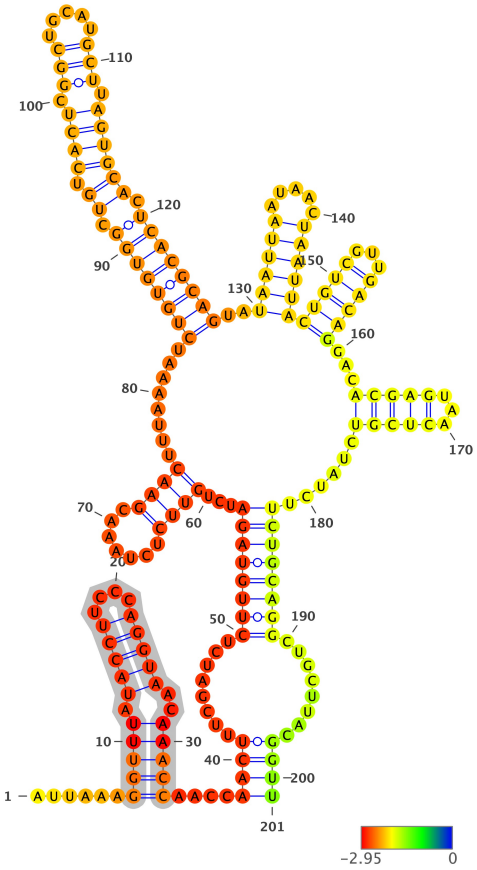
NC_045512.2 (forward strand): Structure number 1 from nt 7 to 33 (nt 7 to 33)

```
5'-GGTTTATACCTTCCCAGGUAACAAACC-3'
5'-(((...(((((....)))))....)))-3'
Motif MFE = -7.0; z-score = -3.72; 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 = -3.36; 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(+)

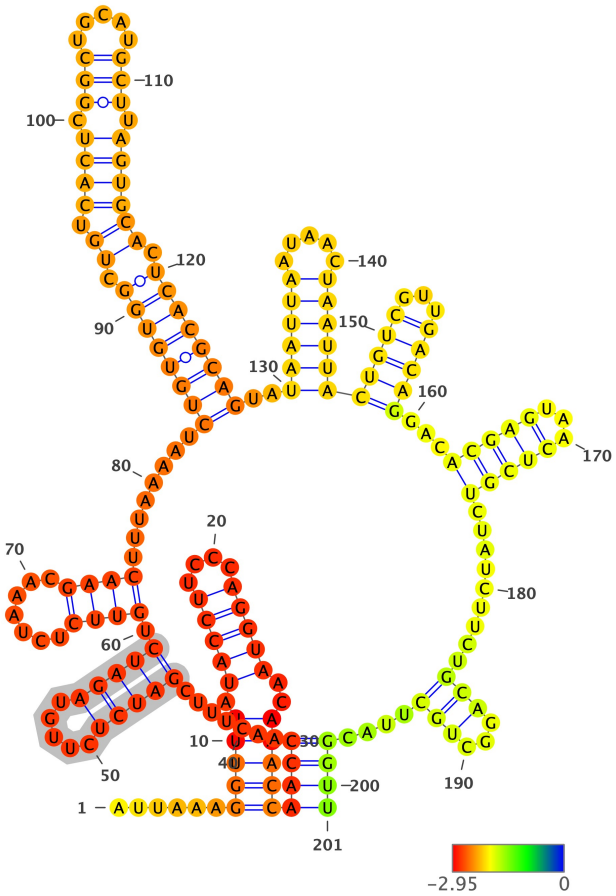
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 = -2.72; 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 = -2.79; 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(+)

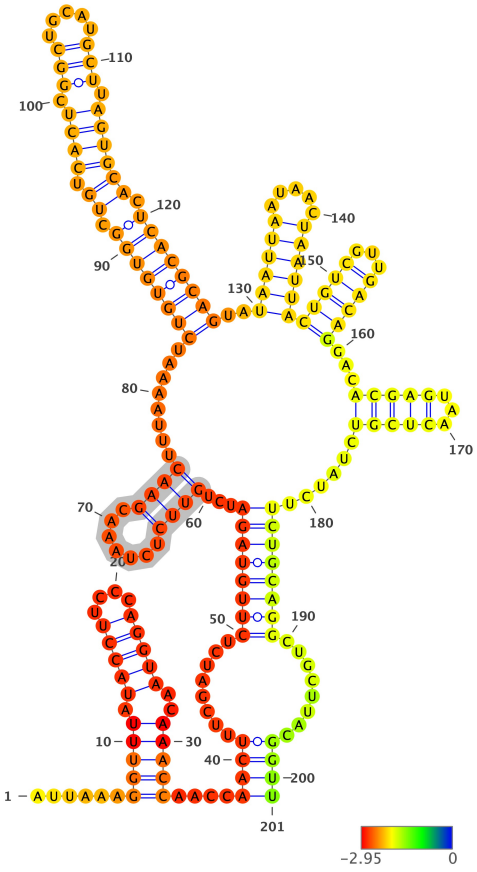
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 61 to 75 (nt 61 to 75)

```
5'-GTTCTCTAAACGAAC-3'
5'-((((.......))))-3'
Motif MFE = -0.9; z-score = -1.37; ED = 1.97
```



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 1 to 201 (motif highlighted in silver):

```
5'-AUUAAAGGUUUAUACCUUCCCAGGUAACAAACCAACCAACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCU
UAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUU-3
5'-......((((((.((((((....))))))..))))))....((((........(((((((((...((((........))))........(((((((((.((.(((((.(((.....)))
.))))))).)))))))))..((((((.....))))))((((((...))))))...((((((...))))))......)))))))).........))))-3'
MFE = -51.1; z-score = -3.12; ED = 21.83
```

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(+)

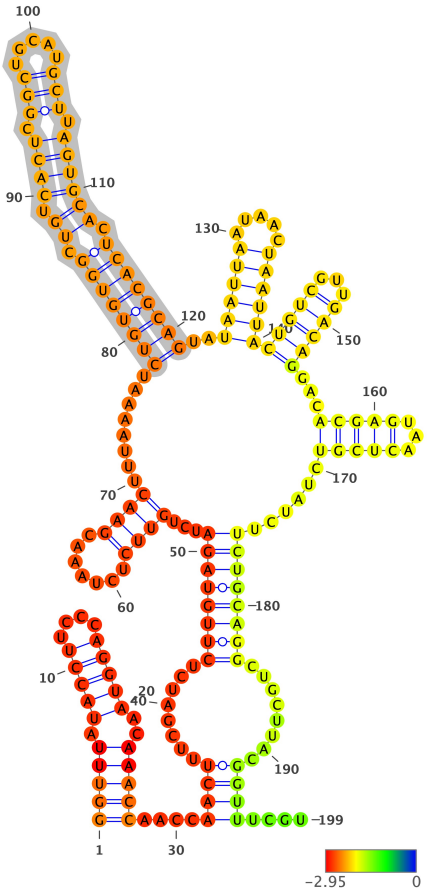
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 4 from nt 84 to 127 (nt 78 to 121)

```
5'-CTGTGTGGCTGTCACTCGGCTGCATGCUTAGUGCACUCACGCAG-3'
5'-((((((((.((.((((.(((.....)).)))))).))))))))-3'
Motif MFE = -20.1; z-score = -3.65; 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 = -2.85; 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(+)

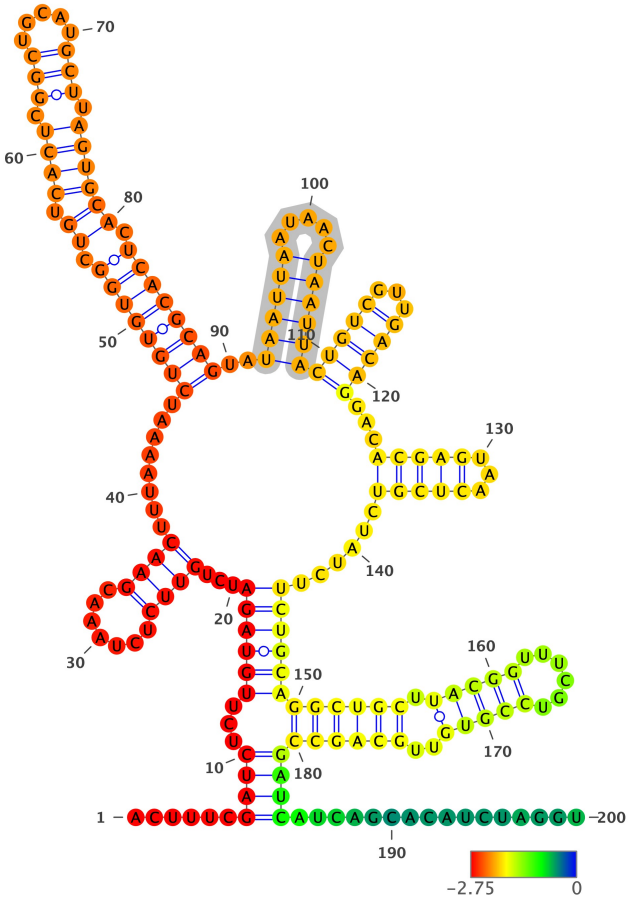
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 5 from nt 130 to 146 (nt 92 to 108)

```
5'-TAATTAATAACUAAUUA-3'
5'-((((((.....))))))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 39 to 238 (motif highlighted in silver):

```
5'-ACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUG
UCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGU-3
5'-......((((...((((((...((((.......))))........((((((((.((.((((.(((.....))).))))))).))))))))..((((((.....))))))(((
((...)))))...(((((...)))))......))))))((((((.(((((......)))))..))))))))))................-3'
MFE = -59.9; z-score = -3.44; ED = 22.48
```

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(+)

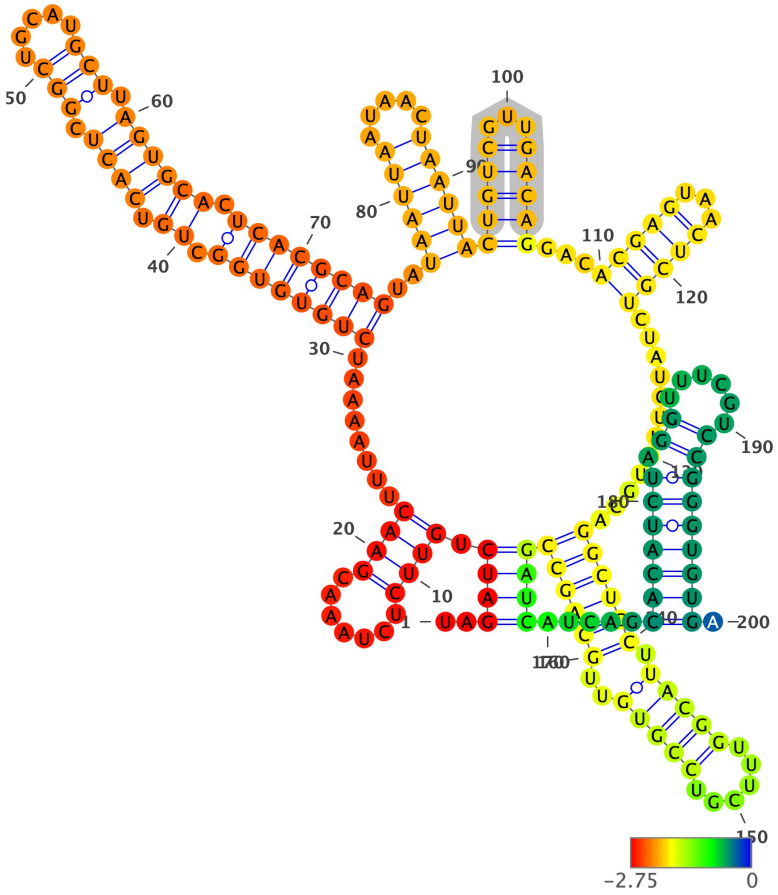
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--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 6 from nt 148 to 158 (nt 95 to 105)

```
5'-TGTCGTTGACA-3'
5'-((((...))))-3'
Motif MFE = -0.8; z-score = -4.05; ED = 1.2
```



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 54 to 253 (motif highlighted in silver):

```
5'-UAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACAC
GAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGA-3
5'-..((((.((((.......)))).........((((((((.((.((((.(((.....))).)))))).))))))))..((((((.....))))))(((((...)))))...((
(((...)))))............((((((.(((((......)))))..)))))))))).....(((((((.((......)))))))))).-3'
MFE = -66.3; z-score = -3.89; ED = 8.53
```

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(+)

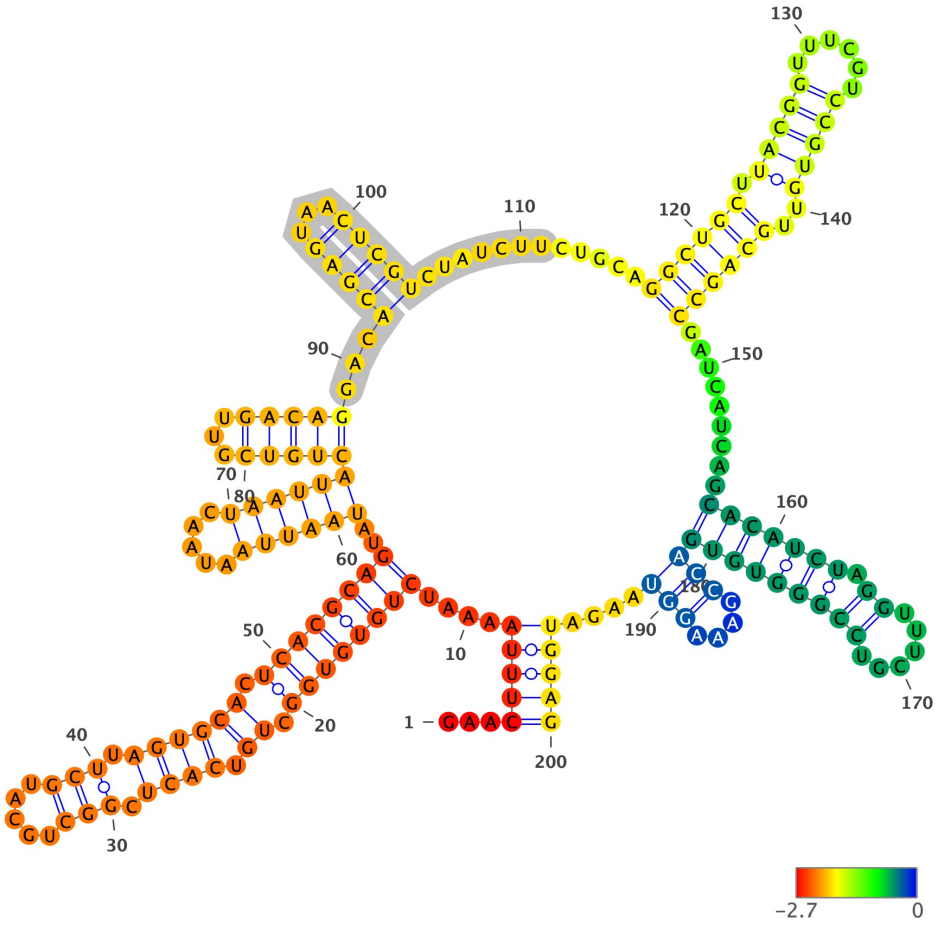
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--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 7 from nt 160 to 182 (nt 89 to 111)

```
5'-GACACGAGTAACUCGUCTATCUU-3'
5'-((.(((((...))))).....))-3'
Motif MFE = -3.8; z-score = -1.71; 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 72 to 271 (motif highlighted in silver):

```
5'-GAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUU
CUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGGAG-3
5'-...(((((....((((((((.((.((((.(((.....))).)))))).))))))))..((((((.....))))))(((((...)))))...(((((...)))))).......
.....((((((.(((((......)))))..))))))..........(((((((.((......)))))))))(((....)))....)))))-3'
MFE = -64.8; z-score = -3.5; ED = 17.07
```

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(+)

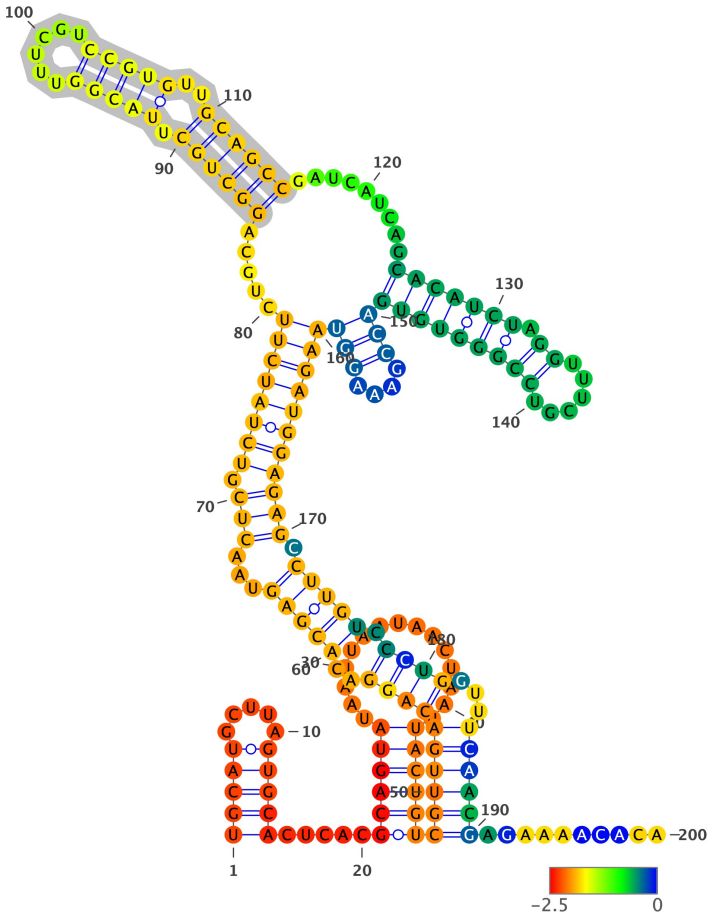
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 8 from nt 188 to 218 (nt 85 to 115)

```
5'-GGCTGCTTACGGTTTCGTCCGUGTTGCAGCC-3'
5'-((((((.(((((.....)))))..)))))))-3'
Motif MFE = -17.2; z-score = -3.8; 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 = -3.03; 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(+)

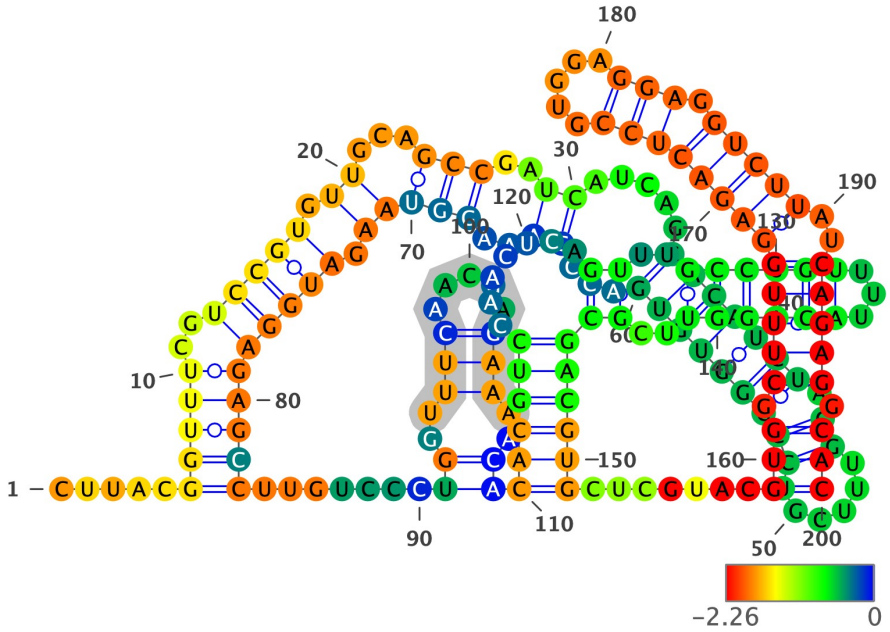
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 9 from nt 286 to 298 (nt 94 to 106)

```
5'-TTTCAACGAGAAA-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.17; ED = 2.03
```



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 193 to 392 (motif highlighted in silver):

```
5'-CUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGGAGAGCCUUGUCCCUGGUUUCAACGAGAAAACACA
CGUCCAACUCAGUUUGCCUGUUUUACAGGUUCGCGACGUGCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCAC-3
5'-.....(((((..(((((.((...(((..((.....(((((((.((......)))))))))...))..))))).))))))))))).......((..(((.....)))..))((
((((.......((..((((((...))))))..))))))))).......(((.((((((((((((.....))).))))).))))).)))-3'
MFE = -57.7; z-score = 0.45; ED = 39.9
```

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 73--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

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

3-- nt 74 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 74 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

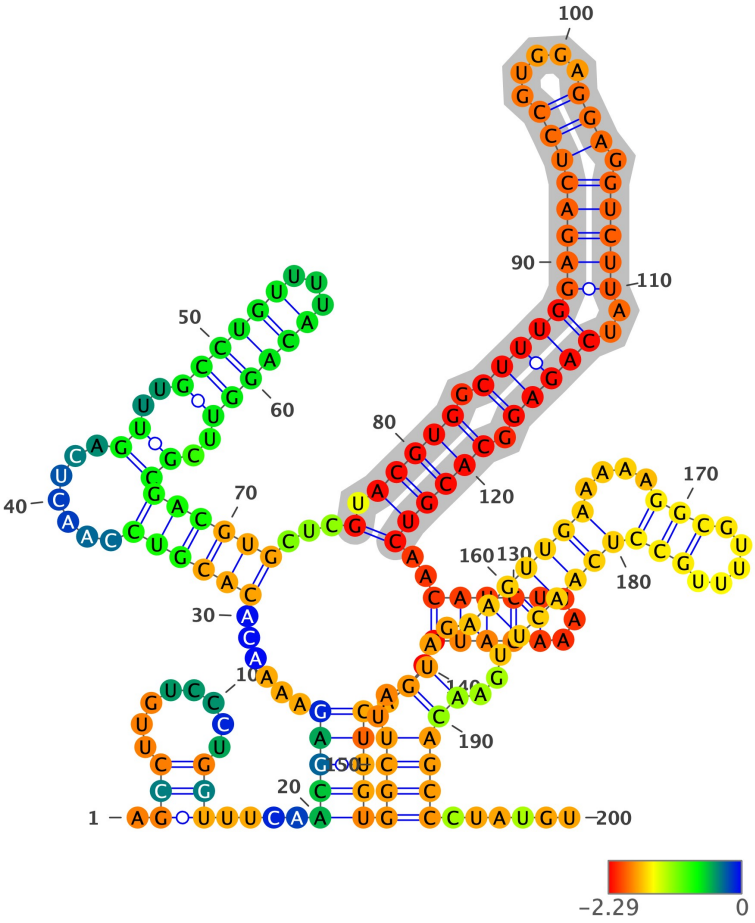
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

5-- nt 74 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 10 from nt 347 to 395 (nt 76 to 124)

```
5'-GTACGTGGCTTTGGAGACTCCGTGGAGGAGGUCUUATCAGAGGCACGUC-3'
5'-(.(((((.(((((((((((((.....))).)))))..)))))).))))))-3'
Motif MFE = -22.6; z-score = -3.58; ED = 3.0
```



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 272 to 471 (motif highlighted in silver):

```
5'-AGCCUUGUCCCUGGUUUCAACGAGAAAACACACGUCCAACUCAGUUUGCCUGUUUUACAGGUUCGCGACGUGCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUA
UCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGU-3
5'-.(((........)))....(((((......((((((.......((..((((((...))))))..))))))))...(.(((((.(((((((((((((.....))).)))))).
.)))))).))))))..(((((...)))))...)))))((((..((..(((((((....(((.....)))))))))..))))))......-3'
MFE = -61.8; z-score = -1.96; ED = 17.64
```

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(+)

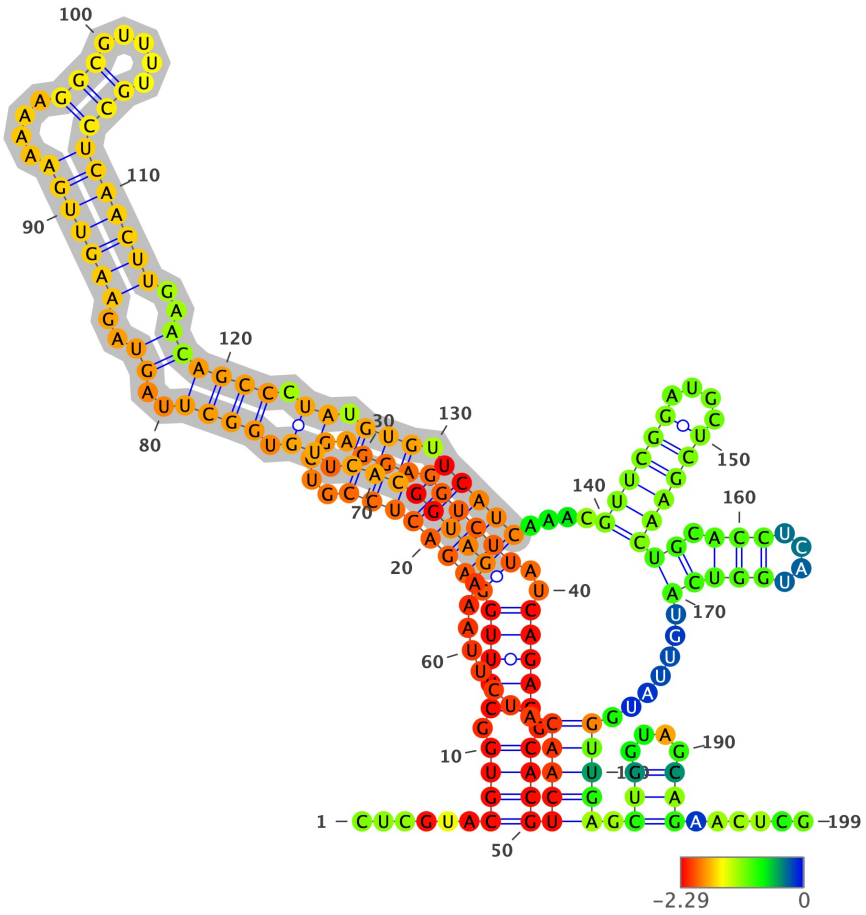
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 11 from nt 407 to 478 (nt 64 to 135)

```
5'-GATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCUCAACUUGAACAGCCCUATGUGTTCAUC-3'
5'-(((..(((.((.((((......(((((((....(((.....)))))))))....)))).)).)))...)))-3'
Motif MFE = -24.6; z-score = -3.24; ED = 4.44
```



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 344 to 542 (motif highlighted in silver):

```
5'-CUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAA
CUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCG-3
5'-......((((.(((((((((((((.....))).)))))..)))))).))))(((((........((((((((.((.((((..((..(((((((....(((.....)))))))
)))..)))))).)).))).)))))....((((((....))))))((.(((....)))))).......)))))).(((....))).....-3'
MFE = -62.0; z-score = -1.6; 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(+)

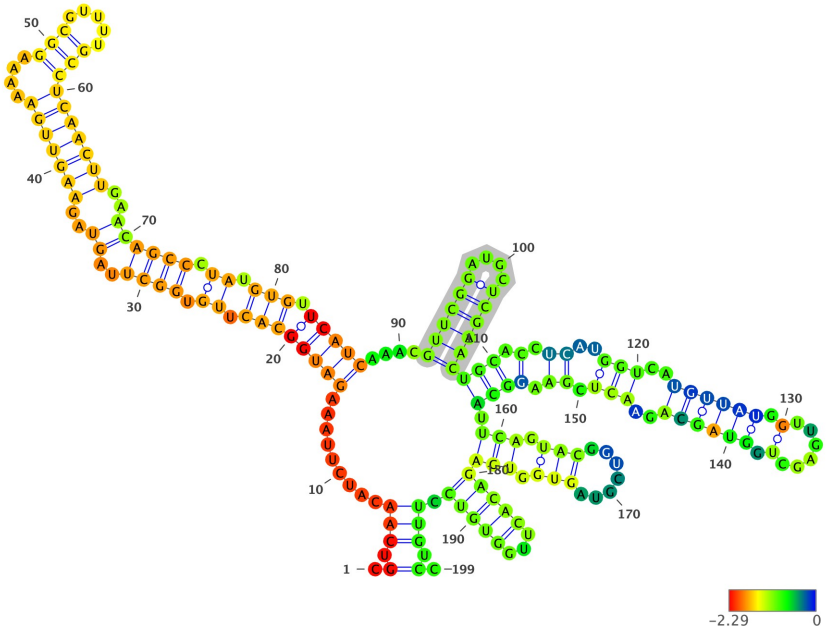
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 12 from nt 483 to 498 (nt 92 to 107)

```
5'-GTTCGGATGCUCGAAC-3'
5'-((((((....))))))-3'
Motif MFE = -4.3; z-score = -2.1; 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 = -0.46; 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(+)

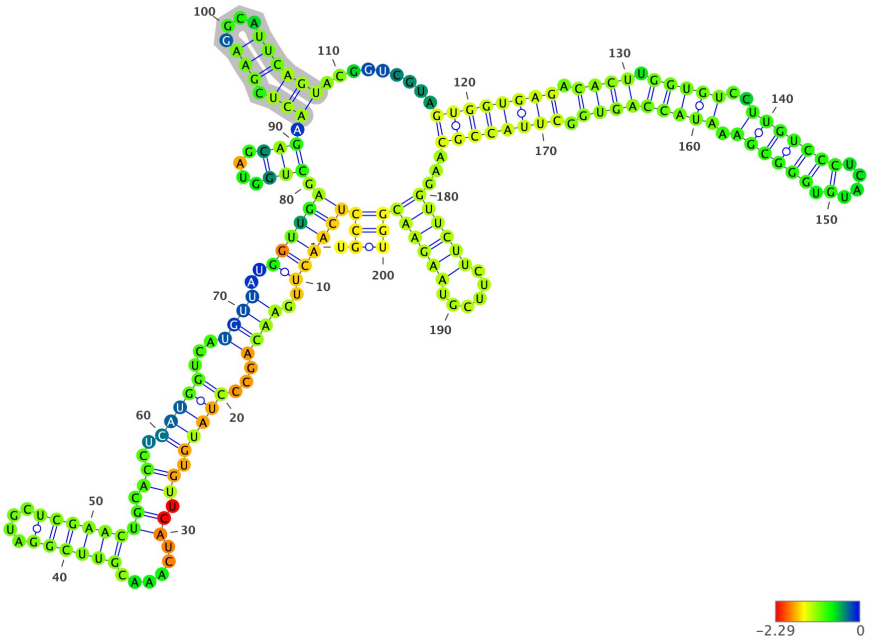
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 13 from nt 538 to 554 (nt 92 to 108)

```
5'-ACTCGAAGGCAUUCAGU-3'
5'-(((.(((....))))))-3'
Motif MFE = -1.0; z-score = -0.3; 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 447 to 646 (motif highlighted in silver):

```
5'-UGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACG
GUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGU-3
5'-.(((((((((..((((...(((((.((.((......((((((....))))))))).))..)))))...))))..)))))).(((....))).(((.(((....))))))...
......((((((((.((((.(((((..(((((((....).))))))).)))))))))).)))))))...((((((......)))))))))-3'
MFE = -60.7; z-score = -1.59; ED = 31.54
```

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, 266-13468(+)

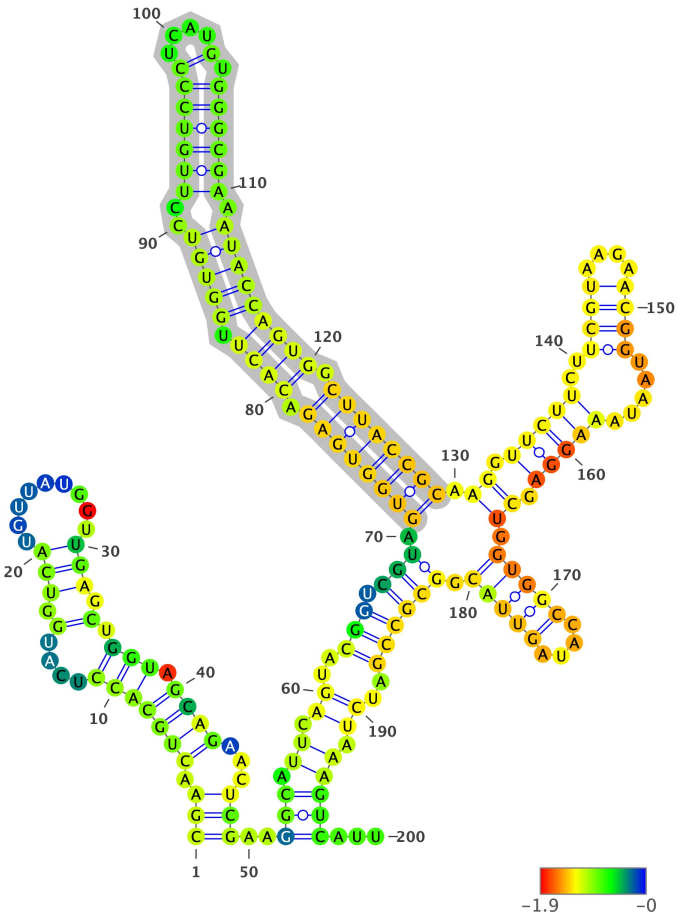
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 14 from nt 564 to 622 (nt 71 to 129)

```
5'-GTGGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAAUACCAGUGGCUUACCGC-3'
5'-((((((((.((((.(((((.....................)))))))))).))))))))-3'
Motif MFE = -28.2; z-score = -4.23; ED = 5.09
```



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 494 to 693 (motif highlighted in silver):

```
5'-CGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAA
AUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUU-3
5'-(((.(((((((....(.(((.........))).).))).))))...))).((((.((.((..(((.(((.(((((((((.((((.(((((..(((((((....).))))))).
))))))))).))))))))).((.(((((..((((....)))).....))))).)).(((((....)))))).))))))..)).)))))...-3'
MFE = -59.2; z-score = -0.15; ED = 59.24
```

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, 266-13468(+)

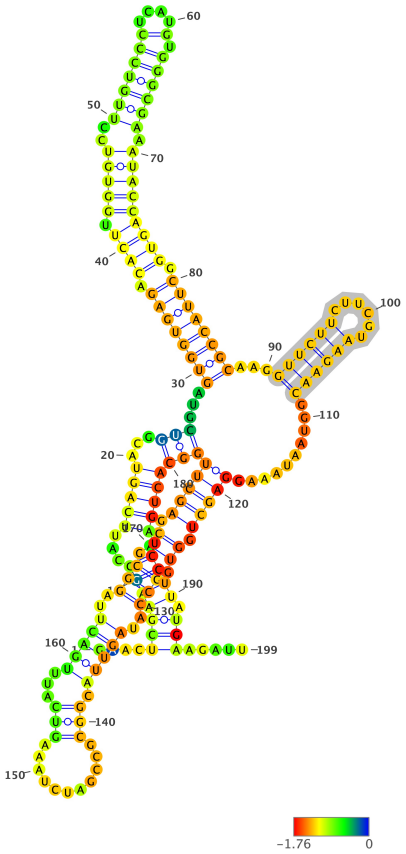
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 626 to 643 (nt 91 to 108)

```
5'-GTTCTTCTTCGTAAGAAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -2.6; 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 = -2.43; 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(+)

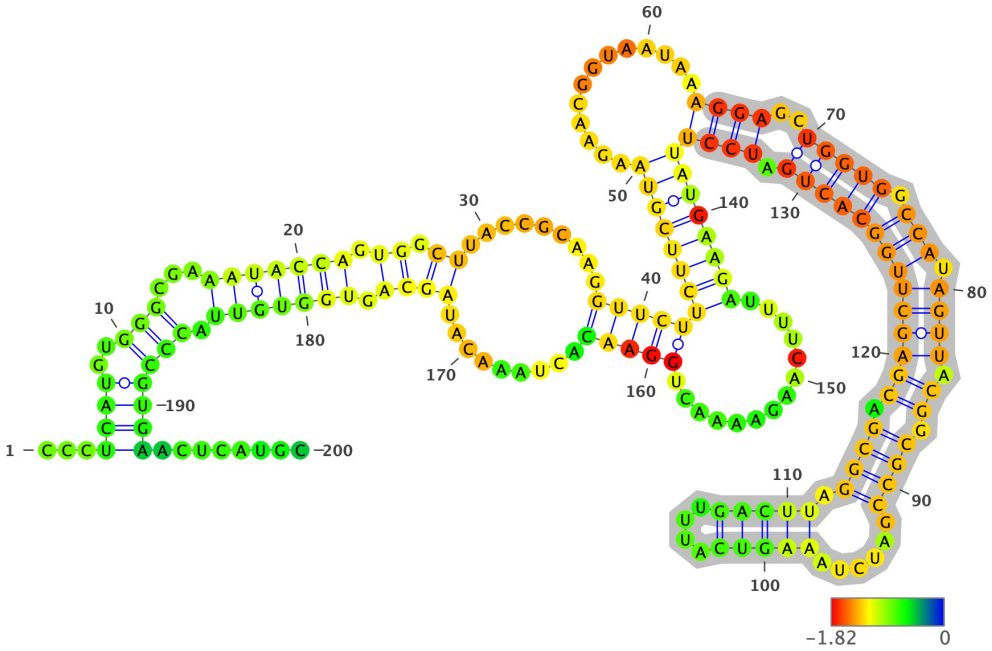
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 16 from nt 653 to 723 (nt 65 to 135)

```
5'-GGAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTTGACUUAGGCGACGAGCUUGGCACUGAUCC-3'
5'-(((..(((((.(((.((((.((.((((......((..........)).)))).)))))))))))))).)))-3'
Motif MFE = -23.8; z-score = -1.26; ED = 6.33
```



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 589 to 788 (motif highlighted in silver):

```
5'-CCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUU
AGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGC-3
5'-...((((..(((...(((((((.((.((.........(((((((((((((.............((((..(((((.(((.((((.((.((((......(((((....)))))
.)))).)))))))))))))).))))))))))))..............)))))........)))).)))))))).)))))))........-3'
MFE = -52.6; z-score = -1.24; ED = 45.29
```

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, 266-13468(+)

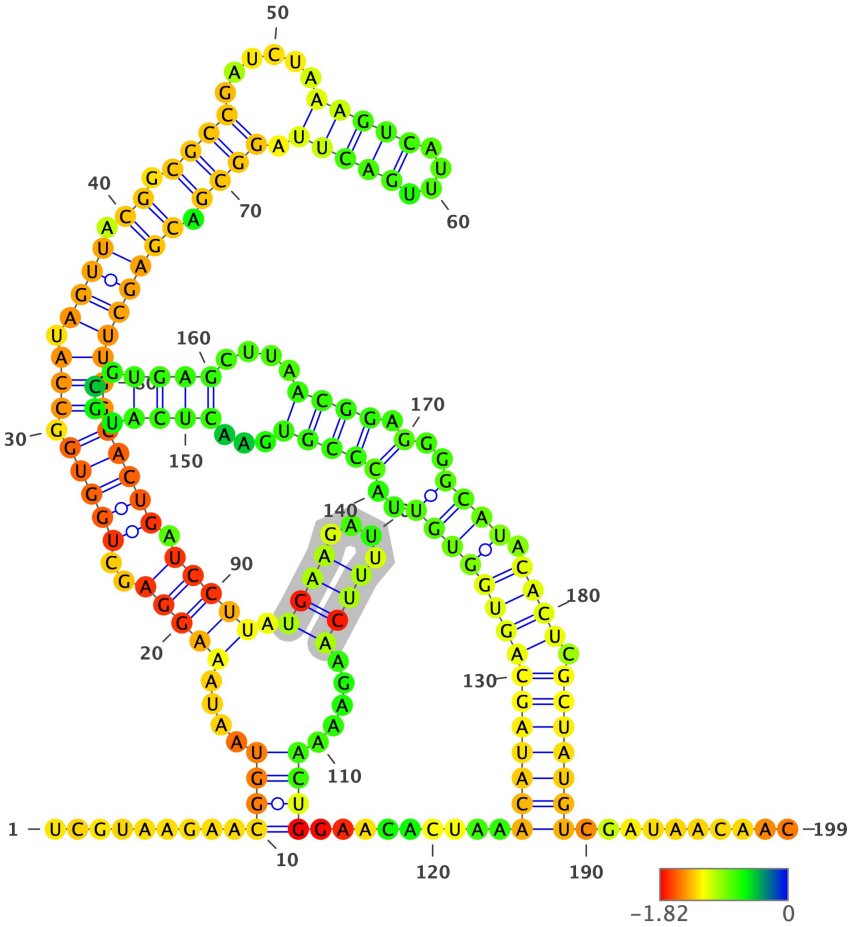
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 17 from nt 727 to 738 (nt 94 to 105)

```
5'-TGAAGATTUUCA-3'
5'-(.((....)).)-3'
Motif MFE = 0.0; z-score = 0.1; ED = 1.97
```



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 634 to 832 (motif highlighted in silver):

```
5'-UCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAA
CUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAAC-3
5'-.........((((....(((((..(((((.(((.((((.((.((((......(((((....))))).)))).))))))))))))).))))).((((....)))).....)
))).........((((((((((((((..(((((...((((....))))....)))).)..)))).)))).)))))))..........-3'
MFE = -55.9; z-score = -2.02; 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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

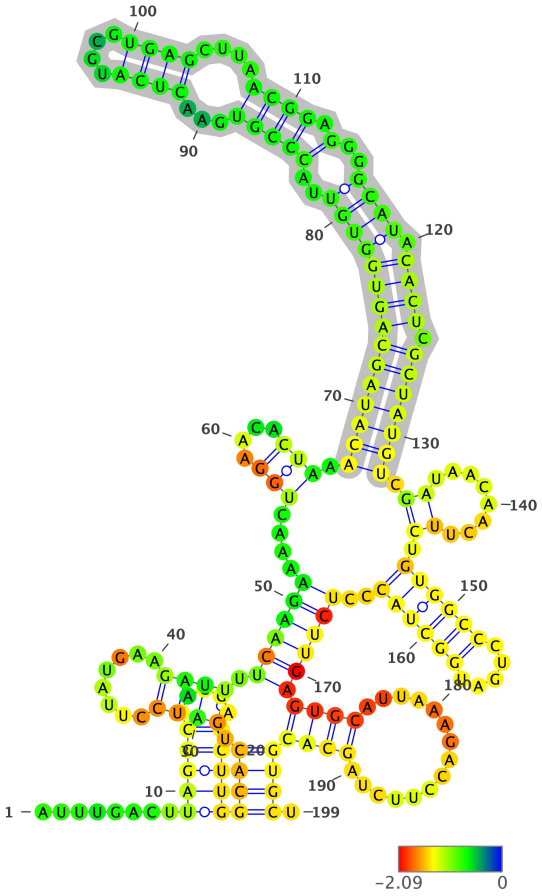
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 18 from nt 757 to 822 (nt 67 to 132)

```
5'-ACATAGCAGTGGTGTTACCCGTGAACTCATGCGUGAGCTTAACGGAGGGGCAUACACUCGCUAUGU-3'
5'-((((((((((.....................................))))).)))))))-3'
Motif MFE = -26.1; z-score = -3.26; ED = 4.18
```



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 691 to 889 (motif highlighted in silver):

```
5'-AUUUGACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGG
AGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCU-3
5'-........(((((.....)))))(((((.((((........)))).((((((....(((....))).((((((((((((((..(((((...((((....))))....)))))
.)..)))).)))).)))))))..((........)).((((((.....))))))..)))))))(((.............)))))))).-3'
MFE = -52.0; z-score = -0.57; ED = 22.15
```

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(+)

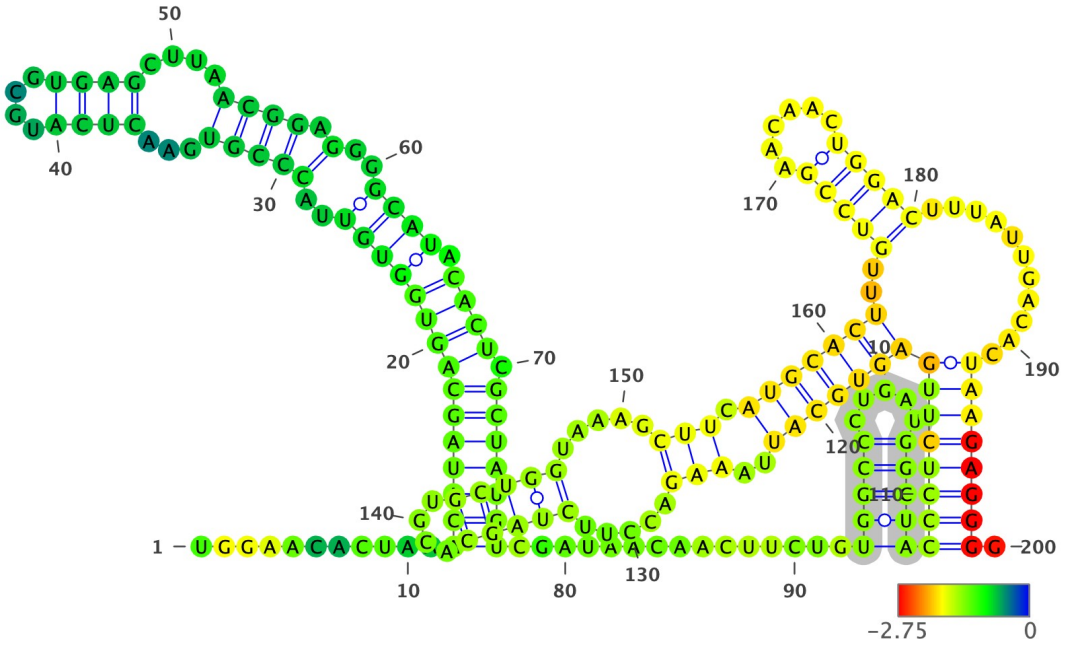
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 19 from nt 838 to 852 (nt 93 to 107)

```
5'-TGGCCCTGATGGCUA-3'
5'-(((((.....)))))-3'
Motif MFE = -4.4; z-score = -2.57; 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 = -2.32; 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(+)

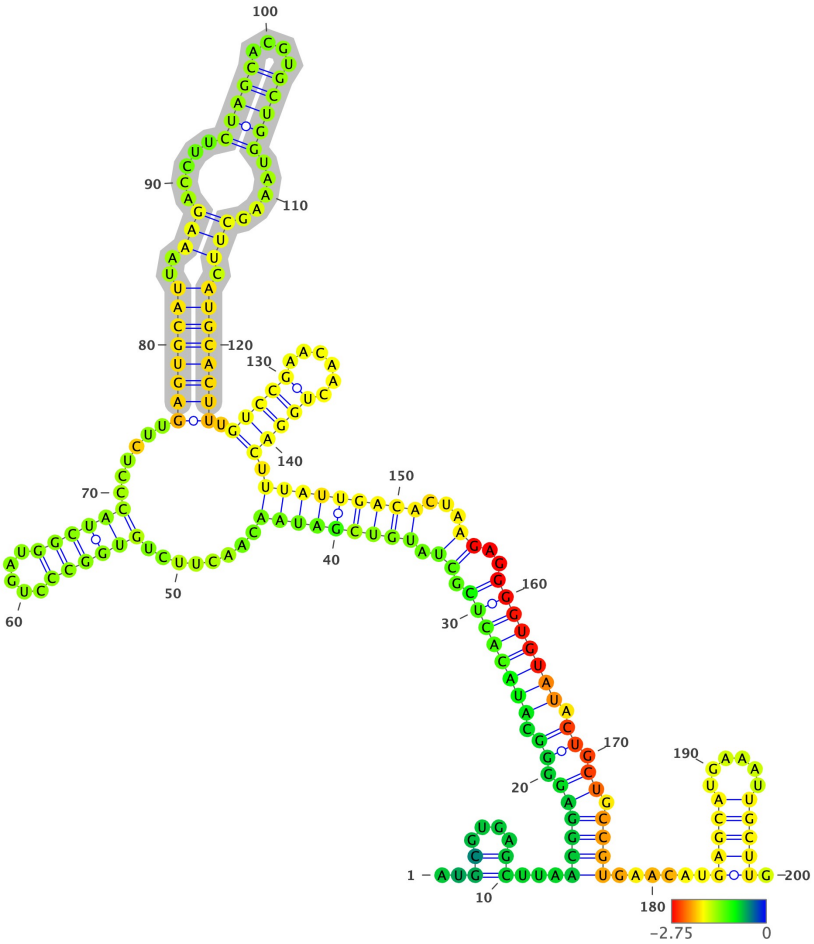
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 20 from nt 861 to 907 (nt 77 to 123)

```
5'-AGTGCATTAAAGACCTTCTAGCACGTGCUGGTAAAGCUUCAUGCACU-3'
5'-(((((((..(((.....(((((....)))))).....))).)))))))-3'
Motif MFE = -15.2; z-score = -3.38; ED = 2.82
```



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 785 to 984 (motif highlighted in silver):

```
5'-AUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAA
GCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUG-3
5'-..((....)).((((((.((.(((((((((.((.(((((((((........((((((.....))))))))).....((((((((..(((.....(((((....)))))).....
.))).)))))))).(((((.....)))))).)))))))))...))..)))))))).)).)).))))......(((((.....))))).-3'
MFE = -65.6; z-score = -2.79; ED = 12.03
```

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, 266-13468(+)

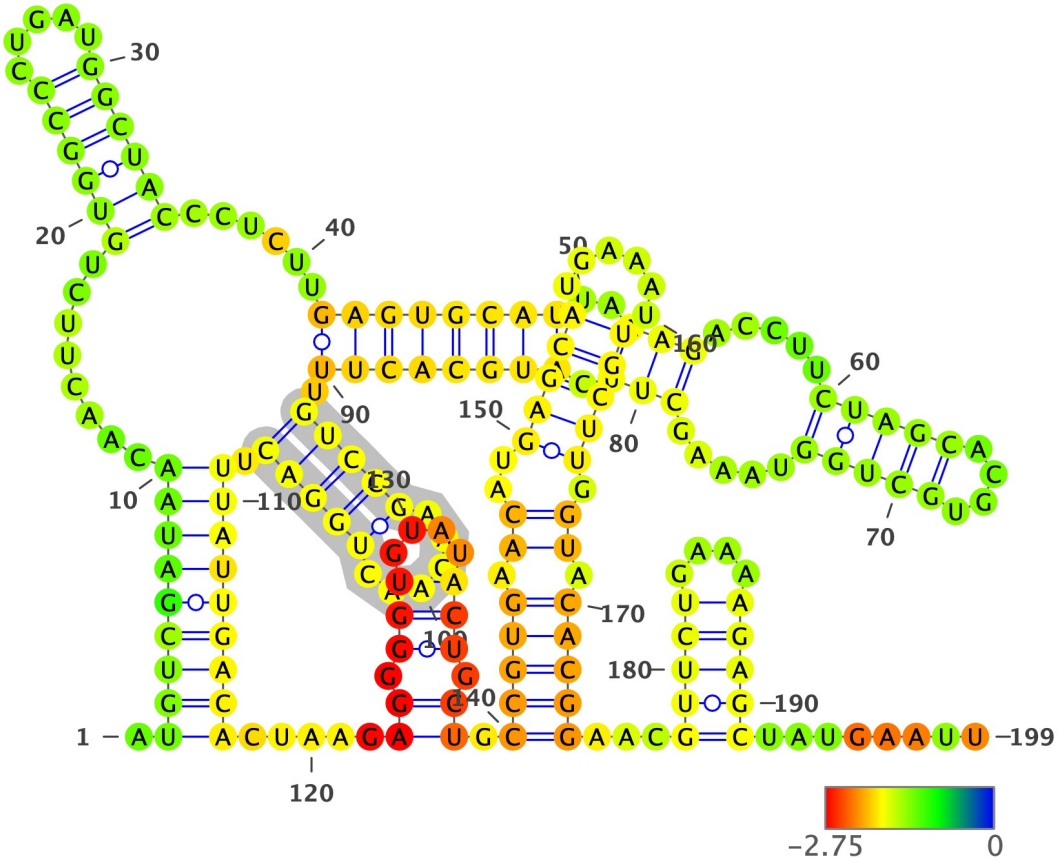
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 21 from nt 910 to 925 (nt 92 to 107)

```
5'-GTCCGAACAACUGGAC-3'
5'-(((((.....)))))-3'
Motif MFE = -4.4; z-score = -4.04; 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 = -2.84; ED = 11.08
```

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(+)

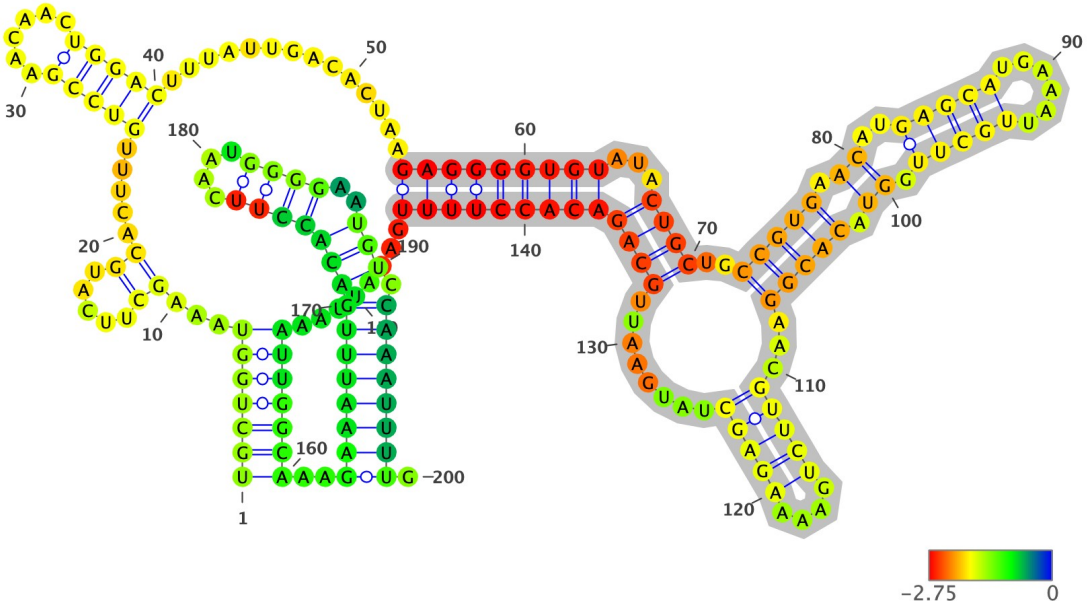
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 22 from nt 940 to 1030 (nt 55 to 145)

```
5'-GAGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATUGCUUGGUACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGACACCUUUU-3'
5'-(((((((((...((((..(((((.((..(((((......))))).)).)))))...(((((....)))))........)))))))))))))-3'
Motif MFE = -32.3; z-score = -3.88; ED = 2.22
```



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 886 to 1085 (motif highlighted in silver):

```
5'-UGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACG
UUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUG-3
5'-(((((((...((.....)).....(((((......)))))..............(((((((((...((((..(((((.((..(((((......))))).)).)))))...(
((((....)))))........)))))))))))))........)))))))..((((((((((((((....))))..))).)))))))).-3'
MFE = -52.0; z-score = -1.74; ED = 15.2
```

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(+)

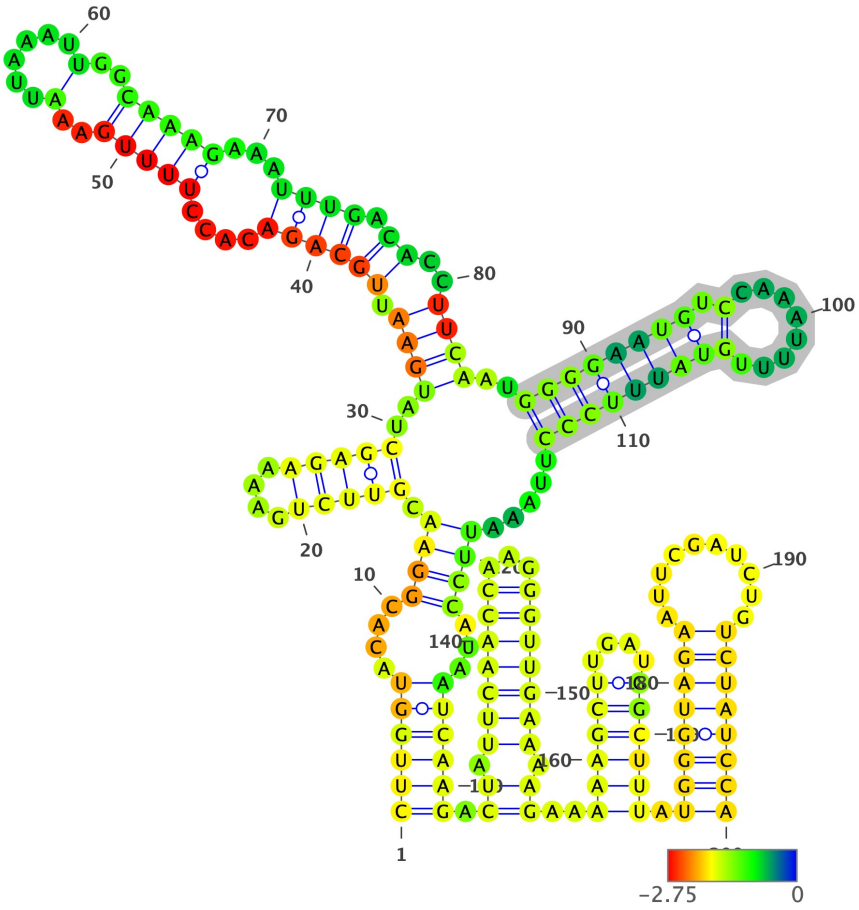
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 23 from nt 1067 to 1093 (nt 87 to 113)

```
5'-GGGGAATGTCCAAATTTTGTATTTCCC-3'
5'-(((......(........).....)))-3'
Motif MFE = -6.4; z-score = -2.39; 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 981 to 1180 (motif highlighted in silver):

```
5'-CUUGGUACACGGAACGUUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUC
CCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCA-3
5'-((((((....((((.(((((....)))))..((((.((((((....(((((..(......)..)))))...)))).))..))))..((((((((.(........)))))))
))).....))))...))))))).((.(((((((...)))))))).))..((((((....)))))).((((((((.........))))))))-3'
MFE = -44.0; z-score = -1.91; ED = 25.18
```

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(+)

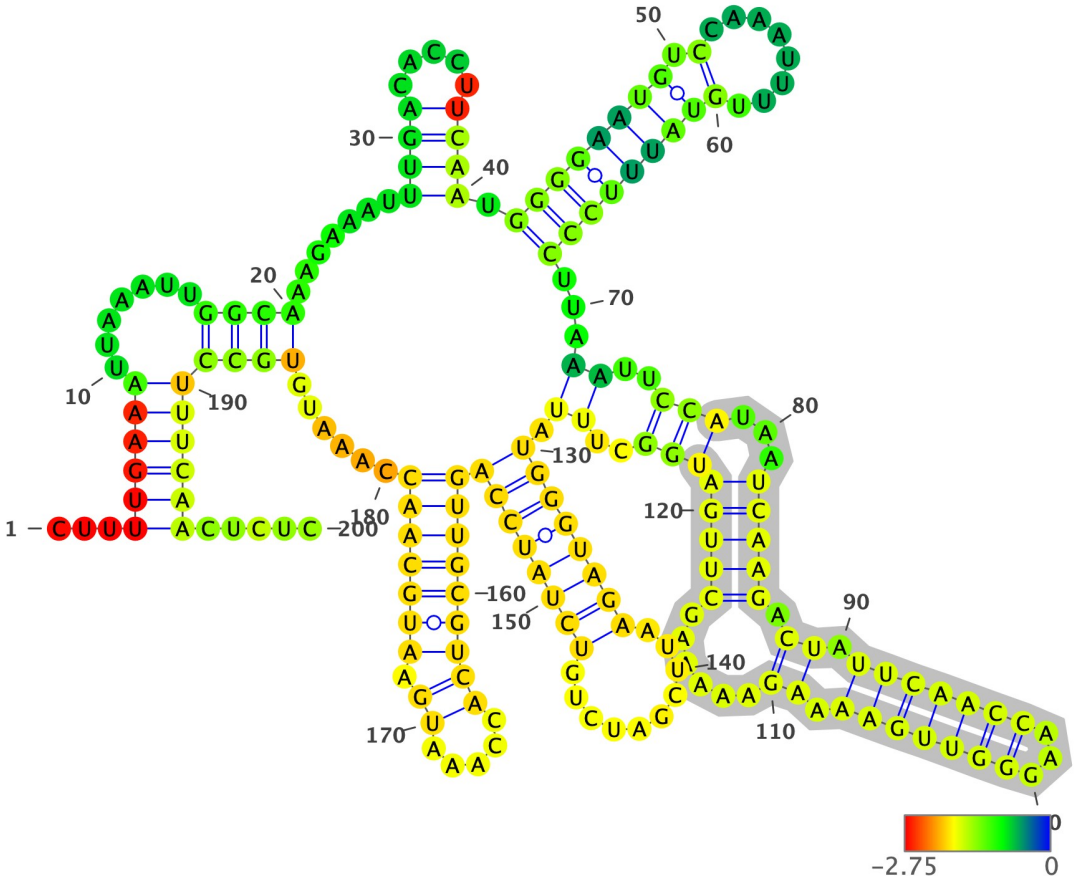
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 24 from nt 1103 to 1147 (nt 78 to 122)

```
5'-ATAATCAAGACTATTCAACCAAGGGUUGAAAAGAAAAAGCUUGAU-3'
5'-(...((((((.((.(((((((...)))))))).)).....))))))-3'
Motif MFE = -9.9; z-score = -3.54; ED = 3.14
```



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 1026 to 1225 (motif highlighted in silver):

```
5'-CUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGA
AAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUC-3
5'-...((((((.......(((.......(((.....)))).(((((((((.(........)))))))))...((..(((...((((((.((.(((((((...)))))))).)).
.....))))))))..)).(((((((((.........)))))))))(((((((((.....)).)))))))......))))))))))).....-3'
MFE = -41.8; z-score = -2.55; ED = 28.19
```

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(+)

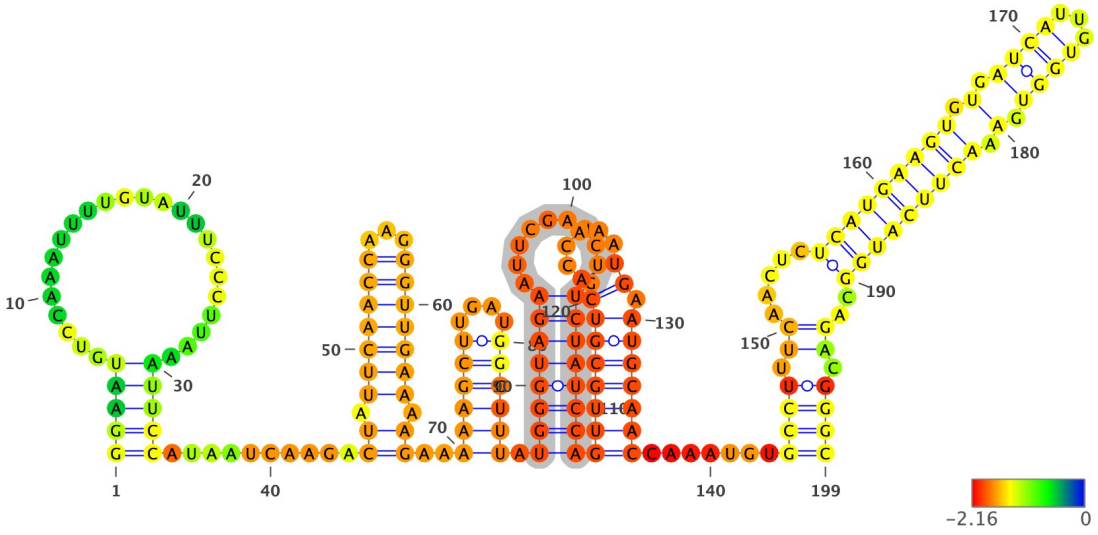
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 25 from nt 1155 to 1180 (nt 87 to 112)

```
5'-TGGGTAGAATTCGATCTGUCUAUCCA-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -7.4; z-score = -3.11; 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
AGUUGCGUCACCAAAUGAAUGCAACCAAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGC-3
5'-(((((.........................))))).........((.(((((((...)))))))).))..((((((....)))))).(((((((.........)))))))
)((((((((.....)).)))))).......((((.((.....(((((((((.(.(((((...)))))).).)))))))))..)).))))-3'
MFE = -49.1; z-score = -1.87; 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(+)

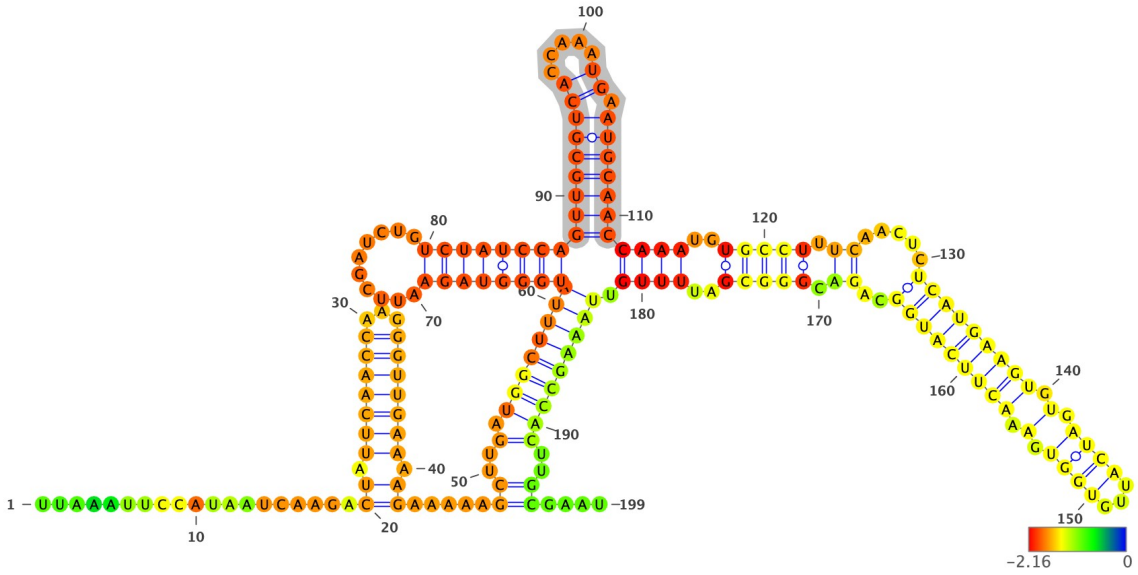
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 26 from nt 1181 to 1204 (nt 88 to 111)

```
5'-GTTGCGTCACCAAAUGAAUGCAAC-3'
5'-(((((((((.....)).)))))))-3'
Motif MFE = -6.5; z-score = -2.97; 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 = -3.4; 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(+)

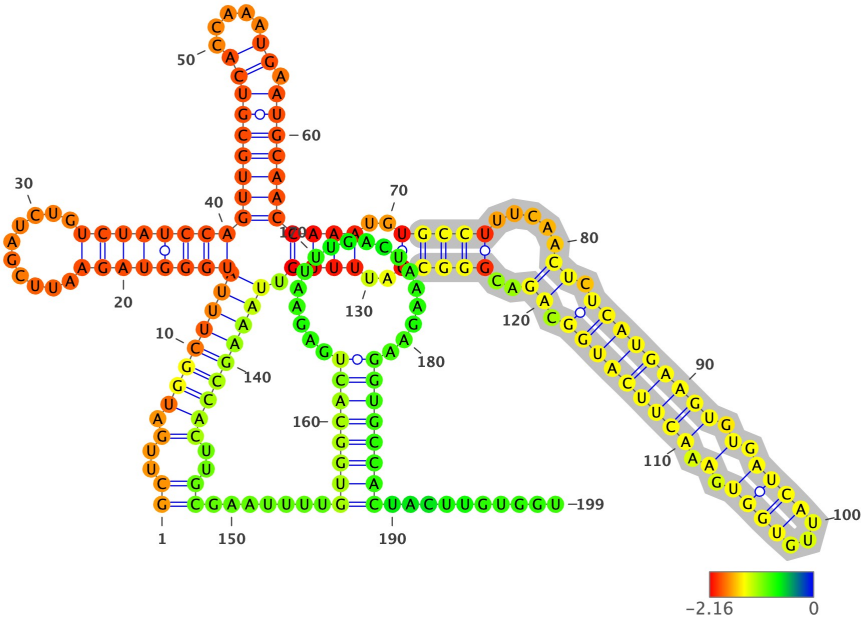
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 27 from nt 1212 to 1267 (nt 72 to 127)

```
5'-GCCTTTCAACTCTCATGAAGTGTGATCATTGUGGUGAAACUUCAUGGCAGACGGGC-3'
5'-(((......((.((((((((((.(.((((...)))).).))))))))).))...)))-3'
Motif MFE = -17.0; z-score = -1.78; 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 = -62.0; z-score = -2.61; ED = 10.54
```

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, 266-13468(+)

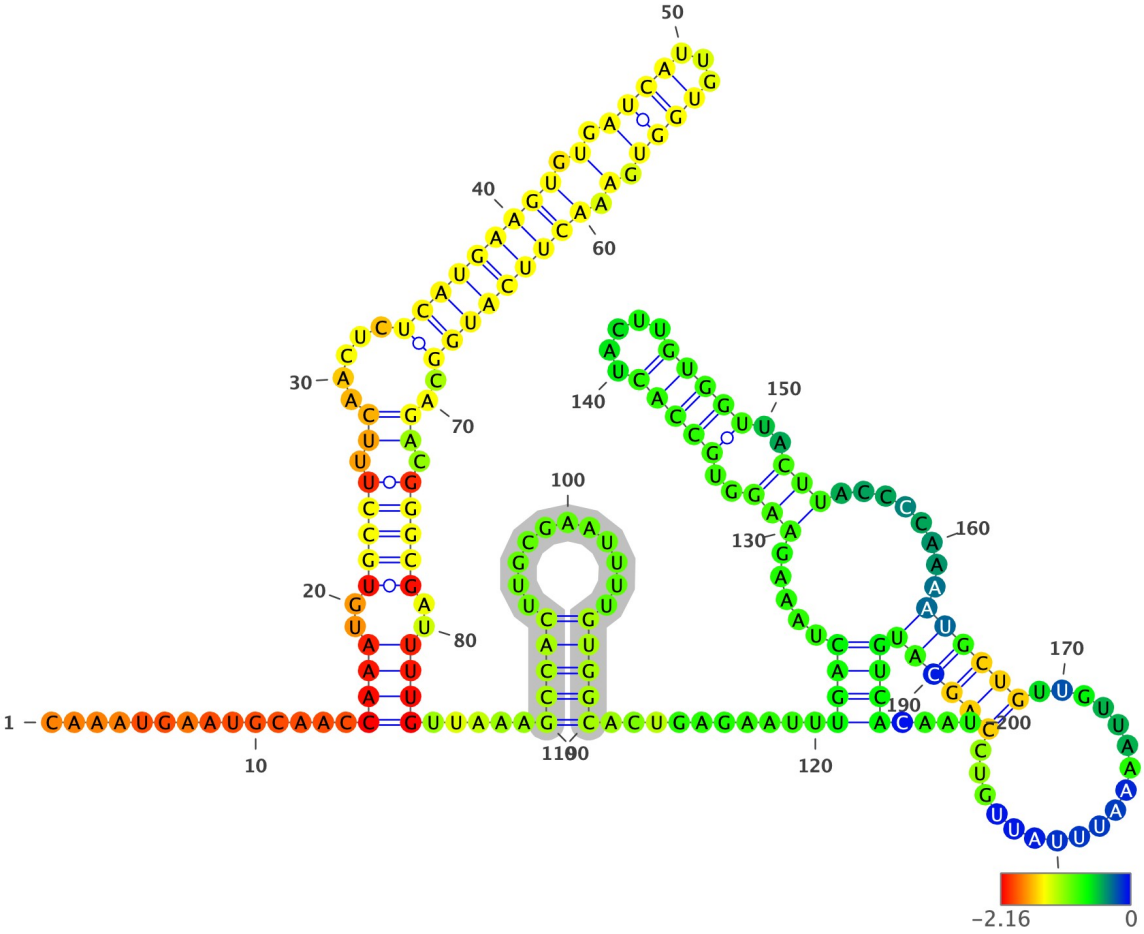
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 1280 to 1300 (nt 90 to 110)

```
5'-GCCACTTGCGAATTTTGUGGC-3'
5'-(((((...........)))))-3'
Motif MFE = -6.5; z-score = -2.0; 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 1191 to 1390 (motif highlighted in silver):

