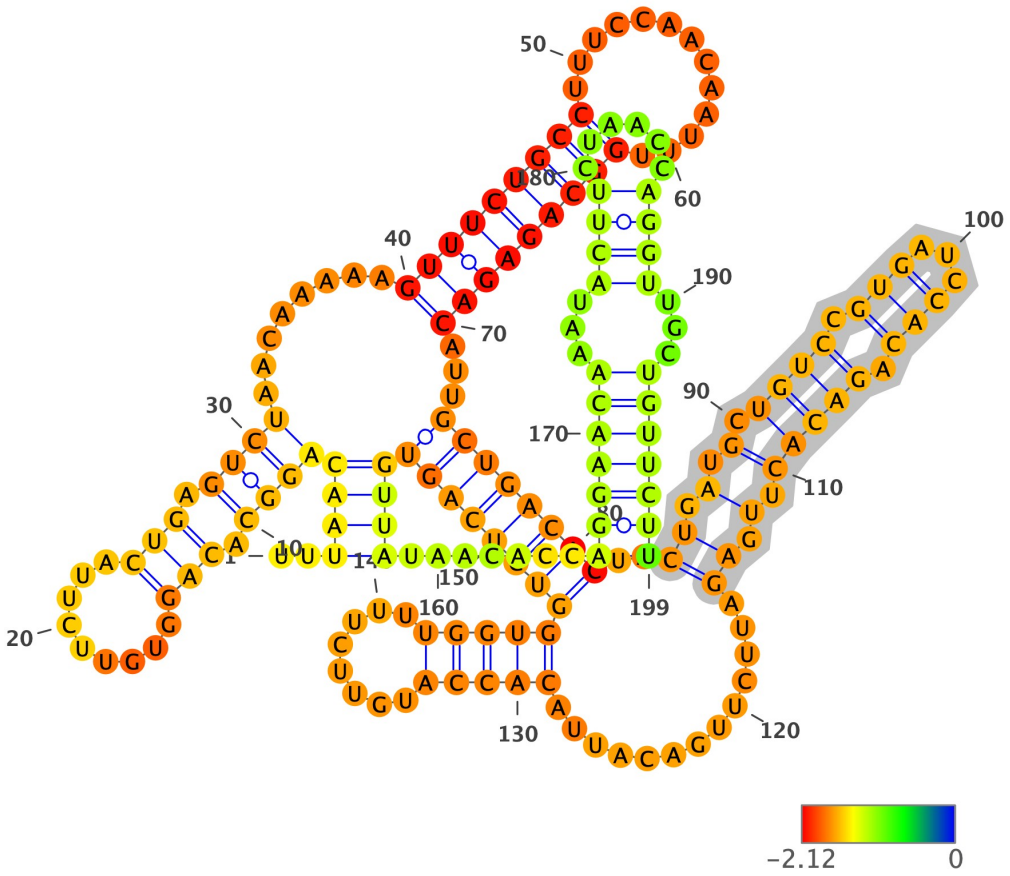
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 367 from nt 23280 to 23311 (nt 84 to 115)

```
5'-CTGATGCTGTCCGTGATCCACAGACACTTGAG-3'
5'-((...(.(((((.(((...))).)))))...))-3'
Motif MFE = -5.5; z-score = -0.18; ED = 2.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23197 to 23395 (motif highlighted in silver):

```
5'-UUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACU
UGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUU-3
5'-..(((((((((.(((.........))).)))).......(((((((((.............)))))))))...(((((((((..((.(.(.(((((.(((...))).)))))).
).)).............(((((........)))))))))))))))).......(((((((...((((......))))...)))))))-3'
MFE = -51.3; z-score = -2.22; ED = 35.16
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

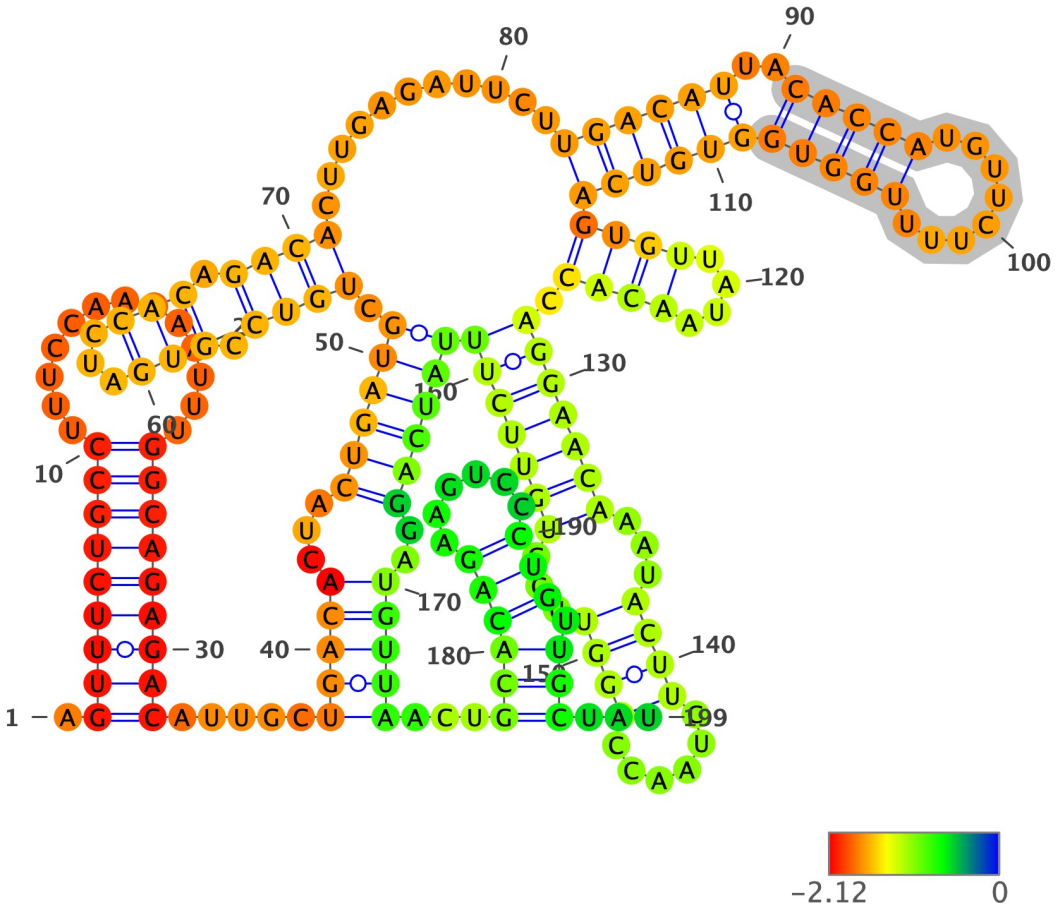
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 368 from nt 23325 to 23342 (nt 91 to 108)

```
5'-CACCATGTTCTTTUGGUG-3'
5'-(((((........)))))-3'
Motif MFE = -5.4; z-score = -5.2; ED = 0.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23235 to 23433 (motif highlighted in silver):

```
5'-AGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUG
UCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAU-3
5'-.(((((((((.............)))))))))).....(((((...((((((.((((.(((...))).)))).........((((((..(((((........)))))))
)))((((....)))).(((((((...((((......))))...)))))))))))))..)))))...((((((......))).)))...-3'
MFE = -56.1; z-score = -2.99; ED = 28.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

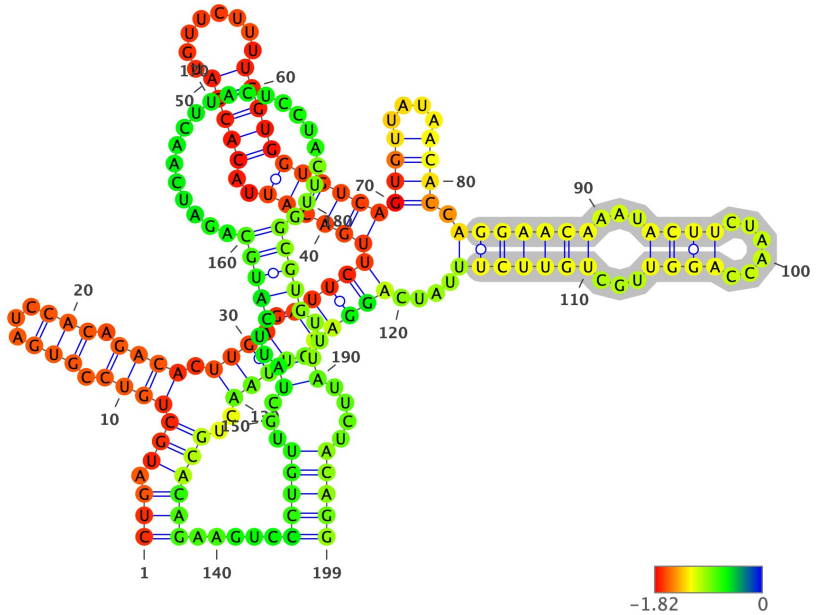
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 369 from nt 23363 to 23394 (nt 84 to 115)

```
5'-GGAACAAATACTTCTAACCAGGUTGCUGUUCU-3'
5'-((((((...((((......))))...))))))-3'
Motif MFE = -6.0; z-score = -1.62; ED = 1.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23280 to 23478 (motif highlighted in silver):

```
5'-CUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUG
UUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGG-3
5'-(((.(((((((.(((...))).)))).((((.(((((((((((..(((((........)))))))))))((((....)))).(((((((...((((......))))...))
)))))....))))).))))..))))))).....(((((...((..(((((.....................)))))..))....)))))-3'
MFE = -45.9; z-score = -0.99; ED = 45.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

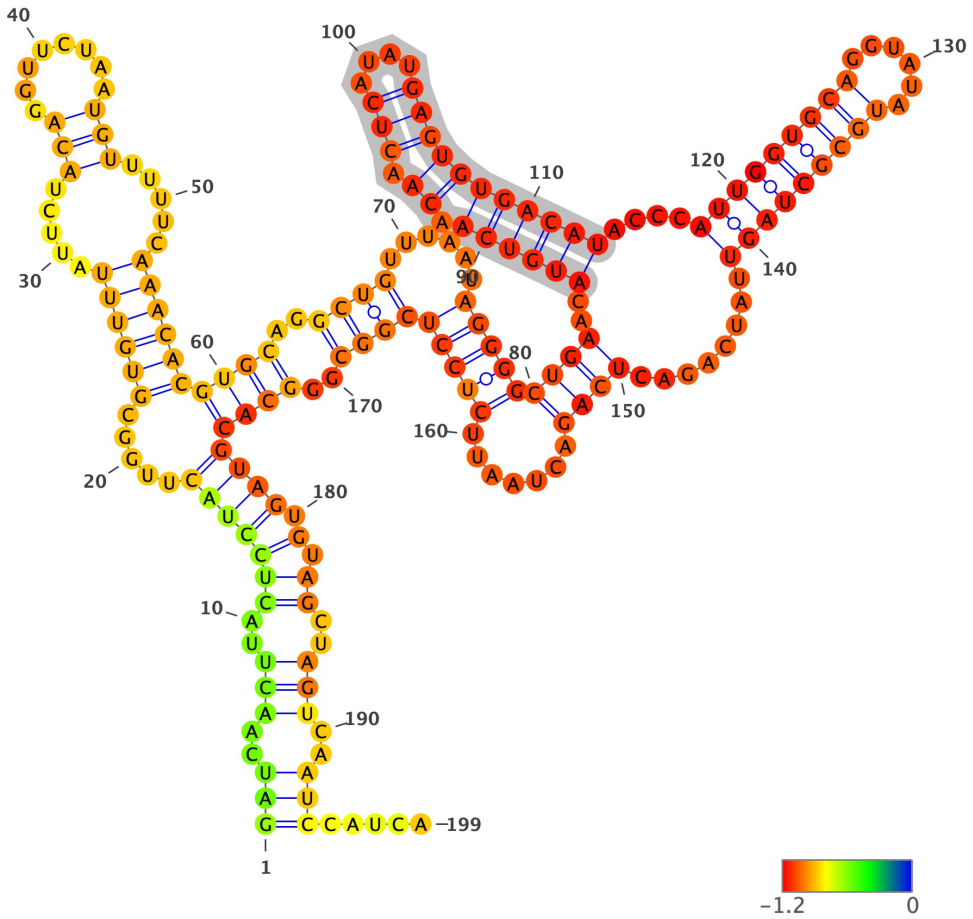
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 370 from nt 23526 to 23553 (nt 86 to 113)

```
5'-ATGTCAACAACTCATATGAGUGUGACAU-3'
5'-((((((.((..((....)).))))))))-3'
Motif MFE = -8.7; z-score = -3.96; ED = 2.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23441 to 23639 (motif highlighted in silver):

```
5'-GAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGAC
AUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCA-3
5'-(((..(((..(((((((.....((((((.....(((.........))).....))))))((((..((((......(((((((((..((((((.((.(((....)))))))))
))....((((((((.....)))))))))........))))........))))))))).))))))))).).))..)))..)))......-3'
MFE = -48.8; z-score = -0.6; ED = 49.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

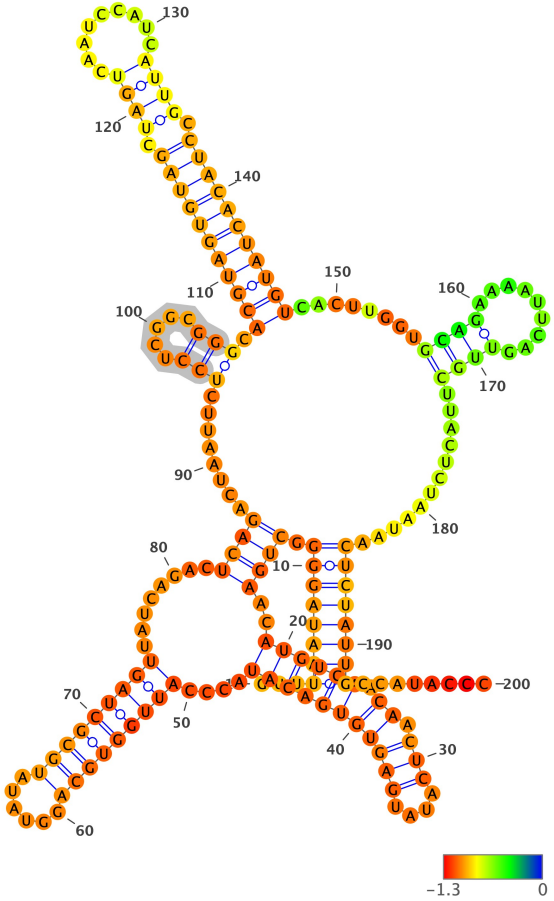
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 371 from nt 23603 to 23611 (nt 96 to 104)

```
5'-CCTCGGCGG-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.39; ED = 0.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23508 to 23707 (motif highlighted in silver):

```
5'-GUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUA
GUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCC-3
5'-...(((((((((.((((..(((((((.((.((((....)))))))))))....((((((((((.....)))))))))).........))))........(((.....))).(((((
((((((.((((.........)))).)))))))))))........((((.........))))............)))))))).........-3'
MFE = -44.5; z-score = -1.51; ED = 39.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

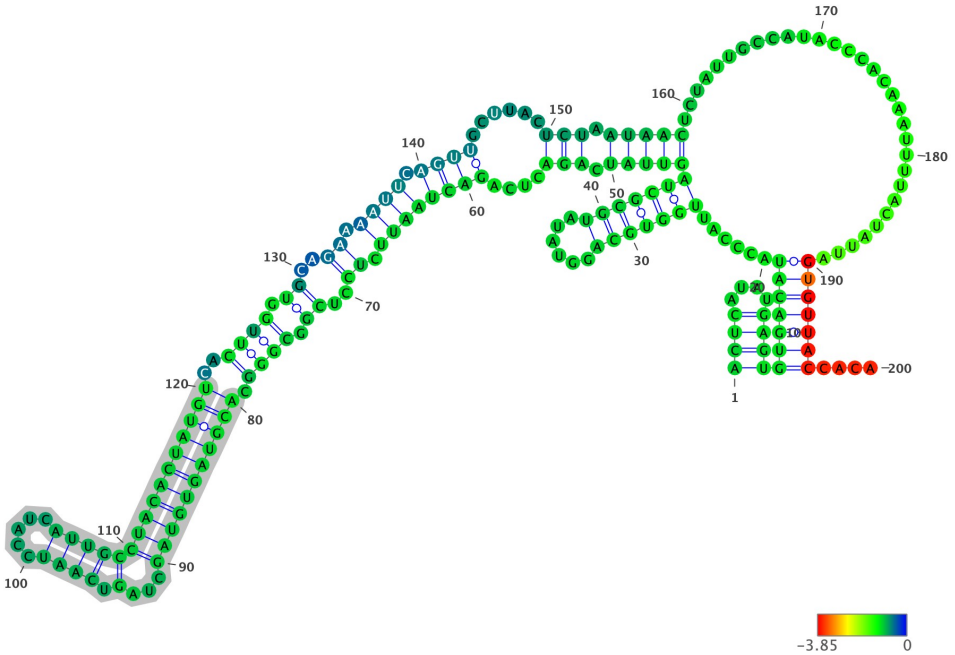
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 372 from nt 23614 to 23654 (nt 80 to 120)

```
5'-ACGTAGTGTAGCTAGTCAATCCATCAUUGCCUACACUAUGU-3'
5'-(((((((((((...(..............)))))))))))-3'
Motif MFE = -13.3; z-score = -3.85; ED = 5.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23535 to 23734 (motif highlighted in silver):

```
5'-ACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCU
ACACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACA-3
5'-((((....))))(((((((.....(((((((......)))))))(((((.(((....((((((((.((..((.((((.((((((((((...(.((((.....)))))))
))))))))..)))).))..)).)))).))))......))).)))))..............................)))))))....-3'
MFE = -43.9; z-score = -1.91; ED = 38.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

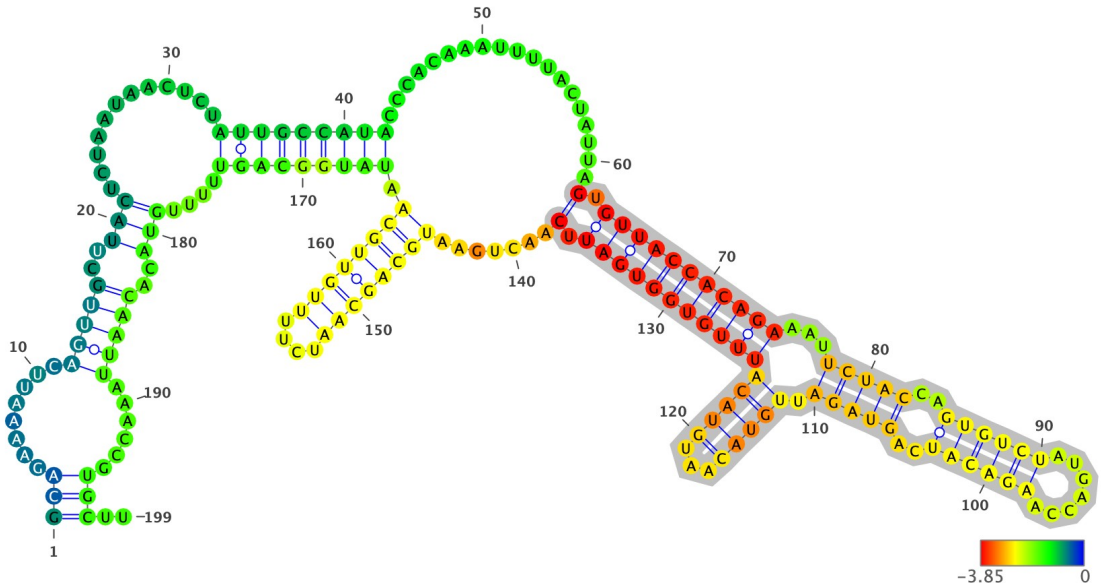
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 373 from nt 23724 to 23799 (nt 62 to 137)

```
5'-GTGTTACCACAGAAATTCTACCAGTGTCTATGACCAAGACAUCAGUAGATTGTACAATGUACAUUUGUGGUGAUTC-3'
5'-(.(((((((((((...(((((..((((((.......))))))..)))))..(((.....))).))))))))))).)-3'
Motif MFE = -25.0; z-score = -4.52; ED = 2.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23663 to 23861 (motif highlighted in silver):

```
5'-GCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAU
UGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUU-3
5'-(((........(((((..(((............(((((((((.................(.(((((((((((...(((((..((((((.......))))))..))))).
(((((...))))))))))))))))).).......((((((((....)))))))).))))))))).....)))..)))))......)))..-3'
MFE = -47.7; z-score = -4.42; ED = 21.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

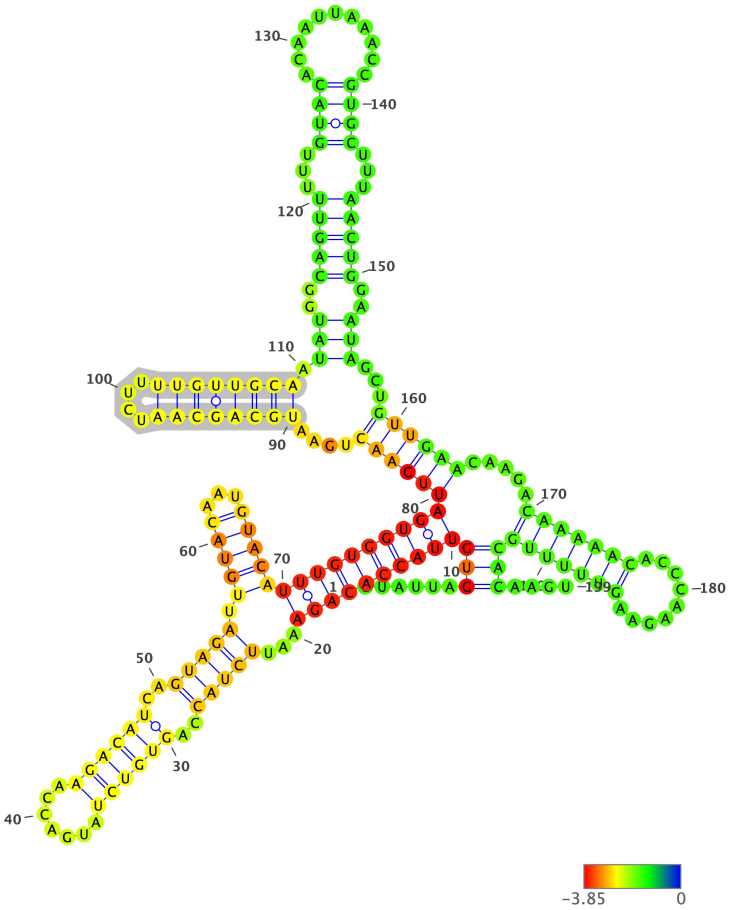
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 374 from nt 23807 to 23826 (nt 90 to 109)

```
5'-TGCAGCAATCTTUUGUUGCA-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.8; z-score = -5.33; ED = 0.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23718 to 23916 (motif highlighted in silver):

```
5'-CUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAU
AUGGCAGUUUUUGUACACAAUUAAACCGUGCUUUAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGU-3
5'-......(((((((((((((...(((((..((((((.......))))))..))))).(((((...))))))))))))))))((((((....((((((((....))))))))).(
((..(((((...((((...........))))...)))))..)))...))))))).....(((((((.........))))))))))....-3'
MFE = -50.2; z-score = -2.83; ED = 32.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

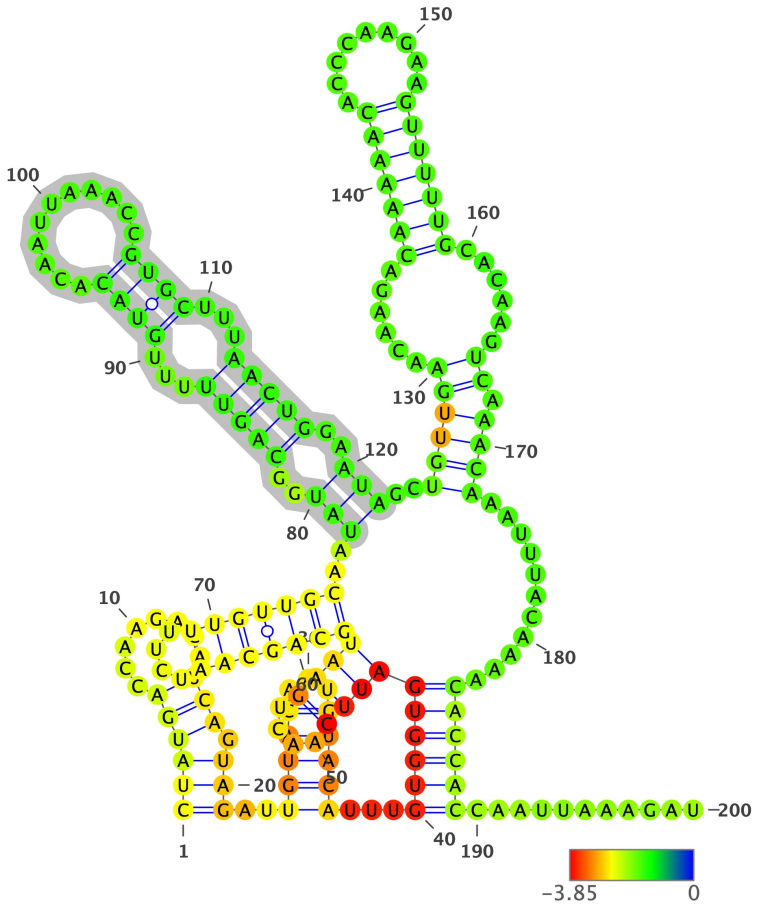
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 375 from nt 23828 to 23872 (nt 78 to 122)

```
5'-TATGGCAGTTTTTGTACACAATTAAACCGUGCTTTAACUGGAAUA-3'
5'-(((..(((((...((((...........))))...)))))..)))-3'
Motif MFE = -7.8; z-score = -1.49; ED = 1.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23751 to 23950 (motif highlighted in silver):

```
5'-CUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUU
UAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGUCAAACAAAUUUACAAAACACCACCAAUUAAAGAU-3
5'-((((((........))).)))..(((((...)))))...(((((((((((....))))(((((((....)))))))..(((..(((((...((((...........))))..
.)))))..)))..((((((......(((((((.........)))))))......)).))))...........))))))...........-3'
MFE = -37.5; z-score = -1.59; ED = 22.5
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

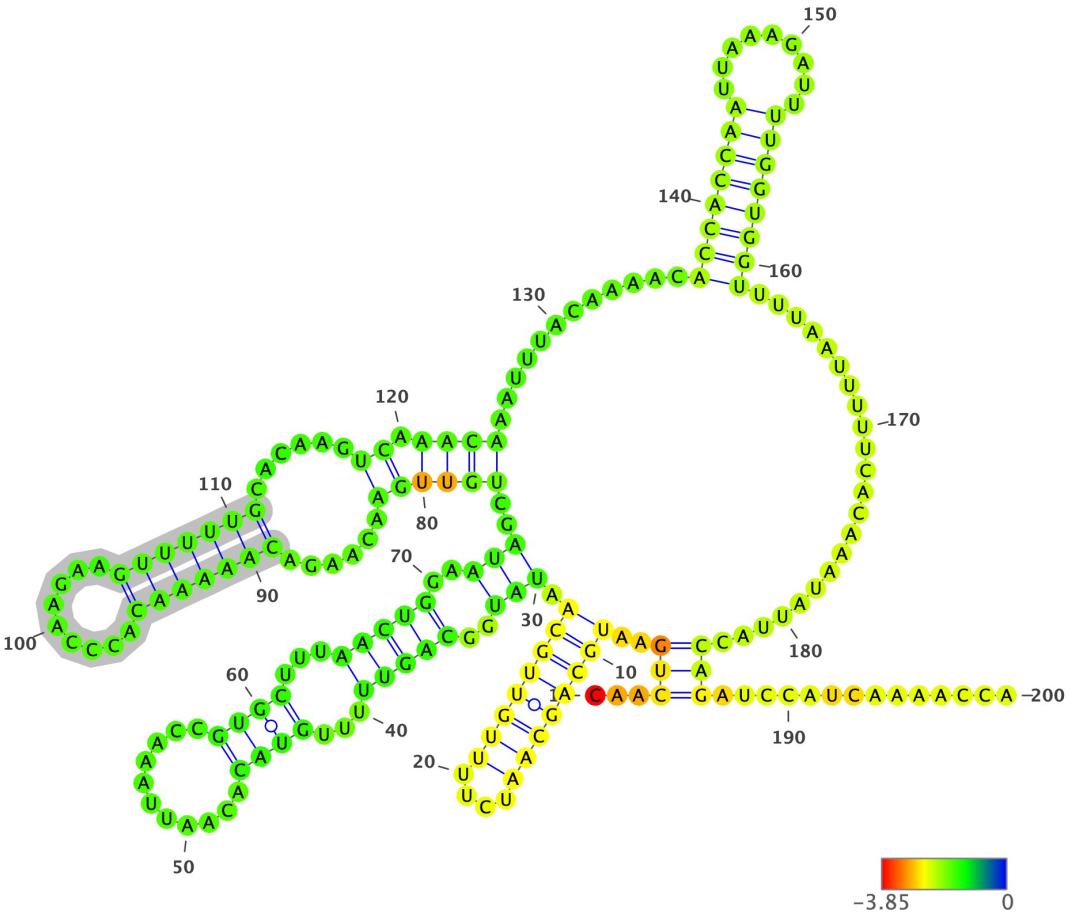
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 376 from nt 23887 to 23909 (nt 89 to 111)

```
5'-CAAAAACACCCAAGAAGUUUUUG-3'
5'-(((((((.........)))))))-3'
Motif MFE = -3.0; z-score = -2.35; ED = 0.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23799 to 23998 (motif highlighted in silver):

```
5'-CAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUUUAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUG
CACAAGUCAAACAAAUUUACAAAACACCACCAAUUAAAGAUUUUGGUGGUUUUAAUUUUUCACAAAUAUUACCAGAUCCAUCAAAACCA-3
5'-...(((..((((((((....)))))))).(((..(((((...((((.............))))...)))))..)))..((((((......(((((((.........)))))))
......)).))))............((((((((.........))))))))......................)))...............-3'
MFE = -37.8; z-score = -2.95; ED = 37.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

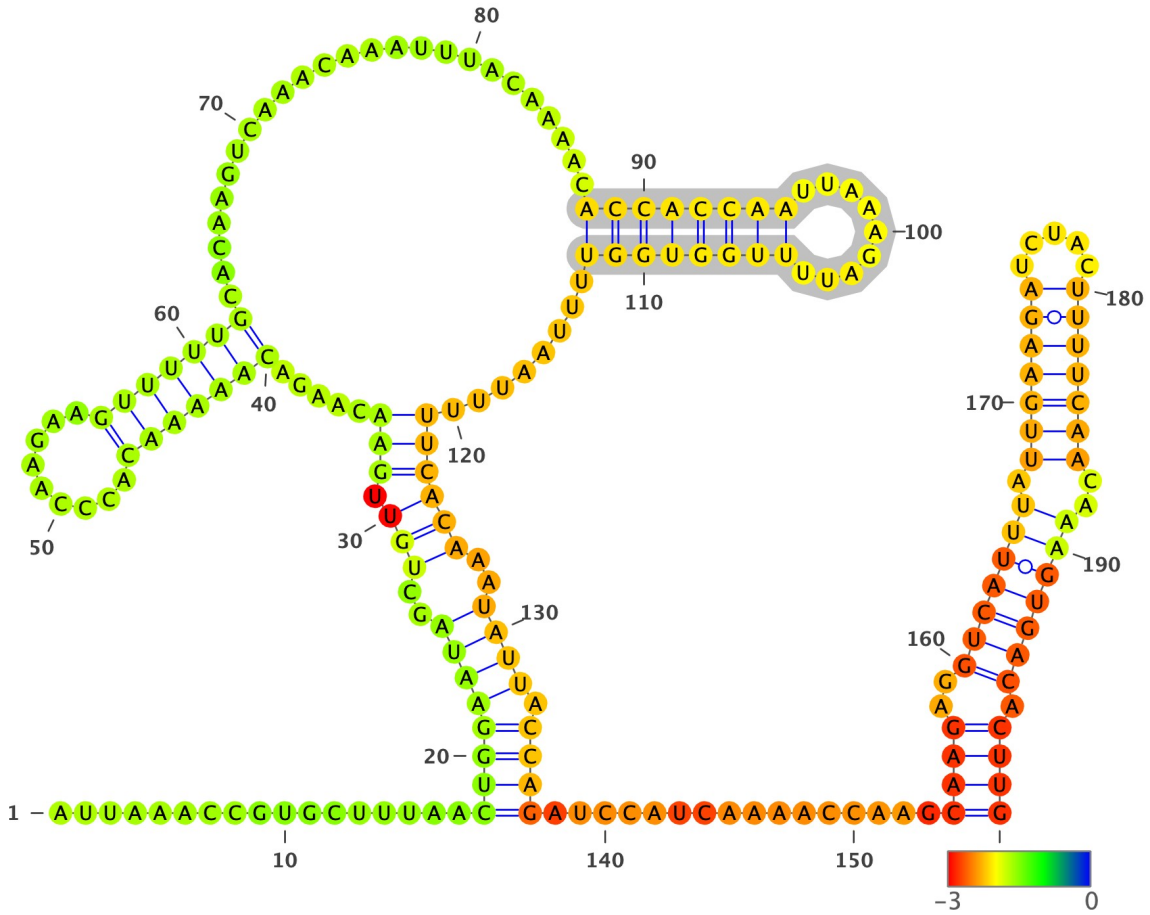
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 377 from nt 23935 to 23959 (nt 88 to 112)

```
5'-ACCACCAATTAAAGATTUUGGUGGU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -10.4; z-score = -5.43; ED = 0.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23848 to 24047 (motif highlighted in silver):

```
5'-AUUAAACCGUGCUUUAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGUCAAACAAAUUUACAAAACACCACCAAUUAAAGAUUUUGGUGG
UUUUAAUUUUUCACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUG-3
5'-.................((((((((..(((.(((.....(((((((.........)))))))..........................((((((((.........)))))))
).......))))))..)))).))))................((((..(((((((.(((((((.....)))))))..)))))))).))))-3'
MFE = -36.6; z-score = -2.61; ED = 20.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

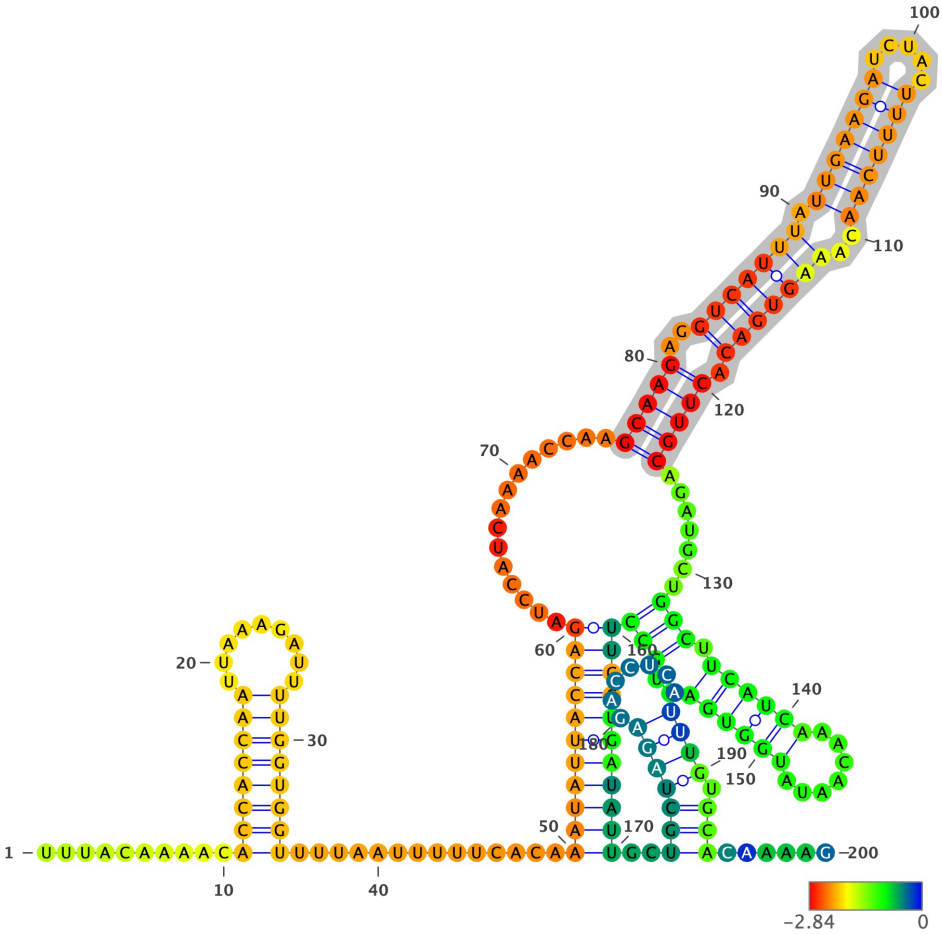
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 378 from nt 24000 to 24048 (nt 76 to 124)

```
5'-GCAAGAGGTCATTTATTGAAGATCTACUUUUCAACAAAGUGACACUUGC-3'
5'-(((((..(((((...(((((((.....)))))))....))))).)))))-3'
Motif MFE = -16.1; z-score = -3.88; ED = 1.88
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23925 to 24124 (motif highlighted in silver):

```
5'-UUUACAAAACACCACCAAUUAAAGAUUUUGGUGGUUUUAAUUUUUCACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACA
AAGUGACACUUGCAGAUGCUGGCUUCAUCAAACAAUAUGGUGAUUGCCUUGGUGAUAUUGCUGCUAGAGACCUCAUUUGUGCACAAAAG-3
5'-..........((((((((.........))))))))..............((((((((((.................(((((..(((((((.(((((((.....)))))))..
)))))))).)))))).......(((.((((((.......))))))..))))))))))))))..(((((((.......)))).)))......-3'
MFE = -49.6; z-score = -3.22; ED = 19.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

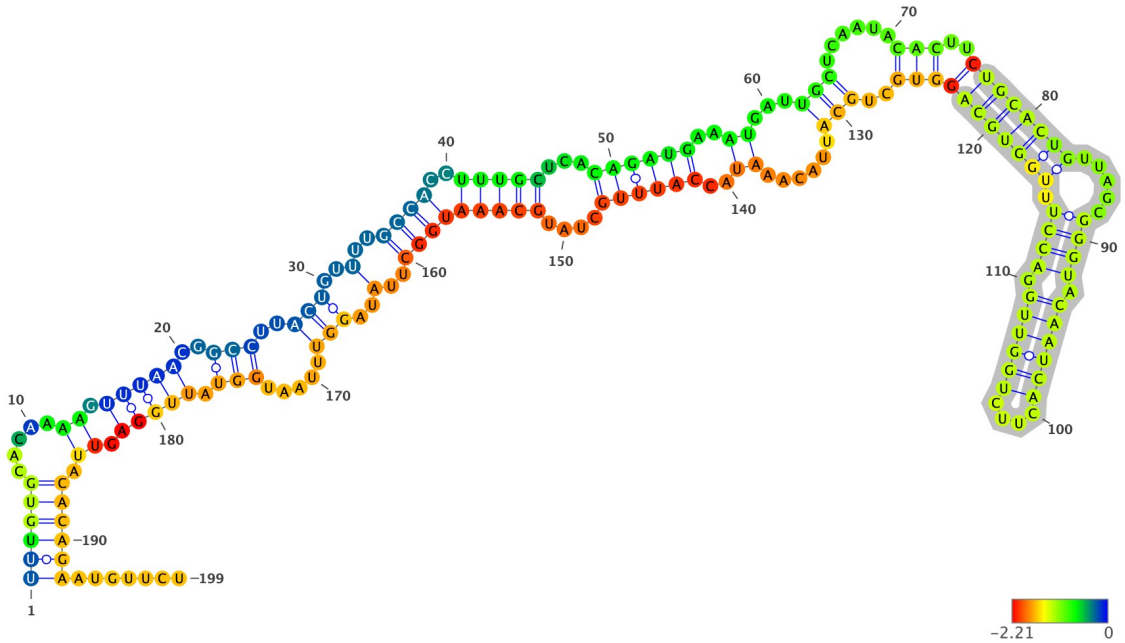
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 379 from nt 24187 to 24232 (nt 77 to 122)

```
5'-TGCACTGTTAGCGGGTACAATCACTTCUGGUUGGACCUTTGGUGCA-3'
5'-(((((.......((((.((((((....)))))).))))...)))))-3'
Motif MFE = -14.3; z-score = -1.84; ED = 3.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24111 to 24309 (motif highlighted in silver):

```
5'-UUUGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGA
CCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCU-3
5'-((((((.....((.(((((..(((..(((..(.(.((((..((((((...((((((..((...(((......(((..((((((((.....((((.((((((....)))))).)
))).))))))))))..)))......))..))))))....))))))))..)..)))).....))).)))))).)).))))))........-3'
MFE = -44.8; z-score = -1.13; ED = 59.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

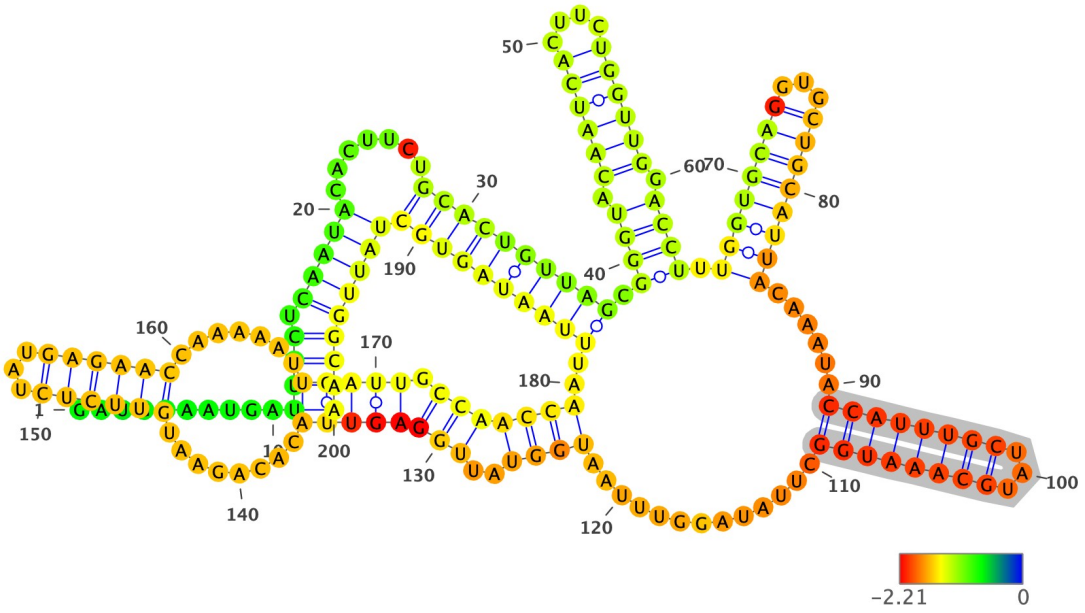
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 380 from nt 24251 to 24269 (nt 91 to 109)

```
5'-CCATTTGCTATGCAAAUGG-3'
5'-(((((((...)))))))-3'
Motif MFE = -8.4; z-score = -5.84; ED = 0.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24161 to 24360 (motif highlighted in silver):

```
5'-GAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCU
UAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3
5'-..........((((.(((((.......((((((((((.((((.((((((....)))))).)))).((((((((...)))))))).....(((((((...)))))))).
..........((((..((((((((.......((((((...)))))).......)))))).)))))))..))))))))))))))))))-3'
MFE = -55.2; z-score = -2.99; ED = 27.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

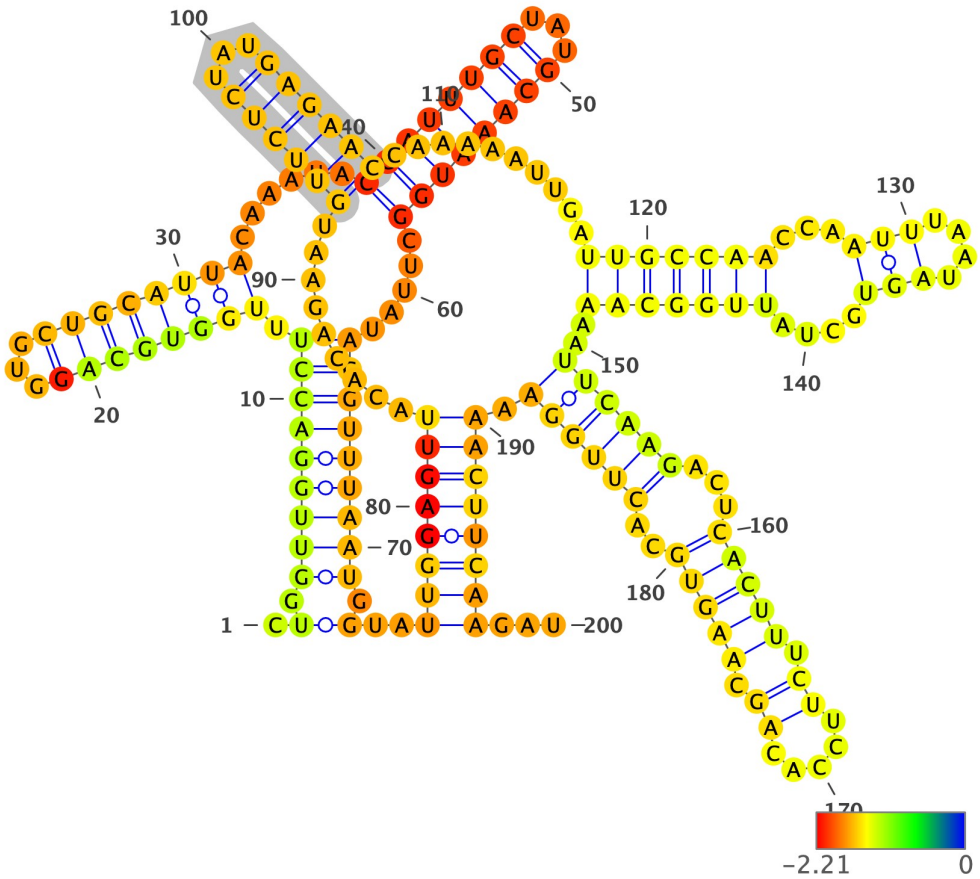
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 381 from nt 24305 to 24319 (nt 93 to 107)

```
5'-GTTCTCTATGAGAAC-3'
5'-((((((...))))))-3'
Motif MFE = -4.6; z-score = -5.0; ED = 0.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24213 to 24412 (motif highlighted in silver):

```
5'-CUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAA
AAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAU-3
5'-.(.(((((((((.(((((((((...)))))))))......(((((((((...)))))))))).....)))))))))..)..((((((((.........((((((...)))))))....
......(((((((...(((....)))....)))))))..((((((...((((((.((.....)).)))))..)))))).))))))))...-3'
MFE = -50.9; z-score = -2.7; ED = 14.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

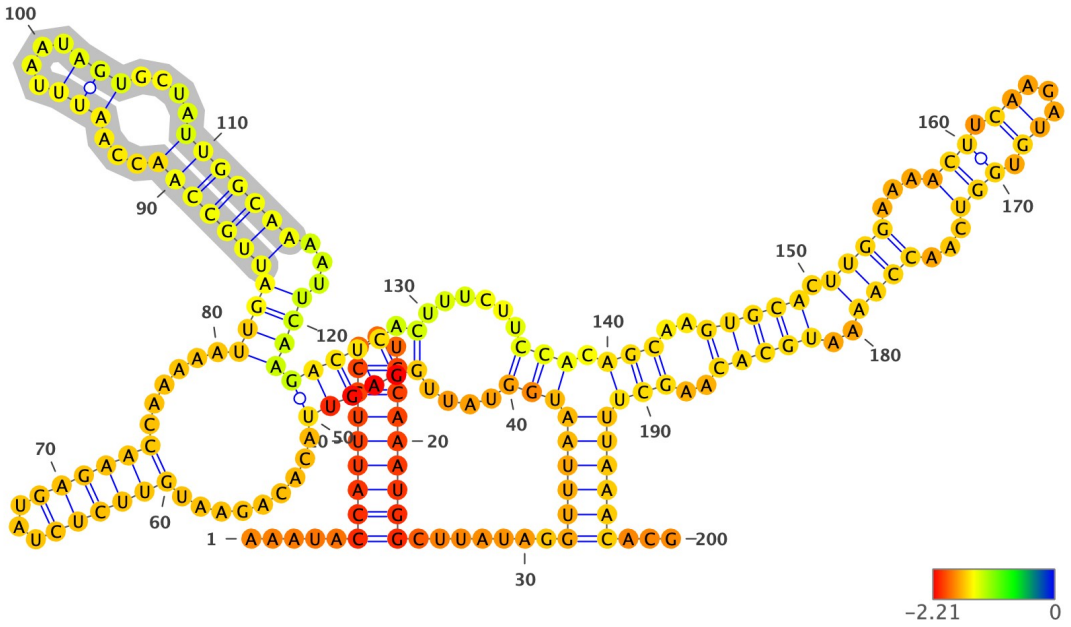
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 382 from nt 24330 to 24360 (nt 85 to 115)

```
5'-TTGCCAACCAATTTAATAGTGCTATUGGCAA-3'
5'-((((((...................))))))-3'
Motif MFE = -6.5; z-score = -2.17; ED = 3.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24246 to 24445 (motif highlighted in silver):

```
5'-AAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUG
GCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACG-3
5'-.....((((((((...))))))))).......(((((((((....((((((.........((((((...))))))......((((((((((...(((....)))....)))
))))...))))))))).).......))).(((..(((((.((((...(((.((...)).)))...)))))..)))))..))))))))))...-3'
MFE = -42.9; z-score = -2.28; ED = 41.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

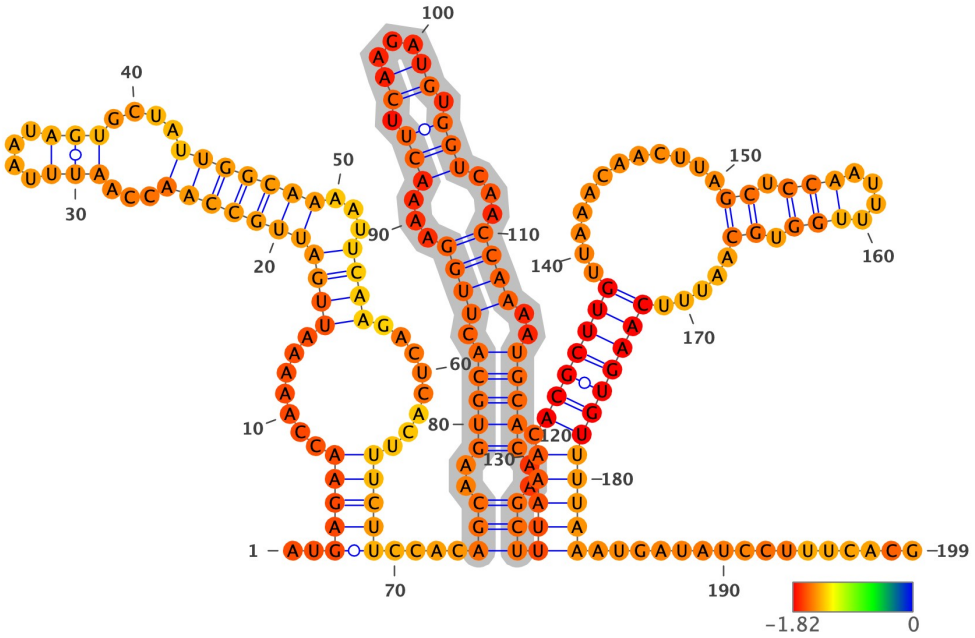
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 383 from nt 24385 to 24436 (nt 74 to 125)

```
5'-AGCAAGTGCACTTGGAAAACTTCAAGATGTGGTCAACCAAAAUGCACAAGCU-3'
5'-(((..(((((.((((....((.(.....).)).....))))..)))))..)))-3'
Motif MFE = -13.3; z-score = -3.35; ED = 6.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24312 to 24510 (motif highlighted in silver):

```
5'-AUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACC
AAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACG-3
5'-..(((((.......((((((((((...(((....))).....)))))))...))))........)))))....(((..(((((.((((...(((.((...)).)))...))
))..)))))..)))(((((.(((((((.............((.(((....))).)).....))))))))))))).................-3'
MFE = -35.9; z-score = -1.25; ED = 24.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

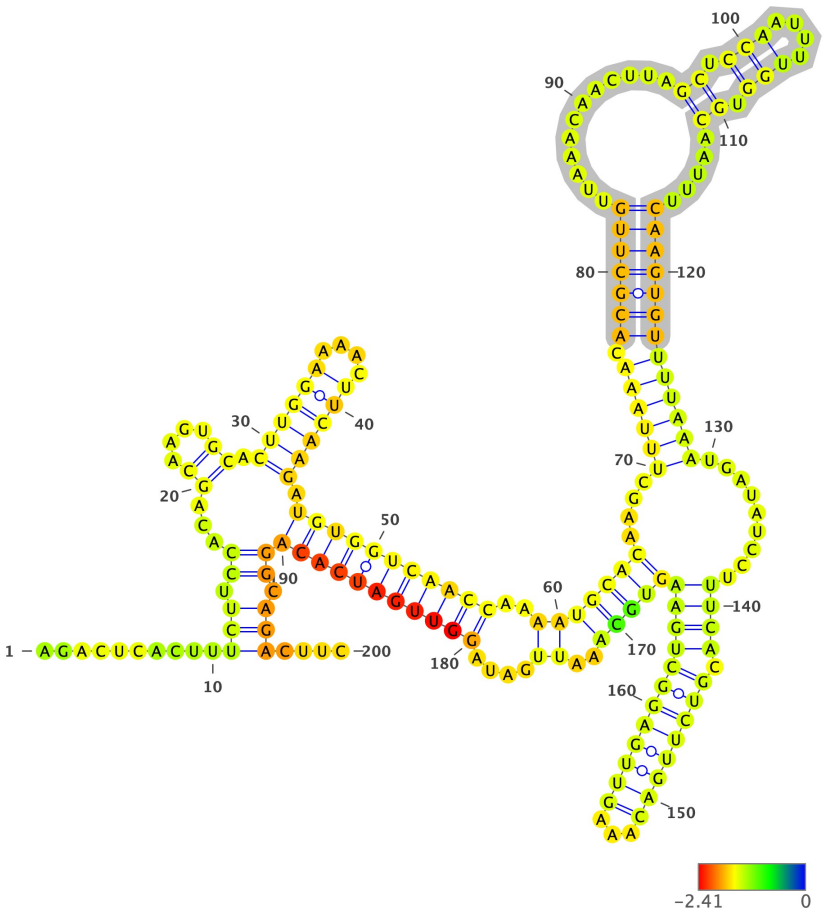
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 384 from nt 24443 to 24489 (nt 77 to 123)

```
5'-ACGCTTGTTAAACAACTTAGCTCCAATTTTGGTGCAATTTCAAGUGU-3'
5'-(((((((............((.((......)).)).....)))))))-3'
Motif MFE = -9.0; z-score = -1.61; ED = 4.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24367 to 24566 (motif highlighted in silver):

```
5'-AGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGC
AAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUC-3
5'-..........(((.((...((....)).((((((....)))))).((((((((((..(((((((....((((((.(((((((.............((.(((....))).))
.....)))))))))))))).........((((.((((((((...)))))))))))))))))..))....)))))))))))))).)))....-3'
MFE = -47.9; z-score = -2.11; ED = 19.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

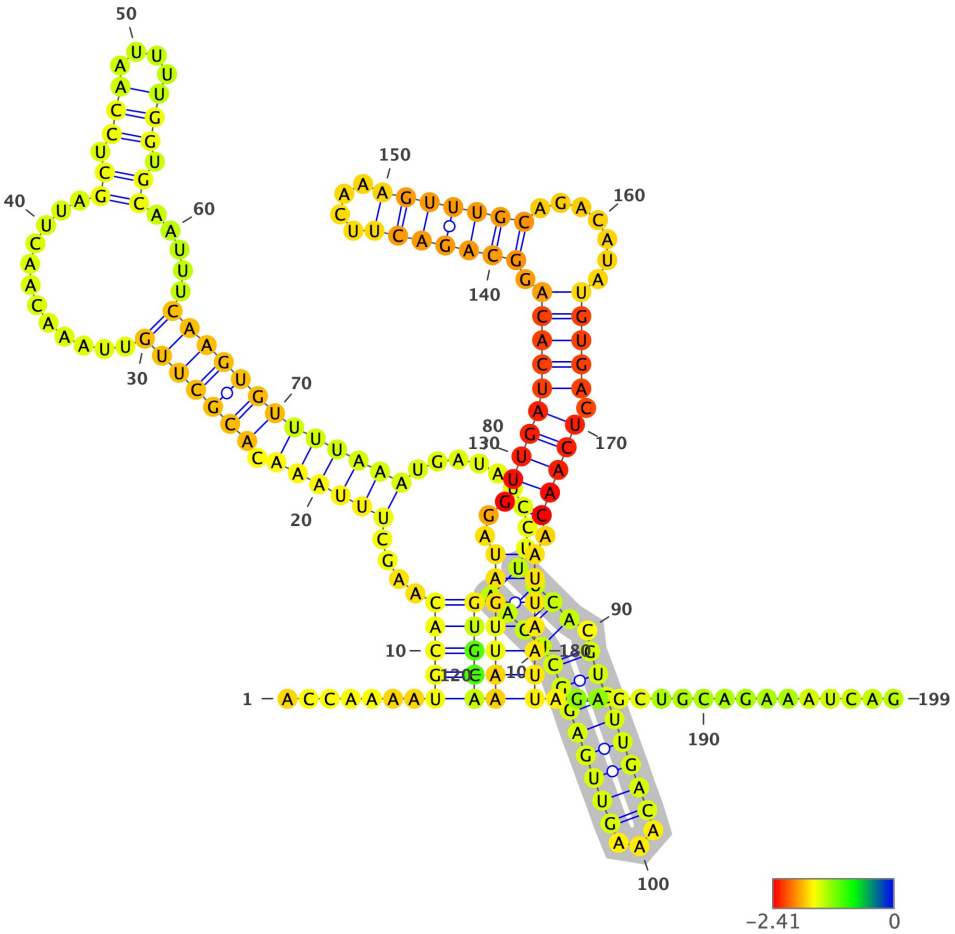
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 385 from nt 24505 to 24532 (nt 86 to 113)

```
5'-TTCACGTCTTGACAAAGUUGAGGCUGAA-3'
5'-((((.((((((((...)))))))))))-3'
Motif MFE = -8.5; z-score = -2.17; ED = 0.87
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24420 to 24618 (motif highlighted in silver):

```
5'-ACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUG
AAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAG-3
5'-.......(((((....((((((.(((((((.............((.(((....))).)).....))))))))))))).........((((.(((((((((...))))))))))
)))))))(((((((..((((((((((.(((((((....)))))))).......))))).))))).)))))))..................-3'
MFE = -45.1; z-score = -2.32; ED = 28.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

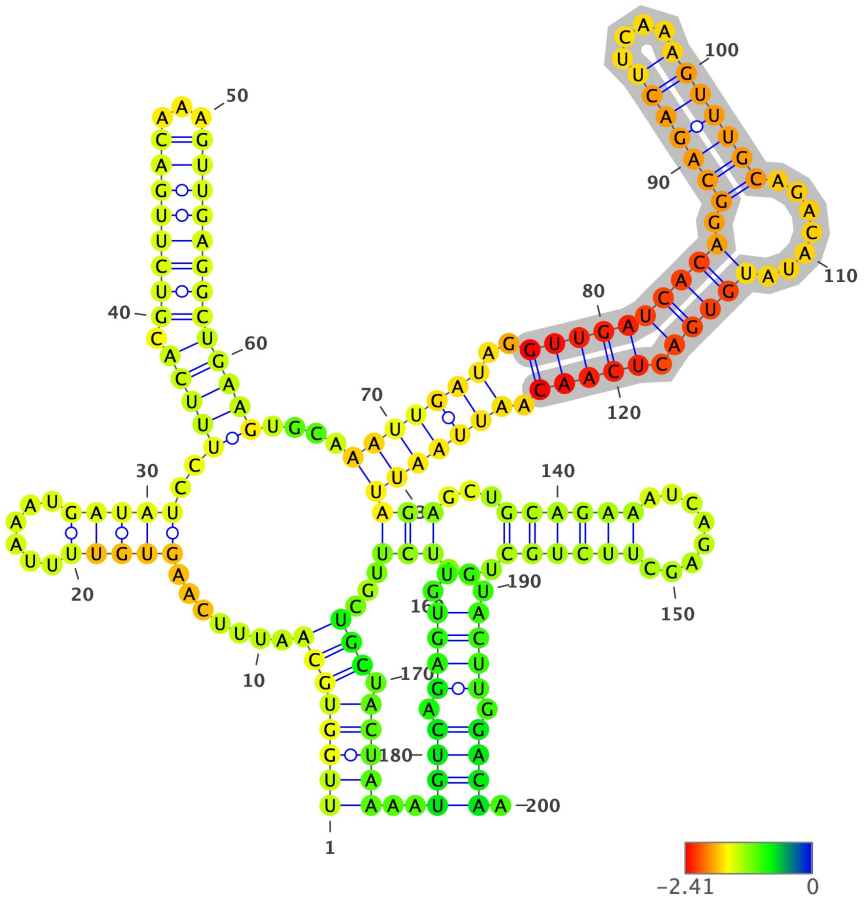
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 386 from nt 24547 to 24593 (nt 77 to 123)

```
5'-GTTGATCACAGGCAGACTTCAAAGUUUGCAGACATATGUGACUCAAC-3'
5'-(((((((((..((((((......))))))........)))).)))))-3'
Motif MFE = -14.0; z-score = -3.05; ED = 1.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24471 to 24670 (motif highlighted in silver):

```
5'-UUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAU
AUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAA-3
5'-((((((((.......(((((......)))))..(((((.((((((((...)))))))))))))....(((((((..((((((((((.(((((((....)))))))......
.))))).))))).)))))))(((...((((((........))))))...)))...))).)))))..((((.((((....)))).)))).-3'
MFE = -50.9; z-score = -2.14; ED = 32.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

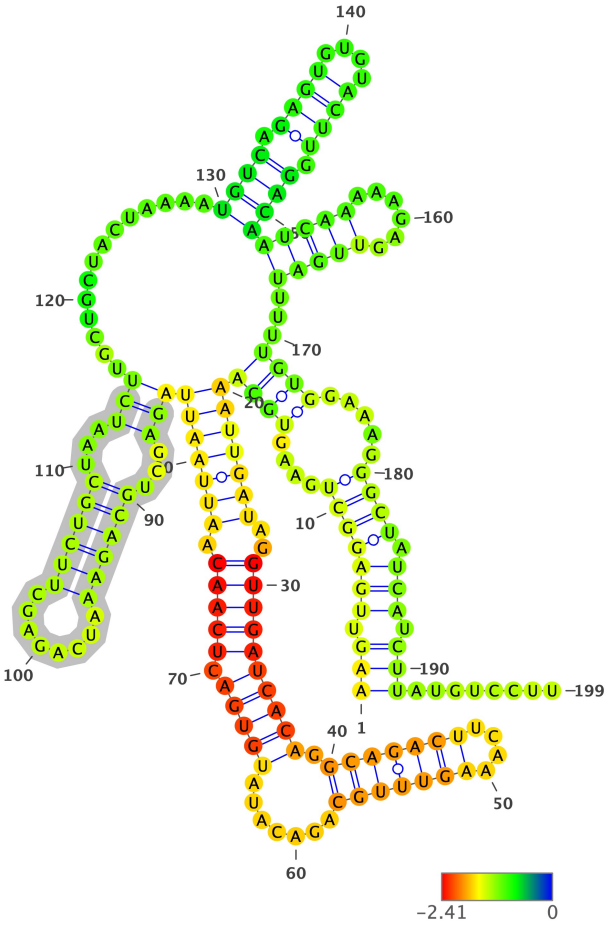
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 387 from nt 24603 to 24632 (nt 85 to 114)

```
5'-GAGCTGCAGAAATCAGAGCUUCUGCTAAUC-3'
5'-((...((((((........))))))...))-3'
Motif MFE = -7.2; z-score = -1.9; ED = 1.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24519 to 24717 (motif highlighted in silver):

```
5'-AAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUA
AUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU-3
5'-(((.(((((((....((((((((((..((((((((((.(((((((....)))))))).......))))).))))).)))))))(((...((((((........))))))..
.))).............((((.((((....)))).))))(((((......)))))...))))).....)))).))).))).........-3'
MFE = -44.8; z-score = -1.18; ED = 37.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

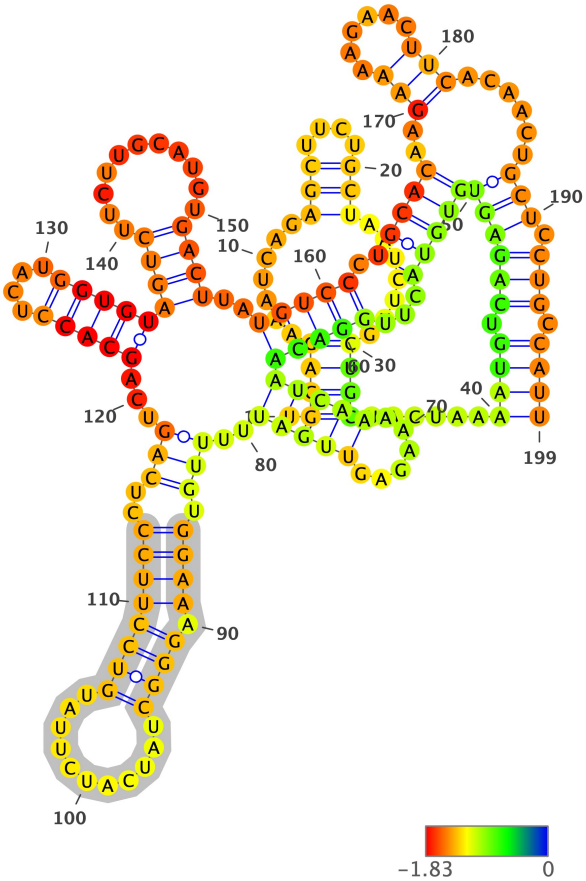
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 388 from nt 24692 to 24719 (nt 86 to 113)

```
5'-GGAAAGGGCTATCATCTTATGUCCUUCC-3'
5'-((((.((((...........))))))))-3'
Motif MFE = -7.7; z-score = -3.05; ED = 3.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24607 to 24805 (motif highlighted in silver):

```
5'-UGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU
CCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUU-3
5'-.((((.......(((....)))........))))......((((.(((((((((((...((((((((((......)))))..(((.((((.((((...........))))))
))..)))...(((((....)))))((((...........))))..)))))).)))))..(((......)))......))).))).))))-3'
MFE = -44.9; z-score = -0.92; ED = 53.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

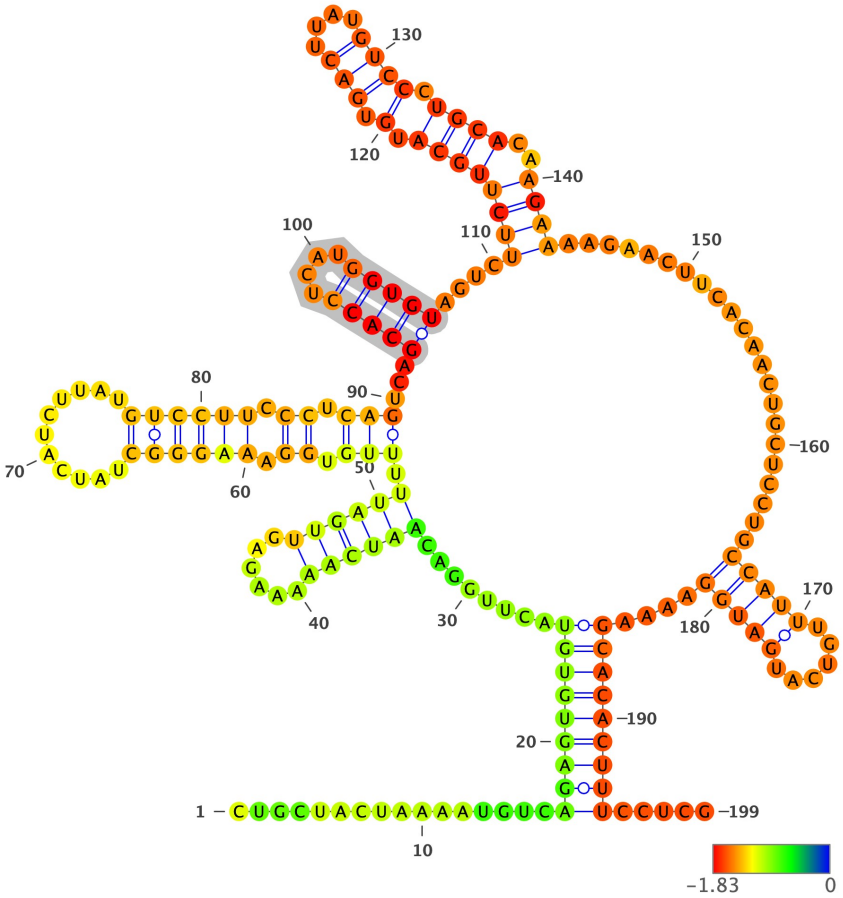
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 389 from nt 24728 to 24741 (nt 93 to 106)

```
5'-GCACCTCATGGUGU-3'
5'-((((......))))-3'
Motif MFE = -6.1; z-score = -4.55; ED = 0.32
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24636 to 24834 (motif highlighted in silver):

```
5'-CUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCU
UCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCG-3
5'-................(((((((((.........((((((......)))))).(((.((.((((((...........)))))).)).)))...(((((....)))))....(
(((((((.(.(((....)))).))))..))))......................(((((......)))))....))))))))).....-3'
MFE = -45.8; z-score = -0.93; ED = 39.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

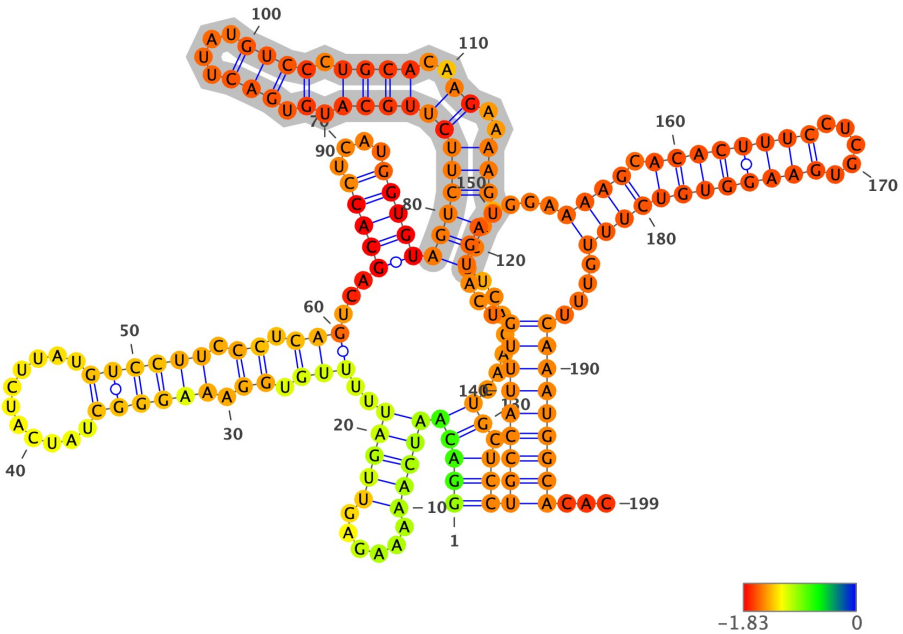
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 390 from nt 24742 to 24785 (nt 78 to 121)

```
5'-AGTCTTCTTGCATGTGACTTATGUCCCUGCACAAGAAAAGAACU-3'
5'-((((((.(((((.(.(((....)))).))))..)...))).)))-3'
Motif MFE = -9.1; z-score = -1.63; ED = 7.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24665 to 24863 (motif highlighted in silver):

```
5'-GGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAA
GAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACAC-3
5'-(((((((((((......)))))..(((.((.((((((...........))))))).)).)))...(((((....)))))((((((((((((.(.(((....)))).))))..)
)..))).))).......)).)))((((((((((.........((((.((((((((.....))))))))))))....))))))))).....-3'
MFE = -51.7; z-score = -2.3; ED = 32.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

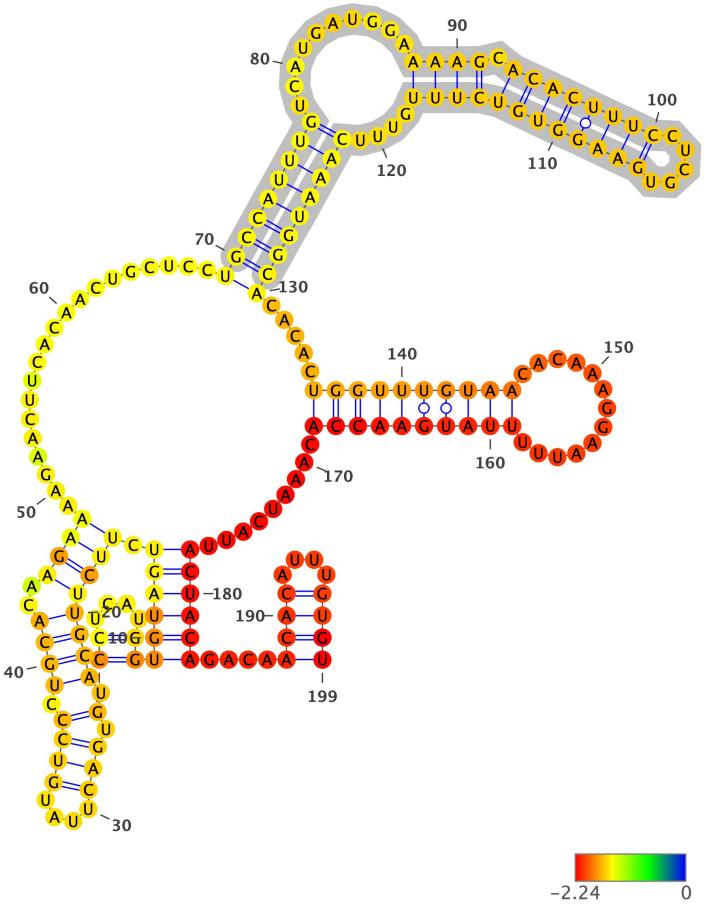
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 391 from nt 24800 to 24859 (nt 70 to 129)

```
5'-GCCATTTGTCATGATGGAAAAGCACACTTTCCTCGTGAAGGUGUCUUUGTTTCAAAUGGC-3'
5'-((((((((.........((((.(((((((.......)))))))))))....))))))))-3'
Motif MFE = -18.9; z-score = -2.66; ED = 10.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24731 to 24929 (motif highlighted in silver):

```
5'-CCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGU
GUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGU-3
5'-((....))((((((.((((((((.(.(((....)))).))))..))))).....................(((((((((.........((((.((((((((.....))))))
))))))....)))))))))).....((((((((((.............))))))))))).........))))))....((((....))))-3'
MFE = -44.1; z-score = -1.47; ED = 32.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

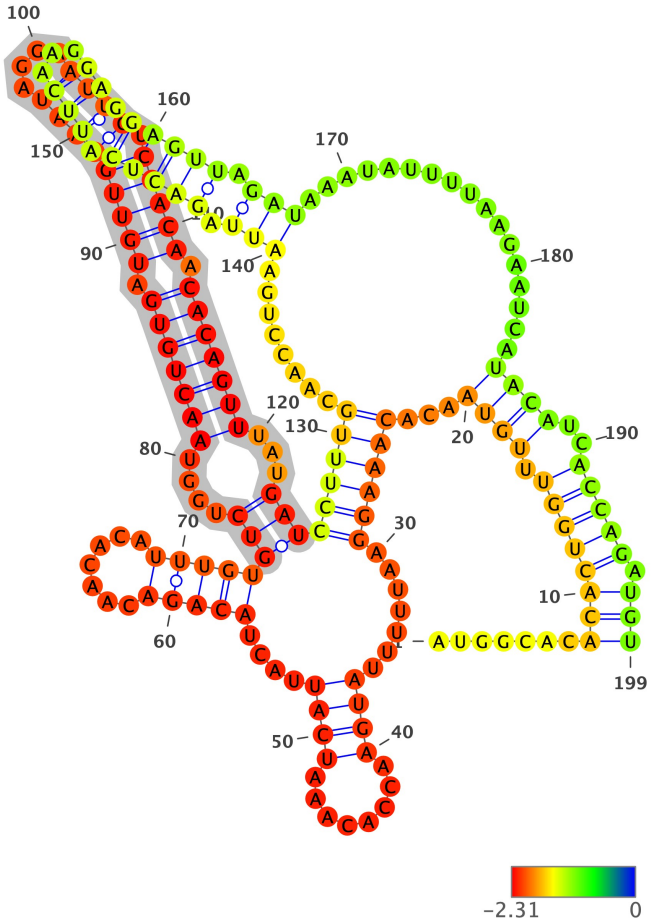
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 392 from nt 24928 to 24979 (nt 74 to 125)

```
5'-GTCTGGTAACTGTGATGTTGTAATAGGAATTGTCAACAACACAGUUTATGAU-3'
5'-(((....(((((((.(((((.............))))).)))))))...)))-3'
Motif MFE = -15.4; z-score = -3.3; ED = 5.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24855 to 25053 (motif highlighted in silver):

```
5'-AUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACA
ACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGU-3
5'-.......((((((((.((((...((((((.......((((........)))).....(((((.......)))))(((....(((((((.(((((((((....)))).)))))
.)))))))...))))))))).........(((.(((((.(((...))))))))).))).................))))..)))))).)))-3'
MFE = -36.5; z-score = -2.12; ED = 28.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

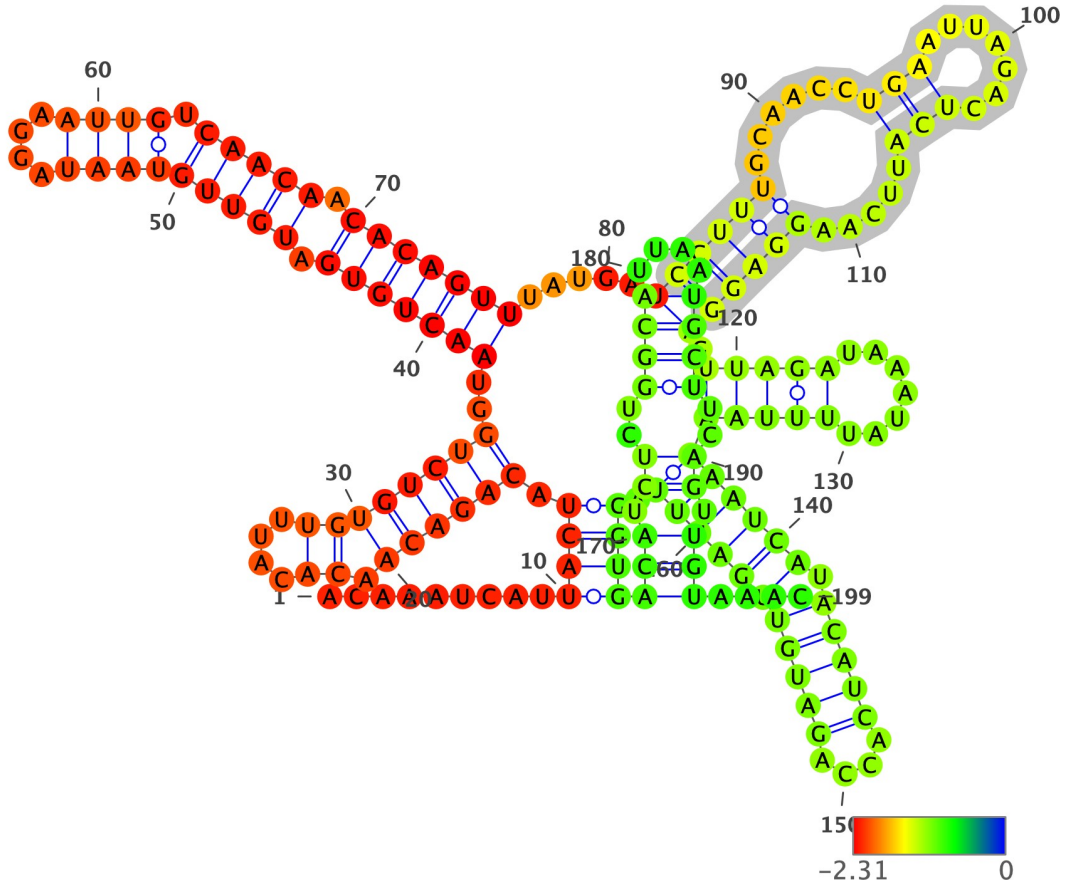
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 393 from nt 24980 to 25013 (nt 83 to 116)

```
5'-CCTTTGCAACCTGAATTAGACTCATTCAAGGAGG-3'
5'-(((((.........................)))))-3'
Motif MFE = -3.3; z-score = 0.18; ED = 7.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24898 to 25096 (motif highlighted in silver):

```
5'-ACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAA
GGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAAC-3
5'-.........((((.(((((((.(((....)))))))).)))))))).(((((((.((((((((((....)))).)))))).)))))))).....((((((.....(((.......))).....
))))))).(((((.....)))))((((((.(((((....)))))))))))).))))))((.((..((((....))))..)).))).....-3'
MFE = -43.8; z-score = -3.15; ED = 27.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

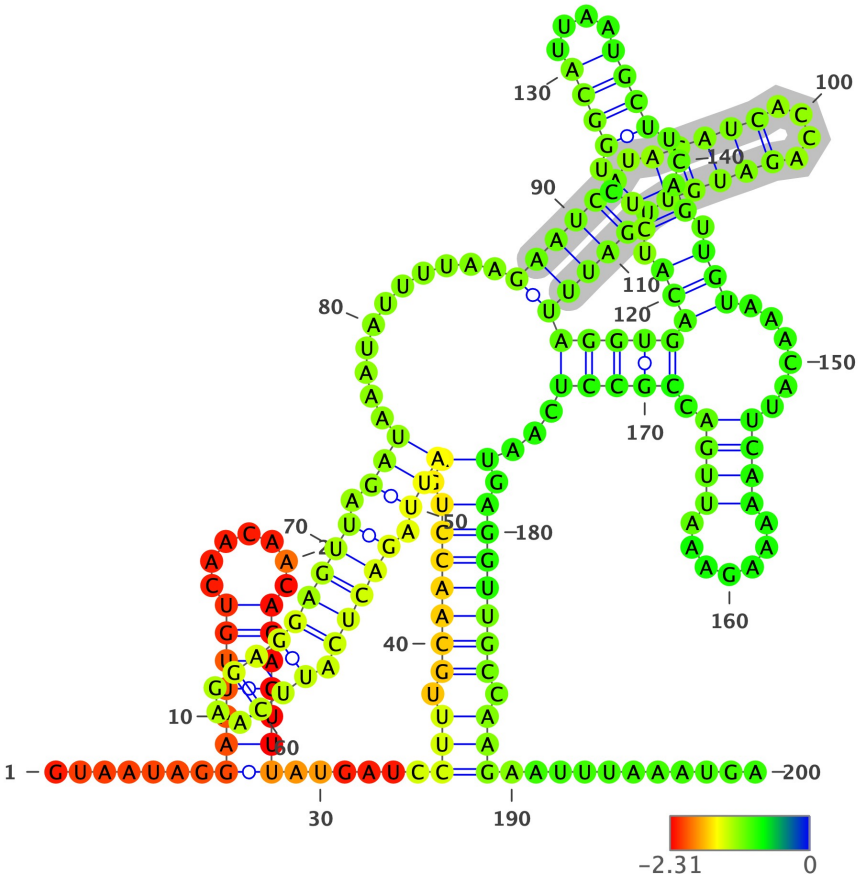
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 394 from nt 25034 to 25058 (nt 88 to 112)

```
5'-AATCATACATCACCAGAUGTUGAUU-3'
5'-(((((..((((....)))).)))))-3'
Motif MFE = -6.8; z-score = -4.85; ED = 0.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24947 to 25146 (motif highlighted in silver):

```
5'-GUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAU
UUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGA-3
5'-.......(((((((.......)))))))......(((.(((((((.((((.(((((.(((...)))))))).))).........((((((.(((((....)))))))))
))((((((((.((..((((....))))..)).)))......((((.......)))).)))))...).)))))))).))).........-3'
MFE = -39.4; z-score = -1.24; ED = 42.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