```
5'-CAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCA
CUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGUUACUUACCCCAAAAUGCUGUUGUUAAAAUUUAUUGUCCAGCAUGUCACAAU-3
5'-..............((((..(((((.((.....(((((((((.(.((((...)))).).))))))))).)).)))))..))))).....(((((...........))))).
.........((((.....(((..(((((.....)))))..)))........((((((.................))))))))))....-3'
MFE = -46.5; z-score = -0.75; ED = 34.79
```

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, 266-13468(+)

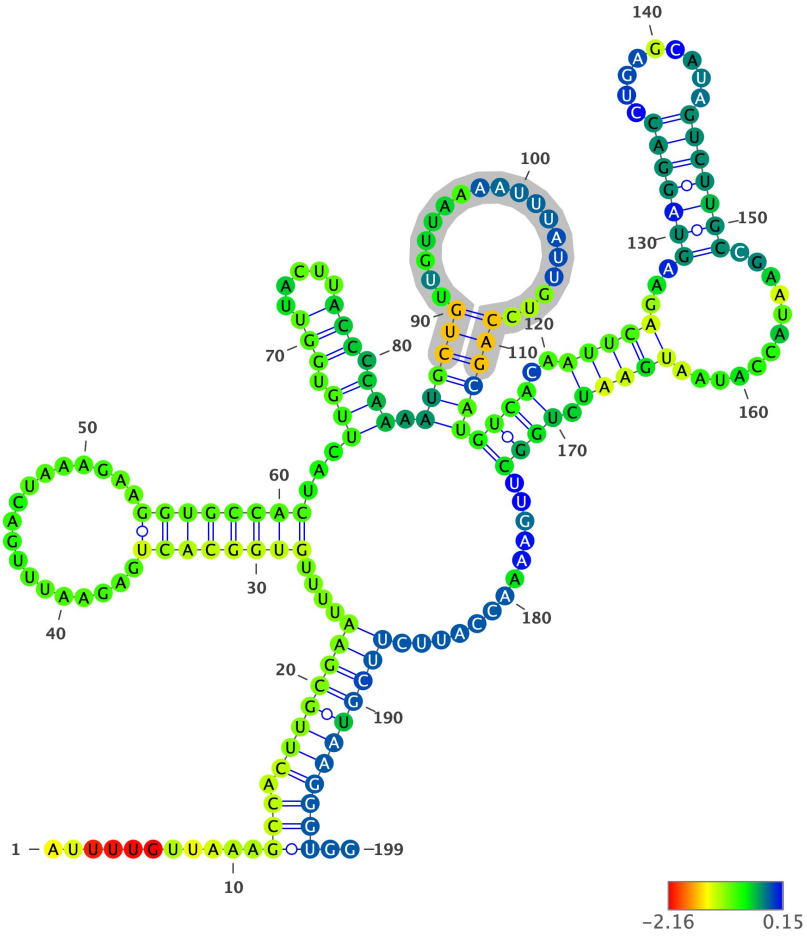
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 29 from nt 1356 to 1379 (nt 88 to 111)

```
5'-CTGTTGTTAAAATTTATTGTCCAG-3'
5'-(((.................)))-3'
Motif MFE = 0.0; z-score = 0.79; 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 1269 to 1467 (motif highlighted in silver):

```
5'-AUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGUUACUUACCCCAAAAUGCUGUUGUUAAAAUUUAUUGUCCAG
CAUGUCACAAUUCAGAAGUAGGACCUGAGCAUAGUCUUGCCGAAUACCAUAAUGAAUCUGGCUUGAAAACCAUUCUUCGUAAGGGUGG-3
5'-...........(((.(((((((((....((((((((.................))))))))...(((.(((.....))).))).((((((.................)))
)))(((((..((((((...(((((((.........)))))))............))))).))))............)))))))))))..-3'
MFE = -44.2; z-score = -0.38; ED = 58.71
```

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, 266-13468(+)

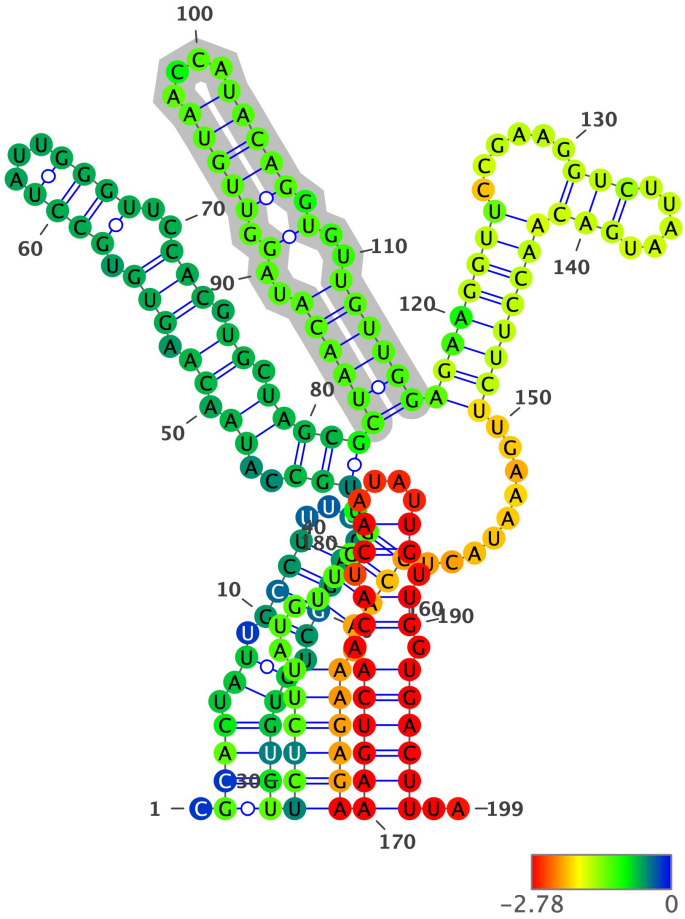
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 1551 to 1584 (nt 83 to 116)

```
5'-CTAACATAGGTTGTAACCAUACAGGUGTUGUUGG-3'
5'-((((((..(.(((((....))))).)..))))))-3'
Motif MFE = -9.6; z-score = -2.28; 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 1469 to 1667 (motif highlighted in silver):

```
5'-CGCACUAUUGCCUUUGGAGGCUGUGUGUUCUCUUAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUU
GUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUA-3
5'-.((((.((.((((....)))).))))))((((((...((((.(((..((.((.(((.((((...)))).)))).)).)))))((((((..(.(((((....))))).)..)
)))))((((((((.....(((.....)))))))))))).........)))).))))))((((((.((.((....)).)).))))))..-3'
MFE = -51.8; z-score = -2.15; ED = 28.64
```

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(+)

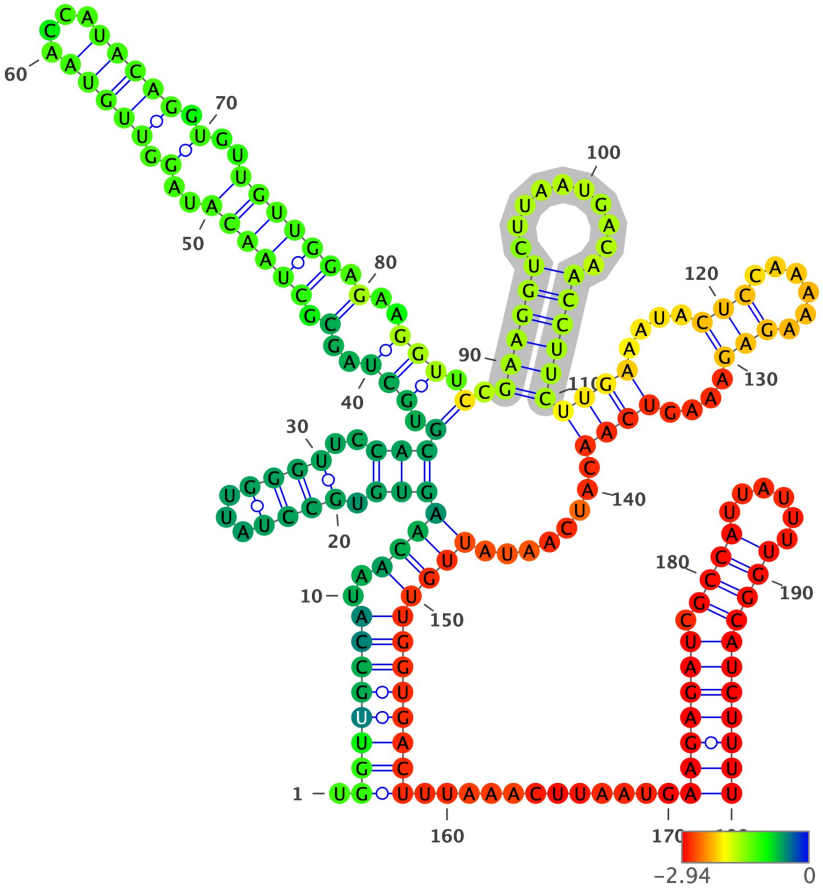
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 31 from nt 1595 to 1616 (nt 89 to 110)

```
5'-GAAGGTCTTAATGACAACCUUC-3'
5'-((((((..........))))))-3'
Motif MFE = -4.6; z-score = -2.48; 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 1507 to 1705 (motif highlighted in silver):

```
5'-UGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCU
UGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUU-3
5'-.((((((((..(((((((.((((...))))..)))(.(((..(.((((((..(.(((((....))))).)..)))))).)..))).).((((((..........))))))(
(((....(((......)))....))))........))))))))))))............(((((((.((((......)))))))))))-3'
MFE = -50.6; z-score = -2.43; ED = 56.72
```

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(+)

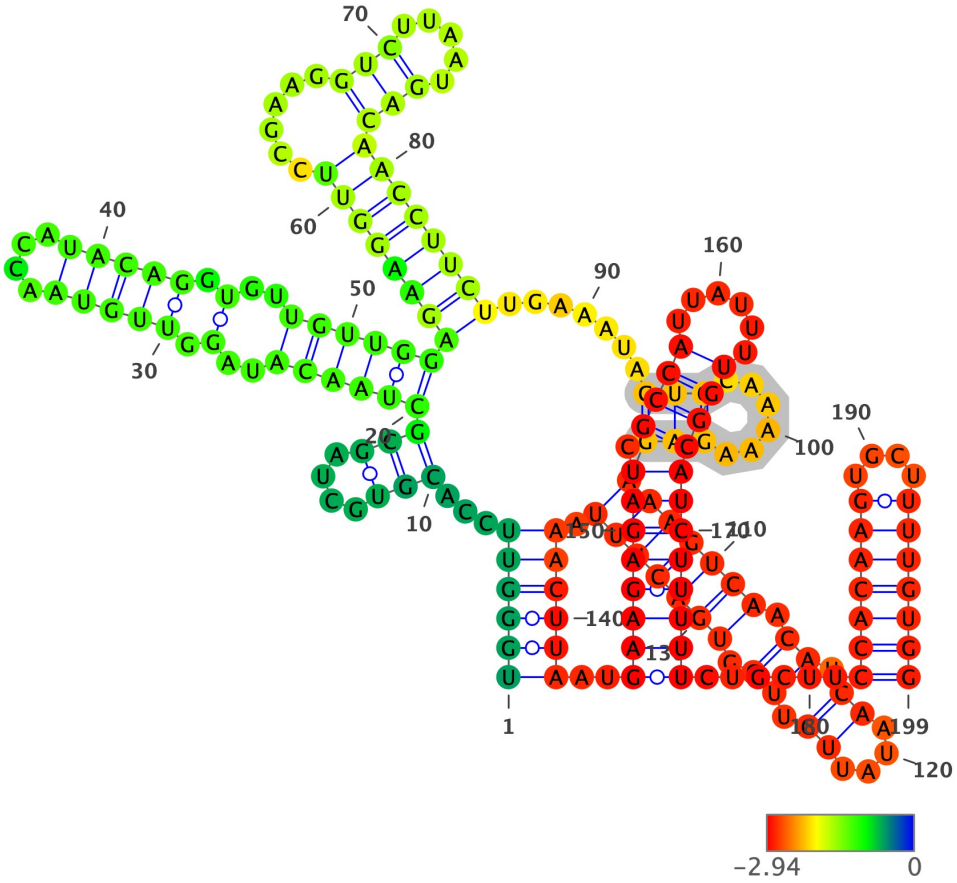
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 32 from nt 1625 to 1636 (nt 94 to 105)

```
5'-CTCCAAAAAGAG-3'
5'-(((.....)))-3'
Motif MFE = -0.1; z-score = -0.41; ED = 1.58
```



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 1532 to 1730 (motif highlighted in silver):

```
5'-UGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUC
AACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGG-3
5'-((((((...(((....)))(((((((..(.(((((....)))))).)..)))))))(((((((.....(((.....)))))))))).....(((.....)))(((((((
(.((.((....)).)).)))))))..)))))).(((((((.(((.....)))))))))))).....(((((((....)))))))-3'
MFE = -54.5; z-score = -2.6; ED = 32.07
```

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(+)

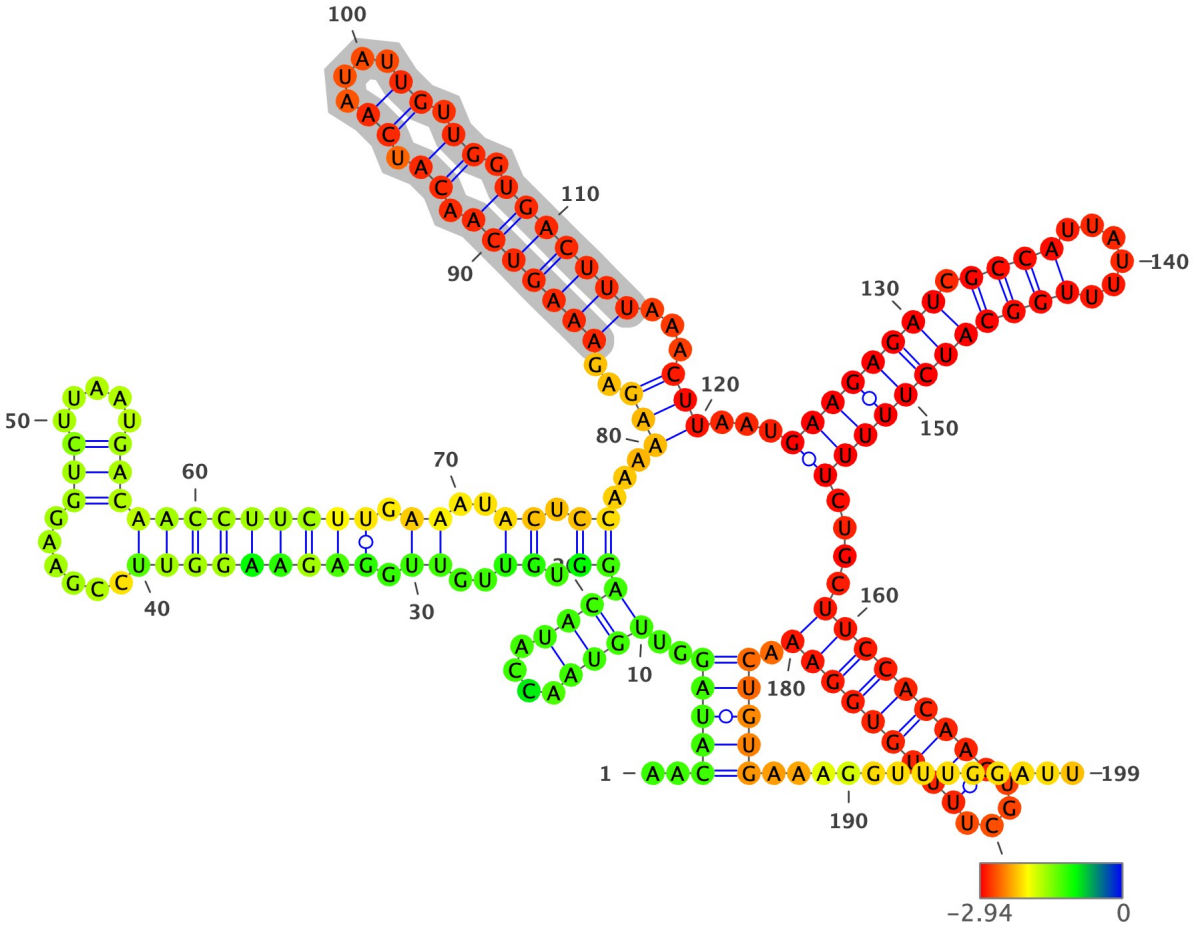
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 33 from nt 1637 to 1666 (nt 85 to 114)

```
5'-AAAGTCAACATCAATATUGTUGGUGACUUU-3'
5'-(((((((.((.((....)).)).)))))))-3'
Motif MFE = -7.2; z-score = -2.58; 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 1553 to 1751 (motif highlighted in silver):

```
5'-AACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGAC
UUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUU-3
5'-..(((((..((((....))))((.((..((.((((((((((.....(((.....)))))))))))).))..)).))...(((..(((((((.((.((....)).)).))))
)))...)))...((((((((.((((.....)))))))))))....(((((((((....)))))))))).)))))............-3'
MFE = -56.2; z-score = -3.39; ED = 31.91
```

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(+)

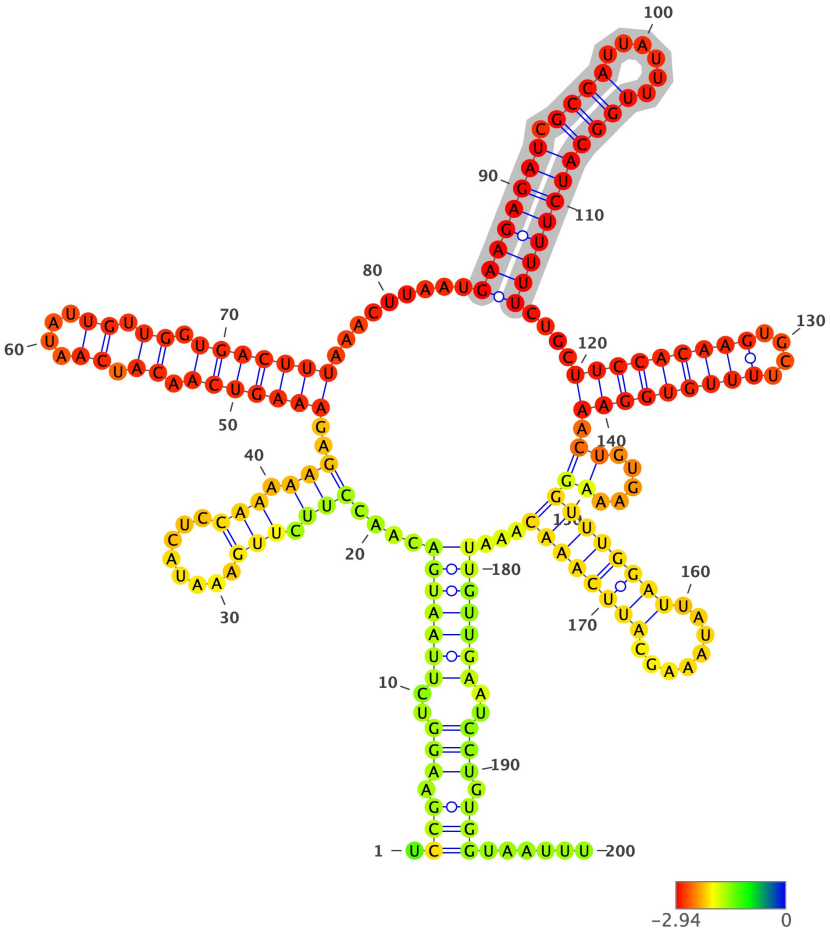
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 34 from nt 1676 to 1706 (nt 85 to 115)

```
5'-GAAGAGATCGCCATTATTTUGGCAUCUUUUU-3'
5'-((((((((.((((......)))))))))))-3'
Motif MFE = -12.1; z-score = -4.75; 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 1592 to 1791 (motif highlighted in silver):

```
5'-UCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCU
UUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUU-3
5'-.(((.(((..(((((((....(((.(((........))).)))..(((((((.((.((....)).)).)))))))..........((((((((.((((......))))))))
))))....((((((((((....)))))))))).((.....))((((((((........))))))))...)))))))..))).)))......-3'
MFE = -49.0; z-score = -2.93; ED = 43.74
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

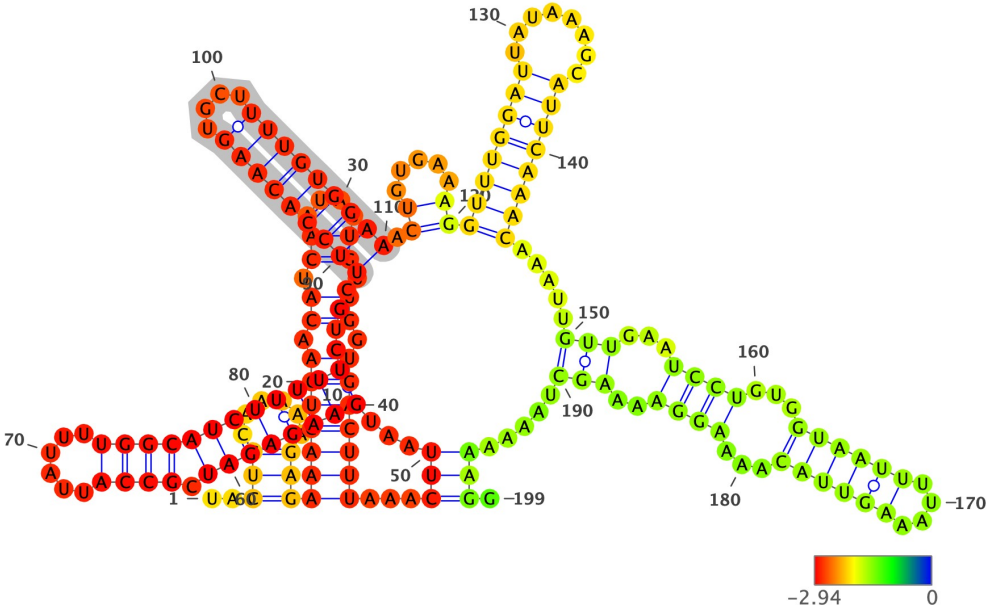
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 35 from nt 1711 to 1732 (nt 89 to 110)

```
5'-TTCCACAAGTGCTUUUGUGGAA-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -9.5; z-score = -4.82; 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'-UACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAA
CUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGG-3
5'-..(((......)))(((((((.((.((....)).)).)))))))...(((...(((((((((.((((......))))))))))))....(((((((((....)))))))))).
((.....))(((((((((........)))))))))).....(((...((((...((((((....))))))...))))..)))).....))).-3'
MFE = -48.5; z-score = -3.16; ED = 33.37
```

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(+)

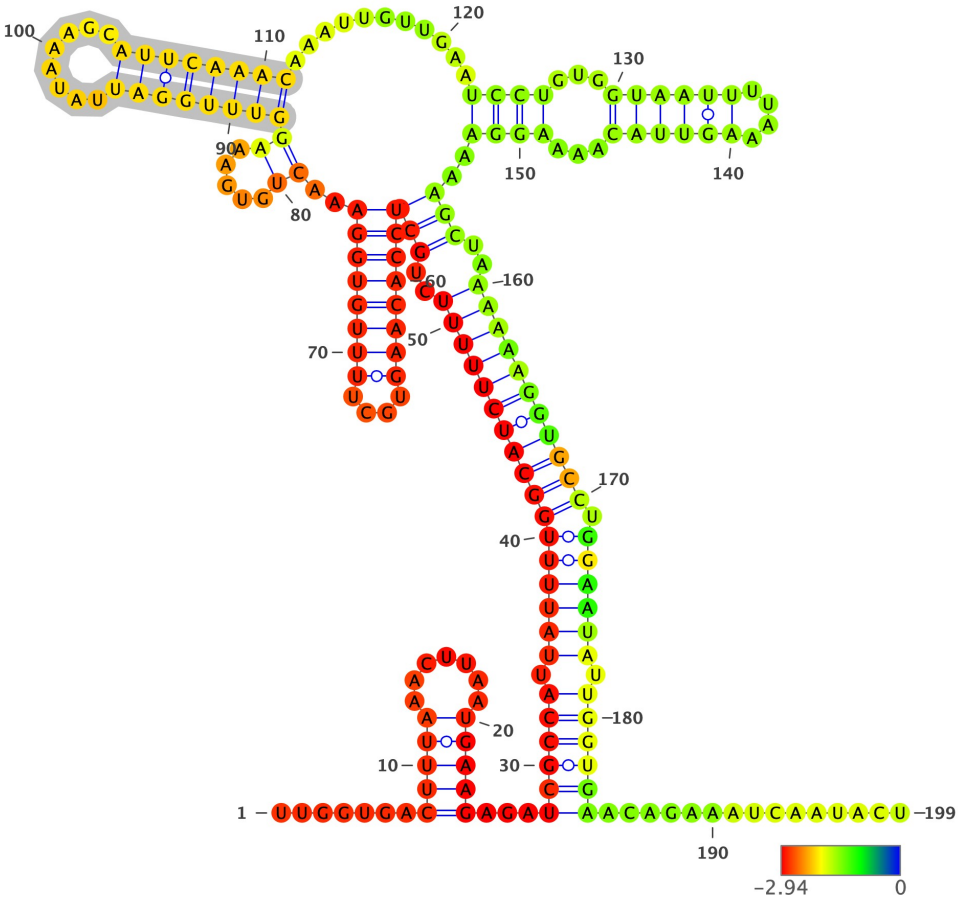
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 36 from nt 1743 to 1766 (nt 88 to 111)

```
5'-GTTTGGATTATAAAGCAUUCAAAC-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -4.6; z-score = -2.09; 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 = -4.26; 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(+)

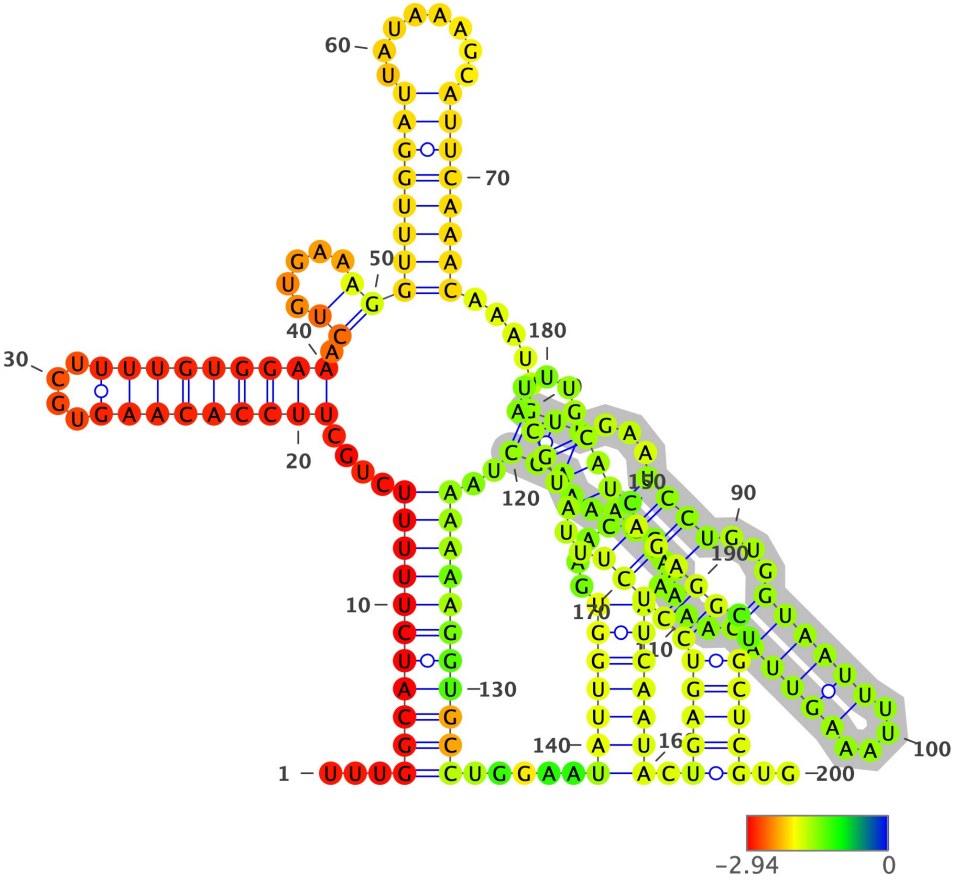
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 37 from nt 1772 to 1812 (nt 80 to 120)

```
5'-GTTGAATCCTGTGGTAATTTTAAAGUUACAAAAGGAAAAGC-3'
5'-(((...(((((...((((((....)))))))...)))))..)))-3'
Motif MFE = -8.2; z-score = -2.27; 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 1693 to 1892 (motif highlighted in silver):

```
5'-UUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAA
AGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUG-3
5'-...((((((((((....((((((((((....))))))))))..((.....))(((((((((........)))))))))).....(((...((((...((((((....)))))))...
))))..))))..))))))))))).....(((((((........)))))))..((((((((((..((((....)))).))))))..))))))..--3'
MFE = -57.7; z-score = -4.44; ED = 11.1
```

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, 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']

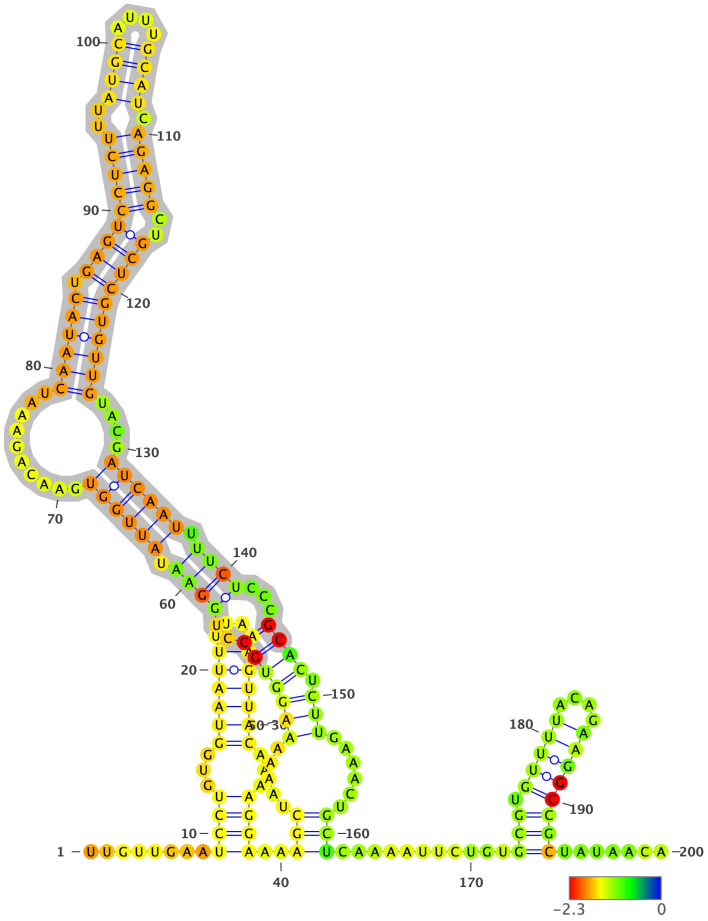
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

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 1823 to 1915 (nt 54 to 146)

```
5'-GCCTGGAATATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCAUCAGAGGCTGCUCGUGUUGTACGAUCAAUTTTCTCCCGC-3'

5'-((...(...((((((..........((((((.((((((((((..((((....)))).)))))..))))))))))....))))))...)....))-3'
Motif MFE = -24.6; z-score = -1.84; 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 1770 to 1969 (motif highlighted in silver):

```
5'-UUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAG
AGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAACA-3
5'-........((((...((((((....))))))...))))..(((.....(((((((..((((.((((((..........((((((.((((((((((..((((....)))).))
)))..))))))))))....)))))).))))...)))).)))......)))...........(((.(((((....))))))))........-3'
MFE = -48.9; z-score = -1.75; 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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

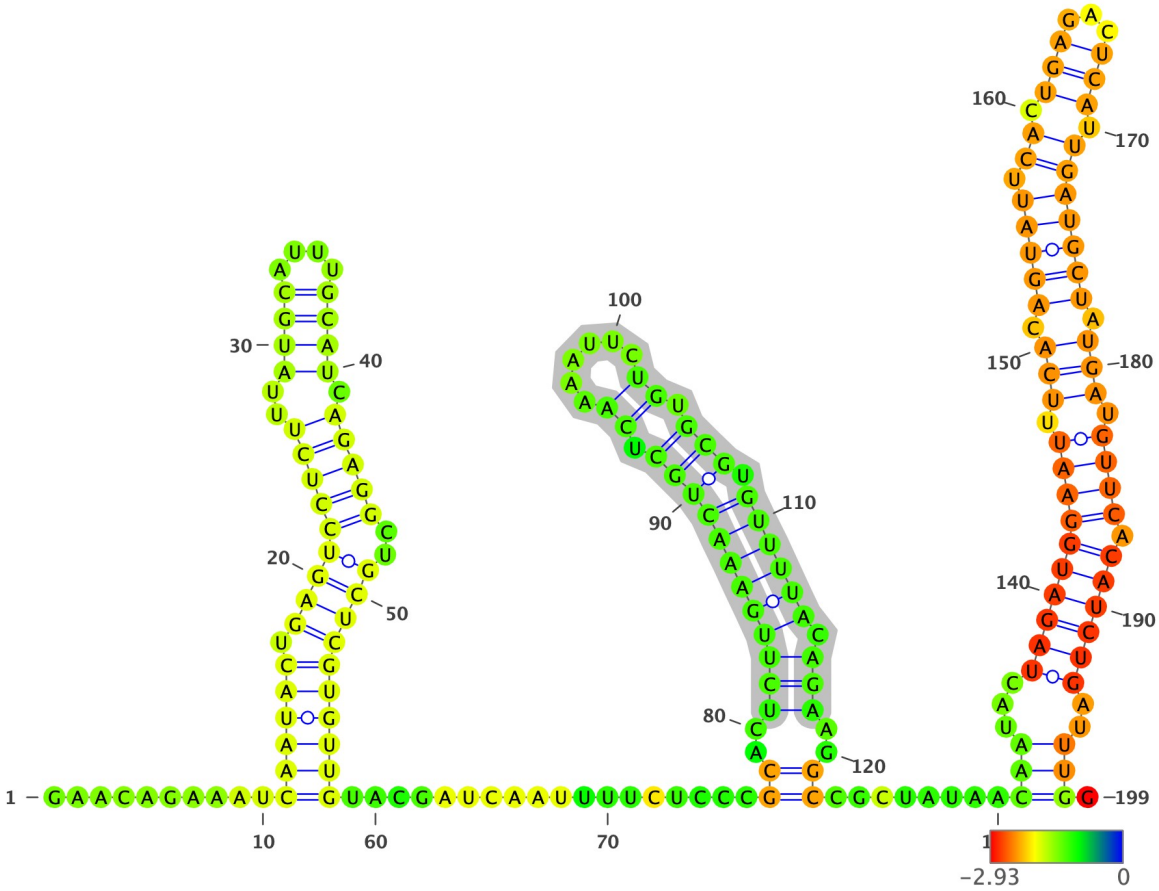
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 39 from nt 1918 to 1955 (nt 81 to 118)

```
5'-TCTTGAAACTGCTCAAAATTCUGTGCGTGUUUUACAGA-3'
5'-(..((((((((((.((......)).)))).)))))))...)-3'
Motif MFE = -7.8; z-score = -1.82; 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 1838 to 2036 (motif highlighted in silver):

```
5'-GAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUU
UUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGG-3
5'-.........((((((.((((((((((..((((....))))).))))))..))))))))))...................((..((((((((((((.((......)).)))).)))
)))).)))..))........(((...((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).))))))..))).-3'
MFE = -50.1; z-score = -2.19; ED = 17.16
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

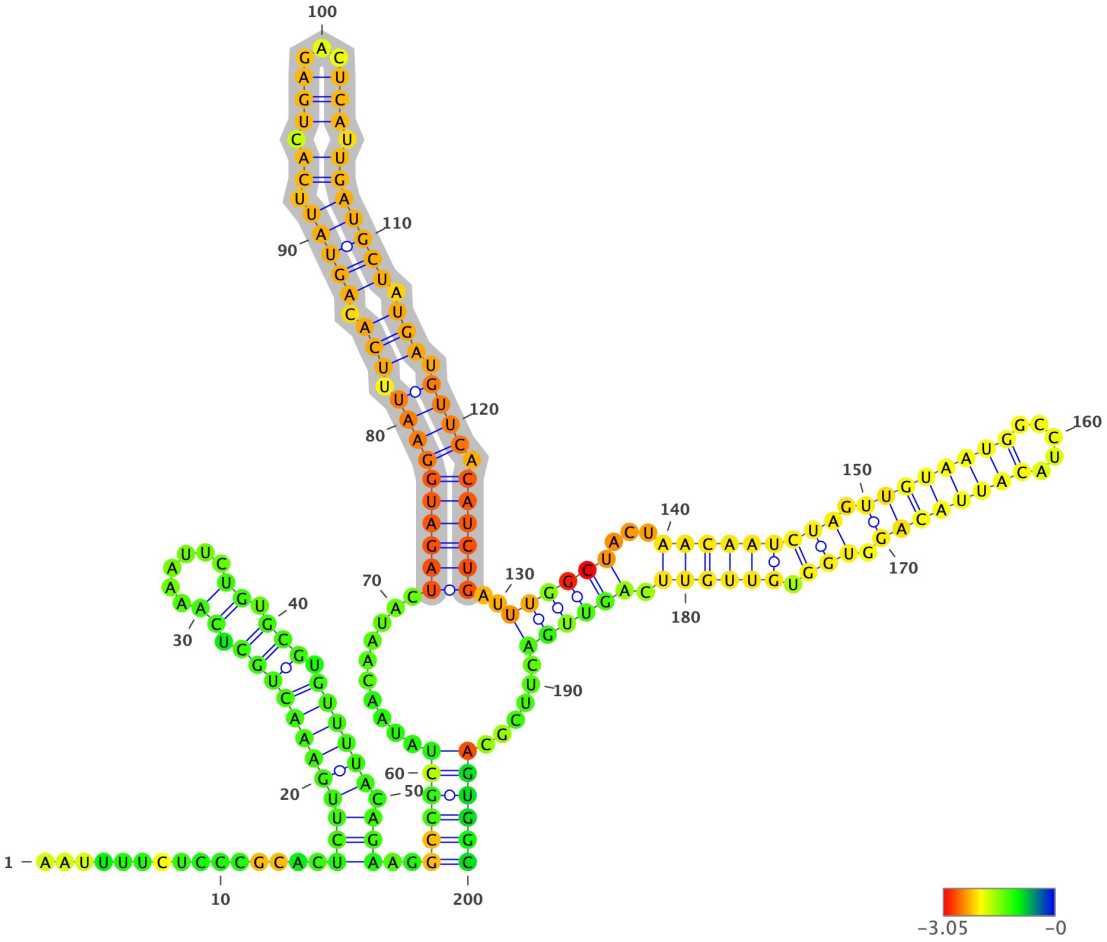
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 40 from nt 1974 to 2030 (nt 72 to 128)

```
5'-TAGATGGAATTTCACAGTATTCACTGAGACUCATUGAUGCUAUGATGUUCACAUCUG-3'
5'-((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).))))))-3'
Motif MFE = -17.5; z-score = -3.8; ED = 3.01
```



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 1903 to 2102 (motif highlighted in silver):

```
5'-AAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGC
UAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGC-3
5'-...............((((((((((((.((......)).))).))))))).)))..((((((..........((((((((((.(((.(((((.((.(((...))).))))))
).))).)))).))))))..((((((...((((((((((.((((((((.....)))))))).))).))))))).))))))......))))))-3'
MFE = -52.4; z-score = -2.13; ED = 25.81
```

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, 266-13468(+)

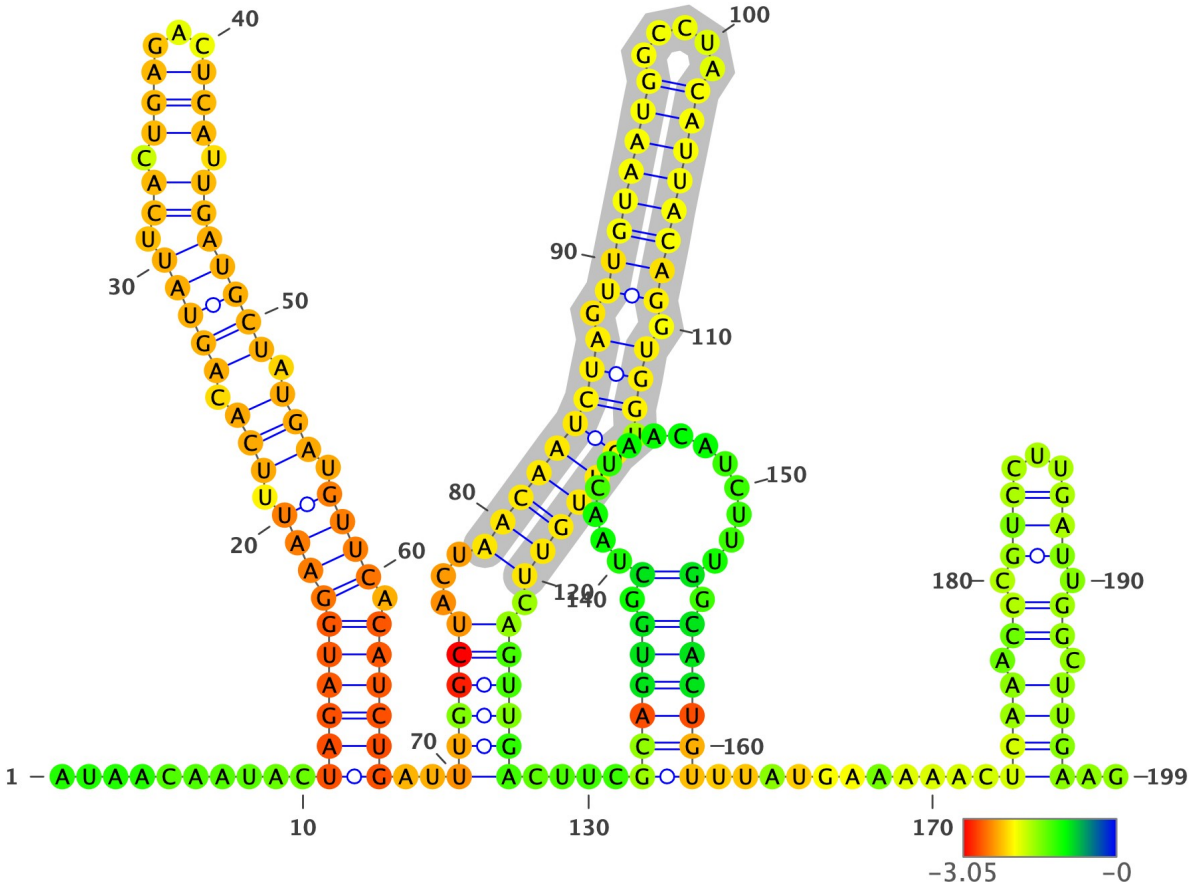
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 41 from nt 2042 to 2083 (nt 79 to 120)

```
5'-AACAATCTAGTTGTAATGGCCTACAUUACAGGUGGTGUUGUU-3'
5'-((((((((((.(((((((((.....)))))))))...))).))))))-3'
Motif MFE = -15.6; z-score = -4.09; ED = 1.11
```



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 1964 to 2162 (motif highlighted in silver):

```
5'-AUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGU
GGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAG-3
5'-..........((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).)))))).(((((((...(((((((((.(((((((((.....)))))))))))))))))))))))).
))).)))))).))))))....((((((.(.............).))))))..........((((.((.(((...))).)).)))))..-3'
MFE = -51.0; z-score = -2.71; ED = 19.64
```

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(+)

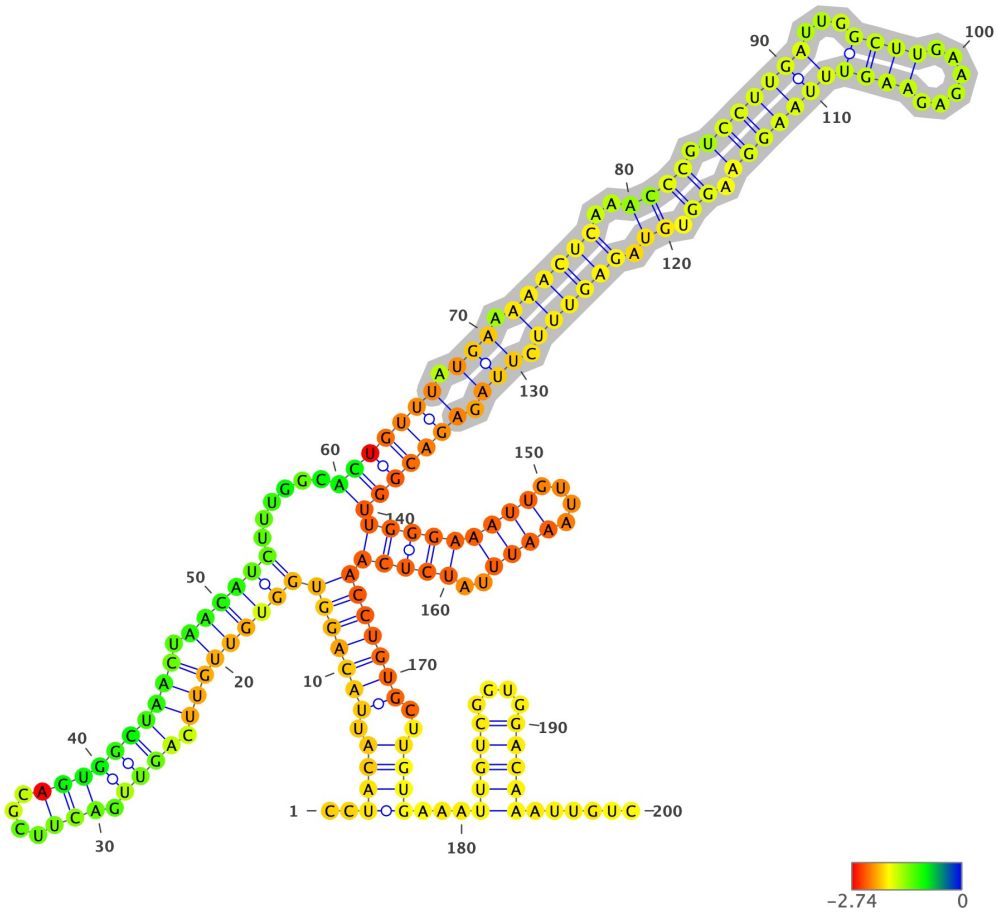
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 42 from nt 2126 to 2194 (nt 66 to 134)

```
5'-TATGAAAAACTCAAACCCGTCCTTGATTGGCTTGAAGAGAAGUUUAAGGAAGGTGTAGAGUUUCUUAGA-3'
5'-(..((.((((((....((..((((((...((((......))))))))))..))....)))))).))..)-3'
Motif MFE = -18.4; z-score = -2.7; ED = 10.24
```



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 = -1.46; ED = 41.58
```

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(+)

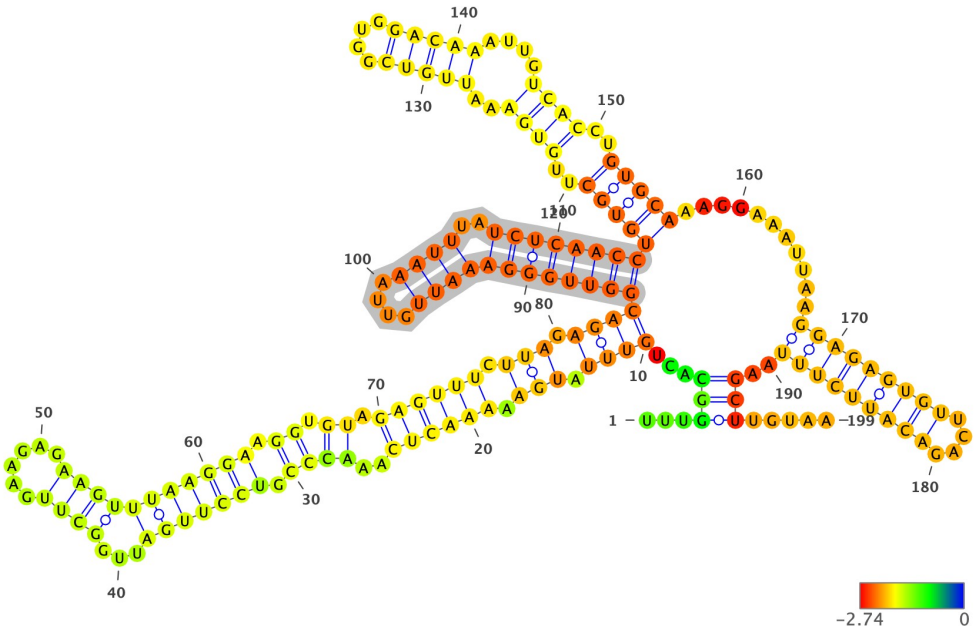
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 43 from nt 2198 to 2227 (nt 85 to 114)

```
5'-GGTTGGGAAATTGTTAAAUUTAUCUCAACC-3'
5'-(((((((((((((....))))..))))))))-3'
Motif MFE = -9.5; z-score = -3.86; ED = 1.98
```



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 2114 to 2312 (motif highlighted in silver):

```
5'-UUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCA
ACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAA-3
5'-...(((...((((.(((.((((((..((((.(((((((...((((......)))))))))))).)).)).)))))).))).))))((((((((((((....))))..)))))
)))(((((..((((..(((((....)))))....))))..)))))...........(((((((((....)))))))))..)))).....-3'
MFE = -56.7; z-score = -3.65; ED = 23.33
```

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(+)

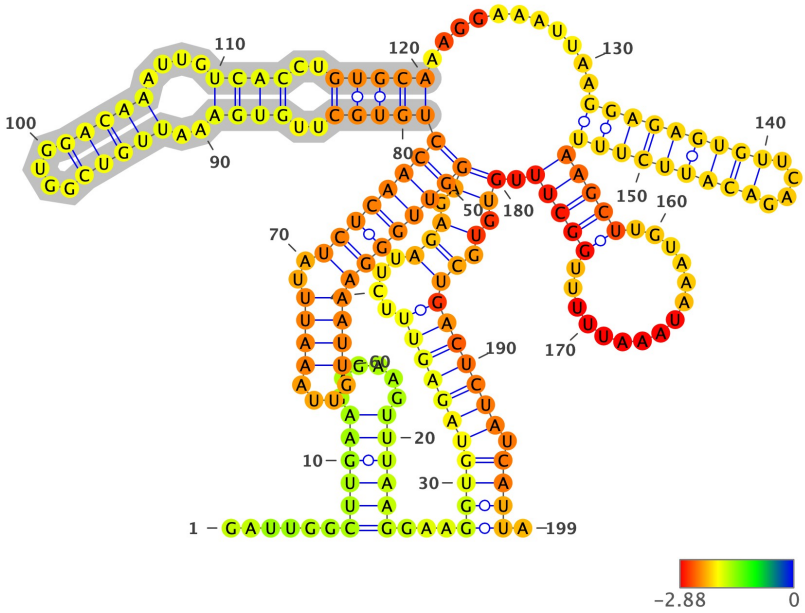
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 44 from nt 2228 to 2269 (nt 79 to 120)

```
5'-TGTGCTTGTGAAATTGTCGGTGGACAAATTGUCACCTGUGCA-3'
5'-(((((..((((..(((((....)))))....))))..)))))-3'
Motif MFE = -13.1; z-score = -2.11; 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 2150 to 2348 (motif highlighted in silver):

```
5'-GAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUC
ACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUA-3
5'-......((((((......))))))...(((((((((((....(((.((((((((((((((....))))..))))))))(((((..((((..(((((....)))))....))
))..)))))...........(((((((((....)))))))))(((((...............)))))).)).).))))))))).)))).-3'
MFE = -48.5; z-score = -1.6; ED = 37.39
```

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(+)

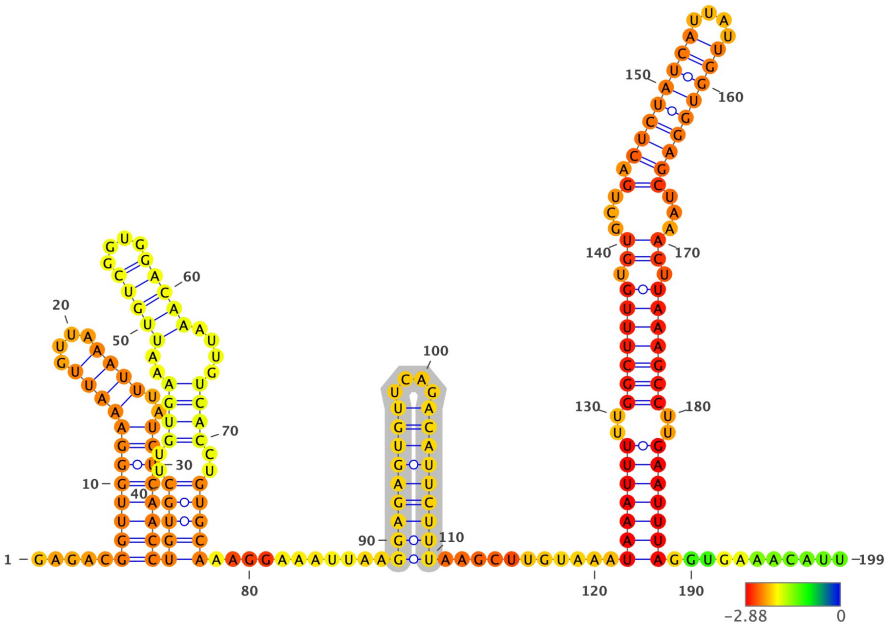
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 45 from nt 2281 to 2302 (nt 89 to 110)

```
5'-GGAGAGTGTTCAGACAUUCUUU-3'
5'-((((((((((....)))))))))-3'
Motif MFE = -6.9; z-score = -3.63; ED = 0.92
```



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 2193 to 2391 (motif highlighted in silver):

```
5'-GAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUA
AGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUU-3
5'-.....(((((((((((....))))..))))))))(((((..((((..(((((....)))))....))))..)))))...........(((((((((....))))))))).
..........(((((((..(((((((.((...(.(((((((((....)))))))))...)).)))))))..)))))))...........-3'
MFE = -57.6; z-score = -3.68; ED = 13.49
```

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(+)

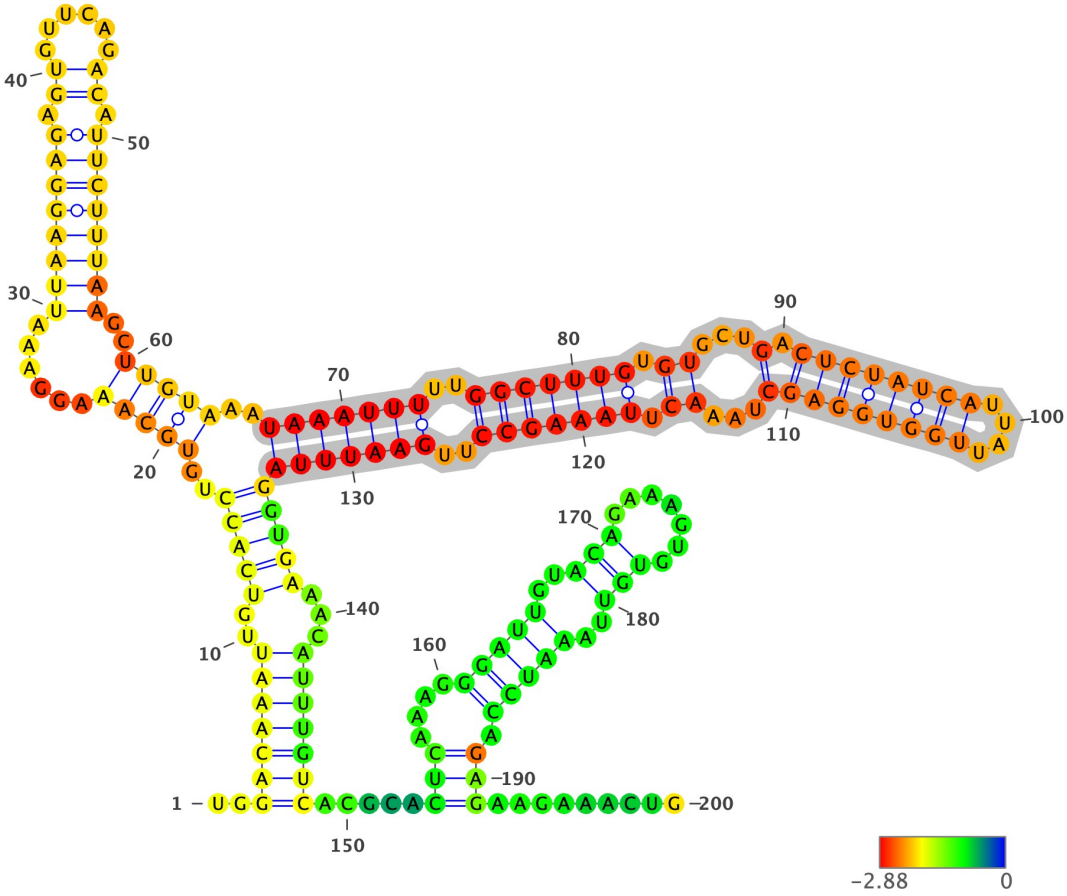
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 46 from nt 2314 to 2380 (nt 67 to 133)

```
5'-TAAATTTTTGGCTTTGTGTGCTGACTCTATCATTATUGGUGGAGCTAAACTUAAAGCCTTGAAUUUA-3'
5'-(((((((..(((((((.((...(.((((((((....)))))))))...)).)))))))..)))))))-3'
Motif MFE = -24.1; z-score = -4.82; 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 = -3.1; 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(+)

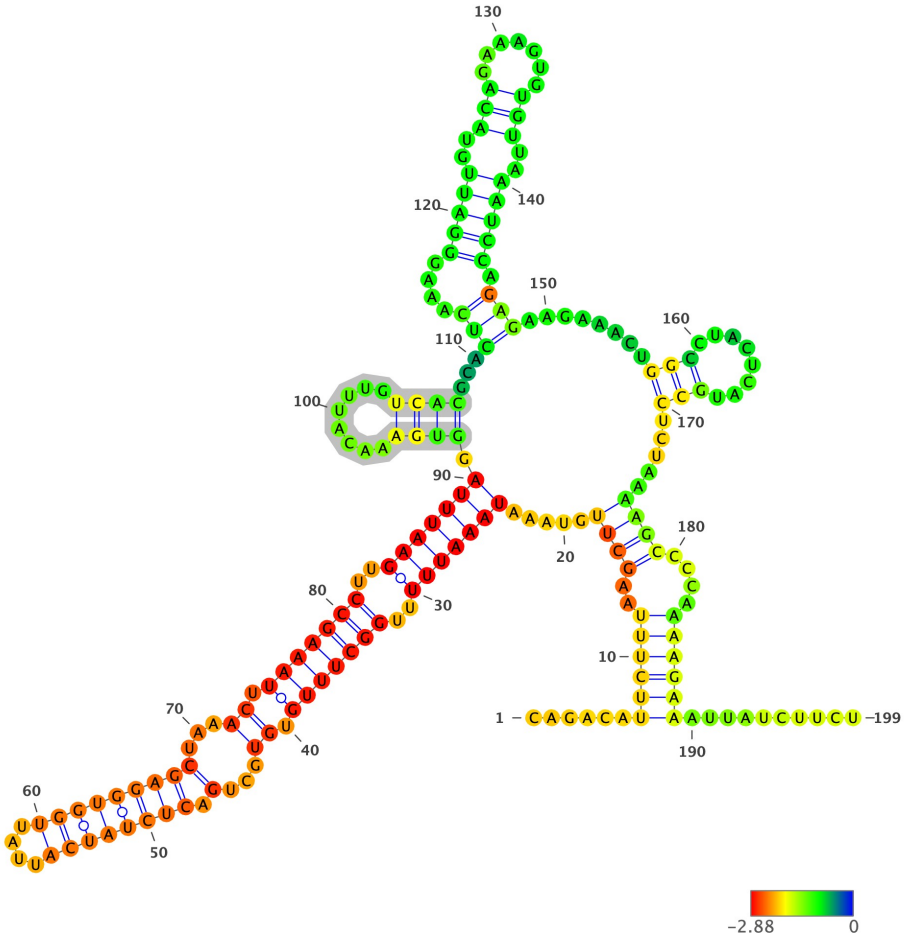
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 47 from nt 2382 to 2397 (nt 92 to 107)

```
5'-GTGAAACATTTGTCAC-3'
5'-((............))-3'
Motif MFE = -1.5; z-score = -2.24; 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 2291 to 2489 (motif highlighted in silver):

```
5'-CAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUUUGUCACGCAC
UCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCU-3
5'-......((((((..((((.....(((((((..(((((((.((...(.((((((((....)))))))))...)).)))))))..)))))))).((((........))))...(
((....(((((..(((.......)))..)))))).)))........(((........)))).....))))....))))))..........-3'
MFE = -45.0; z-score = -1.8; ED = 17.58
```

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(+)

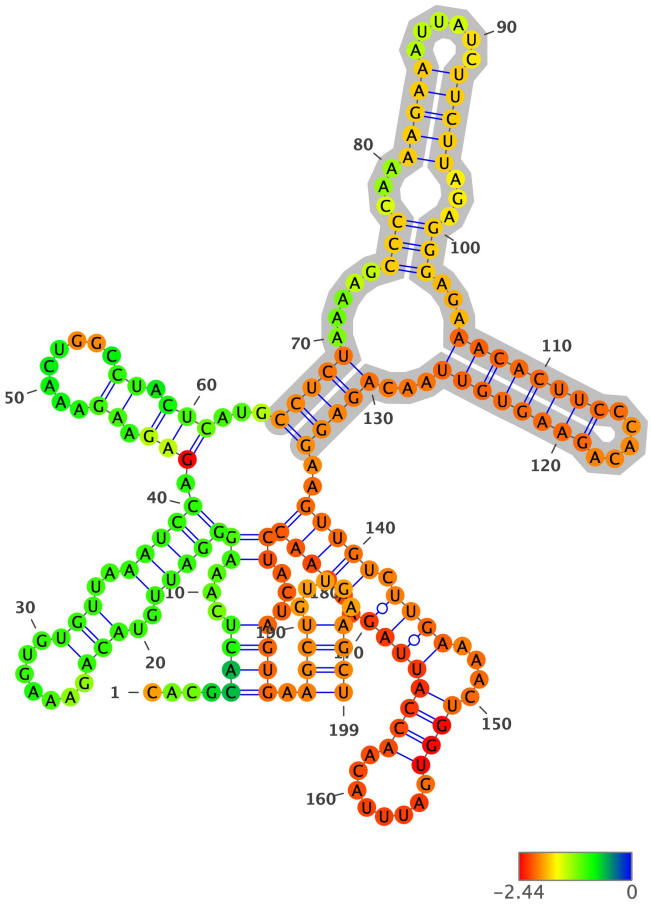
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 48 from nt 2459 to 2528 (nt 65 to 134)

```
5'-CCTCTAAAAGCCCCAAAAGAAATTATCUUCUUAGAGGGAGAAACACTTCCCACAGAAGUGUUAACAGAGG-3'
5'-(((.......(((...(((((.....)))))...)))...((((((((.....)))))))).....)))-3'
Motif MFE = -18.8; z-score = -4.06; ED = 5.36
```



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 2395 to 2593 (motif highlighted in silver):

```
5'-CACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACU
UCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCU-3
5'-....((((...(((((((..(((.......)))..))))).(((.((........)).)))...(((((.....(((...(((((.....)))))...)))...((((((
((.....))))))))...)))))..(((((.((((....((((........))))))))).)))))))...)))).((((.....))))-3'
MFE = -45.3; z-score = -1.63; ED = 13.95
```

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(+)

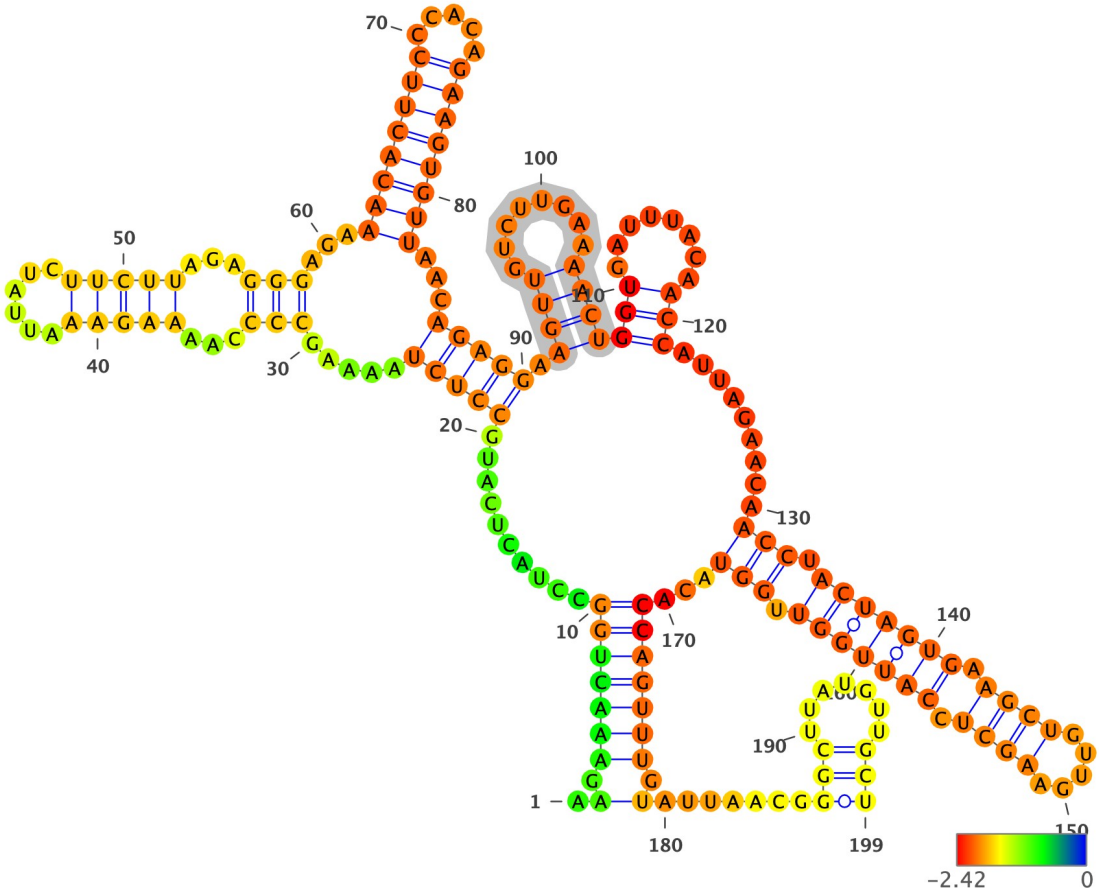
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 49 from nt 2530 to 2545 (nt 92 to 107)

```
5'-AGTTGTCTTGAAAACU-3'
5'-((((........))))-3'
Motif MFE = -0.7; z-score = -0.57; 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 2439 to 2637 (motif highlighted in silver):

```
5'-AAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUG
AUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCU-3
5'-.(.(((((((..........(((((.....(((...(((((......)))))...)))...((((((((.....))))))))...))))).((((........))))(((.
.......)))........(((.(((((((.((((.....)))).)))))))).)))...)))))))).).......(((.......)))-3'
MFE = -51.8; z-score = -2.81; ED = 24.54
```

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, 266-13468(+)

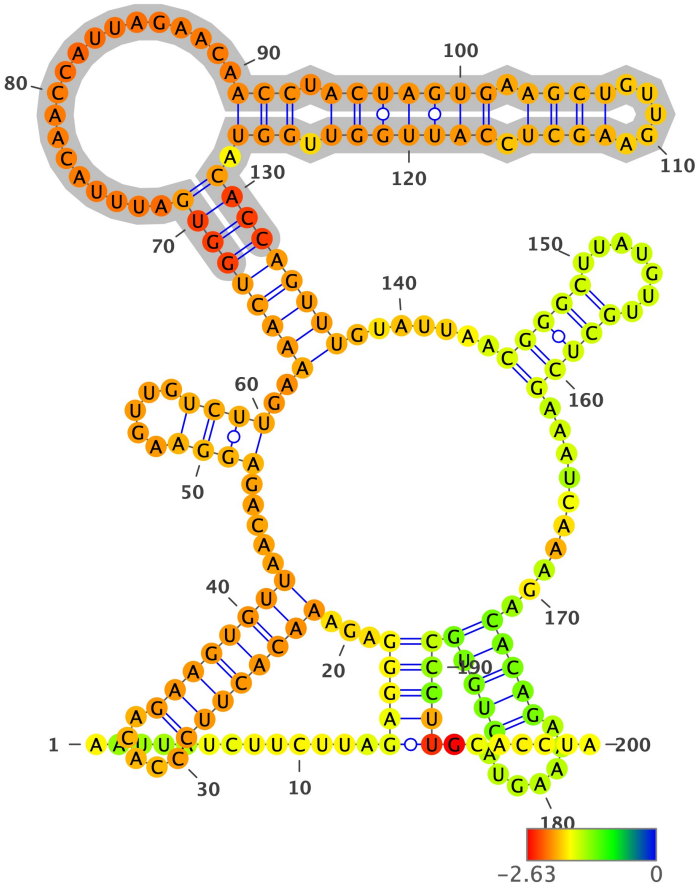
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 50 from nt 2546 to 2610 (nt 68 to 132)

```
5'-GGTGATTTACAACCATTAGAACAACCTACTAGTGAAGCTGTTGAAGCUCCAUUGGUTGGUACACC-3'
5'-(((....................(((.(((((((.((((.....)))).)))))))).)))..)))-3'
Motif MFE = -19.6; z-score = -2.57; 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 2479 to 2678 (motif highlighted in silver):

```
5'-AAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGA
AGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUA-3
5'-.............(((((...((((((((.....))))))))).....((((.....)))).((((((((((.....................(((.(((((((.((((.....
)))).)))))))).))).))))))))).......(((((.......)))))..........(((((.......)))))))))).......-3'
MFE = -53.0; z-score = -2.83; ED = 27.52
```

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(+)

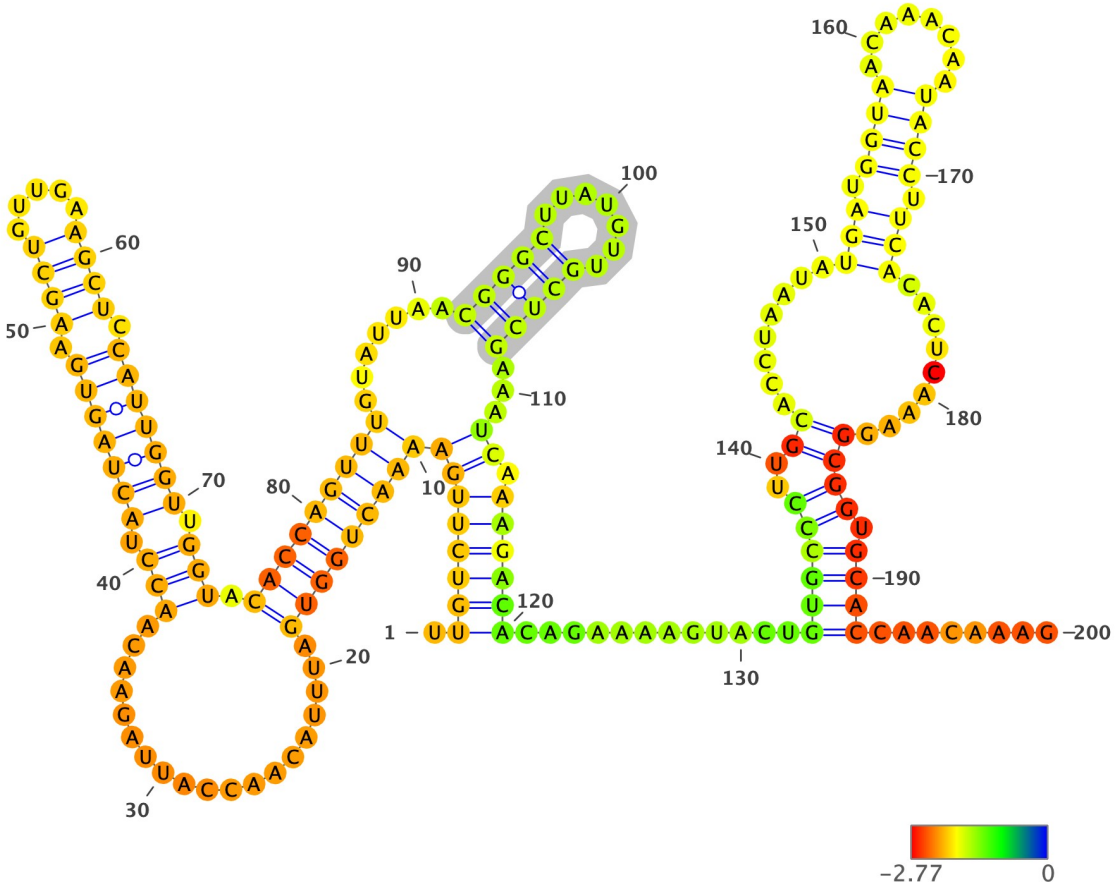
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 51 from nt 2623 to 2639 (nt 92 to 108)

```
5'-CGGGCTTATGTTGCUCG-3'
5'-(((((.......)))))-3'
Motif MFE = -5.5; z-score = -2.95; 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 = -2.62; 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(+)

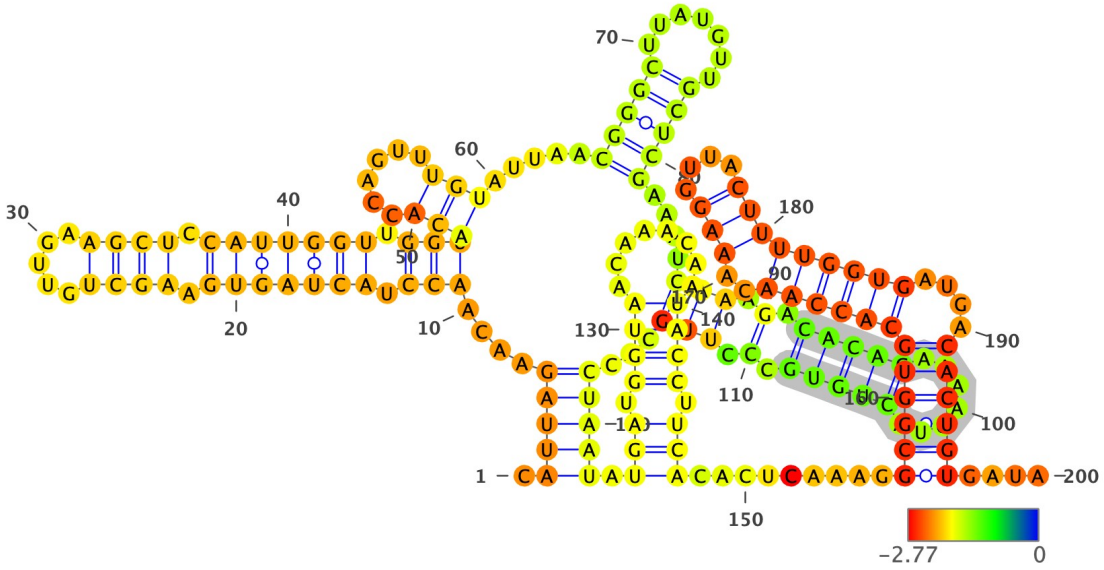
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 52 from nt 2650 to 2666 (nt 92 to 108)

```
5'-CACAGAAAAGTACUGUG-3'
5'-(((((.......)))))-3'
Motif MFE = -3.6; z-score = -4.05; ED = 0.31
```



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 2559 to 2758 (motif highlighted in silver):

```
5'-CAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCC
UUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUA-3
5'-.(((((....(((.(((((((.((((.....)))).)))))))).)))(((......))).....(((((.......)))))....(((.(.(((((.......))))).).
)))...))))).(((.((((.........)))).))).........((((((((((((..(((....)))))))))....))))))....-3'
MFE = -49.3; z-score = -1.79; ED = 42.44
```

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, 266-13468(+)

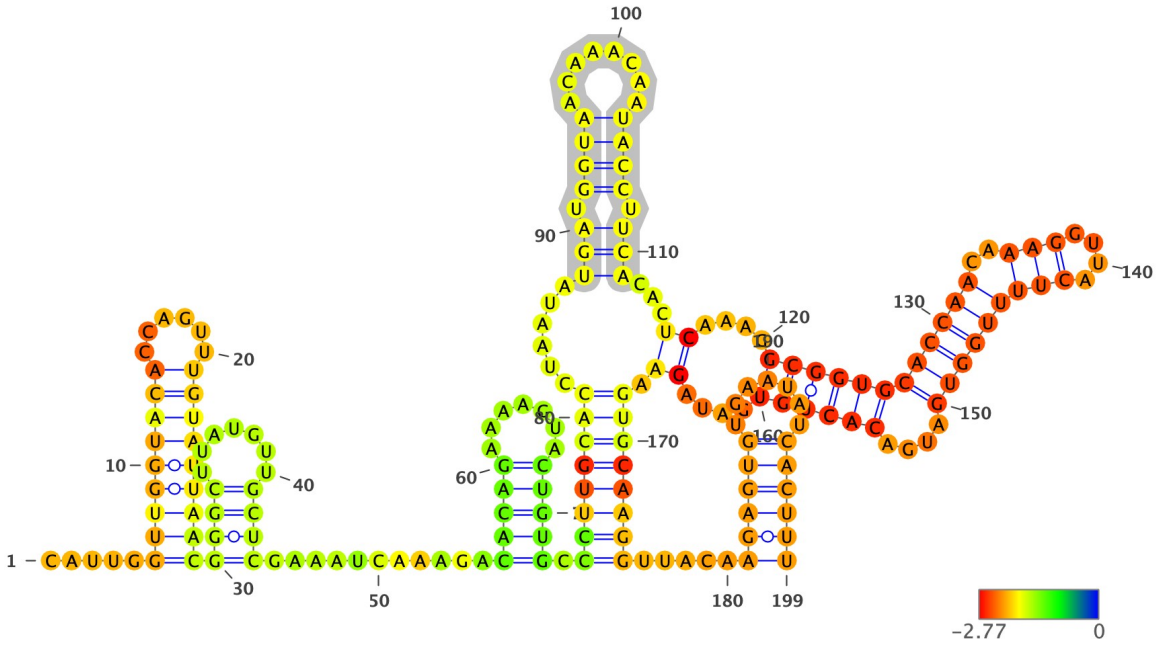
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 2682 to 2705 (nt 88 to 111)

```
5'-TGATGGTAACAAACAAUACCTUCA-3'
5'-(((.((((........)))).)))-3'
Motif MFE = -4.8; z-score = -3.86; 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 2595 to 2793 (motif highlighted in silver):

```
5'-CAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCA
CACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUU-3
5'-.....((((((((((......))))))))))(((.......))))..........(((((.......))))).(((((((((......(((.((((........)))).)))
...((....((((((((((((..(((....)))))))))....))))))....)).)))))))).....((((((.......))))))-3'
MFE = -52.2; z-score = -2.38; ED = 28.92
```

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, 266-13468(+)

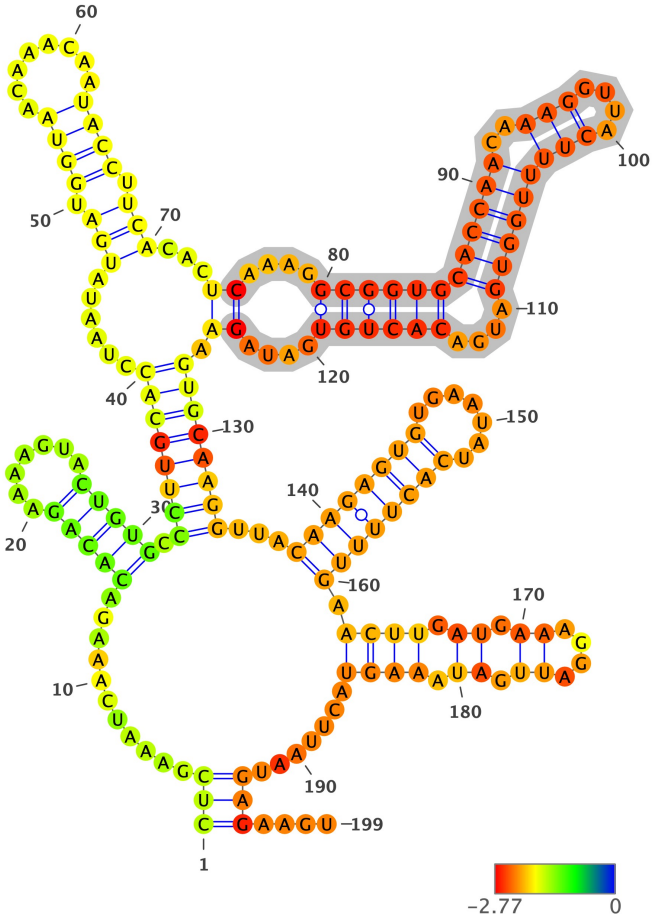
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 54 from nt 2710 to 2759 (nt 75 to 124)

```
5'-CAAAGGCGGTGCACCAACAAAGGTTACUUUUGGUGATGACACUGUGATAG-3'
5'-(....((((((((((((..(((....)))))))))....))))))....)-3'
Motif MFE = -13.7; z-score = -1.96; ED = 3.74
```



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 2636 to 2834 (motif highlighted in silver):

```
5'-CUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAU
GACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGU-3
5'-(((..........(((((.......)))))).(((((((.....(((.((((........)))).))).)))...((....((((((((((((..(((....)))))))))..
..))))))....)).)))))))...(((((((.....)))))))).(((((.((.((....)).)).)))).......))).....-3'
MFE = -47.4; z-score = -2.66; ED = 23.48
```

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(+)

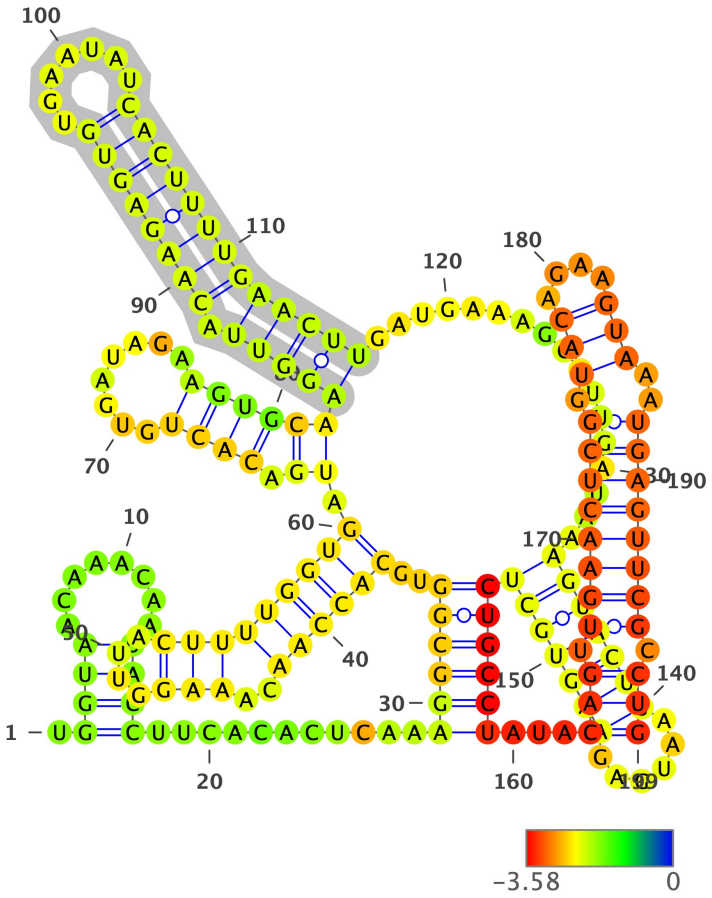
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 55 from nt 2767 to 2800 (nt 83 to 116)

```
5'-AGGTTACAAGAGTGTGAATATCACUUUUGAACUU-3'
5'-(((((.(((((((((.......)))))))))))))))-3'
Motif MFE = -10.9; z-score = -3.73; 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 = -2.89; 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(+)

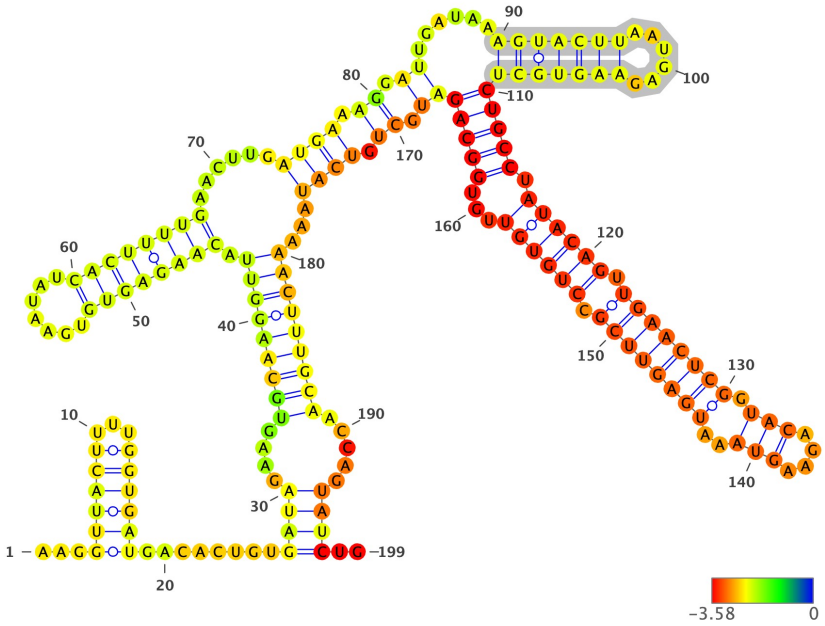
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 56 from nt 2818 to 2837 (nt 90 to 109)

```
5'-AGTACTTAATGAGAAGUGCU-3'
5'-(((((((......)))))))-3'
Motif MFE = -5.4; z-score = -3.84; 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 = -3.74; 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, 266-13468(+)

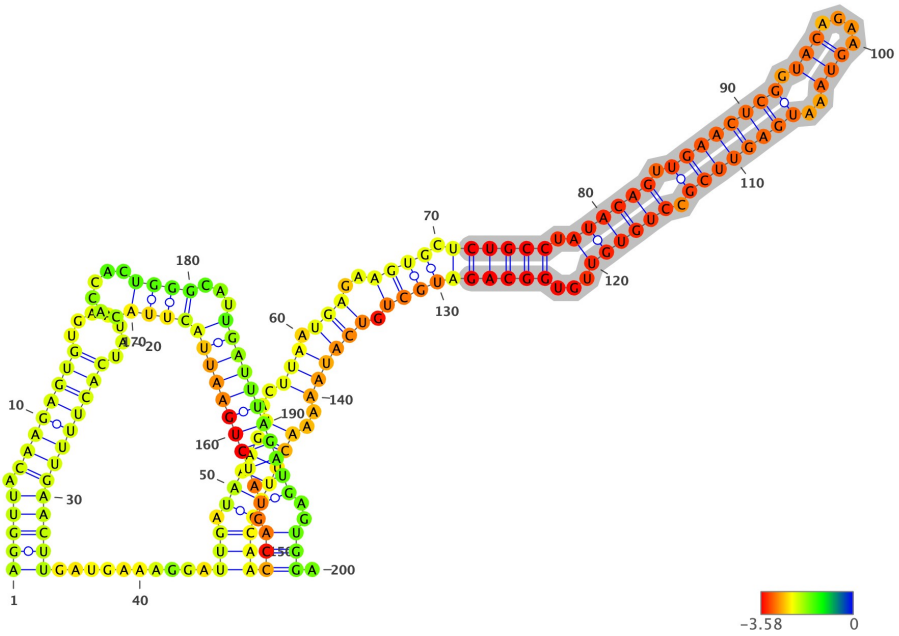
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 2838 to 2894 (nt 72 to 128)

```
5'-CTGCCTATACAGTTGAACTCGGTACAGAAGUAAAUGAGUUCGCCUGUGUTGTGGCAG-3'
5'-(((((.((((((.((((((((.(((....)))..)))))))).))))))...)))))-3'
Motif MFE = -25.1; z-score = -4.17; 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 = -3.81; ED = 19.32
```

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, 266-13468(+)

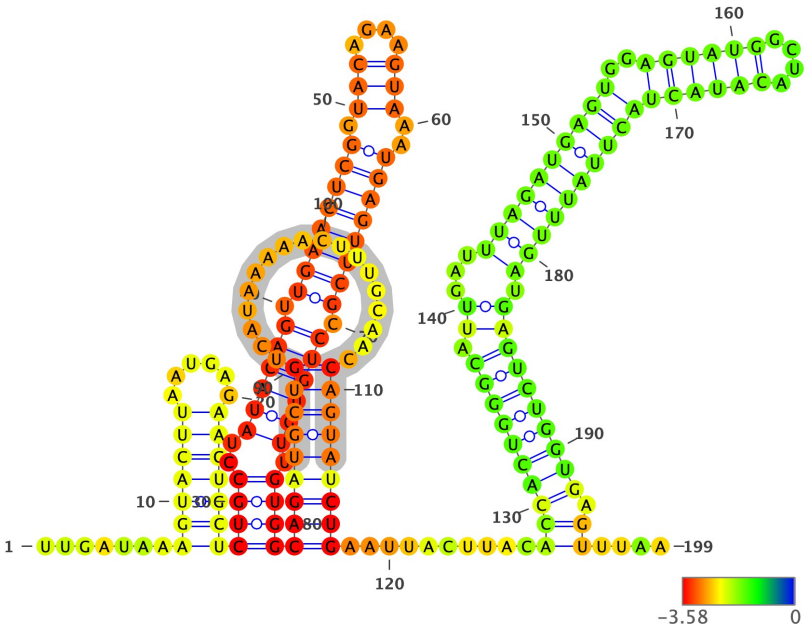
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 2896 to 2923 (nt 86 to 113)

```
5'-TGCTGTCATAAAAACTTTGCAACCAGUA-3'
5'-((((.....................))))-3'
Motif MFE = -1.1; z-score = 0.29; ED = 5.79
```



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 = -3.85; ED = 20.49
```

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(+)

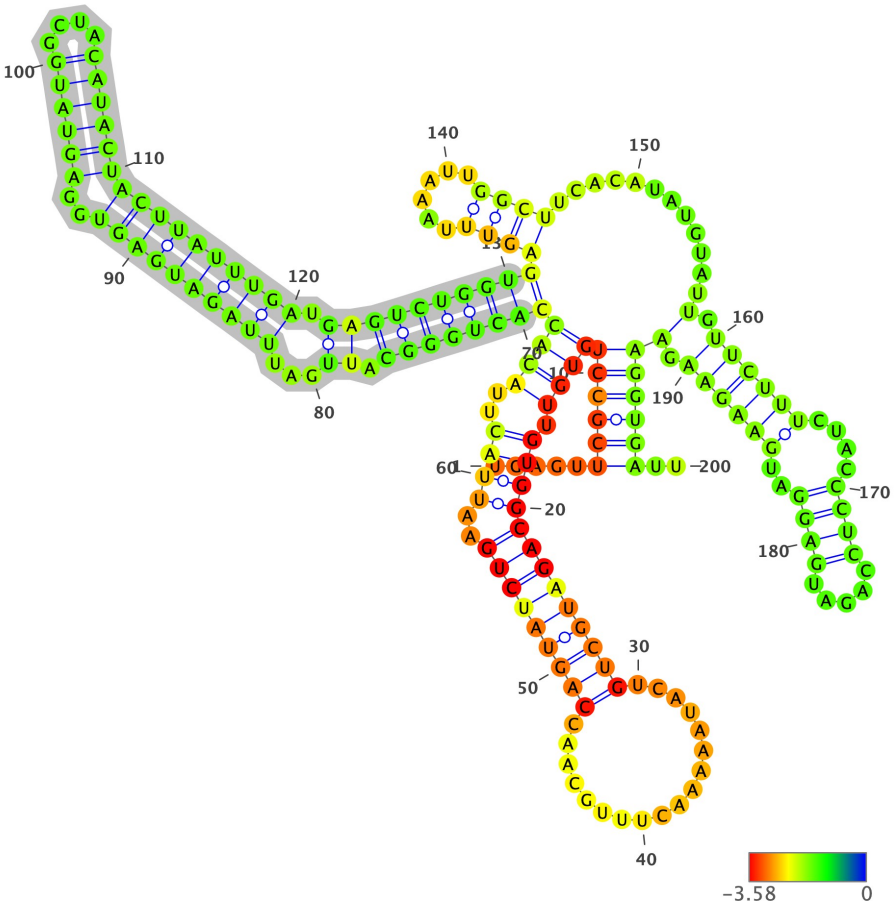
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 59 from nt 2941 to 3001 (nt 70 to 130)

```
5'-ACTGGGCATTGATTTAGATGAGTGGAGTATGGCTACAUACUACUUAUUUGATGAGUCUGGU-3'
5'-(((((((..(...((((((((((..((((((....))))))))))))))).).)))))))-3'
Motif MFE = -19.3; z-score = -3.4; 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 = -1.99; ED = 22.55
```

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(+)

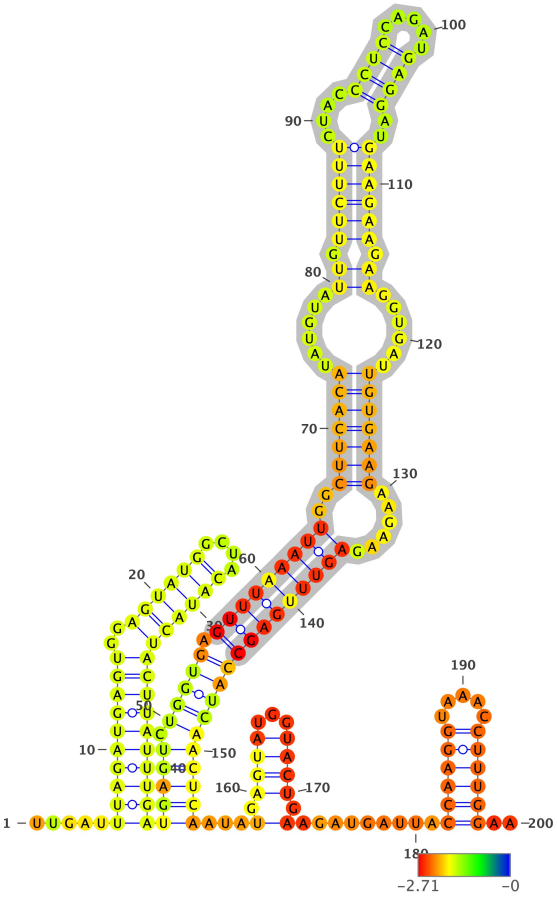
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 60 from nt 3004 to 3092 (nt 56 to 144)

```
5'-GTTTAAATTGGCTTCACATATGTATTGTTCTTTCTACCCTCCAGATGAGGATGAAGAAGAAGGTGATUGUGAAGAAGAAGAGUUTGAGC-3'
5'-((((.((((..(((((((.....((.((((((....((((.....))))..)))))).))......)))))))......)))).))))-3'
Motif MFE = -23.1; z-score = -2.53; ED = 10.85
```



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 2949 to 3148 (motif highlighted in silver):

```
5'-UUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAG
AAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAA-3
5'-.....((((((((((..((((((....))))))))))))))))(((((.(((((.(((((((((..(((((((.....((.((((((....((((.....))))..))))
)).))......)))))))......))))))))))))))))))...(.((((...)))).).........((((((.....))))))..-3'
MFE = -56.1; z-score = -3.99; ED = 14.91
```

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(+)

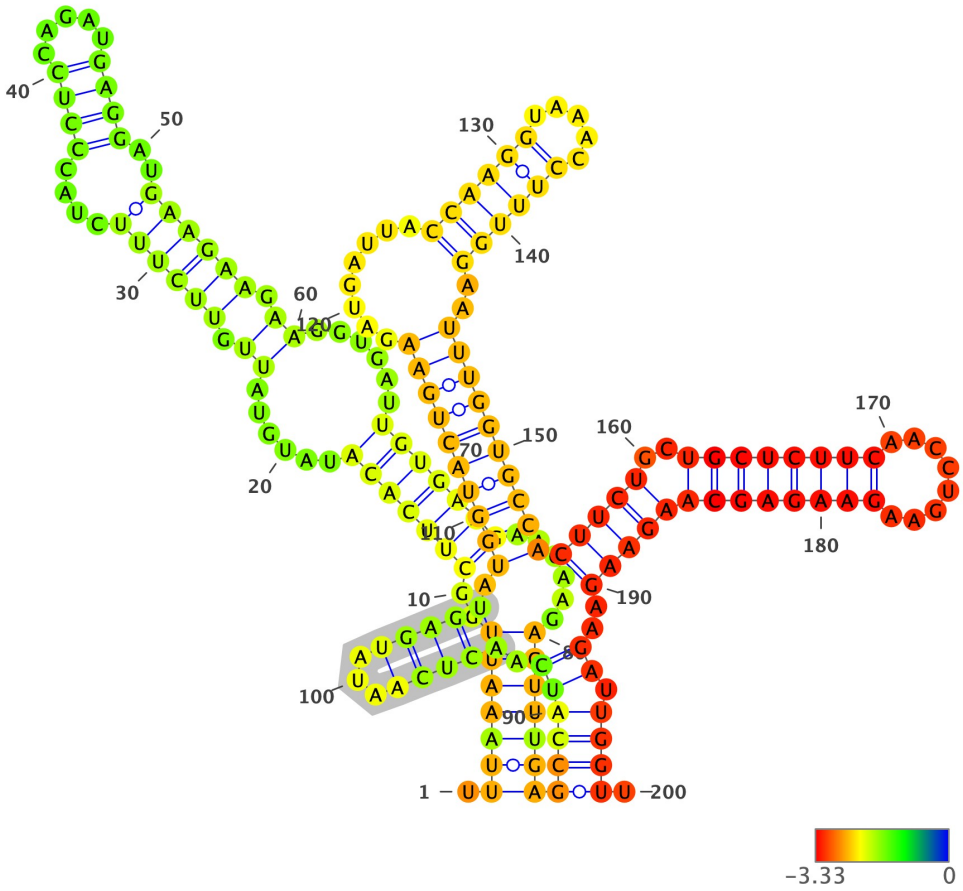
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 61 from nt 3098 to 3110 (nt 94 to 106)

```
5'-ACTCAATATGAGU-3'
5'-((((.....))))-3'
Motif MFE = -2.4; z-score = -7.99; 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 3005 to 3204 (motif highlighted in silver):

```
5'-UUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGU
ACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUU-3
5'-.(((((((..(((((((.....((.((((((....((((.....))))..)))))).))......)))))))......)))))))((((((.(((((...)))))).((((
((((((........((((((.....))))))..))))))))))(((((..(((((((((........)))))))))))))..)).)))).-3'
MFE = -58.0; z-score = -3.38; ED = 35.31
```

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(+)

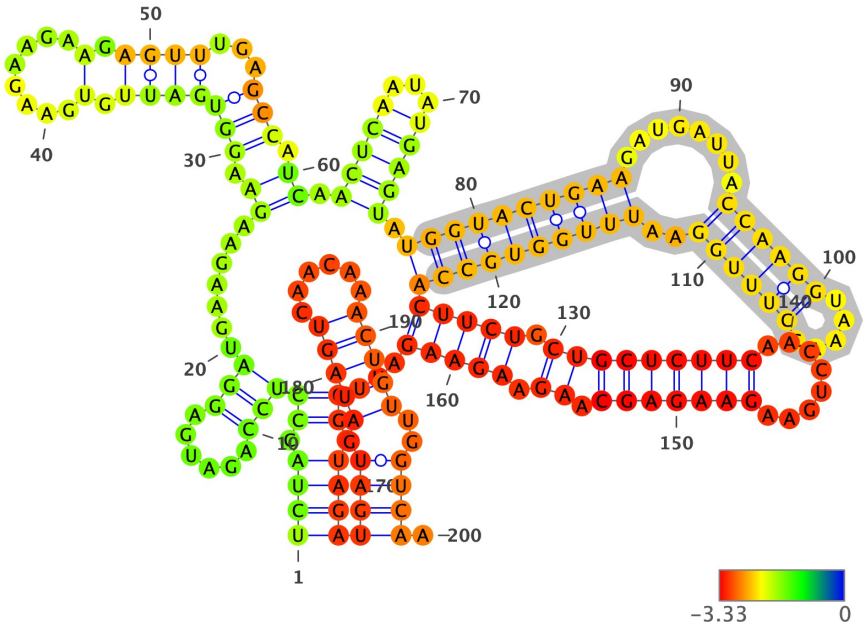
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 62 from nt 3113 to 3157 (nt 78 to 122)

```
5'-GGTACTGAAGATGATTACCAAGGTAAACCUUUGGAAUUUGGUGCC-3'
5'-(((((((((.........((((((.....))))))..)))))))))-3'
Motif MFE = -12.1; z-score = -1.88; ED = 6.69
```



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 3036 to 3235 (motif highlighted in silver):

```
5'-UCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGG
AAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAA-3
5'-((((.(((((......)))).......((.(((((((.(........).))))...))).)).(((((...))))).((((((((((........((((((.....))))))
..))))))))))(((((.(((((((((........)))))))).)).)))))...)).))))((((.(((((......)))))..)))).-3'
MFE = -51.6; z-score = -2.28; ED = 41.56
```

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(+)

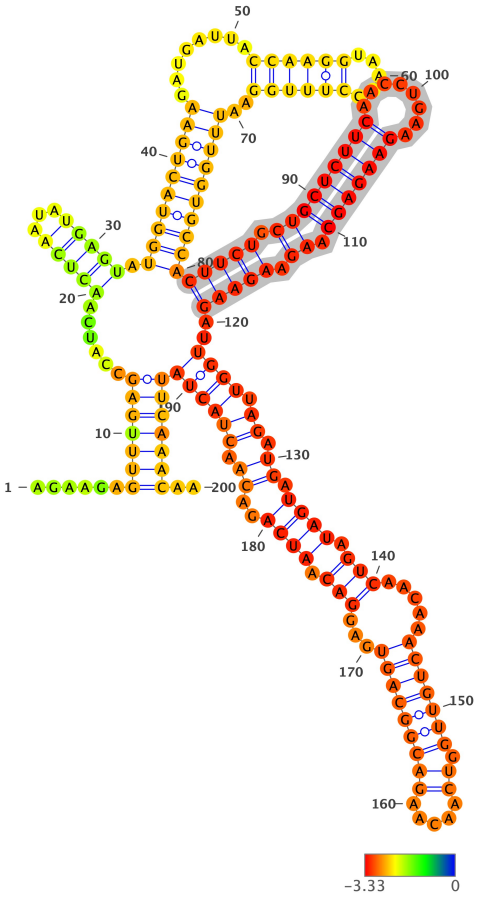
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 63 from nt 3159 to 3197 (nt 81 to 119)

```
5'-CTTCTGCTGCTCTTCAACCTGAAGAAGAGCAAGAAGAAG-3'
5'-(((((.(((((((((.........)))))))).)).)))))-3'
Motif MFE = -16.2; z-score = -4.32; ED = 10.48
```



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 3079 to 3278 (motif highlighted in silver):

```
5'-AGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCA
AGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAA-3
5'-......(((((((......(((((...))))).((((((((((.........((((((.....))))))..))))))))))(((((.(((((((((.........)))))))).
)).)))))..((((.((.((.((((.(((.....(((((((.((.....)))))))))...))).)))).)).)))))))))))))..-3'
MFE = -58.9; z-score = -4.33; ED = 19.16
```

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(+)

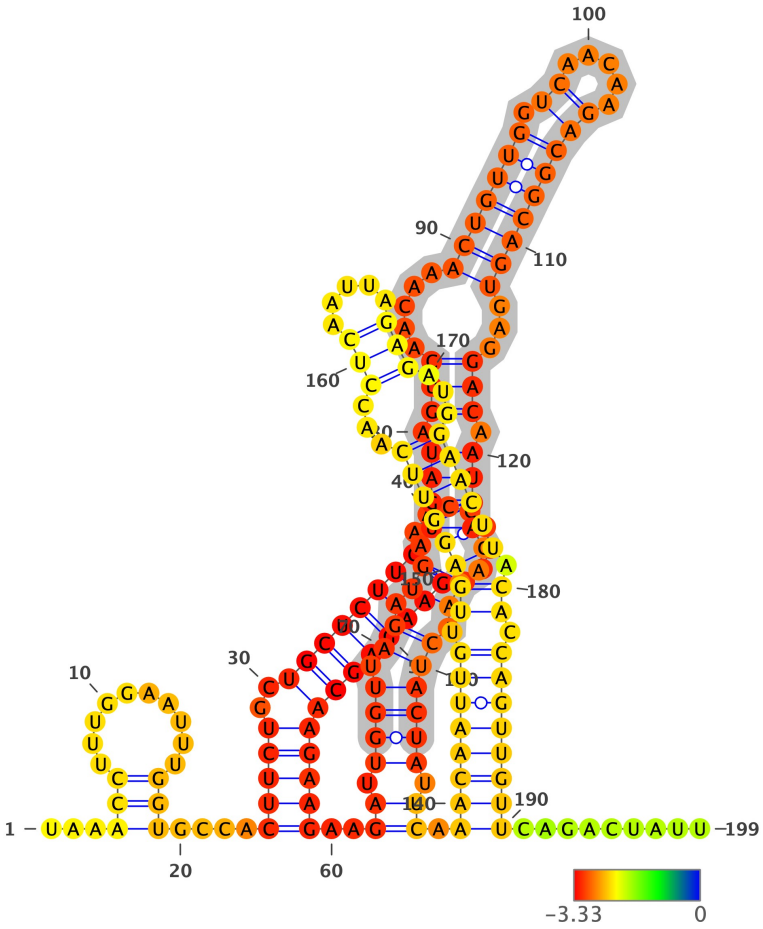
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 64 from nt 3201 to 3268 (nt 66 to 133)

```
5'-GGTTAGATGATGATAGTCAACAAACTGTTGGTCAACAAGACGGCAGUGAGGACAAUCAGACAACTACU-3'
5'-(((.......((((.(((.....(((((((.((.....)))))))))...))))..))))).......)))-3'
Motif MFE = -16.6; z-score = -2.23; ED = 6.83
```



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 3136 to 3334 (motif highlighted in silver):

```
5'-UAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAG
UGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUU-3
5'-...(((..........)))....((((((..(((((((((........)))))))))))))))..((.(((((.((.((.(((((.(((.....(((((((.((.....)))))))
)...)))).)))))..)).)))))).)).(((((((((.(((((((((...(((.....)))...)))))))).)).)))))))).........-3'
MFE = -55.7; z-score = -4.41; ED = 40.68
```

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(+)

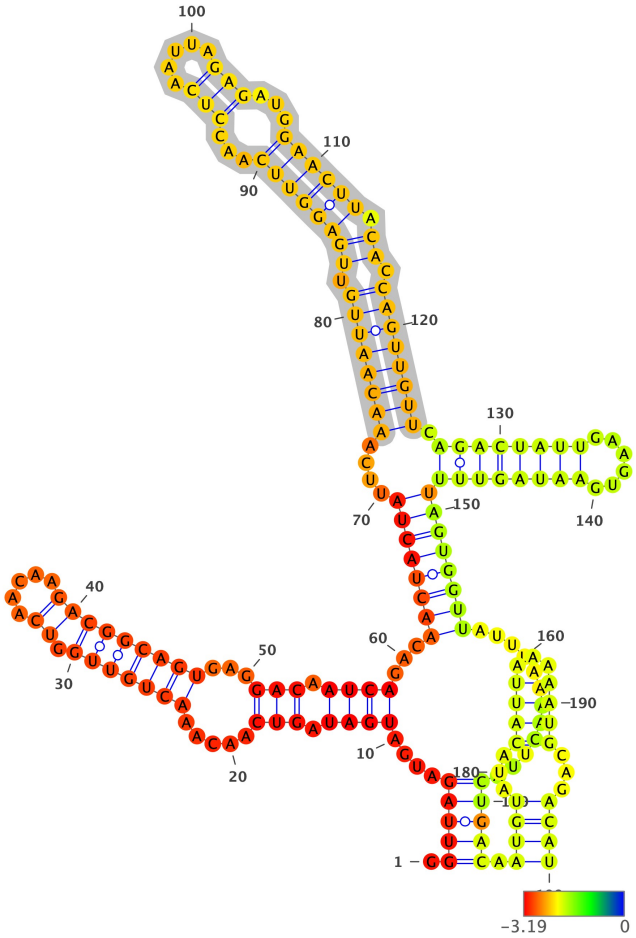
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 65 from nt 3274 to 3325 (nt 74 to 125)

```
5'-AACAATTGTTGAGGTTCAACCTCAATTAGAGATGGAACUUACACCAGUUGUU-3'
5'-(((((((((.(((((((((...(((.....)))...)))))))).)).)))))))-3'
Motif MFE = -16.5; z-score = -3.54; 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 = -47.0; z-score = -2.82; ED = 24.66
```

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(+)

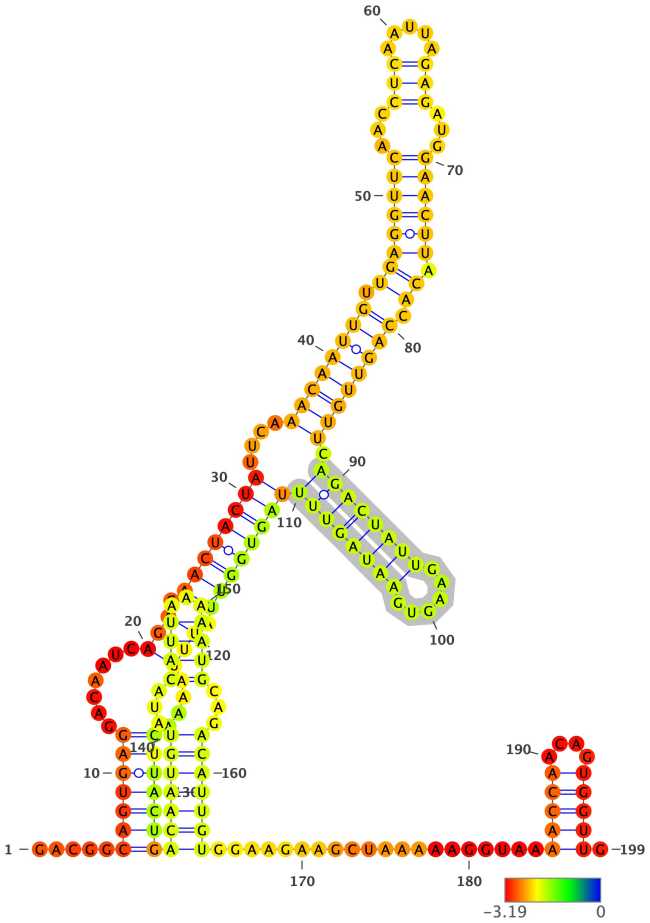
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 66 from nt 3327 to 3348 (nt 89 to 110)

```
5'-AGACTATTGAAGTGAAUAGUUU-3'
5'-((((((((......))))))))-3'
Motif MFE = -5.2; z-score = -4.16; 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 3239 to 3437 (motif highlighted in silver):

```
5'-GACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUU
AGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUG-3
5'-.....(((((((.......(((.((((((((....((((((((.((((((((...(((.....)))...)))))).)).)))))))).((((((((......)))))))))
))))))).)))....)))))))(((((((...((((...))))...)))))))).....................(((((....))))).-3'
MFE = -47.8; z-score = -3.33; ED = 16.85
```

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(+)

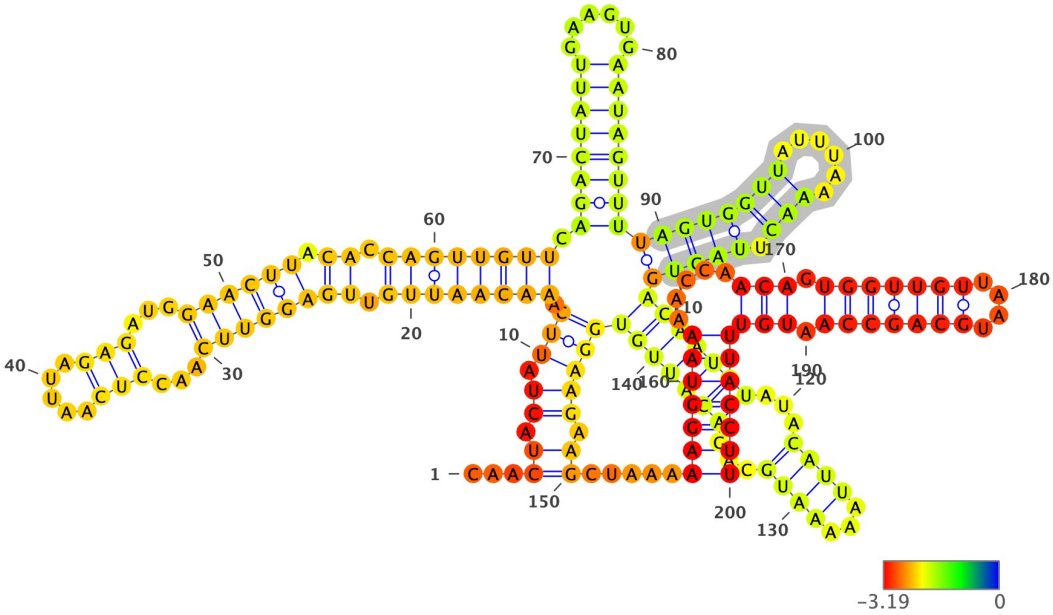
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 67 from nt 3350 to 3370 (nt 90 to 110)

```
5'-AGTGGTTATTTAAAACTUACU-3'
5'-(((((((......))).))))-3'
Motif MFE = -1.3; z-score = -0.7; ED = 2.58
```



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 3261 to 3460 (motif highlighted in silver):

```
5'-CAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUG
ACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUU-3
5'-...((.((.(((.((((((((.((((((((...(((.....)))...)))))).)).))))))))).((((((((......))))))))((((((((......))).)))))
(((((((...((((...))))...))))))))))))).)).....(((((((.....(((.(((((((....)))))))).))))))))))-3'
MFE = -50.8; z-score = -4.62; ED = 16.52
```

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(+)

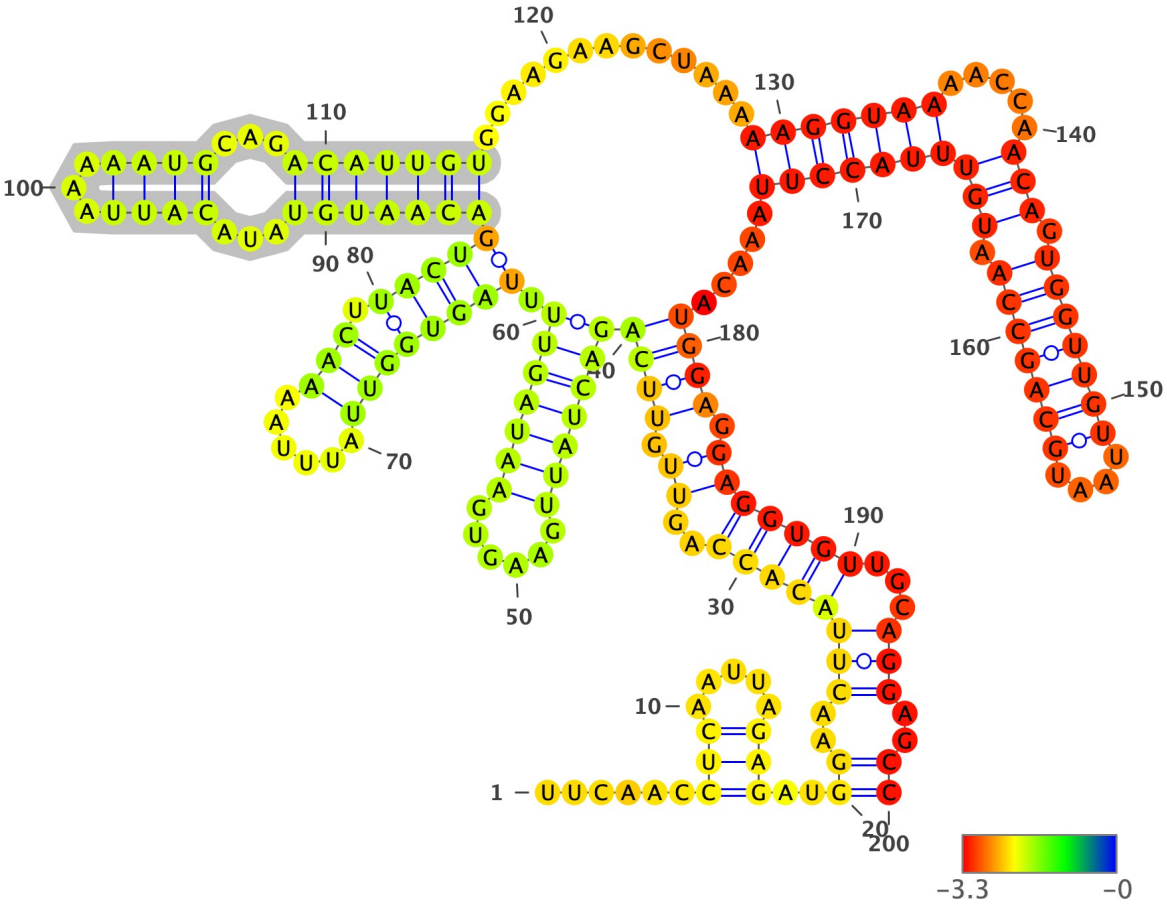
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 68 from nt 3372 to 3402 (nt 85 to 115)

```
5'-ACAATGTATACATTAAAAAUGCAGACAUUGU-3'
5'-(((((((...((((...))))...)))))))-3'
Motif MFE = -6.4; z-score = -3.58; 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 3288 to 3487 (motif highlighted in silver):

```
5'-UUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACA
UUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCC-3
5'-......(((.....)))..((..((((((((..((.(((((((((((.....)))))))).((((((((.....))).)))))(((((((...((((...))))...)))
))))).............(((((((.....(((.(((((((....)))))))).))))))))))).....)))).)))))))...)))..))-3'
MFE = -45.5; z-score = -2.31; ED = 39.27
```

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(+)

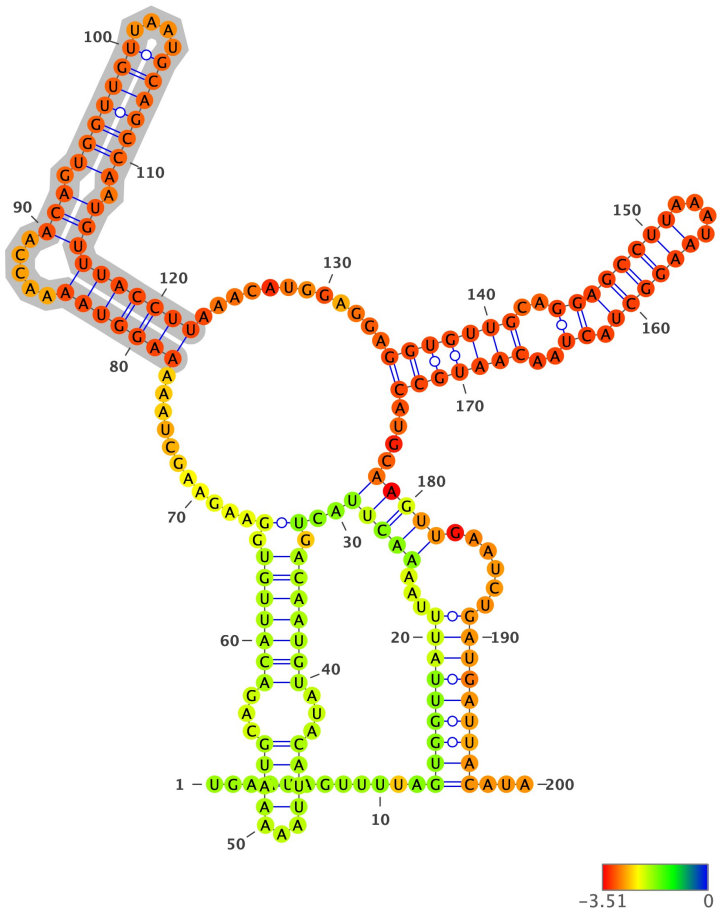
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 69 from nt 3416 to 3460 (nt 78 to 122)

```
5'-AAGGTAAAACCAACAGTGGTTGTTAATGCAGCCAAUGUUUACCUU-3'
5'-(((((((.....(((.(((((((....)))))))..)))))))))-3'
Motif MFE = -16.0; z-score = -4.37; 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 3339 to 3538 (motif highlighted in silver):

```
5'-UGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCA
AUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUA-3
5'-...........((((((((((...((((((..(.(((((((...((((...)))))...)))))))).)...........(((((((.....(((.(((((((....)))))))
.)))))))))).....((((((..(((((((((....)))))))..))..)))))))....))))).....)))))))))...-3'
MFE = -50.2; z-score = -3.3; ED = 29.88
```

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(+)

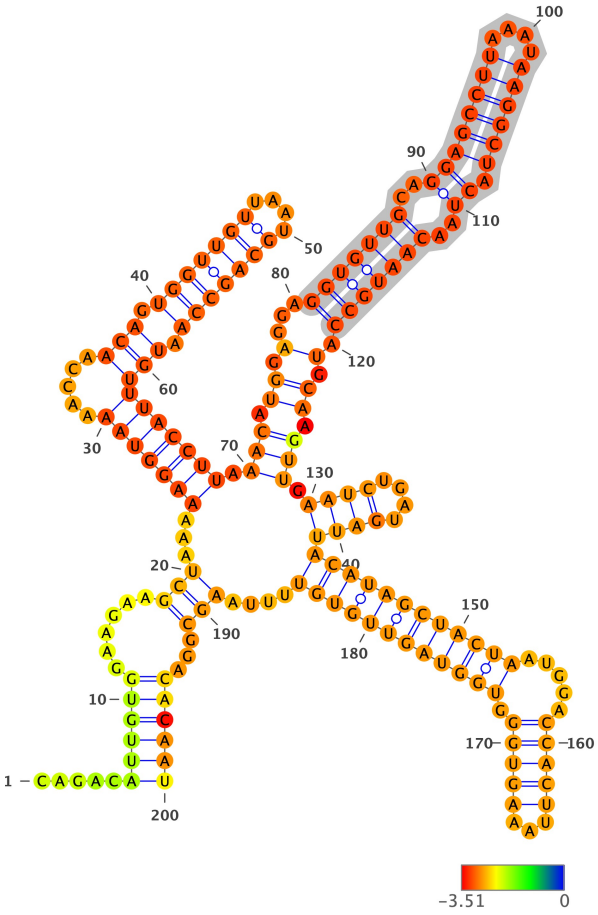
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 70 from nt 3473 to 3511 (nt 81 to 119)

```
5'-GGTGTTGCAGGAGCCTTAAATAAGGCUACUAACAAUGCC-3'
5'-(((((((..((((((((....)))))).))..)))))))-3'
Motif MFE = -15.6; z-score = -3.74; 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 = -61.5; z-score = -4.82; ED = 18.34
```

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(+)

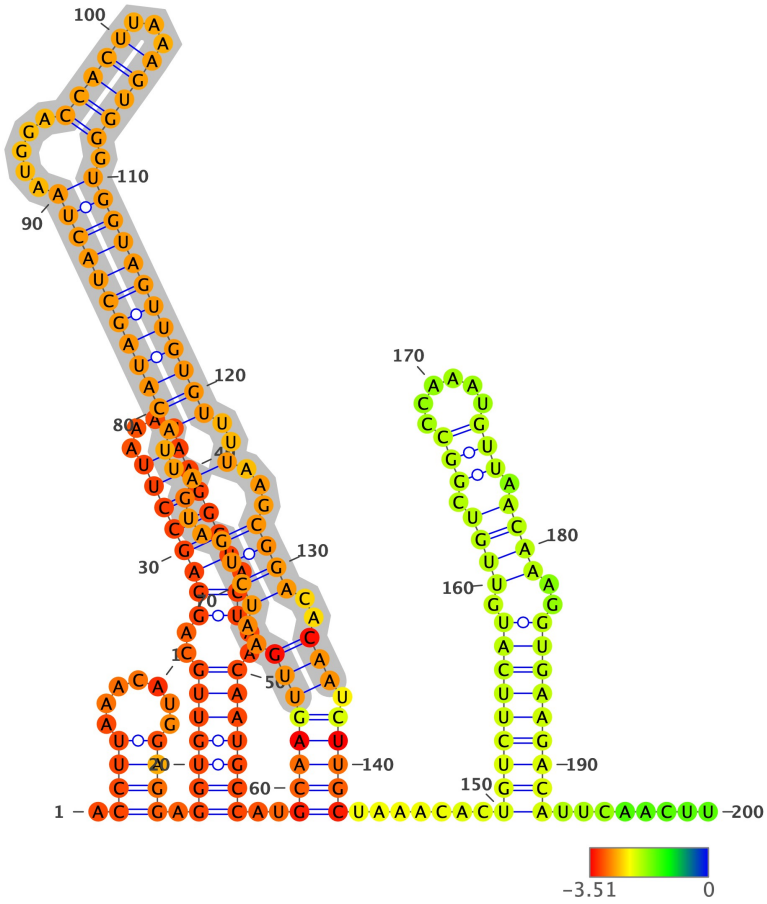
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 71 from nt 3519 to 3591 (nt 64 to 136)

```
5'-TTGAATCTGATGATTACATAGCTACTAATGGACCACTTAAAGUGGGUGGUAGUUGUGUTTUAAGCGGACACAA-3'
5'-((...((.....(..(((((((((((((.....(((((...))))).))))))))))))..).....))...))-3'
Motif MFE = -21.9; z-score = -3.22; ED = 4.19
```



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 3456 to 3655 (motif highlighted in silver):

```
5'-ACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUG
GUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUU-3
5'-.((((.......)))).(((((((..((((((((....))))))).))..)))))))..((((((((..((((...(..(((((((((((.....(((((...))))).))
))))))))))..)...))))..))).)))))).......((((((((.((((.(((.....))).))))..)))))))))........-3'
MFE = -64.9; z-score = -4.4; ED = 11.0
```

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(+)

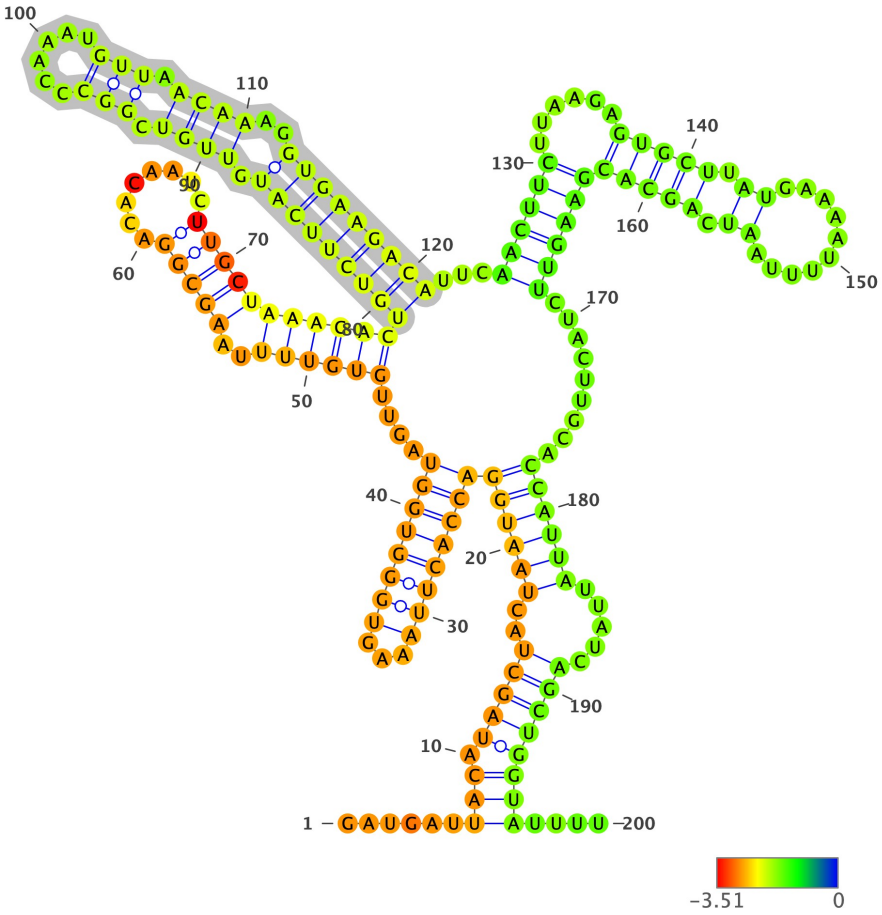
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 72 from nt 3605 to 3647 (nt 79 to 121)

```
5'-TGTCTTCATGTTGTCGGCCCAAATGUUAACAAAGGUGAAGACA-3'
5'-(((((((((.((((.(((......))).)))).)))))))))-3'
Motif MFE = -14.2; z-score = -3.32; 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 = -49.8; z-score = -2.17; ED = 32.88
```

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(+)

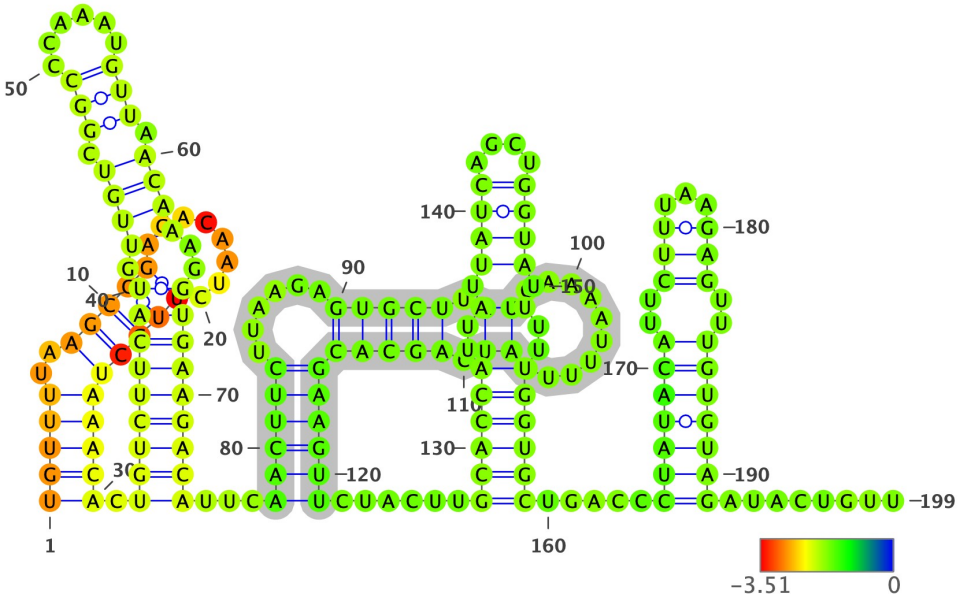
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 73 from nt 3651 to 3694 (nt 78 to 121)

```
5'-AACTTCTTAAGAGTGCTTATGAAAATTTTAAUCAGCACGAAGUU-3'
5'-((((((......((((((.((..........)).)))))))))))-3'
Motif MFE = -7.6; z-score = -1.56; ED = 4.36
```



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 3574 to 3772 (motif highlighted in silver):

```
5'-UGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCA
GCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUU-3
5'-(((((..(((((........)))))))))).(((((((((.((((.(((......))).)))).))))))))))...((((((......((((((.((..........)).)
))))))))))......((((((..(.((((....)))).).))))))).....(((((((..(((...))))..)))))))........-3'
MFE = -49.4; z-score = -2.91; ED = 14.65
```

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(+)

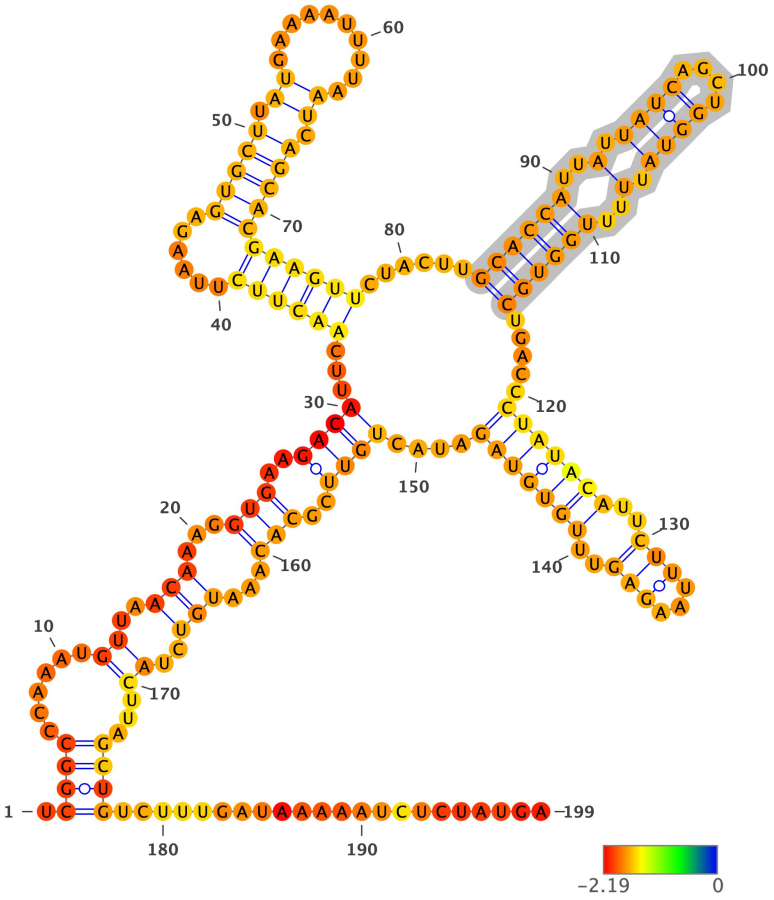
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 74 from nt 3701 to 3732 (nt 84 to 115)

```
5'-GCACCATTATTATCAGCTGGUATUTTUGGUGC-3'
5'-((((((..(.((((....)))))..)..)))))-3'
Motif MFE = -11.2; z-score = -3.88; 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 = -1.03; 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(+)

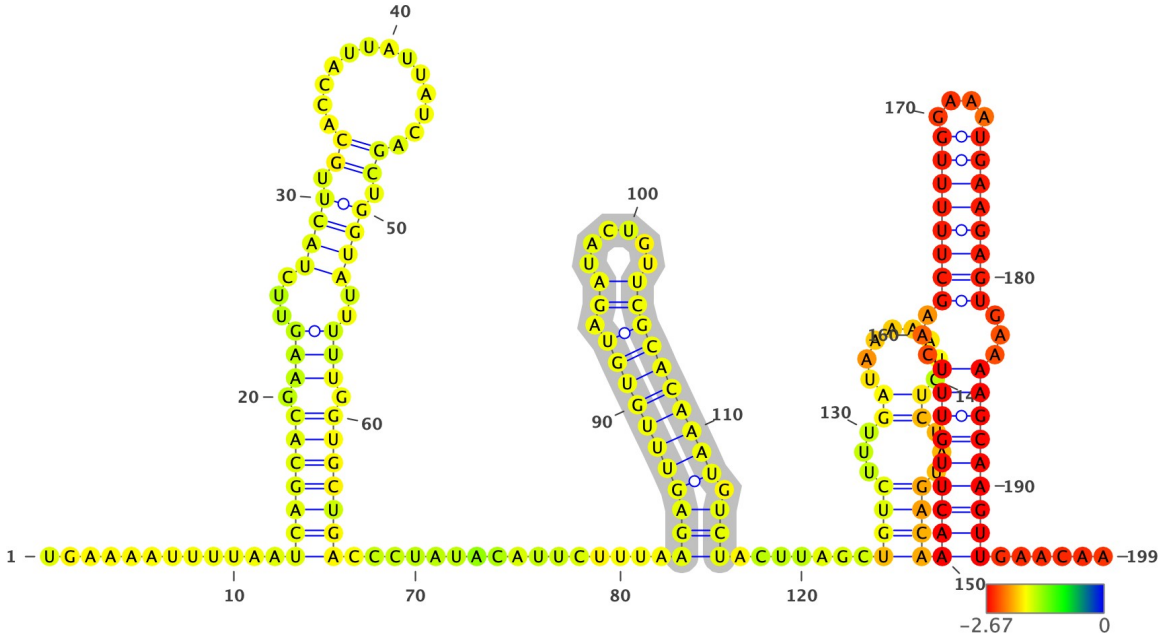
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 75 from nt 3752 to 3785 (nt 83 to 116)

```
5'-AGAGTTTGTGTAGATACTGTUCGCACAAAUGUCU-3'
5'-((((((((((.((.....)))))))))).)))-3'
Motif MFE = -8.7; z-score = -2.49; 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 3670 to 3868 (motif highlighted in silver):

```
5'-UGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAA
UGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAA-3
5'-............(((((((.(((...((((.((............)).)))))..)))).)))))).............((((((((((.((......)))))))))
).))).......((((...((........))...))))((((((((((...(((((((((....)))))))))...))))))))))......-3'
MFE = -43.7; z-score = -2.69; ED = 27.76
```

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(+)

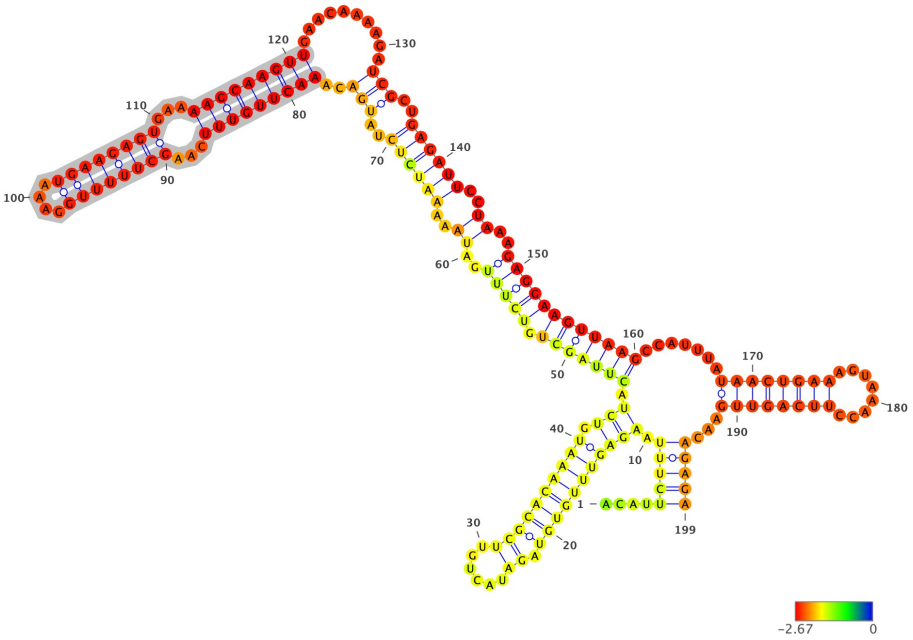
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 76 from nt 3819 to 3862 (nt 78 to 121)

```
5'-AACTTGTTTCAAGCTTTTTGGAAAUGAAGAGUGAAAAGCAAGUU-3'
5'-((((((((((...((((((((....))))))))...)))))))))-3'
Motif MFE = -13.1; z-score = -4.24; 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 = -3.36; 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(+)

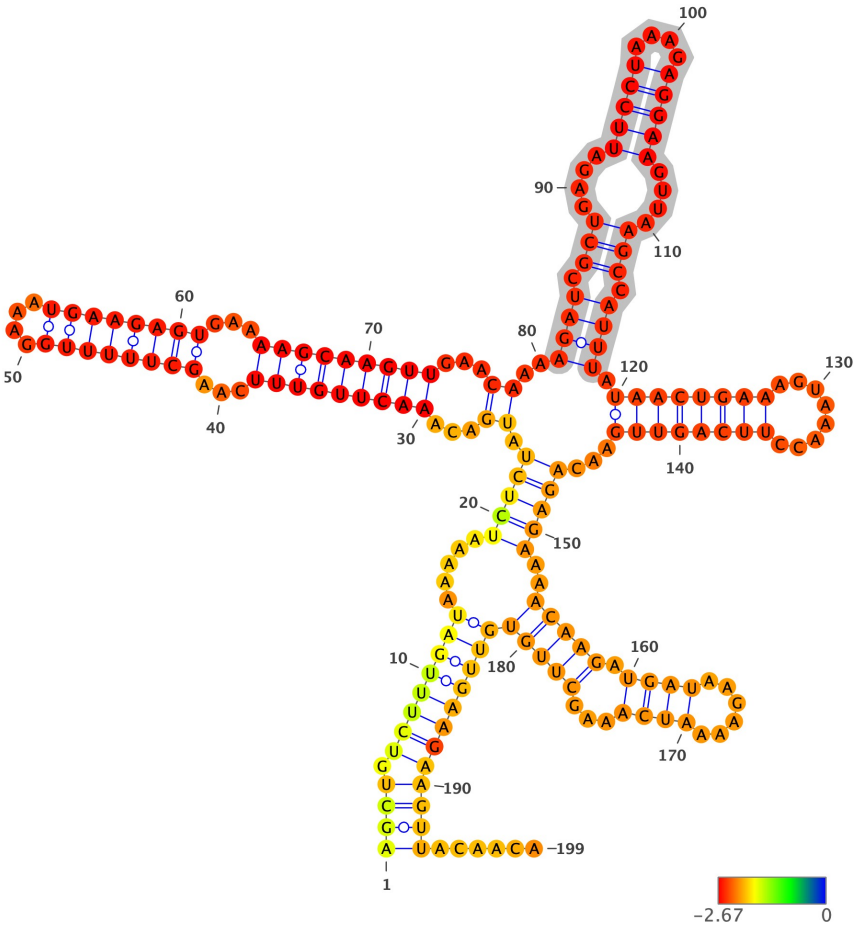
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 77 from nt 3870 to 3907 (nt 81 to 118)