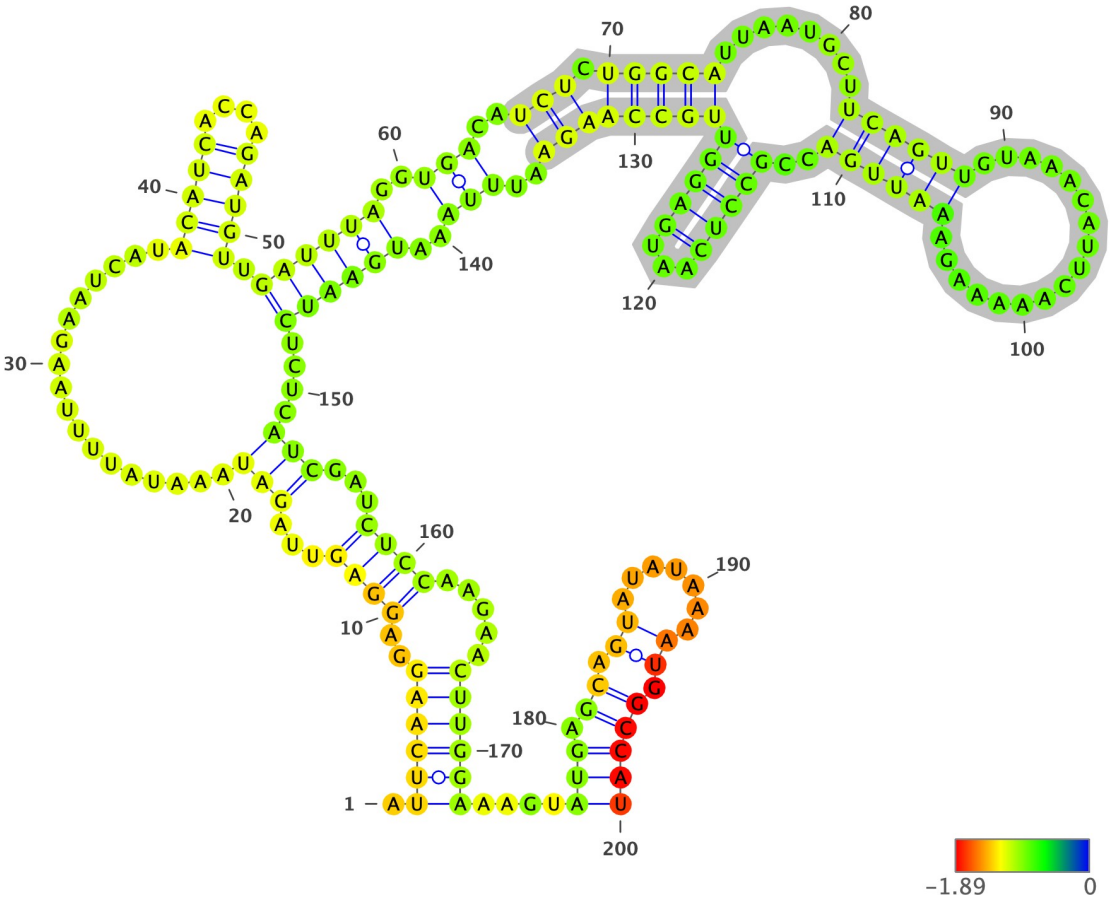
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 395 from nt 25068 to 25136 (nt 66 to 134)

```
5'-TCTCTGGCATTAATGCTTCAGTTGTAAACATTCAAAAAGAAAUUGACCGCCTCAATGAGGUUGCCAAGA-3'
5'-(((.(((((........(((((...................)))))...............))))))))-3'
Motif MFE = -13.2; z-score = -1.51; ED = 16.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25003 to 25202 (motif highlighted in silver):

```
5'-AUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGA
CCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAU-3
5'-.((((((..((((...(((.................(((((....))))).((((((..(((..(((.(((((........((((((.................))))))
..(((((...))))))))))))))..)))..))))))....)))...))))).....))))))....(((.((.((.......)).)))))-3'
MFE = -33.9; z-score = -0.23; ED = 43.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

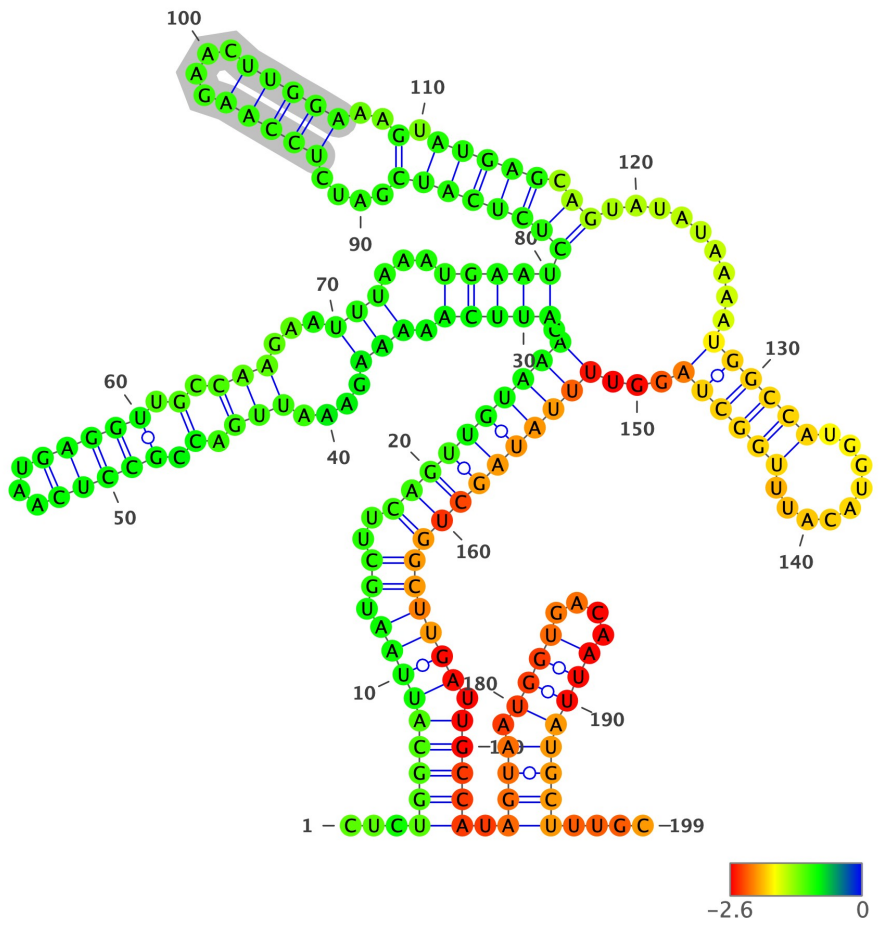
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 396 from nt 25161 to 25174 (nt 93 to 106)

```
5'-TCCAAGAACUUGGA-3'
5'-(((((....)))))-3'
Motif MFE = -3.1; z-score = -5.11; ED = 0.94
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25069 to 25267 (motif highlighted in silver):

```
5'-CUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUA
UGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGC-3
5'-...(((((((((.((..((((((((((.(((((.(((....(((.(.((((((...)))))).).))).)))...))).....))))))((((((((....(((((....)))))..).)
))))).)).........((((((.........)))))).....))))))))))))))))).)))))).(((((.((((....)))))))))....-3'
MFE = -43.8; z-score = -0.94; ED = 48.05
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

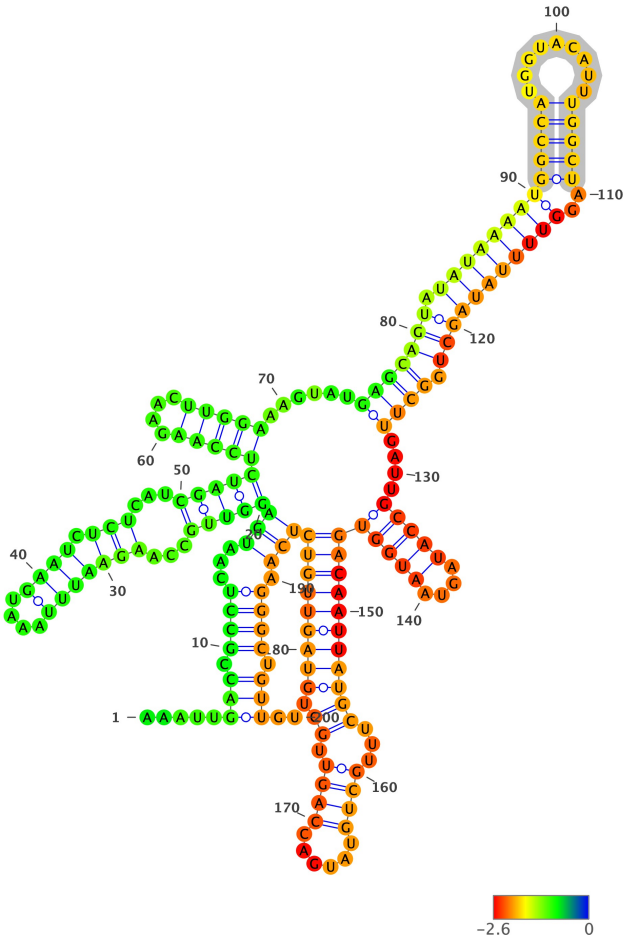
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 397 from nt 25197 to 25215 (nt 91 to 109)

```
5'-GGCCATGGTACATTUGGCU-3'
5'-(((((.........)))))-3'
Motif MFE = -5.2; z-score = -2.18; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25107 to 25306 (motif highlighted in silver):

```
5'-AAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAG
GUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGU-3
5'-.....(((.((((...((((((((...(((((((....)))).)))...)))))(((((....)))))......(((((((.((((((((((((.........)))))..
)))))))))))).))))....(((((....)))))((((((((((...((((......)))).)).))))))))))))).)))).)))..-3'
MFE = -51.6; z-score = -1.41; ED = 62.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

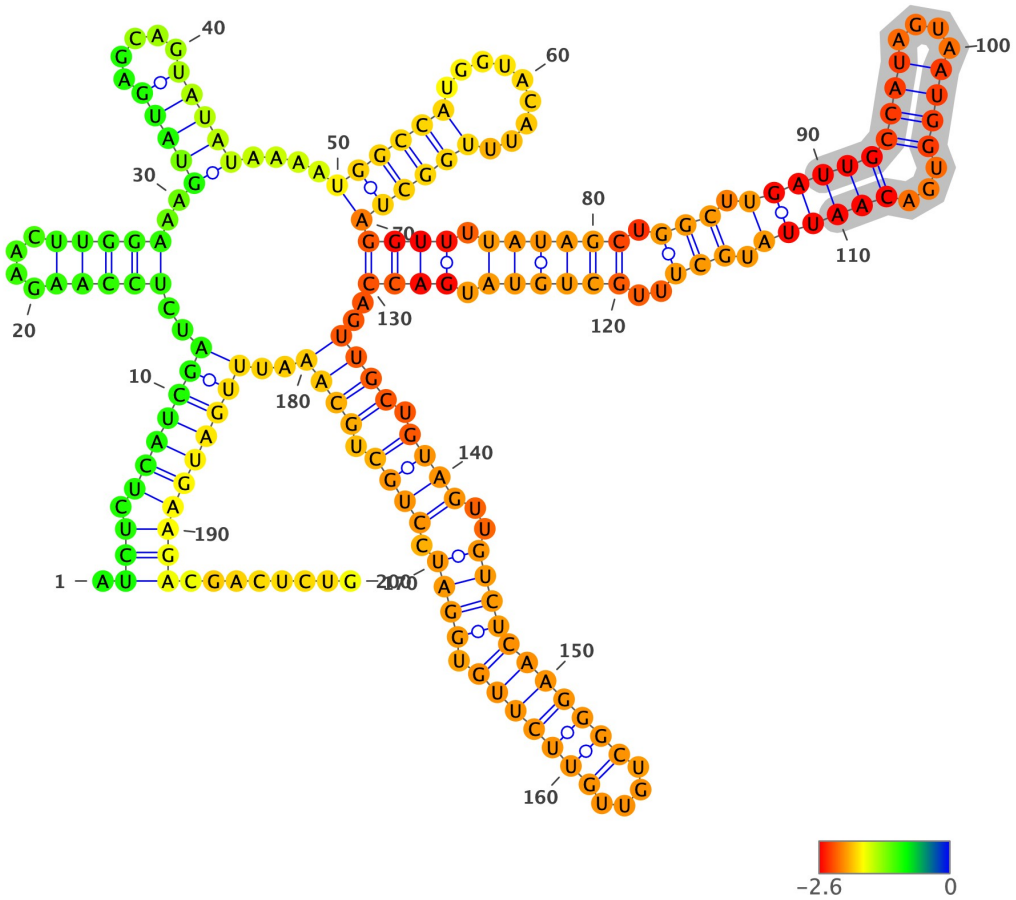
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 398 from nt 25236 to 25256 (nt 90 to 110)

```
5'-TTGCCATAGTAAUGGTGACAA-3'
5'-(((((((....))))...)))-3'
Motif MFE = -4.9; z-score = -3.16; ED = 1.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25147 to 25346 (motif highlighted in silver):

```
5'-AUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAU
UAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUG-3
5'-.(((.(((((((..(((((....)))))..(((((.....)))))....((((((.........))))))((((.((((((.(((.(((((((((((....))))...))))
)).)))..))))))).))))..((((.((((..(((((((((((....)))))))).)))).)))).)))))..))))))))))........-3'
MFE = -61.4; z-score = -3.11; ED = 16.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

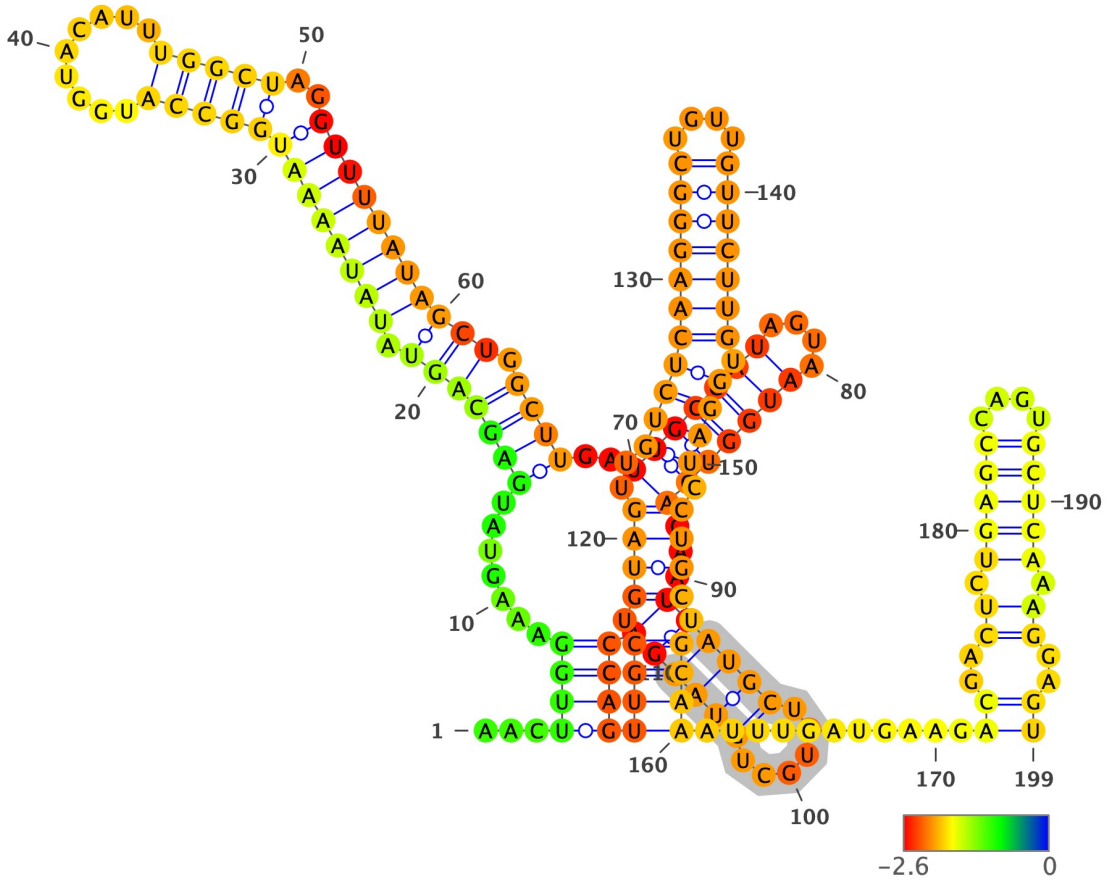
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 399 from nt 25259 to 25272 (nt 93 to 106)

```
5'-ATGCTTTGCTGUAU-3'
5'-((((.....))))-3'
Motif MFE = -0.8; z-score = -1.52; ED = 1.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25167 to 25365 (motif highlighted in silver):

```
5'-AACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCA
GUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGU-3
5'-...((((.......(((((((.(((((((((((((.........)))))..)))))))))))).)))))..(((((((....)))))))...((((((.....)))))))))
)(((((.((((..(((((((((((....)))))))).)))).)))).)))).........((..((.(((((....))))).)).))-3'
MFE = -54.7; z-score = -1.86; ED = 44.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

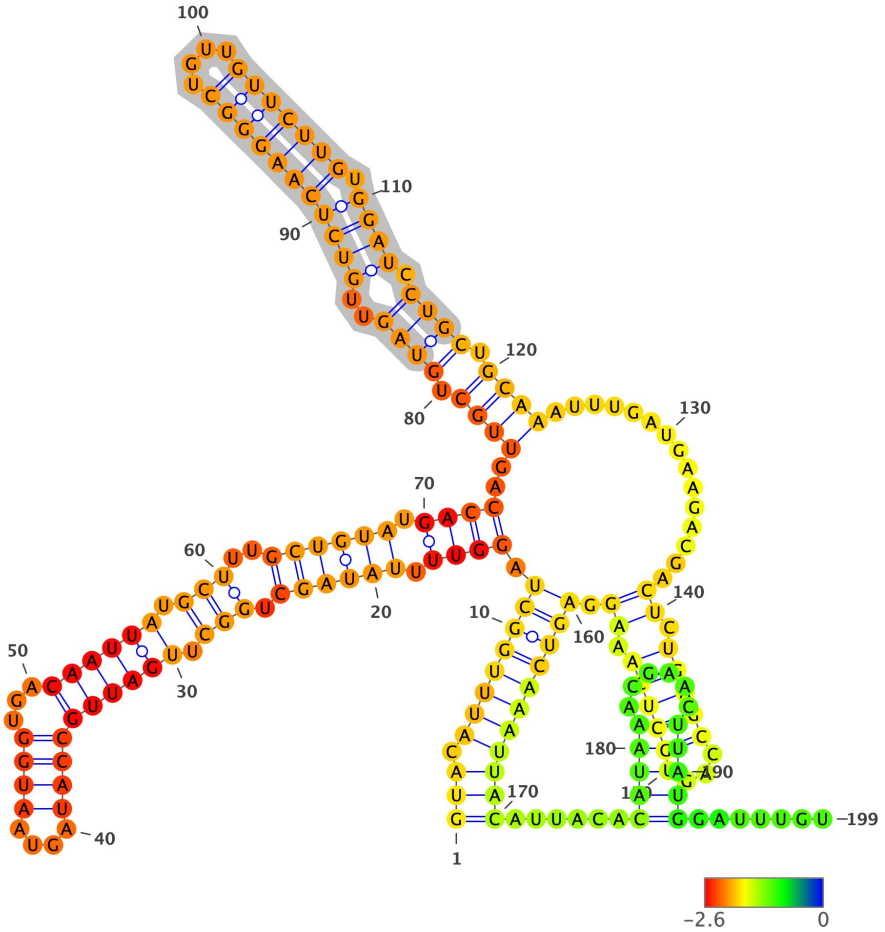
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 400 from nt 25285 to 25320 (nt 82 to 117)

```
5'-TAGTTGTCTCAAGGGCTGTTGUUCUUGTGGAUCCUG-3'
5'-(((..((((((((((....)))))))).))))).)))-3'
Motif MFE = -9.7; z-score = -1.65; ED = 3.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25204 to 25402 (motif highlighted in silver):

```
5'-GUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGG
AUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGU-3
5'-(((.(((((((((.((((.((((((.(((.((((((((((....)))).....)))))))).))))..)))))))).)))).))))..((((.((((..((((((((((....)))))))).))
)).)))).)))).....................((.((((((....)))))).)).)).)))))))))))).....(((((.....)))))).......-3'
MFE = -59.0; z-score = -2.76; ED = 28.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 181--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 181--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 190 to 199--gene, gene-GU280_gp03, 25393-26220(+)

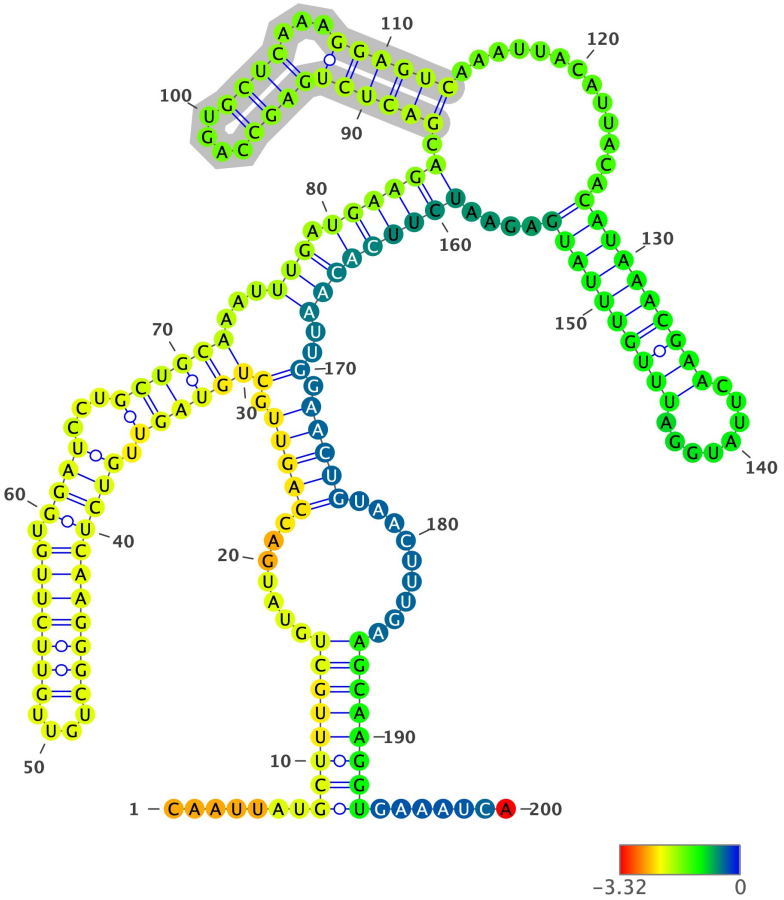
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 190 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 401 from nt 25340 to 25366 (nt 87 to 113)

```
5'-GACTCTGAGCCAGTGCUCAAAGGAGUC-3'
5'-(((((((((((....))))...))))))-3'
Motif MFE = -10.6; z-score = -2.69; ED = 1.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25254 to 25453 (motif highlighted in silver):

```
5'-CAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAG
UCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUAUGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCA-3
5'-.......((((((((.......(((((.(((((((.(((((((((((....)))))))).))))...))))))...(((.((((((.((((((((((....))))...))))
)).............((((((((((........))))))))))....))))))))))..).)))))..........))))))))........-3'
MFE = -55.1; z-score = -2.77; ED = 19.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 131--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 131--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 140 to 200--gene, gene-GU280_gp03, 25393-26220(+)

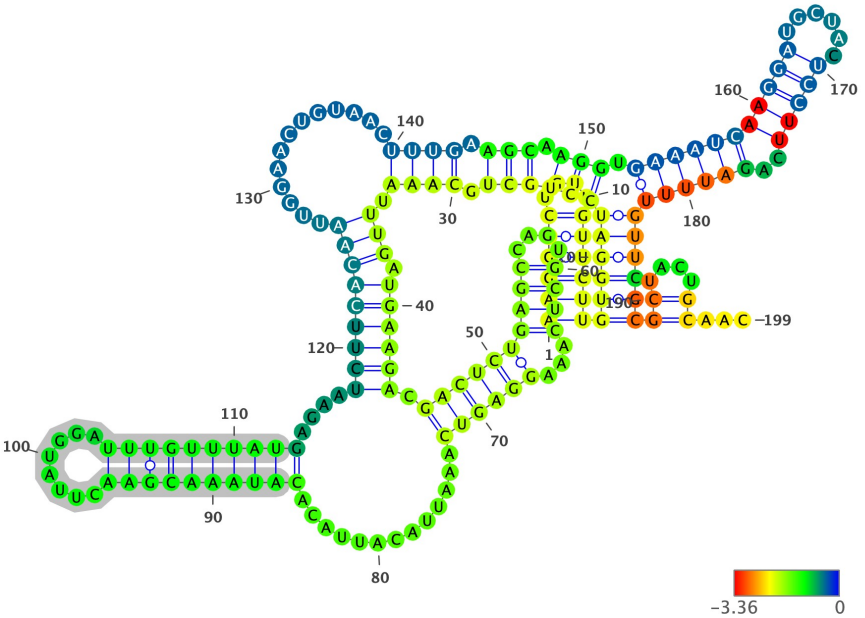
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 140 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 402 from nt 25381 to 25406 (nt 87 to 112)

```
5'-ATAAACGAACTTATGGAUUUGUUUAU-3'
5'-((((((((((........))))))))))-3'
Motif MFE = -4.1; z-score = -2.2; ED = 2.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25295 to 25493 (motif highlighted in silver):

```
5'-AAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUA
UGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAAC-3
5'-((((((....))))))((((((((((((.((((.(((.((((((.((((((((((....))))...))))))..............((((((((((........))))))))
))....))))))))).............)))).))).))).((((((((((((......)))))..))))))))))))((....))...-3'
MFE = -45.8; z-score = -0.93; ED = 48.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 90--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 90--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 99 to 199--gene, gene-GU280_gp03, 25393-26220(+)

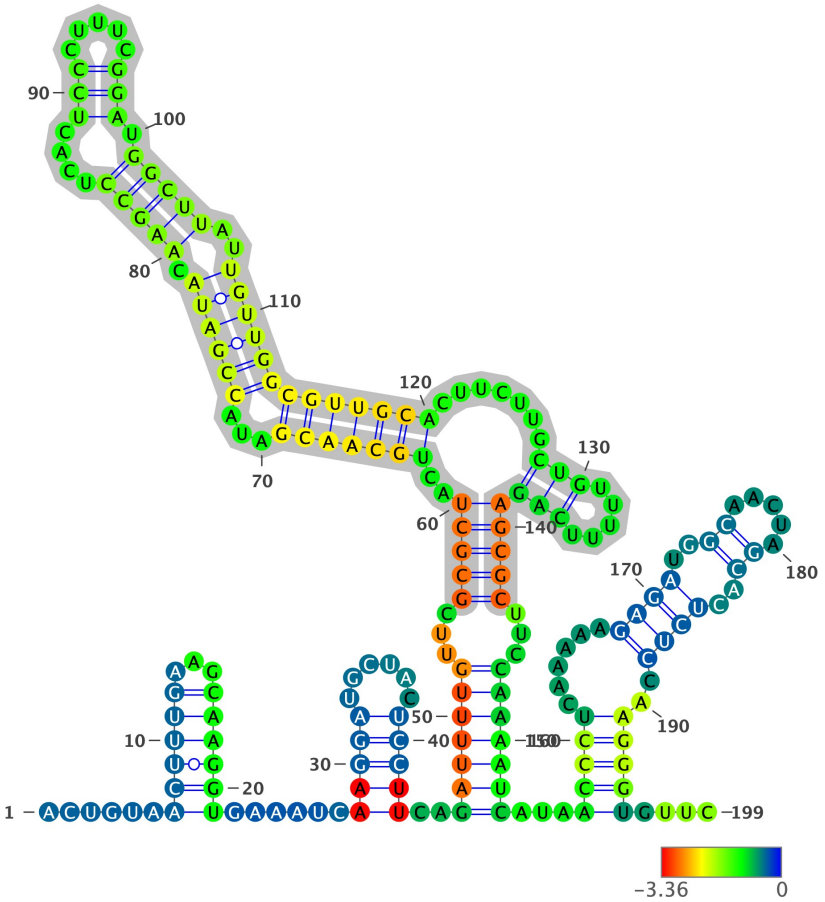
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 99 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 403 from nt 25481 to 25568 (nt 56 to 143)

```
5'-GCGCTACTGCAACGATACCGATACAAGCCTCACTCCCTTTCGGATGGCUUATUGUUGGCGUUGCACTTCTTGCTGTTTTTCAGAGCGC-3'
5'-(((((...((((((...((((((.(((((....(((.....))).)))))..))))))))))))..................)))))-3'
Motif MFE = -27.8; z-score = -2.3; ED = 6.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25426 to 25624 (motif highlighted in silver):

```
5'-ACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAACGAUACCGAUACAAGCCUCACUCCCUUUCGGAUGGCUUAUUGUU
GGCGUUGCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUC-3
5'-......((((((...))))))......(((((......)))))..(((((((...(((((..(((((((...((((((.(((((....(((.....))).)))))..))))
)))))))))).......(((.....))))))))...)))))))...(((((......((((..((.....))..))))..)))))....-3'
MFE = -53.2; z-score = -2.39; ED = 26.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

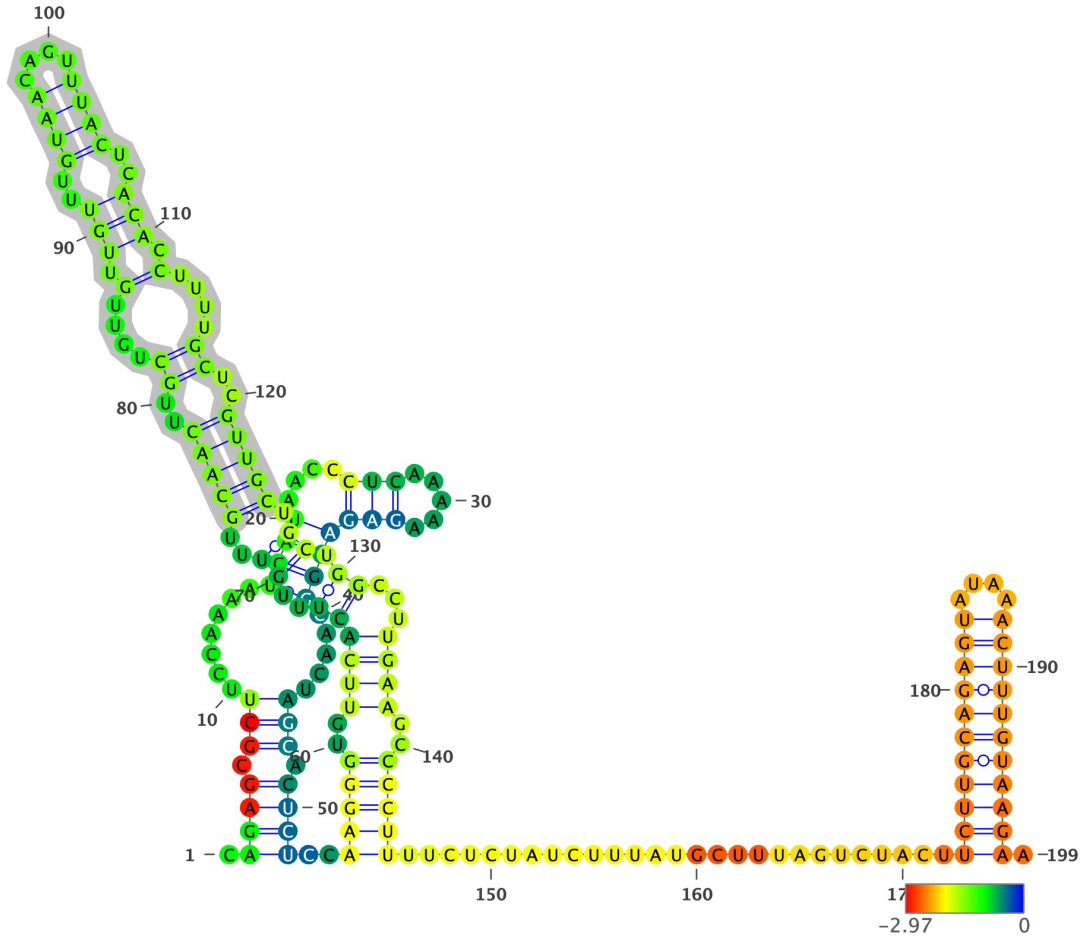
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 404 from nt 25634 to 25685 (nt 74 to 125)

```
5'-GCAACTTGCTGTTGTTGTTTGTAACAGTUUACTCACACCTTTTGCTCGUUGC-3'
5'-(((((..((....(.(((..((((....)))))..))).)....))..)))))-3'
Motif MFE = -11.3; z-score = -2.63; ED = 1.88
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25561 to 25759 (motif highlighted in silver):

```
5'-CAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACAC
CUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAA-3
5'-.((((.(((.......((((....(((.....)))))))).....))).))))..(((((..((((((..((..(((((..((....(.(((..((((....)))).)))).
)....))..)))))).)).))...))))..)))))..........................((((((((((....)))))))))).-3'
MFE = -44.2; z-score = -2.36; ED = 35.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

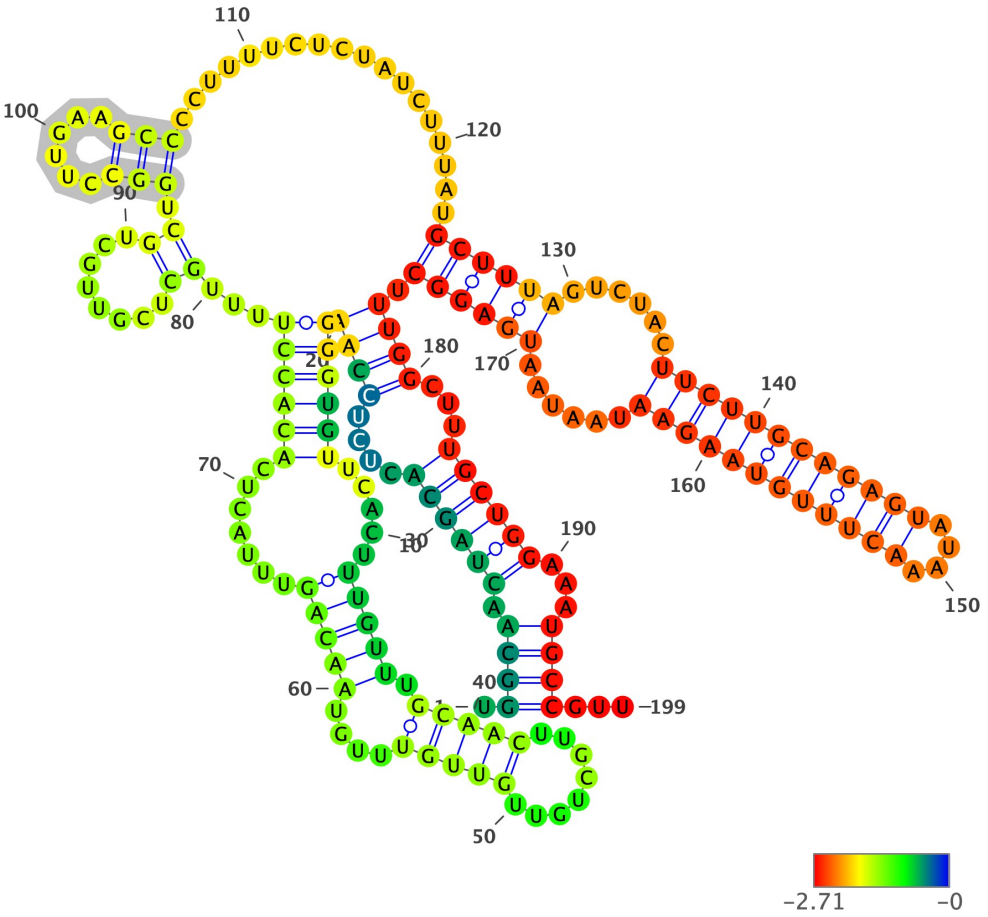
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 405 from nt 25690 to 25701 (nt 94 to 105)

```
5'-GGCCTTGAAGCC-3'
5'-((........))-3'
Motif MFE = -2.3; z-score = -2.75; ED = 0.23
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25597 to 25795 (motif highlighted in silver):

```
5'-UGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUU
CUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUU-3
5'-.((((.((((((....((((((((((.....(((((.(((((........)))))....)))))).......)))))))...((........)).(((......)))).....
............((((((.....((((((((((((....)))))))))))).....)))))).)))))...)))))))...)))))...-3'
MFE = -52.7; z-score = -3.55; ED = 38.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

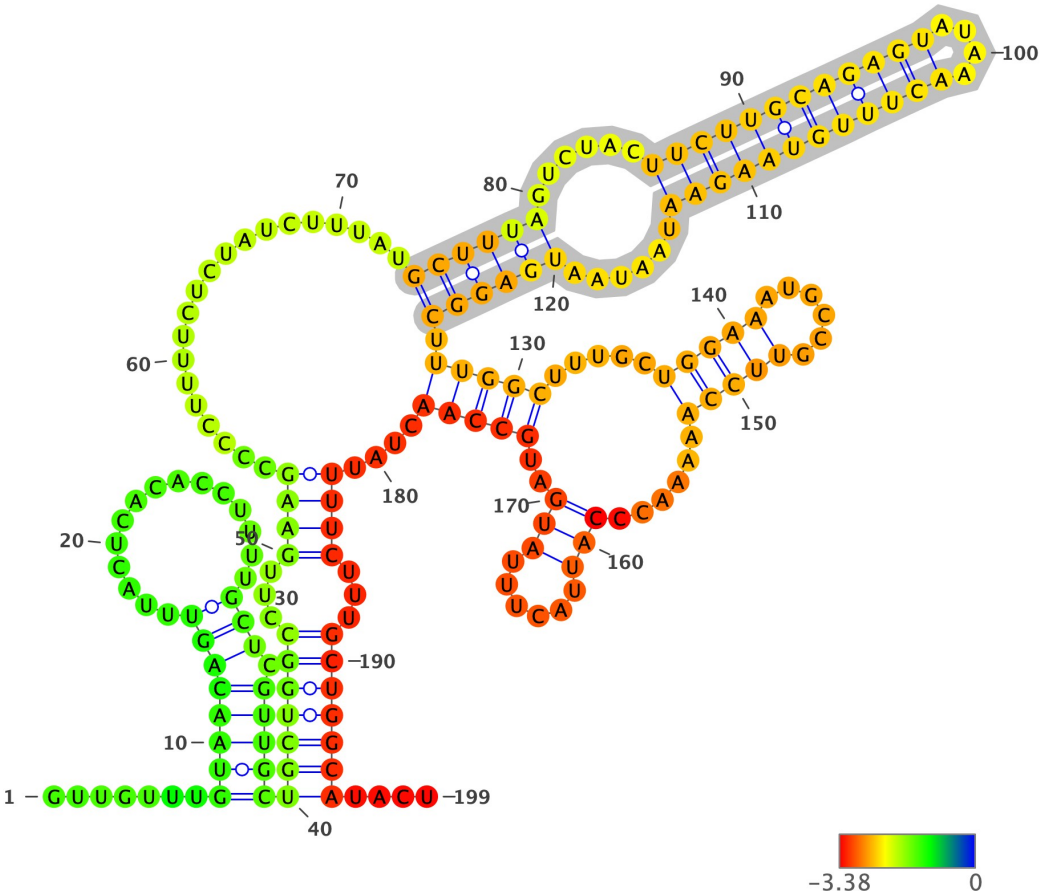
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 406 from nt 25720 to 25771 (nt 74 to 125)

```
5'-GCTTTAGTCTACTTCTTGCAGAGTATAAACUUUGUAAGAATAATAATGAGGC-3'
5'-((((........((((((((((((....))))))))))))........))))-3'
Motif MFE = -18.3; z-score = -4.63; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25647 to 25845 (motif highlighted in silver):

```
5'-GUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAG
AAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACU-3
5'-.......((((((((...............))).)))))(((((((...((((.....................((((((......((((((((((((....))))))))))
))......)))))).(((((.....(((((......)))))......(((......)))..)))))....))))...)))))))....-3'
MFE = -42.2; z-score = -1.72; ED = 39.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

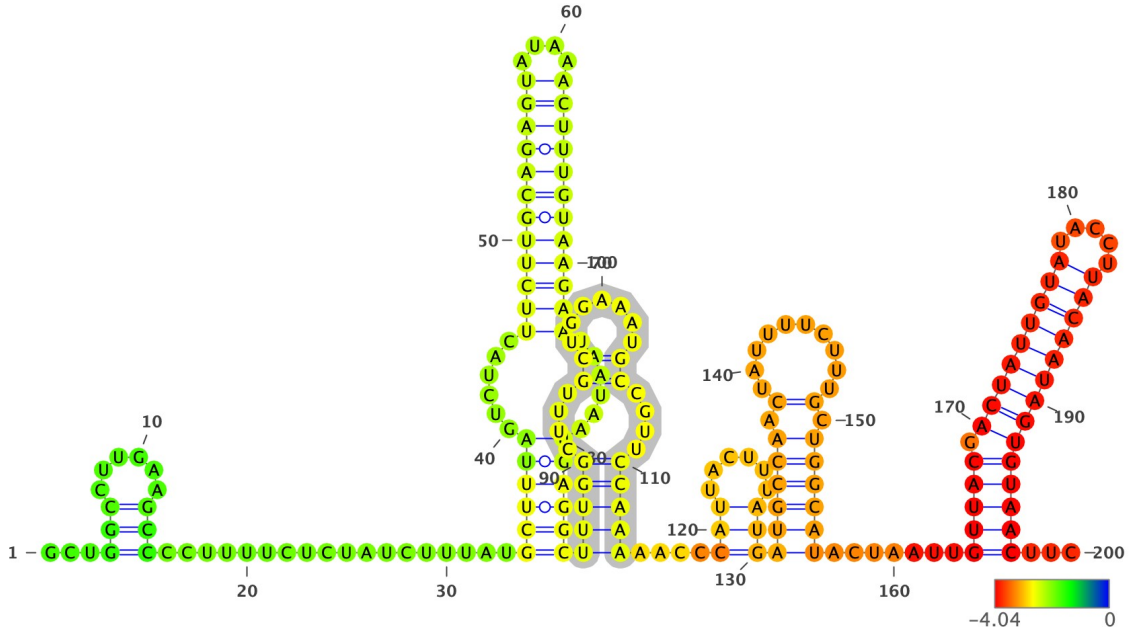
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 407 from nt 25772 to 25800 (nt 86 to 114)

```
5'-TTTGGCTTTGCTGGAAATGCCGTTCCAAA-3'
5'-(((((....((.......)).....)))))-3'
Motif MFE = -4.4; z-score = -0.58; ED = 7.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25687 to 25886 (motif highlighted in silver):

```
5'-GCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCC
AAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUC-3
5'-...(((......)))..................((((((......(((((((((((....)))))))))))).....))))))(((((....((.......)).....))
))).....(((......)))((((((.(..........).))))))......(((((.(((((((((.....)))))))))))))))...-3'
MFE = -49.5; z-score = -4.41; ED = 25.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