```
5'-AGATCGCTGAGATTCCTAAAGAGGAAGTTAAGCCAUUU-3'
5'-((((.(((....(((((....))))).....))).))))-3'
Motif MFE = -8.8; z-score = -2.16; ED = 3.01
```



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 3790 to 3988 (motif highlighted in silver):

```
5'-AGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAA
GCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACA-3
5'-((((.((((((((.....(((((.((...((((((((((...((((((((....))))))))...))))))))))...)).((((.(((....(((((....))))).....)
)).)))).((((((((.........))))))))...)))))..(((((.((((......))))...))))))))))))))))).......-3'
MFE = -45.2; z-score = -3.72; ED = 13.37
```

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(+)

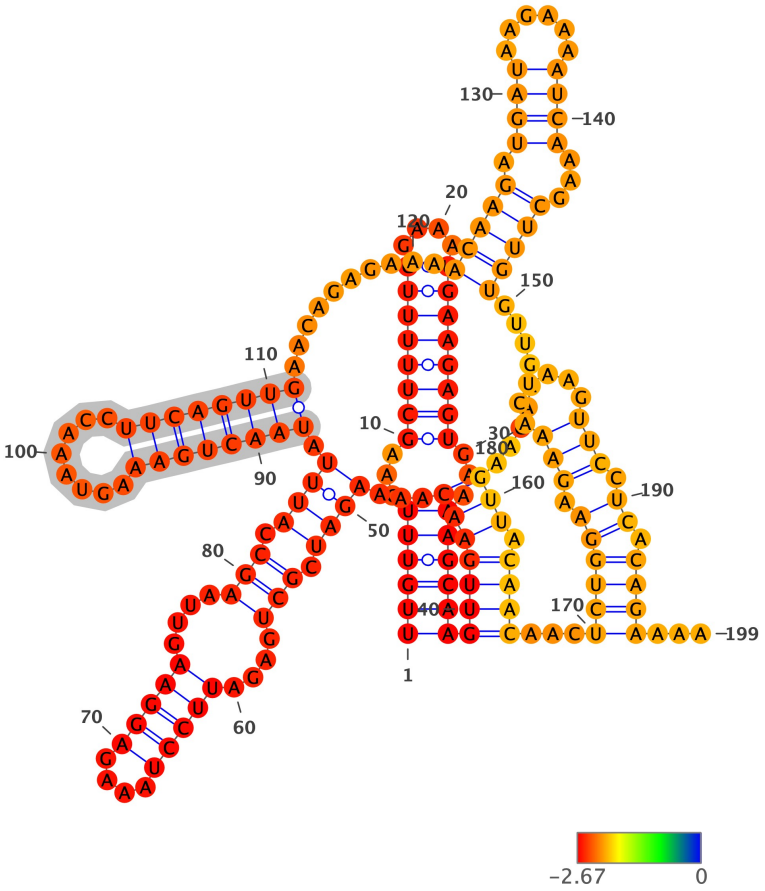
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 78 from nt 3909 to 3932 (nt 88 to 111)

```
5'-TAACTGAAAGTAAACCUUCAGUUG-3'
5'-((((((((........))))))))-3'
Motif MFE = -6.1; z-score = -3.46; 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 3822 to 4020 (motif highlighted in silver):

```
5'-UUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUG
AACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAA-3
5'-((((((...((((((((....))))))))...))))))(((((((...((((.(((....(((((....)))))....))).)))).((((((((........))))))))
..........(((((.((((......))))...)))))..........))).))))...((((((.(((......))).)).))))...-3'
MFE = -40.6; z-score = -3.39; ED = 27.97
```

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(+)

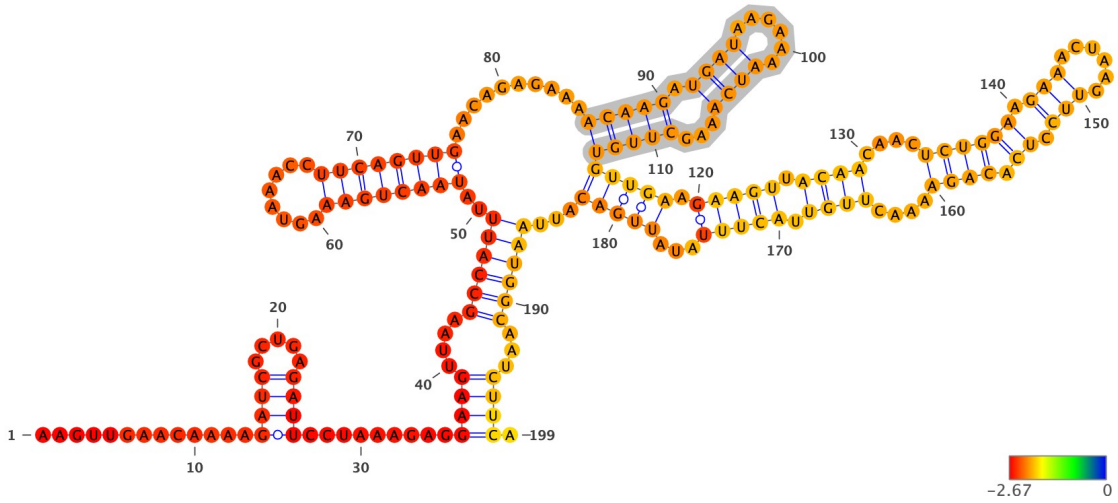
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 79 from nt 3943 to 3970 (nt 86 to 113)

```
5'-ACAAGATGATAAGAAAAUCAAAGCUUGU-3'
5'-(((((.((((......))))...)))))-3'
Motif MFE = -4.5; z-score = -4.36; 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 3858 to 4056 (motif highlighted in silver):

```
5'-AAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUU
GUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCA-3
5'-.............((((.....)))).........((((....((((((..((((((((.........))))))))..........(((((.((((......))))...)))
))(((((.(((((.((((....((((((.(((......))).)).))))....)))).)))))...)))))...))))))...)))).-3'
MFE = -37.5; z-score = -1.92; ED = 32.82
```

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, 266-13468(+)

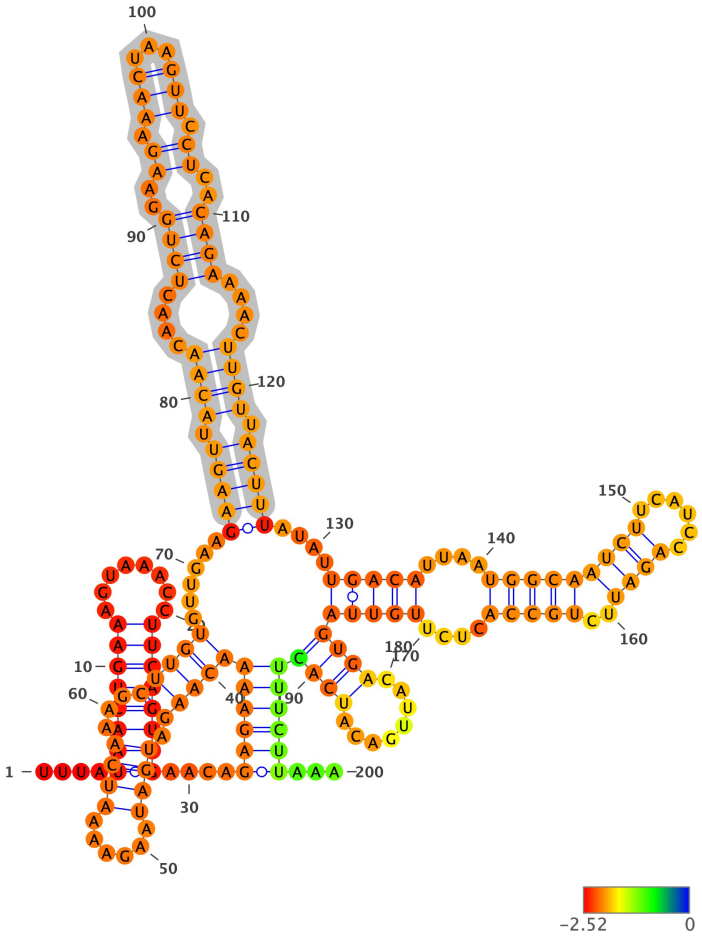
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 3978 to 4030 (nt 74 to 126)

```
5'-AAGTTACAACAACTCTGGAAGAAACTAAGUUCCUCACAGAAAACUUGUTACUU-3'
5'-((((.((((....((((..((.(((...))).))..)))).....)))).))))-3'
Motif MFE = -10.0; z-score = -2.91; 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 = -2.91; ED = 25.76
```

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(+)

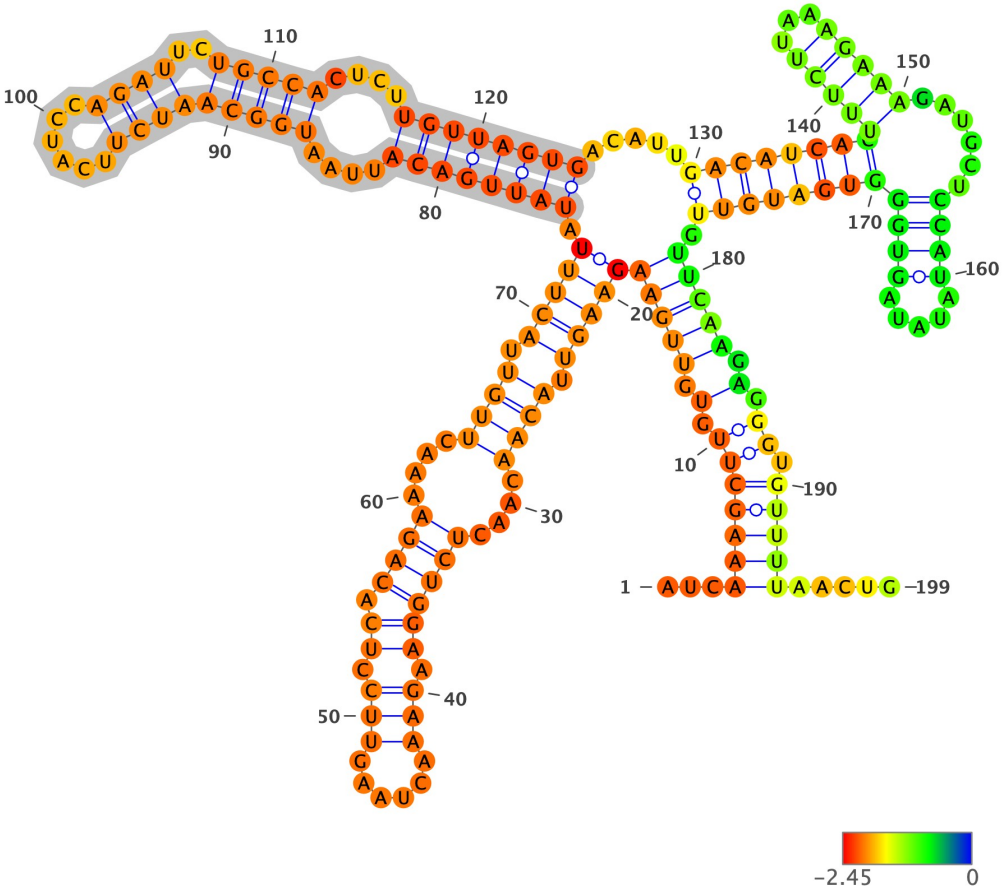
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 81 from nt 4033 to 4082 (nt 75 to 124)

```
5'-TATTGACATTAATGGCAATCTTCATCCAGAUTCUGCCACTCTUGUUAGUG-3'
5'-((((((((....((((((((((......))))..)))))....))))))))-3'
Motif MFE = -13.4; z-score = -3.45; ED = 2.79
```



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 3959 to 4157 (motif highlighted in silver):

```
5'-AUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCC
ACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUG-3
5'-...(((((((.(.((((((((((.((((....((((((.(((......))).)).))))....)))).))))).((((((((....((((((((((......))))..))))
)....))))))))).....((((((((((((...)))))......((((.....)))))))))))).))))).).)).)))))).....-3'
MFE = -44.4; z-score = -1.62; ED = 32.06
```

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(+)

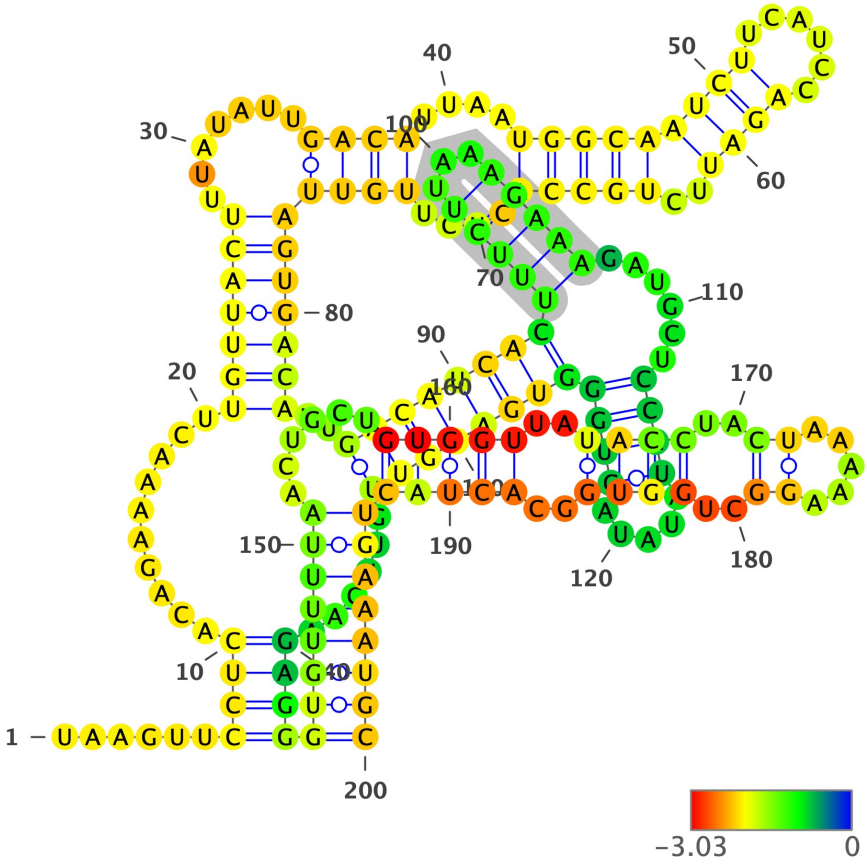
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 82 from nt 4096 to 4108 (nt 94 to 106)

```
5'-TTTCTTAAAGAAA-3'
5'-(((((...)))))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 2.26
```



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 4003 to 4202 (motif highlighted in silver):

```
5'-UAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGC
UCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGC-3
5'-......((((..........(((((((.......((((....((((((((((......))))..)))))....)))))))))))..((((((((((((...)))))).....
.((((.....))))))))))))......))))((((((((.....(((((..((((..((.....))..))))..)))))))))))))-3'
MFE = -42.3; z-score = -0.46; ED = 38.28
```

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(+)

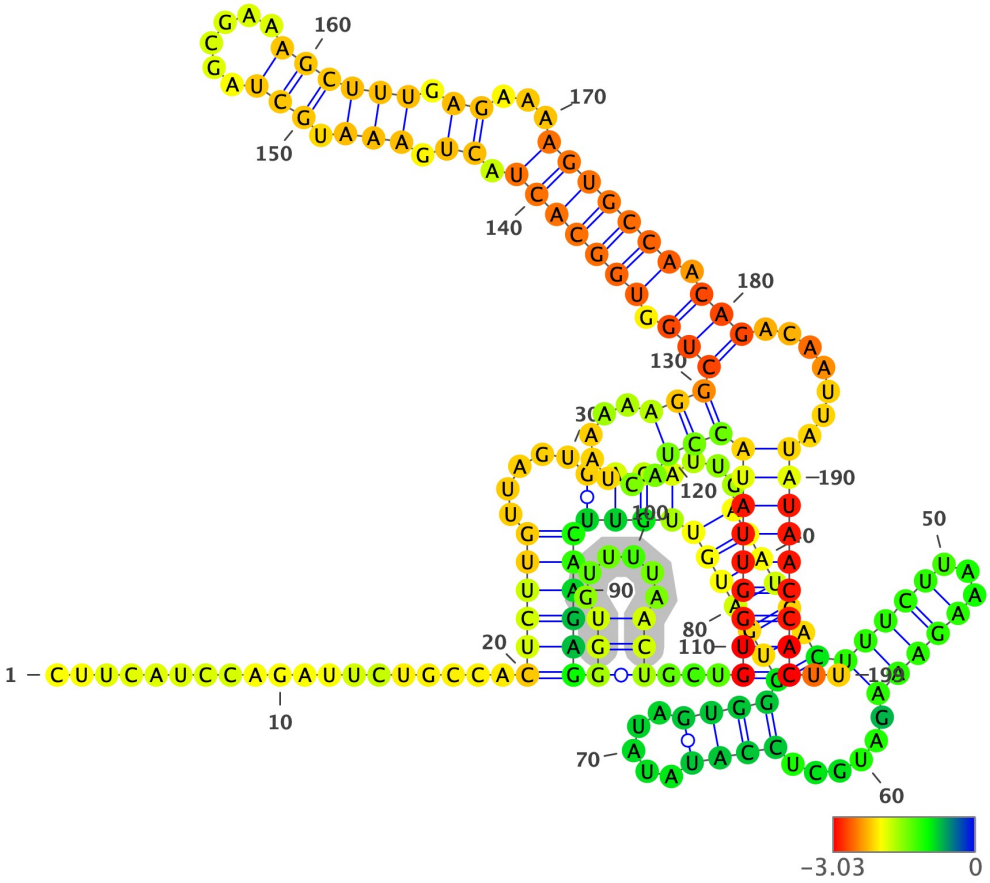
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 83 from nt 4146 to 4155 (nt 95 to 104)

```
5'-GTGTTTTAAC-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.26
```



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 4052 to 4250 (motif highlighted in silver):

```
5'-CUUCAUCCAGAUUCUGCCACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUG
GUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUU-3
5'-...................((((((.....((((...(((((((((((((...)))))).....((((.....)))))))))))))))))))))(((......)))...(((
(((((((((.......)))(((.(((((((.((.(((.(((......))))))).))...)))))))).)))).......)))))))))..-3'
MFE = -49.4; z-score = -2.96; ED = 22.54
```

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, 266-13468(+)

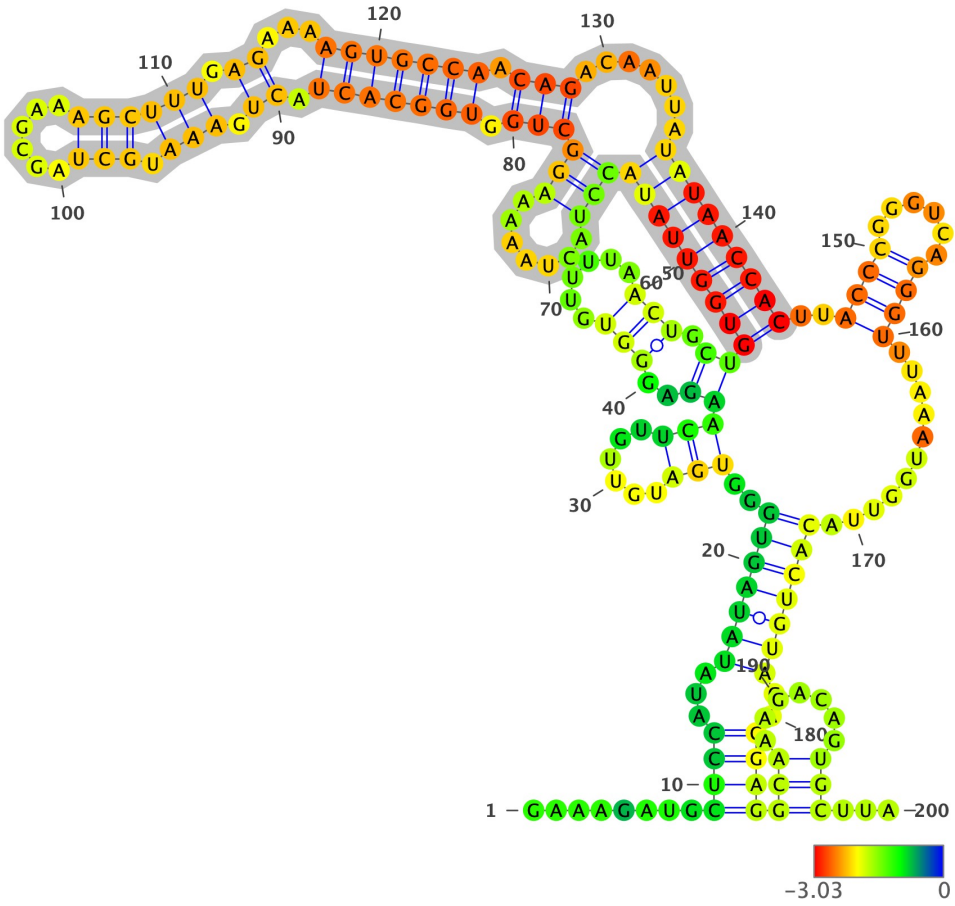
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4160 to 4248 (nt 56 to 144)

```
5'-GTGGTTATACCTACTAAAAAGGCTGGTGGCACTACTGAAATGCTAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAATTATAUAACCAC-3'
5'-(((((((...............(((.(((((((.((.(((.(((......))))))).))...)))))))).)))........)))))))-3'
Motif MFE = -28.9; z-score = -4.73; 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 4105 to 4304 (motif highlighted in silver):

```
5'-GAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUU
GAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUA-3
5'-........((((...(((((((..(((......)))((..(((......))).))((((((((((((.......)))(((.(((((((.((.(((.(((......))))))
.))...)))))))).)))........))))))))..((((......))))...........)))))))..))))(((.......)))...-3'
MFE = -52.3; z-score = -2.19; ED = 22.21
```

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(+)

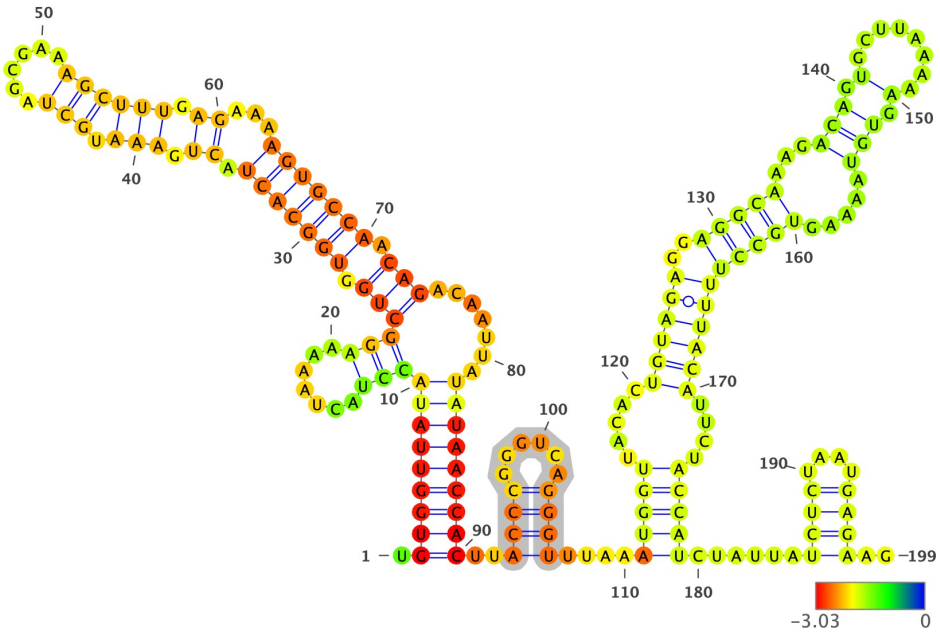
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 85 from nt 4251 to 4264 (nt 93 to 106)

```
5'-ACCCGGGTCAGGGU-3'
5'-(((........)))-3'
Motif MFE = -5.2; z-score = -2.73; ED = 0.42
```



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 4159 to 4357 (motif highlighted in silver):

```
5'-UGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAA
UGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAG-3
5'-.(((((((((((.......)))(((.(((((((.((.(((.(((......)))))).))...)))))))).)))........))))))))..((((......))))....(
((((.....((((((..(((((...(((.(........).)))).....)))))))))))....)))))......((((....))))..-3'
MFE = -56.9; z-score = -3.52; 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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

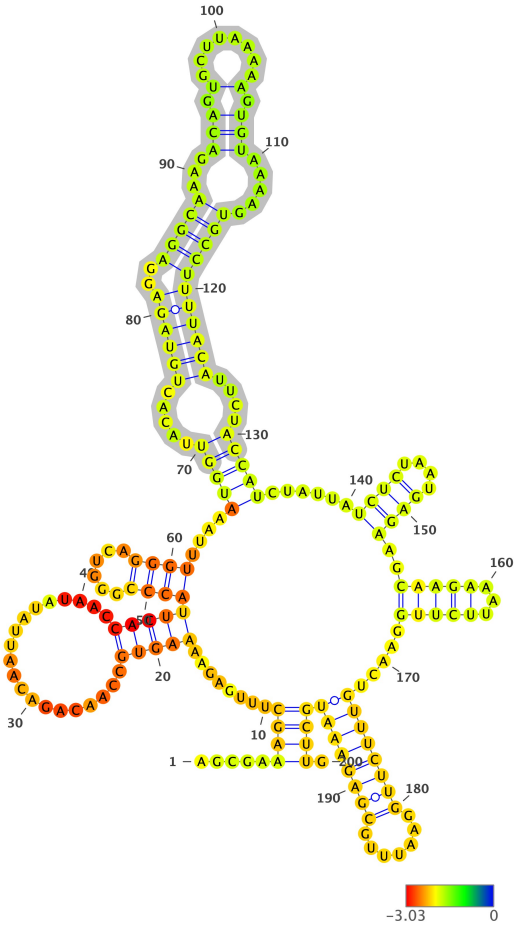
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4272 to 4334 (nt 69 to 131)

```
5'-GTTACACTGTAGAGGAGGCAAAGACAGTGCTTAAAAAGUGUAAAAGUGCCUUUTACATTCTAC-3'
5'-((.....(((.((..(((((...(((.(........).)))).....)))))))).)))....))-3'
Motif MFE = -13.5; z-score = -1.59; ED = 17.5
```



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 4204 to 4403 (motif highlighted in silver):

```
5'-AGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAA
AAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUG-3
5'-.....((((........(((((.....................)))))((((......))))....(((((.....((((((..(((((...(((.(........).)))..
...)))))))))))....)))))......((((....))))..(((((...)))))).....((((((((.......))))))))))).-3'
MFE = -43.2; z-score = -1.48; ED = 34.62
```

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(+)

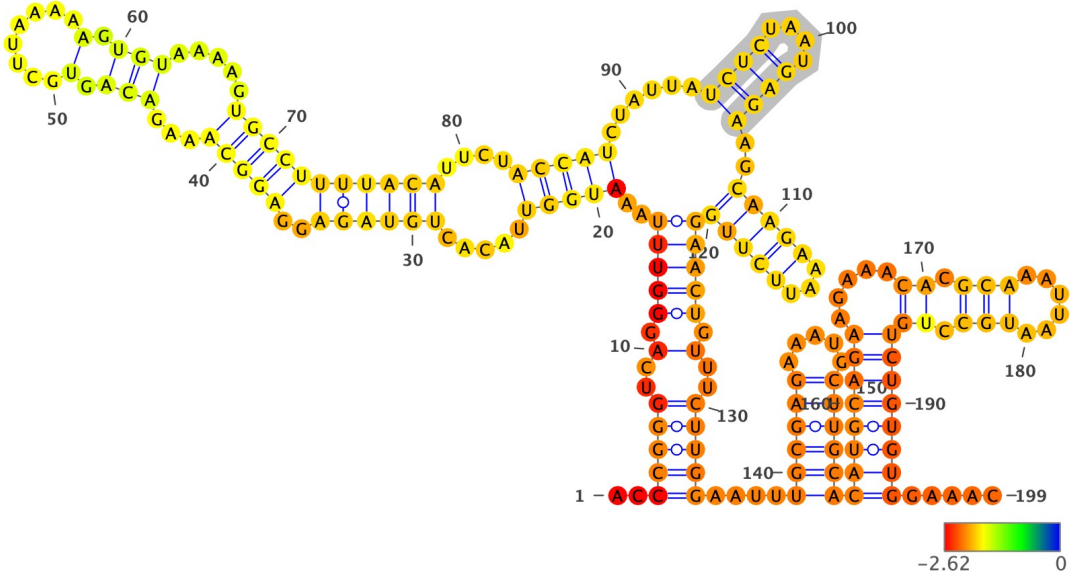
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 87 from nt 4344 to 4355 (nt 94 to 105)

```
5'-TCTCTAATGAGA-3'
5'-((((....))))-3'
Motif MFE = -2.9; z-score = -9.31; 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 4251 to 4449 (motif highlighted in silver):

```
5'-ACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAG
AAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAAC-3
5'-..((((((..(.((((((..((((((.....((((((..((((((...(((.(........).))).....))))))))))))....))))))......((((....)))))..((((
(...))))))))))..)..))))))....((((((.....))))))(((((((((.....((.(((......))).))))))))))).....-3'
MFE = -50.7; z-score = -2.27; ED = 51.41
```

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(+)

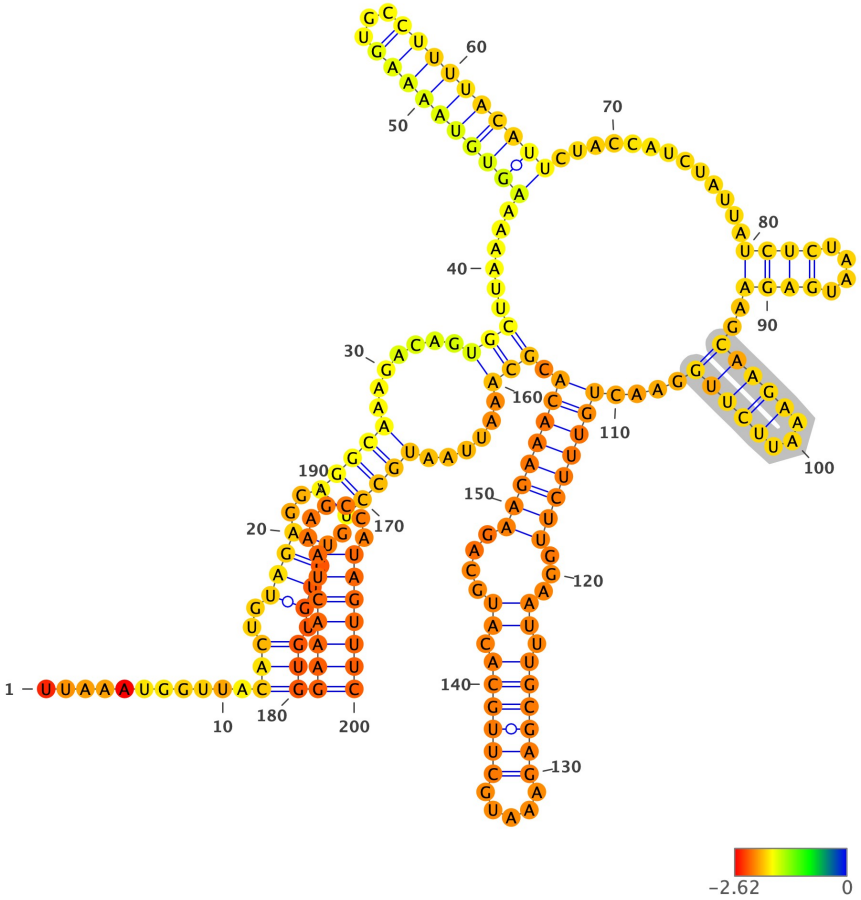
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4358 to 4370 (nt 94 to 106)

```
5'-CAAGAAATUCUTG-3'
5'-(.(((...))).)-3'
Motif MFE = -1.6; z-score = -3.03; ED = 0.92
```



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 4265 to 4464 (motif highlighted in silver):

```
5'-UUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACU
GUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUC-3
5'-...........(((..((((..(((((.......(((......((((((((((...)))))))))).............((((....)))))..((((((...))))))....(
(((((((...((.((((((.....)))))).))....)))))))).)))......)))))).))))(((((((.....)))))))-3'
MFE = -48.9; z-score = -2.66; ED = 42.24
```

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, 266-13468(+)

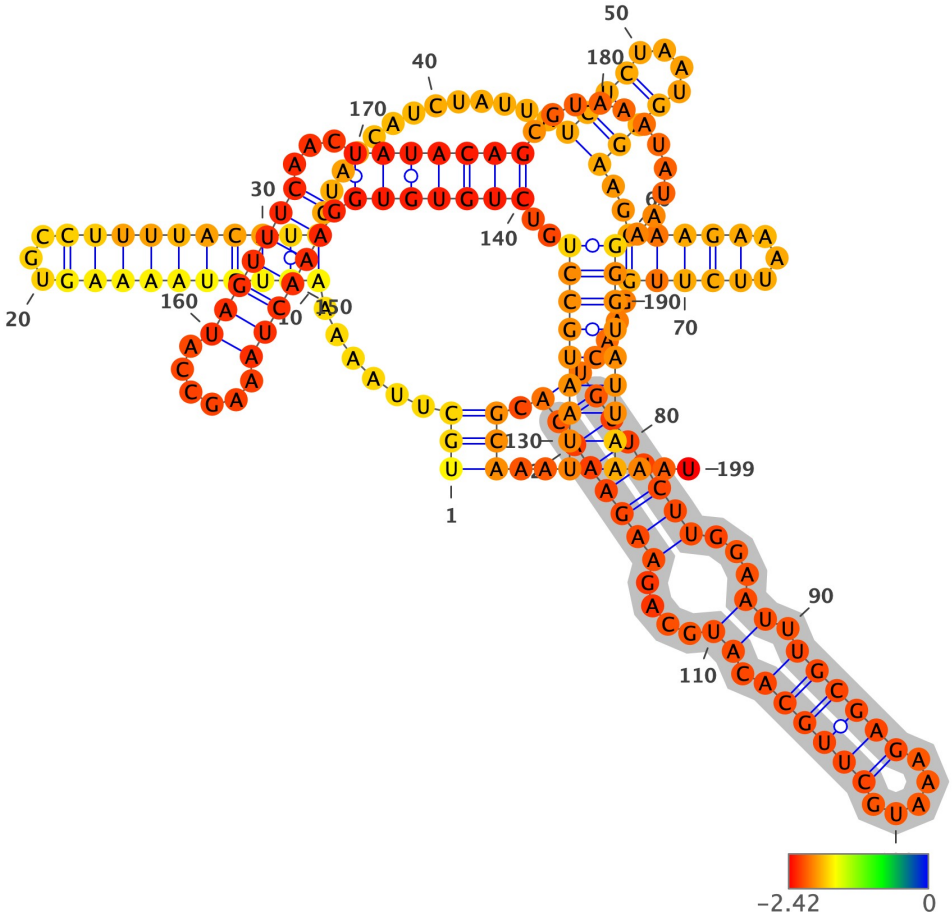
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4376 to 4419 (nt 78 to 121)

```
5'-GTTTCTTGGAATTTGCGAGAAATGCUUGCACAUGCAGAAGAAAC-3'
5'-(.....(...((.((((((.....)))))).))....).....)-3'
Motif MFE = -12.4; z-score = -2.47; 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 4299 to 4497 (motif highlighted in silver):

```
5'-UGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUG
CAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAU-3
5'-(((.....((((((((((...))))))))))).............((((....)))))..(((((...)))))....(((((((...((.((((((.....)))))).)).
...))))))))).)))..(((((((((..(((((((((((((.....)))))))...)))))))).....)))))))))...-3'
MFE = -49.7; z-score = -3.74; ED = 10.08
```

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(+)

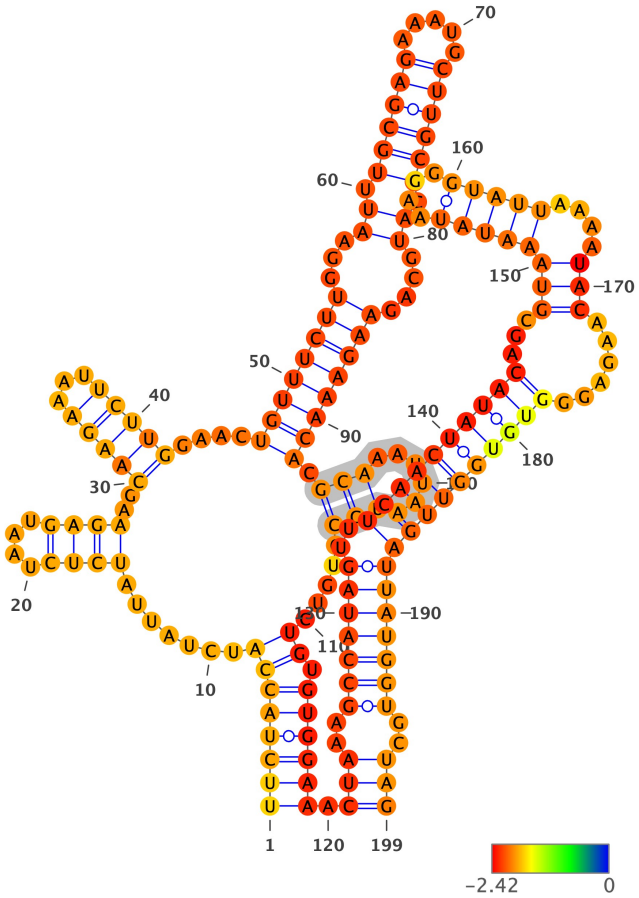
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 90 from nt 4422 to 4433 (nt 94 to 105)

```
5'-GCAAATTAAUGC-3'
5'-(((......)))-3'
Motif MFE = -0.4; z-score = -2.6; 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 4329 to 4527 (motif highlighted in silver):

```
5'-UUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCU
GUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAG-3
5'-((((((((.......((((....))))..(((((...)))))....((((((((...((.((((((.....)))))).))....)))))))).(((......)))).....)
).)))))).((..(((((((..((((((((((...((((((((....)))))....)))......)))))))))))))))))..)))-3'
MFE = -49.1; z-score = -2.25; ED = 38.62
```

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(+)

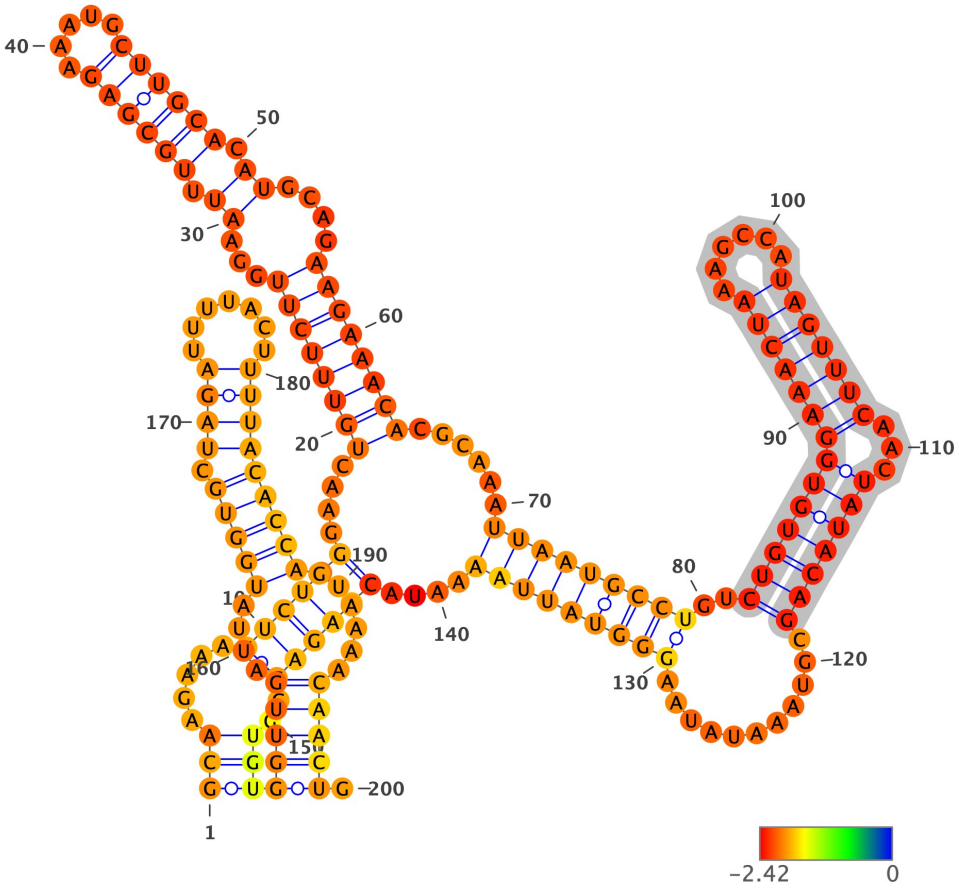
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 91 from nt 4438 to 4474 (nt 82 to 118)

```
5'-CTGTGTGGAAACTAAAGCCAUAGUUUCAACUAUACAG-3'
5'-(((((((((((((.....)))))))...)))))))-3'
Motif MFE = -10.8; z-score = -3.86; 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 4357 to 4556 (motif highlighted in silver):

```
5'-GCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAAC
UAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUG-3
5'-(((.....((((((....((((((((...((.((((((.....)))))).))....))))))))......(((((((((..((((((((((((((.....)))))))...
)))))))...........))))))))....))))))..)))(((((....(((((.((((.......)))))))))......))))).-3'
MFE = -48.5; z-score = -2.36; ED = 23.67
```

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(+)

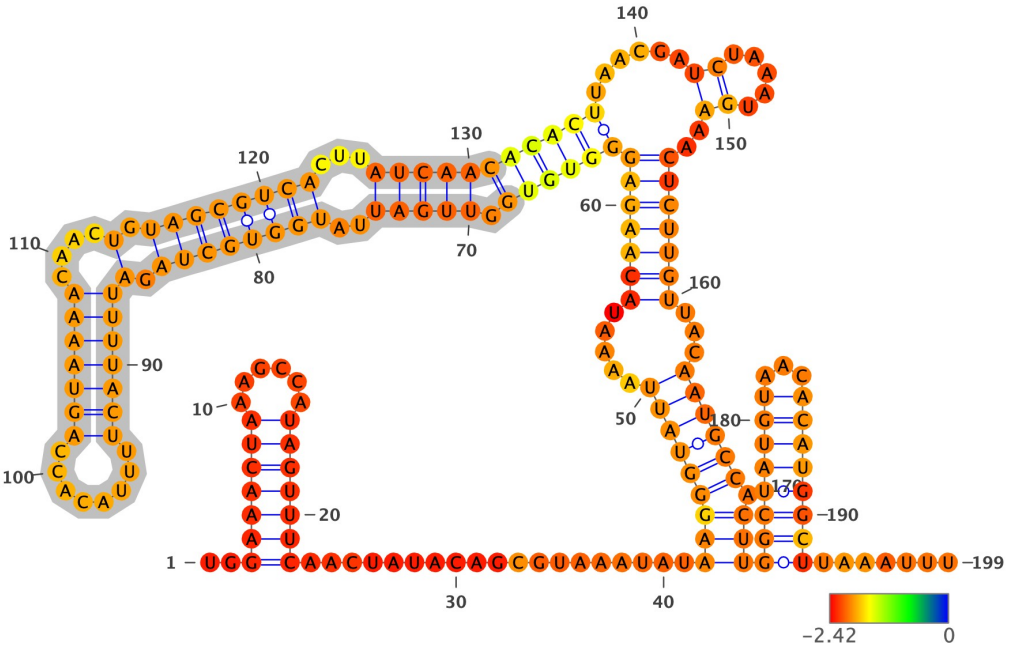
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 92 from nt 4510 to 4573 (nt 68 to 131)

```
5'-GGTTGATTATGGTGCTAGATTTTACTTTTACACCAGUAAAACAACUGUAGCGUCACTTAUCAAC-3'
5'-(.(((((..(((((((((.(((((((((........)))))))))....).)))))))))...)))))-3'
Motif MFE = -14.5; z-score = -2.6; ED = 9.12
```



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 4443 to 4641 (motif highlighted in silver):

```
5'-UGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAA
CUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUU-3
5'-..(((((((......)))))))...................(((((((((.....(((((((((((((.(((((..(((((((((.(((((((((........)))))))))...
.).)))))))))...)))))))))))).....((.....)).)))))))...)))))).)))(((((((((...)))))))))........-3'
MFE = -49.0; z-score = -3.12; ED = 19.52
```

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(+)

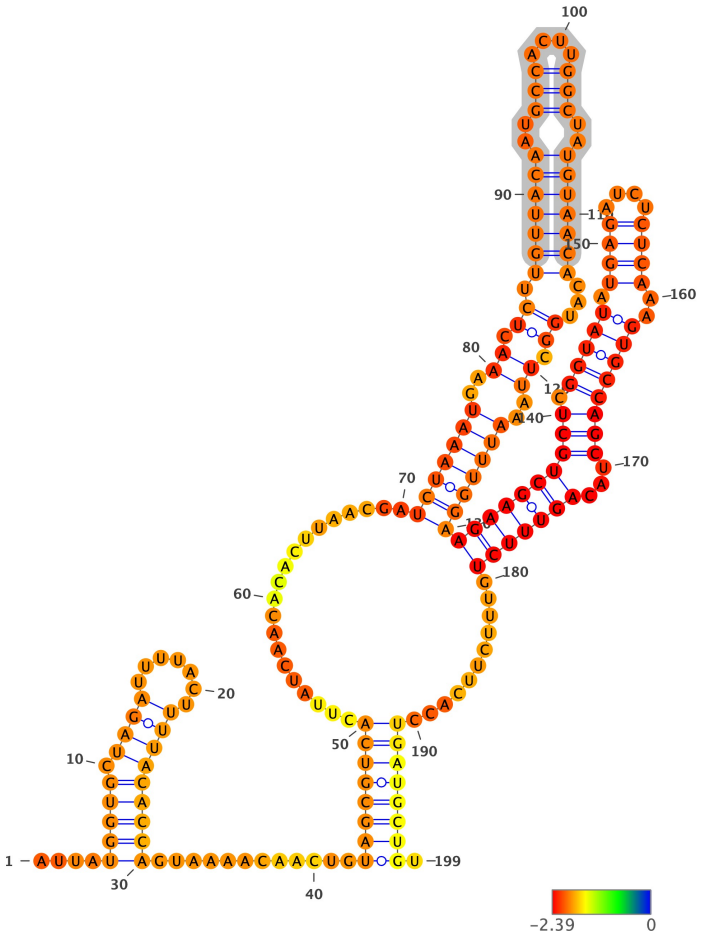
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 93 from nt 4601 to 4626 (nt 87 to 112)

```
5'-GTTACAATGCCACTTGGCTAUGUAAC-3'
5'-((((((..(((....)))..)))))))-3'
Motif MFE = -9.5; z-score = -3.97; 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 = -2.53; 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(+)

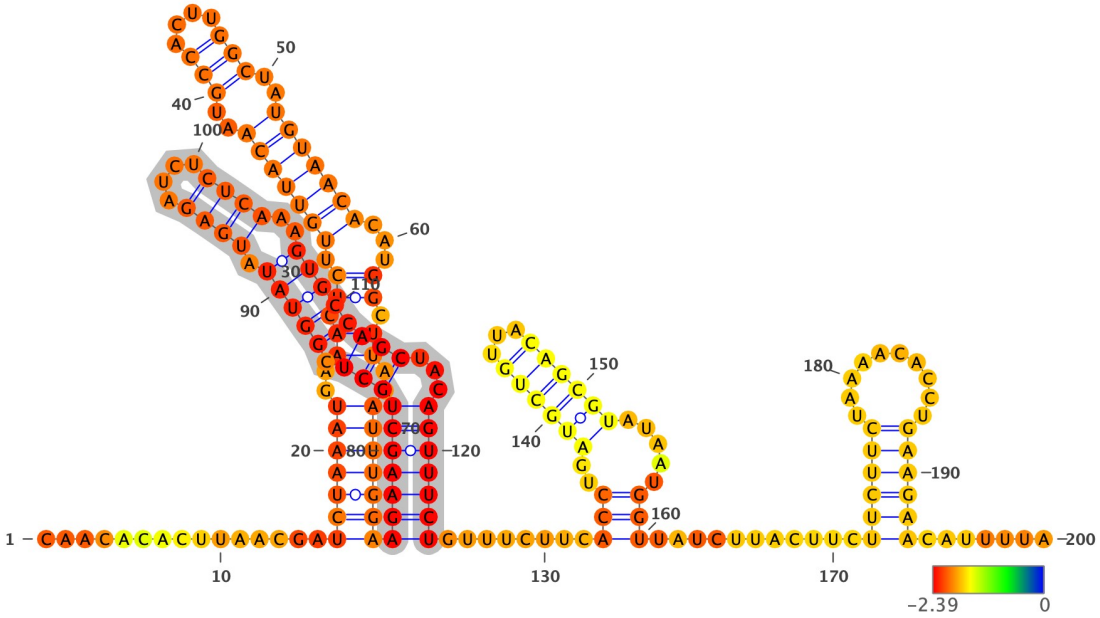
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 94 from nt 4645 to 4693 (nt 76 to 124)

```
5'-AGAAGCTGCTCGGTATATGAGATCTCUCAAAGUGCCAGCTACAGUUUCU-3'
5'-((((((((((.(((((.((((....))))..))))))))...)))))))-3'
Motif MFE = -17.2; z-score = -2.72; 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 = -2.43; ED = 22.08
```

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(+)

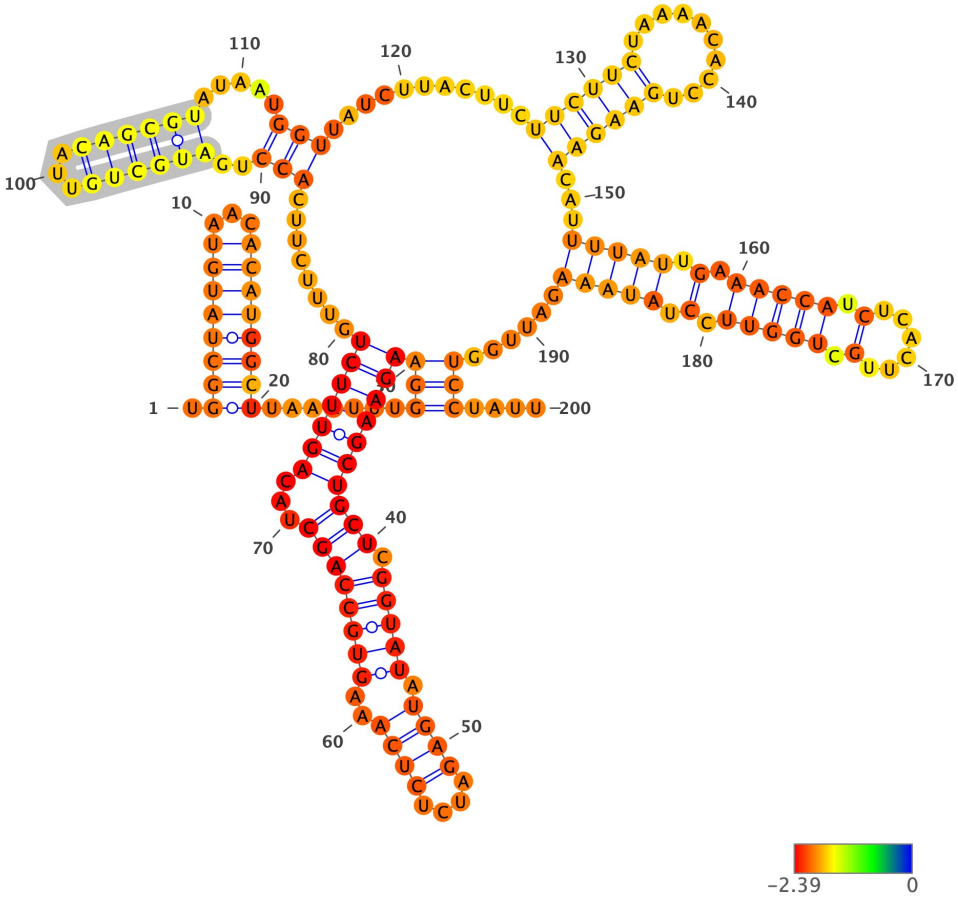
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 95 from nt 4707 to 4721 (nt 93 to 107)

```
5'-ATGCTGTTACAGCGU-3'
5'-((((((...))))))-3'
Motif MFE = -3.0; z-score = -2.18; 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 4615 to 4814 (motif highlighted in silver):

```
5'-UGGCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAA
UGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUU-3
5'-.((((((((...))))))))).......((((((((((((.(((((.((((....)))).)))))))))...)))))))........(((..((((((...))))))....
.))).........((((((.........))))))...(((((.(.(((((.(......).)))))).).)))))......)))....-3'
MFE = -45.5; z-score = -1.76; ED = 25.96
```

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(+)

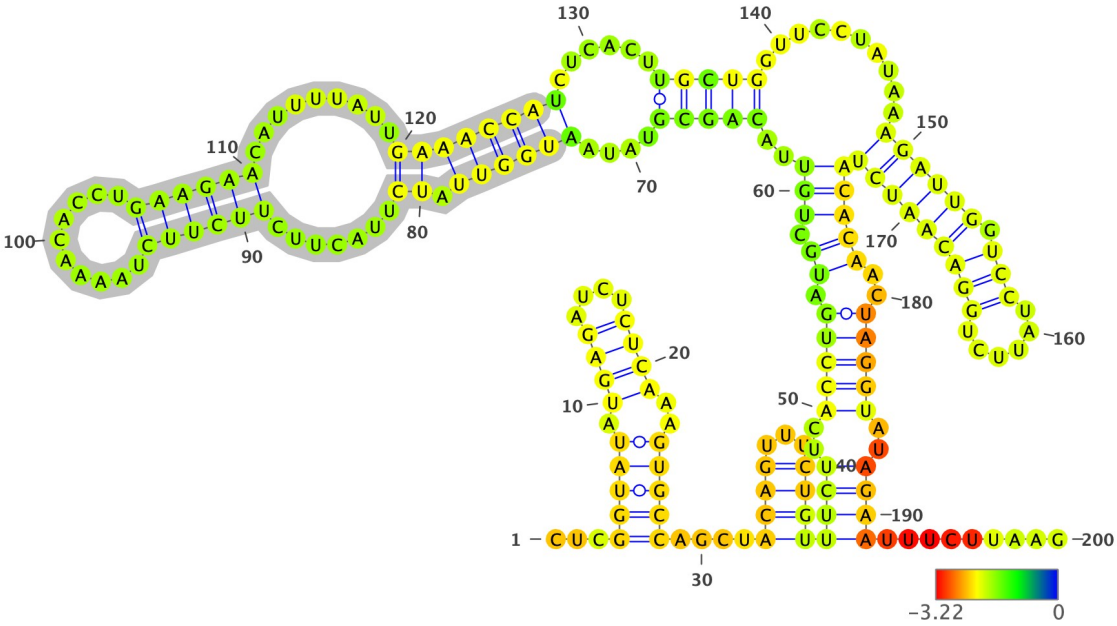
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 96 from nt 4726 to 4778 (nt 74 to 126)

```
5'-TGGTTATCTTACTTCTTCTTCTAAAACACCTGAAGAACATTTTATTGAAACCA-3'
5'-(((((.((.......((((((..........))))))........)))))))-3'
Motif MFE = -7.5; z-score = -2.23; 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 4653 to 4852 (motif highlighted in silver):

```
5'-CUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAAC
AUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAG-3
5'-...(((((.((((....))))..)))))....((((...))))((((..(((((.((.(((..(((((....((((((.((.......((((((..........)))))).
........))))))))......)))))..........((((((.(((......)))))))))))))))..)))))..))))..........-3'
MFE = -41.5; z-score = -2.4; 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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

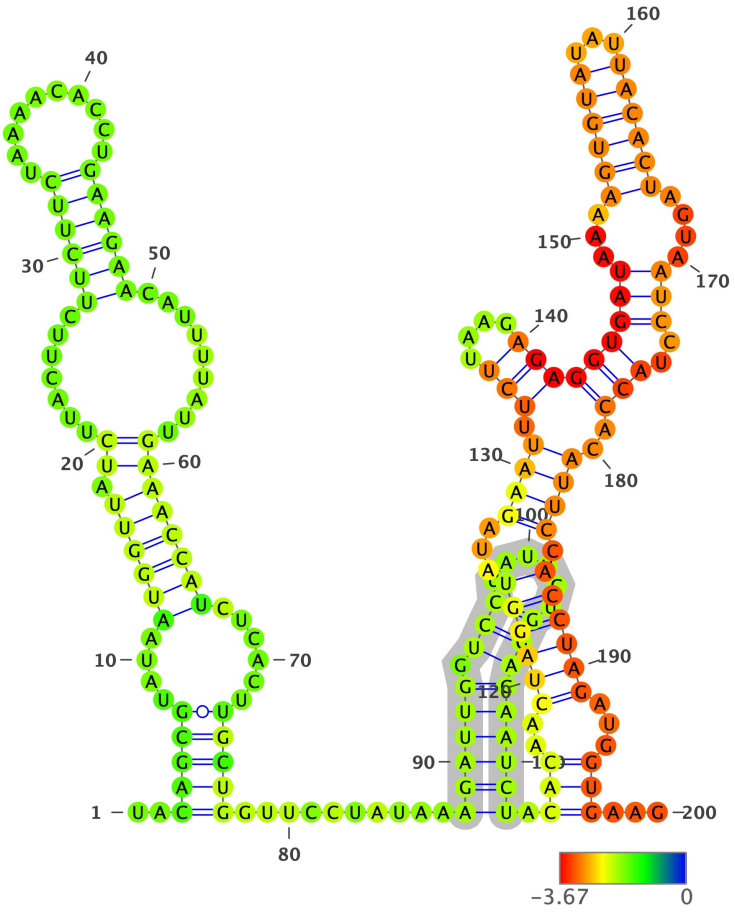
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4801 to 4825 (nt 88 to 112)

```
5'-AGATTGGTCCTATTCTGGACAAUCU-3'
5'-((((((.(((......)))))))))-3'
Motif MFE = -8.9; z-score = -3.61; 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 = -1.92; ED = 36.12
```

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(+)

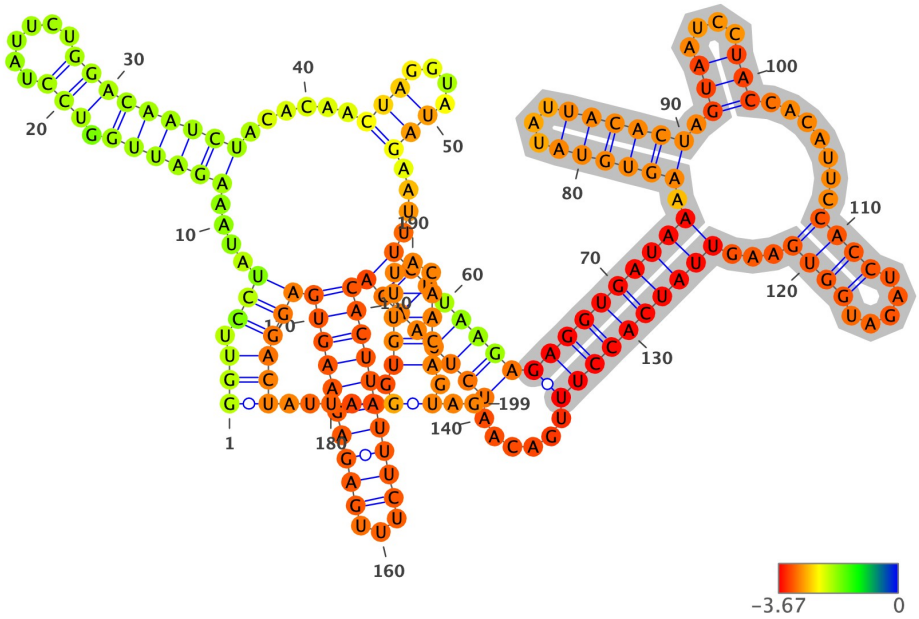
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 98 from nt 4854 to 4923 (nt 65 to 134)

```
5'-GAGGTGATAAAAGTGTATATUACACUAGTAATCCUACCACATTCCACCTAGATGGUGAAGUUAUCACCUU-3'
5'-((((((((((.((((((...)))))).(((....))).......((((.....))))...))))))))))-3'
Motif MFE = -20.2; z-score = -3.45; ED = 8.37
```



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 4790 to 4988 (motif highlighted in silver):

```
5'-GGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCAC
CUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAG-3
5'-(((.(((....((((((.(((......)))))))))......(((....)))....((((((((((((((((((.((((((...)))))).(((....)))).......(((
(.....))))...))))))))))......))))))))((((((((((...)))))))))))))))))).....(.((((...)))).)..-3'
MFE = -54.2; z-score = -3.48; ED = 18.93
```

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(+)

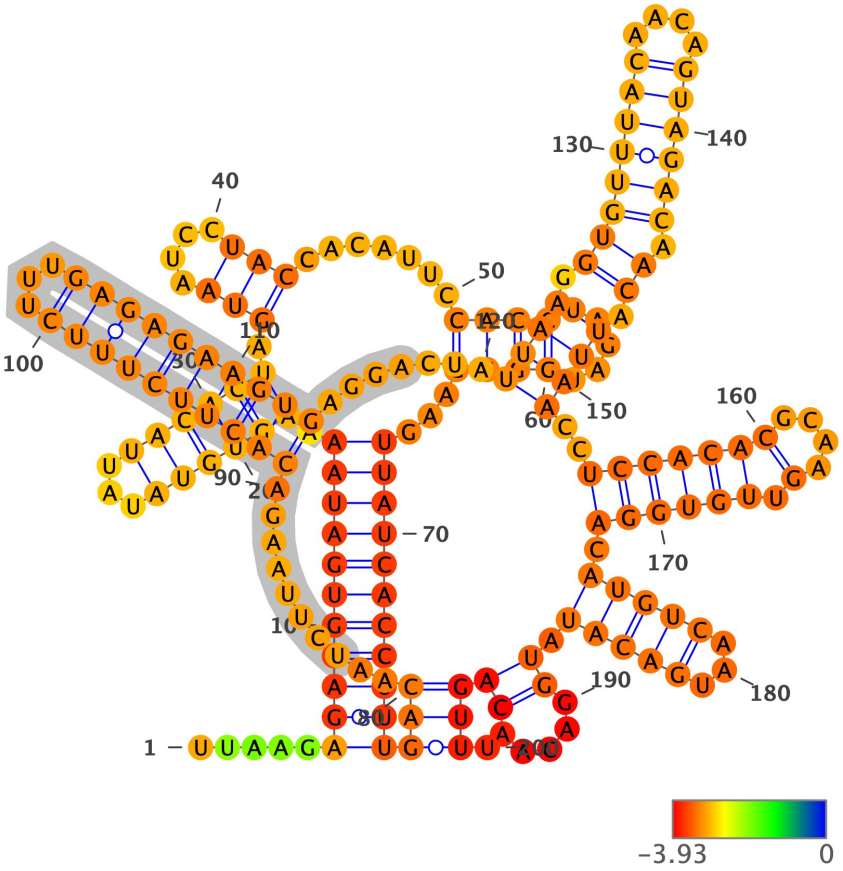
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 99 from nt 4930 to 4964 (nt 83 to 117)

```
5'-TCTTAAGACACTTCTTTCTTTGAGAGAAGUGAGGA-3'
5'-(((.....((((((((((...)))))))))).)))-3'
Motif MFE = -11.8; z-score = -3.56; ED = 2.24
```



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 4848 to 5047 (motif highlighted in silver):

```
5'-UUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAG
UGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUU-3
5'-.....(((((((((((.((((((...)))))).(((....)))).......((((.....))))...)))))))))))(((..........((((((((((...))))))))
)).......((((.((((((((....)))))).)).)))).((((((((....).)))))).(((((...))))).((.....))))).-3'
MFE = -50.2; z-score = -3.59; ED = 27.25
```

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(+)

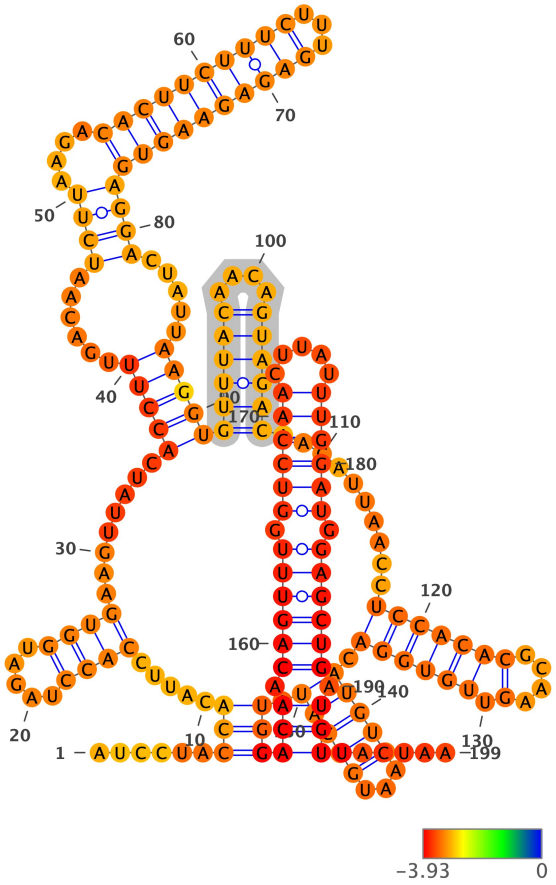
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 100 from nt 4975 to 4990 (nt 92 to 107)

```
5'-GTTTACAACAGUAGAC-3'
5'-((((((....))))))-3'
Motif MFE = -3.5; z-score = -4.35; 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 4884 to 5082 (motif highlighted in silver):

```
5'-AUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACA
UUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAA-3
5'-......(((.....((((.....))))........(((((......((((....((((((((((...)))))))))))))).....)))))((((((....))))))....
......(((((((....).)))))).(((((...))))).)))(((.((((((.((((((.....)))))).)))))).)))......-3'
MFE = -57.0; z-score = -3.76; ED = 32.95
```

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(+)