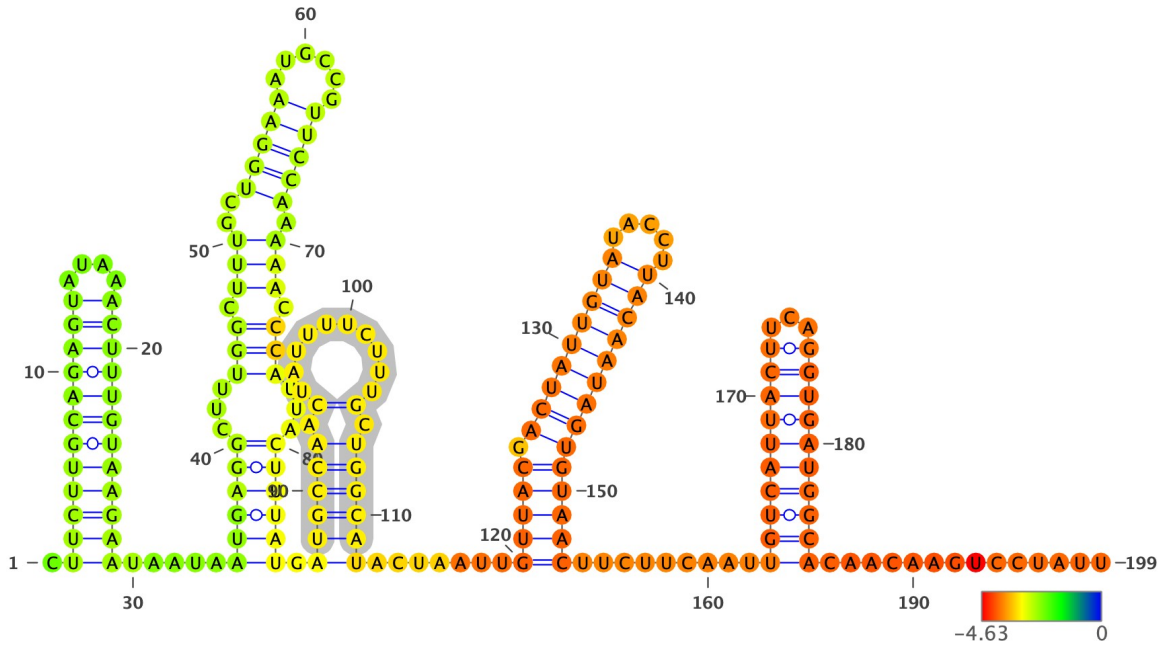
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 408 from nt 25818 to 25841 (nt 88 to 111)

```
5'-TGCCAACTATTTTCTTTGCUGGCA-3'
5'-(((((.(..........).)))))-3'
Motif MFE = -4.8; z-score = -3.07; ED = 1.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25731 to 25929 (motif highlighted in silver):

```
5'-CUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCA
UACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUU-3
5'-.(((((((((((....)))))))))))).....((((((...(((.(((..(((((......))))).))).)))...)))))).((((((.(..........).)))))
).......(((((.(((((((((.....)))))))))))))).........((((((((((...)))))))))).............-3'
MFE = -56.9; z-score = -4.54; ED = 21.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

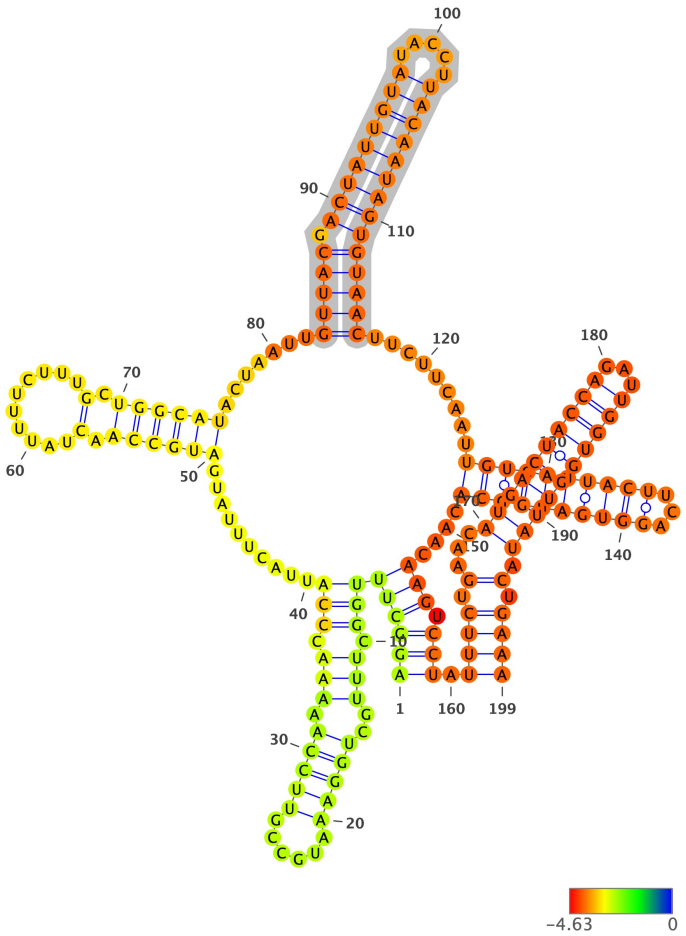
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 409 from nt 25850 to 25883 (nt 83 to 116)

```
5'-GTTACGACTATTGTATACCTUACAAUAGUGUAAC-3'
5'-(((((.(((((((((.....)))))))))))))-3'
Motif MFE = -13.6; z-score = -5.25; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25768 to 25966 (motif highlighted in silver):

```
5'-AGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGU
GUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAA-3
5'-(((((((((.(((..(((((.....))))).))).))).........((((((.(..........).))))))).......(((((.(((((((((.....)))))))))
))))).........((((((((((...)))))))))....))).))).((((.(...((((((((((...)))))))))).).))))-3'
MFE = -53.8; z-score = -3.89; ED = 18.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

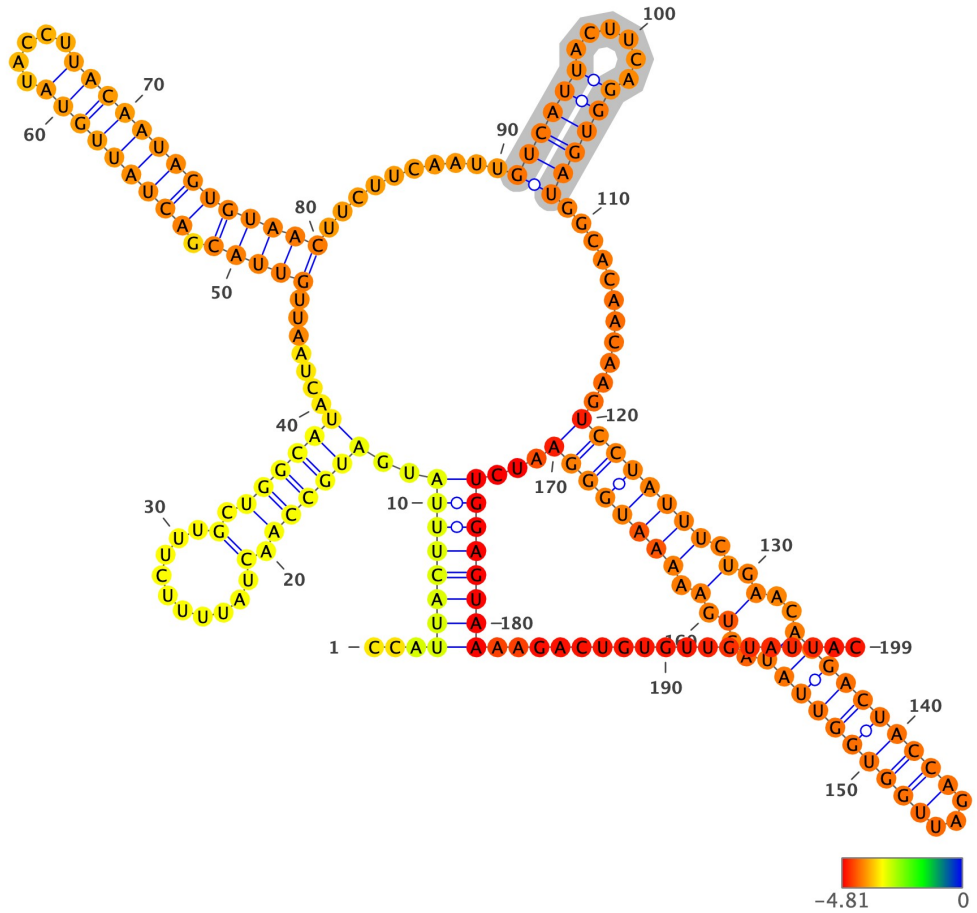
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 410 from nt 25894 to 25911 (nt 91 to 108)

```
5'-GTCATTACTTCAGGUGAU-3'
5'-(((((........)))))-3'
Motif MFE = -2.4; z-score = -1.71; ED = 4.29
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25804 to 26002 (motif highlighted in silver):

```
5'-CCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGC
ACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUAC-3
5'-...((((((((..((((((.(..........).))))))).......(((((.((((((((((.....)))))))))))))).........((((((......))))))...
........((((((((.(.(..((((((((((...)))))))))..).).))))))))...))))))))...................-3'
MFE = -48.7; z-score = -3.83; ED = 23.54
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

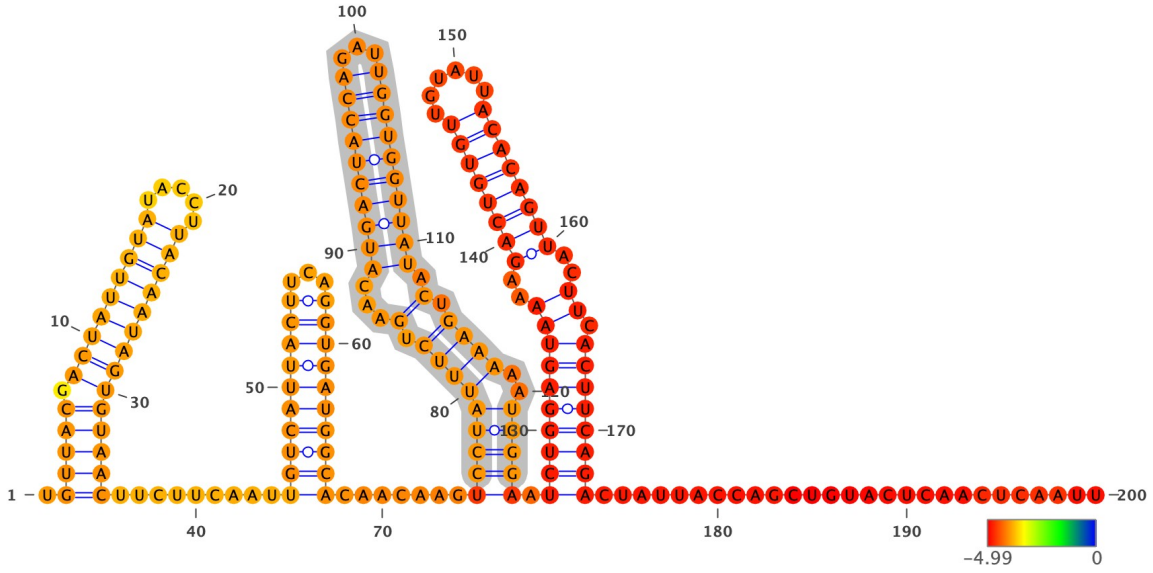
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 411 from nt 25924 to 25972 (nt 76 to 124)

```
5'-CCTATTTCTGAACATGACTACCAGATTGGUGGUUAUACTGAAAAAUGGG-3'
5'-((((((((.(...((((((((((.....)))))))))).).))))..))))-3'
Motif MFE = -15.9; z-score = -3.26; ED = 3.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25849 to 26048 (motif highlighted in silver):

```
5'-UGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAU
ACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUU-3
5'-.(((((.((((((((((.....)))))))))))))).........((((((((((...)))))))))).......((((((((((.(...((((((((((...)))))))))))
.).))))..))))).((((((((((..((((((((.....))))))))..)).))))))))...........................-3'
MFE = -61.1; z-score = -5.53; ED = 17.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

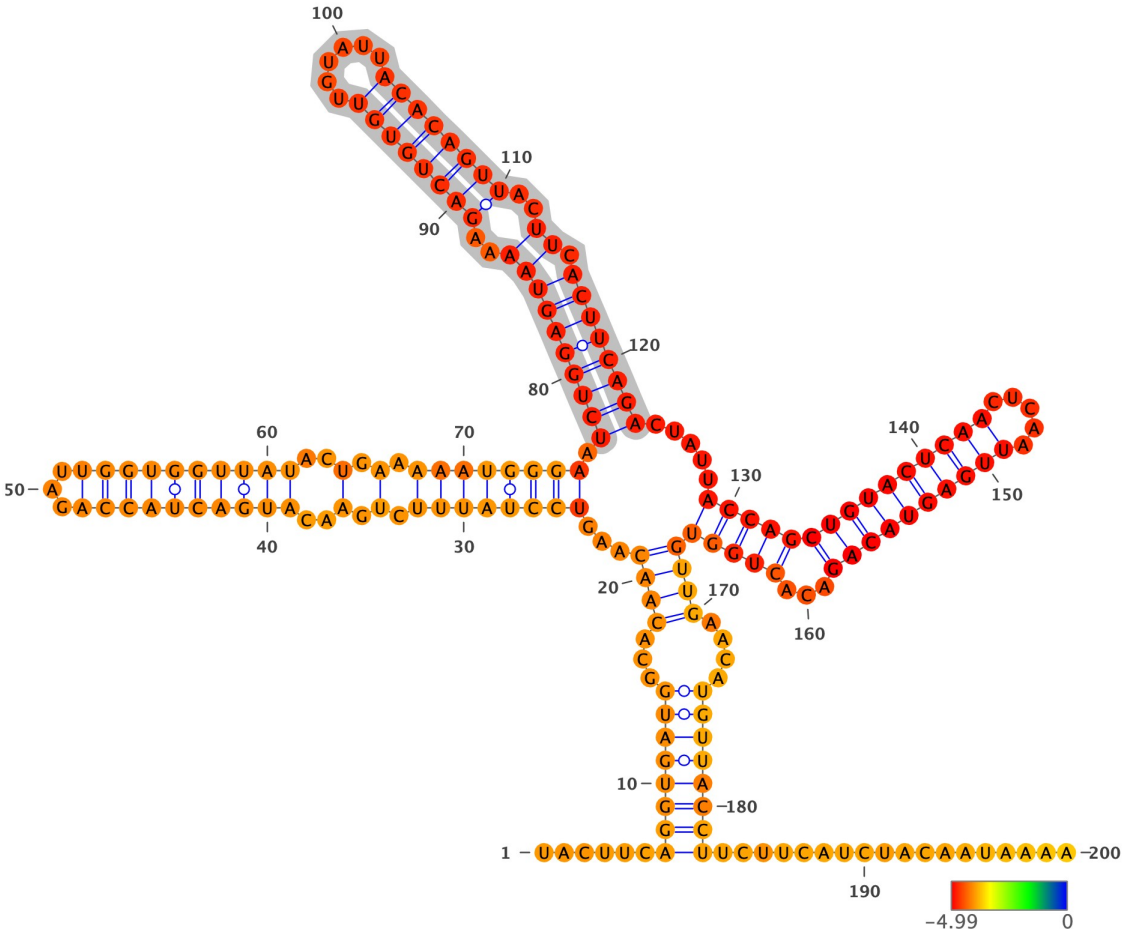
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 412 from nt 25975 to 26021 (nt 77 to 123)

```
5'-TCTGGAGTAAAAGACTGTGTTGTATTACACAGUUACUUCACUUCAGA-3'
5'-((((((((((..((((((((.....))))))))..)).))))))))-3'
Motif MFE = -19.0; z-score = -4.81; ED = 2.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25899 to 26098 (motif highlighted in silver):

```
5'-UACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUA
CUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAA-3
5'-......((((((((...((((...((((((((.(.(..((((((((((...))))))))))..).).))))))))).((((((((((..((((((((......))))))))).
.)).))))))))).....((((((((((((((.....))))))))))...))))))))).....))))))))).................-3'
MFE = -66.5; z-score = -5.48; ED = 11.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

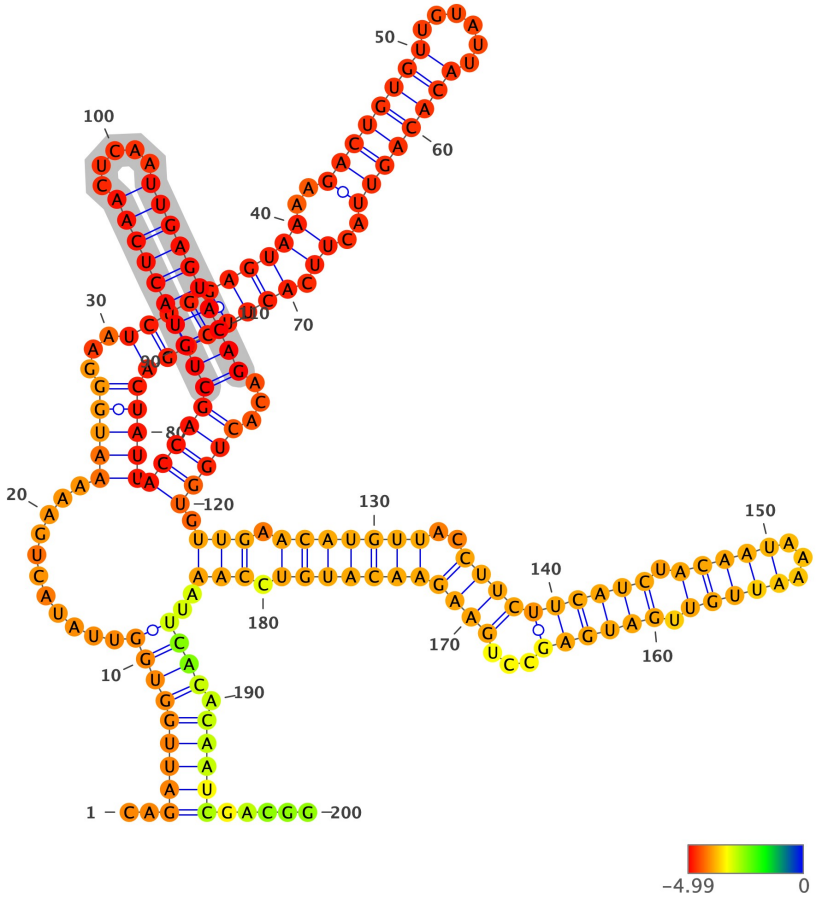
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 413 from nt 26032 to 26056 (nt 88 to 112)

```
5'-CTGTACTCAACTCAAUUGAGUACAG-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -11.8; z-score = -5.84; ED = 0.57
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25945 to 26144 (motif highlighted in silver):

```
5'-CAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACA
GACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGG-3
5'-..((((((((((...........(((((...((((((((((..((((((((.....))))))))..)).))))))))))))((((((((((((((.....)))))))))
)...))))).(((.(((((((..((((((((((.(((((...))))).))))))...))))))))))).)))..)))).)))))).....-3'
MFE = -66.5; z-score = -5.47; ED = 12.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

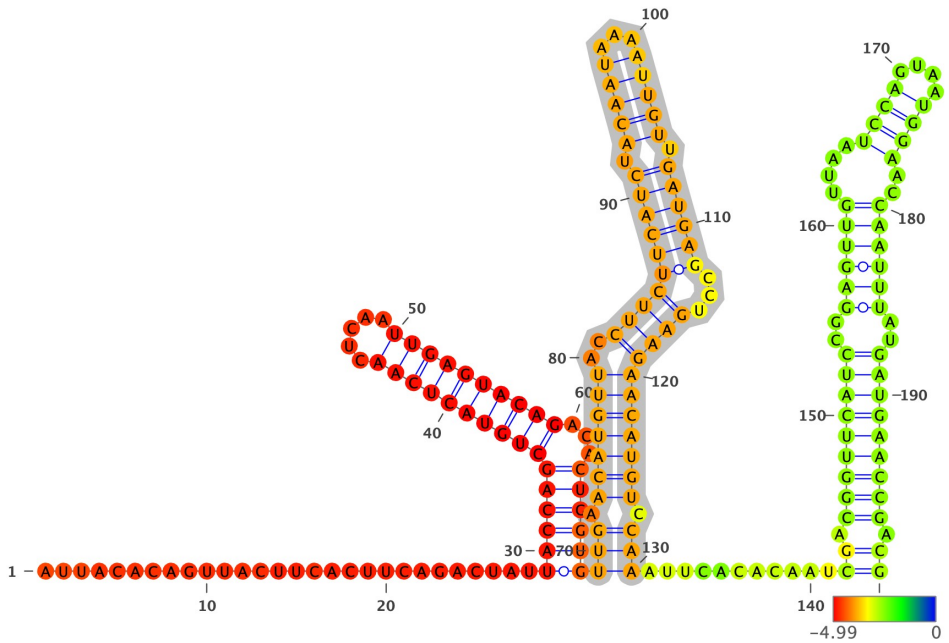
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 414 from nt 26066 to 26127 (nt 69 to 130)

```
5'-TTGAACATGTTACCTTCTTCATCTACAATAAAATUGUTGAUGAGCCTGAAGAACAUGUCCAA-3'
5'-(((.(((((((..((((.(((((.(((.......))).)))))....)))))))))))).)))-3'
Motif MFE = -18.2; z-score = -4.79; ED = 3.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25998 to 26196 (motif highlighted in silver):

```
5'-AUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGA
GCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACG-3
5'-.............................((((((((((((((((.....)))))))))))...))))))(((.(((((((..((((((((((.(((((...))))).)))))
)...)))))))))))).)))...........((.((((((((..((((((....((((....))))..))))))..))))))))).))-3'
MFE = -59.6; z-score = -5.04; ED = 9.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

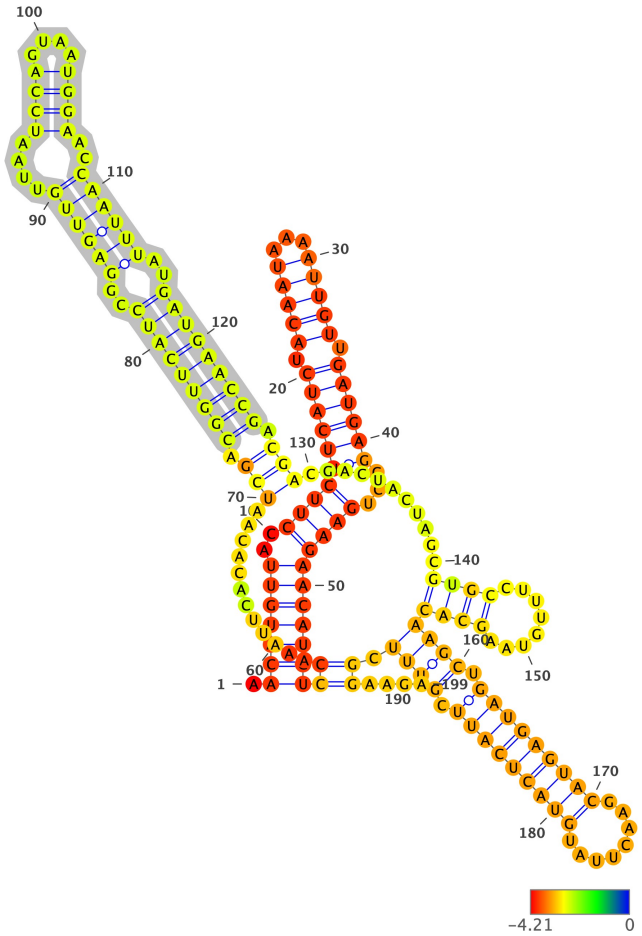
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 415 from nt 26142 to 26193 (nt 74 to 125)

```
5'-CGGTTCATCCGGAGTTGTTAATCCAGTAATGGAACCAAUUUATGAUGAACCG-3'
5'-((((((((..((((((....((........))..))))))..)))))))))-3'
Motif MFE = -19.6; z-score = -4.56; ED = 1.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26069 to 26267 (motif highlighted in silver):

```
5'-AACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAA
UUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGA-3
5'-.(((((((..((((((((((.(((((...))))).))))))...))))))))))((.............(((.((((((((..((((((....((((....))))..)))
)))..))))))))).))).........((((........))))((((.((((((((.........))))))))).)))).)).....-3'
MFE = -59.6; z-score = -3.99; ED = 14.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 152--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 152--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 177 to 199--gene, gene-GU280_gp04, 26245-26472(+)

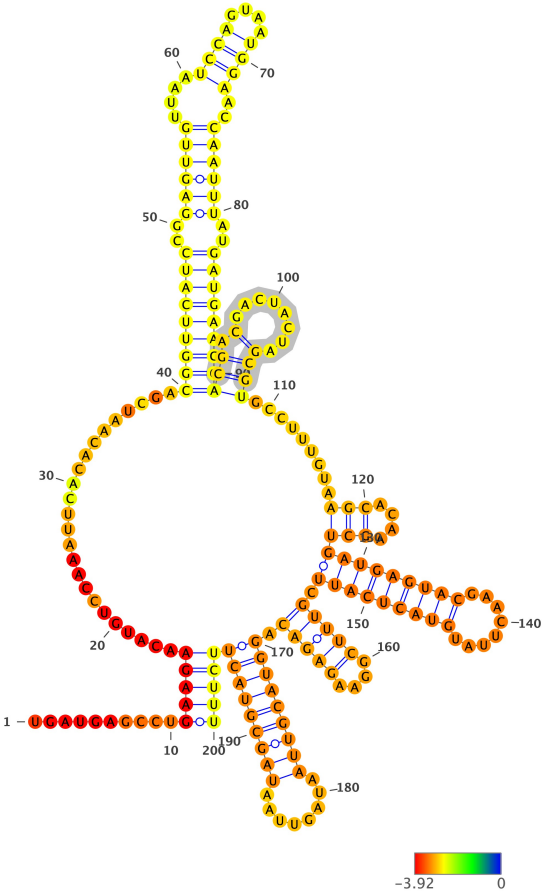
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 177 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 416 from nt 26195 to 26209 (nt 93 to 107)

```
5'-CGACGACTACTAGCG-3'
5'-((.(........)))-3'
Motif MFE = 0.0; z-score = 0.72; ED = 1.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26103 to 26302 (motif highlighted in silver):

```
5'-UGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCC
UUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUU-3
5'-..........(((((.........................(((((((((..((((((....((((....))))..))))))..))))))))))(((.(........))))...
......(((....)))((((((((.........))))))))).(((((....))))).(((((((((.........)))))))))))))-3'
MFE = -53.3; z-score = -2.98; ED = 23.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 118--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 118--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 143 to 200--gene, gene-GU280_gp04, 26245-26472(+)

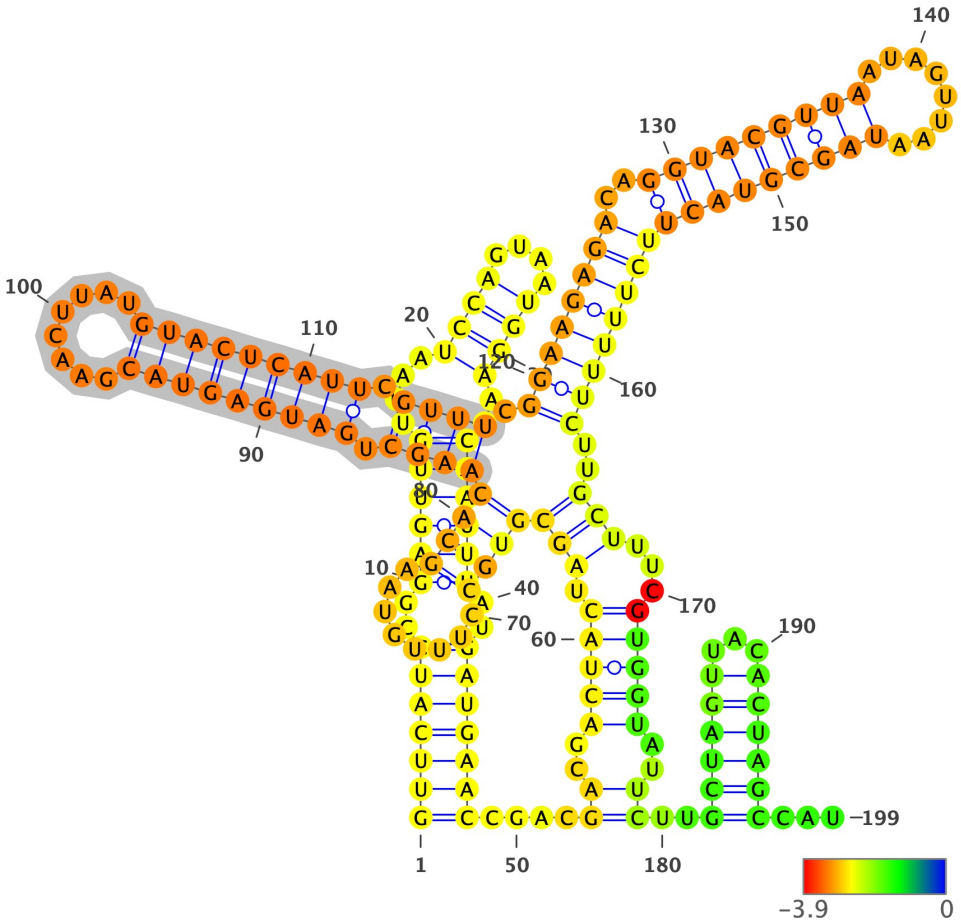
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 143 to 200--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 417 from nt 26225 to 26260 (nt 82 to 117)

```
5'-AAGCTGATGAGTACGAACTTATGUACUCAUUCGUUU-3'
5'-((((.((((((((((........)))))))))).))))-3'
Motif MFE = -13.0; z-score = -4.01; ED = 1.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26144 to 26342 (motif highlighted in silver):

```
5'-GUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAU
UCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAU-3
5'-(((((((..((((((....((((....))))..))))))..)))))))....((..(((((.(((((((........))))((((.(((((((((........))))))))
).)))).((((((((..(((((((((........)))))))))))))))))..)))...)))))..))..((((((...))))))...-3'
MFE = -63.5; z-score = -3.9; ED = 16.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 77--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 77--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 102 to 199--gene, gene-GU280_gp04, 26245-26472(+)

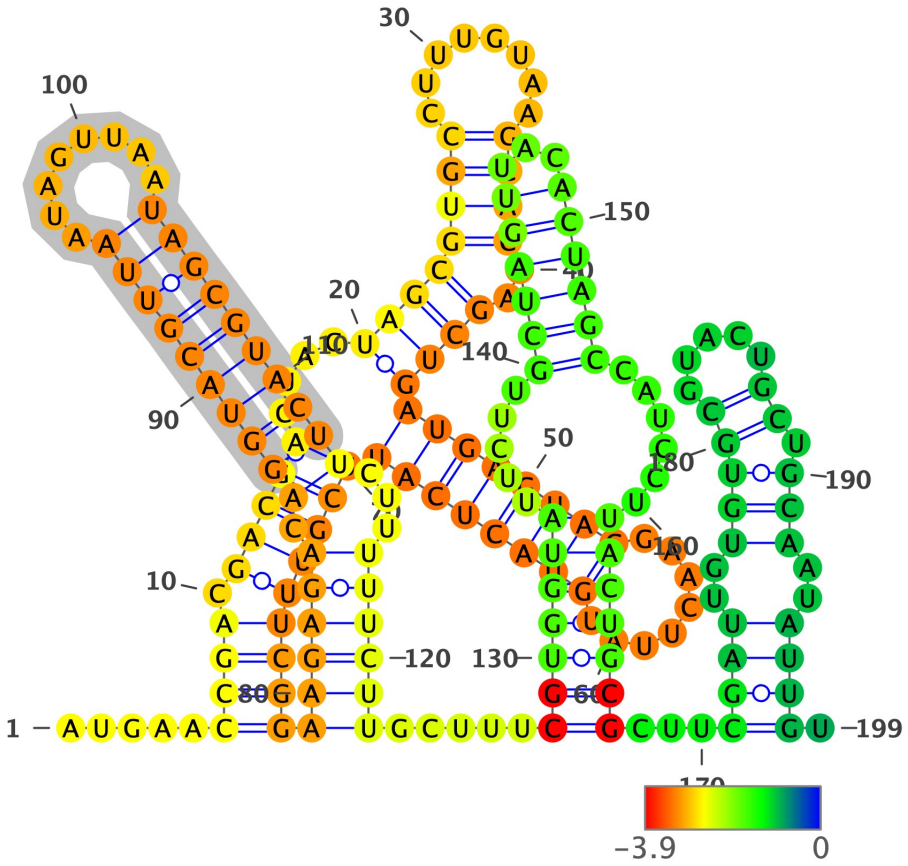
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 102 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 418 from nt 26272 to 26297 (nt 87 to 112)

```
5'-GGTACGTTAATAGTTAAUAGCGUACU-3'
5'-(((((((((........)))))))))-3'
Motif MFE = -8.9; z-score = -4.71; ED = 0.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26186 to 26384 (motif highlighted in silver):

```
5'-AUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUAC
UUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGU-3
5'-.....((((.(((((....((((((((........))))..))))((((((((........))))))))))))))))((((((.((((((((((........))))))))
))...))))))).....(((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..)))).-3'
MFE = -56.3; z-score = -2.64; ED = 36.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 35--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 35--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 60 to 199--gene, gene-GU280_gp04, 26245-26472(+)

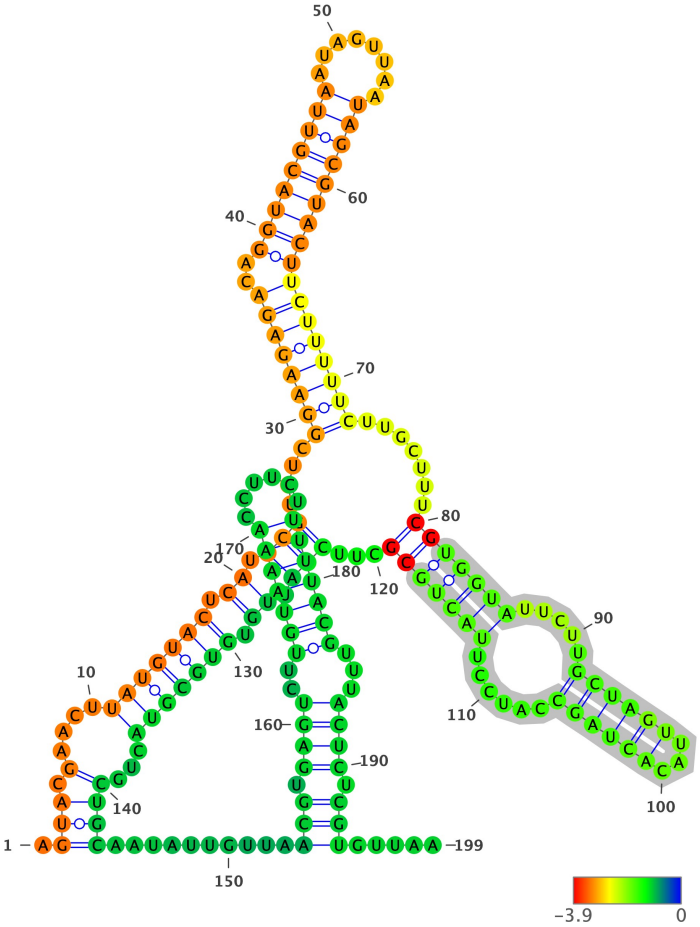
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 60 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 419 from nt 26315 to 26350 (nt 82 to 117)

```
5'-TGGTATTCTTGCTAGTTACACUAGCCATCCTUACUG-3'
5'-(((((.....((((.......)))).....)))))-3'
Motif MFE = -7.8; z-score = -2.34; ED = 2.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26234 to 26432 (motif highlighted in silver):

```
5'-AGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCC
UUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAA-3
5'-.((((.(....(((((((.((.(((....((((((((..(((((((((.......)))))))))))))))))).......(((((((.....((((((...)))))).....
.)))))))...)))).)).)))))))...))))..........(((.((((..(((((((.....)))))))...)))).)))).....-3'
MFE = -50.8; z-score = -3.05; ED = 27.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 12 to 199--gene, gene-GU280_gp04, 26245-26472(+)

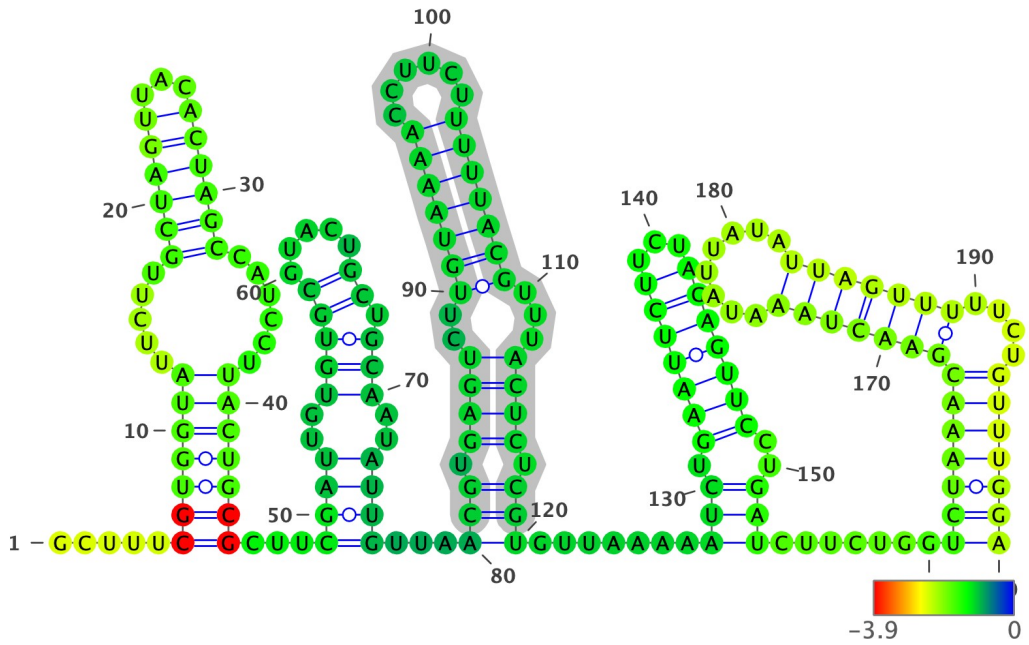
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 12 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 420 from nt 26388 to 26426 (nt 81 to 119)

```
5'-CGTGAGTCTTGTAAAACCTTCTUUUUACGTTTACUCTCG-3'
5'-((.((((..(((((((.....)))))))...)))).))-3'
Motif MFE = -7.9; z-score = -2.06; ED = 1.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26308 to 26507 (motif highlighted in silver):

```
5'-GCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUU
UACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGA-3
5'-.....(((((((.....((((((...)))))).....)))))))...((((..(((((.....)).)))..)))))...(((.((((..(((((((.....)))))))..
.)))).)))).....(((.(((((((...)))))))..)))).....((((((((((((((.....)))))))....)))))))-3'
MFE = -42.5; z-score = -1.66; ED = 21.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 165--gene, gene-GU280_gp04, 26245-26472(+)

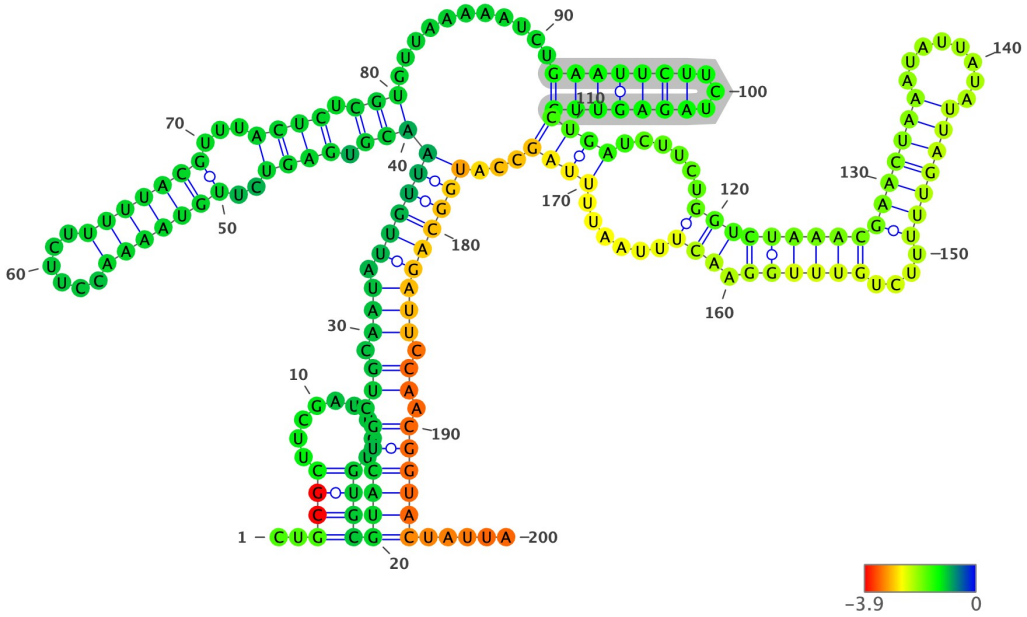
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 165--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 421 from nt 26439 to 26455 (nt 92 to 108)

```
5'-GAATTCTTCTAGAGUUC-3'
5'-(((((((...)))))))-3'
Motif MFE = -3.9; z-score = -5.47; ED = 0.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26348 to 26547 (motif highlighted in silver):

```
5'-CUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUG
AUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUA-3
5'-..((((.........))))((((((.((.(((.(((((((((.((((..(((((((.......)))))))...)))).))).........(((((((...)))))))(((
(......((((((((((((((((.........)))))))....)))))).)))......))))...))))))))).)).))))))).....-3'
MFE = -42.6; z-score = -1.56; ED = 30.5
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 125--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 125--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 176 to 200--gene, gene-GU280_gp05, 26523-27191(+)

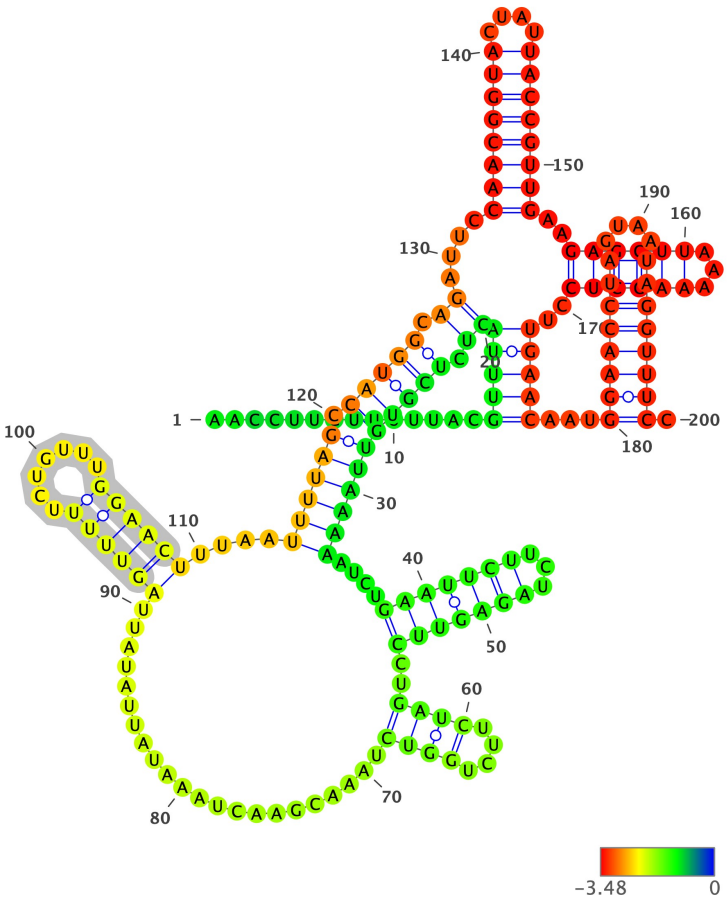
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 176 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 422 from nt 26493 to 26509 (nt 92 to 108)

```
5'-GTTTTTCTGTTTGGAAC-3'
5'-(((((.......)))))-3'
Motif MFE = -0.3; z-score = 0.05; ED = 4.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26402 to 26601 (motif highlighted in silver):

```
5'-AACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUU
AAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCC-3
5'-..............(((((((.((((((((((((....(((((((...)))))))..((((....))))........................((((((.......))))))..
..))))))).))))).))....((((((((....))))))))..((((((...))))))..)))))...((((((((....))))))))).-3'
MFE = -42.1; z-score = -3.98; ED = 39.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 71--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 71--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 122 to 200--gene, gene-GU280_gp05, 26523-27191(+)

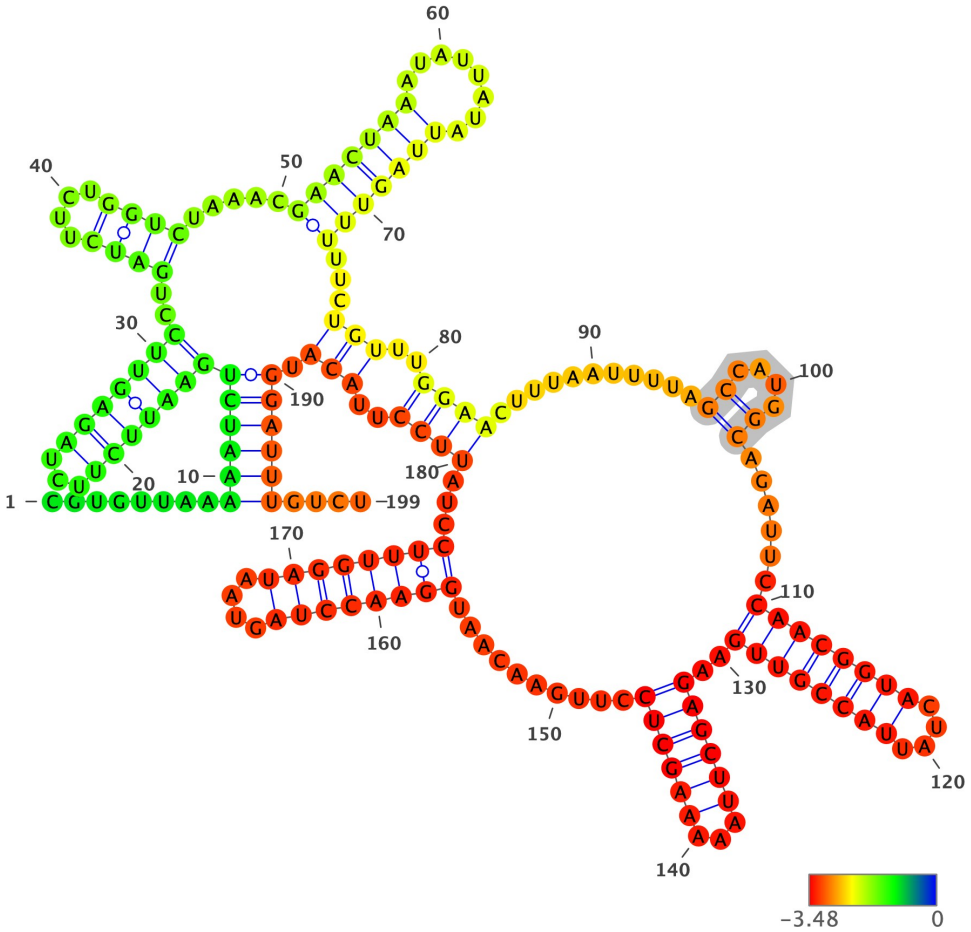
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 122 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 423 from nt 26520 to 26527 (nt 96 to 103)

```
5'-GCCATGGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 0.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26425 to 26623 (motif highlighted in silver):

```
5'-CGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCA
ACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCU-3
5'-........(((((((((((((...)))))))..((((....))))).....(((((((........)))))))...(((..((((...........((....)).....((
((((((....))))))))..((((((...))))))..........((((((((....))))))))...))))..))).))))))....-3'
MFE = -46.8; z-score = -3.91; ED = 37.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 48--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 48--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 99 to 199--gene, gene-GU280_gp05, 26523-27191(+)

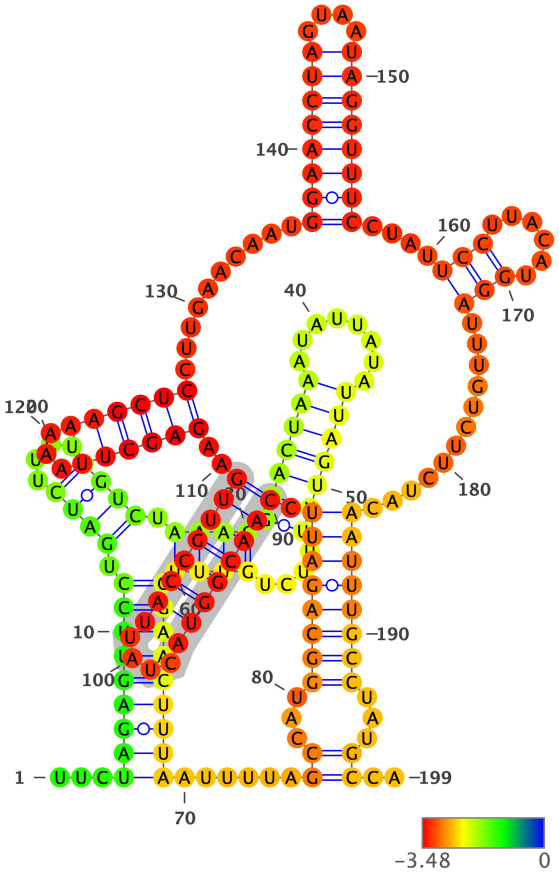
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 99 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 424 from nt 26534 to 26553 (nt 90 to 109)

```
5'-CAACGGTACTATUACCGUUG-3'
5'-((((((((....))))))))-3'
Motif MFE = -9.0; z-score = -4.93; ED = 0.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26445 to 26643 (motif highlighted in silver):

```
5'-UUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAA
GAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCA-3
5'-...(((((((((.((((....)))).(((((((((((........)))))))....))))))))))))).....((...((((((((.((((((((....))))))))..
((((((...))))))..........((((((((....))))))))....(((......)))............))))))))...))..-3'
MFE = -55.1; z-score = -4.63; ED = 18.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 28--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 28--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 79 to 199--gene, gene-GU280_gp05, 26523-27191(+)

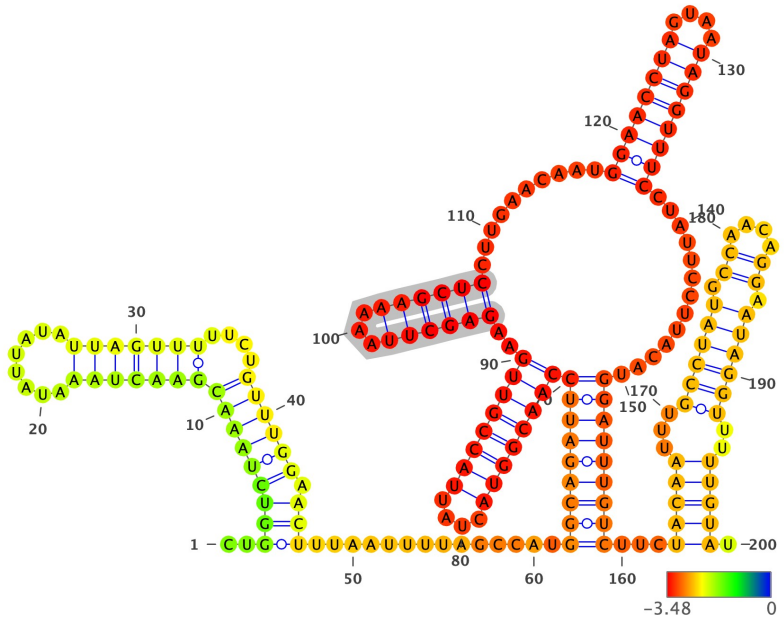
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 79 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 425 from nt 26556 to 26570 (nt 93 to 107)

```
5'-GAGCTTAAAAAGCUC-3'
5'-((((.......))))-3'
Motif MFE = -5.0; z-score = -6.22; ED = 0.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26464 to 26663 (motif highlighted in silver):

```
5'-CUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUG
AACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAU-3
5'-..((((((((((((((((.........)))))))....)))))).)))..............((((((((((((((((....))))))))..((((((...)))))).....
......((((((((....))))))))..............)))))))))...(((((...((((((.((....)).))))))..))))).-3'
MFE = -54.8; z-score = -4.38; ED = 22.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 9--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 9--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 60 to 200--gene, gene-GU280_gp05, 26523-27191(+)

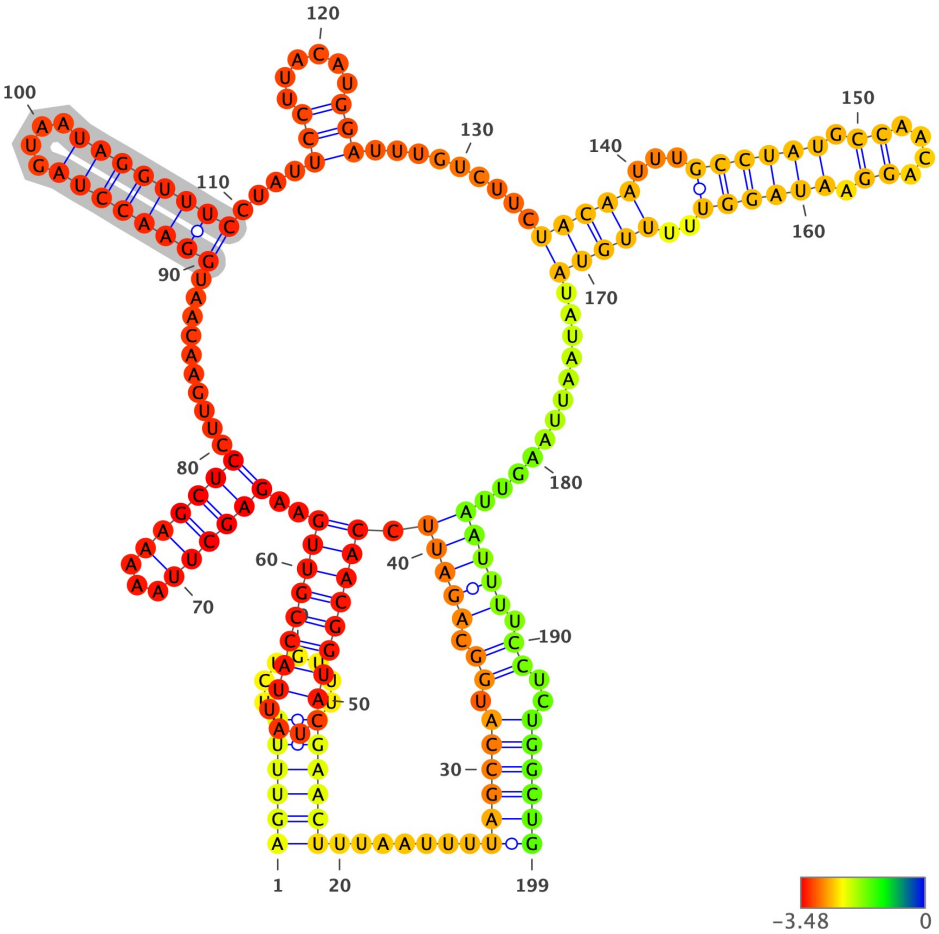
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 60 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 426 from nt 26581 to 26600 (nt 90 to 109)

```
5'-GGAACCTAGTAAUAGGUUUC-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.2; z-score = -4.52; ED = 0.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26492 to 26690 (motif highlighted in silver):

```
5'-AGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCU
AUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUG-3
5'-((((((.......))))))........((((((.((.(((((.((((((((....))))))))..((((((...))))))..........((((((((....))))))))..
..(((......)))..........(((((...((((((.((....)).))))))..)))))............)))))..))..))))))-3'
MFE = -52.9; z-score = -3.7; ED = 25.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 32 to 199--gene, gene-GU280_gp05, 26523-27191(+)

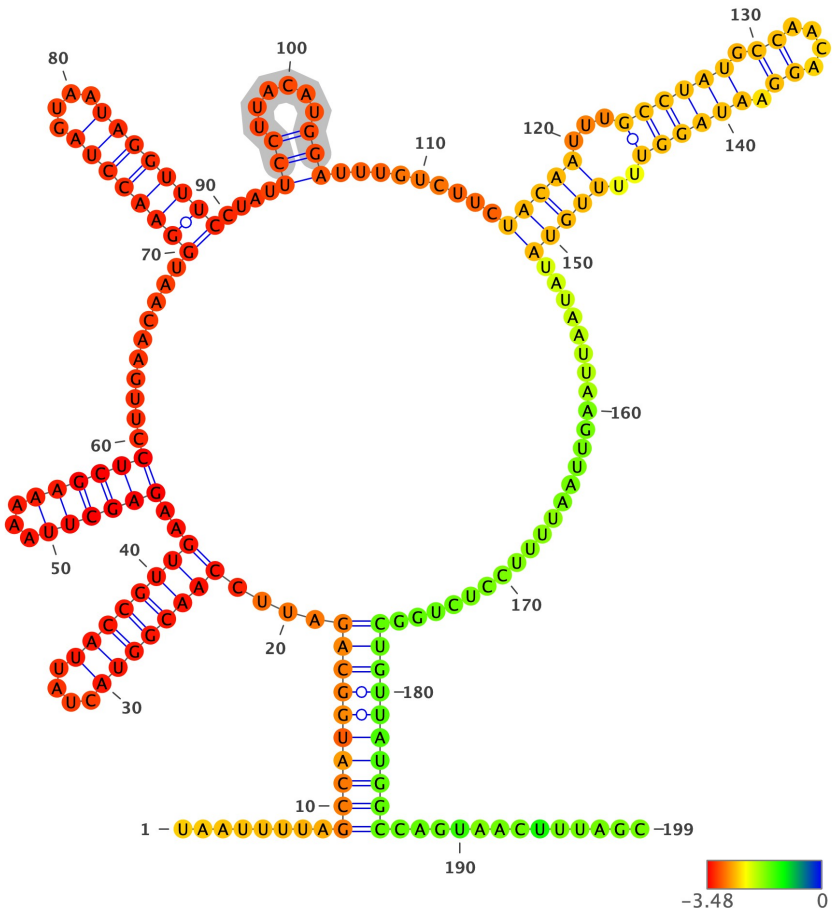
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 32 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 427 from nt 26606 to 26615 (nt 95 to 104)

```
5'-CCTTACATGG-3'
5'-((......))-3'
Motif MFE = 0.0; z-score = 0.16; ED = 1.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26512 to 26710 (motif highlighted in silver):

```
5'-UAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUC
UUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGC-3
5'-........((((((((((....((((((((....))))))))..((((((...))))))..........((((((((....))))))))....(((......)))......
...(((((...((((((.((....)).))))))..)))))........................))))))))))..............-3'
MFE = -56.4; z-score = -4.49; ED = 20.33
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 12 to 199--gene, gene-GU280_gp05, 26523-27191(+)

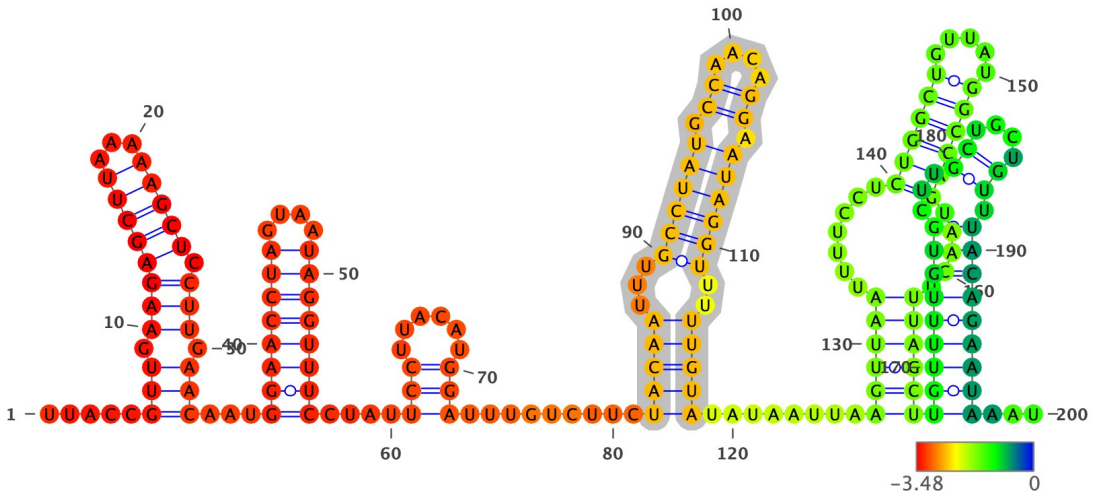
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 12 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 428 from nt 26626 to 26662 (nt 82 to 118)

```
5'-TACAATTTGCCTATGCCAACAGGAAUAGGUTTUUGUA-3'
5'-(((((...((((((.((....)).))))))..)))))-3'
Motif MFE = -10.9; z-score = -3.71; ED = 1.5
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26545 to 26744 (motif highlighted in silver):

```
5'-UUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGU
UUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAU-3
5'-.....(((.((((((((...))))).))).)))...((((((((....))))))))....(((......)))........(((((...((((((.((....)).))))))
..)))))........((((((.......((((((.....))))))).....))))))((((((((...((....)).)))))))))...-3'
MFE = -51.0; z-score = -3.25; ED = 24.18
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

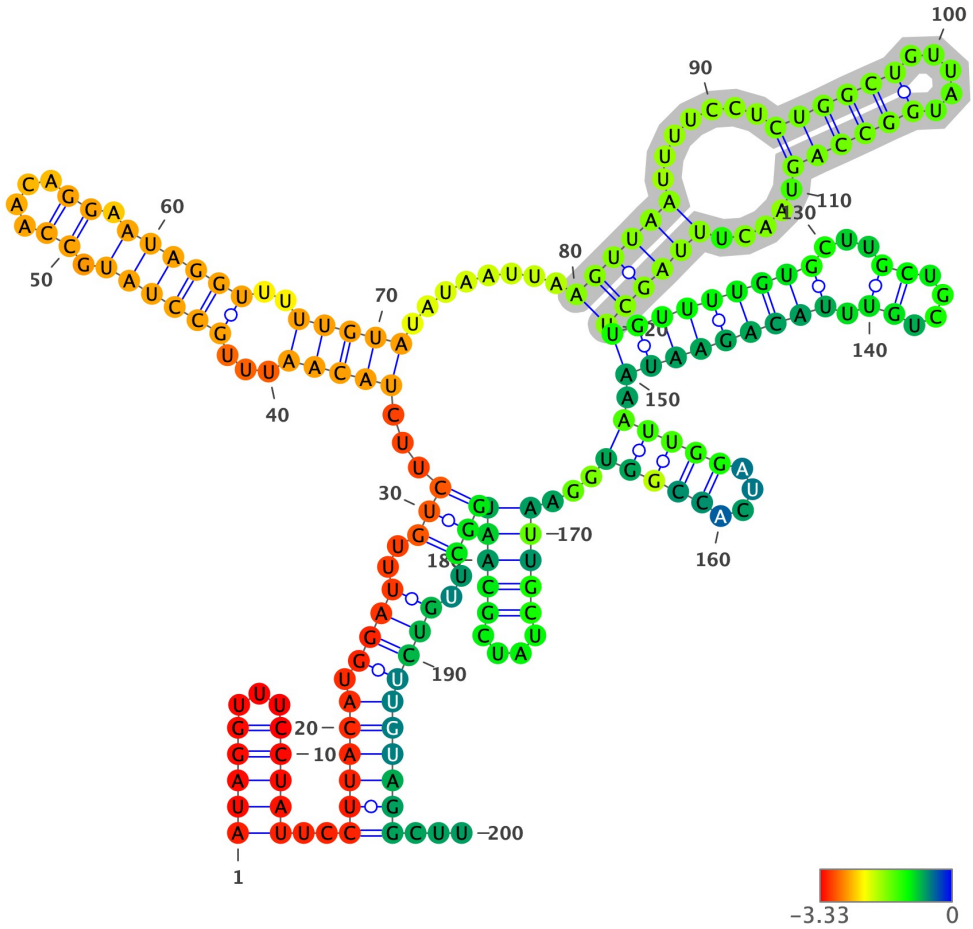
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 429 from nt 26671 to 26711 (nt 80 to 120)

```
5'-AGTTAATTTTCCTCTGGCTGTTATGGCCAGTAACTUUAGCU-3'
5'-((((((.......((((((.....))))))).....))))))-3'
Motif MFE = -11.1; z-score = -3.13; ED = 2.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26592 to 26791 (motif highlighted in silver):

```
5'-AUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUA
ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUU-3
5'-(((((...)))))..((((((.((((..(((...(((((...((((((.((....)).))))))..)))))........((((((.......((((((.....))))))..
...))))))((((((((...((....)).)))))))).(((((....)))))...(((((....)))))))..))))))))))...-3'
MFE = -50.2; z-score = -1.86; ED = 38.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

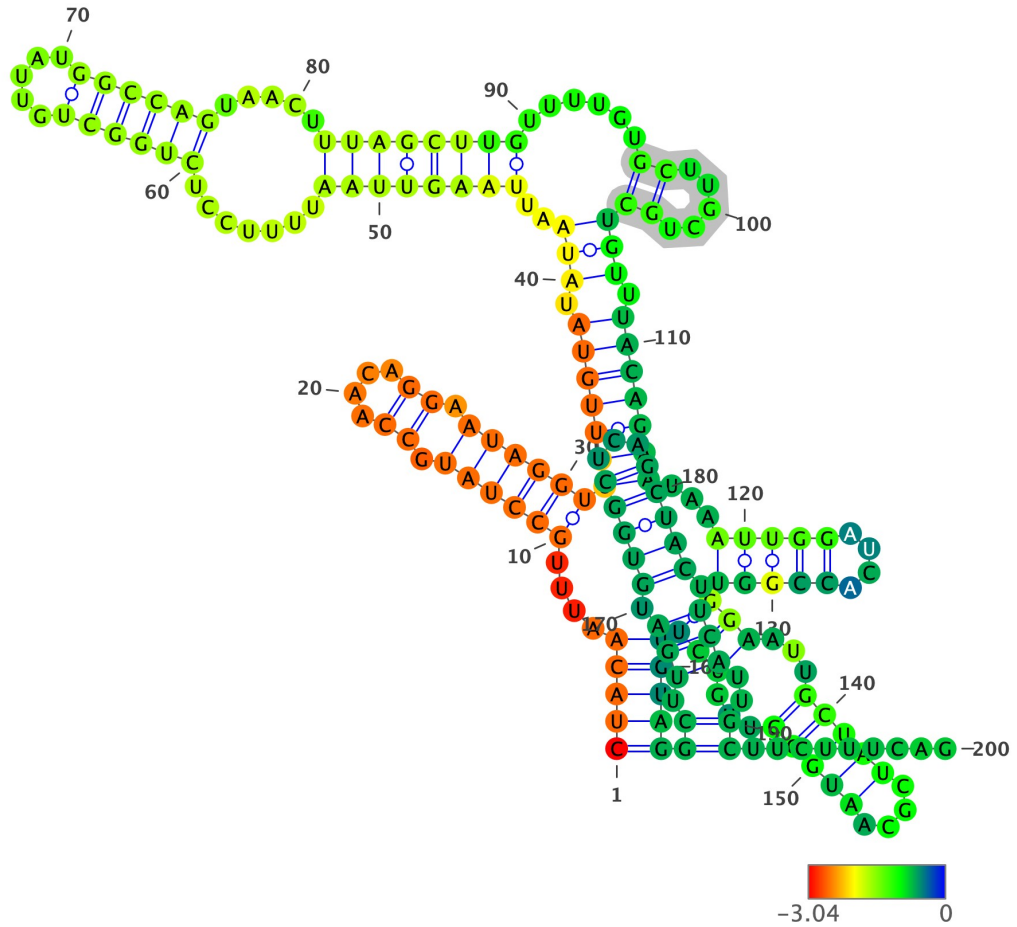
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 430 from nt 26720 to 26728 (nt 96 to 104)

```
5'-GCTTGCTGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.16; ED = 0.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26625 to 26824 (motif highlighted in silver):

```
5'-CUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUAC
AGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUUGCUUCUUUCAG-3
5'-(((((....((((((.((....)).))))))(((((((.(((..((((((((.......((((((.....))))))).....))))))))......((.....))))).)))
))))...(((((....)))))(((...(((((....)))))...))))))))((.(((.(((((...))))).)))..)).........-3'
MFE = -48.4; z-score = -1.24; ED = 43.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

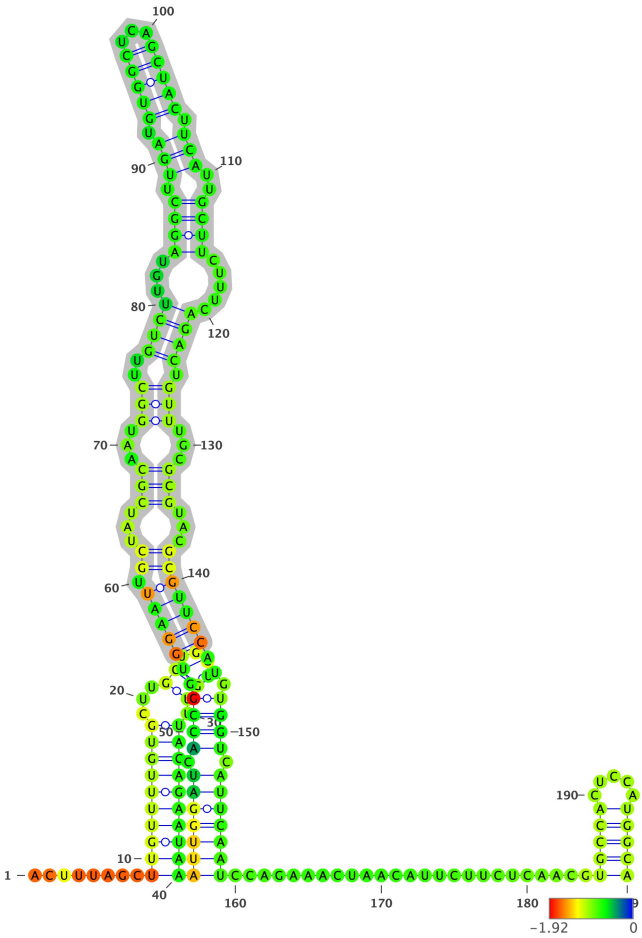
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 431 from nt 26757 to 26846 (nt 55 to 144)

```
5'-GGAATTGCTATCGCAATGGCTTGTCTTGTAGGCTTGATGTGGCTCAGCUACTUCATTGCUUCTTTCAGACTGUUTGCGCGTACGCGTTCC-3'
5'-((..(.((...(((...(((.....................................................)))...)))...)))..))-3'
Motif MFE = -26.4; z-score = -2.2; ED = 10.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26703 to 26901 (motif highlighted in silver):

```
5'-ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUU
GCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCA-3
5'-........((((((((((...((....)).))))))))))(((((((.(((((((((((.((...(((...(((..((((...((((.(((.(((((...))))).)))..
))))).....)))).)))...)))...))))))))).)))).)))))))........................(((((.....)))))-3'
MFE = -51.1; z-score = -1.39; ED = 18.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp05, 26523-27191(+)

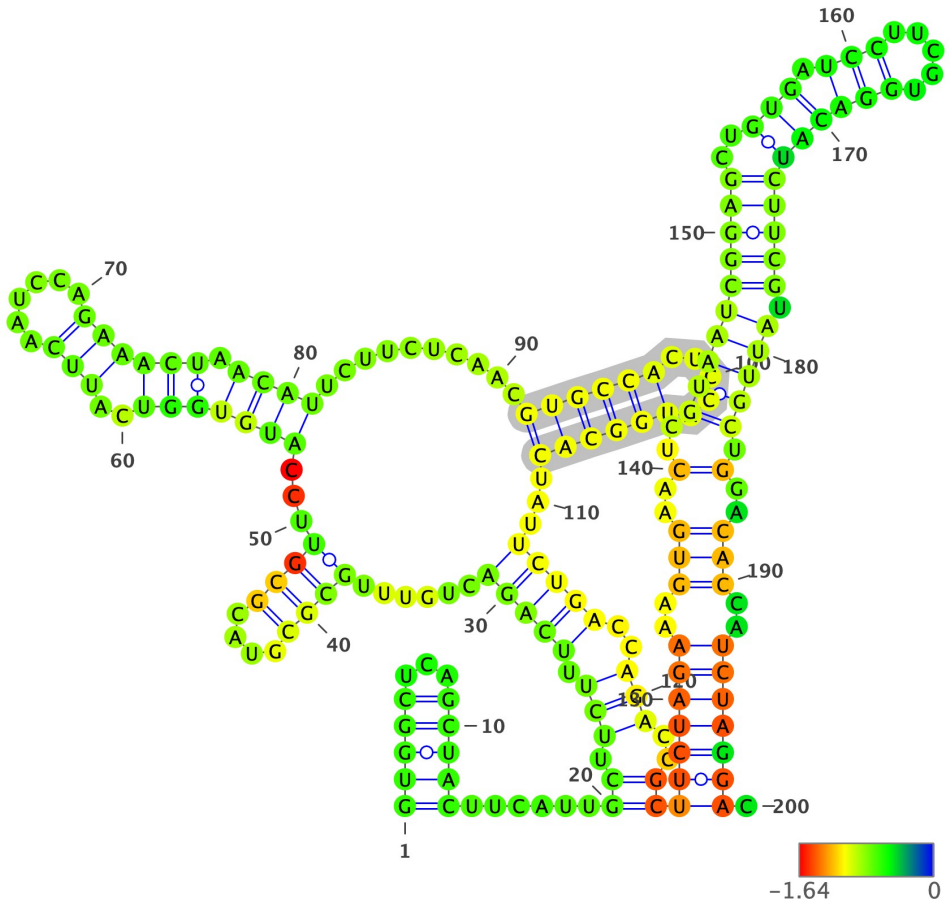
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 432 from nt 26886 to 26902 (nt 92 to 108)

```
5'-GTGCCACTCCATGGCAC-3'
5'-(((((.......)))))-3'
Motif MFE = -7.5; z-score = -4.62; ED = 0.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26795 to 26994 (motif highlighted in silver):

```
5'-GUGGCUCAGCUACUUCAUUGCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAU
UCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGAC-3
5'-(((((...)))))......((.(((.(((((......((((....))))...(((((((..(((......))))))).))))..........((((((.....))))))...
)))))..)))..))(((((((..(((..(..((((((((((..(((.(((.....)))))))))))).))))).)..)))..)))))))).-3'
MFE = -50.5; z-score = -1.38; ED = 36.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

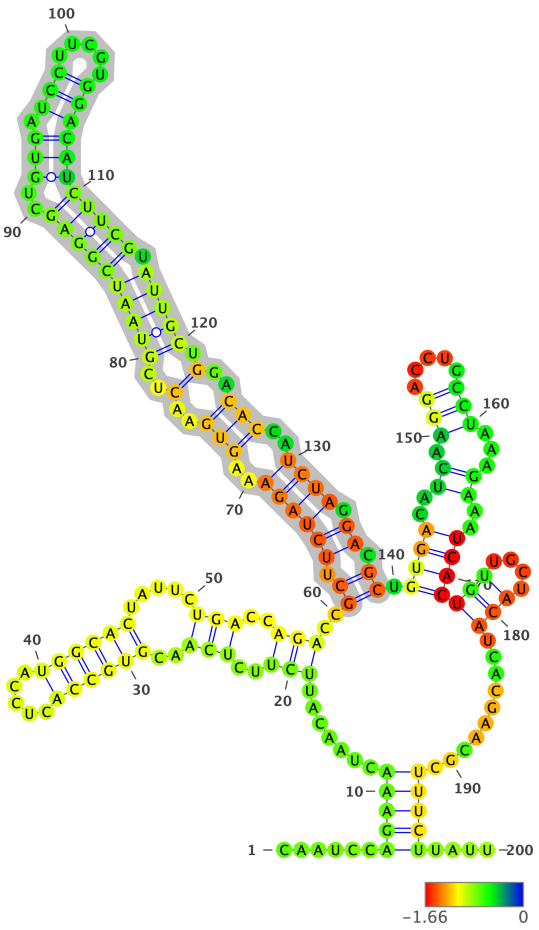
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 433 from nt 26918 to 26996 (nt 61 to 139)

```
5'-GCTTCTAGAAAGTGAACTCGTAATCGGAGCTGTGATCCTTCGTGGACATCUUCGTAUUGCTGGACACCAUCUAGGACGC-3'
5'-((.((((((..(((..(.........................................)..)))..)))).)).))-3'
Motif MFE = -25.9; z-score = -2.49; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26858 to 27057 (motif highlighted in silver):

```
5'-CAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAUUCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCU
UCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUU-3
5'-......(((((.......(((..(((..((((((.....))))))).....)))..)))..((.((((((..(((..(..(((((((((((..(((.(((.....))))))))
))).))))).)..)))..)))).)).)).((((..((.(((.....)))...))..))))(((....)))..........)))))....-3'
MFE = -40.6; z-score = -1.03; ED = 23.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

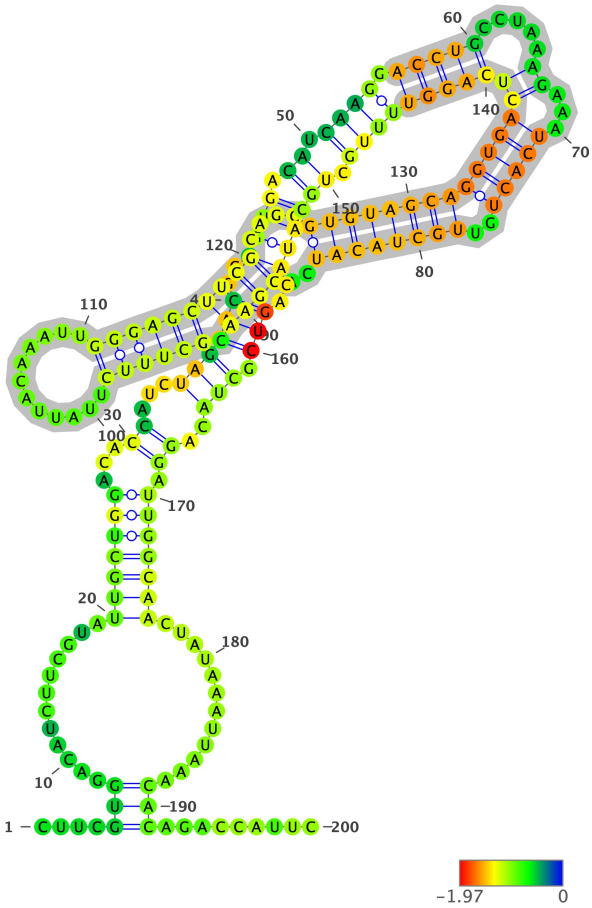
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 434 from nt 27010 to 27098 (nt 56 to 144)

```
5'-ACCTGCCTAAAGAAATCACTGTTGCTACATCACGAACGCTTTCTTATTACAAATTGGGAGCUUCGCAGCGUGUAGCAGGUGACTCAGGU-3'
5'-(.((...........(((((..(((((((((..((((.((((((.............))))))))))....)))))))))))))...)).)-3'
Motif MFE = -27.0; z-score = -2.88; ED = 8.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26955 to 27154 (motif highlighted in silver):

```
5'-CUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUG
GGAGCUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUC-3
5'-....(((.............(((((((...((...((((((..((((.((.((((.(((((.....((...(((((..((((((((..((((.((((((.............)
))))))))....))))))))))))))))))))))).))))))..))).)))..)).)))))))............)))..........-3'
MFE = -48.0; z-score = -0.5; ED = 29.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

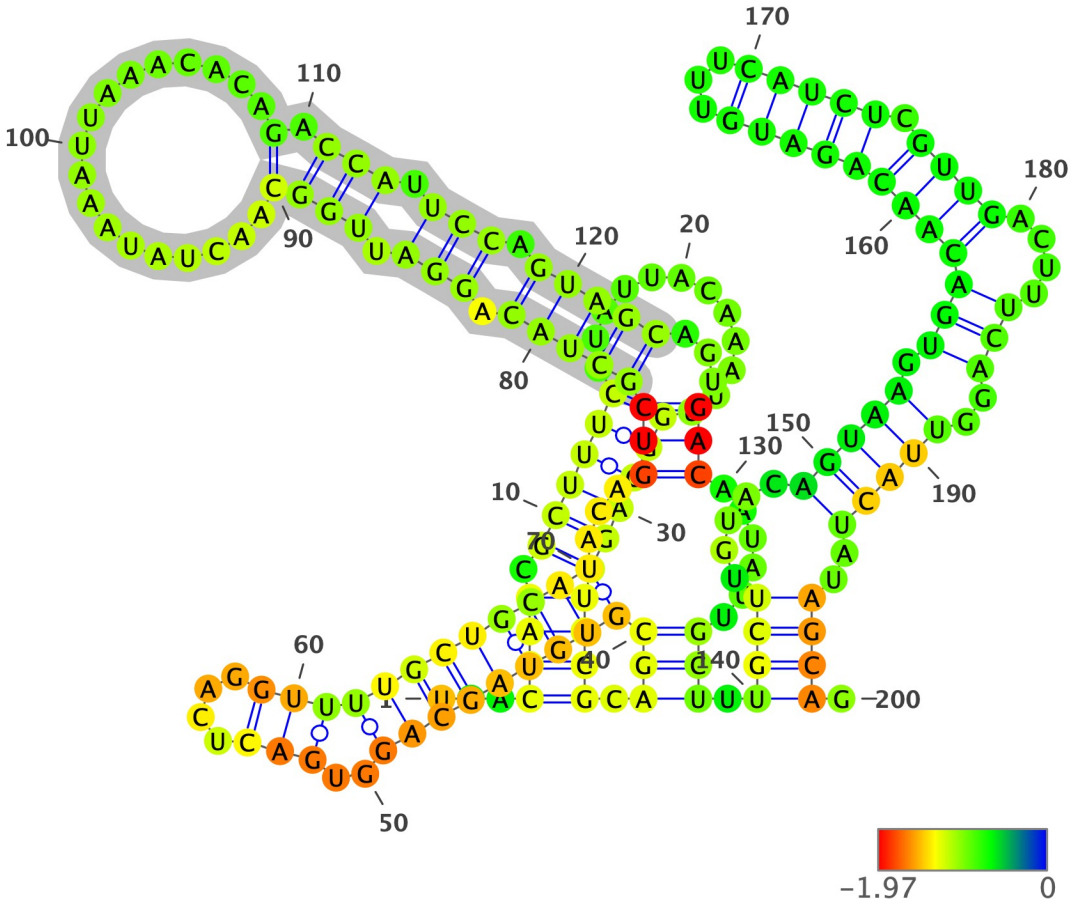
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 435 from nt 27115 to 27161 (nt 77 to 123)

```
5'-GCTACAGGATTGGCAACTATAAATTAAACACAGACCATUCCAGUAGC-3'
5'-(((((.(((.(((.....................))).))).)))))-3'
Motif MFE = -12.0; z-score = -3.35; ED = 1.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27039 to 27238 (motif highlighted in silver):

```
5'-UCACGAACGCUUUCUUAUUACAAAUUGGGAGCUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGAC
CAUUCCAGUAGCAGUGACAAUAUUGCUUUGCUUGUACAGUAAGUGACAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAG-3
5'-...((((.((((((............))))))))).(((((((((((..(((....)))))))))))...((((((((.(((.((((...................).)
)).))).)))))...))).....))).((((.....(((((.(((((((((((...))))).))))....)))..)))))..)))).-3'
MFE = -49.7; z-score = -1.39; ED = 29.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 153--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 153--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

4-- nt 164 to 200--gene, gene-GU280_gp06, 27202-27387(+)

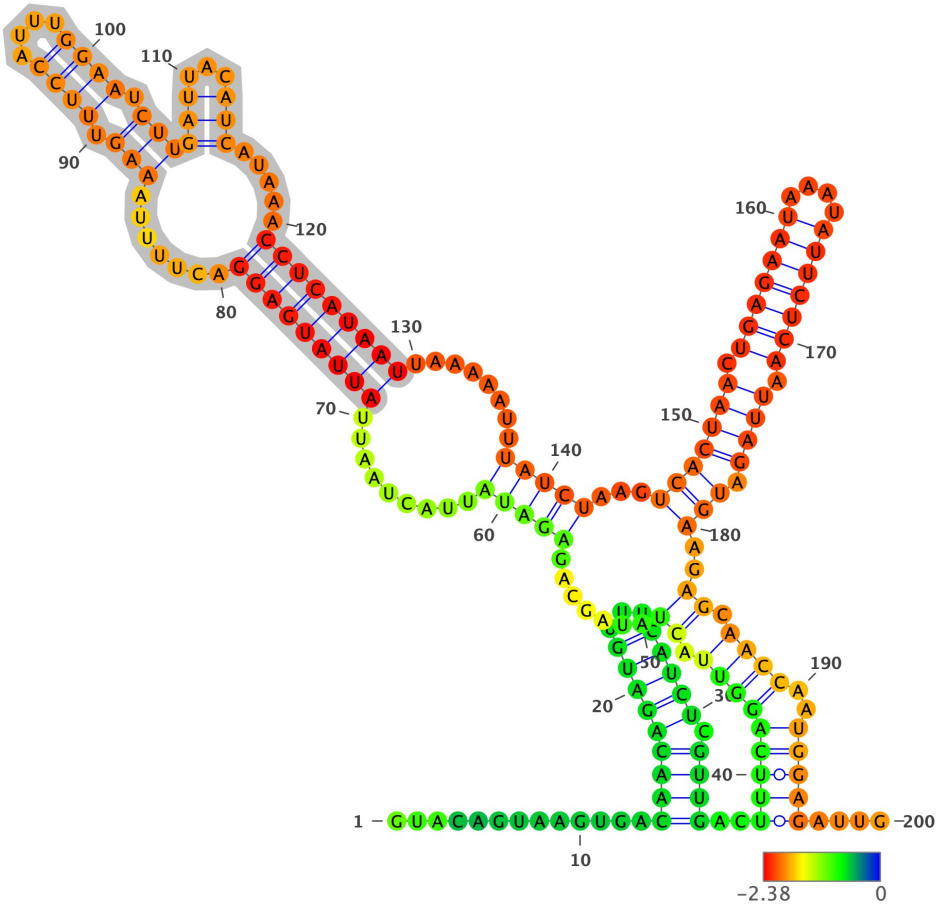
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 164 to 200--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