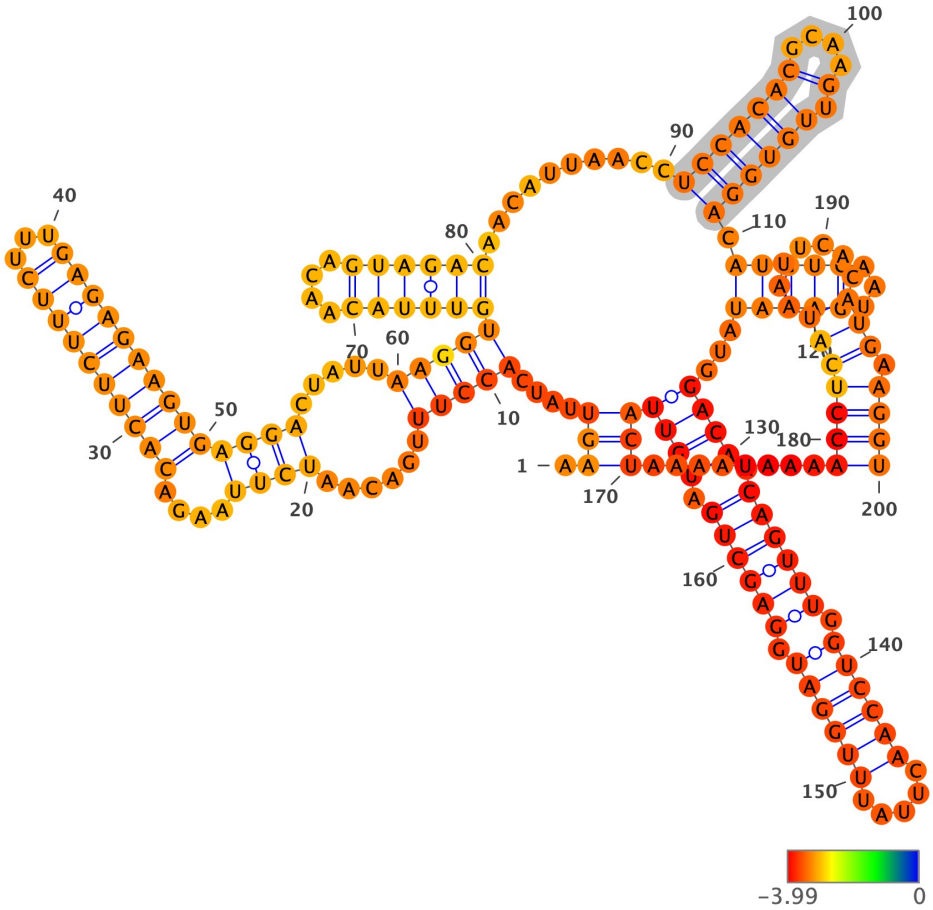
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 101 from nt 5001 to 5019 (nt 91 to 109)

```
5'-TCCACACGCAAGTUGUGGA-3'
5'-(((((((....).))))))-3'
Motif MFE = -6.7; z-score = -3.31; 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 = -3.78; 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(+)

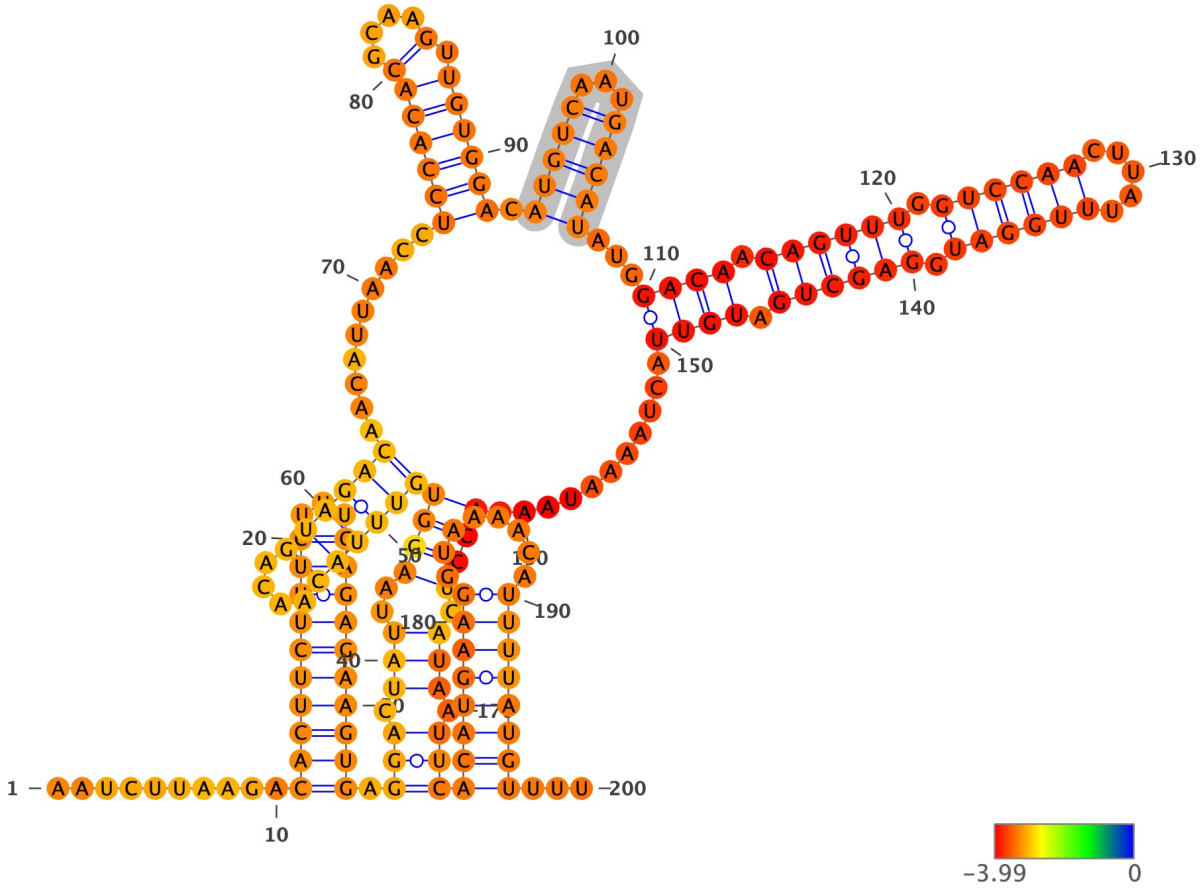
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 102 from nt 5021 to 5033 (nt 94 to 106)

```
5'-ATGTCAATGACAU-3'
5'-(((((...)))))-3'
Motif MFE = -1.9; z-score = -9.28; ED = 0.88
```



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 4928 to 5127 (motif highlighted in silver):

```
5'-AAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGA
CAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUU-3
5'-..........((((((((((...)))))))))).(((.(((..((((((((((....))))))).........(((((((....).)))))).(((((...)))))...((
((.((((((.((((((.....)))))).)))))).)))).........))))).))).)))((((((((........))))))))...-3'
MFE = -55.1; z-score = -4.66; ED = 30.95
```

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(+)

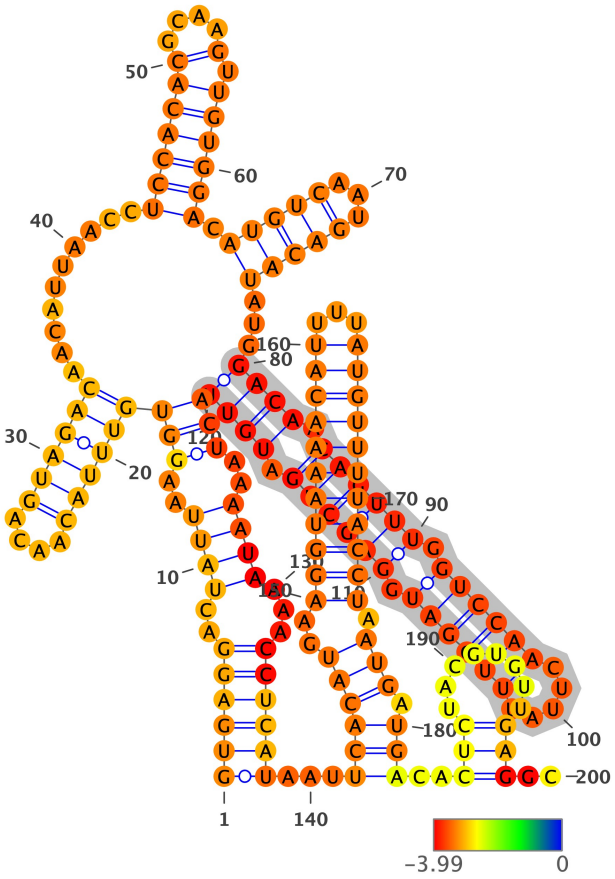
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 103 from nt 5037 to 5077 (nt 80 to 120)

```
5'-GACAACAGTTTGGTCCAACTTATUUGGAUGGAGCUGAUGUU-3'
5'-((((.((((((.((((((.....)))))).)))))).))))-3'
Motif MFE = -17.8; z-score = -4.79; 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 = -4.77; 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(+)

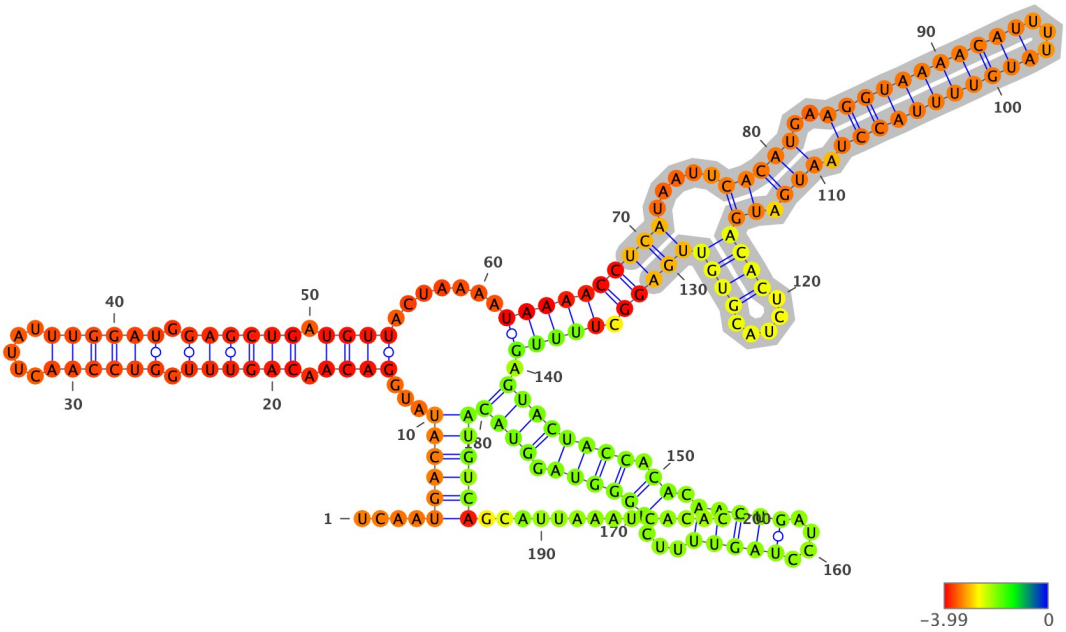
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 104 from nt 5092 to 5154 (nt 69 to 131)

```
5'-TCATAATTCACATGAAGGTAAAACATTTTAUGUUUUACCUAAUGAUGACACTCTACGUGUUGA-3'
5'-(((.....((((((..((((((((((...))))))))))).))).))))(((.....)))))))-3'
Motif MFE = -16.6; z-score = -4.13; ED = 5.57
```



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 5024 to 5223 (motif highlighted in silver):

```
5'-UCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAU
GAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACAC-3
5'-....((((((...((((.((((((.((((((.....)))))).)))))).)))).......((((((((((.....((((((..((((((((((...))))))))))..)))))).))
).))(((((.....)))))))))).)))))).(((((((((.((.((((((....))))))...)))))))))).....(((((((((.....)))))))))).....-3'
MFE = -56.6; z-score = -4.25; ED = 11.63
```

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(+)

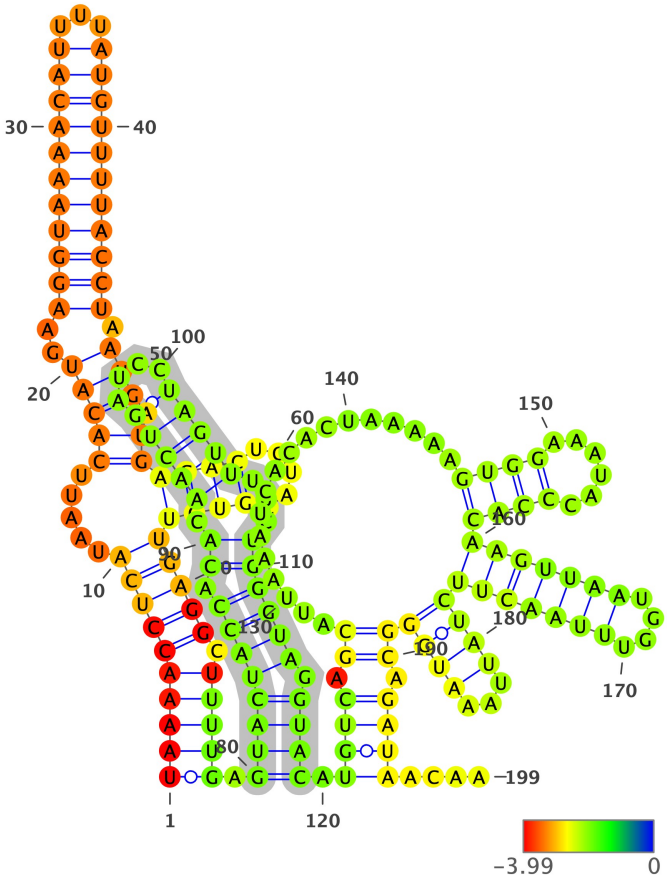
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 105 from nt 5164 to 5203 (nt 80 to 119)

```
5'-GTACTACCACACAACTGATCCUAGUUTTCUGGGUAGGUAC-3'
5'-((((((((.((.(((((....)))))...)))))).))))-3'
Motif MFE = -9.8; z-score = -2.0; 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 = -2.93; ED = 36.54
```

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, 266-13468(+)

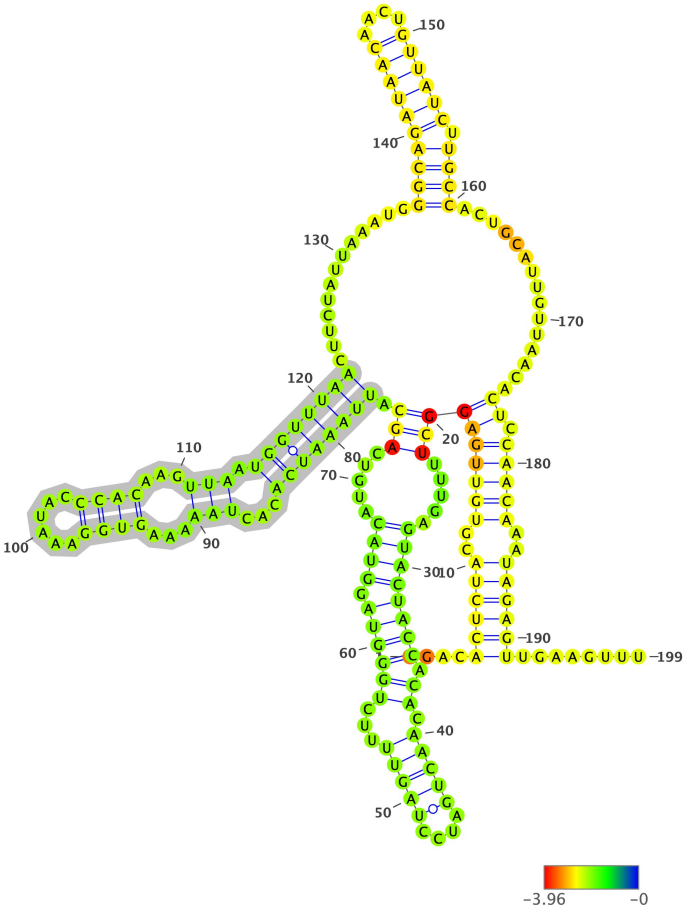
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 106 from nt 5213 to 5258 (nt 77 to 122)

```
5'-TTAAATCACACTAAAAAGTGGAAATACCCACAAGUUAAUGGUUUAA-3'
5'-((((((((...(((...((((......))))...))).))))))))-3'
Motif MFE = -8.9; z-score = -3.74; 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 = -2.93; ED = 18.36
```

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(+)

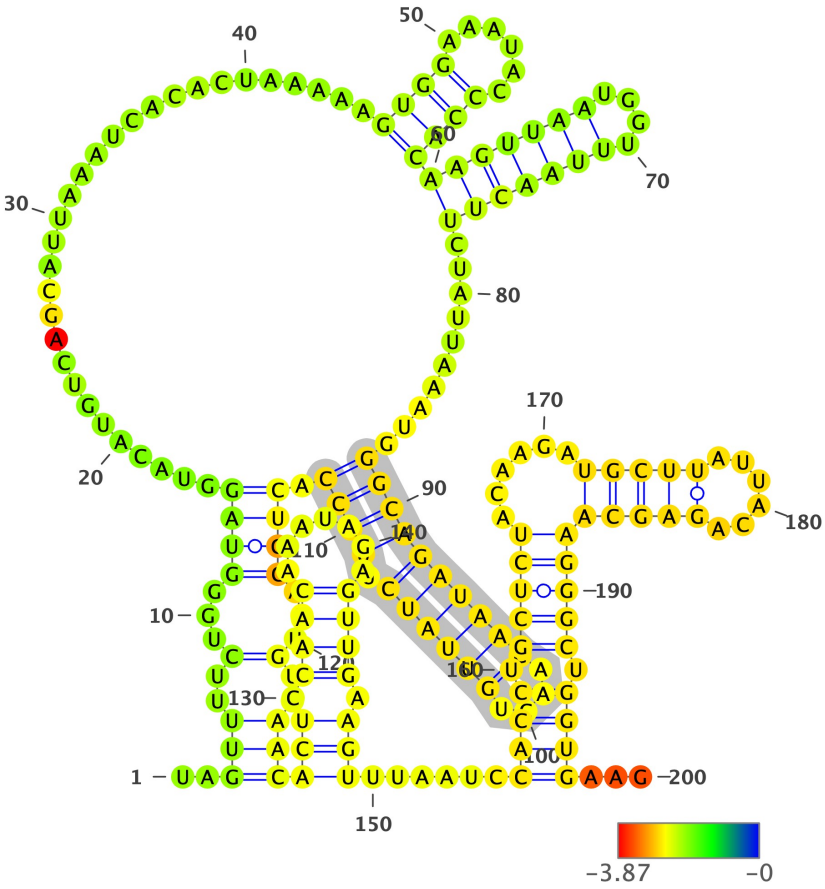
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 107 from nt 5272 to 5296 (nt 88 to 112)

```
5'-GGCAGATAACAACTGUUAUCTUGCC-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -10.9; z-score = -5.35; 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 = -2.21; 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(+)

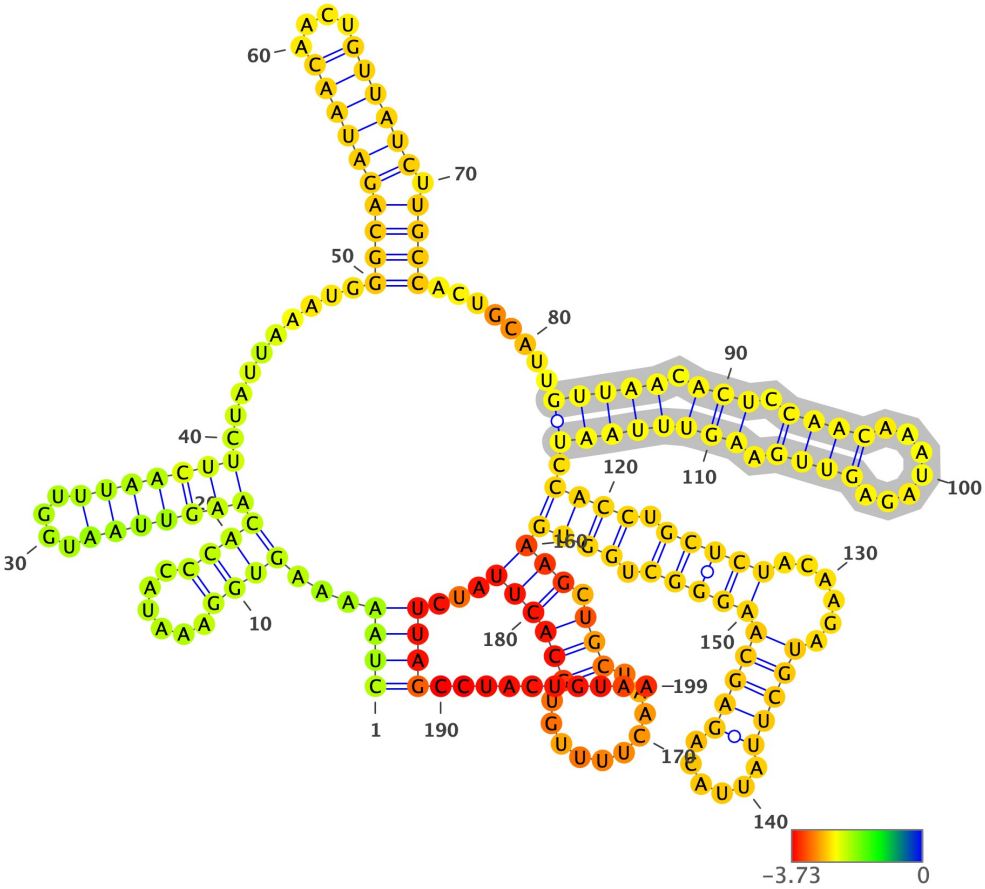
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 108 from nt 5305 to 5338 (nt 83 to 116)

```
5'-GTTAACACTCCAACAAATAGAGUUGAAGUUUAAU-3'
5'-(((((.(((.((((.......)))).))))))))-3'
Motif MFE = -4.9; z-score = -1.46; 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 5223 to 5421 (motif highlighted in silver):

```
5'-CUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGU
UUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAA-3
5'-((((...((((......))))(((((((....)))))))..........((((((((((....)))))).))))........(((((.(((.((((.......)))).)))
))))).((((.(((((......(((((......)))))))))).))))(((.(((..........))))))...))))..........-3'
MFE = -48.6; z-score = -2.8; ED = 35.88
```

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(+)

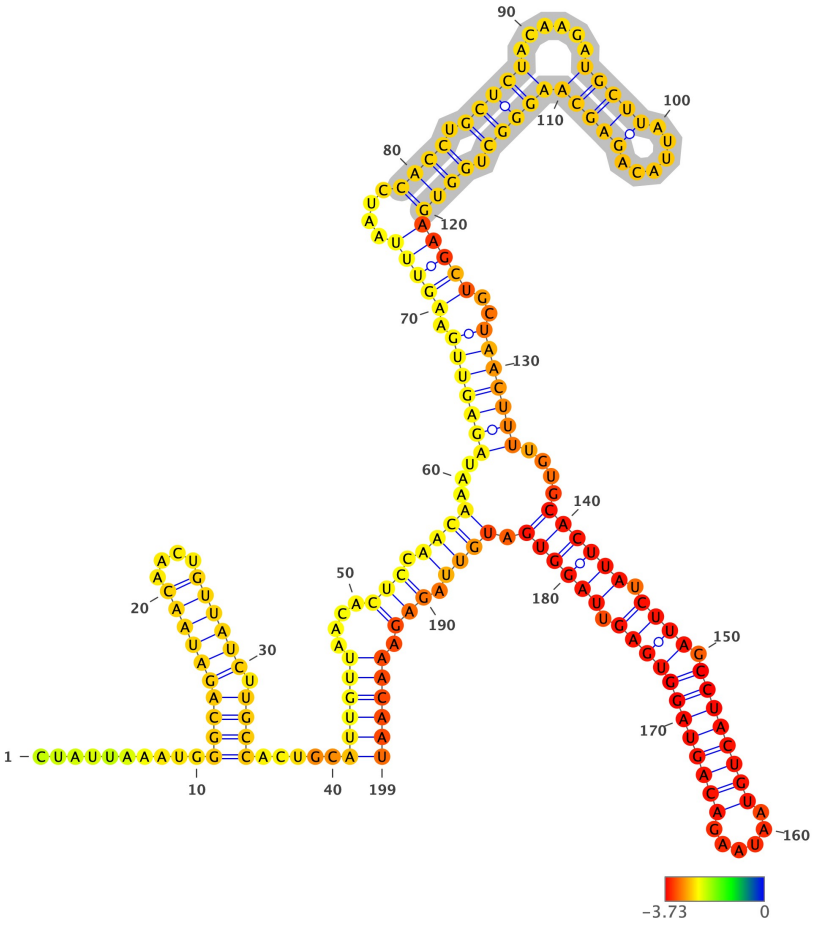
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 109 from nt 5340 to 5381 (nt 79 to 120)

```
5'-CACCTGCTCTACAAGATGCTTATTACAGAGCAAGGGCTGGUG-3'
5'-((((.(((((......(((((......)))))))))).))))-3'
Motif MFE = -14.9; z-score = -2.43; ED = 0.36
```



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 5262 to 5460 (motif highlighted in silver):

```
5'-CUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAA
GGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAU-3
5'-..........((((((((((....))))))).))))......((((((....(((.((((((...(((((((.(((((....((((.(((((......(((((......)))))))))))))).))))))))).
))))).)))))))))..)))))))....((((((.((((.(((((((((.....))))))))))).)))))).))))).))))))-3'
MFE = -61.4; z-score = -5.01; ED = 17.84
```

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(+)

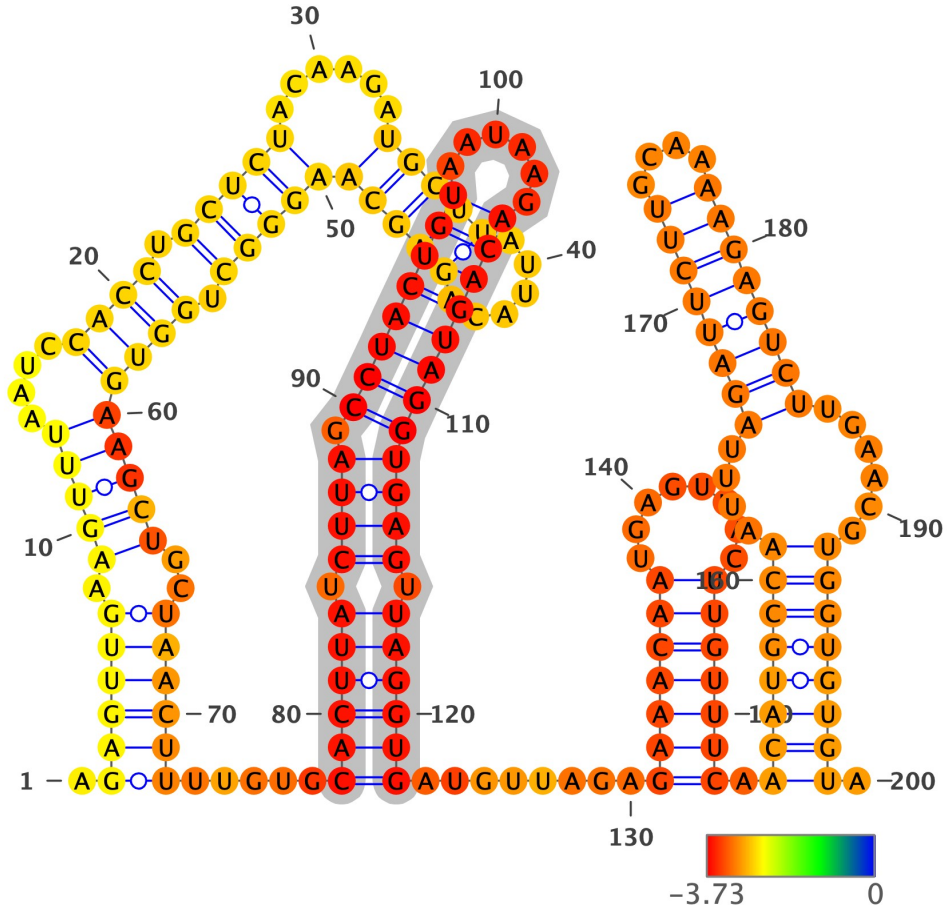
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 110 from nt 5400 to 5444 (nt 78 to 122)

```
5'-CACTTATCTTAGCCTACTGTAATAAGACAGUAGGUGAGTUAGGUG-3'
5'-((((((.((((.((((((((......)))))))))))).))))))-3'
Motif MFE = -20.7; z-score = -5.81; 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 5323 to 5522 (motif highlighted in silver):

```
5'-AGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGG
UGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUA-3
5'-.((((((.(((((....((((.(((((......(((((......)))))))))).)))))))))..))))))).....((((((.((((.((((((((......))))))))
)))).))))))........(((((((........))))))).((((((((....((((((((....))))))))......)))))))).-3'
MFE = -67.6; z-score = -5.45; ED = 10.94
```

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(+)

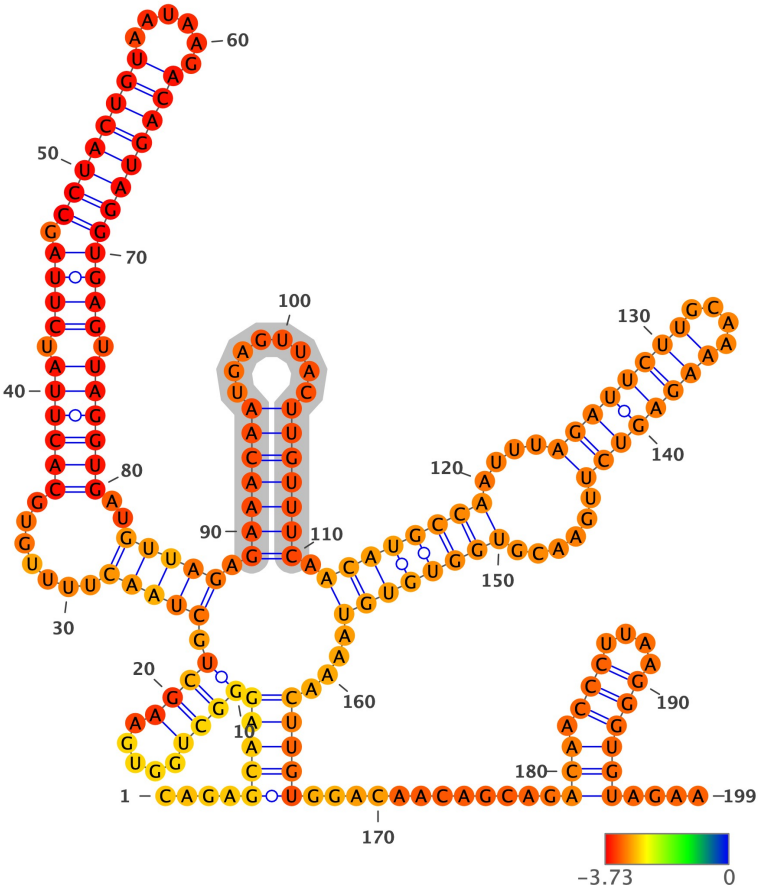
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 111 from nt 5453 to 5474 (nt 89 to 110)

```
5'-GAAACAATGAGTTACUUGUUUC-3'
5'-(((((((........)))))))-3'
Motif MFE = -4.2; z-score = -2.61; 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 5365 to 5563 (motif highlighted in silver):

```
5'-CAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCA
ACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAA-3
5'-....((((((((((.....)))).(((((.......((((((.((((.((((((((((.....))))))))))).)))))))..))))))..(((((((........)))))))).
(((((((((....(((((((((....)))))))))......)))))))))....)))))............(((.(((....)))))))....-3'
MFE = -61.5; z-score = -3.86; ED = 29.05
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

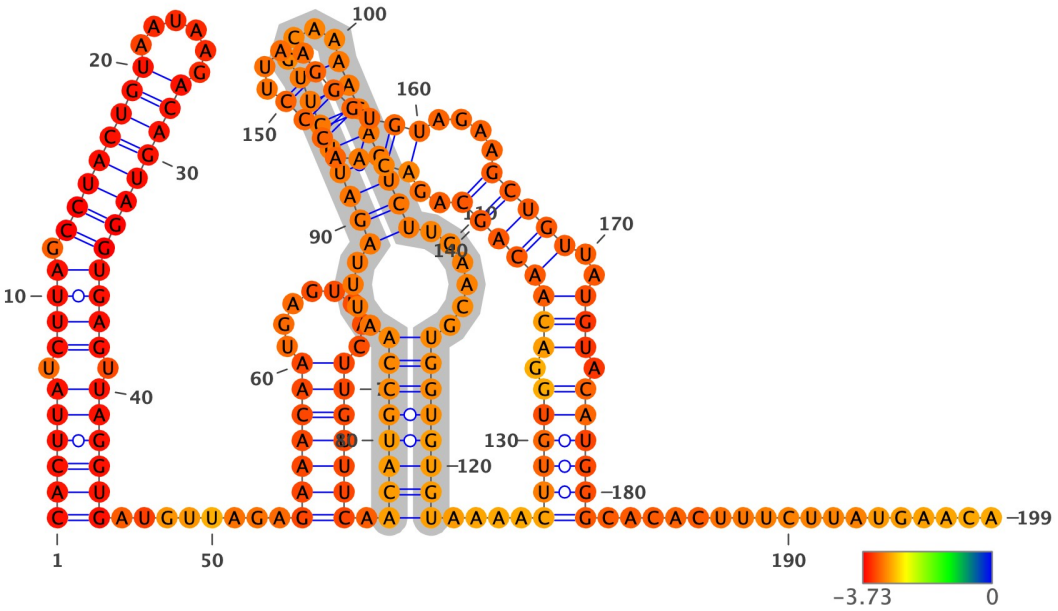
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 112 from nt 5476 to 5521 (nt 77 to 122)

```
5'-ACATGCCAATTTAGATTCTTGCAAAAGAGUCUTGAACGUGGUGUGU-3'
5'-(((((((((....(((((((((....)))))))))......)))))))))-3'
Motif MFE = -16.9; z-score = -4.43; ED = 3.32
```



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 5400 to 5598 (motif highlighted in silver):

```
5'-CACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGA
ACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACA-3
5'-((((((.((((.(((((((((.....)))))))))))).)))))).......(((((((........)))))))..(((((((((....(((((((((....)))))))))...
...)))))))))....((((((.(((((((((..(((.(((....)))))))....))))))..))).)))))).................-3'
MFE = -63.0; z-score = -4.8; ED = 24.97
```

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(+)

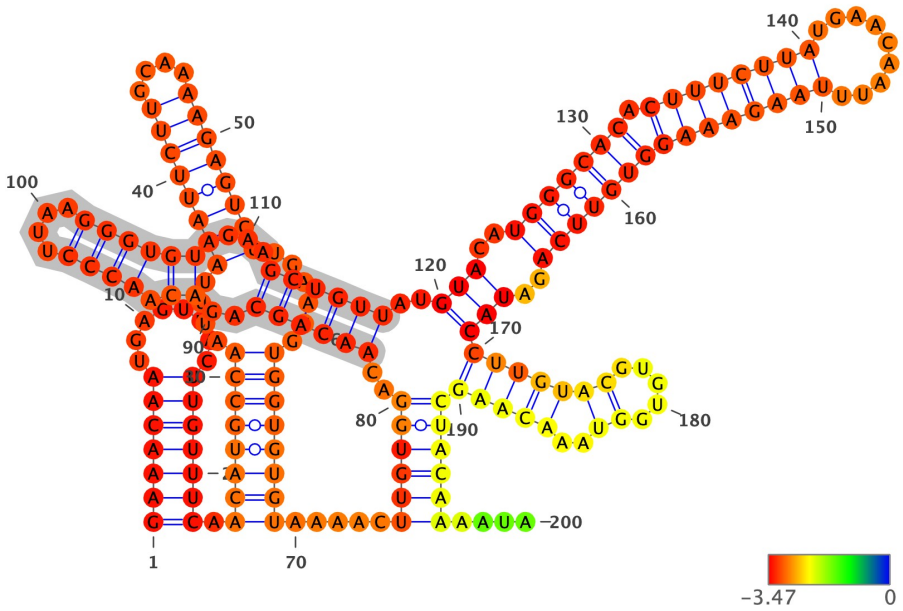
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 113 from nt 5535 to 5569 (nt 83 to 117)

```
5'-AACAGCAGACAACCCTTAAGGGUGTAGAAGCUGUU-3'
5'-((((((.....((((....)))).....))))))-3'
Motif MFE = -11.8; z-score = -3.26; 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 5453 to 5652 (motif highlighted in silver):

```
5'-GAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAA
GCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUA-3
5'-(((((((........)))))))..(((((((((....(((((((((....)))))))))......)))))))).....((((((..((((((..((.((((....))))))).....
))))))..(((..(((((((.(((((((((.........))))))))))))))))..)))(((((((.....)).))))))))))....-3'
MFE = -62.7; z-score = -4.57; 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(+)

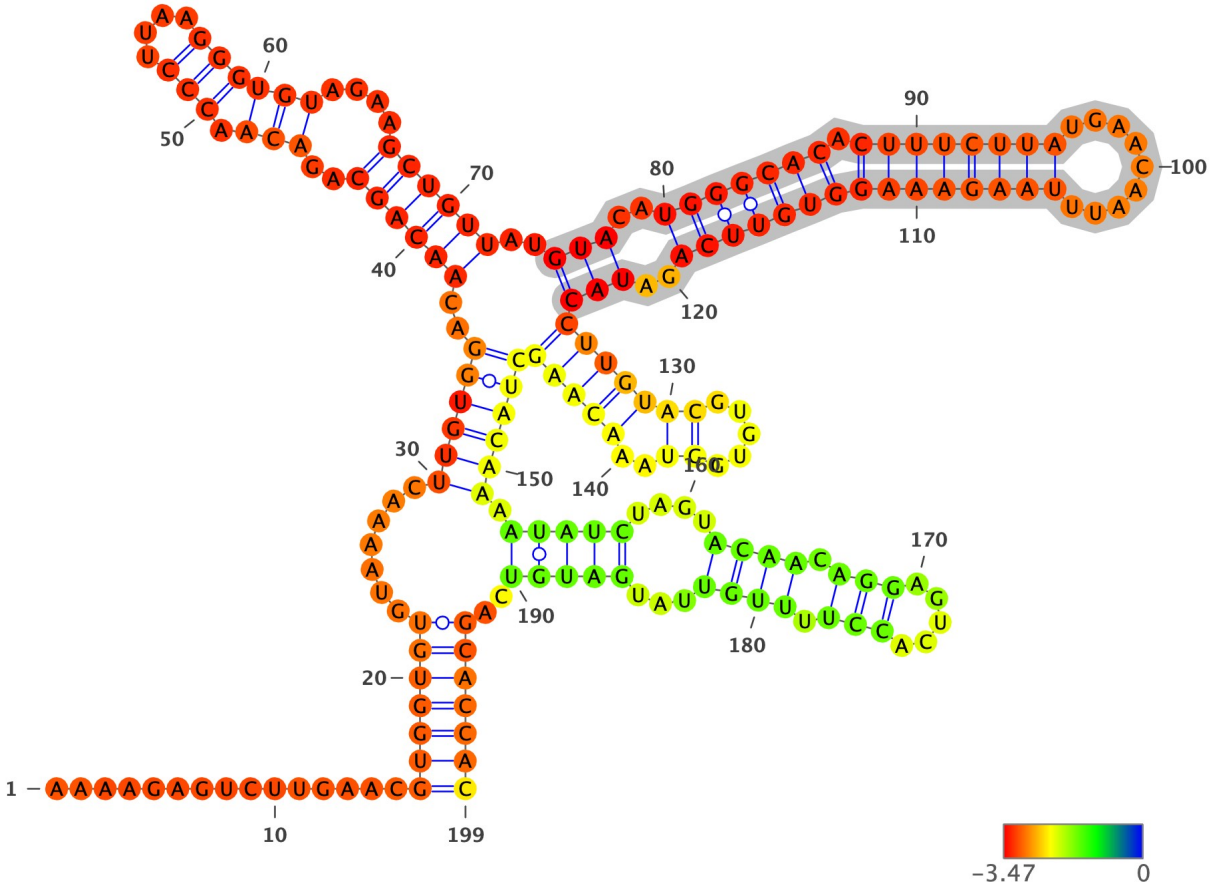
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 114 from nt 5572 to 5621 (nt 75 to 124)

```
5'-GTACATGGGCACACTTTCTTATGAACAATTUAAGAAAGGUGUUCAGAUAC-3'
5'-(((..(((((((.(((((((((.........)))))))))))))))..)))-3'
Motif MFE = -18.0; z-score = -4.32; 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 5498 to 5696 (motif highlighted in silver):

```
5'-AAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAA
GGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCAC-3
5'-...............(((((((.......((((((..((((((..(((.(((....)))))))....))))))..(((..(((((((.(((((((.........)))))))
))))))))..)))(((((((.....))..)))))))))).((((((....((((.((.....)).)))))...))))))..)))))))-3'
MFE = -55.0; z-score = -3.42; ED = 25.31
```

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(+)

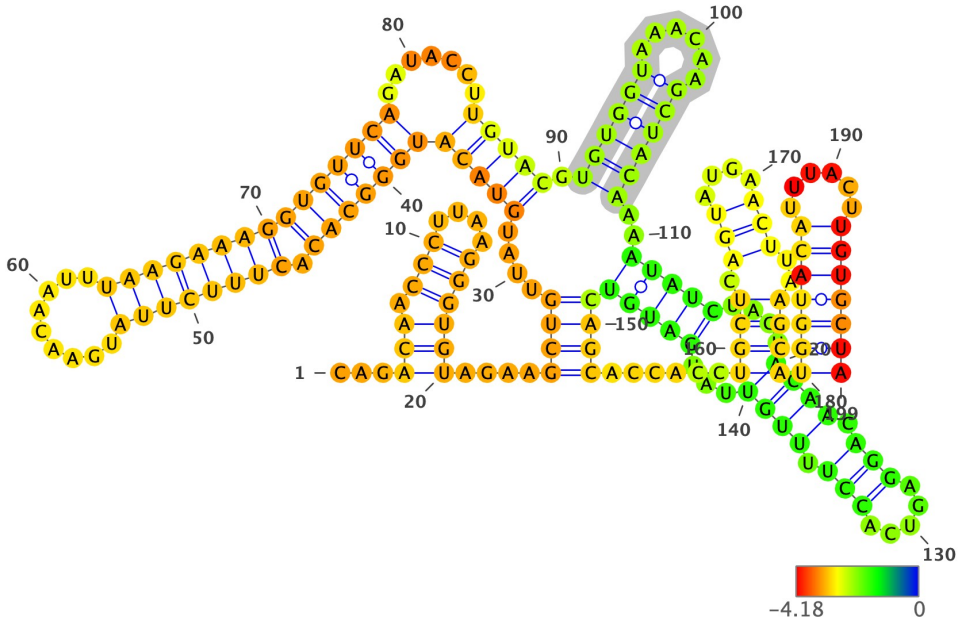
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 115 from nt 5630 to 5647 (nt 91 to 108)

```
5'-TGTGGTAAACAAGCUACA-3'
5'-((((((......))))))-3'
Motif MFE = -4.5; z-score = -4.24; 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 = -2.93; 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(+)

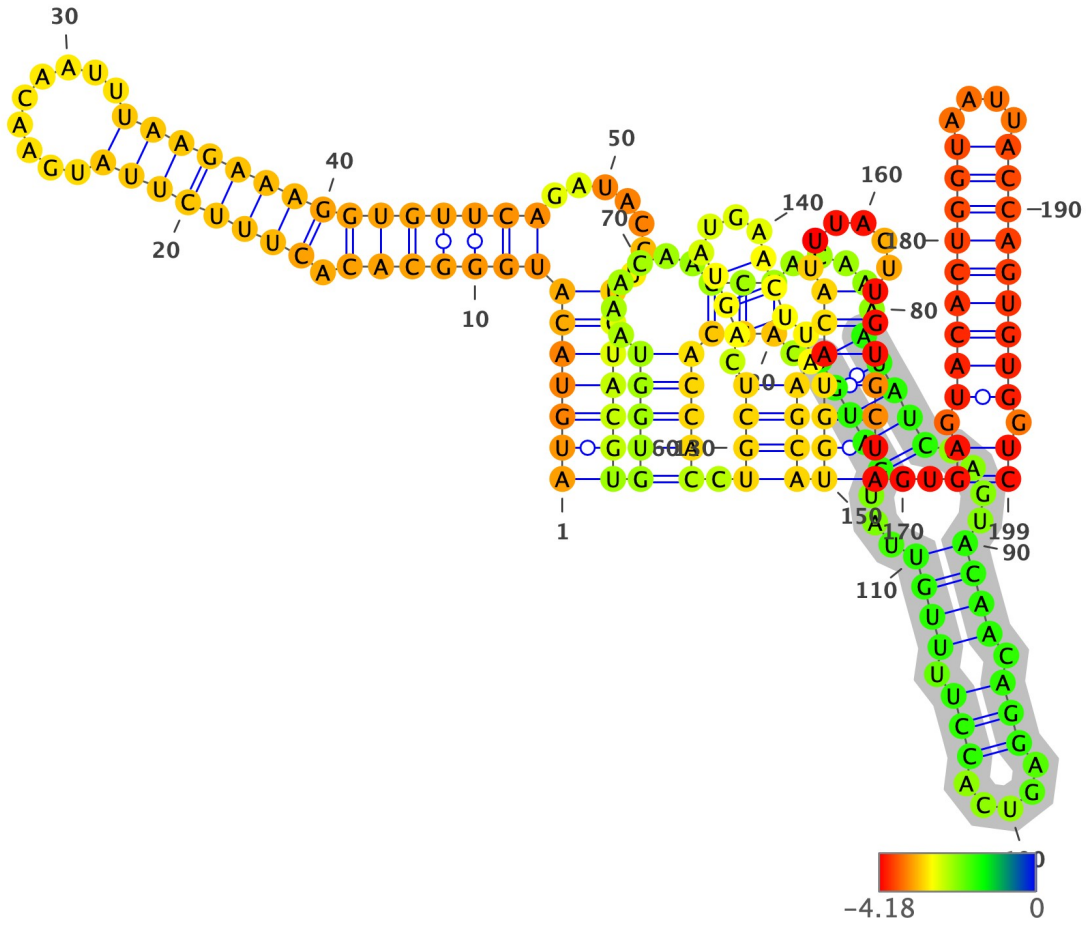
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 116 from nt 5650 to 5687 (nt 81 to 118)

```
5'-ATATCTAGTACAACAGGAGTCACCUTUUGUTATGAUGU-3'
5'-(((((....((((.(((.....))).))))...)))))-3'
Motif MFE = -7.3; z-score = -1.87; ED = 4.99
```



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 5570 to 5768 (motif highlighted in silver):

```
5'-AUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUU
AUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUC-3
5'-(((((((((((((.((((((((.........))))))))))))))).......)))))))(((((......(((.....(((((....((((.(((.....))).)))).
..))))).)))))))).((((.(((....)))..))))(((((((......)))))))..((.((((((((....))))))))).))-3'
MFE = -59.6; z-score = -4.17; ED = 32.51
```

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(+)

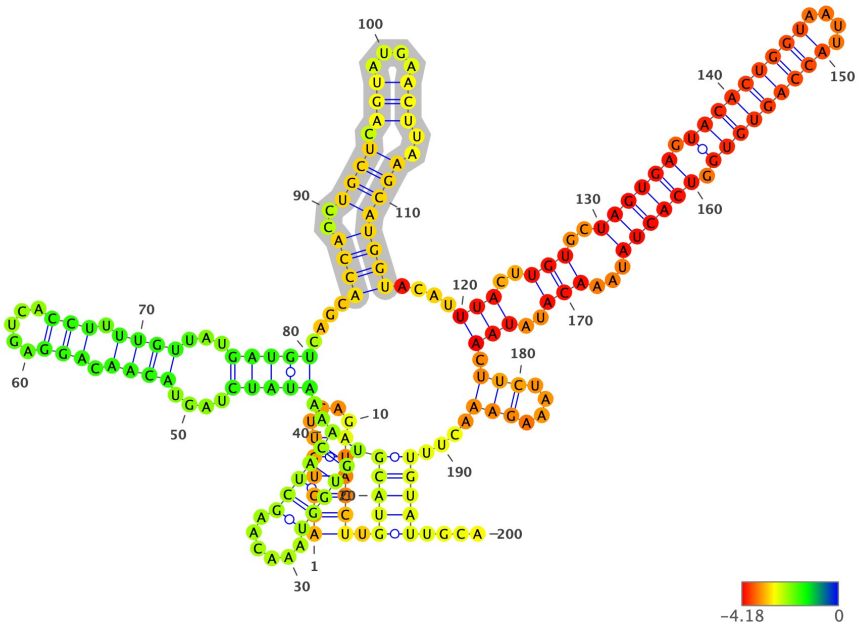
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 117 from nt 5692 to 5722 (nt 85 to 115)

```
5'-ACCACCTGCTCAGTATGAACUTAAGCAUGGU-3'
5'-((((..((((.(((....)))..))))))))-3'
Motif MFE = -6.7; z-score = -1.83; 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 = -3.55; 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(+)

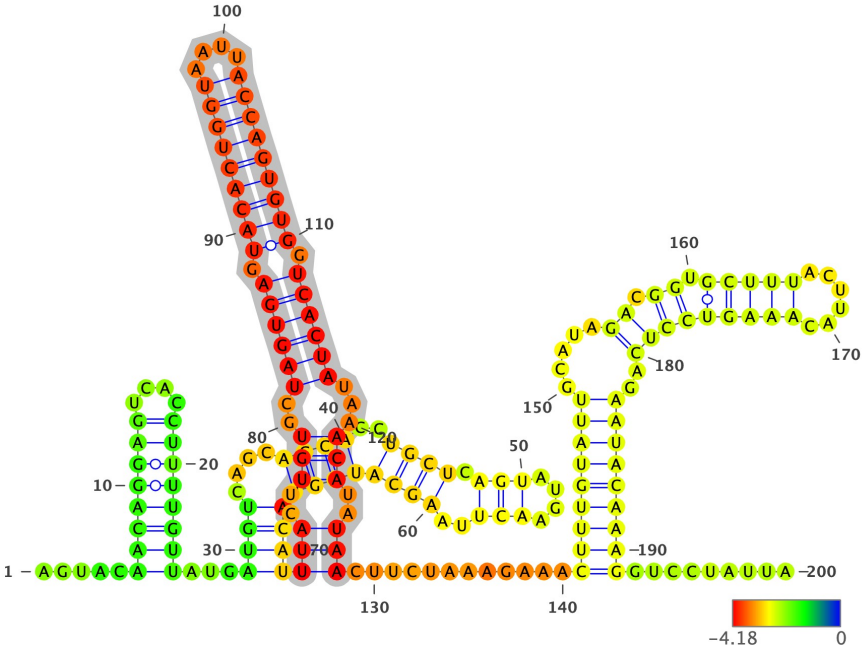
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 118 from nt 5727 to 5783 (nt 72 to 128)

```
5'-TTACTTGTGCTAGTGAGTACACTGGTAATTACCAGUGUGGUCACUATAAACATAUAA-3'
5'-(((..(((..(((((((.(((((((((....)))))))))).))))))...)))..)))-3'
Motif MFE = -24.5; z-score = -5.5; ED = 2.72
```



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 5656 to 5855 (motif highlighted in silver):

```
5'-AGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGG
UCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUA-3
5'-.....((((((((....))))))))...((((....((((..((((.(((....)))..)))))))))))))(((..(((..((((((.(((((((((....)))))))))).
))))))...)))..)))............(((((((((.....((.((.(((((......)))))))))..)))))))))..........-3'
MFE = -50.9; z-score = -3.52; ED = 47.69
```

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 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(+)

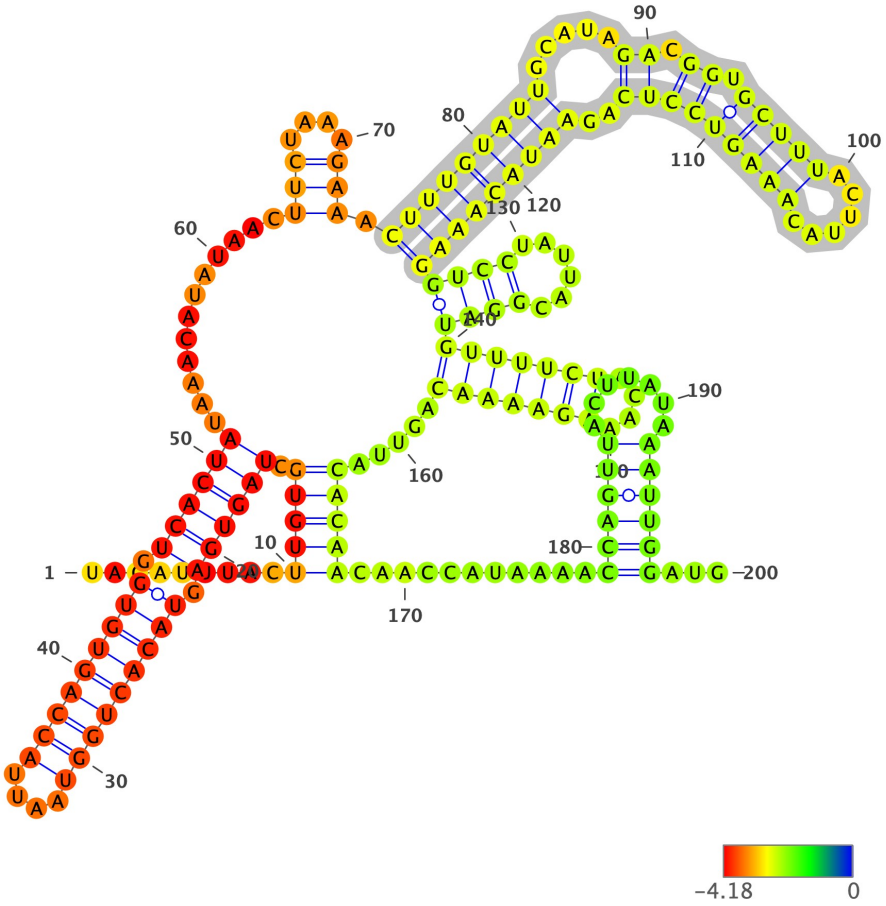
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 119 from nt 5796 to 5846 (nt 75 to 125)

```
5'-CTTTGTATTGCATAGACGGTGCTTTACTTACAAAGUCCUCAGAAUACAAAG-3'
5'-((((((((((.....((.((.(((((.....))))))))).))))))))))-3'
Motif MFE = -10.9; z-score = -2.5; 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 5722 to 5921 (motif highlighted in silver):

```
5'-UACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUC
CUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUG-3
5'-.........(((((.((((((.((((((((((....)))))))))).))))))............(((....))).(((((((((.....((.((.(((((.....))))))
)))..)))))))))((((.....))))(((((((....)))))))).....)))))...........((((((.......))))))...-3'
MFE = -52.5; z-score = -4.87; ED = 15.13
```

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(+)

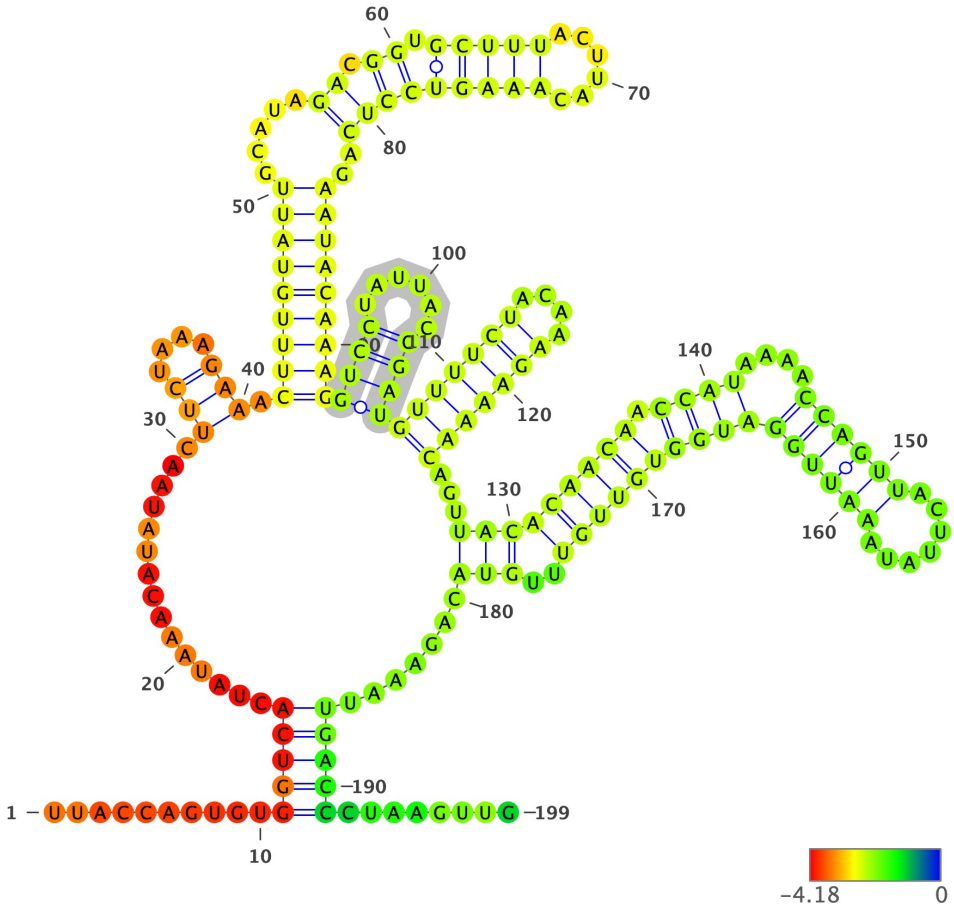
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 120 from nt 5847 to 5860 (nt 93 to 106)

```
5'-GTCCTATTACGGAU-3'
5'-((((......))))-3'
Motif MFE = -2.6; z-score = -4.77; 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 = -2.72; 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(+)

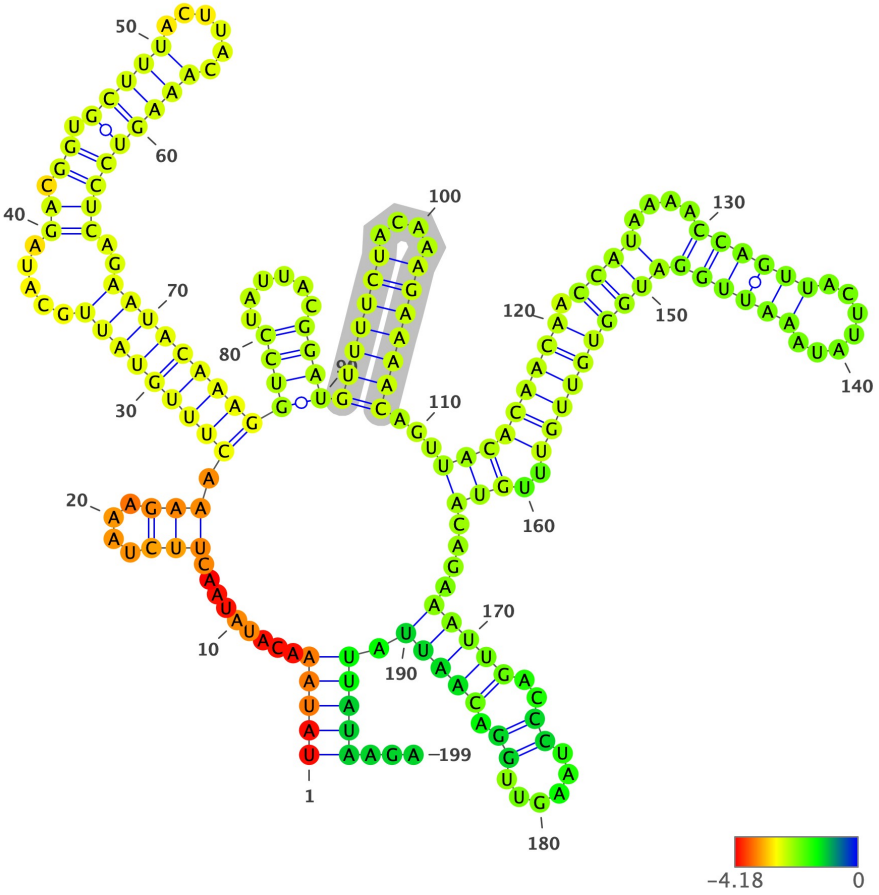
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 121 from nt 5861 to 5878 (nt 91 to 108)

```
5'-GTTTTCTACAAAGAAAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -5.98; 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 = -3.16; 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(+)

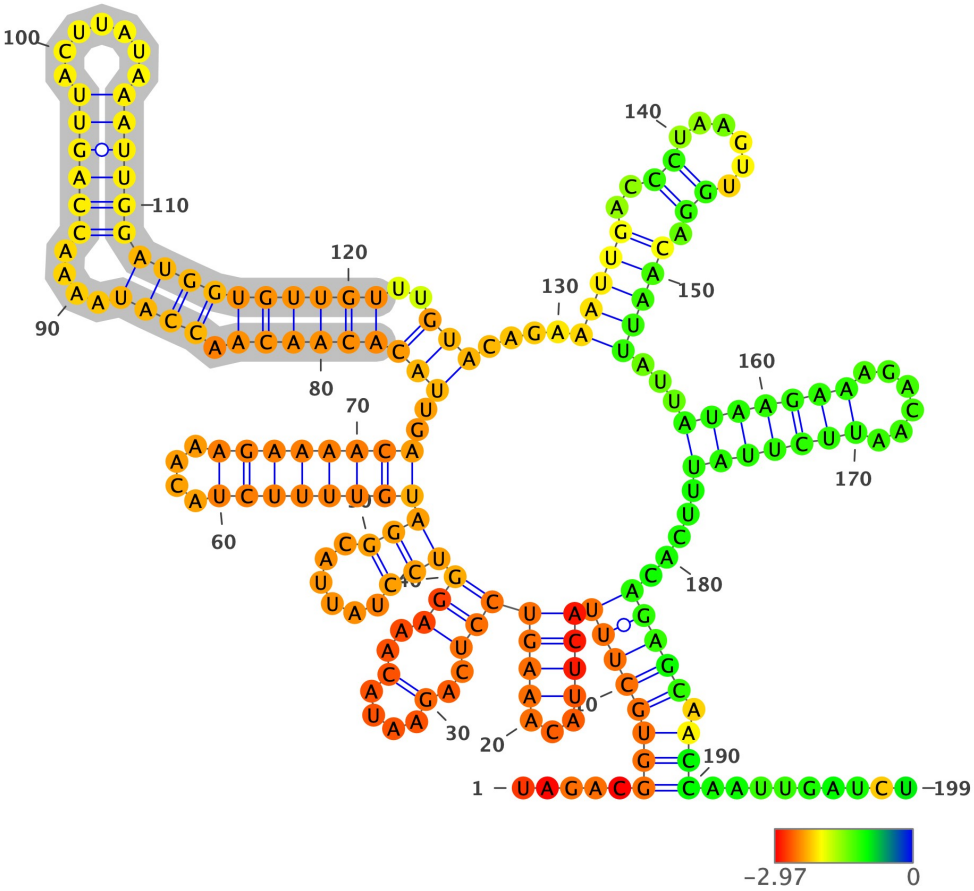
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 122 from nt 5885 to 5928 (nt 78 to 121)

```
5'-ACAACAACCATAAAACCAGTTACTTATAAAUUGGAUGGUGUUGU-3'
5'-((((((.((((....((((((.......))))))))))))))))-3'
Motif MFE = -12.6; z-score = -4.15; 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 5808 to 6006 (motif highlighted in silver):

```
5'-UAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGG
AUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCU-3
5'-.....((((((((((((...))))))((..(....)..)))(((......)))(((((((((....)))))))))..((((((((((.((((....((((((.......))))))
))))))))))..))).....((((((..((.......)).))))))...(((((((.....)))))))).....))))).)))).........-3'
MFE = -39.1; z-score = -2.24; ED = 19.67
```

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(+)

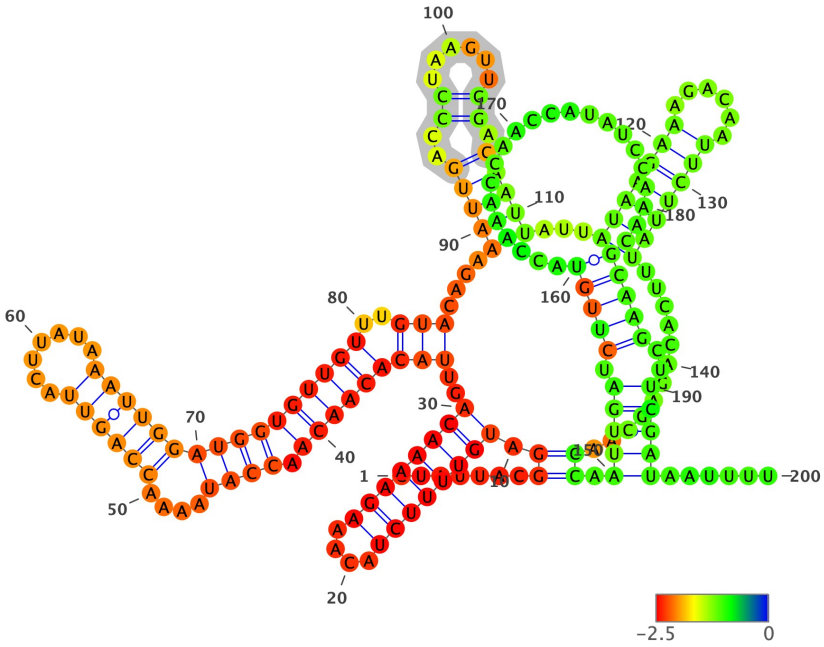
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 123 from nt 5942 to 5956 (nt 93 to 107)

```
5'-GACCCTAAGTTGGAC-3'
5'-(.............)-3'
Motif MFE = -1.5; z-score = -0.91; 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 5850 to 6049 (motif highlighted in silver):

```
5'-CUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUU
AUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUU-3
5'-.......((.(((((((((....)))))))))..((((((((((.((((....((((((.......))))))))))))))))))..))).....((((((..((......)).))))))
...(((((((......)))))))............)).(((((.(((((.....................)))))..)))))......-3'
MFE = -33.2; z-score = -1.91; ED = 36.42
```

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(+)

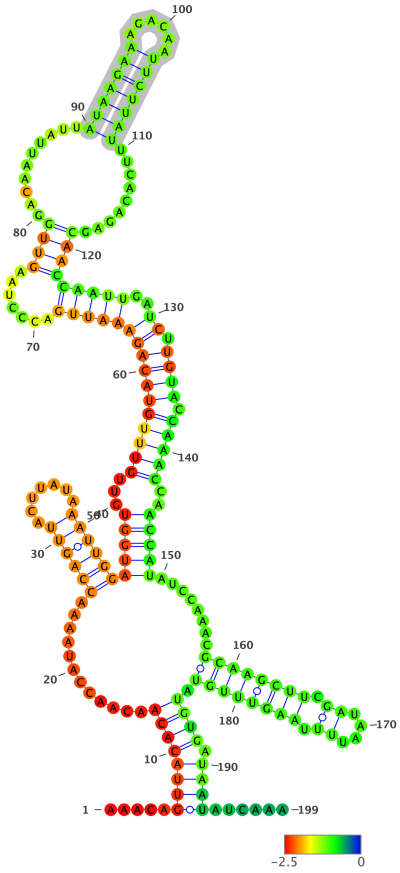
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 124 from nt 5964 to 5983 (nt 90 to 109)

```
5'-ATAAGAAAGACAAUUCUUAU-3'
5'-(((((((......)))))))-3'
Motif MFE = -3.1; z-score = -3.47; 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 5875 to 6073 (motif highlighted in silver):

```
5'-AAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUU
CACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUGUAUGUGAUAAUAUCAAA-3
5'-.....((((((((.............((((((.......))))))(((((...((((((((((((((((.......((((..........(((((((......)))))))..
.......))))))))).))).)))).)))))..)))))........((((((((.((....)).)))))))).)))).))))......-3'
MFE = -34.7; z-score = -2.42; ED = 45.11
```

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(+)

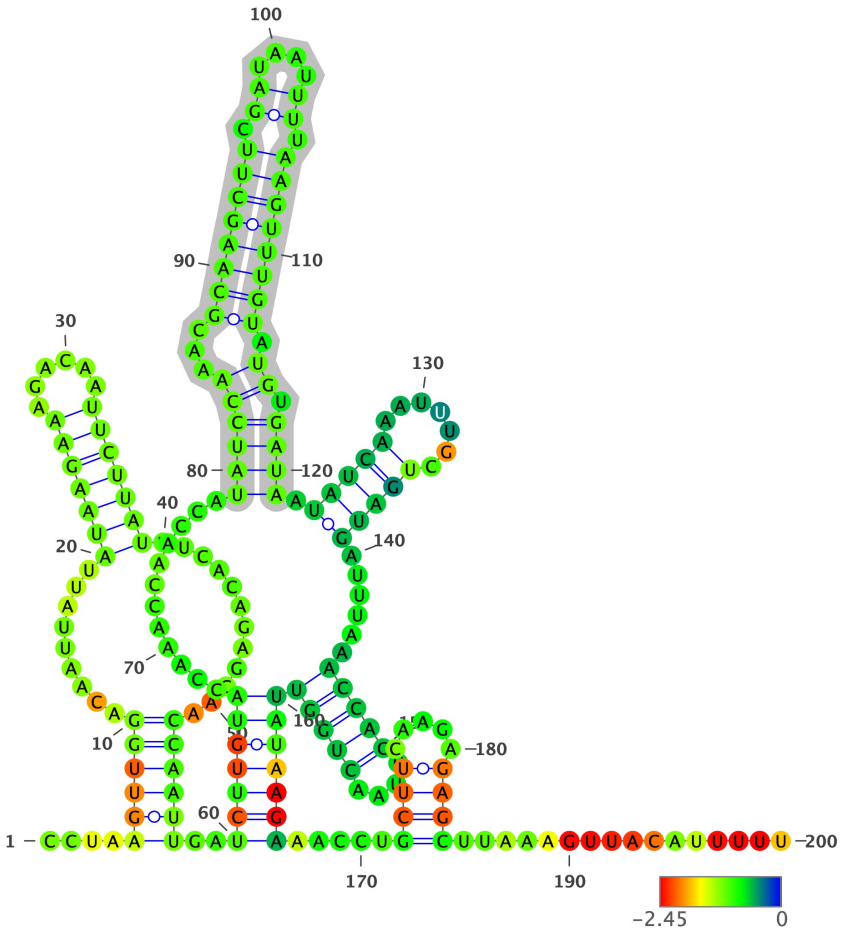
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 125 from nt 6023 to 6065 (nt 79 to 121)

```
5'-TATCCAAACGCAAGCTTCGATAATUUTAAGUUUGUAUGTGAUA-3'
5'-((((((...((((((((.((....)).))))))))).)).))))-3'
Motif MFE = -8.8; z-score = -2.22; ED = 4.18
```



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 5945 to 6144 (motif highlighted in silver):

```
5'-CCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUU
GUAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUU-3
5'-....((((((.........(((((((......)))))))............))))))..(((((((............((((((...((((((((.((....)).))))))
)).)).)))).(((((.......)))))......(((((....))))))))))))).....((((.....))))................-3'
MFE = -29.6; z-score = -0.22; ED = 40.44
```

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, 266-13468(+)

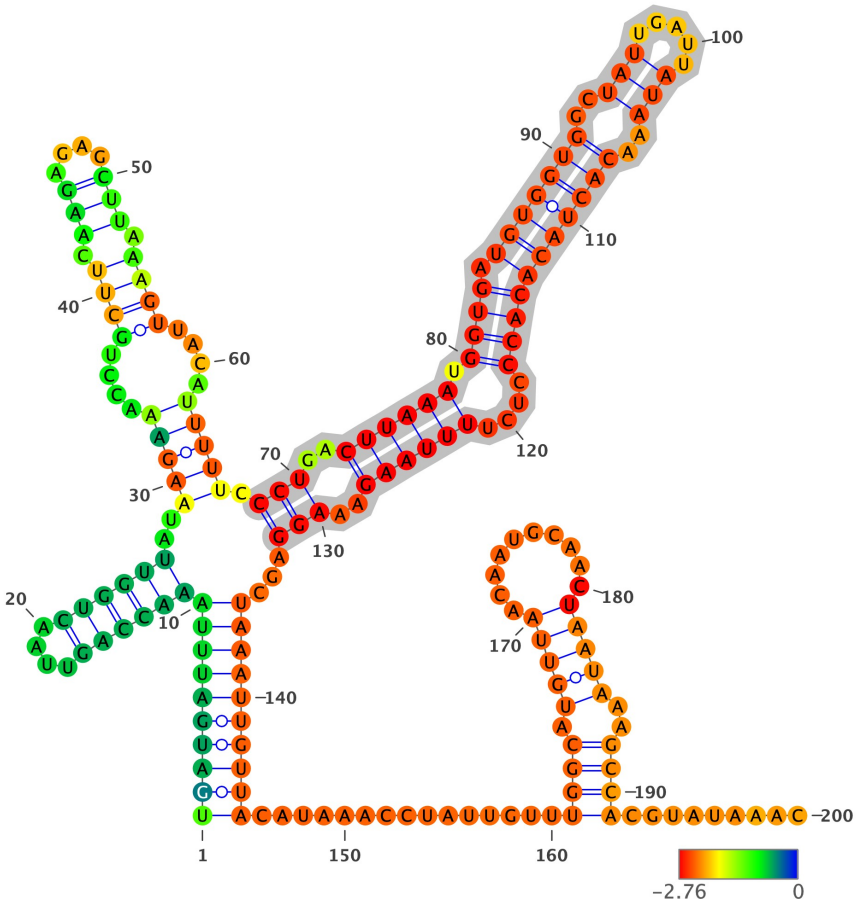
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 126 from nt 6146 to 6210 (nt 68 to 132)

```
5'-CCTGACTTAAATGGTGATGTGGTGGCTATTGATTAUAAACACUACACACCCTCTUUUAAGAAAGG-3'
5'-(((..(((((((.(((((.(((((((..(((.....)))..)))))))))))).....)))))))..)))-3'
Motif MFE = -21.2; z-score = -3.99; 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 = -2.2; ED = 39.58
```