NC_045512.2 (forward strand): Structure number 436 from nt 27253 to 27311 (nt 71 to 129)

```
5'-ATTATGAGGACTTTTAAAGTTTCCATTTGGAATCUUGATTACATCATAAACCUCAUAAU-3'
5'-(((((((((.......(((.((((....)))).)))..............)))))))))-3'
Motif MFE = -12.7; z-score = -3.5; ED = 6.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27183 to 27382 (motif highlighted in silver):

```
5'-GUACAGUAAGUGACAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAGAGAUAUUACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUA
CAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUG-3
5'-.............(((((((((...))))).))))..(((((((((.((.......(((((.........(((((((((.......(((.((((....)))).)))(((..
.)))).....))))))))).......))))).....(((((((.(((((((....)))))))).)))).)))..)).))))..)))))....-3'
MFE = -39.0; z-score = -2.3; ED = 25.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 9--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 9--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

4-- nt 20 to 200--gene, gene-GU280_gp06, 27202-27387(+)

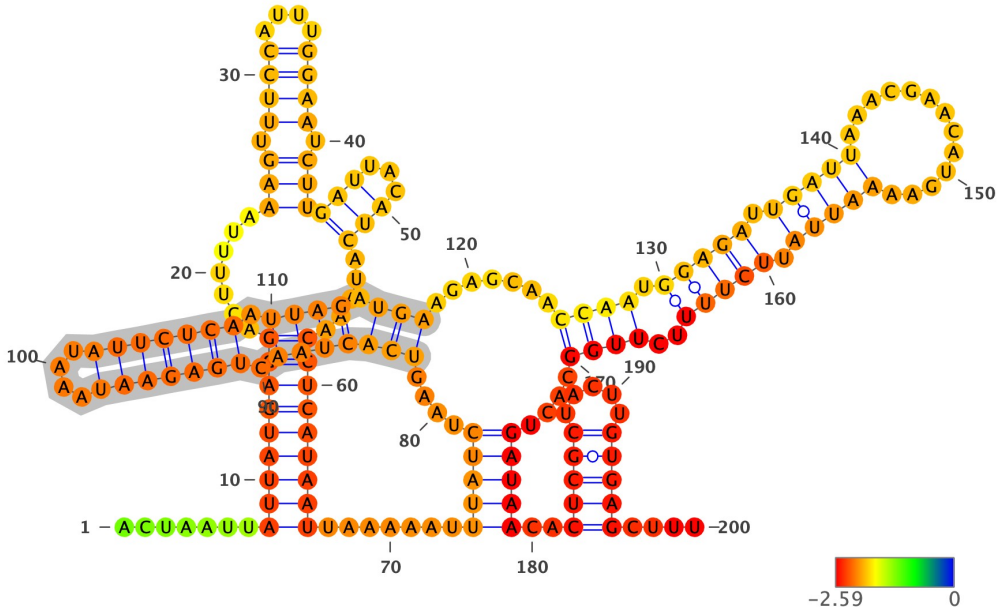
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 20 to 200--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

NC_045512.2 (forward strand): Structure number 437 from nt 27328 to 27362 (nt 83 to 117)

```
5'-TCACTAACTGAGAATAAATAUUCUCAAUUAGAUGA-3'
5'-(((((((.((((((.....)))))).)))).)))-3'
Motif MFE = -10.5; z-score = -5.24; ED = 1.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27246 to 27445 (motif highlighted in silver):

```
5'-ACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUACAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUU
AGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUU-3
5'-.......(((((((((.......(((.((((....)))).)))(((...))).....)))))))))).......(((((....(((((((.(((((((....)))))))).))
)).)))......((((.(((((.(((((.............)))))).)))))..)))).....)))))..(((((.....)))))....-3'
MFE = -38.4; z-score = -2.66; ED = 19.82
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 142--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 142--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 149 to 200--gene, gene-GU280_gp07, 27394-27759(+)

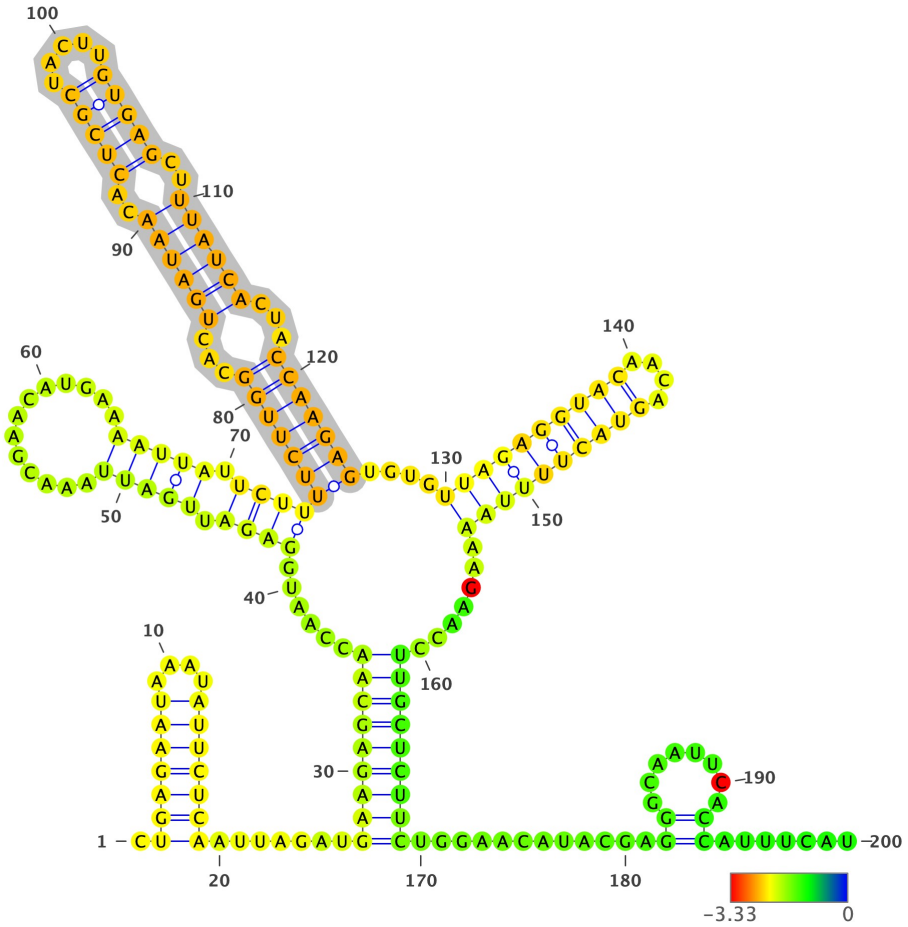
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 149 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 438 from nt 27409 to 27459 (nt 75 to 125)

```
5'-TTCTTGGCACTGATAACACTCGCTACTTGUGAGCTUUAUCACTACCAAGAG-3'
5'-(((((((...((((((..(((((.....)))))..)))))))...)))))))-3'
Motif MFE = -19.5; z-score = -4.58; ED = 1.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27335 to 27534 (motif highlighted in silver):

```
5'-CUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUU
AUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAU-3
5'-.(((((((....)))))))......(((((((((.....((((.(((((.............)))))).))))(((((((...((((((..(((((.....)))))..))
))))).....)))))))....((((((((((....)))))))))).....)))))))).............((........)).......-3'
MFE = -51.2; z-score = -3.68; ED = 21.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 53--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 53--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 60 to 200--gene, gene-GU280_gp07, 27394-27759(+)

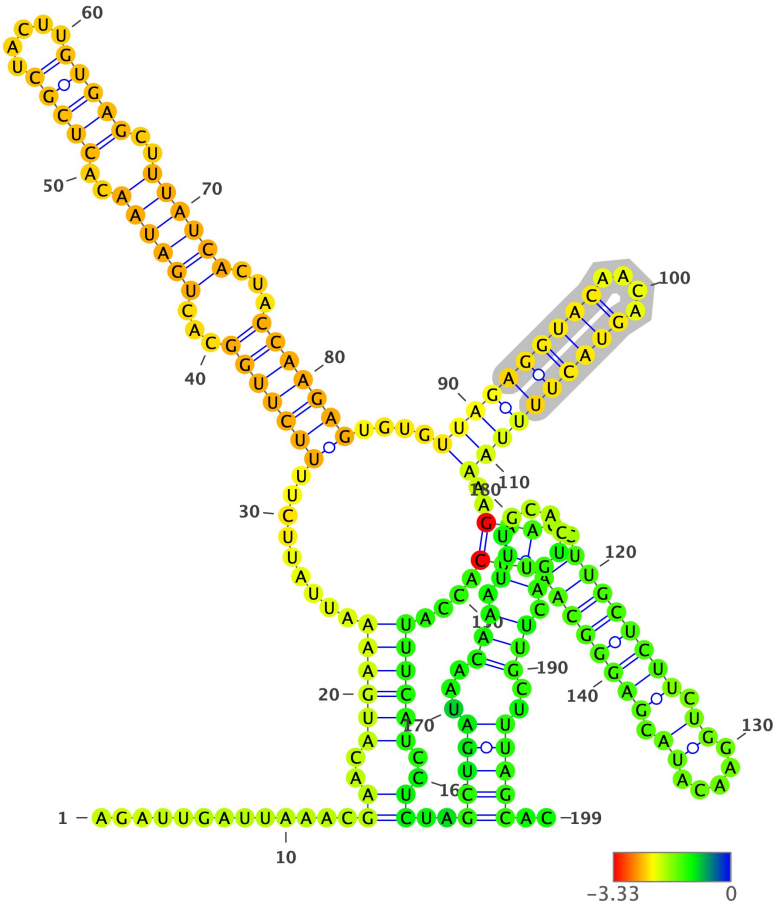
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 60 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 439 from nt 27468 to 27483 (nt 92 to 107)

```
5'-AGGTACAACAGUACUU-3'
5'-((((((....))))))-3'
Motif MFE = -3.9; z-score = -4.61; ED = 0.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27377 to 27575 (motif highlighted in silver):

```
5'-AGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAA
AAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCAC-3
5'-.............((..((((((.........(((((((...((((((..(((((.....)))))..))))))...)))))))....((((((((((....))))))))))
..(((..((((((((.((.....)).))))))))))....))))))..))..(((((...(((.((......)).)))..)))))..-3'
MFE = -44.6; z-score = -2.61; ED = 22.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 11--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 11--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 18 to 199--gene, gene-GU280_gp07, 27394-27759(+)

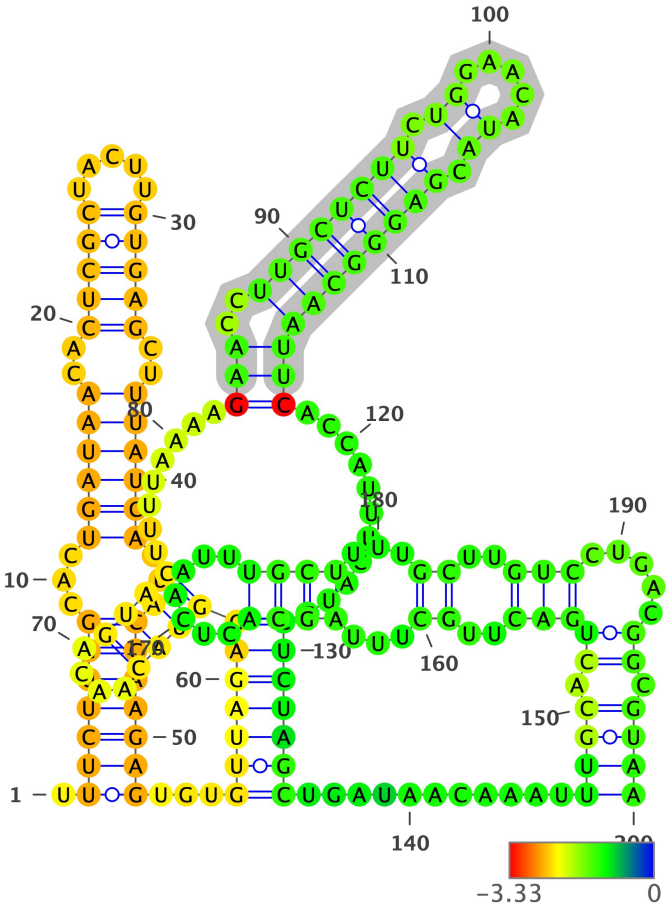
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 18 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 440 from nt 27491 to 27523 (nt 84 to 116)

```
5'-AACCTTGCTCTTCTGGAACATACGAGGGCAAUU-3'
5'-((..(((((((.............)))))))))-3'
Motif MFE = -8.1; z-score = -2.32; ED = 3.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27408 to 27607 (motif highlighted in silver):

```
5'-UUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGG
CAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAA-3
5'-.(((((((...((((((..(((((.....)))))..))))))...)))))))...((((((((((....))))........(((..((((((((.((.....)).)))))
))))))...........)))))))...........((((.(((((..((...((((.......))))...))..)))).....)).))))-3'
MFE = -49.0; z-score = -2.51; ED = 28.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp07, 27394-27759(+)

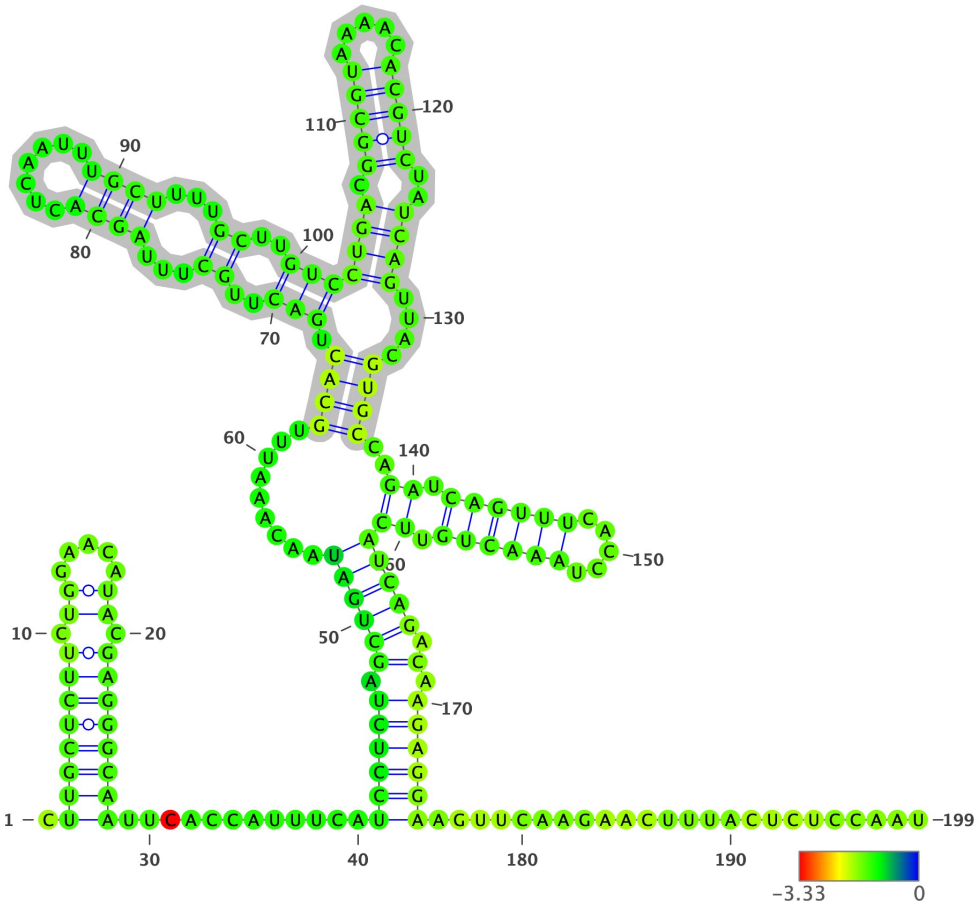
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 441 from nt 27556 to 27629 (nt 63 to 136)

```
5'-GCACTGACTTGCTTTAGCACTCAATTTGCUTTTGCTTGUCCTGACGGCGTAAAACACGUCTAUCAGTTACGUGC-3'
5'-((((.(((..((...(((.........)))...))..)))((((.(((((.....)))))..))))....))))-3'
Motif MFE = -19.8; z-score = -2.25; ED = 1.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27494 to 27692 (motif highlighted in silver):

```
5'-CUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCG
UAAAACACGUCUAUCAGUUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAU-3
5'-.((((((((.((.....)).)))))))).............((((((.((((((.........((((.(((..((...((((.......))))...))..)))((((.((((
(.....)))))..))))....))))..((.((((((.....)))))).)))))))).).))))))........................-3'
MFE = -46.7; z-score = -2.44; ED = 13.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp07, 27394-27759(+)

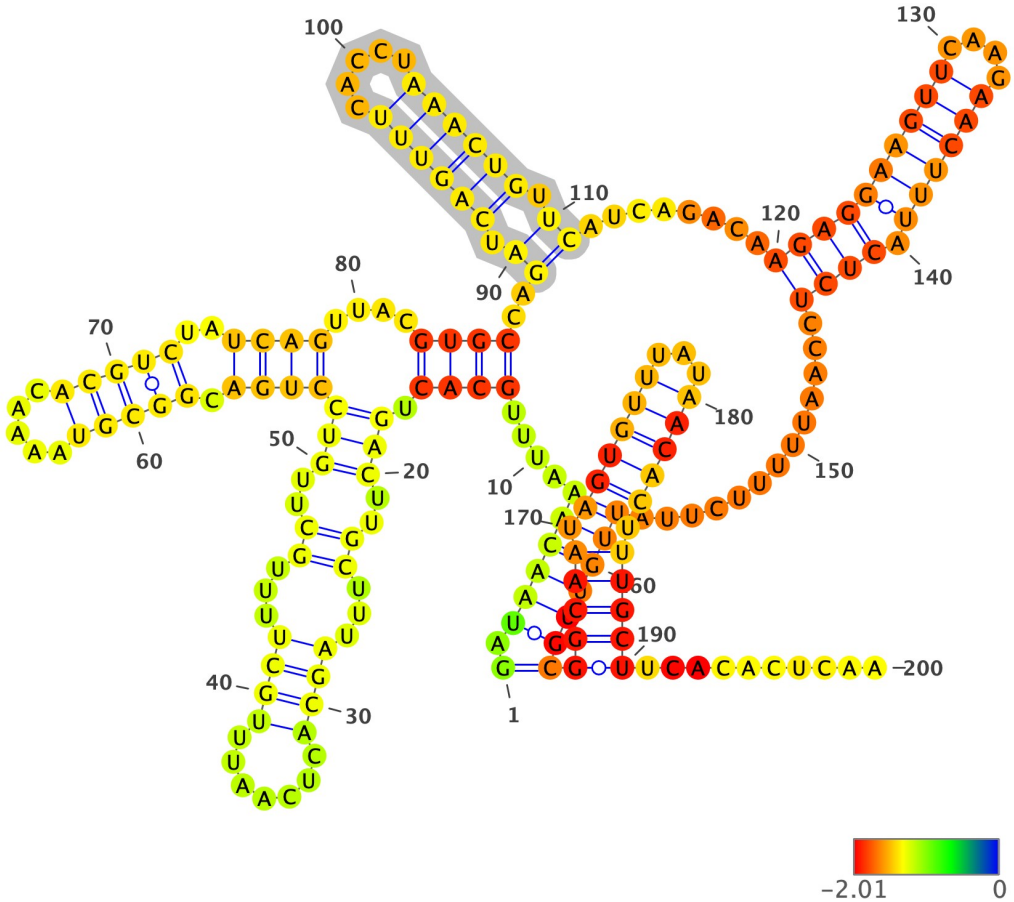
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 442 from nt 27632 to 27654 (nt 89 to 111)

```
5'-GATCAGTTTCACCTAAACUGTUC-3'
5'-((.((((((.....)))))).))-3'
Motif MFE = -4.1; z-score = -3.56; ED = 1.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27544 to 27743 (motif highlighted in silver):

```
5'-GAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAAAACACGUCUAUCAGUUACGUGCCAGAUCAGUUUCACCUAAACUGUUC
AUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCUUCACACUCAA-3
5'-(.((((((....((((.(((..((...((((.......))))...))..)))((((.(((((.....)))))..))))....))))..((.((((((.....)))))).))
........((((((((((....)))))).))))............)))))))(((((.((((((...)))))))))))..........-3'
MFE = -44.1; z-score = -2.68; ED = 22.94
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp07, 27394-27759(+)

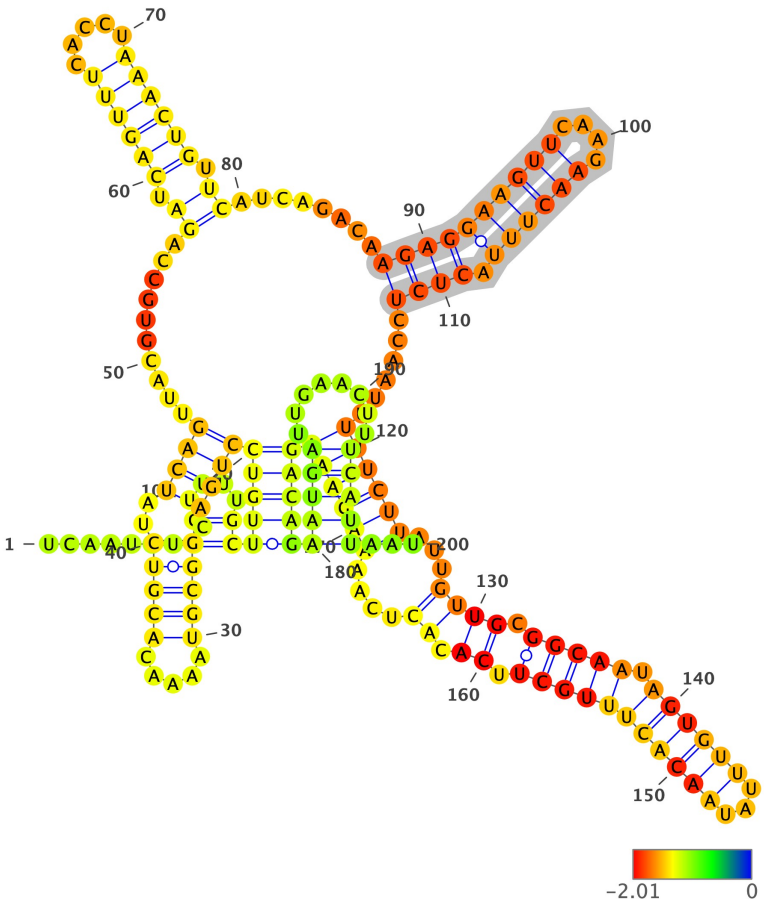
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 443 from nt 27663 to 27687 (nt 88 to 112)

```
5'-AGAGGAAGTTCAAGAACTTTACUCU-3'
5'-((((...(((....)))....))))-3'
Motif MFE = -5.8; z-score = -3.0; ED = 1.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27576 to 27775 (motif highlighted in silver):

```
5'-UCAAUUUGCUUUUGCUUGUCCUGACGGCGUAAAACACGUCUAUCAGUUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUC
UCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCUUCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAU-3
5'-.......((....))(((((((((.(((((.....)))))..))))..........((.((((((.....)))))).)).........((((((((((....)))))).)))
).....((((((...((((.(((((.((((((...)))))))))))).)).))....))))))))))))(((((........)))))...-3'
MFE = -42.1; z-score = -2.64; ED = 34.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 184--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 184--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 181 to 200--gene, gene-GU280_gp08, 27756-27887(+)

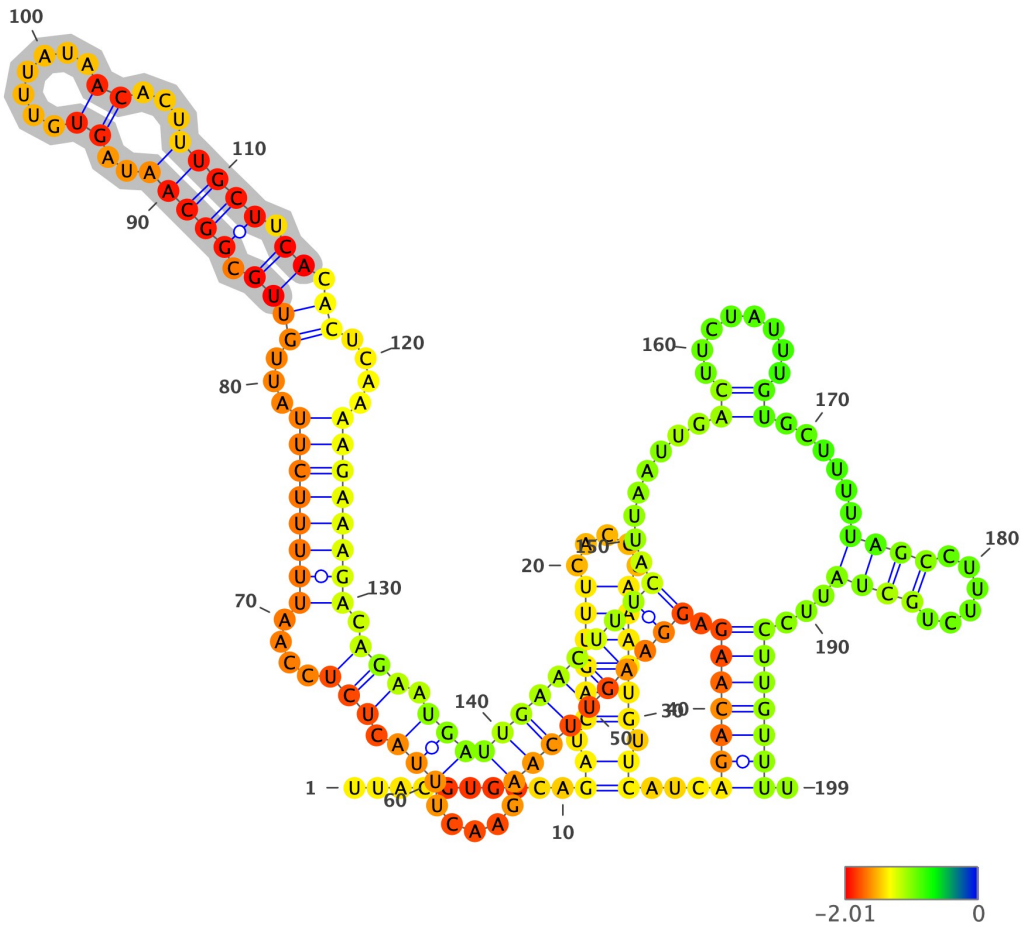
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 181 to 200--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

NC_045512.2 (forward strand): Structure number 444 from nt 27705 to 27736 (nt 84 to 115)

```
5'-TGCGGCAATAGTGTTTATAACACTTUGCUTCA-3'
5'-((.((((...((.......)).....)))).))-3'
Motif MFE = -9.6; z-score = -2.99; ED = 1.95
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27622 to 27820 (motif highlighted in silver):

```
5'-UUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGC
UUCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUU-3
5'-..........((.((((((.....)))))).))...(((((((.(((((((((.....(((.(((....(((((((((...((((.(((((..((.......)).....))))
).)).))....))))))))).))).))))))))))))).........((........)).....(((.....)))).....)))))))).-3'
MFE = -32.9; z-score = -2.13; ED = 33.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 138--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 138--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 135 to 199--gene, gene-GU280_gp08, 27756-27887(+)

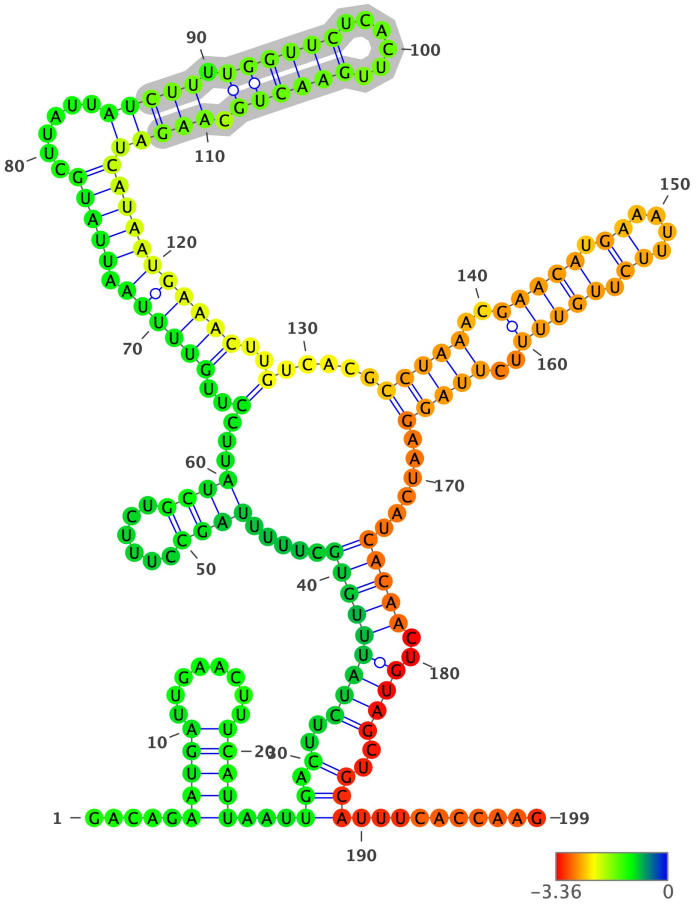
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 135 to 199--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

NC_045512.2 (forward strand): Structure number 445 from nt 27836 to 27861 (nt 87 to 112)

```
5'-CTTTTGGTTCTCACTTGAACUGCAAG-3'
5'-(((.((((((......))))))).)))-3'
Motif MFE = -5.1; z-score = -2.01; ED = 2.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27750 to 27948 (motif highlighted in silver):

```
5'-GACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAA
GAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAG-3
5'-.....(((((.........)))))...((.(..(((((((((.....((((......))))...(..((((((.(((((......(((((.((((((......))))))).))
))))))))))))))..).....(((((..(((((.((....)).)))))..)))))......)))))..))))..))).........-3'
MFE = -33.5; z-score = -1.03; ED = 24.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 10--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 10--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 7 to 138--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 7 to 138--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

6-- nt 145 to 199--gene, gene-GU280_gp09, 27894-28259(+)

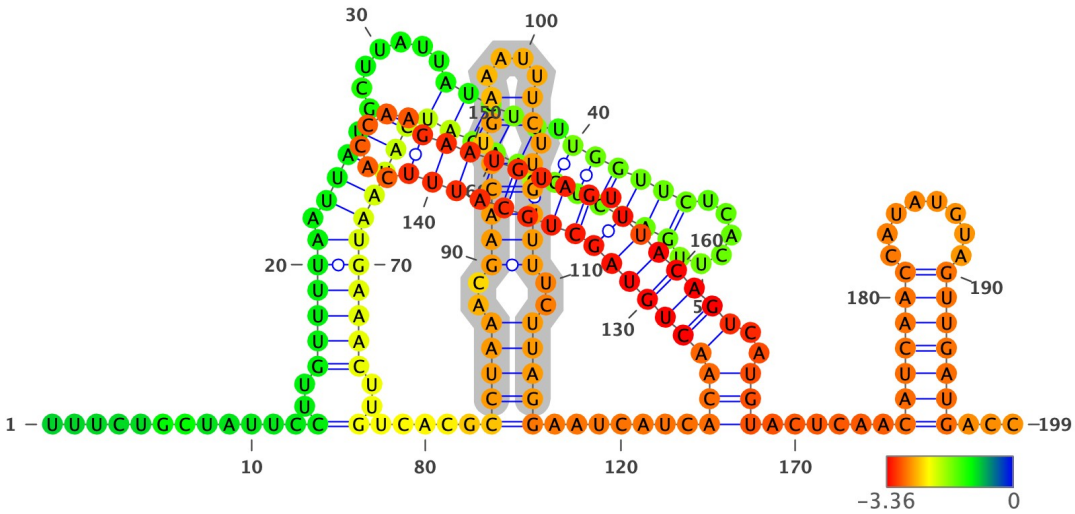
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 145 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 446 from nt 27884 to 27915 (nt 84 to 115)

```
5'-CTAAACGAACATGAAATTTCTUGUUUTCUUAG-3'
5'-((((..(((((.(......).)))))..))))-3'
Motif MFE = -4.7; z-score = -1.76; ED = 1.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27801 to 27999 (motif highlighted in silver):

```
5'-UUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUC
UUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACC-3
5'-............(..((((((.(((((......(((((.((((((......))))))).))))))))))))))))..).....(((((..(((((.((....)).)))))..
)))))).......((((((((((((((((((.....)))))))).)))))))..))).....(((((((........)))))))...-3'
MFE = -46.6; z-score = -4.09; ED = 12.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 87--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 87--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 94 to 199--gene, gene-GU280_gp09, 27894-28259(+)

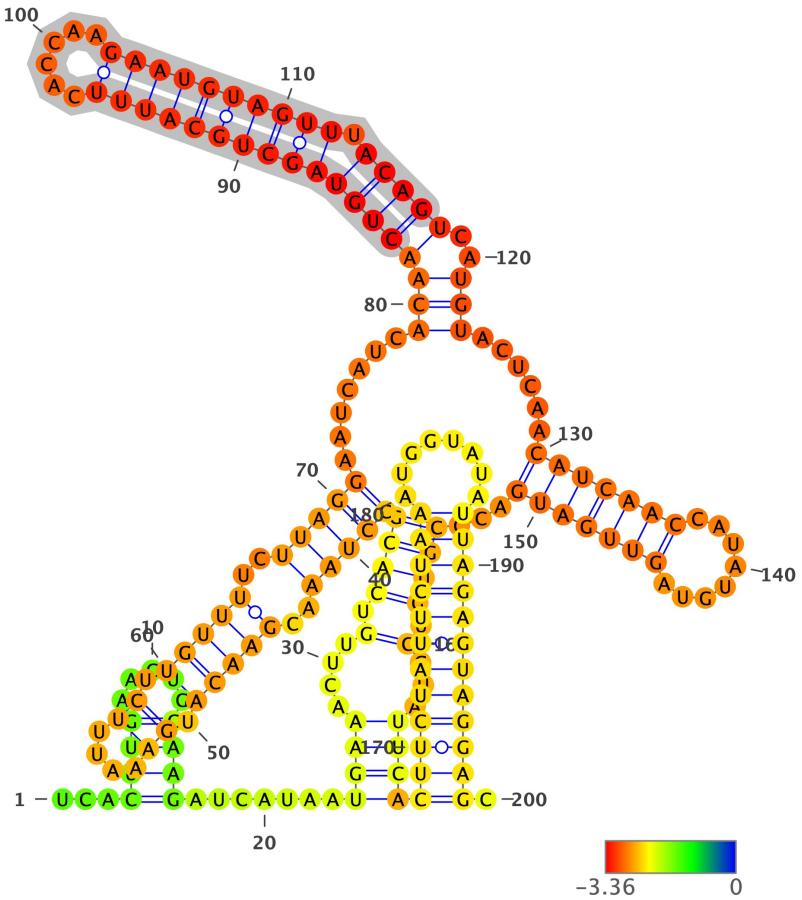
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 94 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 447 from nt 27928 to 27962 (nt 83 to 117)

```
5'-CTGTAGCTGCATTTCACCAAGAAUGUAGUUTACAG-3'
5'-(((((((((((((.....)))))))))))).))))-3'
Motif MFE = -12.8; z-score = -4.58; ED = 3.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27846 to 28045 (motif highlighted in silver):

```
5'-UCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGU
UUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGC-3
5'-...((((.....)))).......((((....(.(((((((((..(((((.((....)).)))))..)))))).......((((((((((((((((.....)))))))))
).)))))..)))......(((((((.......)))))))...)))).)...))))((((((((((((.......)))))))))))).-3'
MFE = -51.6; z-score = -4.34; ED = 18.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 42--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 42--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 49 to 200--gene, gene-GU280_gp09, 27894-28259(+)

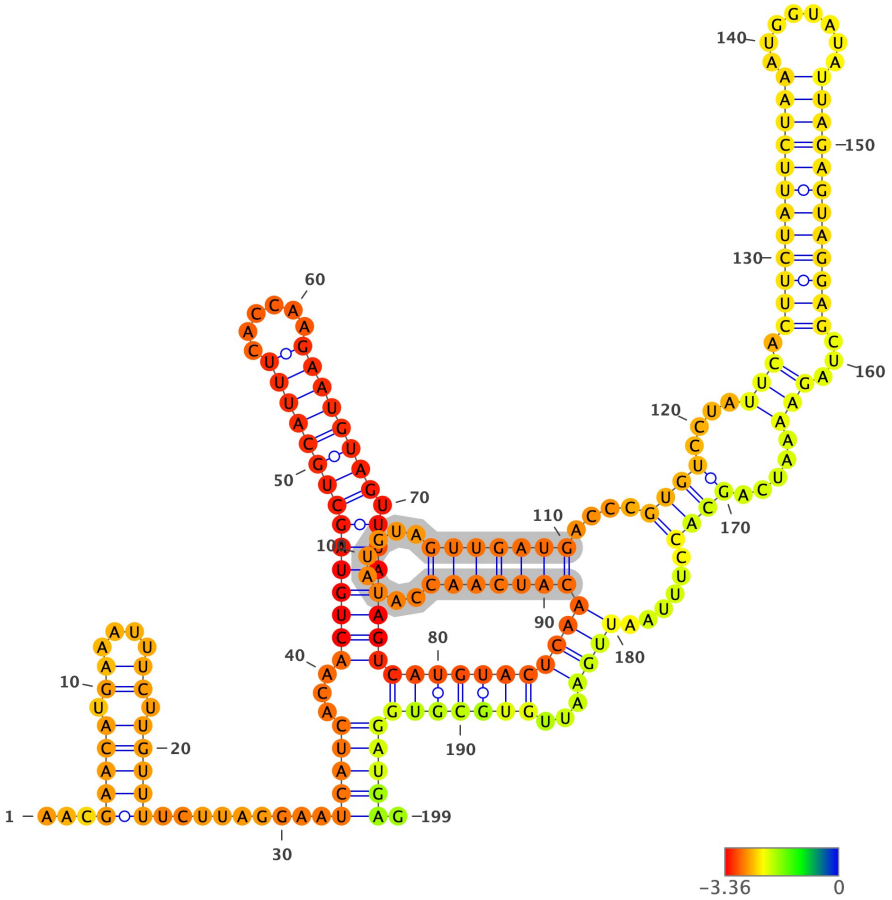
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 49 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 448 from nt 27975 to 27996 (nt 89 to 110)

```
5'-CATCAACCATATGTAGUUGAUG-3'
5'-(((((((........)))))))-3'
Motif MFE = -6.3; z-score = -3.1; ED = 0.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27887 to 28085 (motif highlighted in silver):

```
5'-AACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGA
CCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAG-3
5'-...(((((.((....)).)))))..........(((((...(((((((((((((((.....))))))))).)))))))((((((((((((((((.........)))))))).
...((((....(((.(((((((((((.........)))))))))))))...)))).....))))......))))...)))))))))))).-3'
MFE = -52.4; z-score = -3.51; ED = 23.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 1--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 1--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 8 to 199--gene, gene-GU280_gp09, 27894-28259(+)

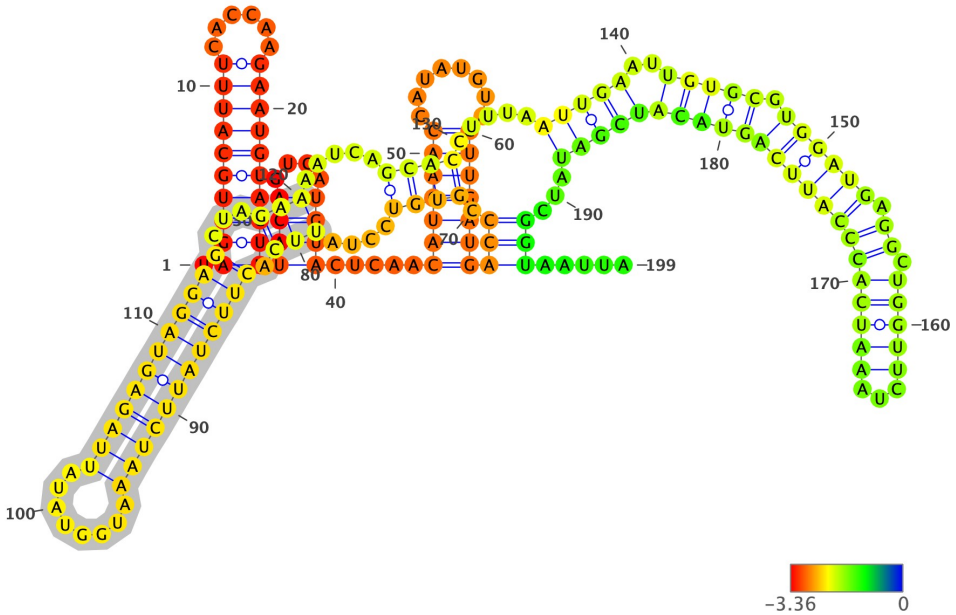
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 8 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 449 from nt 28009 to 28050 (nt 79 to 120)

```
5'-TTCACTTCTATTCTAAATGGTATATUAGAGUAGGAGCTAGAA-3'
5'-(((.(((((((((((.........))))))))))...)))-3'
Motif MFE = -12.9; z-score = -3.93; ED = 2.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27931 to 28129 (motif highlighted in silver):

```
5'-UAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAG
GAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAUAUCGGUAAUUA-3
5'-.(((((((((((......)))))))))((((....)))).....(((((((........)))))))(((.((((....(((.(((((((((((((........)))))))))
)))...)))).....)))).....(((((..(((((.((((((.((.(((((...)))))))))))))))))))))))...)))).....-3'
MFE = -52.9; z-score = -3.33; ED = 23.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp09, 27894-28259(+)

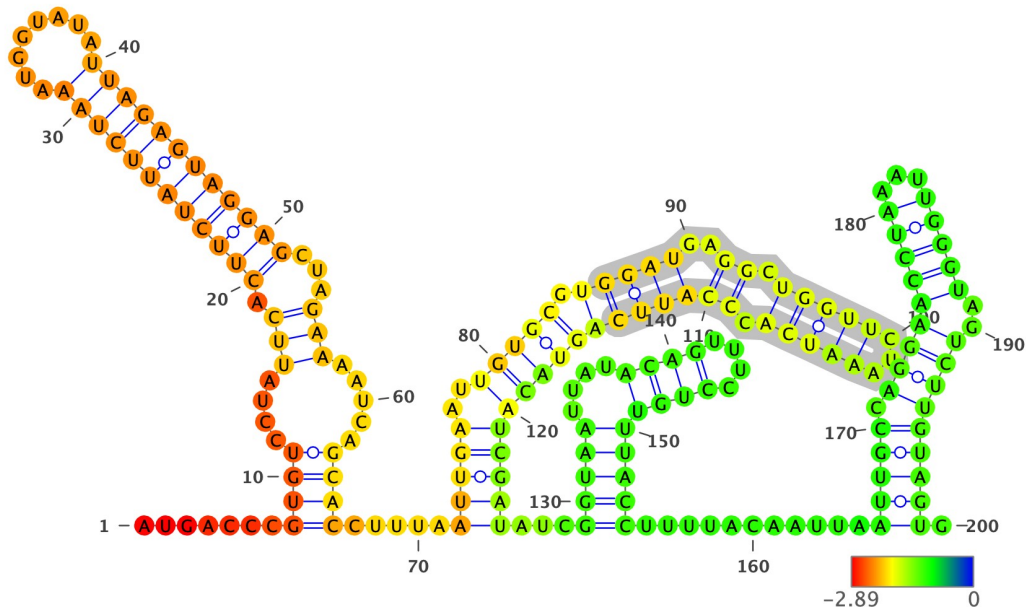
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 450 from nt 28079 to 28107 (nt 86 to 114)

```
5'-GGATGAGGCTGGTTCTAAAUCACCCAUUC-3'
5'-((((..((.(((.......))).))))))-3'
Motif MFE = -7.2; z-score = -2.02; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27994 to 28193 (motif highlighted in silver):

```
5'-AUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCA
UUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUG-3
5'-.......((((....(((.((((((((((((.........)))))))))))...)))).....)))).....(((((..(((((.(((((..((.(((((...))))).)))
))))))))))))))...(((((....((((....)))))))))...........(((((.(((((((((...)))))..))))))))).-3'
MFE = -44.8; z-score = -1.97; ED = 23.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp09, 27894-28259(+)

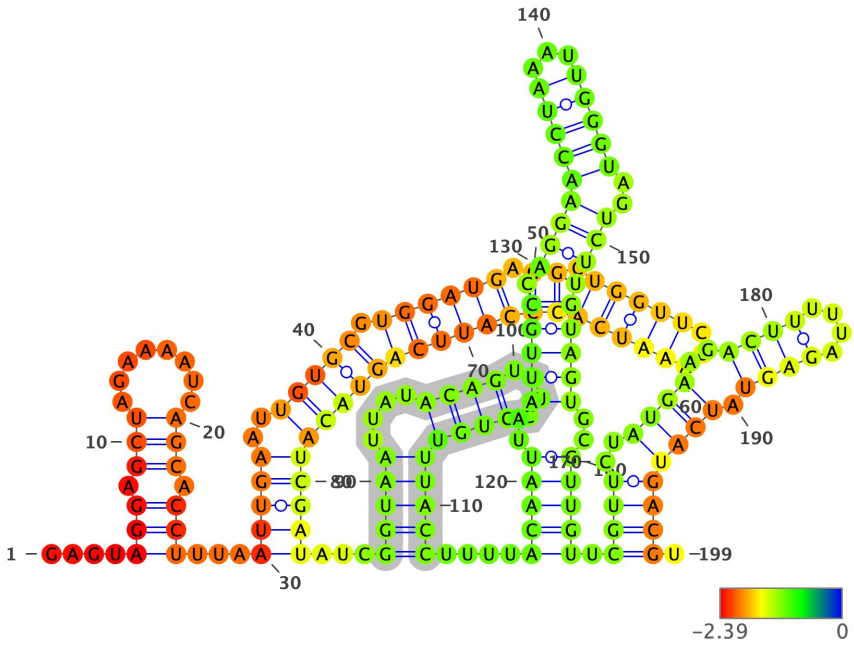
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 451 from nt 28122 to 28147 (nt 87 to 112)

```
5'-GGTAATTATACAGTTTCCTGTUUACC-3'
5'-(((((................)))))-3'
Motif MFE = -4.9; z-score = -2.13; ED = 0.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28036 to 28234 (motif highlighted in silver):

```
5'-GAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUAC
CUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGU-3
5'-....(((.(((........))).)))...(((((..(((((.((((((.((.(((((...)))))))))))))))))))))...(((((....((((....))))))))
)....(((((..(((((.((((((((...)))))..)))))))))..))))).((((..((((..((((....)))).)))))))).-3'
MFE = -47.5; z-score = -1.24; ED = 15.9
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp09, 27894-28259(+)

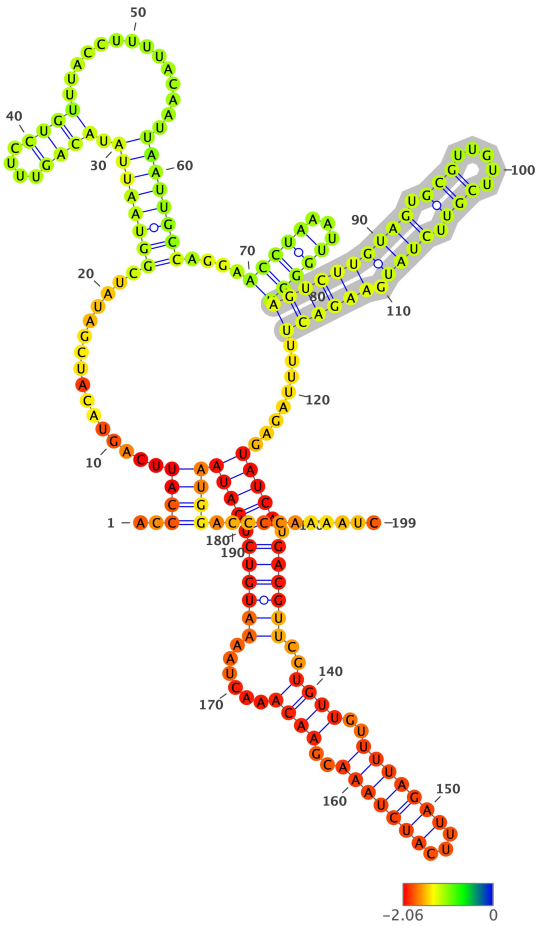
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 452 from nt 28182 to 28215 (nt 83 to 116)

```
5'-AGTCTTGTAGTGCGTTGTTCGUTCUAUGAAGACU-3'
5'-((((((((((.(((.....))).)))).))))))-3'
Motif MFE = -11.3; z-score = -3.23; ED = 2.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28100 to 28298 (motif highlighted in silver):

```
5'-ACCCAUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGA
AGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUC-3
5'-..((((................((((((((.((((....))))..............))))))))....(((((...)))))((((((((((.(((.....))).)))).)
)))))........(((((.(((((((..(((((..(((((((...)))))))..))))......))))))))))))))).....-3'
MFE = -40.9; z-score = -1.63; ED = 44.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 160--gene, gene-GU280_gp09, 27894-28259(+)

Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 160--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

4-- nt 175 to 199--gene, gene-GU280_gp10, 28274-29533(+)

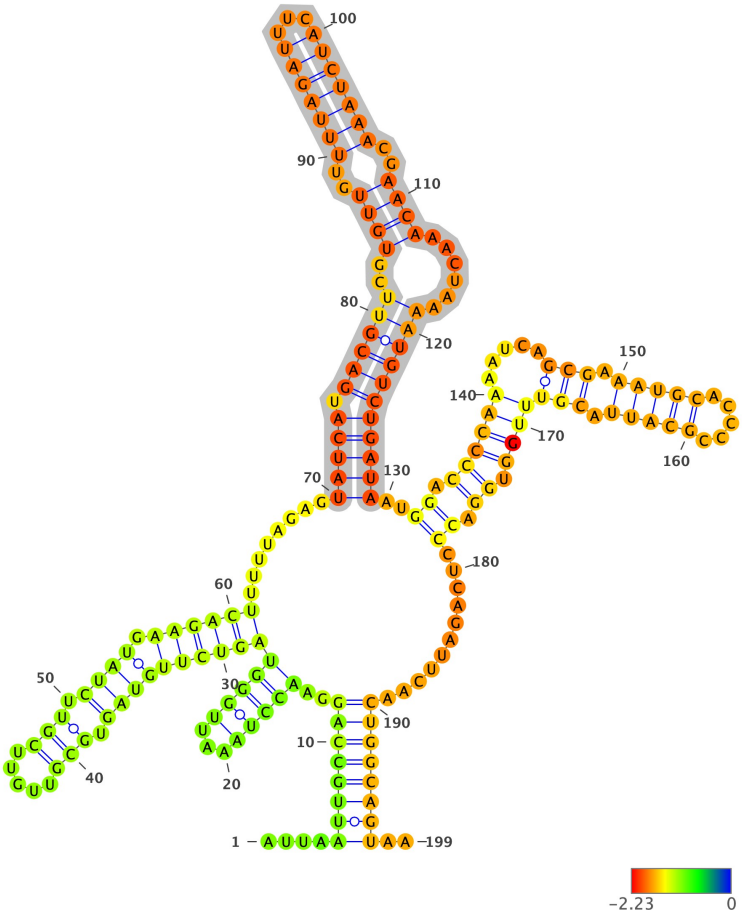
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 175 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 453 from nt 28224 to 28283 (nt 70 to 129)

```
5'-TATCATGACGTTCGTGTTGTTTTAGATTTCAUCUAAACGAACAAACTAAAAUGUCUGAUA-3'
5'-(((((.((((....((((..(((((((...)))))))..))))........)))))))))-3'
Motif MFE = -14.7; z-score = -2.72; ED = 9.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28155 to 28353 (motif highlighted in silver):

```
5'-AUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAAC
AAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAA-3
5'-....((((((((..(((((...)))))((((((((((.(((.....))).)))).))))))........(((((.((((((..((((..(((((((...)))))))..)))
).....))))))))))..((.((((((.....(((.(((((.....))))).)))))))).)).)).........))))))))..-3'
MFE = -57.2; z-score = -3.74; ED = 16.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 105--gene, gene-GU280_gp09, 27894-28259(+)

Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 105--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

4-- nt 120 to 199--gene, gene-GU280_gp10, 28274-29533(+)

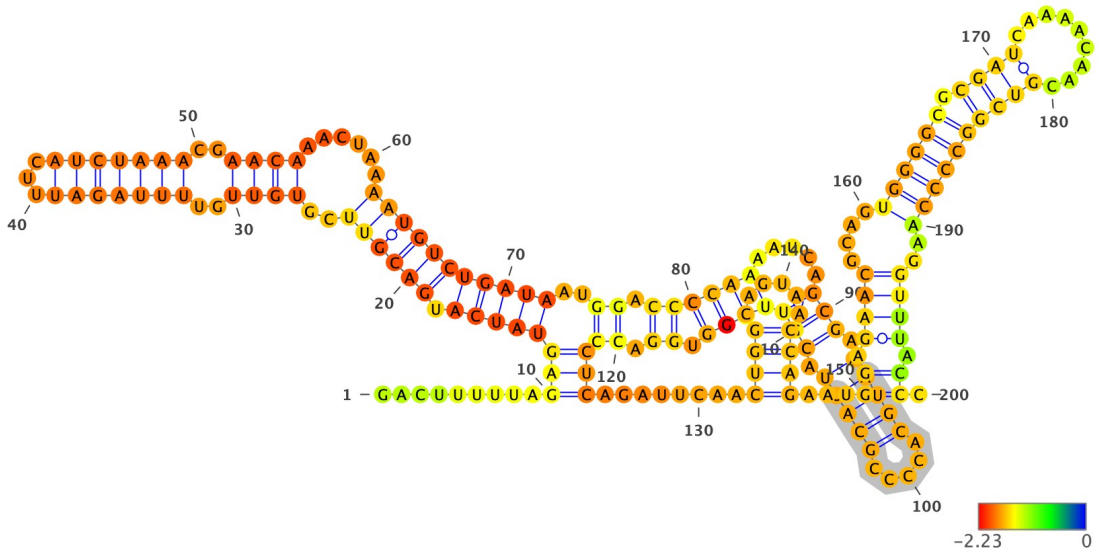
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 120 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 454 from nt 28305 to 28317 (nt 94 to 106)

```
5'-ATGCACCCCGCAU-3'
5'-((((.....))))-3'
Motif MFE = -1.9; z-score = -4.77; ED = 0.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28212 to 28411 (motif highlighted in silver):

```
5'-GACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGU
UUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCC-3
5'-.........(((((((.((((((..(((((..(((((((...)))))))..)))).....)))))))))))..((.((((((.....(((.(((((.....)))))).)))
)))).)).)))))........((((.....)))).....((.((((....((((((.((((.........)))))))))))..)))).)).-3'
MFE = -54.2; z-score = -2.2; ED = 43.05
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 48--gene, gene-GU280_gp09, 27894-28259(+)

Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 48--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

4-- nt 63 to 200--gene, gene-GU280_gp10, 28274-29533(+)

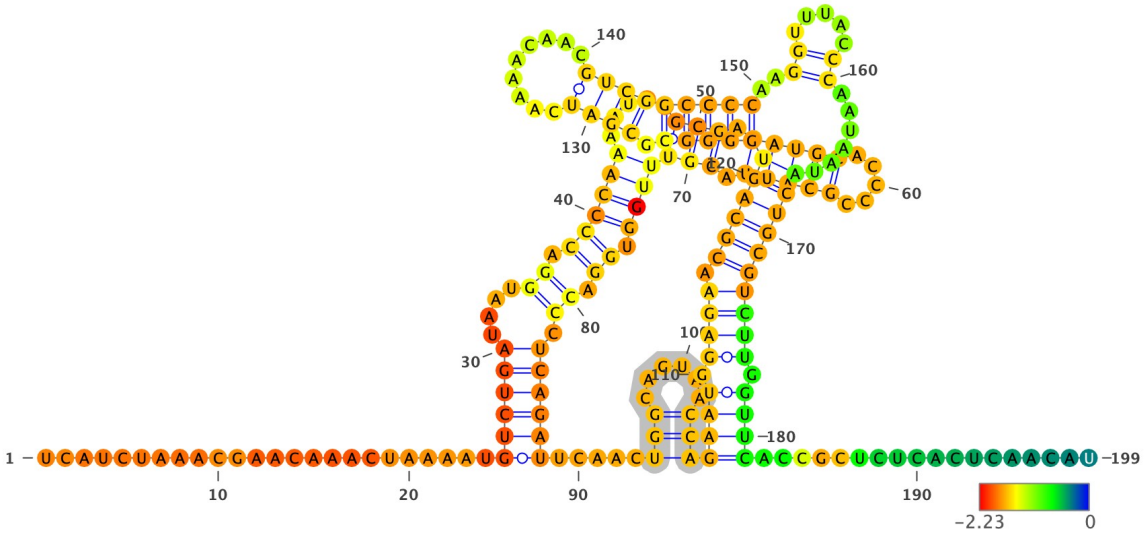
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 63 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 455 from nt 28345 to 28356 (nt 94 to 105)

```
5'-TGGCAGTAACCA-3'
5'-(((......)))-3'
Motif MFE = -0.6; z-score = -1.15; ED = 1.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28252 to 28450 (motif highlighted in silver):

```
5'-UCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGG
AGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAU-3
5'-.......................((((((....((.((((((.....(((.(((((.....)))))).)))))))).)).)).)))))).....((.....)))((((.(
(((.((((((((((.((((.........)))))))))..((.....)).....)))))))))).)))).................-3'
MFE = -52.4; z-score = -2.82; ED = 32.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 8--gene, gene-GU280_gp09, 27894-28259(+)

Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 8--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

4-- nt 23 to 199--gene, gene-GU280_gp10, 28274-29533(+)

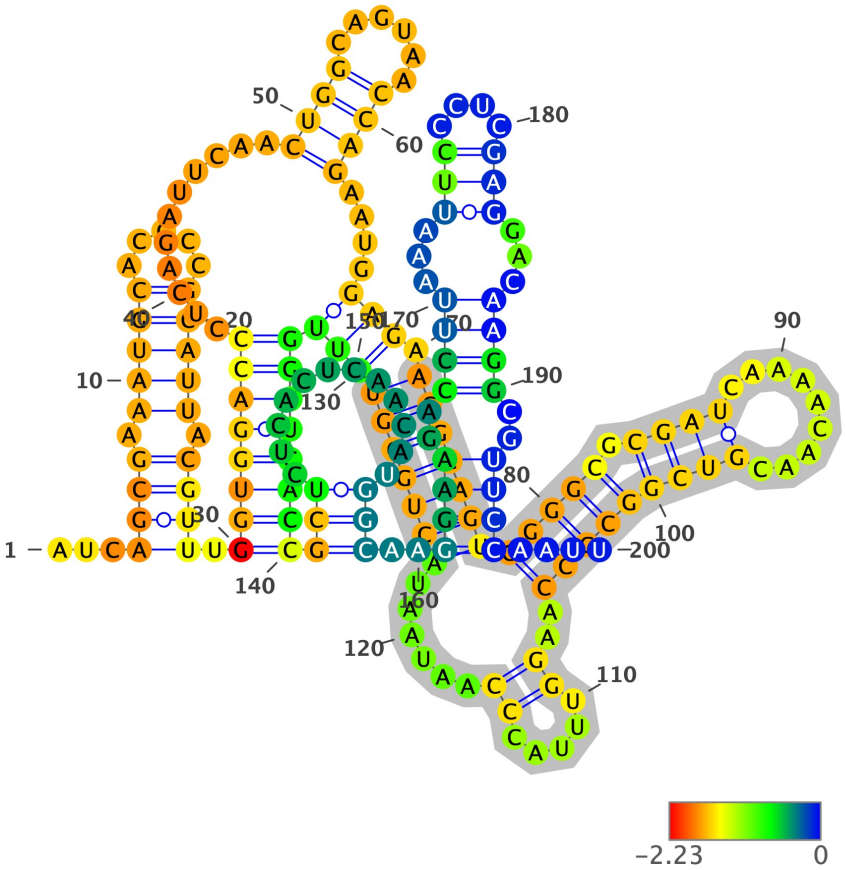
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 23 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 456 from nt 28366 to 28424 (nt 71 to 129)

```
5'-ACGCAGTGGGGCGCGATCAAAACAACGUCGGCCCCAAGGTTTACCCAATAATACUGCGU-3'
5'-((((((.((((..((((.........)))).)))).((.....)).......))))))-3'
Motif MFE = -21.9; z-score = -3.01; ED = 4.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28296 to 28495 (motif highlighted in silver):

```
5'-AUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUU
UACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAUU-3
5'-...((((.(((((.....))))).)))).((((((((...........((((......))))....(((.(((((((((((.((((.........)))))))))..((..
...)).....))))))))))))))))))(((............)))..((((..((((...(((....)))...))))..))))....-3'
MFE = -59.0; z-score = -2.11; ED = 16.41
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

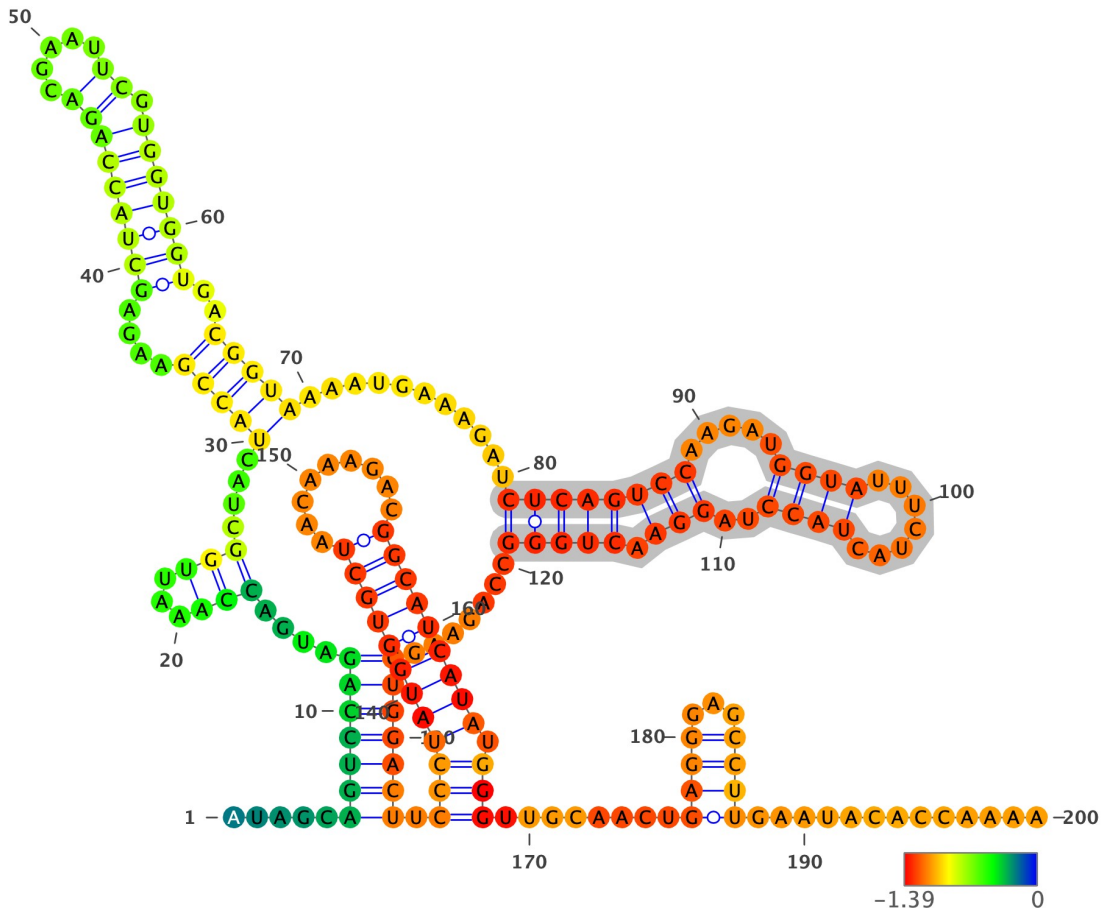
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 457 from nt 28583 to 28621 (nt 81 to 119)

```
5'-CTCAGTCCAAGATGGTATTTCTACUACCTAGGAACUGGG-3'
5'-((((((((.....((((.......))))..))).)))))-3'
Motif MFE = -12.9; z-score = -3.07; ED = 2.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28503 to 28702 (motif highlighted in silver):

```
5'-AUAGCAGUCCAGAUGACCAAAUUGGCUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAG
GAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAA-3
5'-.....(((((((....(((...))).....(((((....(((((((((.....)).)))))))..)))))...........((((((((.....((((.......))))..)
)).)))))).......))))))).((((((((((((.........))))))))).))).........((((...))))..............-3'
MFE = -52.0; z-score = -2.19; ED = 20.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

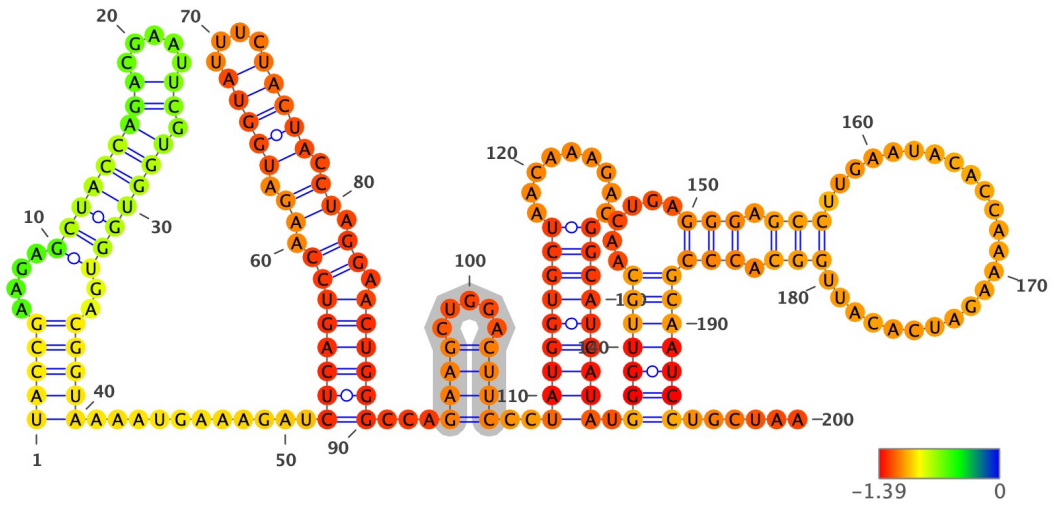
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 458 from nt 28625 to 28637 (nt 94 to 106)

```
5'-GAAGCTGGACUUC-3'
5'-((((.....))))-3'
Motif MFE = -0.8; z-score = -0.64; ED = 1.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28532 to 28731 (motif highlighted in silver):

```
5'-UACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAU
GGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAA-3
5'-(((((....((((((((.....)).)))))))..)))))...........((((((((.((.(((((....))))).)).)).))))))...((((.....))))..(((
((((((.........)))))))))).(((((((......(((.(((.......................))).)))))))))).......-3'
MFE = -55.9; z-score = -2.64; ED = 11.58
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

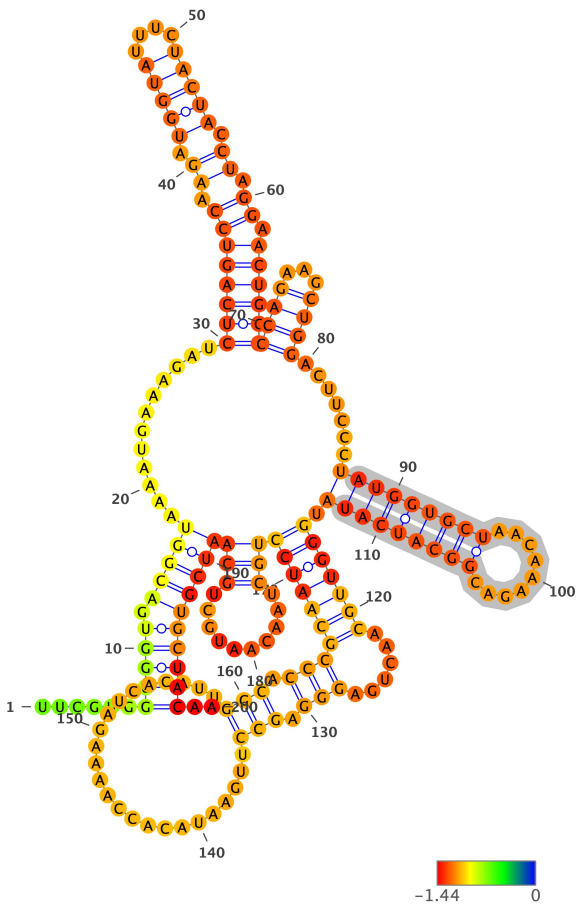
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 459 from nt 28641 to 28665 (nt 88 to 112)

```
5'-ATGGTGCTAACAAAGACGGCAUCAU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -7.1; z-score = -2.68; ED = 0.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28554 to 28753 (motif highlighted in silver):

```
5'-UUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCA
UAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAA-3
5'-......(((((.(((((............((((((((.((.(((((....))))).)).)).))))))((((...))))).......(((((((((.........)))))))
)).(((((((......(((.(((.......................))).))))))))))(((..........)))))))))))))..-3'
MFE = -54.6; z-score = -1.39; ED = 30.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

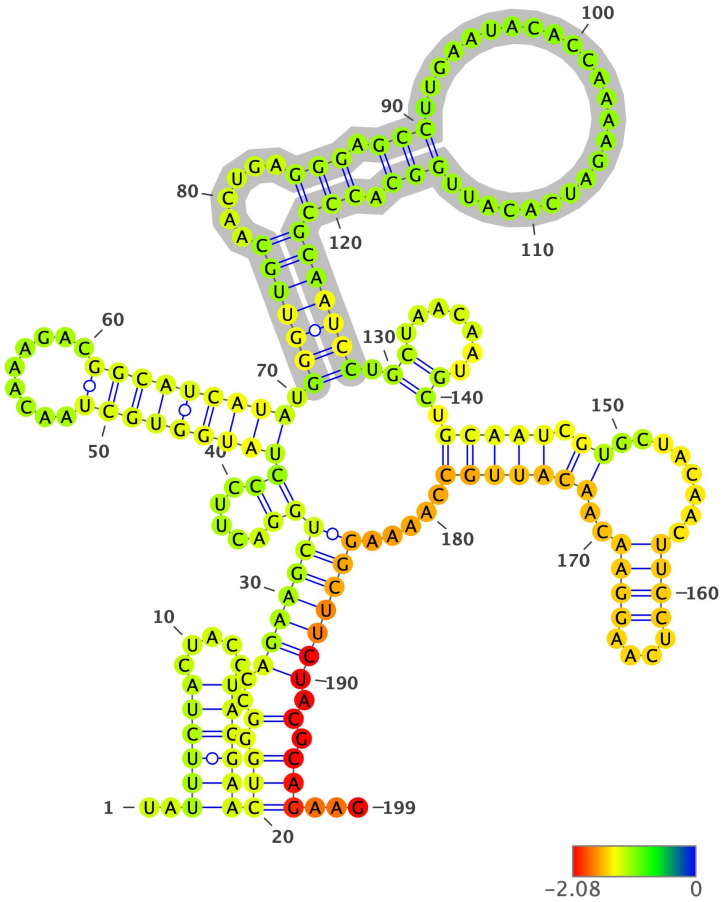
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 460 from nt 28668 to 28725 (nt 71 to 128)

```
5'-GGGTTGCAACTGAGGGAGCCTTGAATACACCAAAAGATCACATTGGCACCCGCAATCC-3'
5'-(...(((......(((.(((.......................))).))))))...)-3'
Motif MFE = -15.3; z-score = -1.62; ED = 2.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28598 to 28796 (motif highlighted in silver):

```
5'-UAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCAC
AUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAG-3
5'-..((((((.....))))))(((.(..((((((((((.....))(((((((((.........)))))))))).(((((((......(((.(((.....................
...))).))))))))))).((.......)).(((((.((........((((....))))..)))))))).....)))))))).).)))...-3'
MFE = -46.9; z-score = -1.27; ED = 33.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

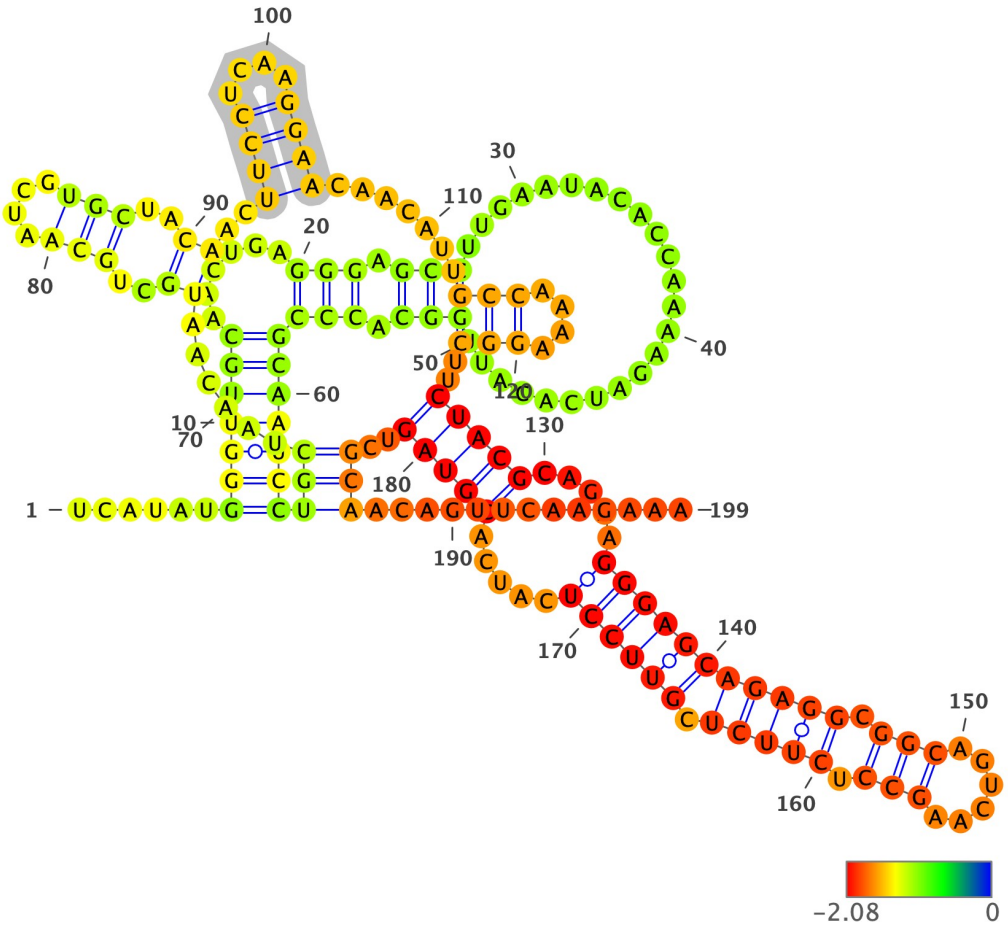
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 461 from nt 28755 to 28766 (nt 94 to 105)

```
5'-TTCCTCAAGGAA-3'
5'-((((....))))-3'
Motif MFE = -1.6; z-score = -7.88; ED = 0.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28662 to 28860 (motif highlighted in silver):

```
5'-UCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAU
UGCCAAAAGGCUUCUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAA-3
5'-......(((((((......(((.(((.......................))).))))))))))(((......((..(((....)))..))..((((....))))......
.(((....)))..(((((.....((((((((((.(((......))).)))))).))))))).....)))))..)))............-3'
MFE = -52.1; z-score = -1.89; ED = 37.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

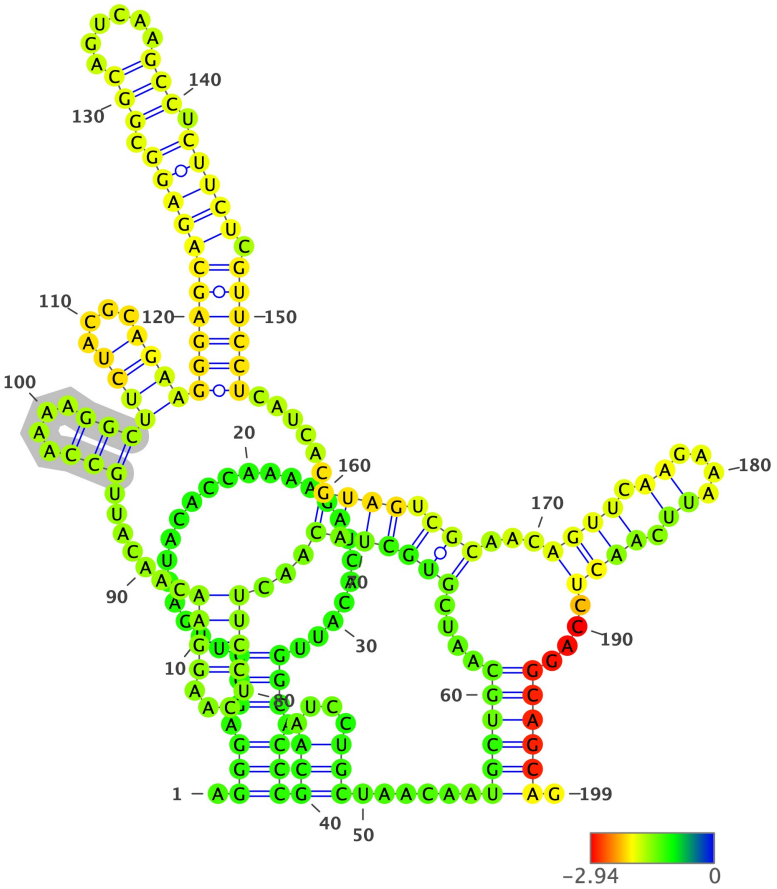
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 462 from nt 28774 to 28783 (nt 95 to 104)

```
5'-GCCAAAAGGC-3'
5'-(((....)))-3'
Motif MFE = -2.6; z-score = -6.41; ED = 0.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28680 to 28878 (motif highlighted in silver):

```
5'-AGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACG
CAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAAUUCAACUCCAGGCAGCAG-3
5'-.(((.(((.......................))).)))((....)))......((((((....(((((((...((((....))))).......((....)))((((...
.))))(((((((((((.(((......))).)))))).))))))......)))).)))...((((.((....)).)))).....)))))).-3'
MFE = -51.7; z-score = -1.67; ED = 21.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

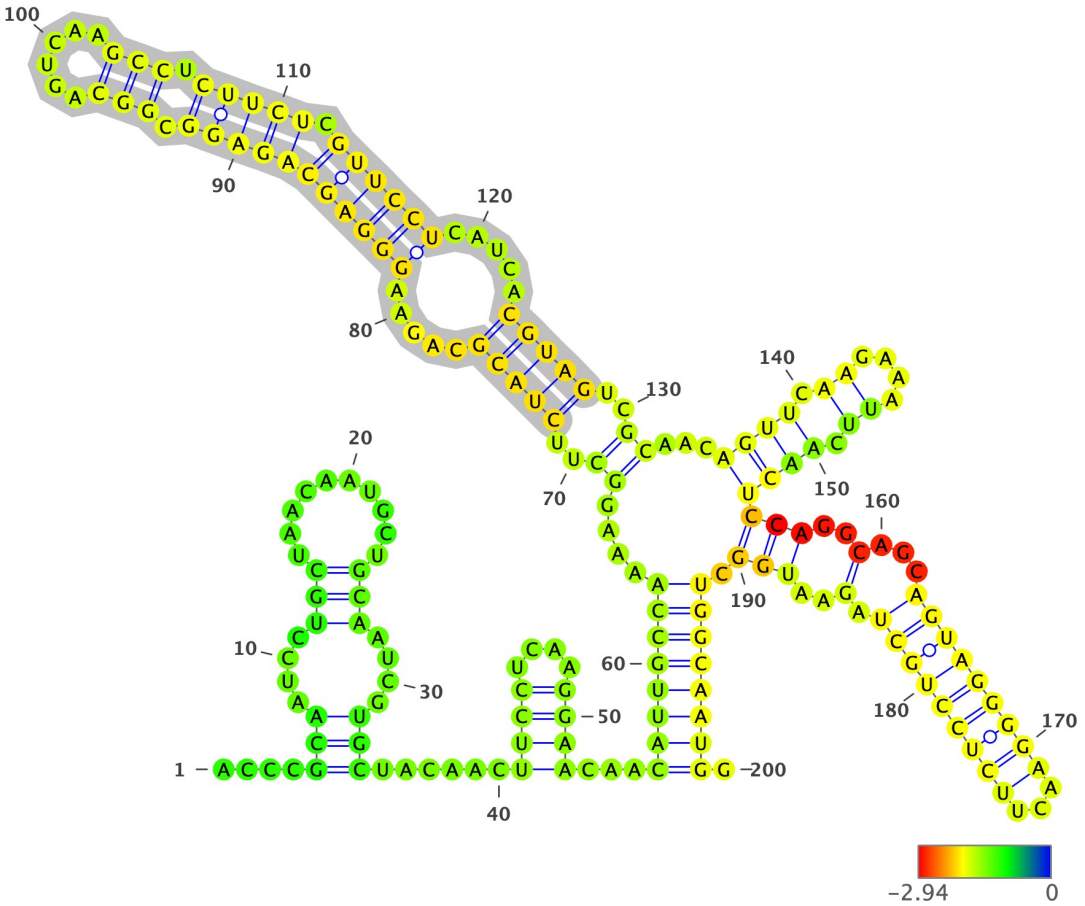
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 463 from nt 28786 to 28842 (nt 72 to 128)

```
5'-CTACGCAGAAGGGAGCAGAGGCGGCAGTCAAGCCTCUUCUCGUUCCUCATCACGUAG-3'
5'-(((((.....(((((((((((.(((......))).))))).))))))).....)))))-3'
Motif MFE = -24.0; z-score = -3.4; ED = 2.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28715 to 28914 (motif highlighted in silver):

```
5'-ACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCU
CGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAAUUCAACUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGG-3
5'-....(((....(((..........)))....)))......((((....))))...((((((((....((..(((((.....(((((((((((.(((......))).)))))
.))))))).....)))))..))...((((.((....)).))))(((..(...((((((((((...)))))))))).)..))).)))))))).-3'
MFE = -61.5; z-score = -3.12; ED = 20.59
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

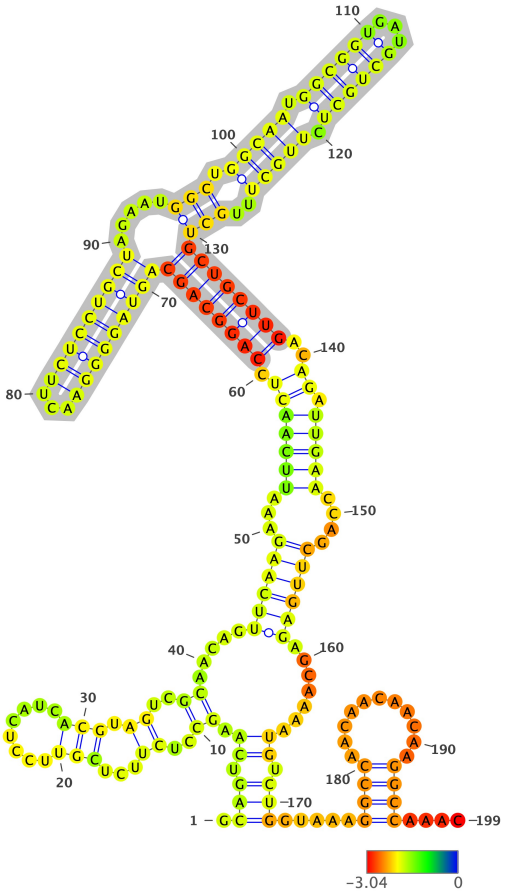
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 464 from nt 28869 to 28946 (nt 61 to 138)

```
5'-CAGGCAGCAGTAGGGGAACTTCUCCUGCUAGAATGGCTGGCAATGGCGGTGATGCUGCUCUUGCUTTGCUGCUGCUUG-3'
5'-(((((((((((((((.....))))))))).....(((.(((((.(((((.....))))).))))).))))))))))))-3'
Motif MFE = -37.9; z-score = -3.96; ED = 9.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28809 to 29007 (motif highlighted in silver):