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(+)

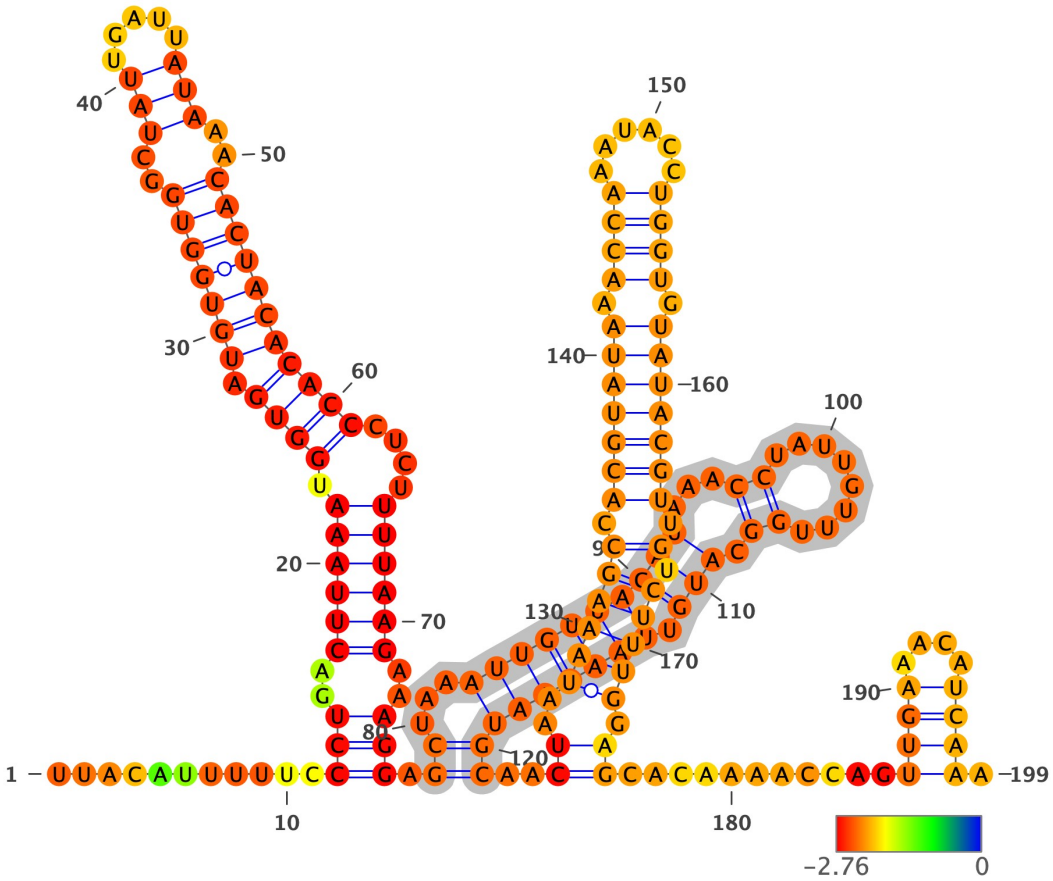
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 127 from nt 6212 to 6255 (nt 78 to 121)

```
5'-GCTAAATTGTTACATAAACCTATTGTTTGGCAUGTUAACAAUGC-3'
5'-((...((((((((((...((........)).)))).))))))))-3'
Motif MFE = -7.6; z-score = -2.07; 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 = -3.73; ED = 17.43
```

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(+)

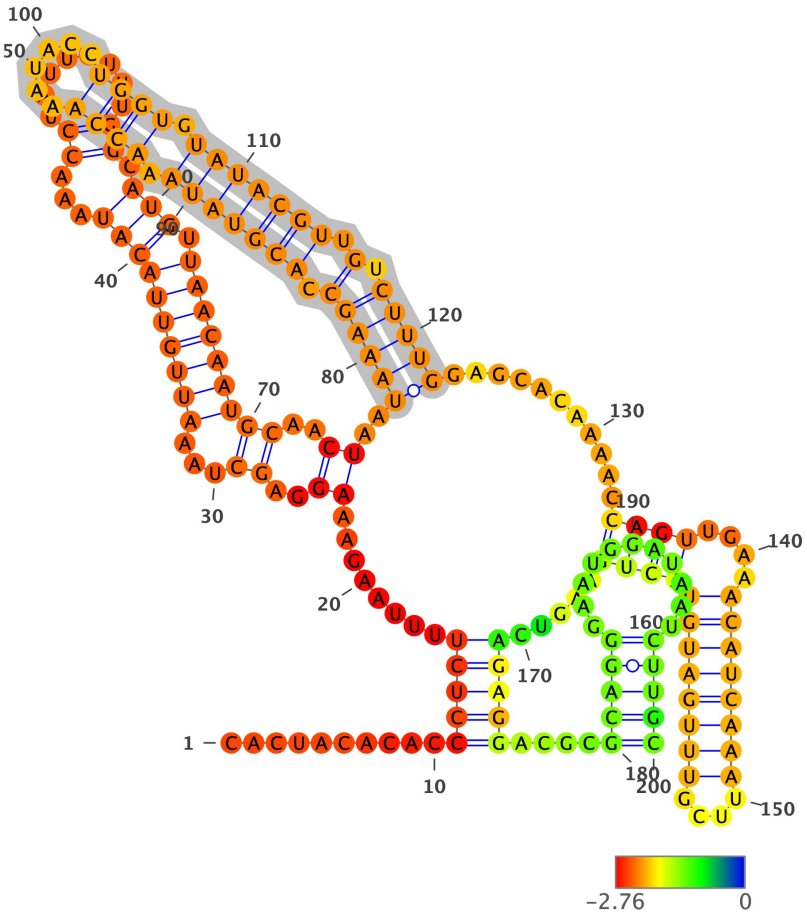
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 128 from nt 6262 to 6306 (nt 78 to 122)

```
5'-TAAAGCCACGTATAAACCAAATACCUGGUGUAUACGUTGTCUUUG-3'
5'-((((((.(((((((.((((......)))).)))))))).).)))))-3'
Motif MFE = -14.1; z-score = -3.87; 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 6185 to 6384 (motif highlighted in silver):

```
5'-CACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUA
CGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGC-3
5'-..........(((((........((..((...((((((((((...((........)).))).)))))))))..)).((((((.(((((((.((((......)))).))))
))).).)))))...........((((....((((((((....))))))))))))).....)))))....(((((...........)))))-3'
MFE = -43.0; z-score = -1.32; ED = 29.12
```

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(+)

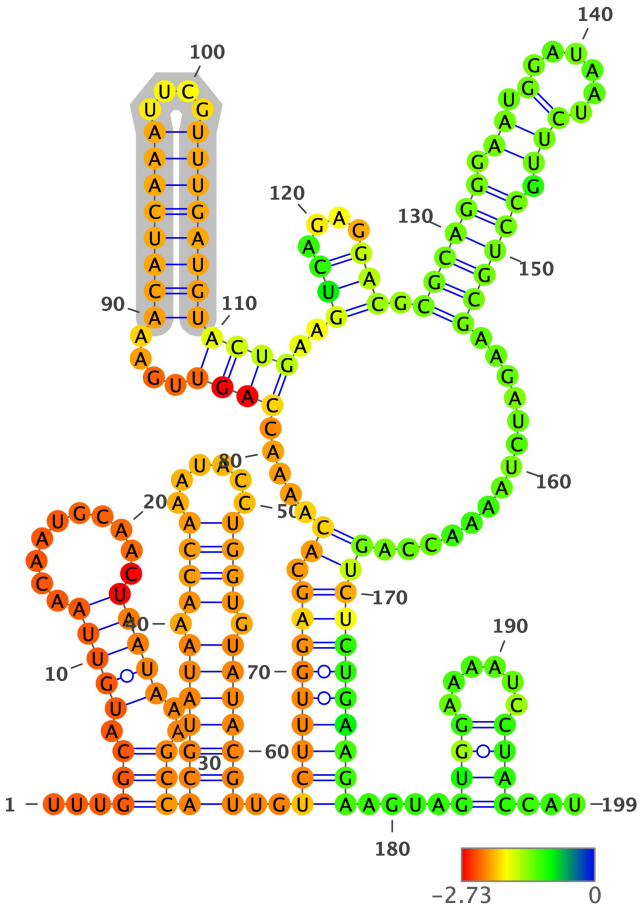
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 129 from nt 6326 to 6345 (nt 90 to 109)

```
5'-ACATCAAATTCGUUUGAUGU-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -5.7; z-score = -5.81; ED = 1.06
```



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 6237 to 6435 (motif highlighted in silver):

```
5'-UUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUAC
UGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAU-3
5'-...(((.(((((..........)))))..)))(((((((.((((......)))).)))))))..(((((((((.((.....((((....((((((((....)))))))))
))..(((....))).((((((.((.(......)).)))))).............))))))))))....((((......))))...-3'
MFE = -50.1; z-score = -2.41; ED = 31.82
```

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, 266-13468(+)

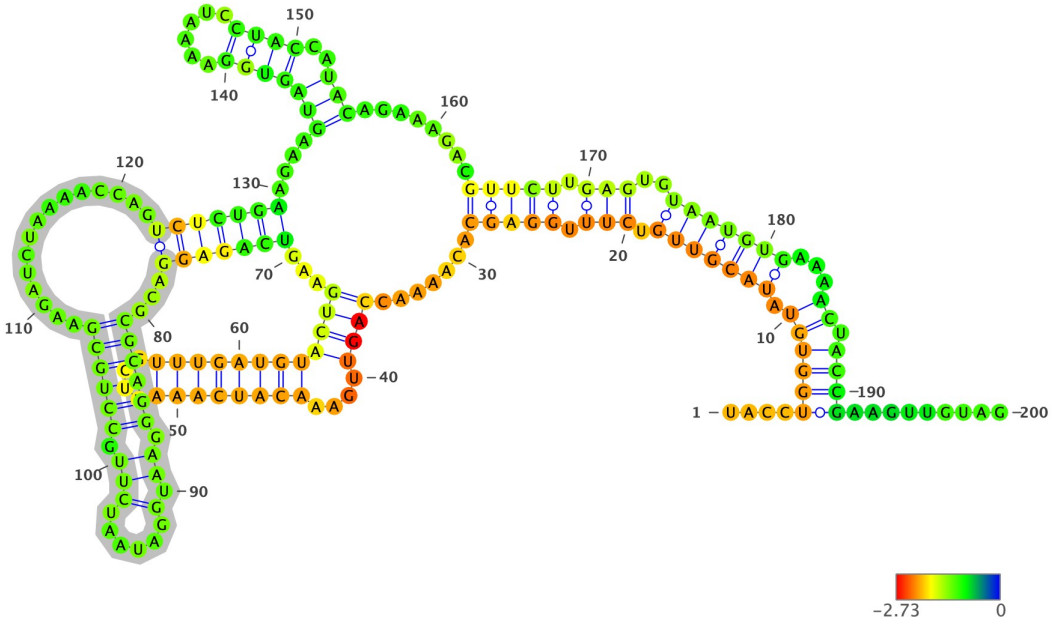
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 6359 to 6405 (nt 77 to 123)

```
5'-GACGCGCAGGGAATGGATAATCUUGCCUGCGAAGATCTAAAACCAGU-3'
5'-(...(((((((.((.(......))).)))))))..............)-3'
Motif MFE = -11.3; z-score = -1.32; ED = 4.32
```



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 6283 to 6482 (motif highlighted in silver):

```
5'-UACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGA
UCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAG-3
5'-....((((((.(((((((.(((.(((((.......((((....(((((((((....)))))))))))))...(((((((...((((((.((.(......))).)))))))....
..........)))))))....(((((((......))))..)))........))))).))))..)))))))...)).))))).........-3'
MFE = -45.1; z-score = -0.62; ED = 20.6
```

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(+)

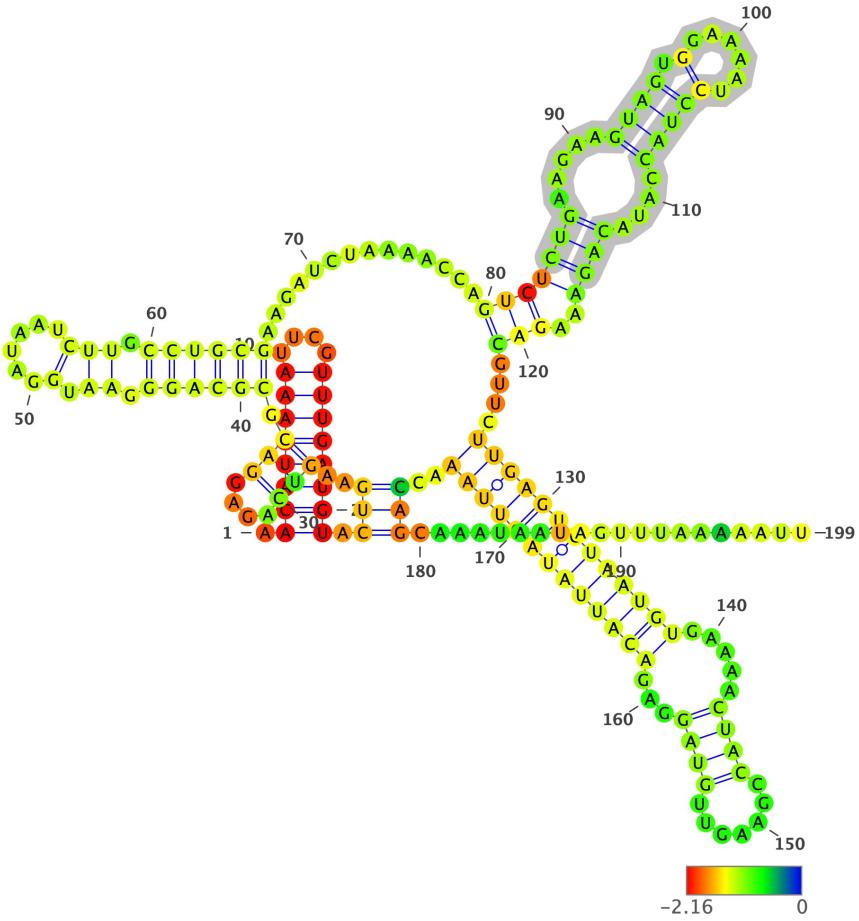
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 131 from nt 6408 to 6439 (nt 84 to 115)

```
5'-CTGAAGAAGTAGTGGAAAATCCUACCATACAG-3'
5'-(((.....((((.........))))....)))-3'
Motif MFE = -3.1; z-score = -0.29; ED = 9.19
```



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 6325 to 6523 (motif highlighted in silver):

```
5'-AACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAU
ACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUU-3
5'-.((((((((....)))))))).(((..(((....))).((((((.((.(......))).))))))..............(((((((.....((((.(......)))))...
.))))..)))....((((((((((((.....((((.......))))...)))))))))))))..)))....................-3'
MFE = -45.5; z-score = -2.62; ED = 23.15
```

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(+)

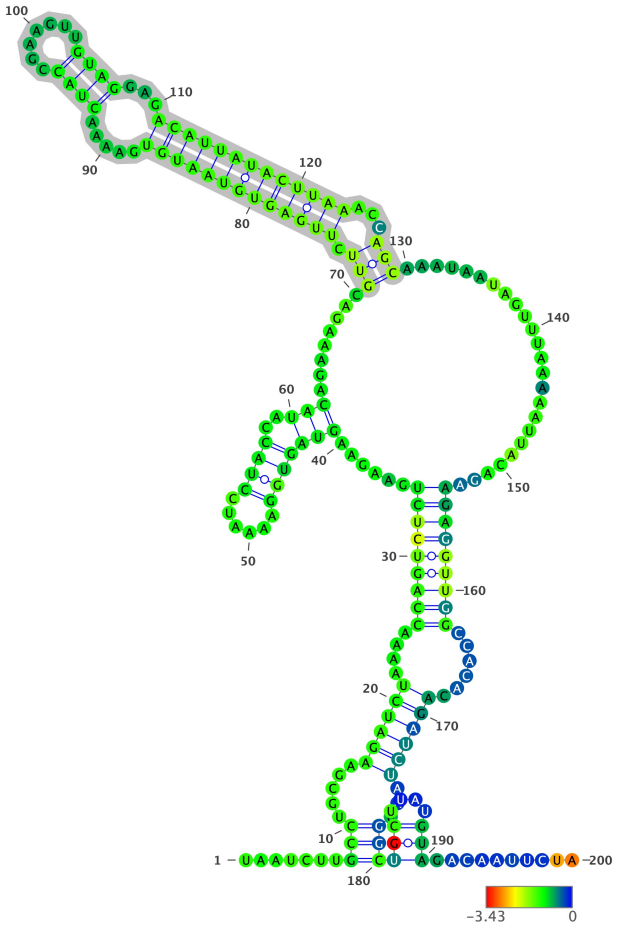
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 132 from nt 6446 to 6504 (nt 71 to 129)

```
5'-GTTCTTGAGTGTAATGTGAAAACTACCGAAGTTGUAGGAGACAUUAUACUUAAACCAGC-3'
5'-(((.(((((((((((((.....((((.......))))...)))))))))))))...)))-3'
Motif MFE = -16.2; z-score = -2.82; 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 6376 to 6575 (motif highlighted in silver):

```
5'-UAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGA
CAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUA-3
5'-.......(((.....((((((....(((((((((.....(((((((.....))))..))).........(((.(((((((((((((.....((((.......))))...)
))))))))))))...))).......................)))))))))......))))))...)))(((....))).........-3'
MFE = -37.0; z-score = -0.62; 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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

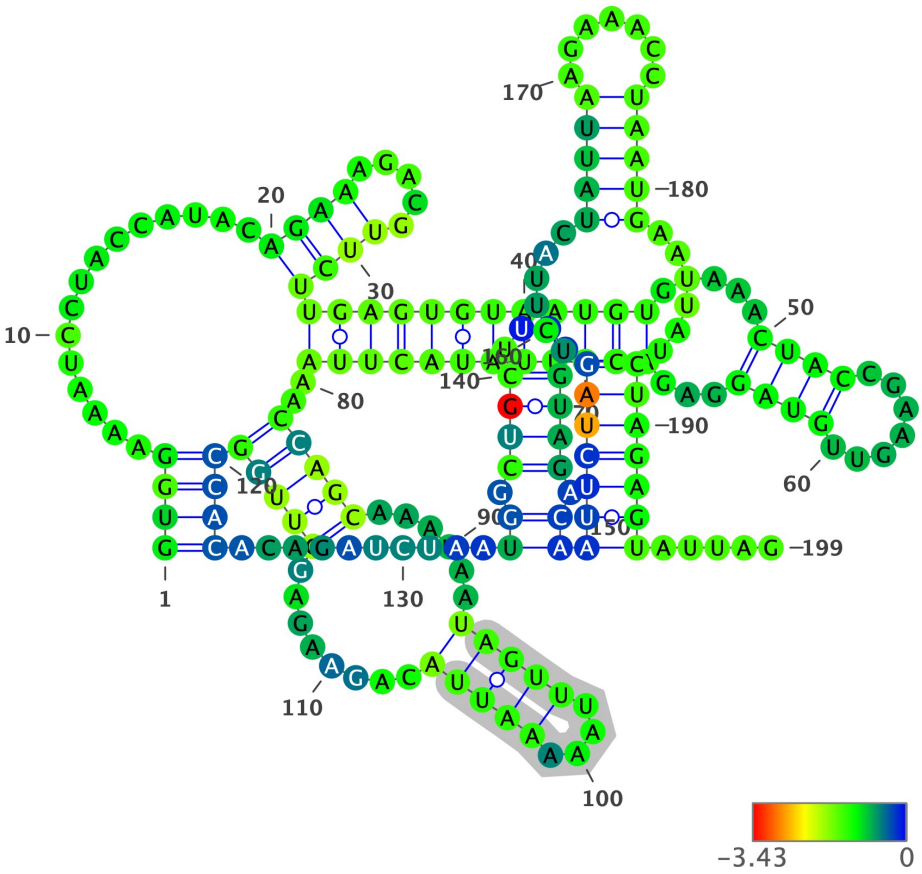
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 6512 to 6523 (nt 94 to 105)

```
5'-AGTTTAAAAATU-3'
5'-(..........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 6419 to 6617 (motif highlighted in silver):

```
5'-GUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAA
GAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAG-3
5'-((((..............((((.....))))((((((((((((.....((((.......))))...))))))))))))..(((((......(((((....)))))).....
...))))))))).........((.((((....)))).))(((((((.....(((((.......)))))).....)))))))).....-3'
MFE = -35.1; z-score = -1.0; ED = 43.36
```

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(+)

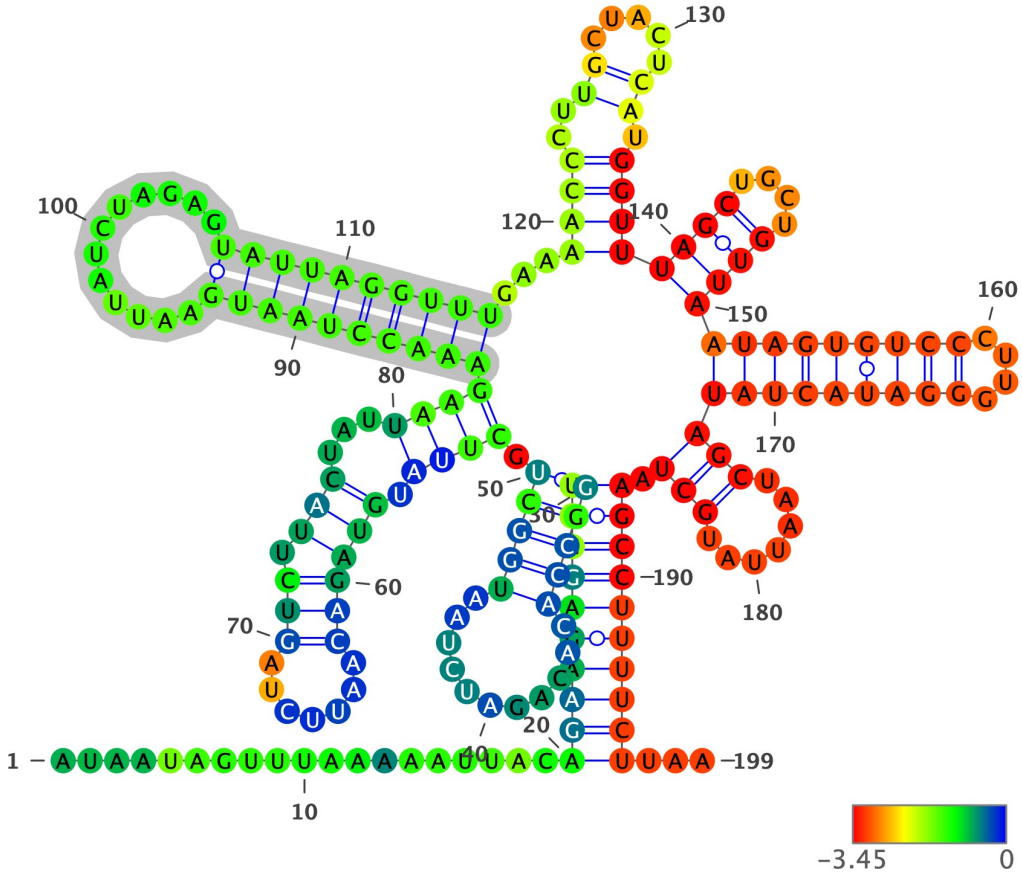
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 134 from nt 6590 to 6621 (nt 84 to 115)

```
5'-AAACCTAATGAATTATCTAGAGUAUUAGGUUU-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -6.8; z-score = -3.2; 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 = -2.45; 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(+)

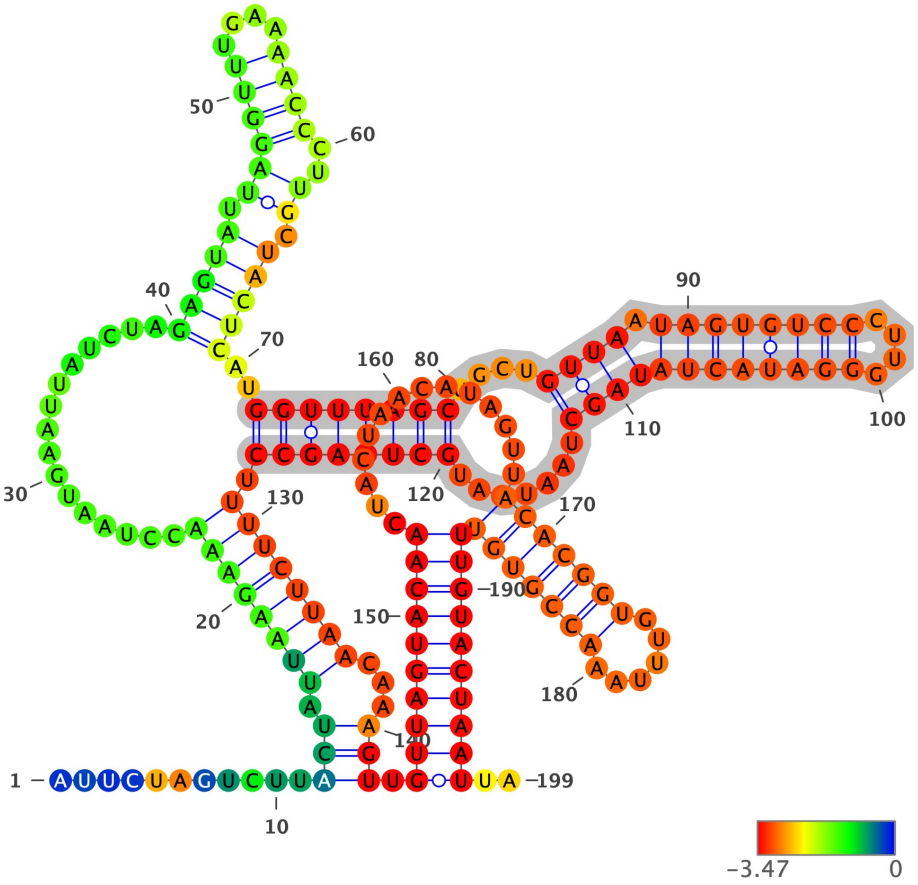
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 135 from nt 6641 to 6696 (nt 72 to 127)

```
5'-GGTTTAGCTGCTGTTAATAGTGTCCCTTGGGAUACUAUAGCTAATTATGCUAAGCC-3'
5'-((((((((....((((.((((((((....))))))))))))).......))))))))-3'
Motif MFE = -21.7; z-score = -4.2; 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 = -51.4; z-score = -3.77; ED = 38.36
```

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(+)

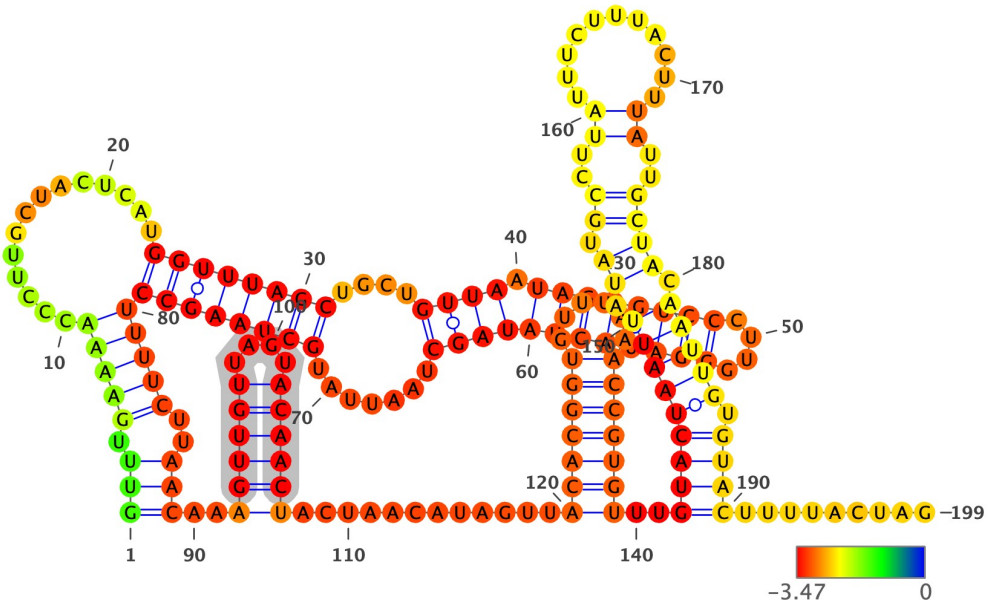
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 136 from nt 6710 to 6723 (nt 93 to 106)

```
5'-GTTGTTAGTACAAC-3'
5'-((((.....))))-3'
Motif MFE = -2.7; z-score = -4.14; ED = 0.36
```



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 6618 to 6816 (motif highlighted in silver):

```
5'-GUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUA
ACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAG-3
5'-(((.(((((.............(((((((((....((((.(((((((((....)))))))))))).......))))))))))))..))))..((((((....))))))....
........(((((((......)))))))..(((((((((.((.((..((..........))..)))))..)))))).))))).........-3'
MFE = -44.5; z-score = -3.03; ED = 26.99
```

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(+)

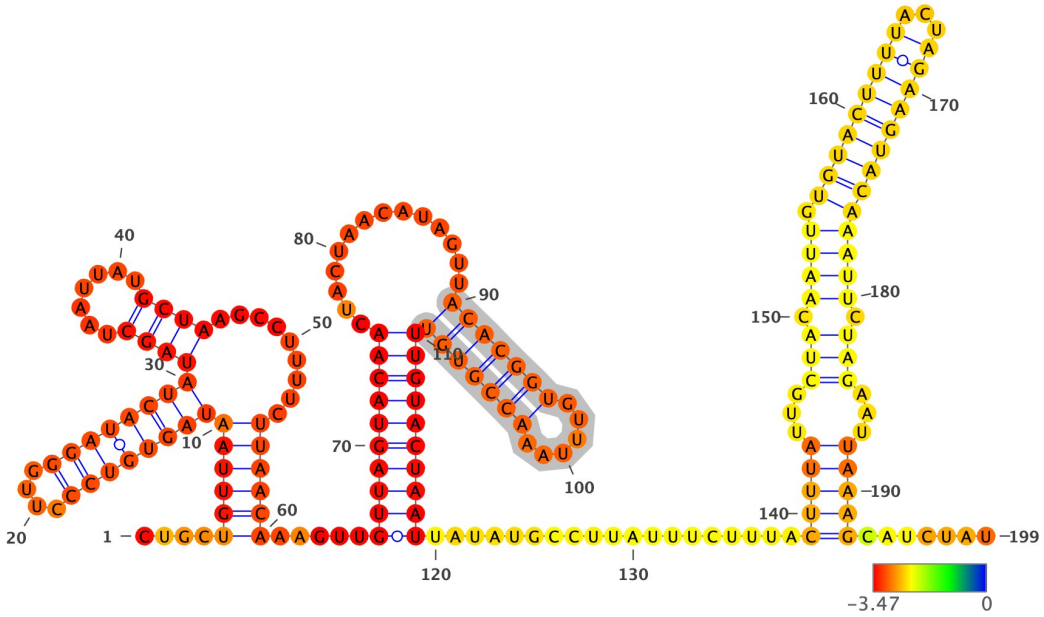
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 137 from nt 6737 to 6756 (nt 90 to 109)

```
5'-ACACGGTGTTTAAACCGUGU-3'
5'-(((((((......)))))))-3'
Motif MFE = -10.0; z-score = -5.23; 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 6648 to 6846 (motif highlighted in silver):

```
5'-CUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUU
GUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAU-3
5'-....(((((((((((((....))))))))((((.......))))........))))))).....((((((((((..............(((((((......)))))))))
))))))))...................(((((...(((.((((.((((((((((...)))))))))))))).)))...)))))).......-3'
MFE = -45.9; z-score = -3.97; ED = 46.4
```

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(+)

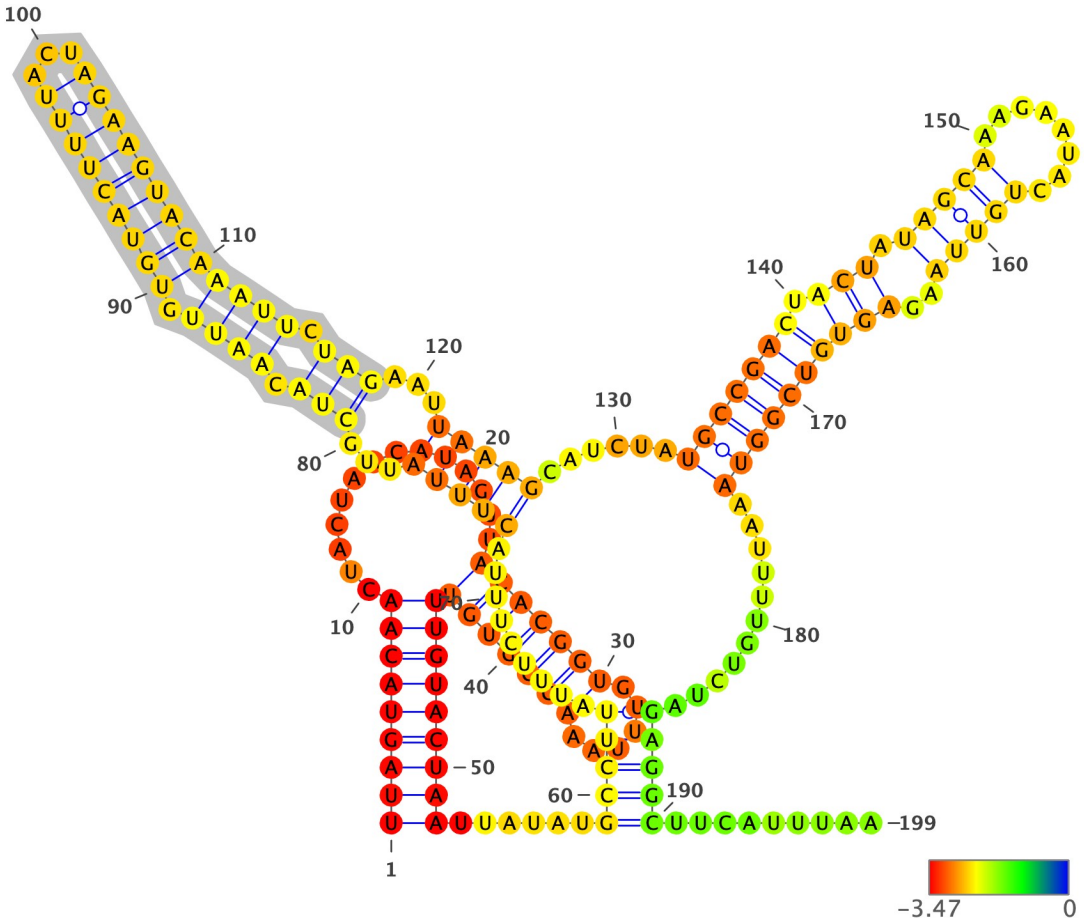
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 138 from nt 6794 to 6831 (nt 81 to 118)

```
5'-CTACAATTGTGTACTTTTACTAGAAGUACAAAUUCUAG-3'
5'-(((.(((((.((((((((((...))))))))))))))).)))-3'
Motif MFE = -8.3; z-score = -2.75; 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 = -4.44; 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(+)

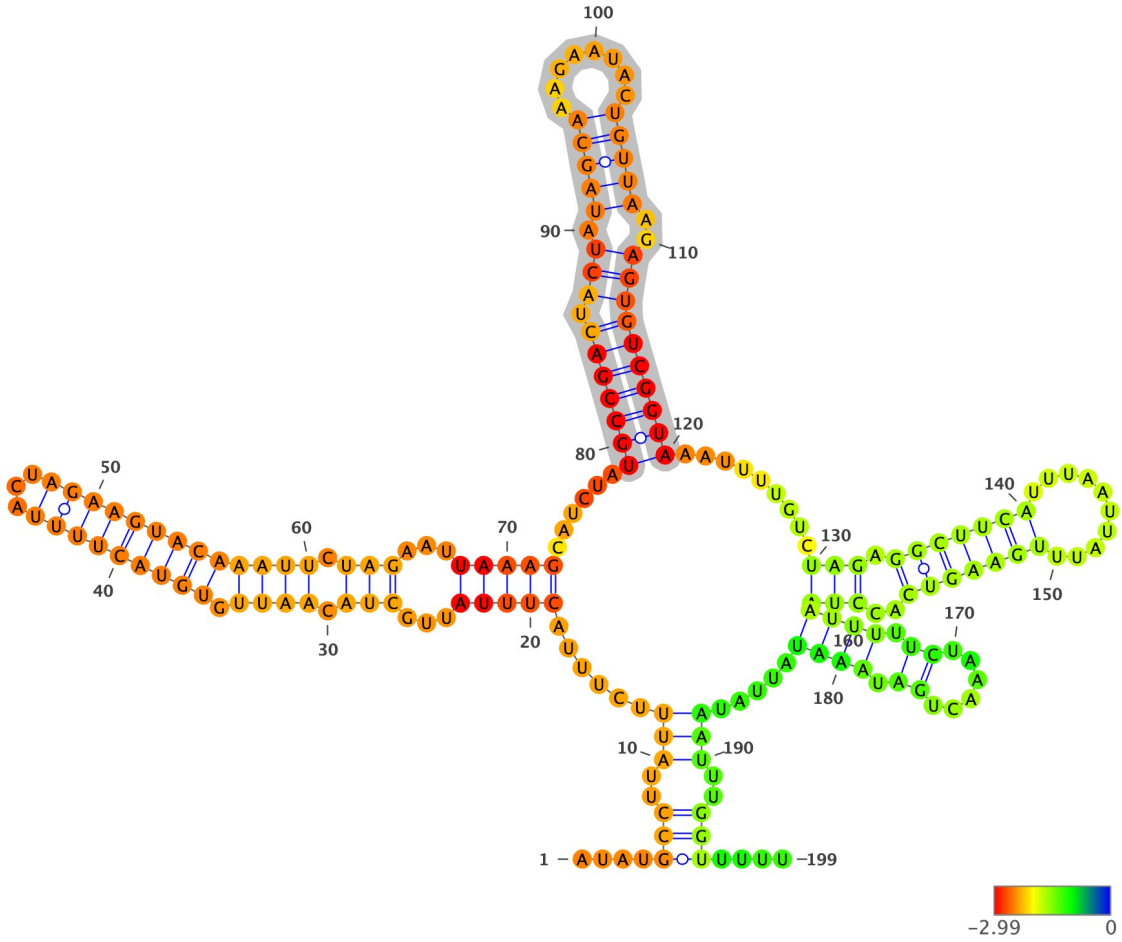
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 139 from nt 6846 to 6887 (nt 79 to 120)

```
5'-TGCCGACTACTATAGCAAAGAATACUGUUAAGAGTGUCGGUA-3'
5'-((((((...((.(((((........)))))..))..)))))))-3'
Motif MFE = -14.8; z-score = -3.7; 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 = -2.64; ED = 21.82
```

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, 266-13468(+)

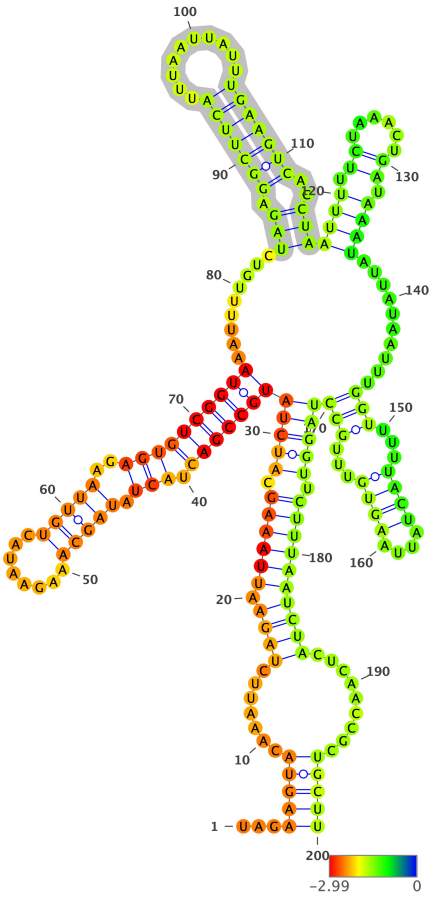
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 140 from nt 6897 to 6929 (nt 84 to 116)

```
5'-TAGAGGCTTCATTTAATTATTUGAAGUCACCUA-3'
5'-(((.(((((((.........)))))))..)))-3'
Motif MFE = -7.7; z-score = -3.1; 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 6814 to 7013 (motif highlighted in silver):

```
5'-UAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUC
ACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUU-3
5'-...(((((.......((((.((((((.(((((((((((.(((.(((((........))))).)).)))))))))).........(((.(((((((.........)))))))
..)))(((((.((......)).)))).........(((...((((....))))...)))))))).)))))))).........))))-3'
MFE = -40.0; z-score = -2.17; ED = 30.72
```

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(+)

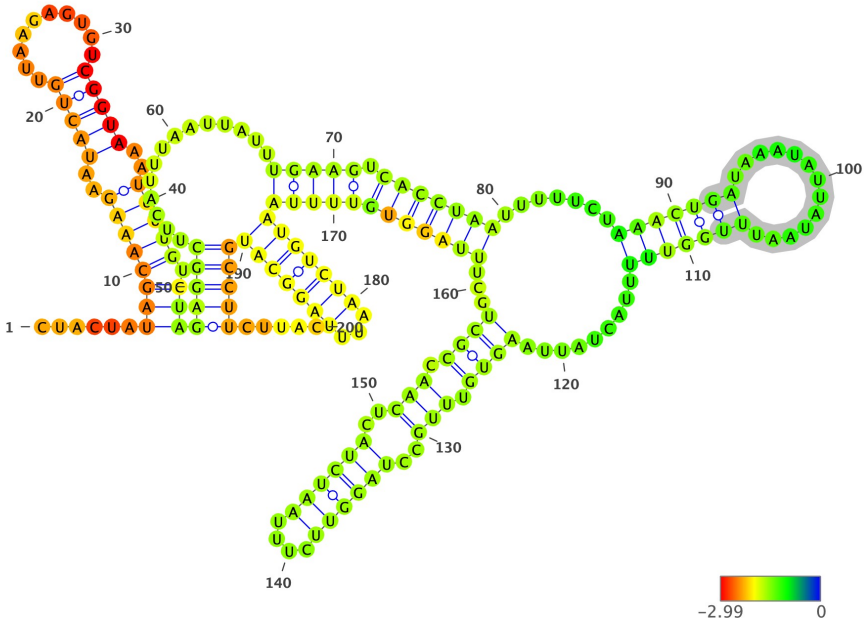
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 141 from nt 6943 to 6959 (nt 92 to 108)

```
5'-GATAAATATTATAATUU-3'
5'-((.............))-3'
Motif MFE = 0.0; z-score = 0.22; ED = 0.8
```



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 6852 to 7051 (motif highlighted in silver):

```
5'-CUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGU
UUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUAC-3
5'-......(((((((((..(((((..........)))))..))))))..)))))(((((.............(((((.(((((((.......(((((((.............)))))))
)).........((((.(((..(((((((....)))))))..))).)))))...)))))))))))))))(((((((...)))))))))))))).....-3'
MFE = -35.1; z-score = -0.8; ED = 39.68
```

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(+)

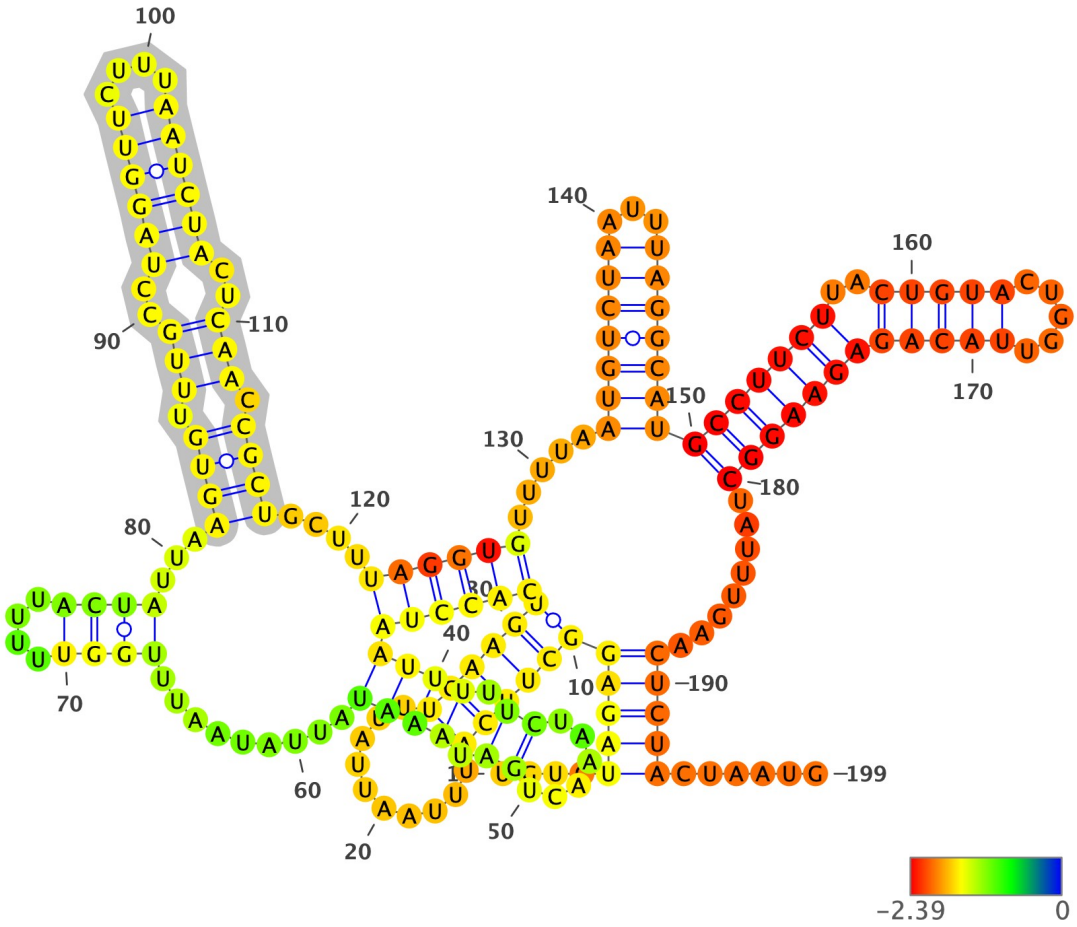
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 6974 to 7009 (nt 82 to 117)

```
5'-AGTGTTTGCCTAGGTTCTTTAAUCUACTCAACCGCU-3'
5'-((((.(((..(((((((....)))))))..))).))))-3'
Motif MFE = -7.2; z-score = -2.19; 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 6893 to 7091 (motif highlighted in silver):

```
5'-UGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCA
ACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUG-3
5'-....((((((((((.........))))))((((((((((.((......)).)))).........((((....))))))...((((.(((..(((((((....)))))))..))
).))))....))))))).....(((((((...)))))))((((((..(((((.....)))))))))))).......))))).....-3'
MFE = -46.1; z-score = -2.98; ED = 19.3
```

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(+)

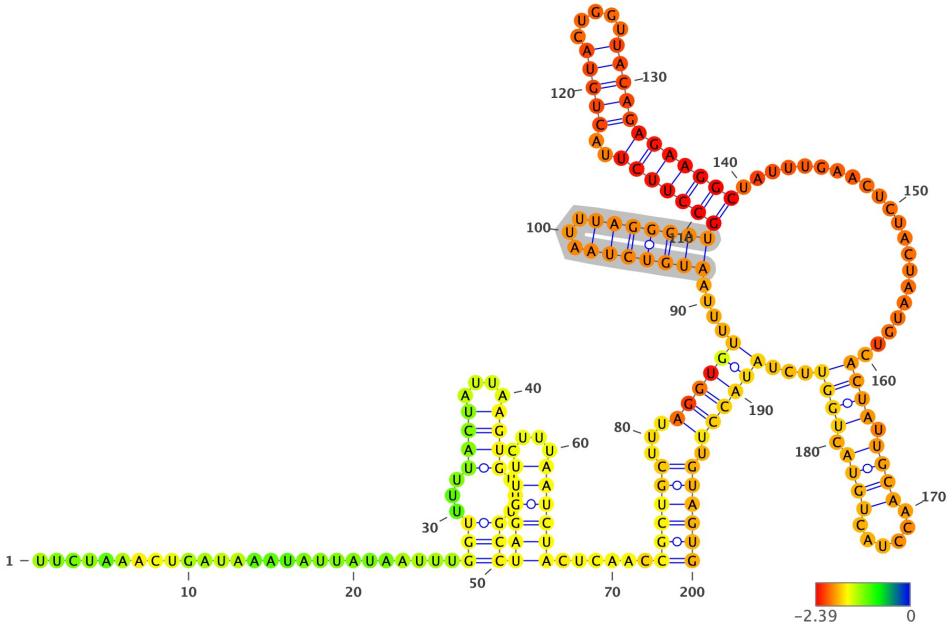
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 143 from nt 7025 to 7041 (nt 92 to 108)

```
5'-ATGTCTAATTUAGGCAU-3'
5'-(((((((...)))))))-3'
Motif MFE = -4.2; z-score = -5.77; 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 = -1.71; 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(+)

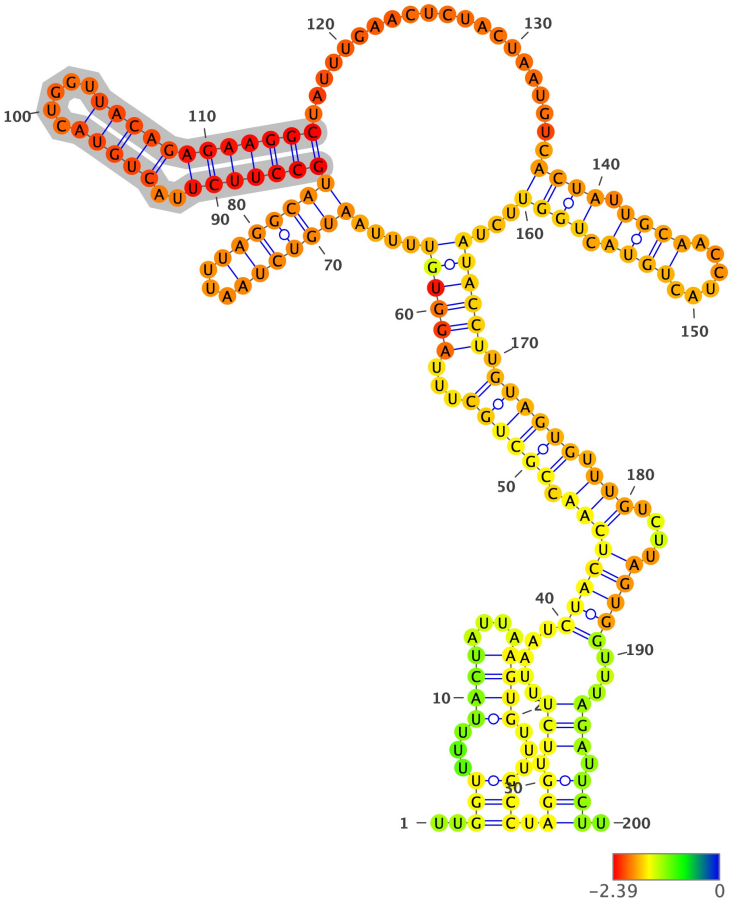
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 144 from nt 7042 to 7072 (nt 85 to 115)

```
5'-GCCTTCTTACTGTACTGGTUACAGAGAAGGC-3'
5'-(((((((..(((((.....)))))))))))-3'
Motif MFE = -13.1; z-score = -3.97; 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 = -3.65; 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(+)

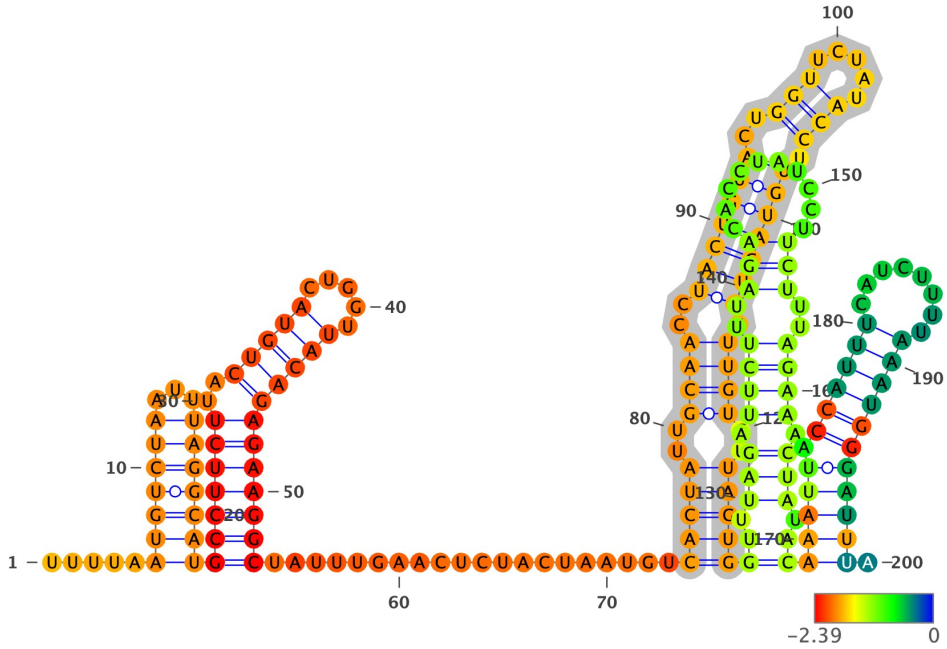
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 145 from nt 7093 to 7145 (nt 74 to 126)

```
5'-CACTATTGCAACCTACTGTACTGGTTCTATACCTUGUAGUGTUUGUCTUAGUG-3'
5'-(((((..((((..(((((((..(((.....))).)))))))).))))..)))))-3'
Motif MFE = -12.3; z-score = -2.45; 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 = -45.2; z-score = -3.19; ED = 16.57
```

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 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(+)

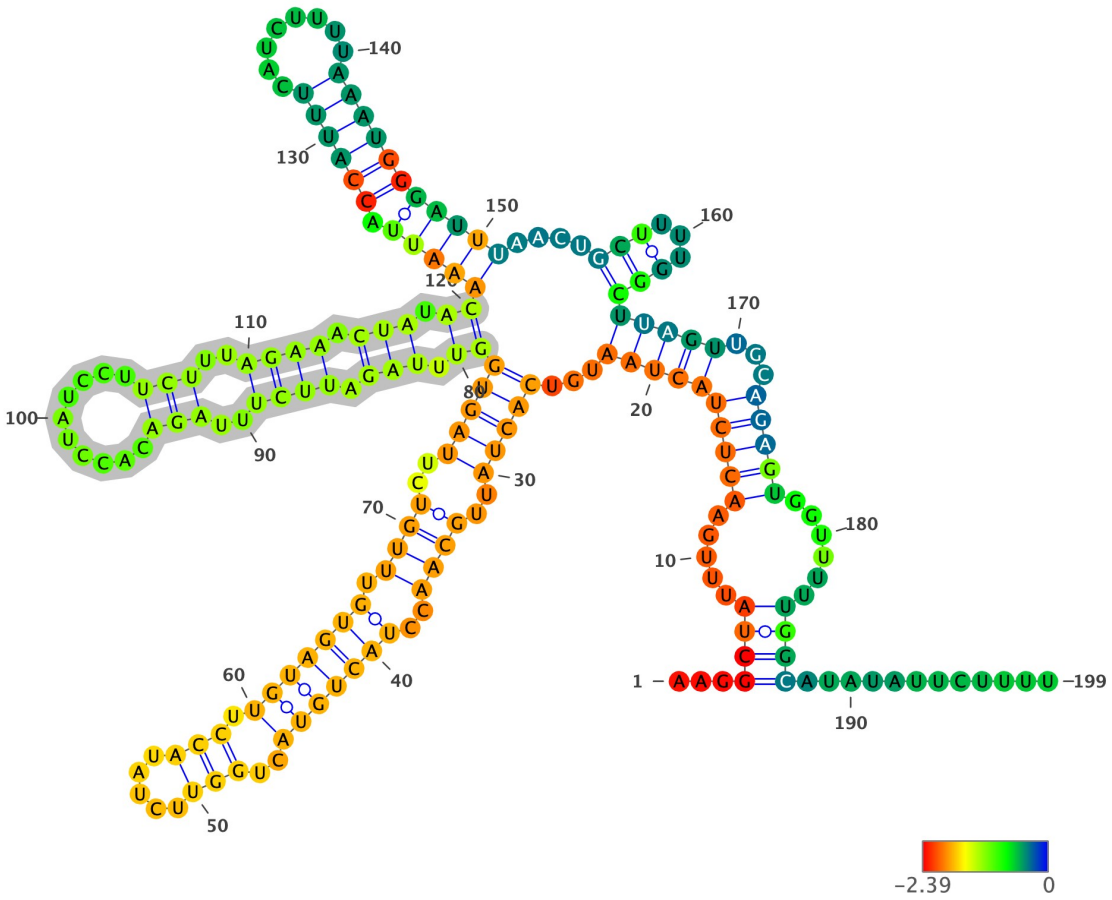
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7146 to 7187 (nt 79 to 120)

```
5'-GTTTAGATTCTTTAGACACCTATCCTUCUTTAGAAACUATAC-3'
5'-((.(((.((((..(((..........)))..)))).))).))-3'
Motif MFE = -5.4; z-score = -2.16; 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 7068 to 7266 (motif highlighted in silver):

```
5'-AAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAG
AAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUU-3
5'-...((((.....((((((((((...(((((..((((..(((((((..(((.....))).)))))))).))))..)))))((.(((.((((..(((..........)))..))
)).))).))(((((.((((((........)))))))))))....(((...)))))))))...)))))......))))............-3'
MFE = -37.9; z-score = -1.54; ED = 33.06
```

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(+)

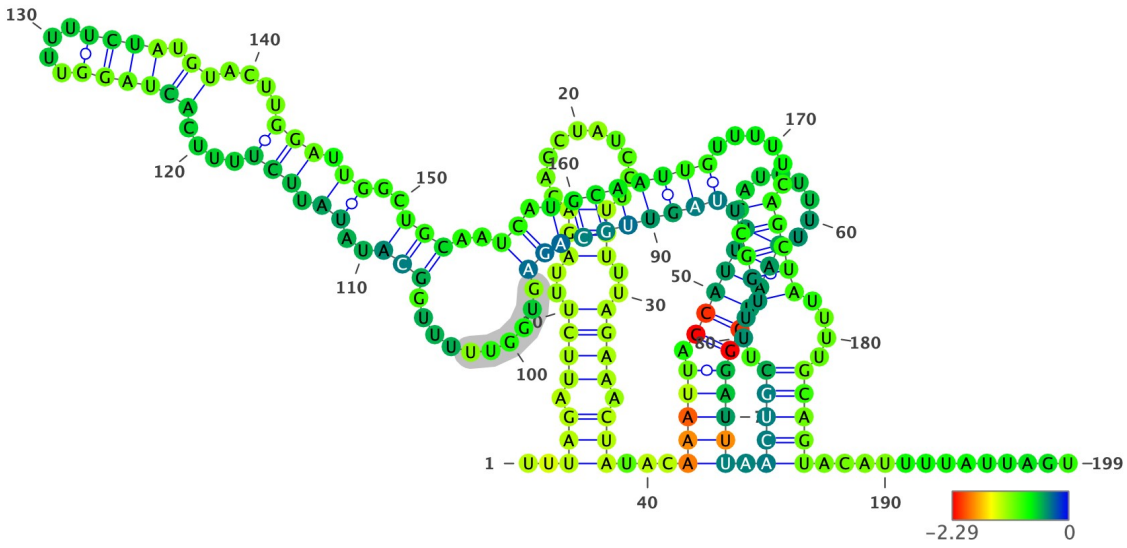
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 147 from nt 7243 to 7248 (nt 97 to 102)

```
5'-GTGGTU-3'
5'-(....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.0
```



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 7147 to 7345 (motif highlighted in silver):

```
5'-UUUAGAUUCUUUAGACACCUAUCCUUCUUUAGAAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUA
UAUUCUUUUCACUAGGUUUUUCUAUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAGCUAUUUUGCAGUACAUUUUAUUAGU-3
5'-..(((.(((((..(((..........)))..)))))..)))...((((((.((((((........))))))))))).((((((...((((((((((((((.........(((..
((.(((....((((((....)))))..))....)))).))..))))..)).)))))))).....))))).....))))).............-3'
MFE = -33.7; z-score = -0.99; ED = 47.31
```

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(+)

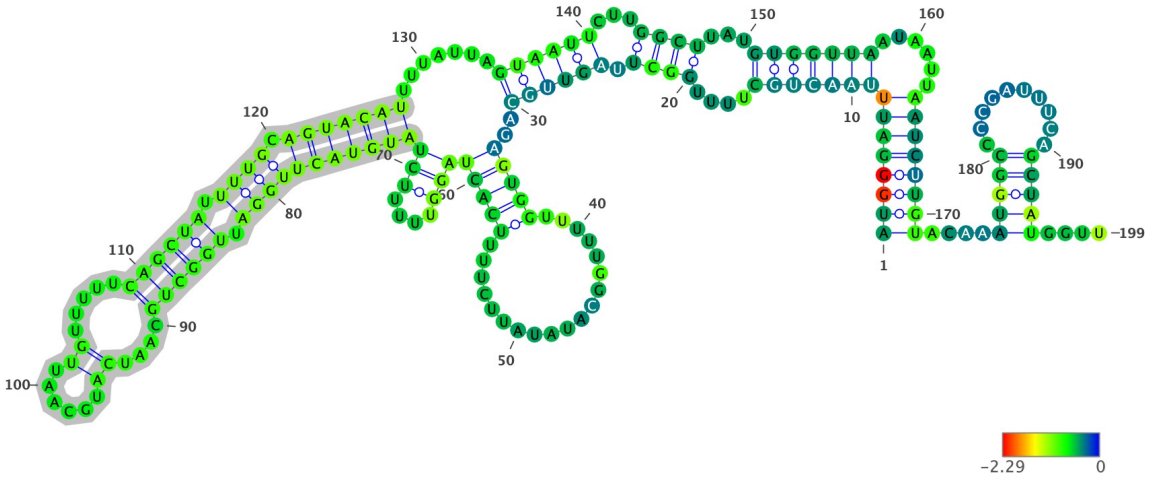
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 148 from nt 7281 to 7336 (nt 72 to 127)

```
5'-ATGTACTTGGATTGGCTGCAATCATGCAATUGTTTTTCAGCUATUUUGCAGUACAU-3'
5'-(((((((((((.................................)))).)))))))-3'
Motif MFE = -14.5; z-score = -2.83; 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 = -34.8; z-score = 0.27; ED = 64.48
```

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(+)

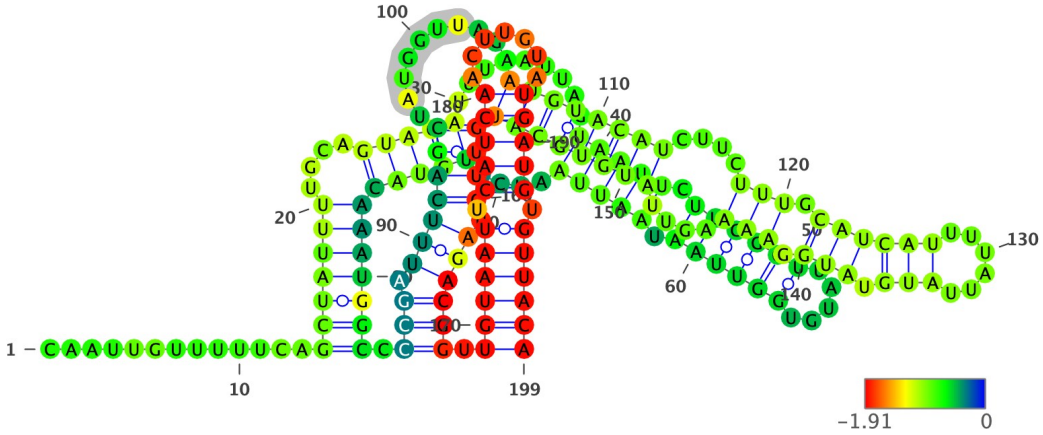
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 149 from nt 7403 to 7408 (nt 97 to 102)

```
5'-ATGGTU-3'
5'-(....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.0
```



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 7307 to 7505 (motif highlighted in silver):

```
5'-CAAUUGUUUUUCAGCUAUUUUGCAGUACAUUUUAUUAGUAAUUCUUGGCUUAUGUGGUUAAUAAUUAAUCUUGUACAAAUGGCCCCGAUUUCAGCUAUGGUUAGAAUGUAC
AUCUUCUUUGCAUCAUUUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACA-3
5'-............(((((((....(((((.........(((((.(((((.....)))))).)))))....)))))))))))).(((.(((((((..........((((((
((....(((.((((((......))).))).))).....))))))))))))).)))))).((((((.(((((.......))))).)))))).)))))-3'
MFE = -39.2; z-score = -0.81; ED = 42.19
```

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(+)

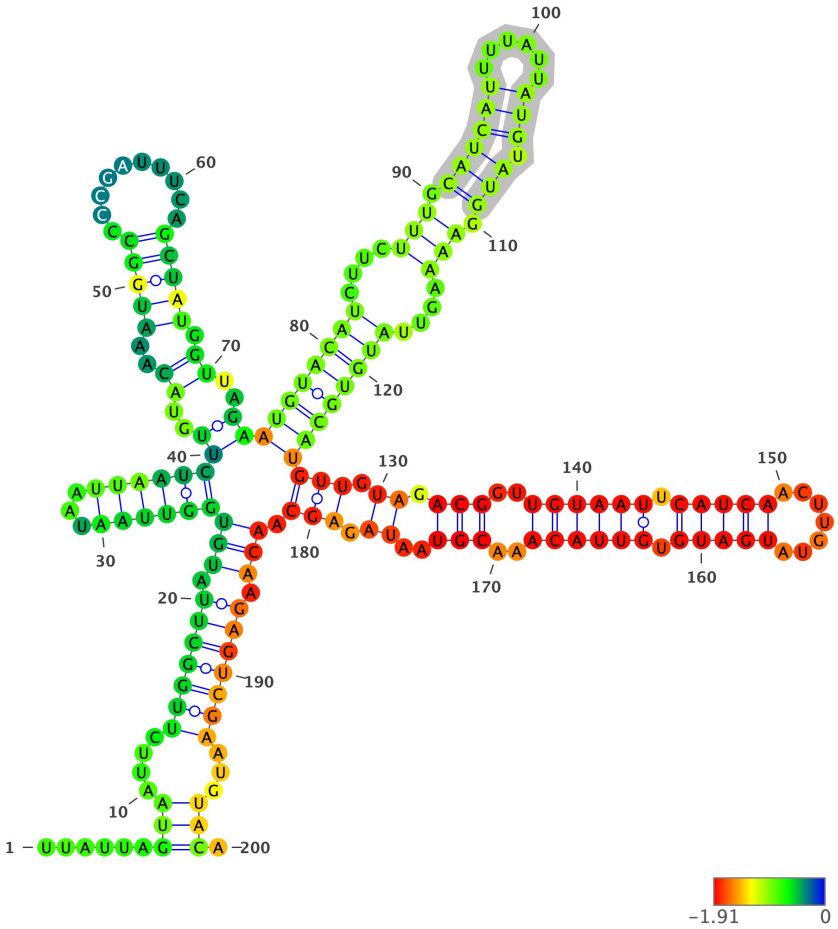
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 150 from nt 7428 to 7446 (nt 91 to 109)

```
5'-CATCATTTTATTAUGTAUG-3'
5'-((((((......))).)))-3'
Motif MFE = -0.5; z-score = -0.72; 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 7338 to 7537 (motif highlighted in silver):

```
5'-UUAUUAGUAAUUCUUGGCUUAUGUGGUUAAUAAUUAAUCUUGUACAAAUGGCCCCGAUUUCAGCUAUGGUUAGAAUGUACAUCUUCUUUGCAUCAUUUUAUUAUGUAUGGA
AAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACA-3
5'-......(((....(((((((.(((((((((...))))))((..((..(((((..........))))).))..))((((((((....(((.((((((......))).))).)
))....))))))))(((.((.(((..((((((.(((((.......))))).))))))..)))..)).))).))).)))))))...))).-3'
MFE = -45.4; z-score = -1.78; ED = 23.65
```

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, 266-13468(+)

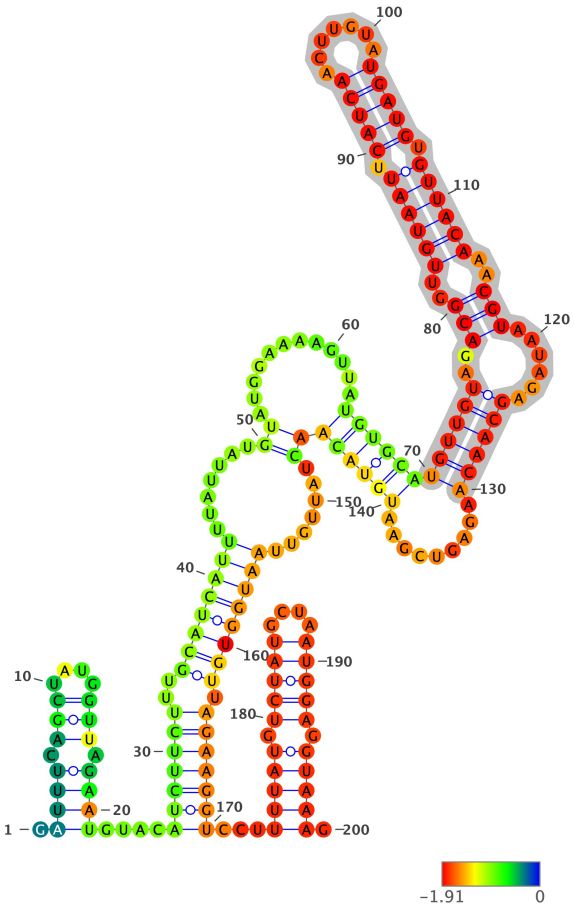
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7462 to 7522 (nt 70 to 130)