```
5'-GCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAAUUCAACUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUG
AUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAAAC-3
5'-.(((.((.((..((...(((.........))).))..)).....((((((...(((((((.((((((((((((((((...)))))))))).....(((.(((((.((((((.
..)))))).)))))..))))))))))))..)).)))))....))))))).......)).)))).....((((...........))))....-3'
MFE = -59.2; z-score = -1.63; ED = 27.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

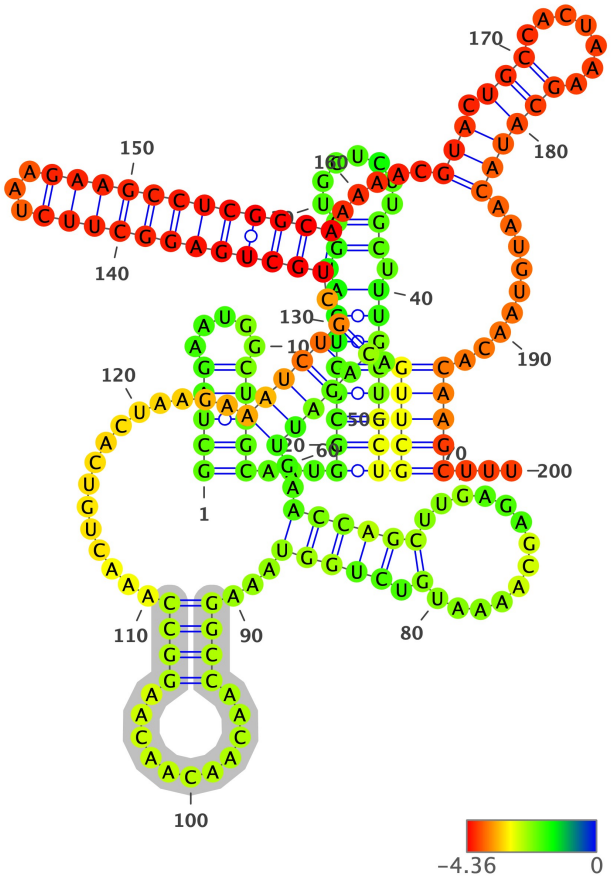
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 465 from nt 28985 to 29003 (nt 91 to 109)

```
5'-GGCCAACAACAACAAGGCC-3'
5'-((((...........))))-3'
Motif MFE = -4.9; z-score = -5.69; ED = 0.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28895 to 29094 (motif highlighted in silver):

```
5'-GCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAA
ACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUU-3
5'-(((((.....)))))...((((((((.((.......)).))))))))(((((.((((((..((((((.............).)))))...((((...........))))..
.............)))))).((((((((((((...)))))))))))).....(((.(((.......))))))..........)))))...-3'
MFE = -61.2; z-score = -3.34; ED = 46.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

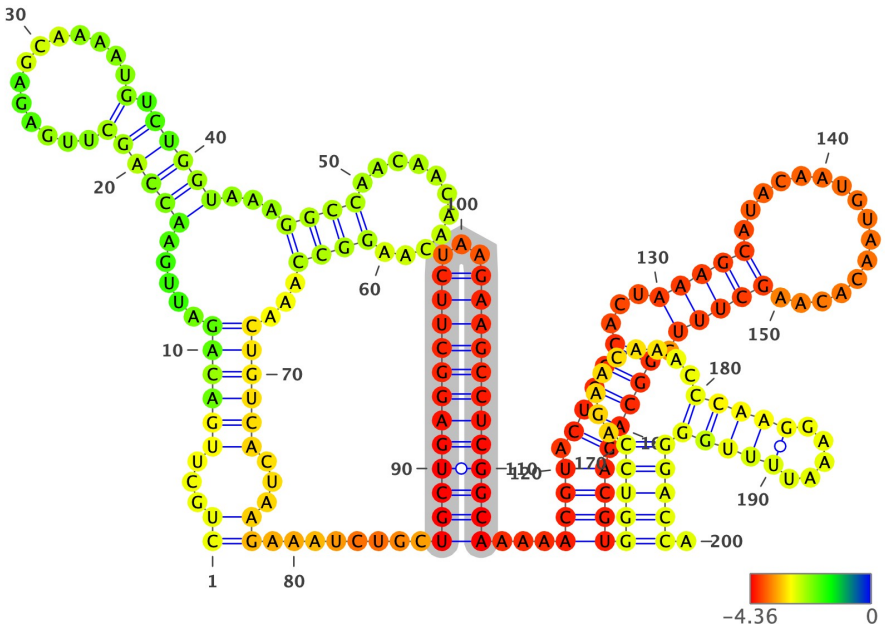
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 466 from nt 29026 to 29052 (nt 87 to 113)

```
5'-TGCTGAGGCTTCTAAGAAGCCUCGGCA-3'
5'-(((((((((((...)))))))))))-3'
Motif MFE = -19.7; z-score = -6.12; ED = 0.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28940 to 29139 (motif highlighted in silver):

```
5'-CUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGG
CAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCA-3
5'-((...((((((.....((((((.............).)))))...((((...........))))...))))))...)).........(((((((((((...)))))))))))
))...((((.(((((...(((((................))))).))))))))))(((((.........(((((.....)))))))))).-3'
MFE = -63.7; z-score = -4.78; ED = 14.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

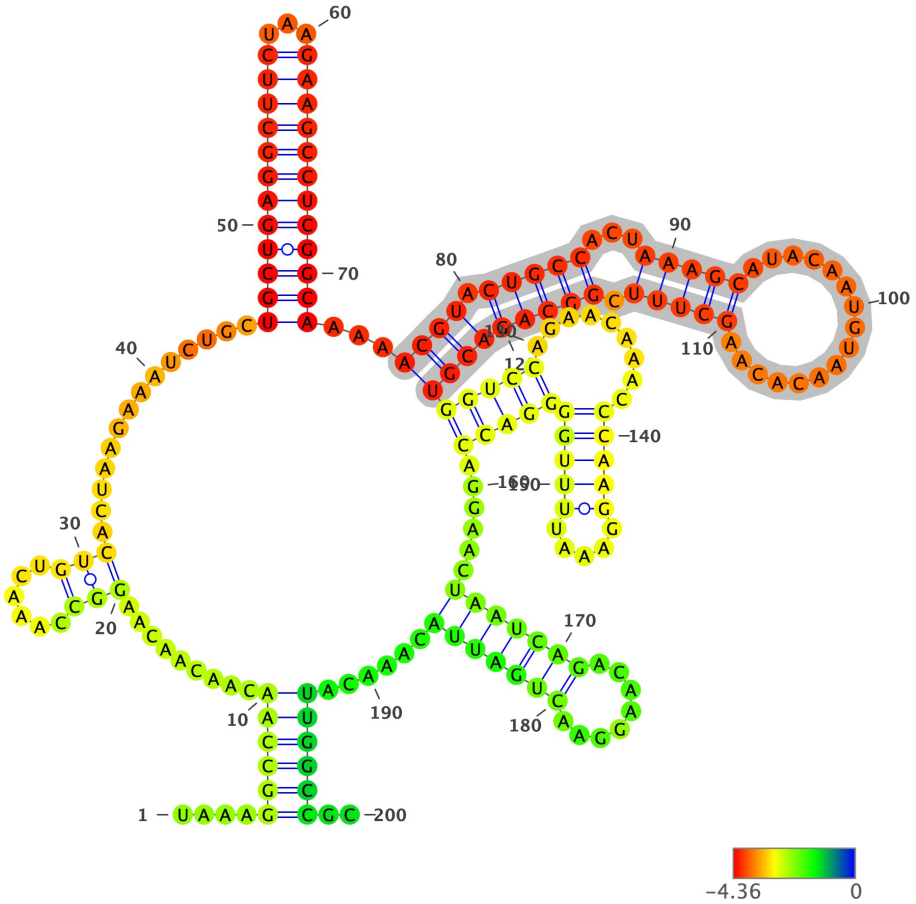
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 467 from nt 29056 to 29104 (nt 76 to 124)

```
5'-ACGTACTGCCACTAAAGCATACAATGTAACACAAGCUUUCGGCAGACGU-3'
5'-((((.(((((...(((((.................))))).)))))))))-3'
Motif MFE = -14.6; z-score = -4.53; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28981 to 29180 (motif highlighted in silver):

```
5'-UAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGC
UUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGC-3
5'-....((((((.........(((......)))..............((((((((((((...)))))))))))))...((((.(((((...(((((.................))
))).)))))))))(((((.........(((((.....)))))))))).....(((((((........)))))))......))))))..-3'
MFE = -63.2; z-score = -5.12; ED = 14.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

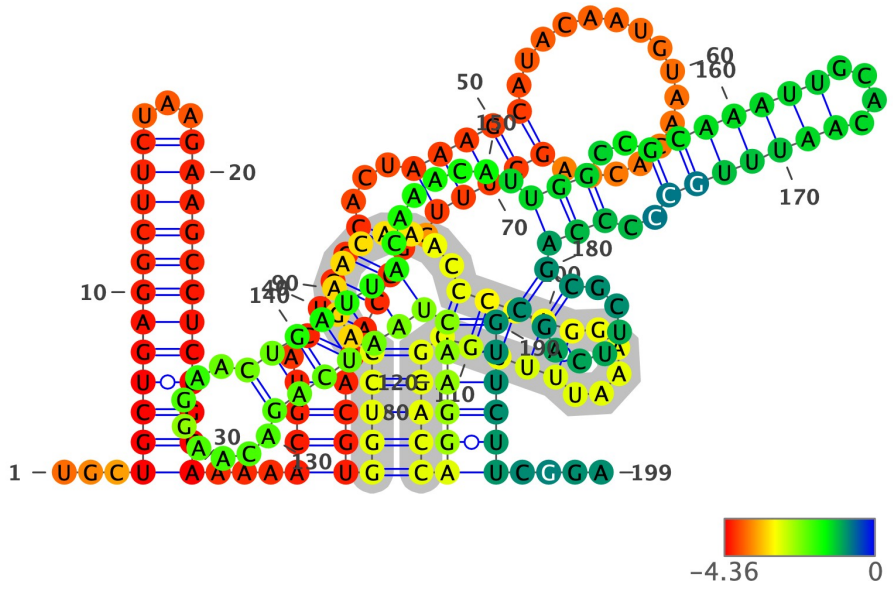
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 468 from nt 29105 to 29138 (nt 83 to 116)

```
5'-GGTCCAGAACAAACCCAAGGAAATTTTGGGGACC-3'
5'-(((((.......................)))))-3'
Motif MFE = -8.1; z-score = -1.67; ED = 3.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29023 to 29221 (motif highlighted in silver):

```
5'-UGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGG
GGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGA-3
5'-...(((((((((((...)))))))))))...((((.(((((...(((((...............)))))).)))))))))((((.........(((((.....)))))
)))))((((((((((((.......)))))))).......(((..(((((((....)))))))..)))((.....)))))))....-3'
MFE = -66.0; z-score = -4.93; ED = 13.36
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

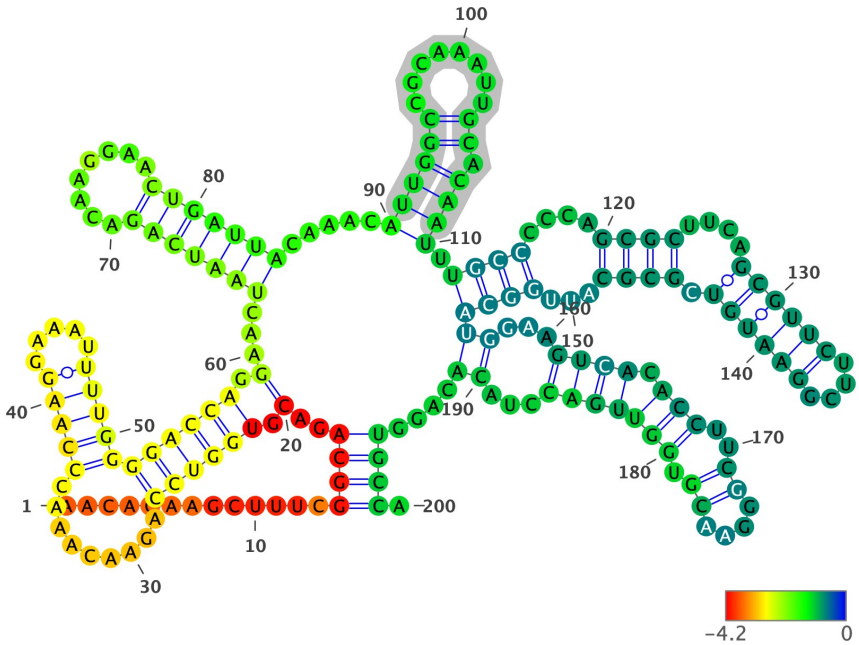
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 469 from nt 29173 to 29191 (nt 91 to 109)

```
5'-TTGGCCGCAAATTGCACAA-3'
5'-(((((........)).)))-3'
Motif MFE = -1.1; z-score = 0.03; ED = 4.08
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29083 to 29282 (motif highlighted in silver):

```
5'-AACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUU
UGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCA-3
5'-............((((..(.((((((.........(((((.....)))))))))))).)...(((((((.......)))))))).....((((((........)).)))).
((((....((((....((((((....)))))).)))).....))))((...((((.(((..((....)).)))))))...)).....)))).-3'
MFE = -51.8; z-score = -1.08; ED = 25.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

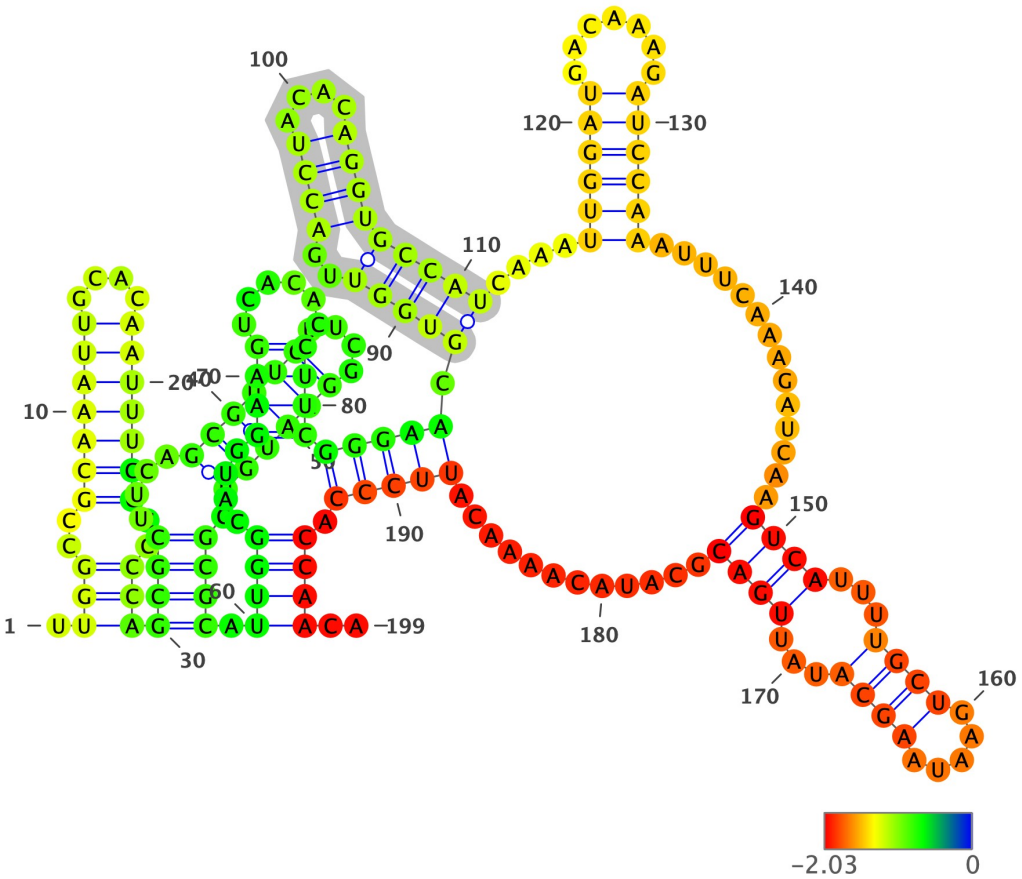
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 470 from nt 29260 to 29283 (nt 88 to 111)

```
5'-GTGGTTGACCTACACAGGUGCCAU-3'
5'-(((((..(((......))))))))-3'
Motif MFE = -7.3; z-score = -2.04; ED = 1.08
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29173 to 29371 (motif highlighted in silver):

```
5'-UUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAU
CAAAUUGGAUGACAAAGAUCCAAAUUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUGACGCAUACAAAACAUUCCCACCAACA-3
5'-.(((..(((((((....)))))))..)))((((....((((((....)))))).)))).((((....((((......))))(((((.(((((..((((....)))))))))
....((((((.......))))))..............((((...((((.....))))...))))............))))).))))..-3'
MFE = -51.8; z-score = -2.29; ED = 21.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

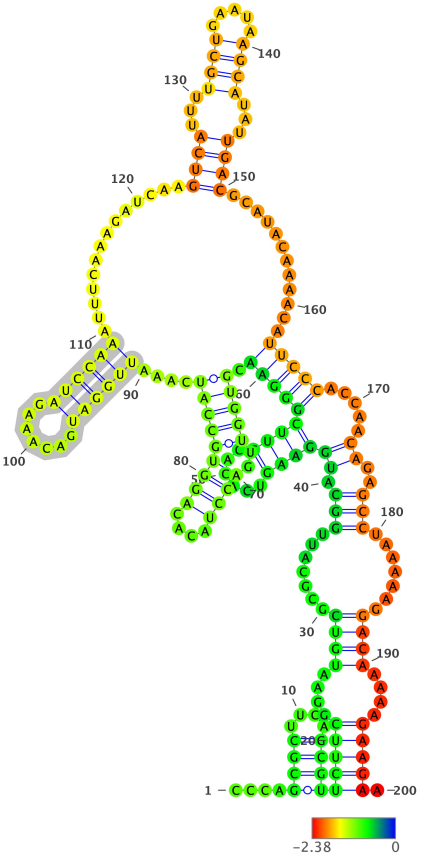
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 471 from nt 29288 to 29306 (nt 91 to 109)

```
5'-TTGGATGACAAAGAUCCAA-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -3.84; ED = 0.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29198 to 29397 (motif highlighted in silver):

```
5'-CCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAUCAAAUUGGAUGACAAAGAUCCAAAU
UUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAA-3
5'-....((((....))))(((((....((((.......(((.((((((......))))(((((.(((((..((((....)))))))))....((((((.......))))))..
............((((...((((.....))))...))))............)))))).....))..)))).......))))....)))))).-3'
MFE = -48.7; z-score = -2.75; ED = 16.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

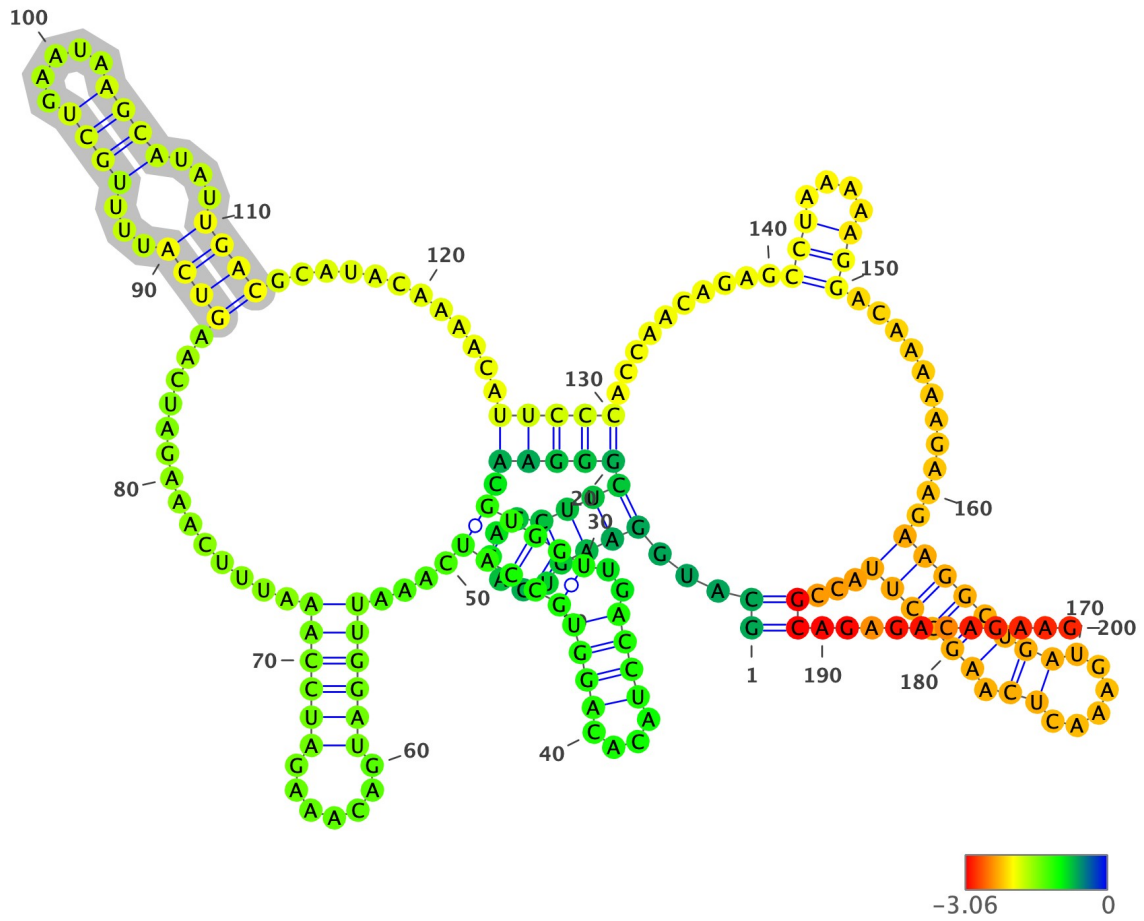
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 472 from nt 29321 to 29347 (nt 87 to 113)

```
5'-GTCATTTTGCTGAATAAGCATATUGAC-3'
5'-((((....(((.....)))....))))-3'
Motif MFE = -7.9; z-score = -3.31; ED = 0.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29235 to 29434 (motif highlighted in silver):

```
5'-GCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAUCAAAUUGGAUGACAAAGAUCCAAAUUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUG
ACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAG-3
5'-((...((((.....))))(((((.(((((..((((....)))))))))....((((((.......))))))..............((((...((((.....))))...))
)).............)))))..........(((....)))...........((((((((......)).)))))))...)).............-3'
MFE = -42.6; z-score = -2.19; ED = 18.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

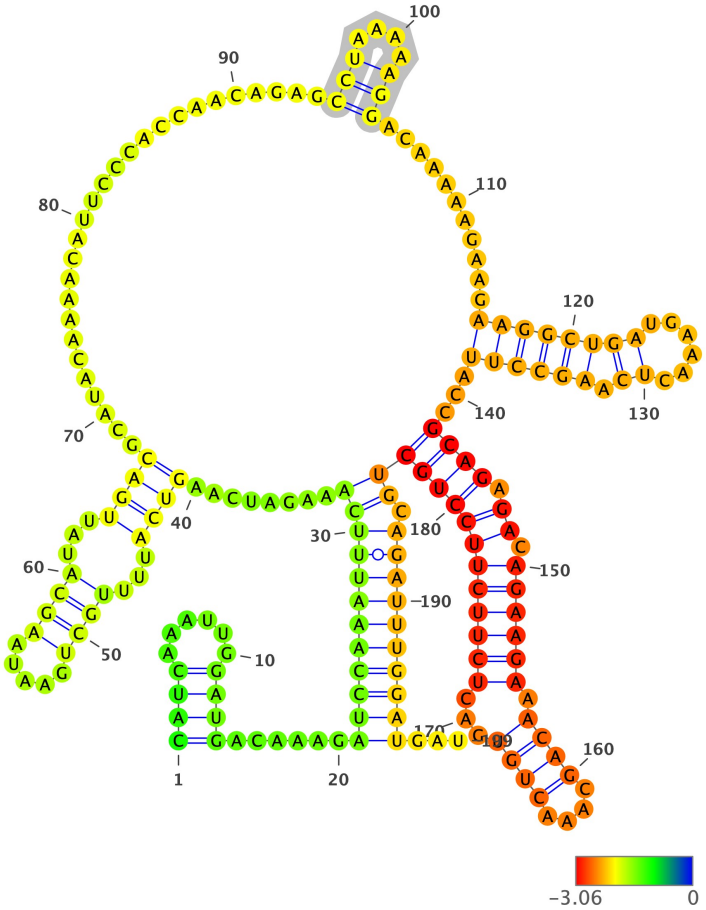
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 473 from nt 29375 to 29384 (nt 95 to 104)

```
5'-CCTAAAAAGG-3'
5'-((......))-3'
Motif MFE = -0.3; z-score = -1.98; ED = 1.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29281 to 29479 (motif highlighted in silver):

```
5'-CAUCAAAUUGGAUGACAAAGAUCCAAAUUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAA
GAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAU-3
5'-((((......))))......(((((((((((.........((((...((((.....))))...))))..........................(((....)))........
....((((((((......)).))))))...((((.((.((((((.((((....))))...)))))))))))))).))))))))))...-3'
MFE = -48.5; z-score = -3.98; ED = 15.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

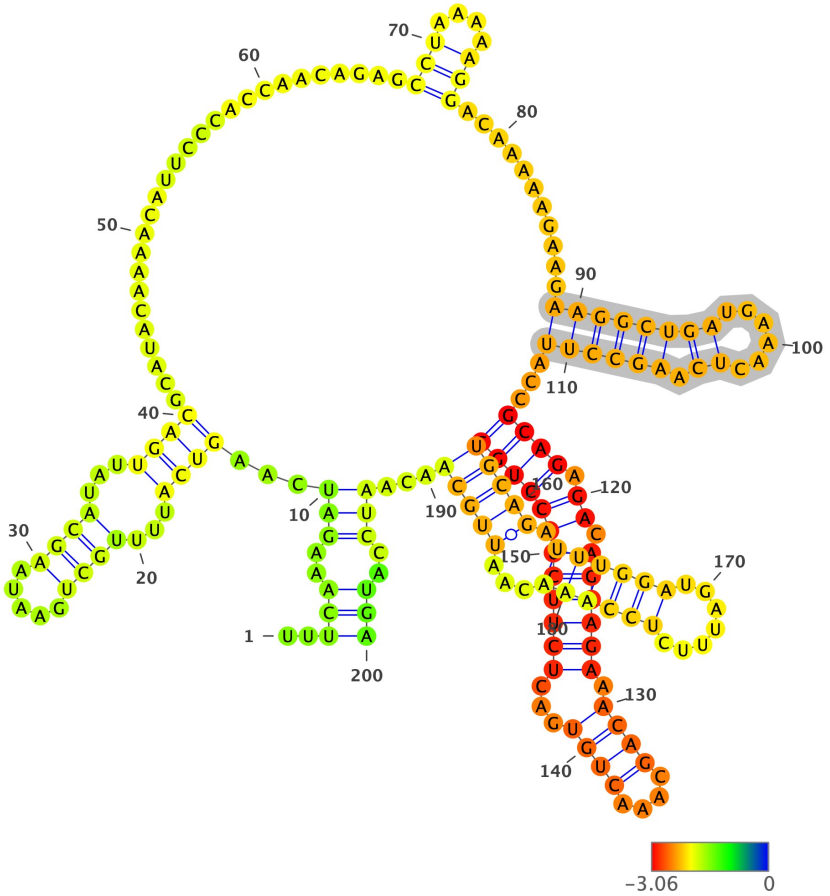
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 474 from nt 29396 to 29418 (nt 89 to 111)

```
5'-AAGGCTGATGAAACUCAAGCCUU-3'
5'-((((((((......)).))))))-3'
Motif MFE = -6.9; z-score = -3.52; ED = 3.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29308 to 29507 (motif highlighted in silver):

```
5'-UUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUU
ACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGA-3
5'-..(((..(((...((((...((((.....))))...))))..........................(((....)))...........((((((((......)).))))))
...((((.((.((((((.((((....))))...)))))))))))))(((((.((((((.......))))))...)))))...)))..)))-3'
MFE = -46.0; z-score = -3.98; ED = 10.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

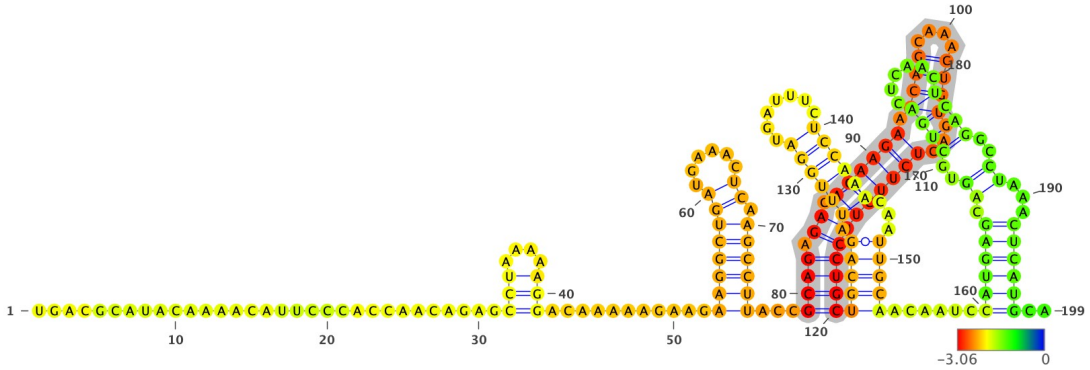
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 475 from nt 29422 to 29463 (nt 79 to 120)

```
5'-GCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGC-3'
5'-((((.((.(((((((.((((....))))...))))))))))))-3'
Motif MFE = -14.7; z-score = -3.92; ED = 1.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29344 to 29542 (motif highlighted in silver):

```
5'-UGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCU
UCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCA-3
5'-...............................(((....)))...........((((((((......)).))))))...((((.((.(((((((.((((....))))...)))
))))))))((((((.(((((((.......))))))...)))))......((((((.((..((((......))))..))...))))))..-3'
MFE = -46.0; z-score = -3.12; ED = 14.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 190--gene, gene-GU280_gp10, 28274-29533(+)

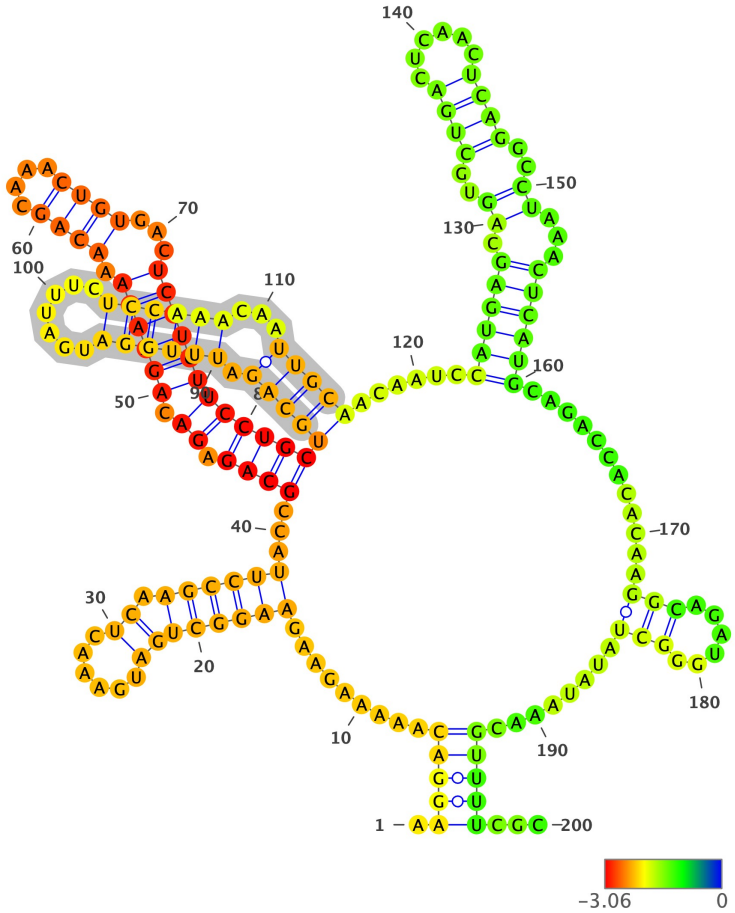
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 190--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 476 from nt 29465 to 29495 (nt 85 to 115)

```
5'-GCAGATTTGGATGATTTCUCCAAACAAUUGC-3'
5'-((((....(((.......)))......))))-3'
Motif MFE = -6.3; z-score = -1.98; ED = 1.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29381 to 29580 (motif highlighted in silver):

```
5'-AAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAA
UUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGC-3
5'-.(((((.........((((((((......)).))))))...((((.((.((((((.((((....))))...))))))))))))(((((.((((((.......))))))...
)))))......((((((.((..((((......))))..))...))))))............(((......)))........)))))...-3'
MFE = -48.8; z-score = -2.29; ED = 29.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 153--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 153--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 178 to 200--gene, gene-GU280_gp11, 29558-29674(+)

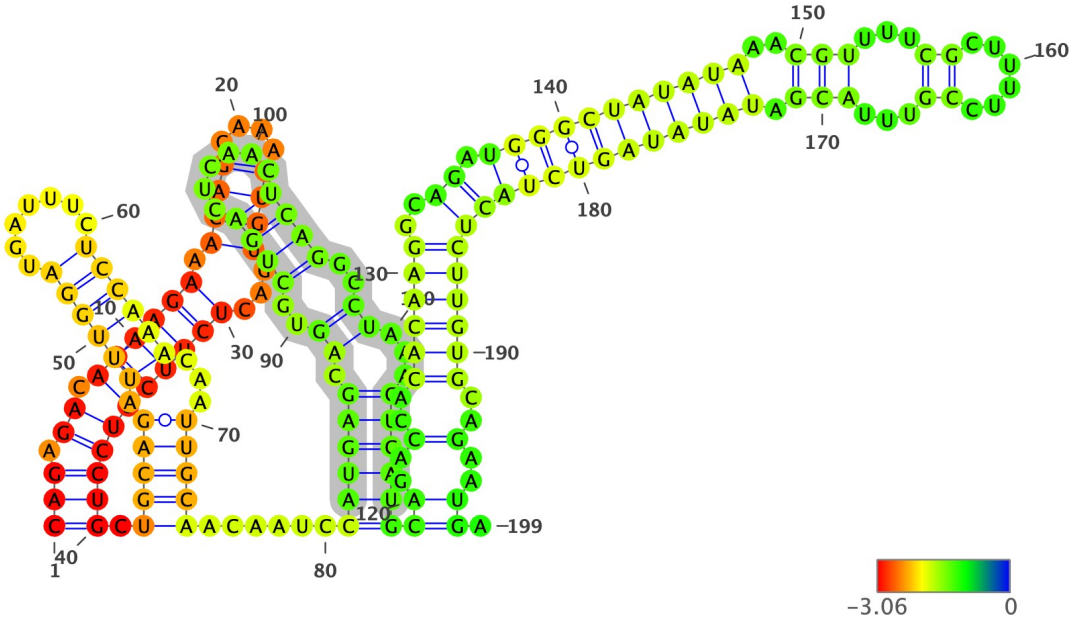
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 178 to 200--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

NC_045512.2 (forward strand): Structure number 477 from nt 29504 to 29539 (nt 82 to 117)

```
5'-ATGAGCAGTGCTGACTCAACUCAGGCCTAAACUCAU-3'
5'-(((((..(..((((......))))..)....)))))-3'
Motif MFE = -8.1; z-score = -2.04; ED = 2.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29423 to 29621 (motif highlighted in silver):

```
5'-CAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAA
ACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGA-3
5'-(((.((.((((((.((((....))))...)))))))))))).(((((.((((((.......))))))...)))))......((((((.((..((((......))))..))..
.))))))((..(..((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))))..)..)).-3'
MFE = -53.2; z-score = -2.59; ED = 12.16
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 111--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 111--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 136 to 199--gene, gene-GU280_gp11, 29558-29674(+)

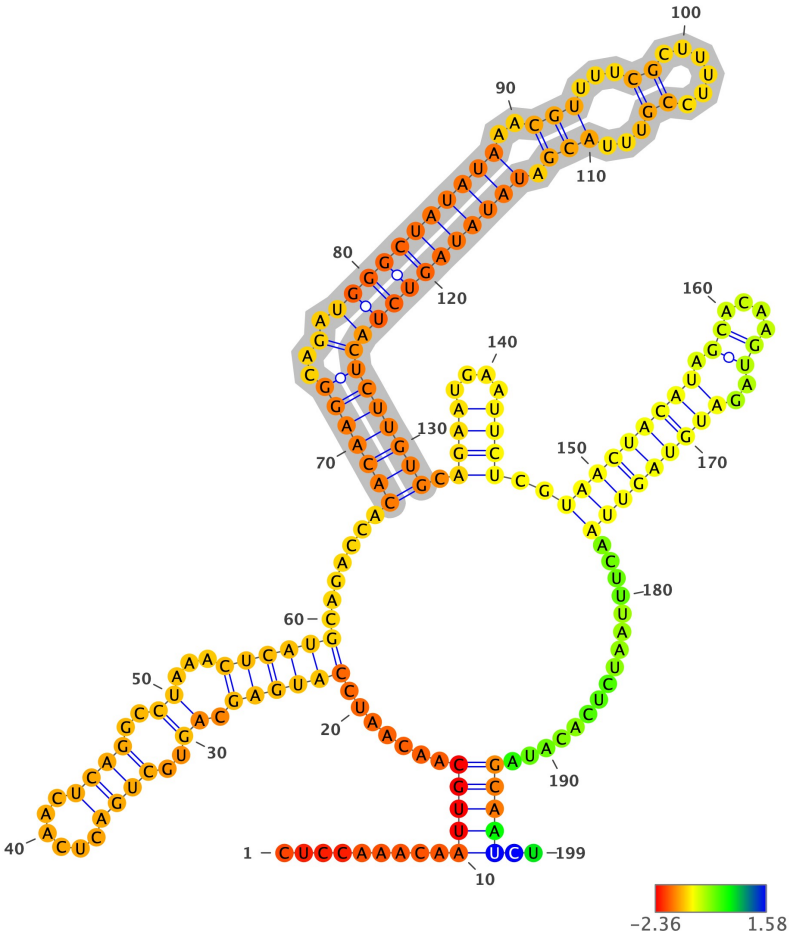
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 136 to 199--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

NC_045512.2 (forward strand): Structure number 478 from nt 29548 to 29613 (nt 67 to 132)

```
5'-CACAAGGCAGATGGGCTATATAAACGTTTTCGCTTTTCCGTTTACGAUAUAUAGUCUACUCUUGUG-3'
5'-(((((((.....((((((((((..(((...((......))...))).))))))))))..)))))))-3'
Motif MFE = -19.7; z-score = -3.07; ED = 3.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29482 to 29680 (motif highlighted in silver):

```
5'-CUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUAC
GAUAUAUAGUCUACUCUUGUGCAGAAUGAAUUCUCGUAACUACAUAGCACAAGUAGAUGUAGUUAACUUUAAUCUCACAUAGCAAUCU-3
5'-.........(((((.......((((((.((..((((......))))..))...))))))).......(((((((..(.(((((((((((..(((...((......))...))
).))))))))))))))))))).((((....))))..(((((((((.((....))..)))))))))..................)))))..-3'
MFE = -45.3; z-score = -3.33; ED = 11.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 52--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 52--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 77 to 193--gene, gene-GU280_gp11, 29558-29674(+)

Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 77 to 193--CDS, cds-YP_009725255.1, 29558-29674(+)

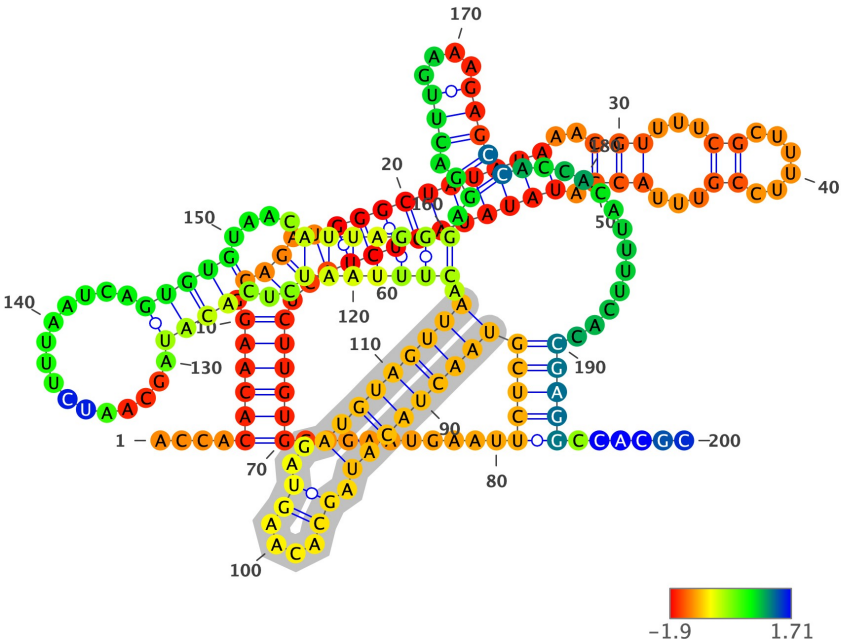
Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

6-- nt 194 to 199--three_prime_UTR, id-NC_045512.2:29675..29903, 29675-29903(+)

Attributes: ['ID=id-NC_045512.2:29675..29903', "gbkey=3'UTR"]

NC_045512.2 (forward strand): Structure number 479 from nt 29629 to 29657 (nt 86 to 114)

```
5'-TAACTACATAGCACAAGTAGAUGUAGUUA-3'
5'-((((.....))))-3'
Motif MFE = -8.5; z-score = -5.41; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29544 to 29743 (motif highlighted in silver):

```
5'-ACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGAAUUCUCGUAACUACAUAGCACAAGUAGAUGUAG
UUAACUUUAAUCUCACAUAGCAAUCUUUAAUCAGUGUGUAACAUUAGGGAGGACUUGAAAGAGCCACCACAUUUUCACCGAGGCCACGC-3
5'-....((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))).........((((((((((((.((....)).)))))))
))).(((((((..(((((.............)))))....)))))))).((.(((....)))))............)))))......-3'
MFE = -42.8; z-score = -0.96; ED = 35.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 15 to 131--gene, gene-GU280_gp11, 29558-29674(+)

Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

3-- nt 15 to 131--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

4-- nt 132 to 200--three_prime_UTR, id-NC_045512.2:29675..29903, 29675-29903(+)

Attributes: ['ID=id-NC_045512.2:29675..29903', "gbkey=3'UTR"]