```
5'-TGTTGTAGACGGTTGTAATTCATCAACTTGTAUGAUGTGUUACAAACGUAATAGAGCAACA-3'
5'-((((((..(((..((((((.(((((.......))))).))))))..)))......))))))-3'
Motif MFE = -18.7; z-score = -3.8; 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 7393 to 7592 (motif highlighted in silver):

```
5'-GAUUUCAGCUAUGGUUAGAAUGUACAUCUUCUUUGCAUCAUUUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUA
CAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAG-3
5'-.((((.(((....))).))))....(((((((..((((((((.......((............(((((((((((..(((..((((((.(((((.......))))).))))
))..)))......))))))).........))))))))).......))))))))).)))))))...(((((.(((((....))))).))))).-3'
MFE = -44.0; z-score = -2.23; 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, 266-13468(+)

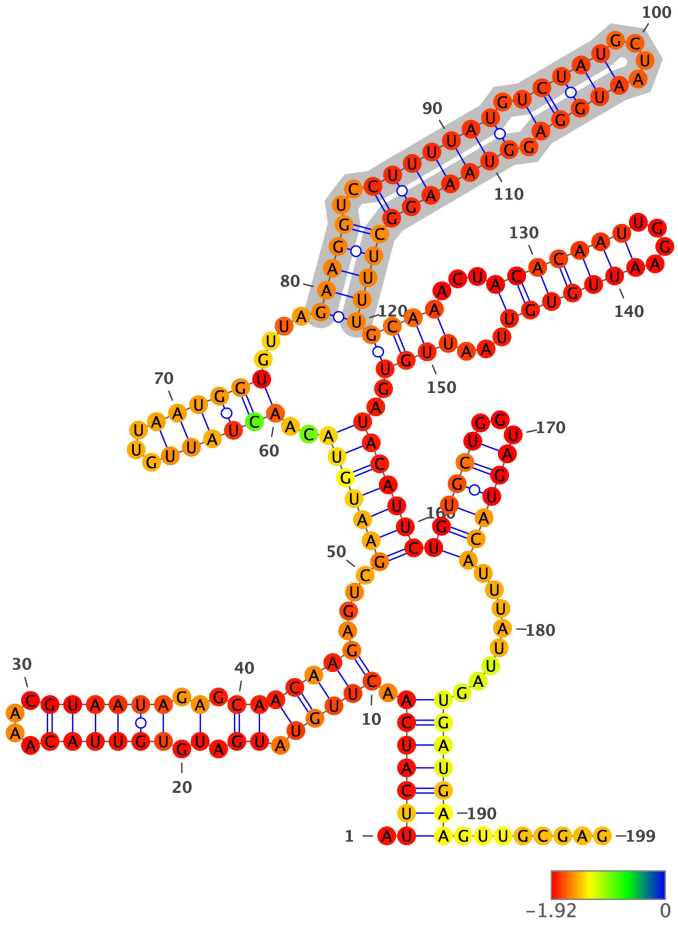
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 152 from nt 7557 to 7598 (nt 79 to 120)

```
5'-GAAGGTCCTTTTATGTCTATGCTAAUGGAGGUAAAGGCUUUU-3'
5'-((((...(((((((.(((((....))))).)))))))).))))-3'
Motif MFE = -13.3; z-score = -3.47; ED = 4.92
```



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 7479 to 7677 (motif highlighted in silver):

```
5'-AUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUA
AAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAG-3
5'-.(((((((.(((((.((.(.((((((....)))))).).)))))))....(((((((..((((((...)))))).....(((((..(((((((.(((((....))))).)))
))))))))))((((...(((((((....)))))))...)))).)))))))((((((...)))))).........)))))))........-3'
MFE = -48.5; z-score = -2.93; ED = 43.33
```

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(+)

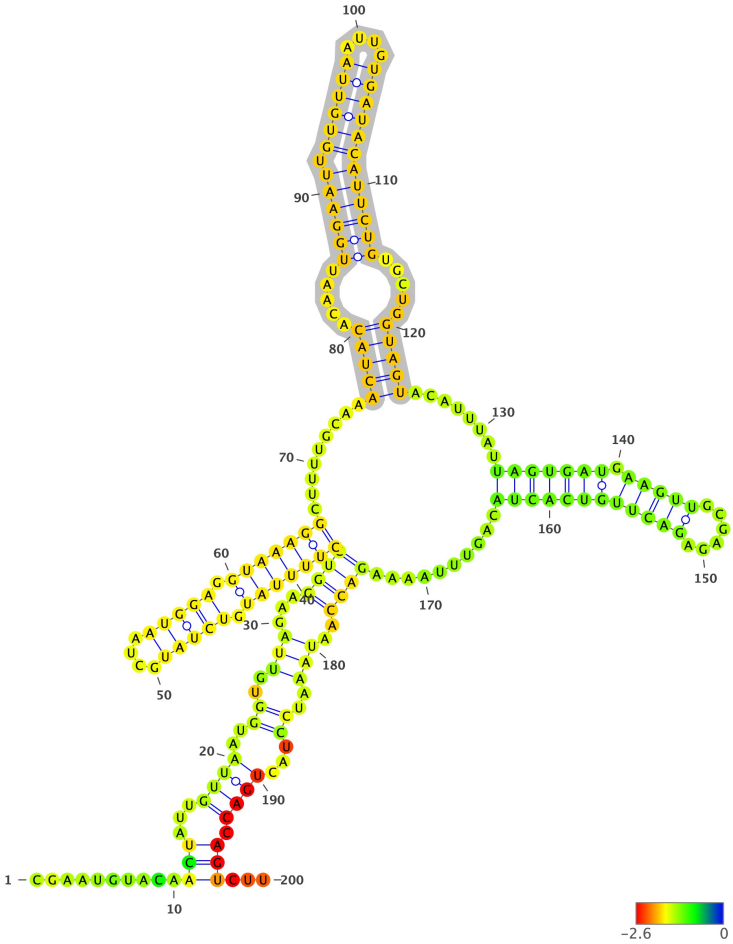
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 153 from nt 7603 to 7651 (nt 76 to 124)

```
5'-ACTACACAATTGGAATTGTGTTAATTGUGAUACAUUCUGTGCTGGUAGU-3'
5'-(((((.....((((((.((((((....))))))))))))).....)))))-3'
Motif MFE = -11.6; z-score = -2.08; ED = 5.96
```



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 7528 to 7727 (motif highlighted in silver):

```
5'-CGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUU
CUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUU-3
5'-..........(((...((((..((..(((...(((((((((((.(((((....))))).)))))))).........(((((.....((((((.((((((....)))))))))
)))).....)))))........(((((((.(((((......))))))))))))..........))))..)))..))...)))).)))...-3'
MFE = -43.5; z-score = -2.14; ED = 50.34
```

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(+)

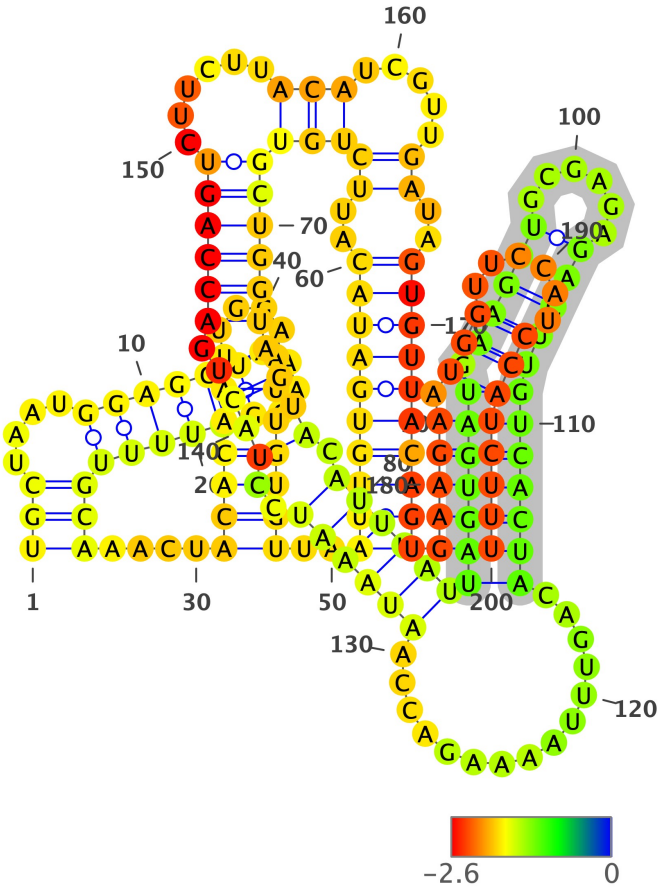
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 154 from nt 7660 to 7690 (nt 85 to 115)

```
5'-TAGTGATGAAGTTGCGAGAGACUUGUCACUA-3'
5'-(((((((.(((((.....)))))))))))))-3'
Motif MFE = -10.2; z-score = -3.28; ED = 2.13
```



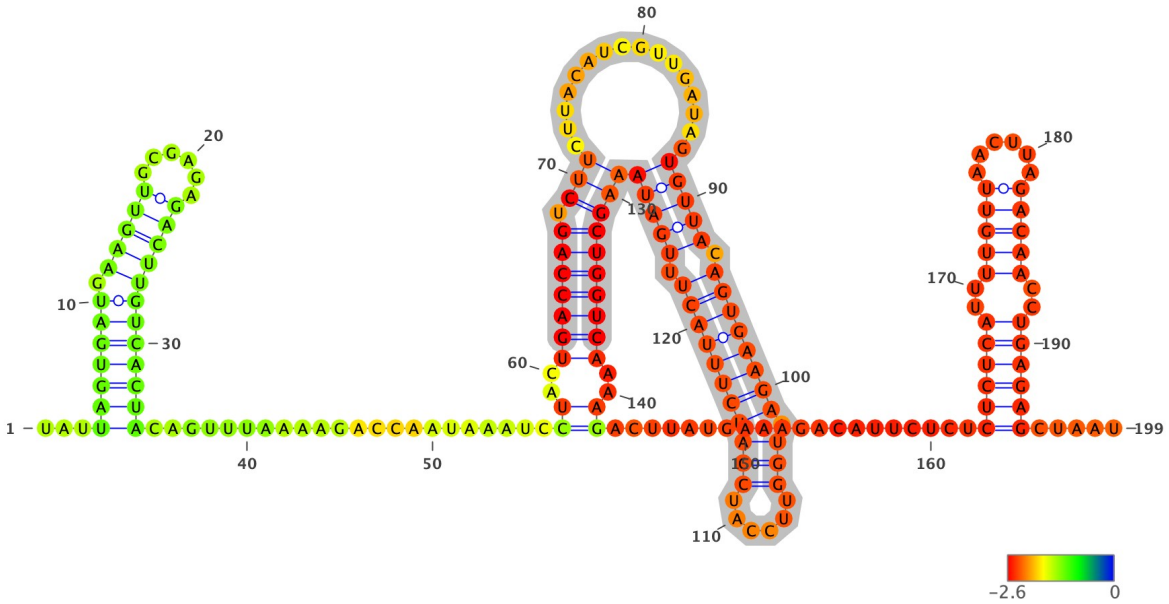
Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 7576 to 7775 (motif highlighted in silver):

```
5'-UGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUC
ACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUU-3
5'-(((....((((((....))))))))).....(((((((....))))))).(((((((((..((((((((((((((.((((((((((((.(((((.....)))))))))))))
```

NC_045512.2 (forward strand): Structure number 155 from nt 7718 to 7793 (nt 62 to 137)

```
5'-GACCAGTCTTCTTACATCGTTGATAGTGTTACAGTGAAGAATGGTTCCATCCAUCUUUACUTUGAUAAAGCUGGUC-3'
5'-((((((.(.................(((((.(((((((((.(((.....)))))))))))).))))))..)))))))-3'
Motif MFE = -22.0; z-score = -3.32; ED = 8.09
```



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 7657 to 7855 (motif highlighted in silver):

```
5'-UAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAU
CCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAU-3
5'-...(((((((.(((((.....)))))))))))).....................((..(((((((.(((.................(((((.(((((((((.(((.....
)))))))))))).)))))))))))))..))...................(((((((..(((((.....)))))))..)))))).....-3'
MFE = -46.8; z-score = -3.21; 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 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(+)

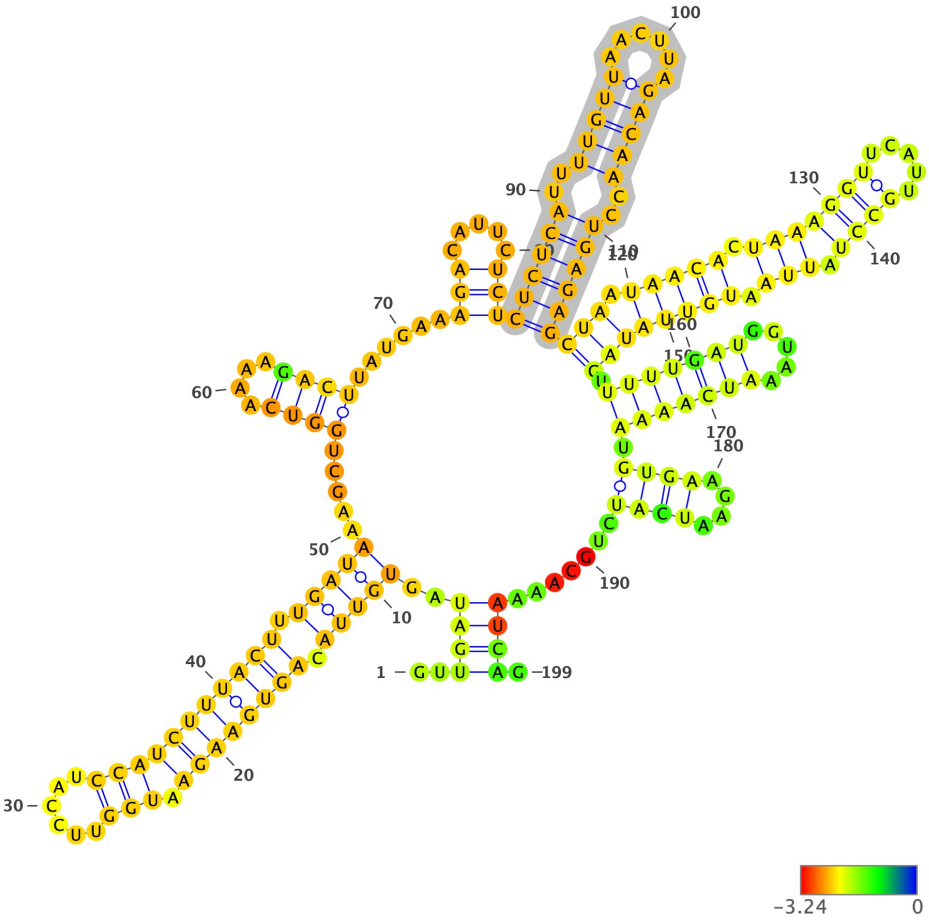
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 156 from nt 7819 to 7850 (nt 84 to 115)

```
5'-CTCTCATTTTGTTAACTTAGACAACCUGAGAG-3'
5'-((((((..(((((......)))))..))))))-3'
Motif MFE = -10.3; z-score = -4.67; 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 = -2.57; ED = 30.63
```

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, 266-13468(+)

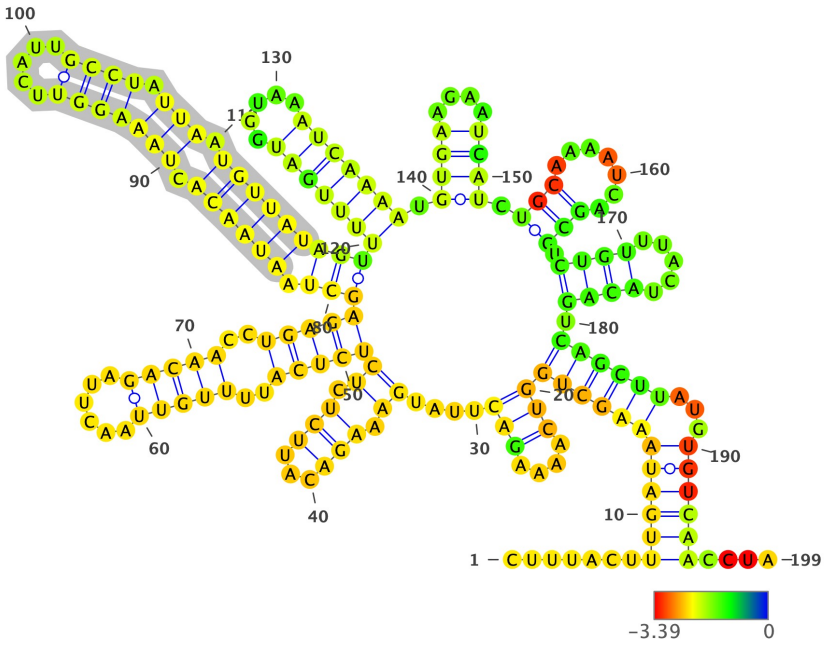
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7854 to 7887 (nt 83 to 116)

```
5'-ATAACACTAAAGGTTCATTGCCUAUUAAUGUUAU-3'
5'-((((((.(((((((.....)))).))).))))))-3'
Motif MFE = -7.6; z-score = -3.23; 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 7772 to 7970 (motif highlighted in silver):

```
5'-CUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAU
GUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUA-3
5'-.......((((((((((((((....)))....((.(((...))).))(((((..(((((......)))))..)))))(((.((((((.(((((((.....)))).))).)
))))))))(((((((.....)))))))).((((....)))).(((.......))).((((.....)))).))))))...))))))....-3'
MFE = -43.5; z-score = -2.52; ED = 29.25
```

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, 266-13468(+)

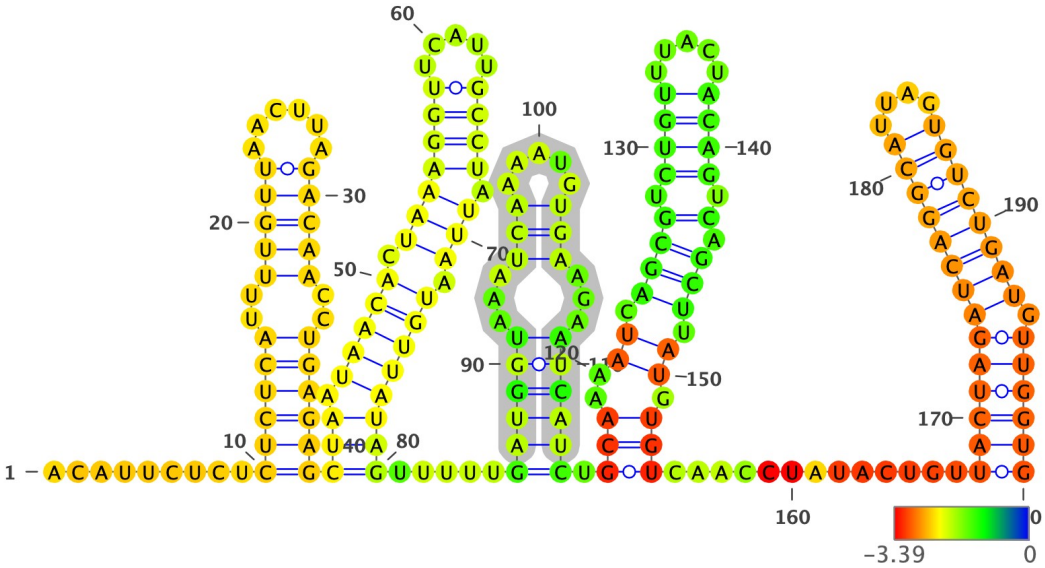
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 158 from nt 7896 to 7922 (nt 87 to 113)

```
5'-ATGGTAAATCAAAATGUGAAGAAUCAU-3'
5'-((.(....(((.....))).....).))-3'
Motif MFE = -1.3; z-score = -0.45; ED = 4.46
```



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 7810 to 8009 (motif highlighted in silver):

```
5'-ACAUUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUC
AUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUG-3
5'-.........((((((..(((((.....)))))..)))))))(((.(((((.(((((((.....)))))).))).))))))))).....((((((...(((.....)))...)))
))).(((..((.((((.((((.....)))).).))).)).))).............((((((((((((((....))))))))).)))))-3'
MFE = -44.9; z-score = -1.87; ED = 19.44
```

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, 266-13468(+)

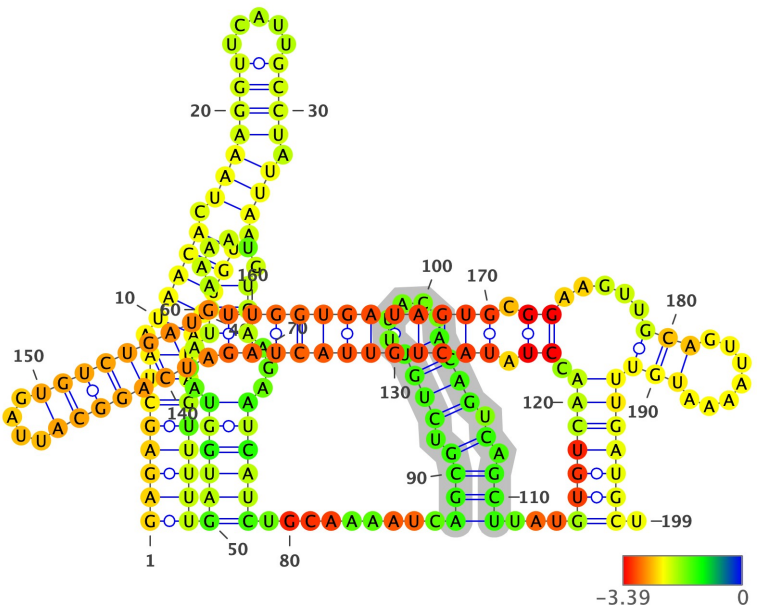
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7933 to 7956 (nt 88 to 111)

```
5'-AGCGTCTGTTTACTACAGTCAGCU-3'
5'-((((.((((.....)))).).)))-3'
Motif MFE = -5.8; z-score = -2.38; 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 7846 to 8044 (motif highlighted in silver):

```
5'-GAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCU
UAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCU-3
5'-(((((((.(((((.(((((((.....)))).))).)))))))))))))(((((((...(((.....)))...)))))))........((((.((((.....)))).).)))
...(((((((.((.((((((((((((((((((....))))))))).)))))))))))))).))).....(((.......)))))))))).-3'
MFE = -53.0; z-score = -2.8; ED = 30.28
```

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

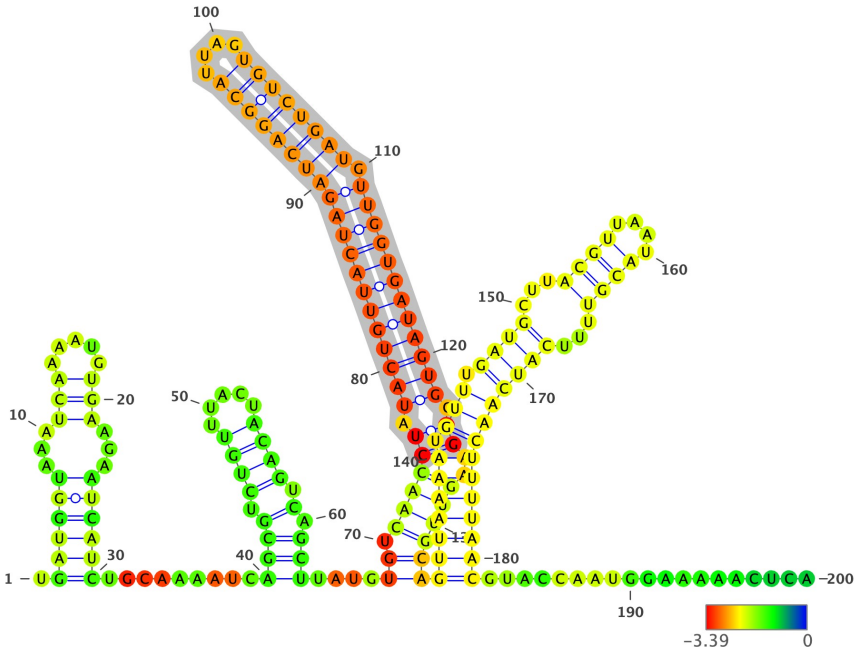
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7968 to 8018 (nt 75 to 125)

```
5'-CTATACTGTTACTAGATCAGGCATTAGUGUCUGAUGUUGGUGAUAGUGCGG-3'
5'-((.(((((((((((((((((((....)))))))).))))))))))))).))-3'
Motif MFE = -21.9; z-score = -5.02; ED = 2.66
```



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 7894 to 8093 (motif highlighted in silver):

```
5'-UGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGU
UGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCA-3
5'-.((((((...(((.....)))...))))))........((((.((((.....)))).).)))....((.((((((.((((((((((((((((((((....)))))))).)
))))))))))).))..))))))(((((((.(((.((((...((((....))))...)))))))))))))).....................-3'
MFE = -51.9; z-score = -2.7; ED = 24.93
```

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(+)

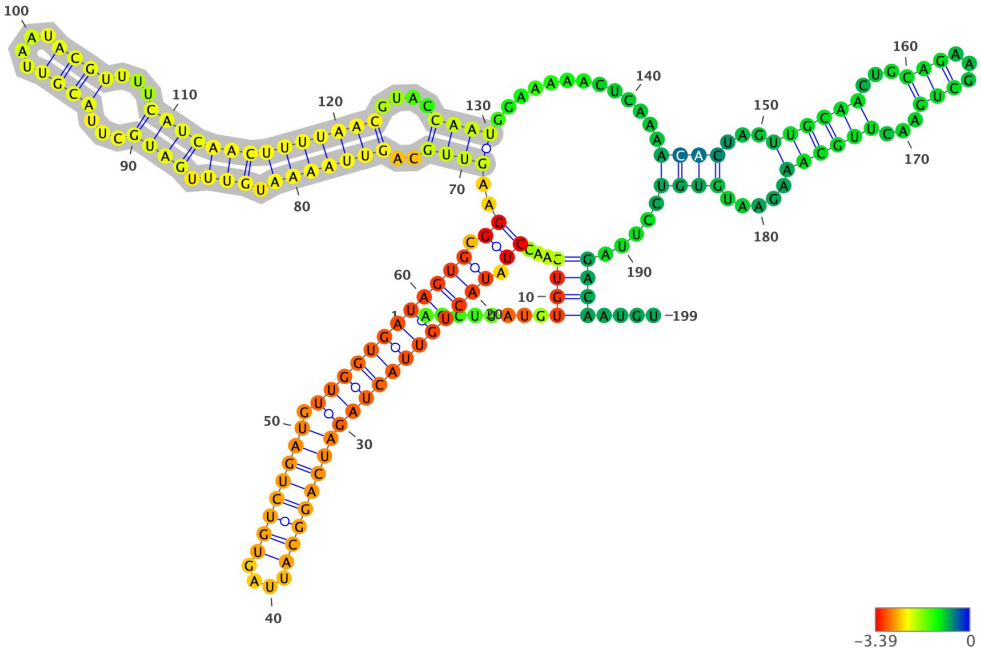
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 8021 to 8082 (nt 69 to 130)

```
5'-GTTGCAGTTAAAATGTTTGATGCTTACGTTAATACGUTTTCAUCAACUUUUAACGTACCAAU-3'
5'-((((..(((((((.(((.((((...((((....))))...))))))))))))))....))))-3'
Motif MFE = -15.0; z-score = -3.54; 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 7953 to 8151 (motif highlighted in silver):

```
5'-AGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAU
CAACUUUUAACGUACCAAUGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUGU-3
5'-........((((...((.((((((((((((((((((((....))))))))).))))))))))))).))..((((..(((((((.(((.((((...((((....))))...)))
))))))))))....))))..............((((...((((((...(((...)))...))))))).....))))).....))))....-3'
MFE = -51.0; z-score = -2.16; ED = 15.32
```

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(+)

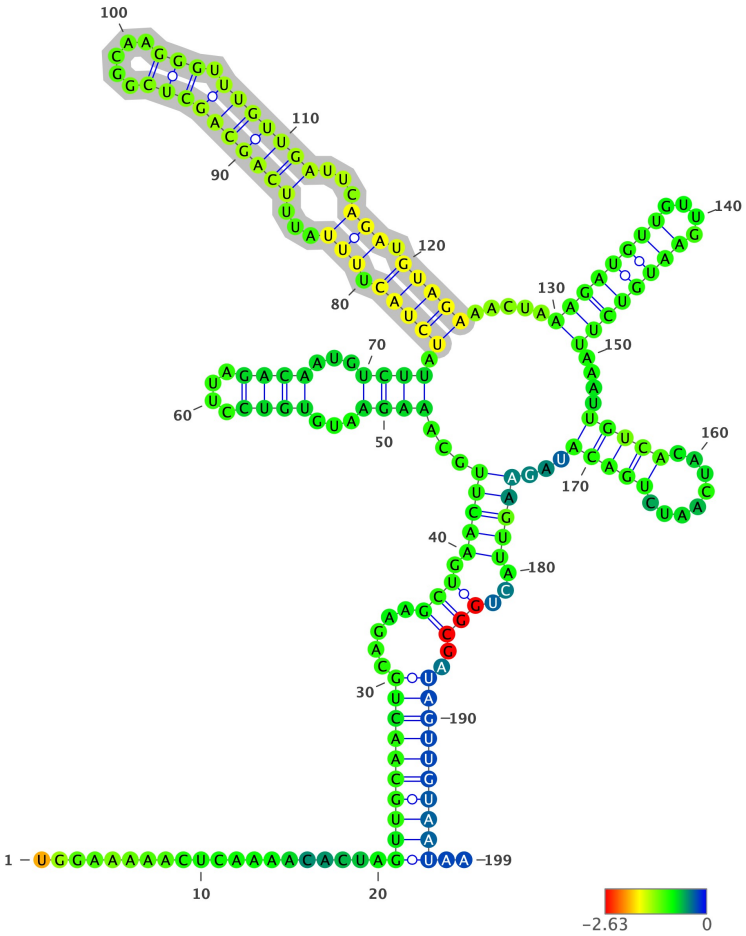
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 162 from nt 8156 to 8205 (nt 75 to 124)

```
5'-TCTACTTTTATTTCAGCAGCTCGGCAAGGGTUUGUUGATTCAGATGUAGA-3'
5'-(((((.(((...((((((((((.....))).)))))))...))).)))))-3'
Motif MFE = -15.0; z-score = -3.16; 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 8082 to 8280 (motif highlighted in silver):

```
5'-UGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUG
AUUCAGAUGUAGAAACUAAAGAUGUUGUUGAAUGUCUUAAAUUGUCACAUCAAUCUGACAUAGAAGUUACUGGCGAUAGUUGUAAUAA-3
5'-....................((((((((((.....(((.(((((...((((...((((....))))...)))).(((((.(((...((((((((((.....))).))))))
)...))).)))))).....((((((((....))))))))....(((((........)))))...)))))...)))..)))))))))..-3'
MFE = -45.8; z-score = -1.99; ED = 26.36
```

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(+)

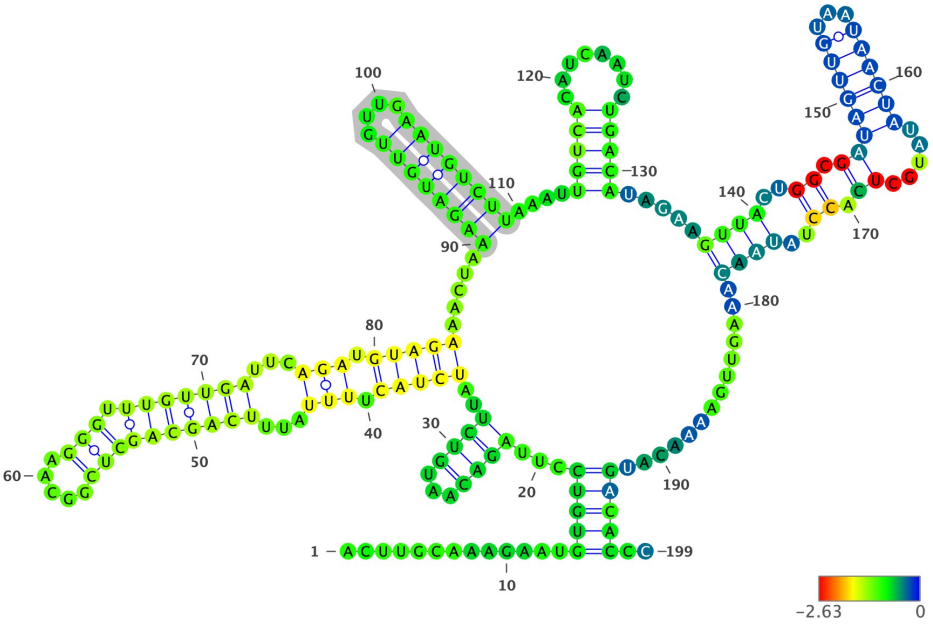
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 163 from nt 8211 to 8230 (nt 90 to 109)

```
5'-AAGATGTTGTTGAAUGUCUU-3'
5'-((................))-3'
Motif MFE = -4.2; z-score = -3.68; ED = 0.74
```



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 8122 to 8320 (motif highlighted in silver):

```
5'-ACUUGCAAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAUUCAGAUGUAGAAACUAAAGAUGUUGUUGAAUGUCUUAA
AUUGUCACAUCAAUCUGACAUAGAAGUUACUGGCGAUAGUUGUAAUAACUAUAUGCUCACCUAUAACAAAGUUGAAAACAUGACACCC-3
5'-............(((((...((((...)))))..(((((.(((...((((((((((.....))).)))))))...)))).)))))).....(((((((....)))))))).
..(((((........)))))).....((((..((.(((((((...))))))).....)).)).))))..............))))))..-3'
MFE = -40.4; z-score = -1.51; ED = 35.47
```

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(+)

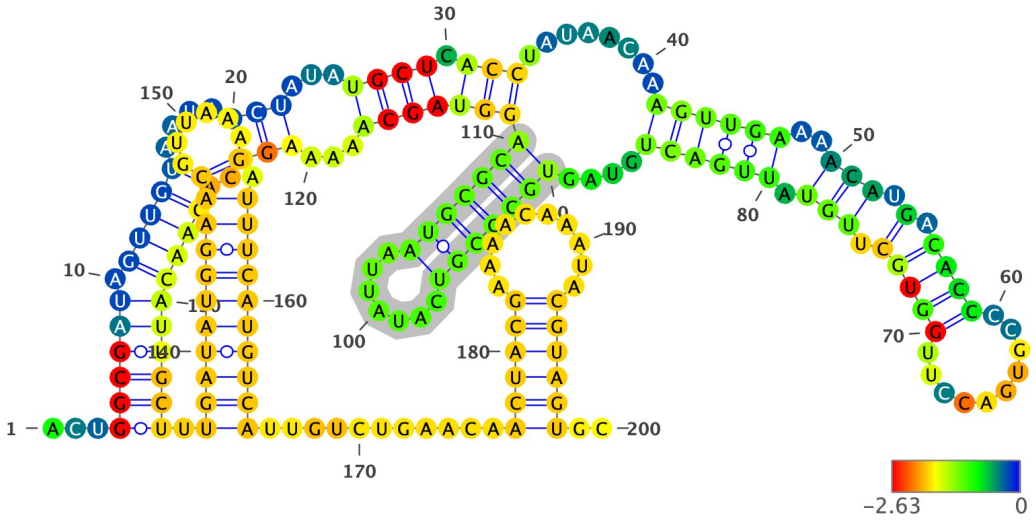
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 164 from nt 8350 to 8370 (nt 90 to 110)

```
5'-TGCGCGTCATATTAAUGCGCA-3'
5'-(((((((.......)))))))-3'
Motif MFE = -7.8; z-score = -3.99; 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 = -2.16; 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(+)

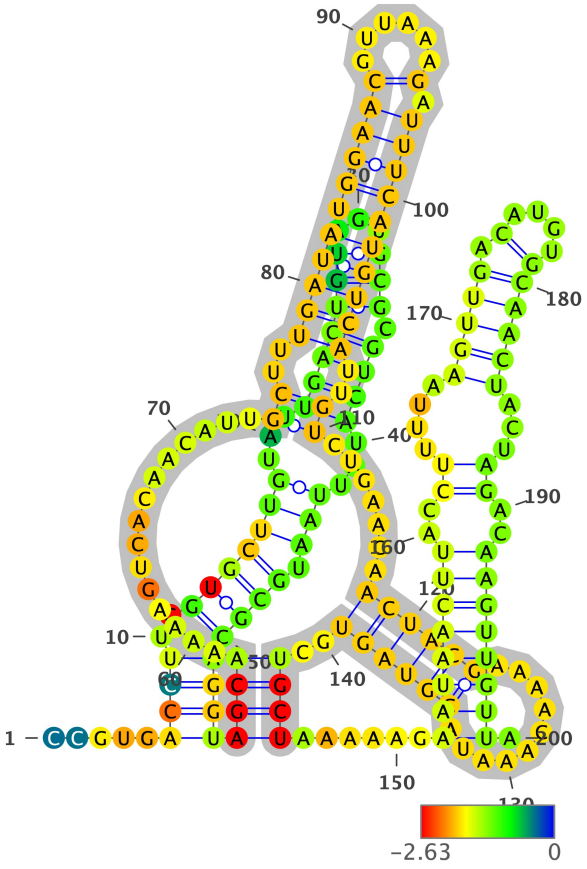
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 165 from nt 8374 to 8464 (nt 55 to 145)

```
5'-AGCAAAAAGTCACAACATTGCTTTGATATGGAACGTTAAAGAUUUCAUGUCATTGUCTGAACAACTACGAAAACAAATACGUAGUGCTGCU-3'
5'-(((................((..(((((((((((......).))))))))))..)).......((((((..........))))))...)))-3'
Motif MFE = -17.9; z-score = -2.28; ED = 12.47
```



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 8320 to 8519 (motif highlighted in silver):

```
5'-CCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUC
UGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUA-3
5'-.....((((..(((((((...(((((((...))).))))...))).))))))))((((................((..(((((((((((......).))))))))))..)).
......((((((..........))))))..))))......((((((((..((....(((((.(....))))))...))..)))))))).-3'
MFE = -41.5; z-score = -1.68; ED = 44.43
```

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(+)

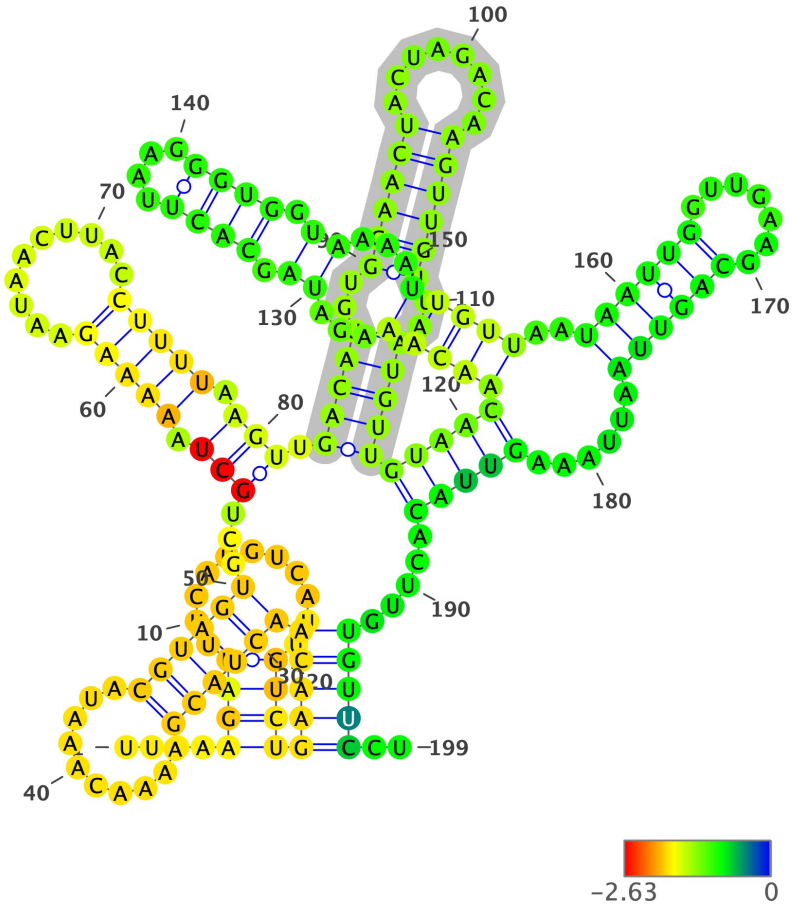
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 166 from nt 8491 to 8524 (nt 83 to 116)

```
5'-GACATGTGCAACTACTAGACAAGUUGUTAAUGUU-3'
5'-((((((..((((((........)))))))..))))))-3'
Motif MFE = -9.3; z-score = -2.78; 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 8409 to 8607 (motif highlighted in silver):

```
5'-UUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUA
AUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAAUUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUACACUUGUGUUCCU-3
5'-....((((..........))))((((((((((((.........))))))...(((.(((((.........))))).))).((((((..((((((........))))))..
))))))((((((((((...((.((((....)))).)).)...))))))..((((((.......))))))......))))).....))))))..-3'
MFE = -35.2; z-score = -0.66; ED = 36.38
```

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(+)

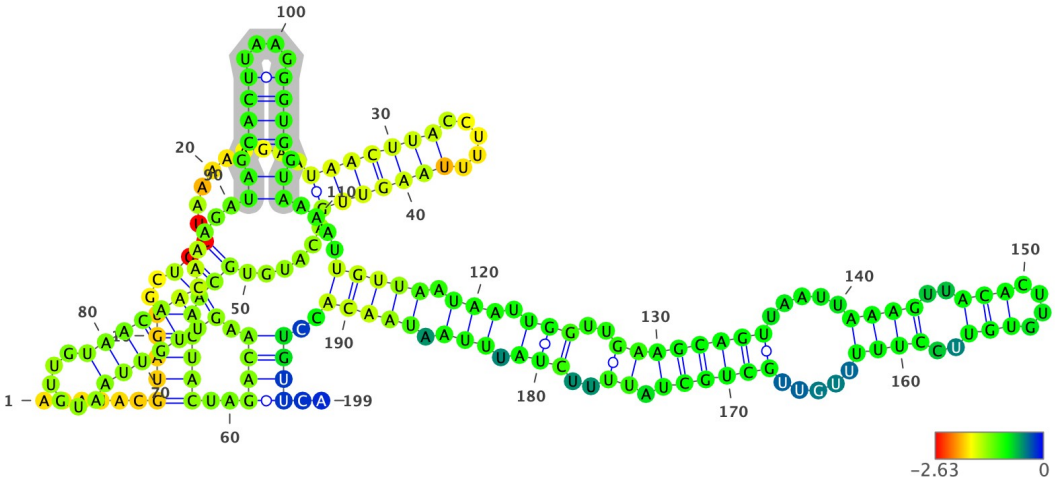
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 167 from nt 8538 to 8555 (nt 91 to 108)

```
5'-TAGCACTTAAGGGUGGUA-3'
5'-((.((((....)))).))-3'
Motif MFE = -3.2; z-score = -2.21; ED = 1.14
```



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 8448 to 8646 (motif highlighted in silver):

```
5'-AAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAA
UUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUACACUUGUGUUCCUUUUUGUUGCUGCUAUUUUCUAUUUAAUAACACCUGUUCA-3
5'-......(((((..(((.........(((((((.....)))))))......))))))))..((((.(((((((......)))))))).....((.((((....)))).))...
.(((((.(((.(((..((((((((.....((((..(((....)))..)))).....)))))).))..))).))).)))))..)))))..-3'
MFE = -37.0; z-score = -0.98; ED = 41.23
```

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, 266-13468(+)

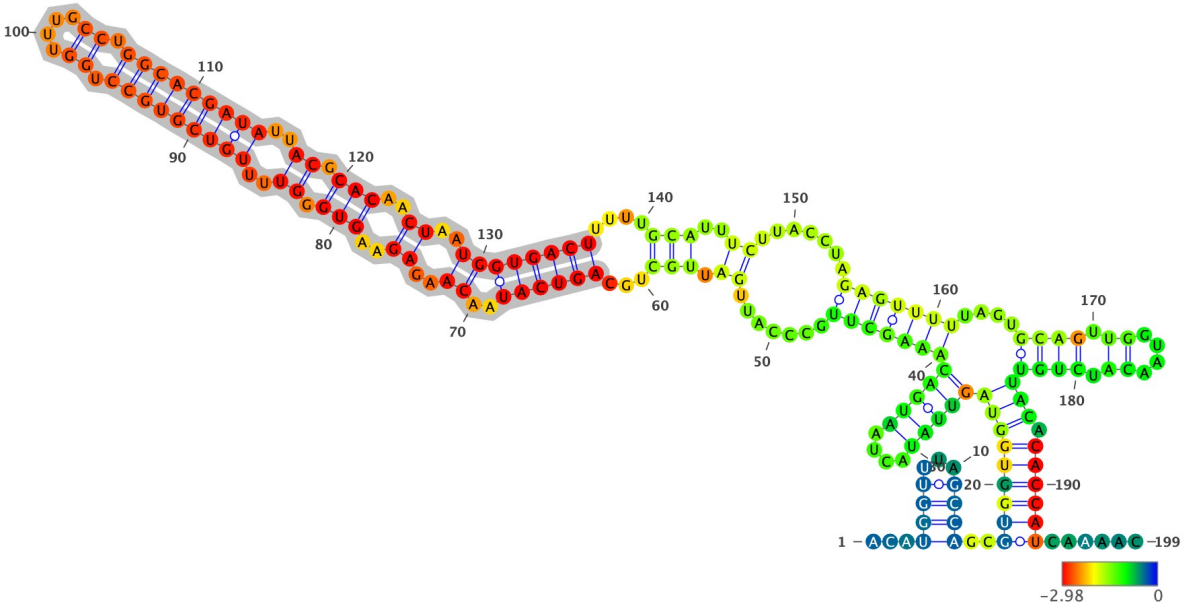
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 168 from nt 8833 to 8906 (nt 63 to 136)

```
5'-AGTCATAACAAGAGAAGTGGGTTTTGTCGTGCCTGGTTTGCCTGGCACGAUATTACGCACAACUAAUGGUGACU-3'
5'-((((((..((..((..(((.((..((((((((((.((....)).)))))))))..)).))))..))..))))))))-3'
Motif MFE = -32.0; z-score = -5.05; 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 8771 to 8969 (motif highlighted in silver):

```
5'-ACAUGGUUUAGCCAGCGUGGUGGUAGUUAUACUAAUGACAAAGCUUGCCCAUUGAUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACG
AUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGUGCAGUUGGUAACAUCUGUUACACACCAUCAAAAC-3
5'-...((((...))))..((((((((((((((....))))))(((((((.......((.(((...(((((((..((..((..((((.((..(((((((((.((....)).))))))
)))..))..))))..))..))))))))....)))..))).......)))))))....((((.((....)).)))))))..))))))......-3'
MFE = -59.2; z-score = -2.87; ED = 35.14
```

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(+)

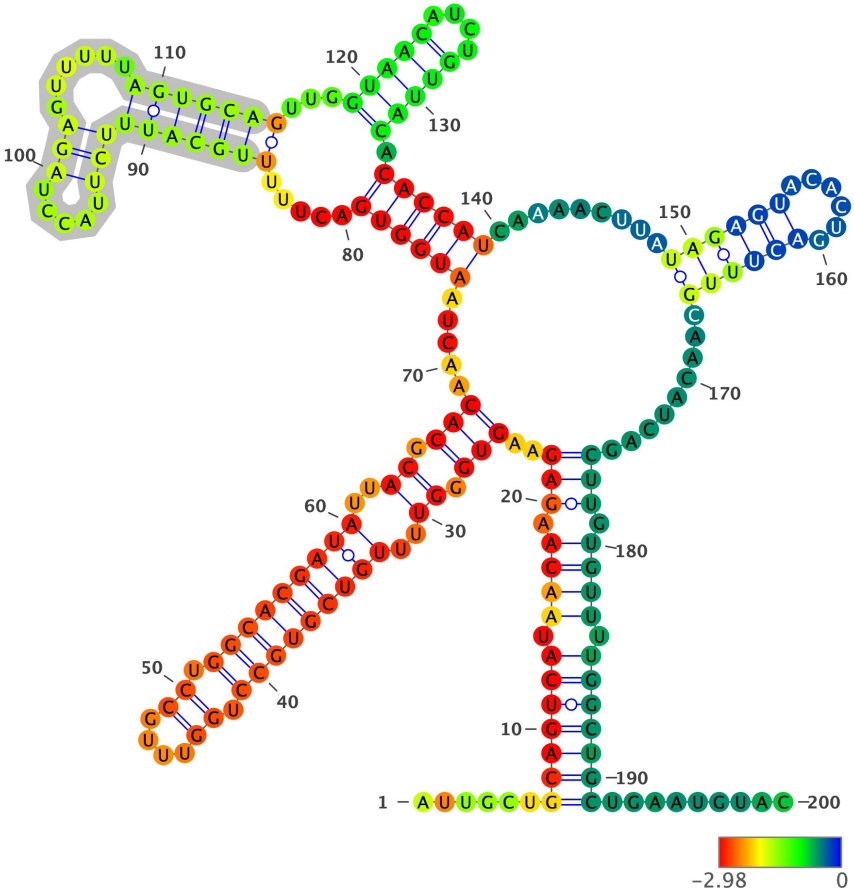
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 169 from nt 8910 to 8938 (nt 86 to 114)

```
5'-TGCATTTCTTACCTAGAGTTTTTAGUGCA-3'
5'-((((((((((.....)))......))))))-3'
Motif MFE = -4.1; z-score = -1.07; 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 8825 to 9024 (motif highlighted in silver):

```
5'-AUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGU
GCAGUUGGUAACAUCUGUUACACACCAUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUAC-3
5'-......(((((((.((((.(((..(((.((..((((((((((.((....)).))))))))).))).))).....((((((.....((((((((((.....)))......)))
))))...(((((....))))).))))))).........((((((......))))))).........))).)))).)))))))).........-3'
MFE = -58.1; z-score = -2.7; ED = 21.23
```

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(+)

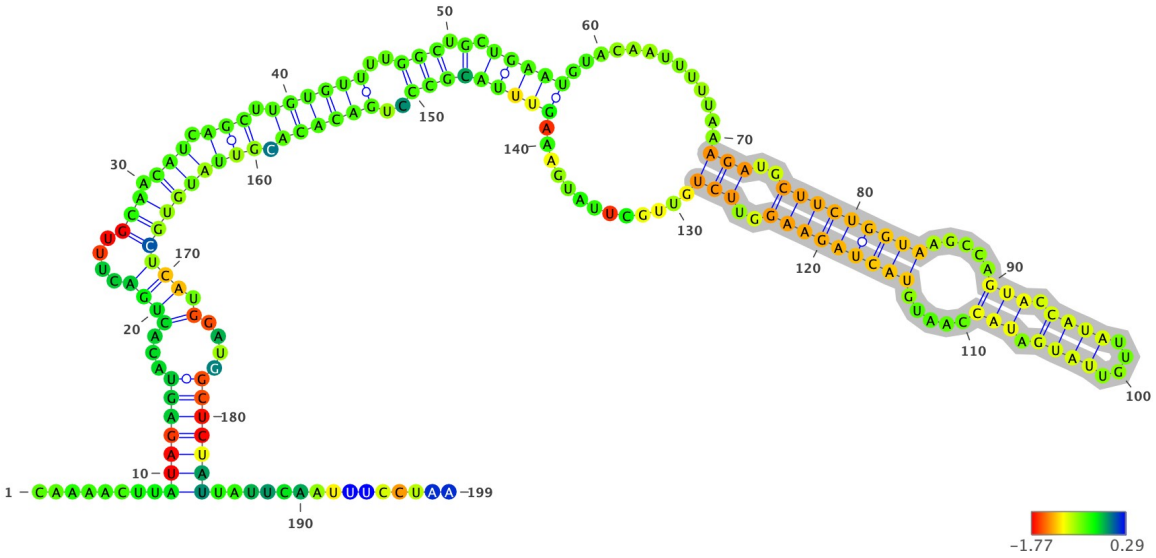
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 170 from nt 9034 to 9091 (nt 71 to 128)

```
5'-AGATGCTTCTGGTAAGCCAGTACCATATTGTUAUGAUACCAATGUACUAGAAGGTUCU-3'
5'-(((..(((((((((.....(((..............)))).....)))))))))..)))-3'
Motif MFE = -17.4; z-score = -3.14; ED = 1.27
```



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 8964 to 9162 (motif highlighted in silver):

```
5'-CAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCA
AUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGCCCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAA-3
5'-........(((((((...((((....(((.(((.(((((((..(((.(.(((((.............(((..(((((((((.....(((.((((....)))).)))..
...)))))))))..)))............)))))))))..)))))).))))))))))))).)....)))))))...............-3'
MFE = -46.2; z-score = -1.94; ED = 17.59
```

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(+)

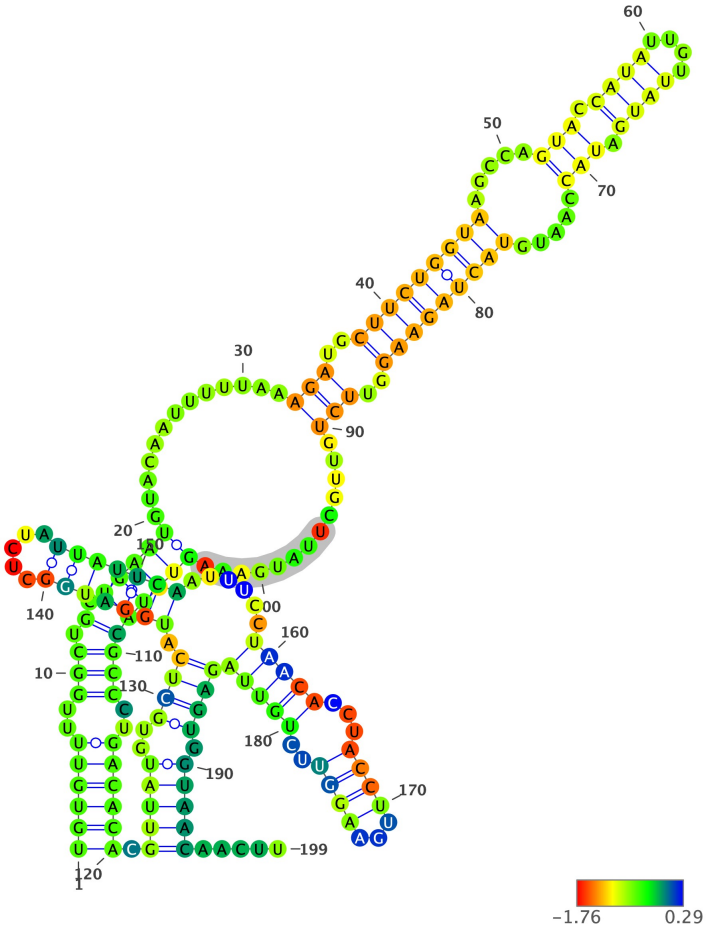
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 171 from nt 9097 to 9104 (nt 96 to 103)

```
5'-TTATGAAA-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 9002 to 9200 (motif highlighted in silver):

```
5'-UGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCAAUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGC
CCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAACACCUACCUUGAAGGUUCUGUUAGAGUGGUAACAACUU-3
5'-((((((..(((.(.(((((.............(((..((((((((((.....(((.((((....)))).)))).....)))))))))..)))..............))))))))
)..)))))).(((((..(((((.(((((((.....)))))))......(((((...((((...))))..)))))))))).)))))).....-3'
MFE = -44.9; z-score = -0.93; ED = 21.18
```

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(+)

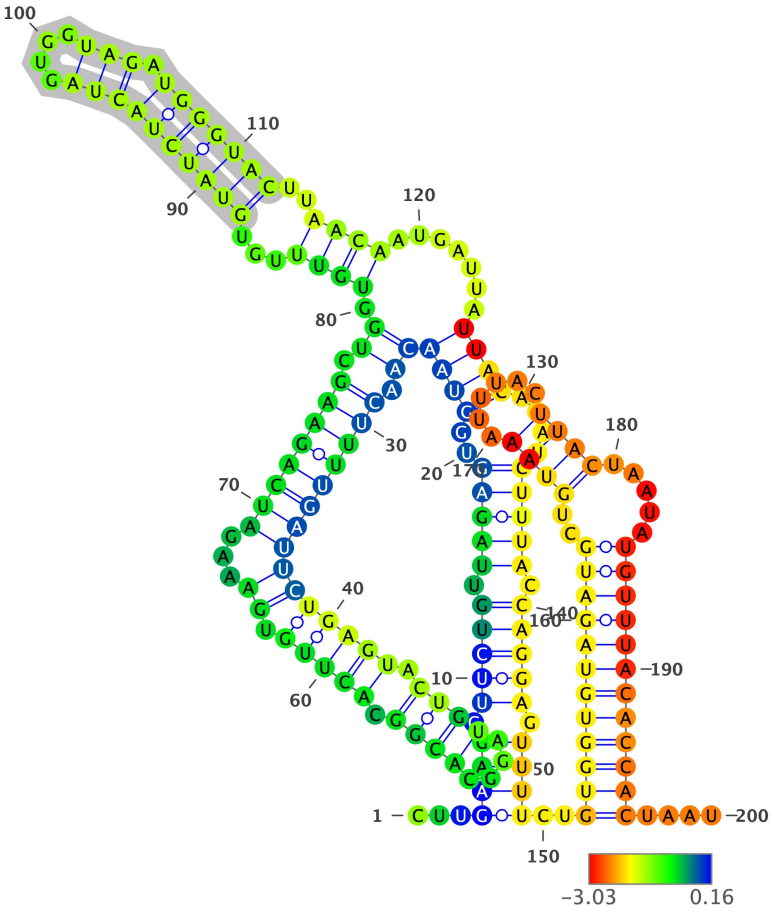
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 9257 to 9281 (nt 88 to 112)

```
5'-GTATCTACTAGTGGUAGAUGGGUAC-3'
5'-((((((((((....))).)))))))-3'
Motif MFE = -6.8; z-score = -2.61; ED = 8.97
```



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 9170 to 9369 (motif highlighted in silver):

```
5'-CUUGAAGGUUCUGUUAGAGUGGUAACAACUUUUGAUUCUGAGUACUGUAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUA
CUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAU-3
5'-...((((.(((((.(((((..((((((.(((((((((((((((.((((....)))).)))))).))...)))))))))).)).((((...((((((((((....))).))))))
)..))))).......))))....))))).)))))..((((((((((((..((((.....)))).....))))))))))))....-3'
MFE = -49.4; z-score = -2.02; ED = 41.39
```

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(+)

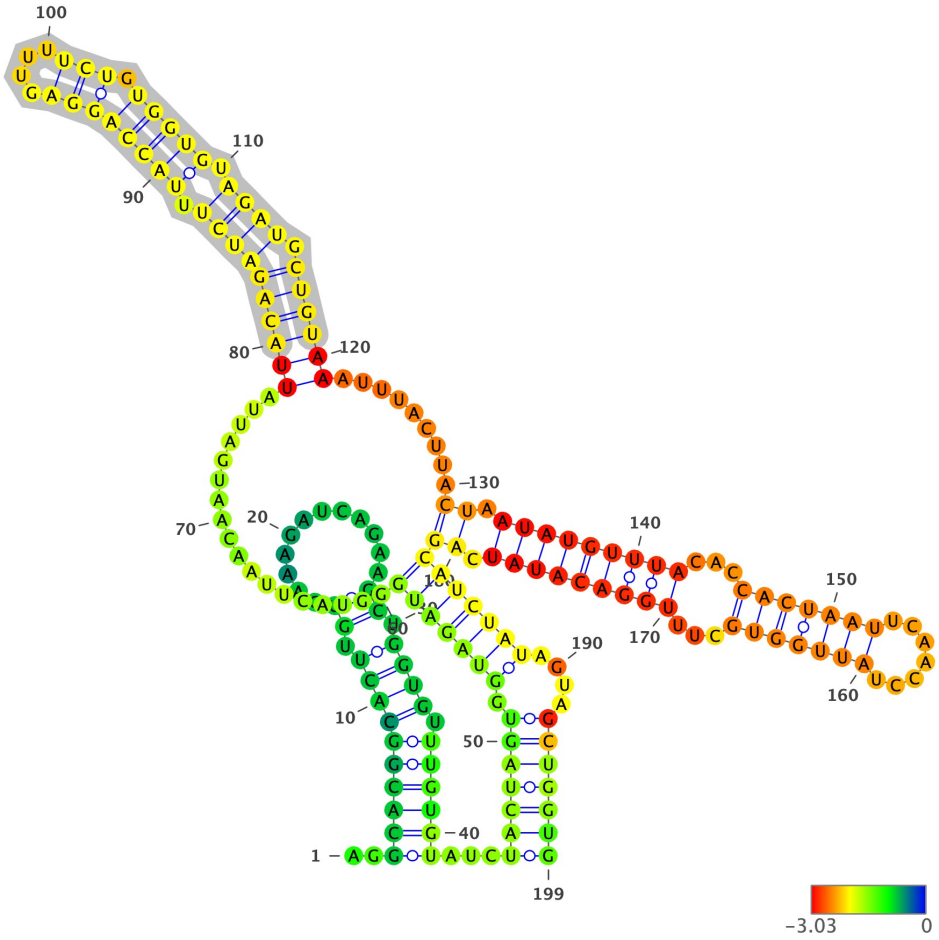
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 173 from nt 9297 to 9336 (nt 80 to 119)

```
5'-ACAGATCTTTACCAGGAGTTTUCUGUGGUGTAGAUGCUGU-3'
5'-((((((((.((((((((....))).)))))).)))).))))-3'
Motif MFE = -13.3; z-score = -3.11; ED = 3.37
```



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 9218 to 9416 (motif highlighted in silver):

```
5'-AGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUA
GAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG-3
5'-..(((((((((((.((.............)).)))).))))))...(((((((.(((((((.................(((((((((.((((((((....))).)))))).)
))).))))))).........((.(((((((((...(((((((.......)))))))...))))))))).))))))))).....)))))))-3'
MFE = -50.3; z-score = -2.34; ED = 51.97
```

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(+)

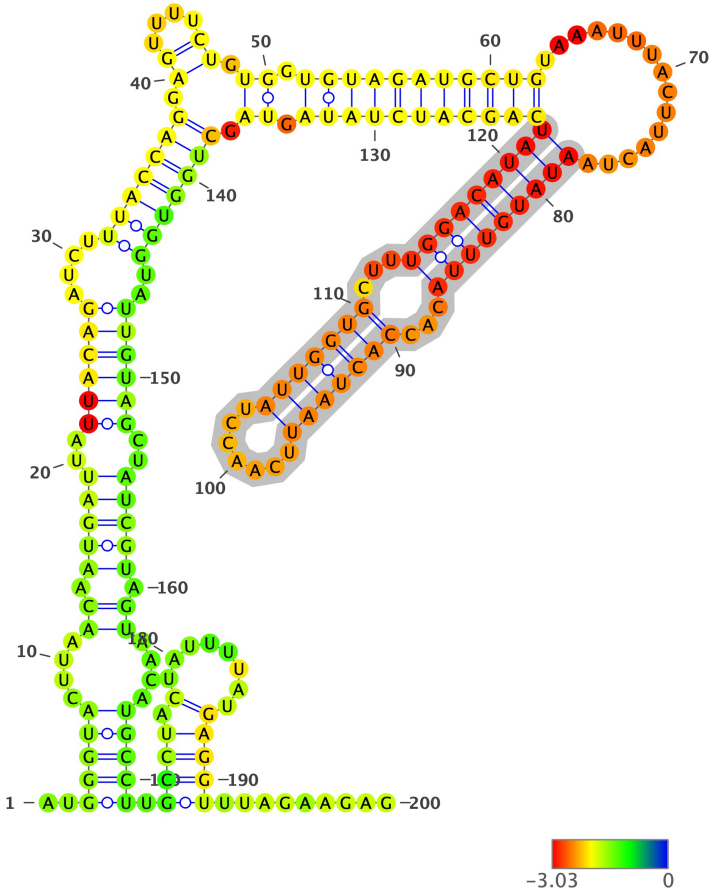
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 174 from nt 9351 to 9395 (nt 78 to 122)

```
5'-ATATGTTTACACCACTAATTCAACCTAUUGGUGCTTUGGACAUAU-3'
5'-((((((((((...(((((((.......)))))))...)))))))))-3'
Motif MFE = -11.7; z-score = -3.97; 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 9274 to 9473 (motif highlighted in silver):

```
5'-AUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGC
UUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAG-3
5'-..(((((....((.(((((..((((((....(((((((.((....)).((.((((((((((((.................(((((((((...(((((((.......)))))))).
..))))))))))))))))))).)).)))))))..)))))).)))))).))....))))).((((.(........)))))..........-3'
MFE = -48.3; z-score = -1.75; ED = 56.63
```

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(+)

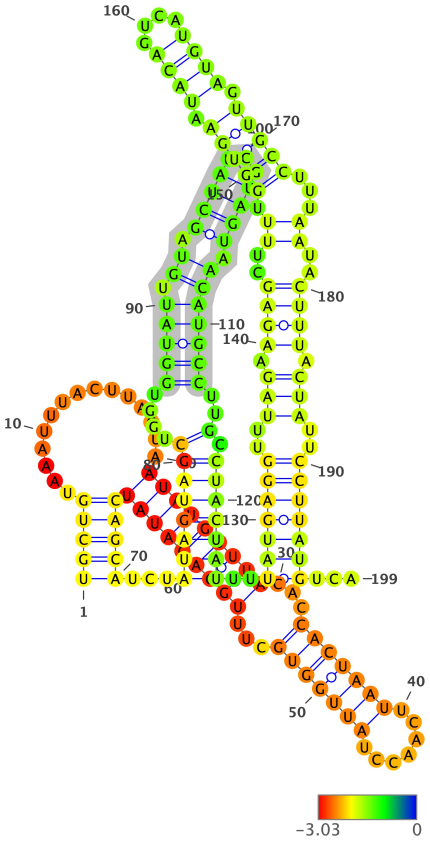
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 175 from nt 9416 to 9443 (nt 86 to 113)

```
5'-GGTATTGTAGCTATCGUAGUAACAUGCC-3'
5'-((((((.((.(((((...))))).)))))))-3'
Motif MFE = -6.5; z-score = -1.89; 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 = -3.34; 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(+)

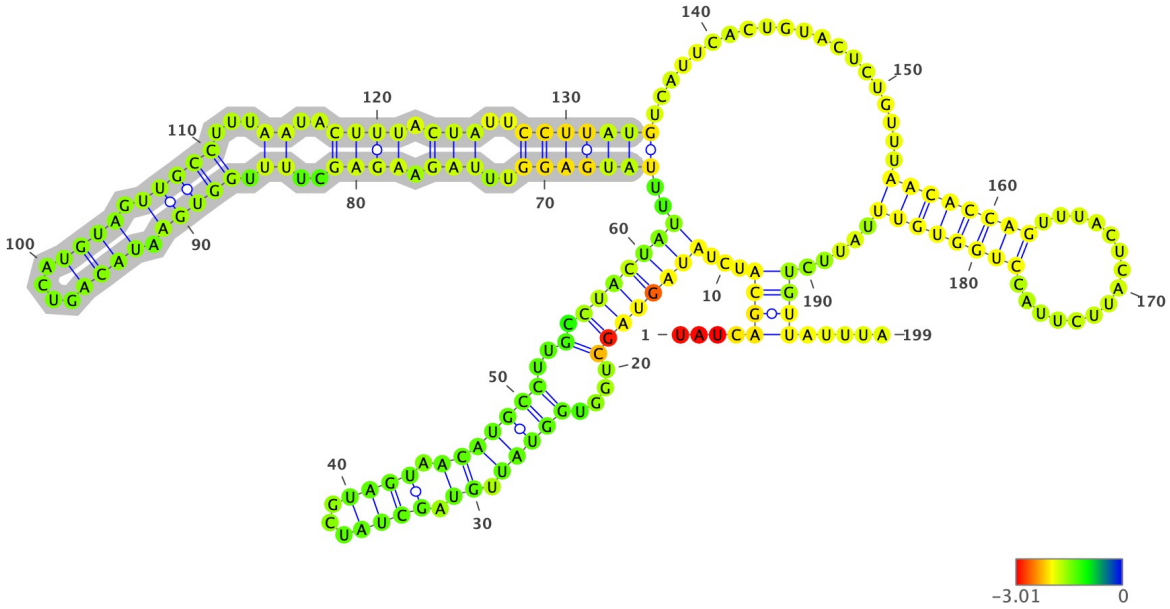
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 176 from nt 9458 to 9525 (nt 66 to 133)

```
5'-ATGAGGTTTAGAAGAGCTTTTGGTGAATACAGTCAUGUAGUUGCCTTTAATACUUUACUATTCCTTAU-3'
5'-((......(((.((((..((.(((((.((((....)))).)))))...))..)))).)))......))-3'
Motif MFE = -17.7; z-score = -3.33; 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 9393 to 9591 (motif highlighted in silver):

```
5'-UAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCU
UUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUA-3
5'-....((((...((((((((....(((((.((.((((...)))).)))))))..).)))))))..(((((((..(((.((((..((.(((((.((((....)))).)))))).
..))..)))).)))..)))))))....................((((((((...............))))))))).....))))).....-3'
MFE = -42.6; z-score = -1.9; ED = 22.54
```

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, 266-13468(+)

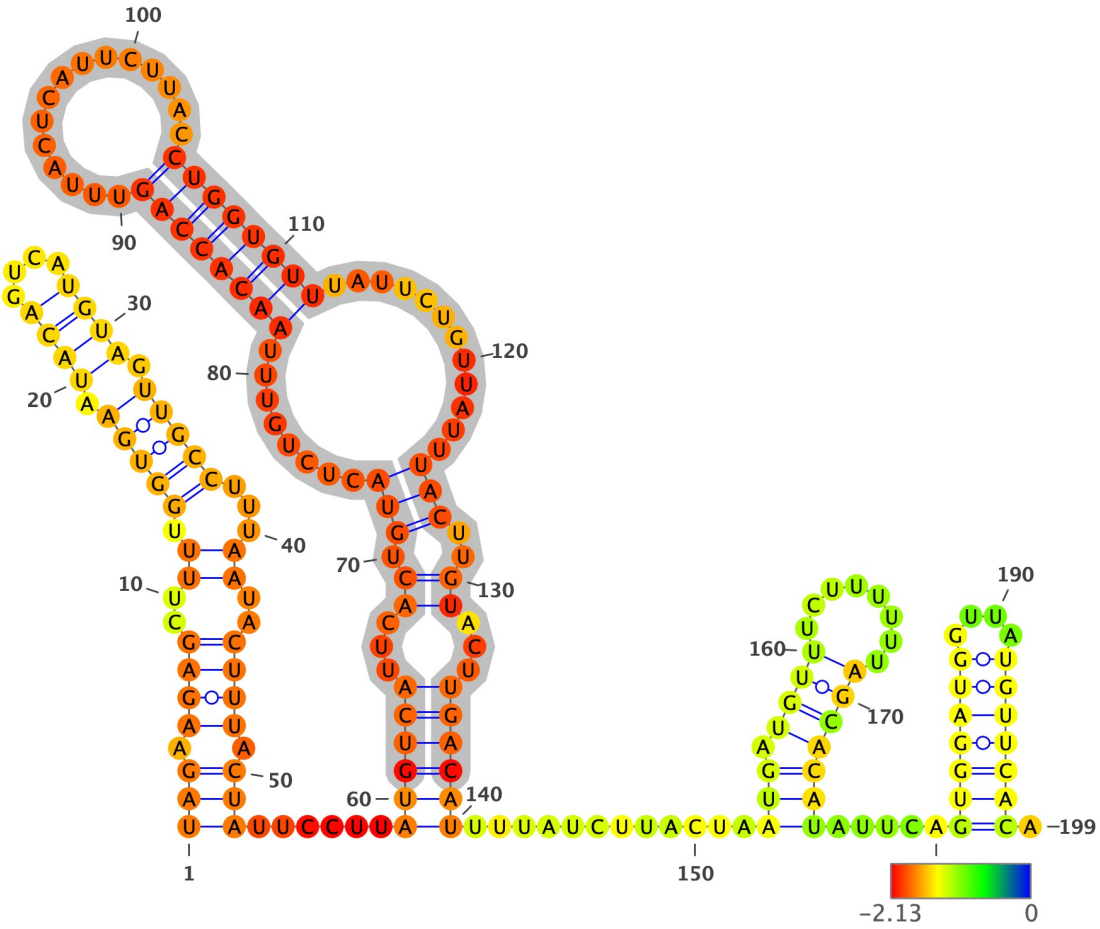
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 9526 to 9603 (nt 61 to 138)

```
5'-GTCATTCACTGTACTCTGTTTAACACCAGTTTACTCATTCTTACCUGGUGUUTATTCTGTTATTTACTTGTACTTGAC-3'
5'-(....................((((((((...............))))))))........................)-3'
Motif MFE = -11.3; z-score = -1.98; ED = 13.62
```



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 9466 to 9664 (motif highlighted in silver):

```
5'-UAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGU
UUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACA-3
5'-(((.((((..((.(((((.((((....)))).)))))...))..)))).))).....((((((...((.(((........((((((((...............)))))))
).............)))..))...))))))............(((.((((........)))))))).....(((((((....)))))))).-3'
MFE = -31.1; z-score = -1.0; ED = 39.08
```

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(+)

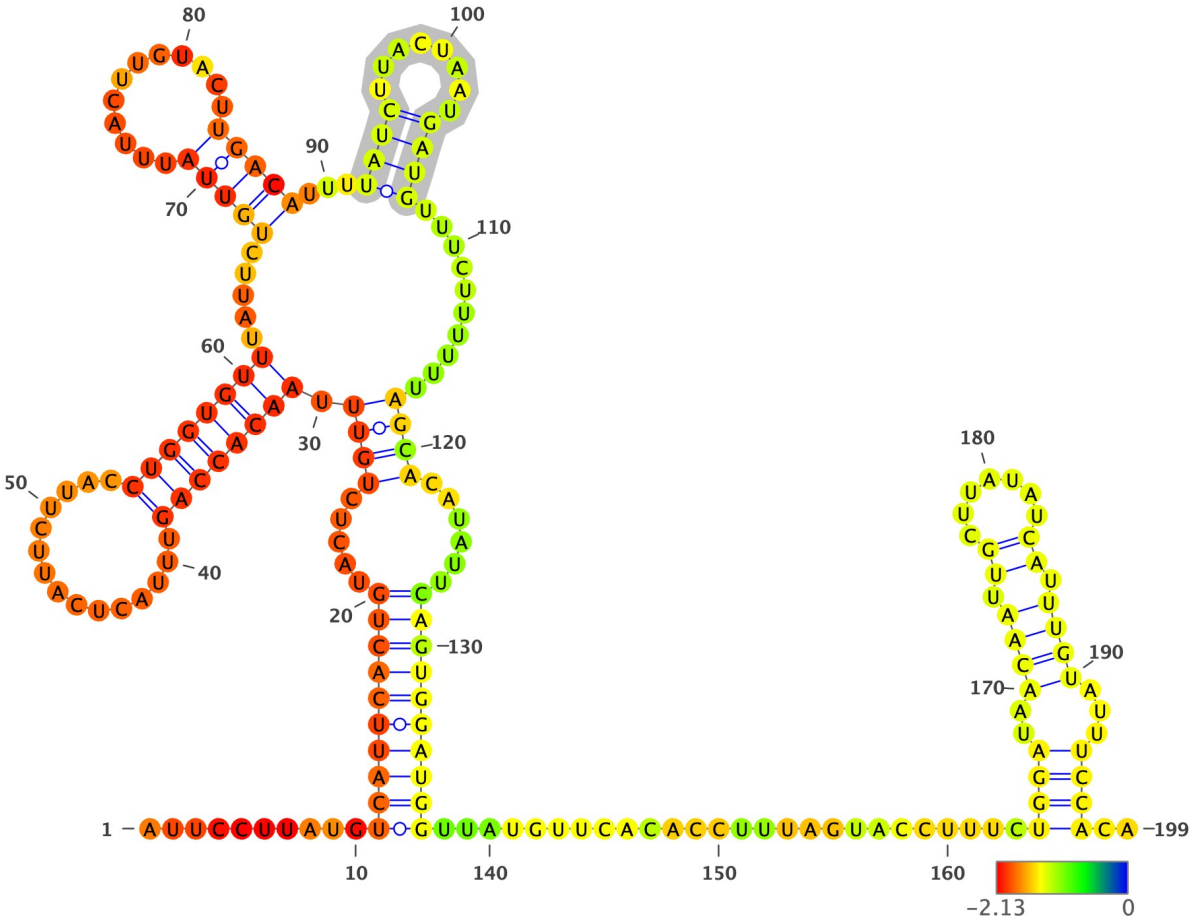
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 178 from nt 9608 to 9623 (nt 92 to 107)

```
5'-TATCTTACTAATGAUG-3'
5'-((((........))))-3'
Motif MFE = -0.6; z-score = -0.59; 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 9517 to 9715 (motif highlighted in silver):

```
5'-AUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUC
UUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACA-3
5'-..........((((((((((.....((((.((((((((.................))))))))).....(((((.............)))))...((((........))))....
......))))......))))))))))........................((((..((((.((.......)).))))...))))..-3'
MFE = -28.8; z-score = -1.77; ED = 17.38
```

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(+)

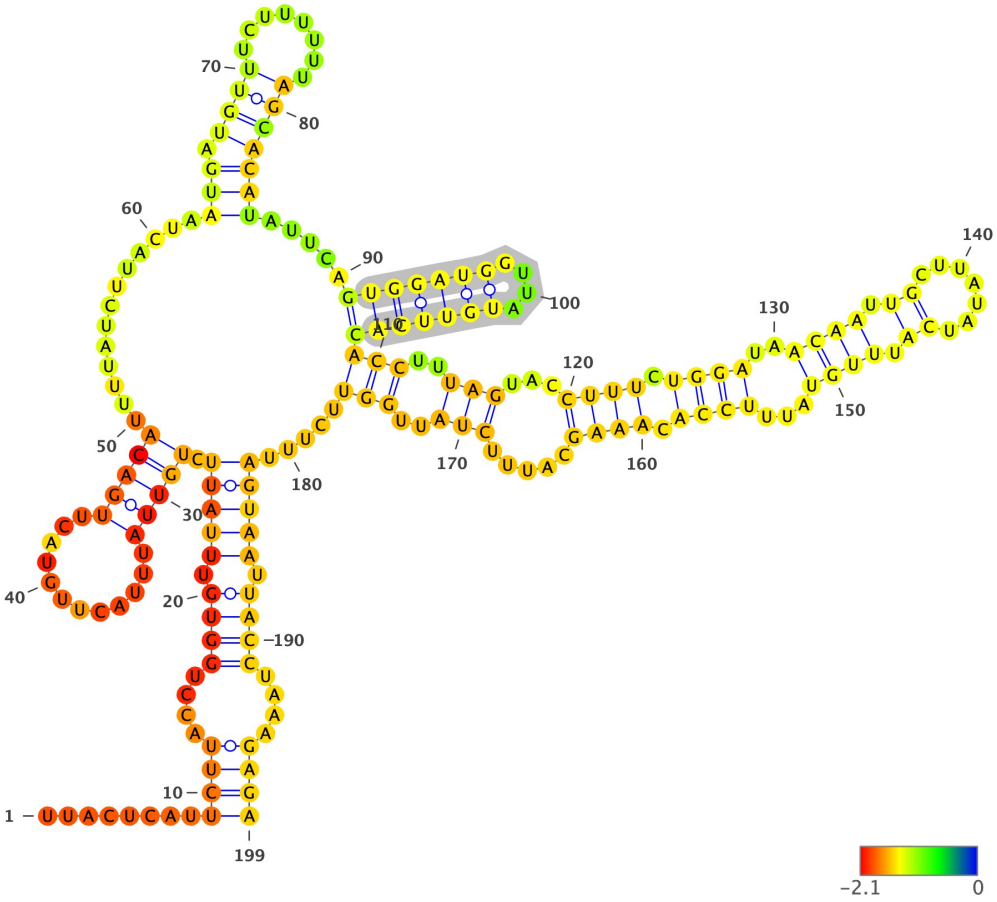
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 179 from nt 9647 to 9662 (nt 92 to 107)

```
5'-TGGATGGTTAUGUUCA-3'
5'-((((((....))))))-3'
Motif MFE = -0.9; z-score = -1.47; ED = 1.9
```



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 9556 to 9754 (motif highlighted in silver):

```
5'-UUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACC
UUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGA-3
5'-........((((....((((.(((((.(((((.............)))))..............(((.((((........)))))))).....(((((((....)))))))(((
..(((...((((.((((..((((.((.......)).))))...)))).)))).....)))..)))).....)))))).)))).....))))-3'
MFE = -29.7; z-score = -0.79; ED = 29.4
```

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(+)

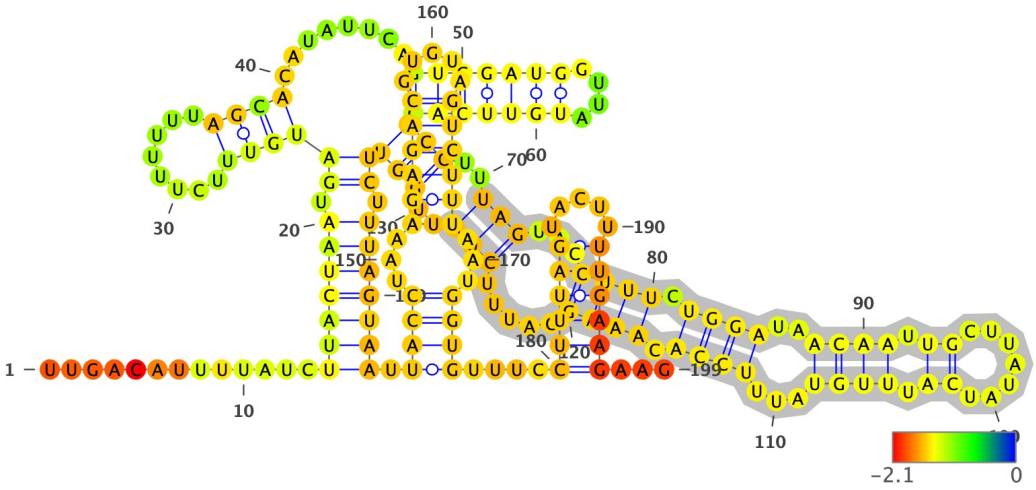
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 180 from nt 9669 to 9726 (nt 71 to 128)

```
5'-TAGTACCTTTCTGGATAACAATTGCTTATATCATUUGUATTUCCACAAAGCATTTCUA-3'
5'-(((...((((.((((..((((.((.......)).))))...)))).)))).....)))-3'
Motif MFE = -7.4; z-score = -1.47; ED = 4.22
```



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 9599 to 9797 (motif highlighted in silver):

```
5'-UUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUU
UCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAG-3
5'-.............(((((((.((((((........))))........(((((((....)))))))(((..(((...((((.((((..((((.((.......)).))))...
)))).)))).....)))..))))).))))))).((((...((((((.....))))))...)))).....((((((.....))))))...-3'
MFE = -36.1; z-score = -1.17; ED = 52.61
```

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(+)

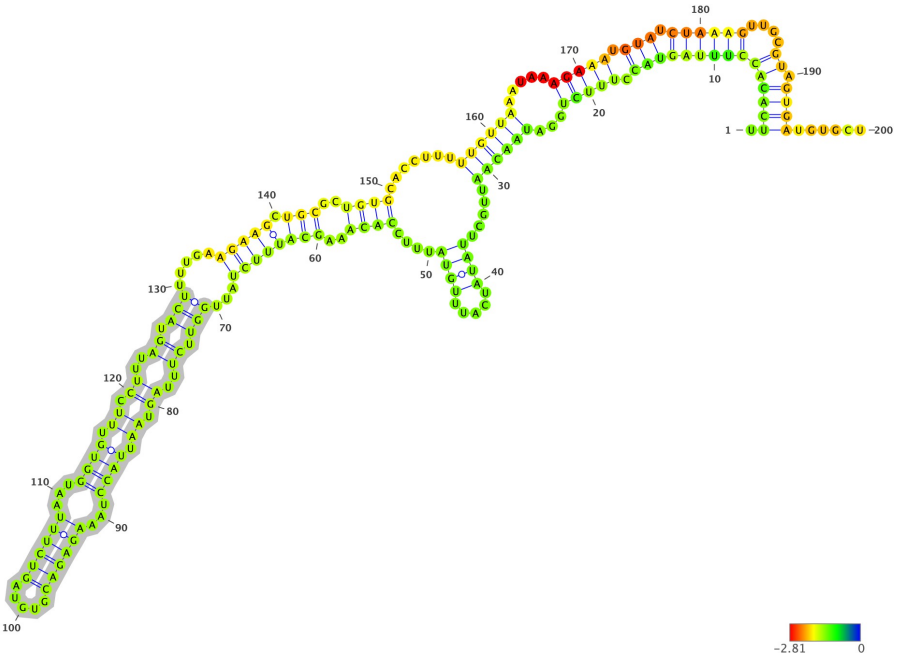
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 181 from nt 9729 to 9787 (nt 71 to 129)

```
5'-GGTTCTTTAGTAATTACCTAAAGAGACGTGTAGUCUUUAATGGUGTUUCCUTTAGTACU-3'
5'-(((.((..((.((.((((...((((((.....))))))...)))).)).))..)).)))-3'
Motif MFE = -13.8; z-score = -2.24; ED = 2.72
```



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 9659 to 9858 (motif highlighted in silver):

```
5'-UUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAU
GGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCU-3
5'-.(((((((((((((((.(((((...((((((.....((((.....))))....((((..((((((((...(((.((..((.((.((((...((((((.....))))))...
)))).)).))..)).))).....))))).)))..))))).......))))))).....))))).))).))))))....)).))))......-3'
MFE = -40.2; z-score = -1.35; ED = 41.8
```

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(+)

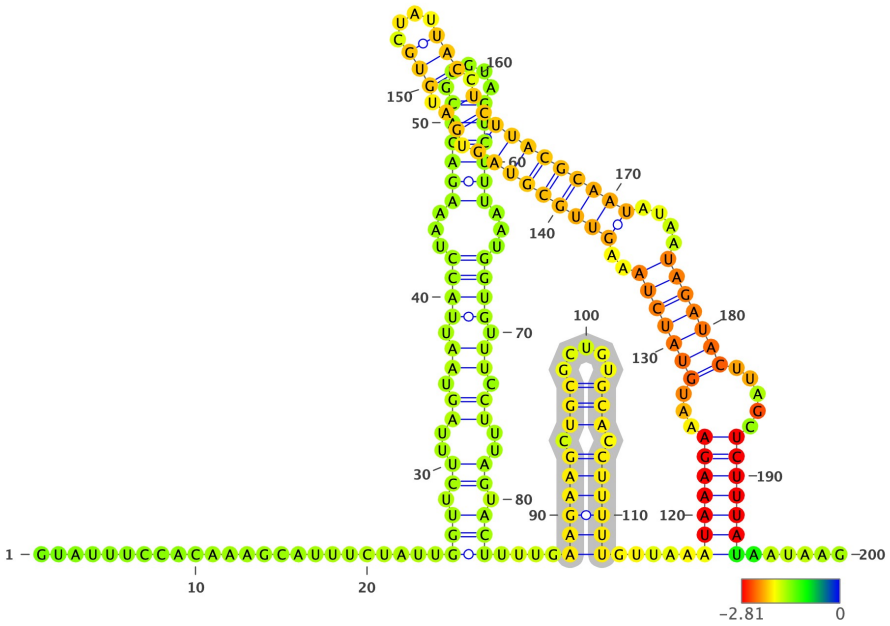
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 182 from nt 9792 to 9816 (nt 88 to 112)

```
5'-AAGAAGCTGCGCTGTGCACCUUUUU-3'
5'-((((((.(((.....))).))))))-3'
Motif MFE = -5.4; z-score = -1.22; ED = 1.48
```



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 9705 to 9904 (motif highlighted in silver):

```
5'-GUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUU
UGUUAAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAG-3
5'-.......................(((.((..((.((.((((...((((((.....))))))...))))).)).))..)).))).....((((((.(((.....))).)))))
).....(((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....)))))))......-3'
MFE = -43.9; z-score = -3.01; ED = 23.79
```

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, 266-13468(+)

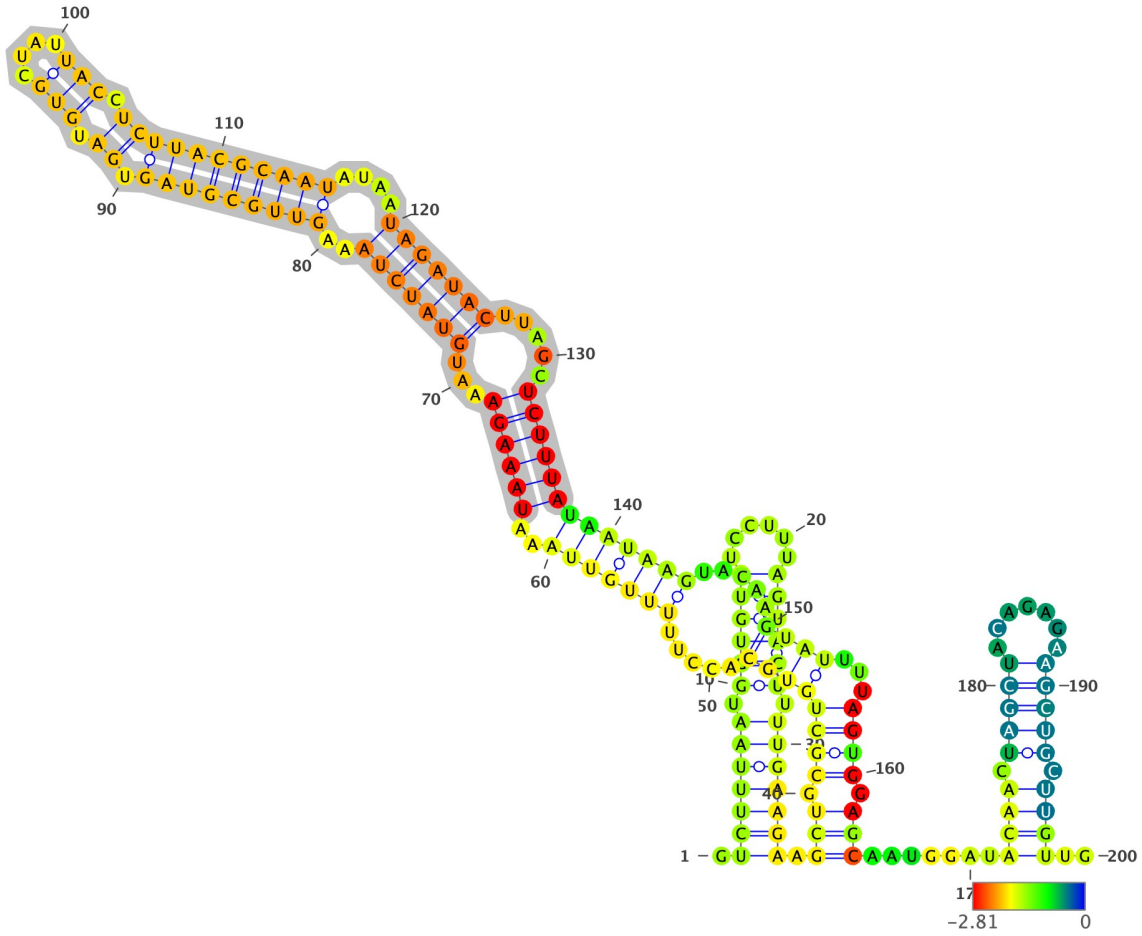
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 183 from nt 9823 to 9897 (nt 63 to 137)

```
5'-TAAAGAAATGTATCTAAAGTTGCGTAGTGATGTGCTATUACCUCUUACGCAAUATAAUAGAUACTTAGCUCUUUA-3'
5'-((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....))))))-3'
Motif MFE = -20.9; z-score = -3.42; 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 = -2.35; 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(+)

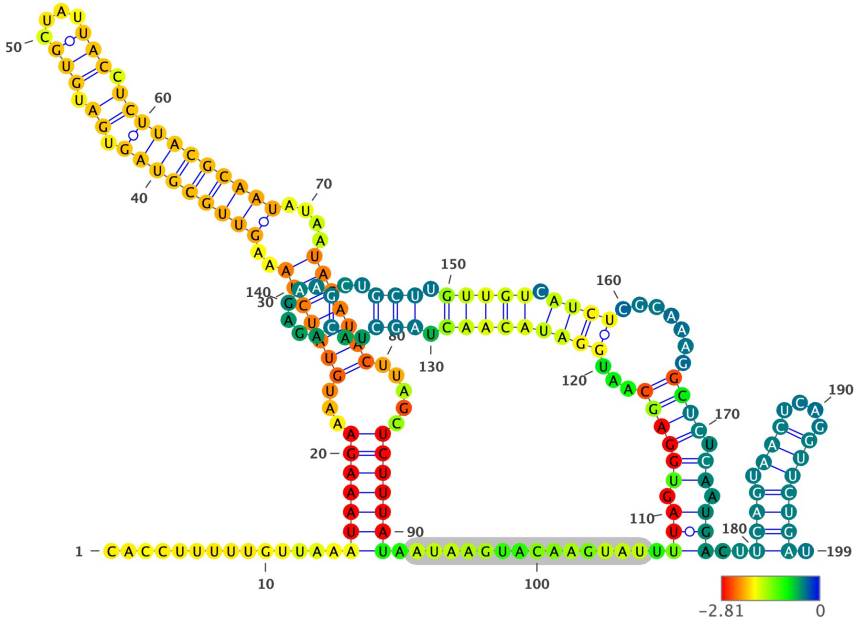
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 184 from nt 9900 to 9913 (nt 93 to 106)

```
5'-ATAAGTACAAGUAU-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.24; ED = 0.12
```



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 9808 to 10006 (motif highlighted in silver):

```
5'-CACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAG
UGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUUGUCAUCUCGCAAAGGCUCUCAAUGACUUCAGUAACUCAGGUUCUGAU-3
5'-..............(((((((...(((((((..((((((((((.((.(((....))).))))))))))....)))))))).....)))))))................(((.
((((((...((((((((((.(((..(......)..))).))))).))))).......)))).)).)))..((((.(((....)))))))).-3'
MFE = -43.8; z-score = -2.06; ED = 35.15
```

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(+)

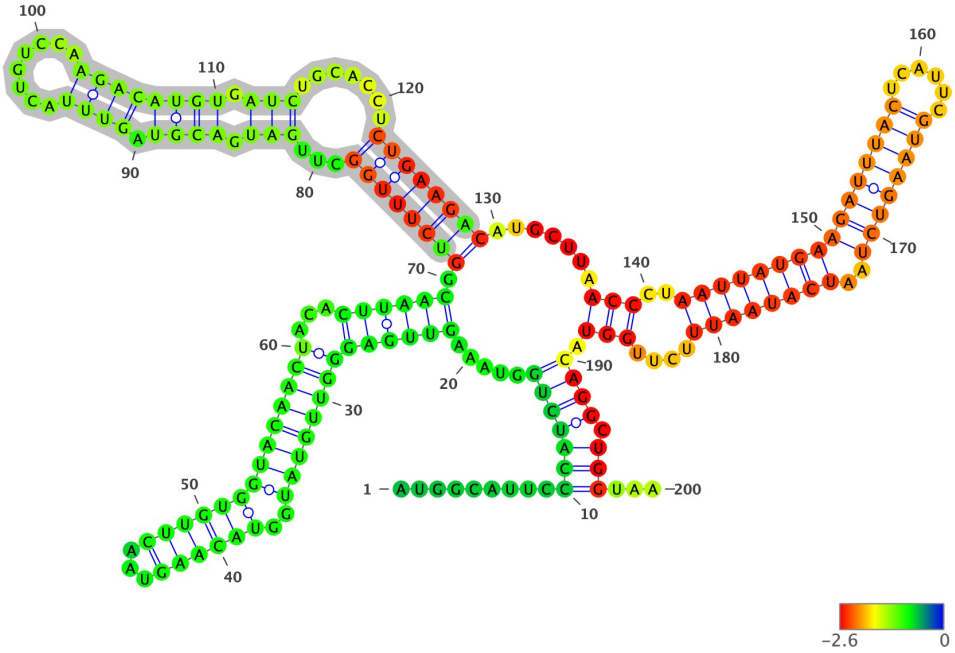
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 185 from nt 10141 to 10197 (nt 72 to 128)

```
5'-TCTTTGGCTTGATGACGTAGTTTACTGTCCAAGACAUGUGAUCTGCACCTCTGAAGA-3'
5'-(.........(((.((((.((((........))))))))).)))............)-3'
Motif MFE = -11.6; z-score = -0.54; ED = 12.4
```



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 10070 to 10269 (motif highlighted in silver):

```
5'-AUGGCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUG
AUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAA-3
5'-.........(((((((.....((((((((((((((..((((((...)))))))))))))))...)))))).((((((((...(((.((((.((((........))))))))).
)))).......))))))))).......(((..((((((((((((((((.....))))))))..))))))))....))).)))).)))...-3'
MFE = -52.1; z-score = -2.59; ED = 18.28
```

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(+)

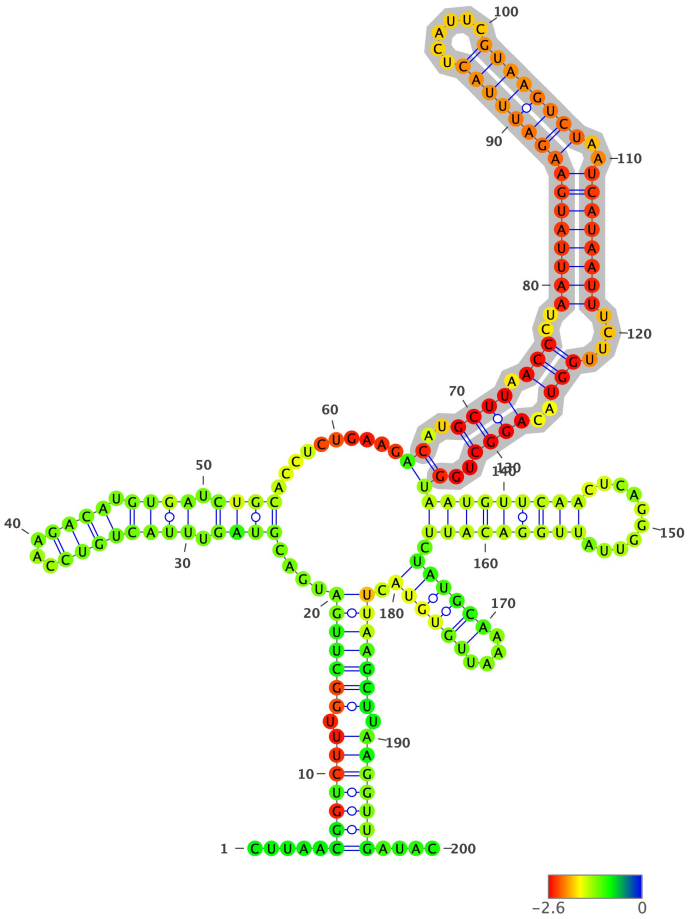
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 186 from nt 10198 to 10266 (nt 66 to 134)

```
5'-CATGCTTAACCCTAATTATGAAGATTTACTCATTCGUAAGUCUAAUCAUAAUUTCTTGGUACAGGCTGG-3'
5'-(..((((.(((..((((((((((((((((.....))))))))..))))))))....)))..)))))..)-3'
Motif MFE = -19.2; z-score = -4.13; ED = 2.85
```



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 10133 to 10332 (motif highlighted in silver):

```
5'-CUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAU
CAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUAC-3
5'-.....(((((((.(((((((....((((.((((((((...)))).)))).))))..........((..((((.(((..((((((((((((((((.....))))))))..)
)))))))....)))..))))..))((((((((.........))))))))).((((((....)))))).))))))).))))))....-3'
MFE = -49.6; z-score = -3.25; ED = 17.45
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

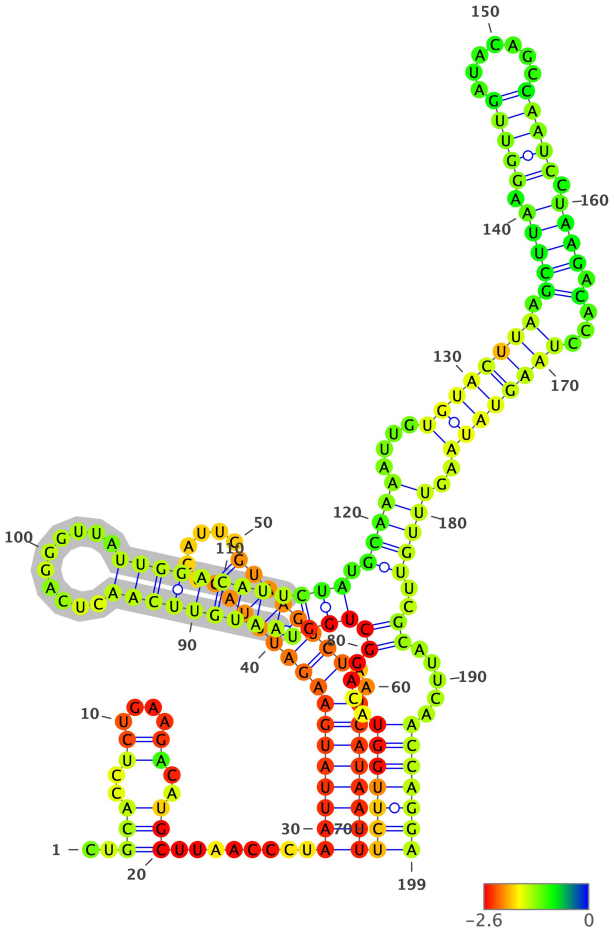
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 187 from nt 10268 to 10295 (nt 86 to 113)

```
5'-AATGTTCAACTCAGGGTTAUUGGACAUU-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -5.2; z-score = -1.76; 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 = -1.73; 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(+)

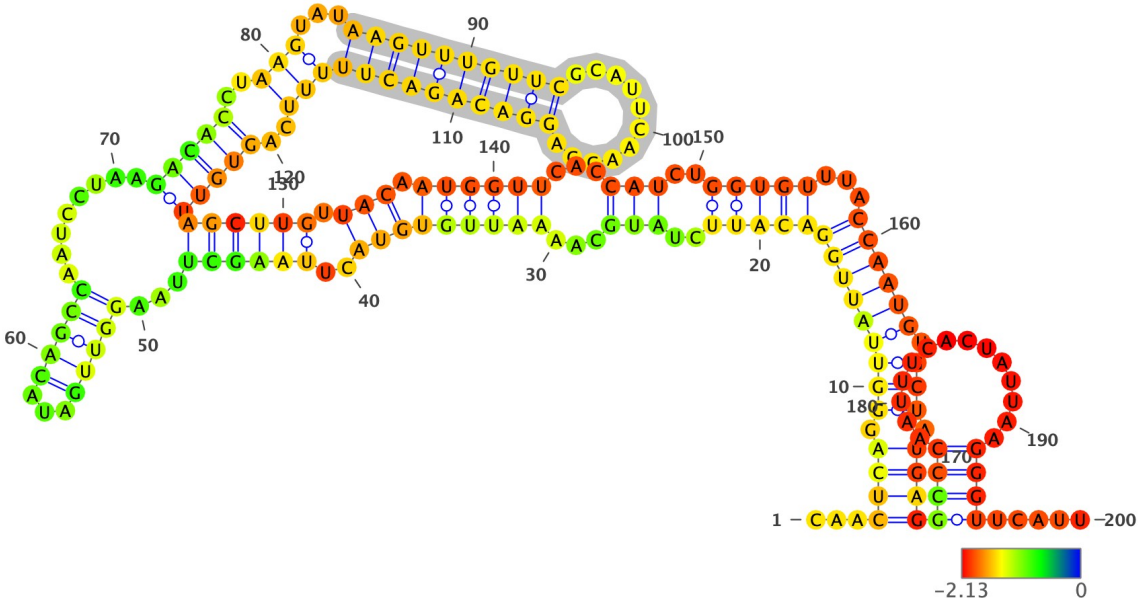
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 188 from nt 10358 to 10388 (nt 85 to 115)

```
5'-AAGTTTGTTCGCATTCAACCAGGACAGACUU-3'
5'-((((((((((...........))))))))))-3'
Motif MFE = -9.4; z-score = -3.06; ED = 0.74
```



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 10274 to 10473 (motif highlighted in silver):

```
5'-CAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAG
ACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUU-3
5'-...((((.(((((((((((((..(((...((((((((((..((((((...(((((...)))))........(((((..(((...((((((((((.........))))))
)))))))..))))))))))).))).))))))...)))..)))))...))))))).))).))))((((..............))))).....-3'
MFE = -44.5; z-score = -1.14; ED = 60.64
```

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(+)

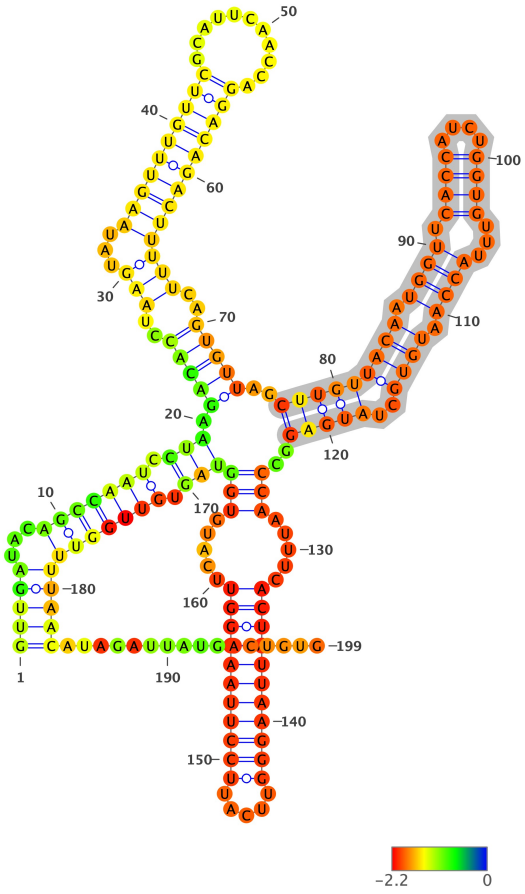
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 189 from nt 10401 to 10446 (nt 77 to 122)

```
5'-CTTGTTACAATGGTTCACCATCTGGUGTTTACCAAUGUGCTATGAG-3'
5'-(....((((.((((.((((....))))...)))).)))).....)-3'
Motif MFE = -12.2; z-score = -2.22; ED = 4.25
```



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 10325 to 10523 (motif highlighted in silver):

```
5'-GUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAA
UGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUG-3
5'-(((((...(((((((.(((.(((((..(((...((((((((((.....)))))))))))))..)))))..((((((((.((((.((((....))))...)))).
))))..)))))..(((.....((((((((((.....))))))))))).....))))))).))))))))))))).................-3'
MFE = -53.0; z-score = -2.76; ED = 16.07
```

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(+)

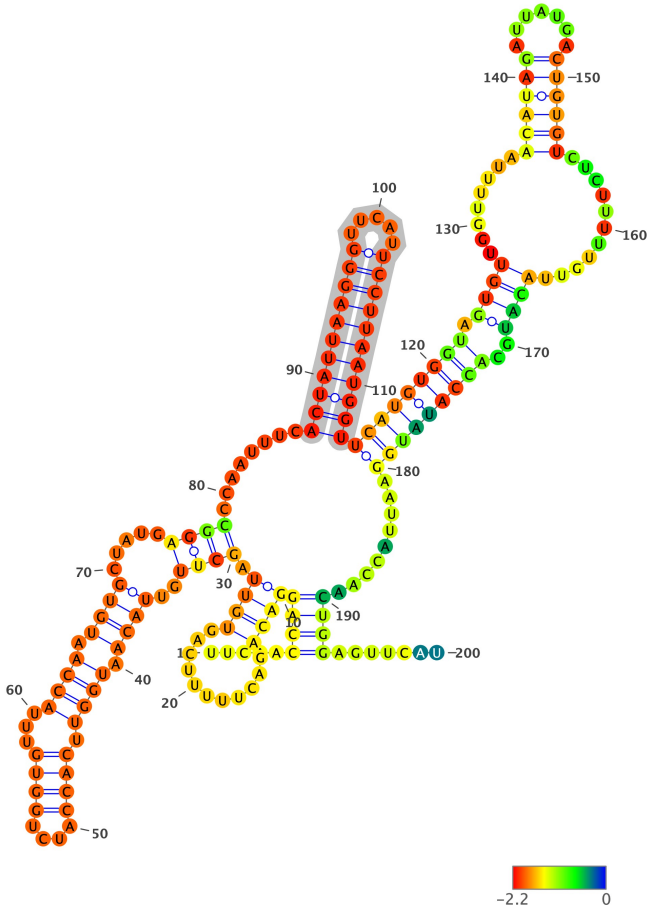
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 10457 to 10483 (nt 87 to 113)

```
5'-ACTATTAAGGGTTCATUCCUUAAUGGU-3'
5'-(((((((((((.....)))))))))))-3'
Motif MFE = -11.2; z-score = -5.04; 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 10371 to 10570 (motif highlighted in silver):

```
5'-UUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUG
GUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAU-3
5'-.....((((((((...........)))).((((..((((.((((.((((....))))...)))).)))).....))))........(((((((((((.....)))))))))
))(((((((((.((((........((((((.......))))))...........))))..))))))))).........))))........-3'
MFE = -48.6; z-score = -1.87; ED = 43.31
```

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(+)

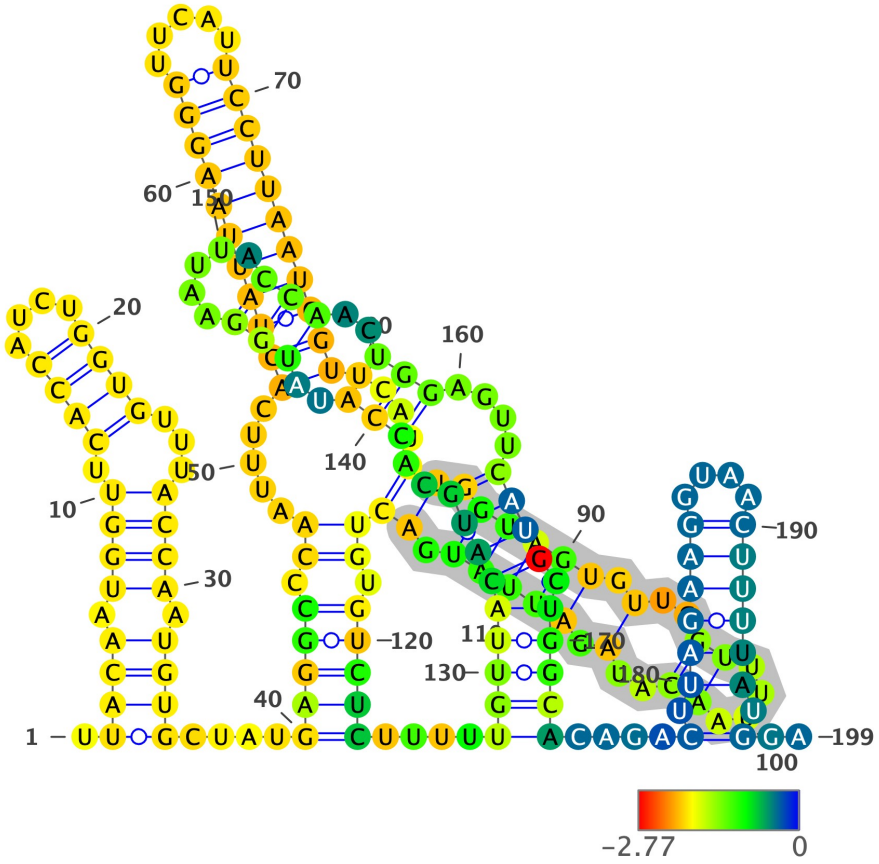
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 191 from nt 10489 to 10518 (nt 85 to 114)

```
5'-TGGTAGTGTTGGTTTTAACATAGATTATGA-3'
5'-(.....(.(..........<.).).....)-3'
Motif MFE = -3.0; z-score = -1.26; ED = 7.71
```



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 10405 to 10603 (motif highlighted in silver):

```
5'-UUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUA
UGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGA-3
5'-.((((.((((.((((....))))...)))).))))....(((((.((.....((((((((((.....)))))))))))....((.(((((.(..((....))..).))))
).)))).)))))....((((((((..(((..(((.....)))..)))....)))).)))))....(.((((((....)))))).)..-3'
MFE = -49.0; z-score = -2.37; ED = 39.83
```

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(+)

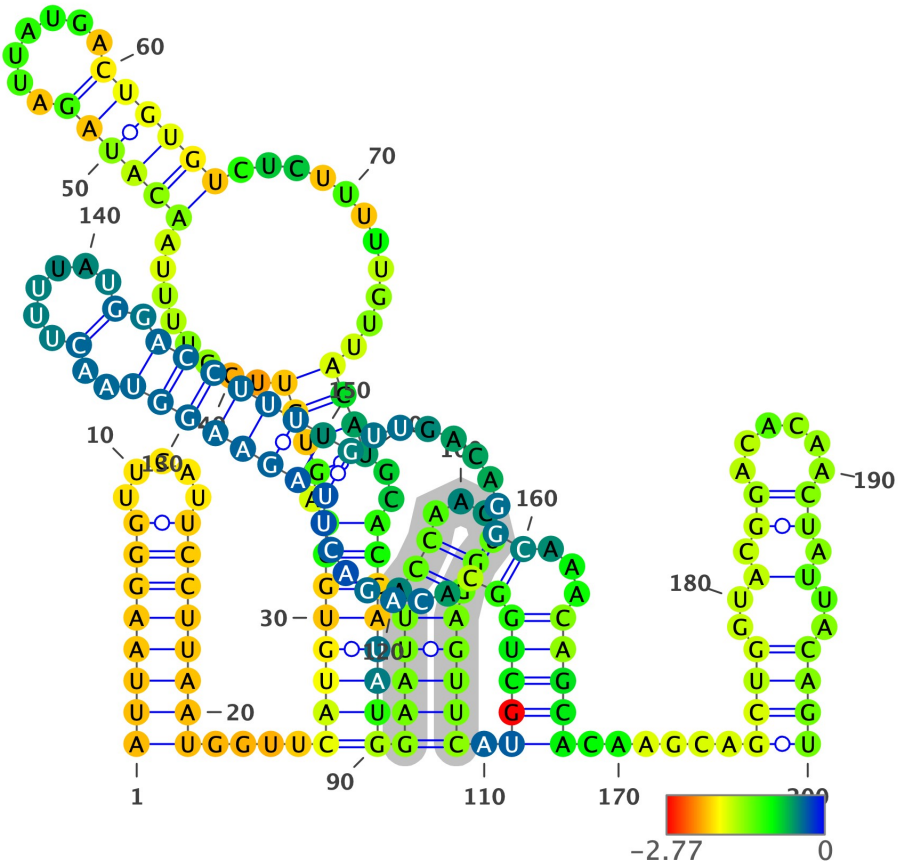
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 192 from nt 10550 to 10568 (nt 91 to 109)

```
5'-GAATTACCAACTGGAGUUC-3'
5'-(((((.((....)))))))-3'
Motif MFE = -3.1; z-score = -1.79; ED = 0.42
```



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 10460 to 10659 (motif highlighted in silver):

```
5'-AUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAU
GCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGU-3
5'-(((((((((.....)))))))))....(((((((((.((((........((((((.......))))))..........))))..)))))))))((((((.((....)))))))).(
((((((.......(((((((((..(......).)))))))).......))...)))))).....(((((..(.((......)).).)..))))-3'
MFE = -44.1; z-score = -0.53; ED = 59.63
```

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(+)

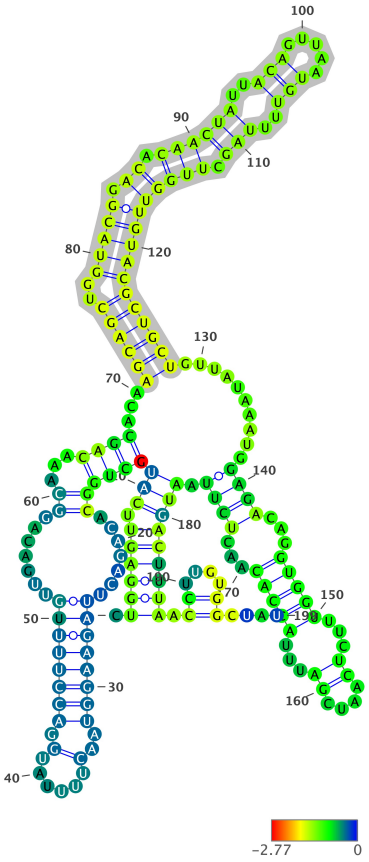
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 193 from nt 10630 to 10687 (nt 71 to 128)

```
5'-AGCAGCTGGTACGGACACAACTATTACAGTTAAUGUTTUAGCUUGGUUGUACGCUGCU-3'
5'-((((((..((((((.((.(((((((..(((.....))))..))))..))))))))))))))))-3'
Motif MFE = -19.9; z-score = -3.39; ED = 2.99
```



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 10560 to 10758 (motif highlighted in silver):

```
5'-CUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAG
CUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCACAACUCUUAAUGACUUUAACCUUGUGGCUAU-3
5'-.((((((.(((((((((.......(((((((((..(......).)))))))).......)).)))))...((((((..((((((.((.(((((((..(((.....))))..)))
.)))))))))))))))).........((((...((((((...((....))...))))))...)))))).)))))))))..((....))....-3'
MFE = -49.3; z-score = -0.91; ED = 23.99
```

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(+)

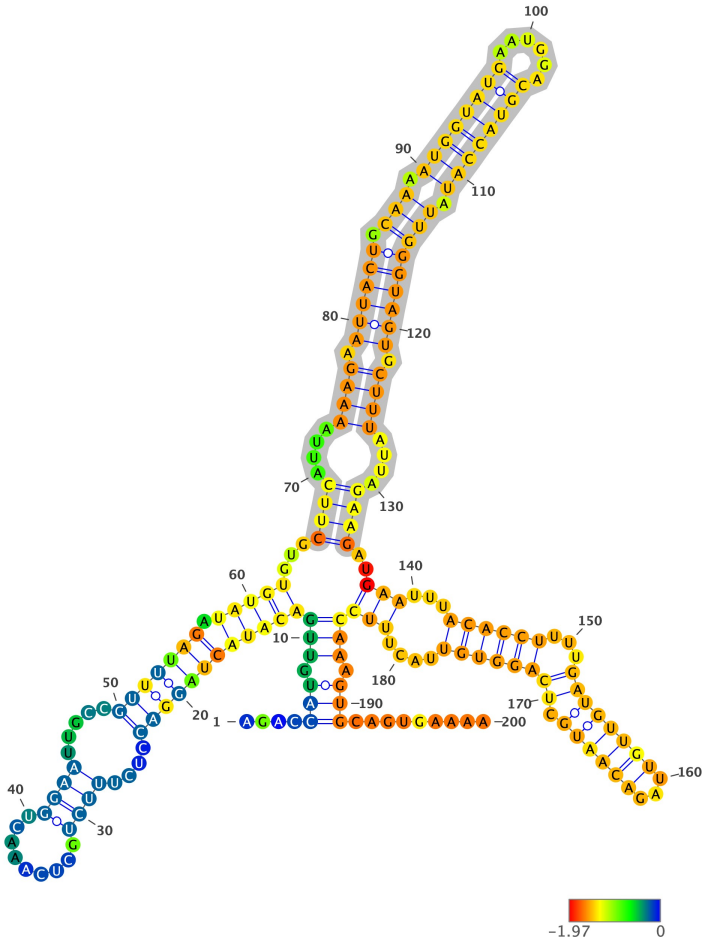
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 194 from nt 10851 to 10919 (nt 66 to 134)

```
5'-CTTCATTAAAAGAATTACTGCAAAATGGTATGAATGGACGUACCAUAUUGGGUAGUGCUUUATTAGAAG-3'
5'-(.......((((.(((((((.(((.(((((((((.....))))))))).))))))))).)))).......)-3'
Motif MFE = -20.0; z-score = -4.48; 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 10786 to 10985 (motif highlighted in silver):

```
5'-AGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUAUGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAU
AUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAA-3
5'-....(((.((((((((((((((....((((.........))))).....)))))))).)))))...((((....((((.((((((.(((.((((((((.....))))))))
.)))))))))).))))....))))..(((...((((((...((((((((...)))))).))))))))....)))))).)))..........-3'
MFE = -42.2; z-score = -0.24; ED = 25.95
```

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(+)

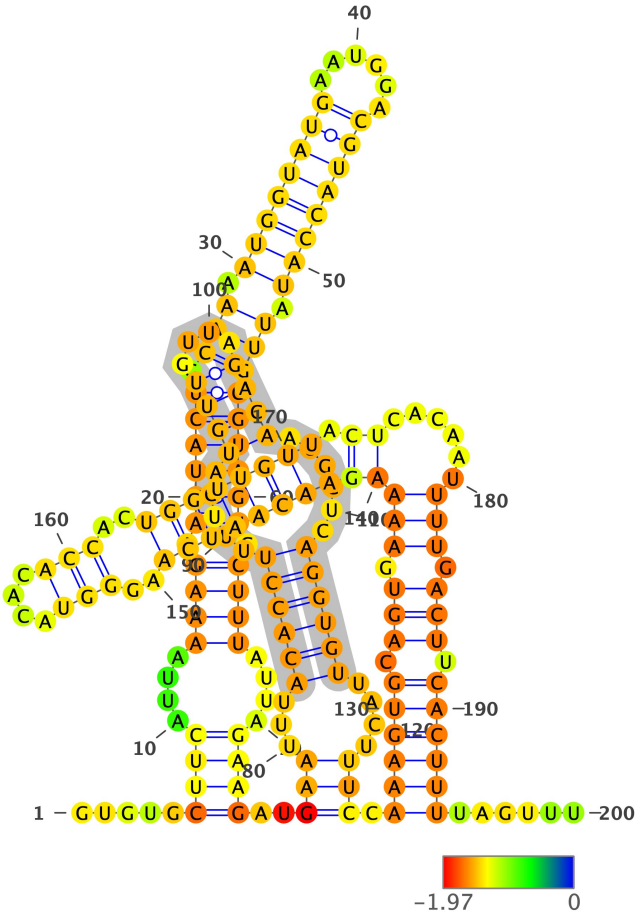
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 195 from nt 10928 to 10962 (nt 83 to 117)

```
5'-ACACCTTTTGATGTTGTTAGACAATGCTCAGGUGU-3'
5'-((((((.....((((....))))......))))))-3'
Motif MFE = -8.1; z-score = -1.67; 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 = -50.3; z-score = -2.63; ED = 26.34
```

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(+)

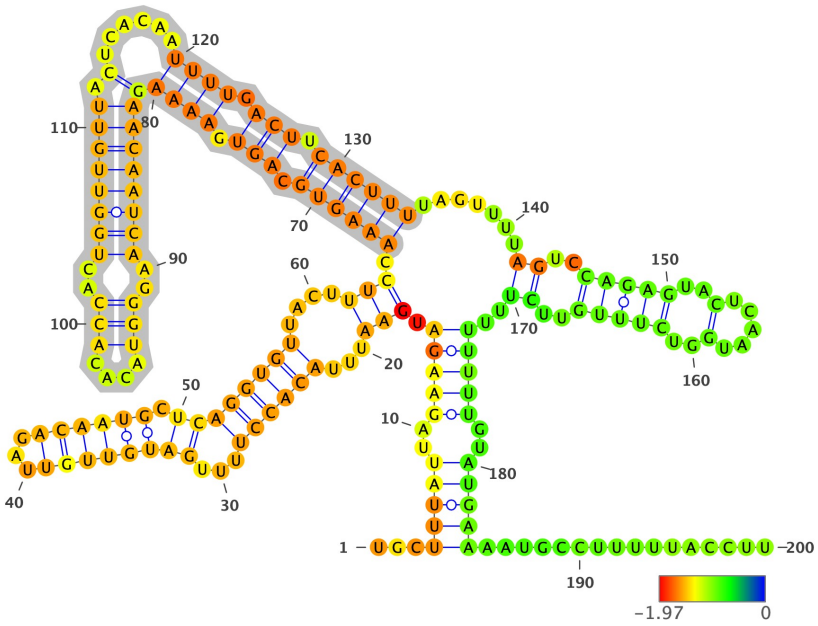
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 196 from nt 10971 to 11039 (nt 66 to 134)

```
5'-AAAGTGCAGTGAAAAGAACAATCAAGGGTACACACCACUGGUUGUUACTCACAAUUUUGACUTCACUUU-3'
5'-((((((.(((.((((.((((((((..(((....)))..))))))))........)))).))).))))))-3'
Motif MFE = -19.0; z-score = -3.23; 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 = -0.89; ED = 37.43
```

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(+)

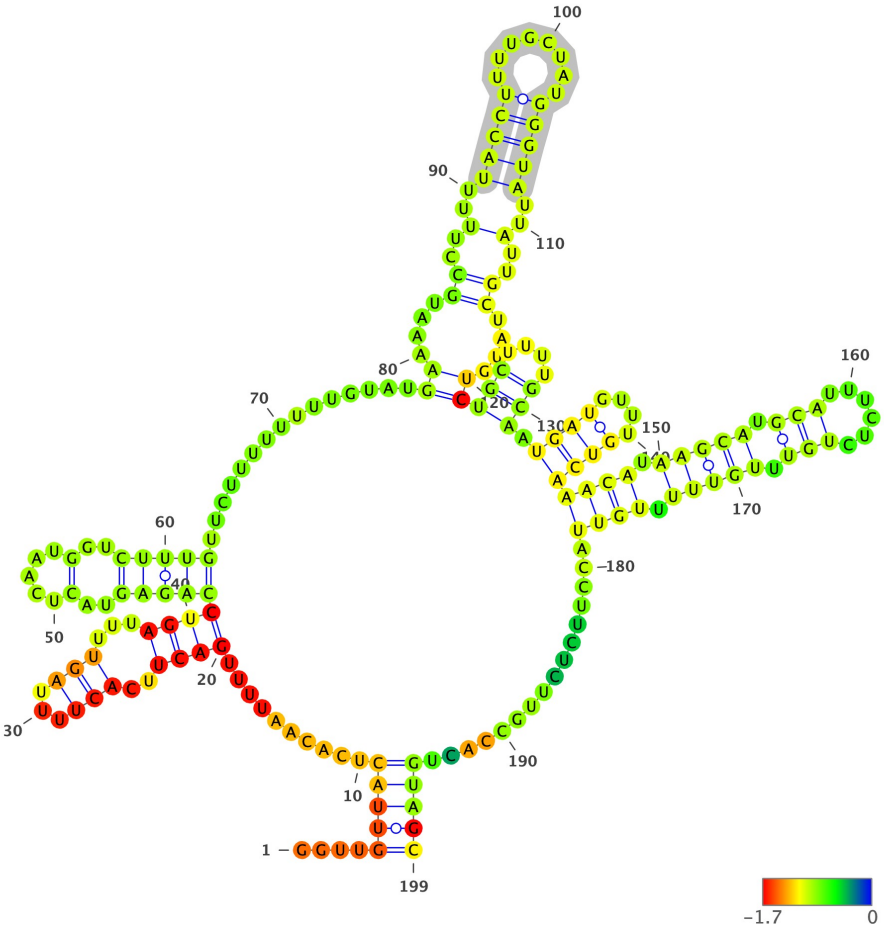
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 197 from nt 11100 to 11117 (nt 91 to 108)

```
5'-TACCTTTTGCTATGGGUA-3'
5'-(((((........)))))-3'
Motif MFE = -3.8; z-score = -3.62; 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 11010 to 11208 (motif highlighted in silver):

```
5'-GGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUA
UUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGC-3
5'-....(((((..........((((..(((...)))...))))(((((..(.....)..)))))...............((....((..(..(((((........)))))..)
..))....))(((....))).((((....))))((((.(((((.(((......))).)))))).))))................)))))-3'
MFE = -31.5; z-score = -0.59; ED = 44.01
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

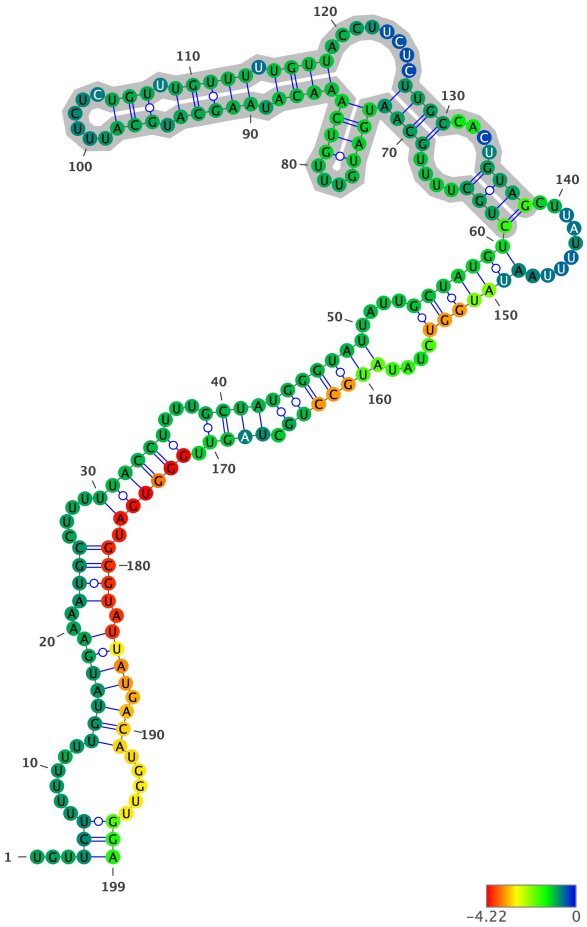
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 198 from nt 11130 to 11207 (nt 61 to 138)

```
5'-CTGCTTTTGCAATGATGTTTGUCAAACATAAGCATGCATTTCTCUGUTUGUUUTUGUUACCTTCTCTTGCCACTGTAG-3'
5'-(...........((((....))))((((.((....................)).))))...................)-3'
Motif MFE = -14.0; z-score = -1.4; ED = 9.27
```



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 11070 to 11268 (motif highlighted in silver):

```
5'-UGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGU
UUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGA-3
5'-...(((......(((((((..((((....((((((...((((((((((((....((((((((((((....((((((((....))))((((.(((((.(((......))).)))
)).))))........))))....))))).........)))))))....)))))))).)))).)))))).)))).)))).)))).....)))-3'
MFE = -37.2; z-score = -1.19; ED = 20.46
```

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(+)

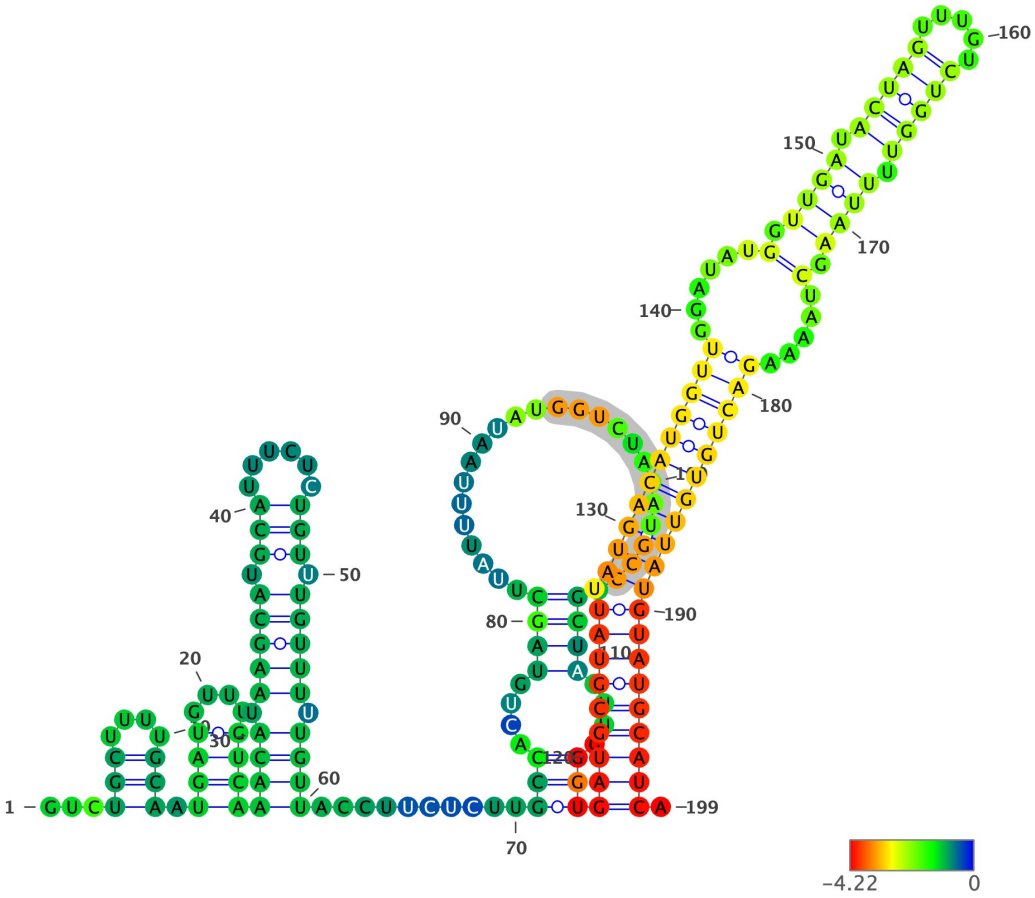
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 199 from nt 11221 to 11232 (nt 94 to 105)

```
5'-GGTCTATATGCC-3'
5'-(((......)))-3'
Motif MFE = -0.4; z-score = -0.37; 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 11128 to 11326 (motif highlighted in silver):

```
5'-GUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAG
UUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCA-3
5'-...(((....))).((((....))))((((.(((((.(((......))).))))).))))..........(((....((((.........................)))).
...)))(((((((((.((((((((((.......(.((((.(((((.....))))).)))).).....)))))))))))))))))))).-3'
MFE = -49.6; z-score = -2.94; 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, 266-13468(+)

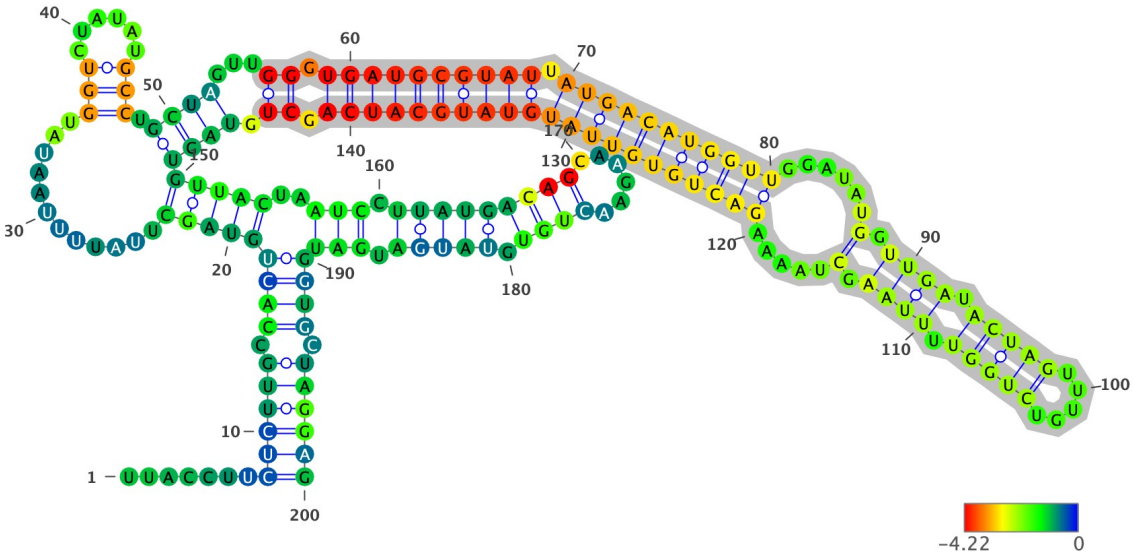
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 200 from nt 11241 to 11329 (nt 56 to 144)

```
5'-GGGTGATGCGTATTATGACATGGTTGGATATGGTTGATACTAGTTTGTCUGGUTUUAAGCTAAAAGACUGUGUUAUGUAUGCAUCAGCU-3'
5'-((.((((((((((.((((((((((.......(.((((.(((((.....))))).)))).).....)))))))))))))))))))).))-3'
Motif MFE = -35.3; z-score = -5.67; ED = 6.13
```



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 11186 to 11385 (motif highlighted in silver):

```
5'-UUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUU
AAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAG-3
5'-.......((((((.(((((((((.............(((......))).((((...((.((((((((((.((((((((((.......(.((((.(((((.....))))).))
)).).....))))))))))))))))))))).)).))))))))..(((.((((((((.......)))).))))).)))))))).))))))-3'
MFE = -56.4; z-score = -2.46; ED = 28.59
```

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, 266-13468(+)

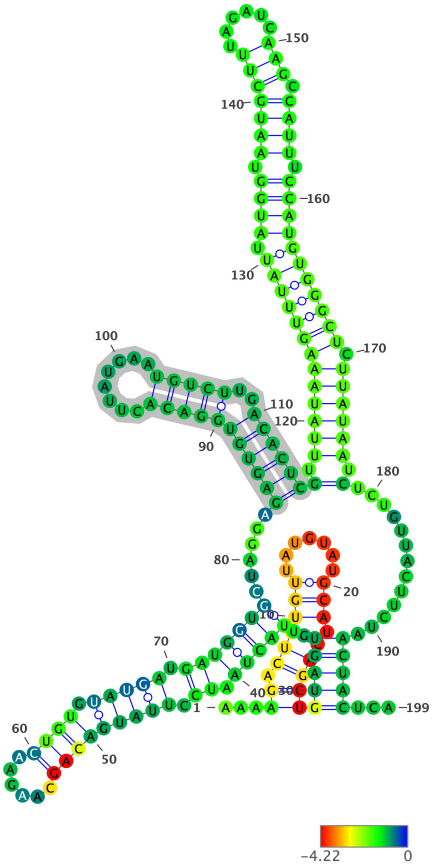
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 201 from nt 11385 to 11416 (nt 84 to 115)

```
5'-GAGTGTGGACACTTATGAAUGUCUTGACACUC-3'
5'-(((((((((((.........)))))..))))))-3'
Motif MFE = -10.6; z-score = -2.75; 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 = -0.58; 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(+)

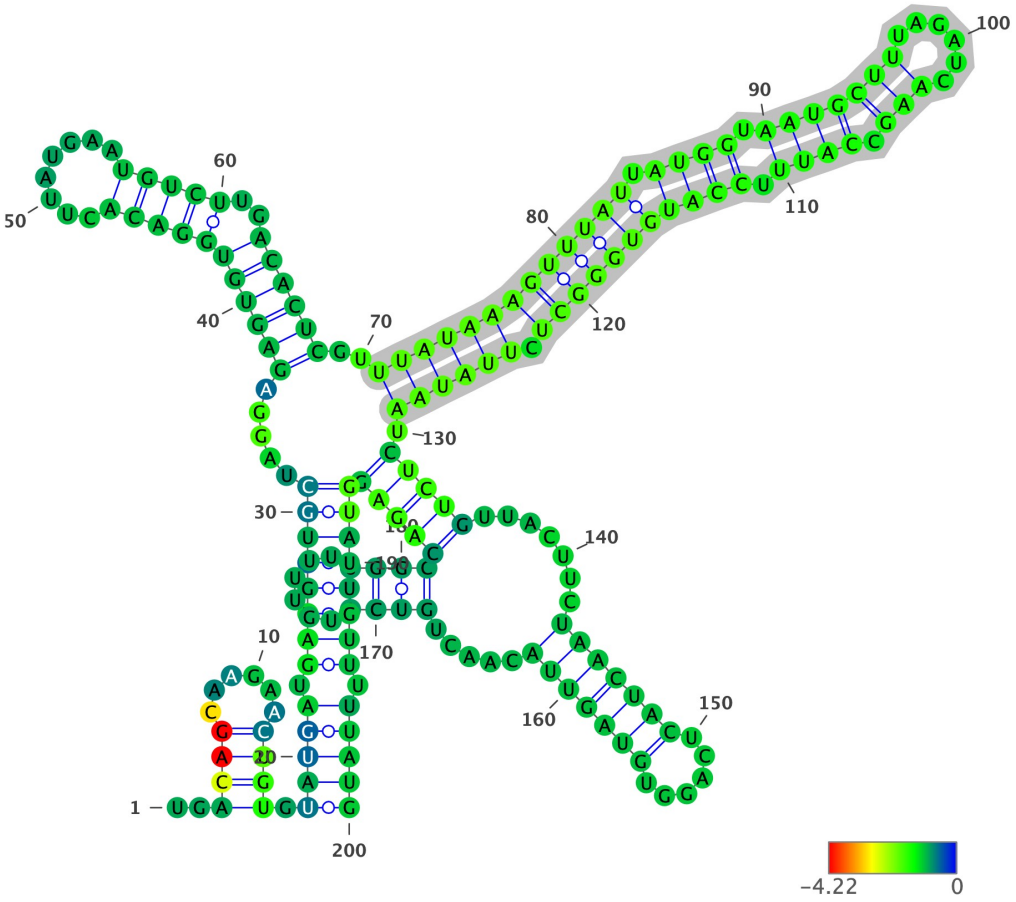
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 202 from nt 11419 to 11477 (nt 71 to 129)

```
5'-TTATAAAGTTTATTATGGTAATGCTTTAGATCAAGCCAUUTCCAUGUGGGCUCUUAUAA-3'
5'-(((((((((((((.((((.(((((((.....))).)))).)))))))))))).)))))-3'
Motif MFE = -14.1; z-score = -2.63; ED = 4.41
```



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 11349 to 11548 (motif highlighted in silver):

```
5'-UGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAGAGUGUGGACACUUAUGAAUGUCUUGACACUCGUUUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUU
CCAUGUGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUG-3
5'-..((((......)))).(((((.(((((((((.....((((((((((........))))))..))))))..((((((((((((.((((.(((((((.....))).)))).
))))))))))).)))))).(((((.......(((((((.....)))))))).....((((.....))))))))))))))))))).)))))-3'
MFE = -49.4; z-score = -1.72; 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(+)

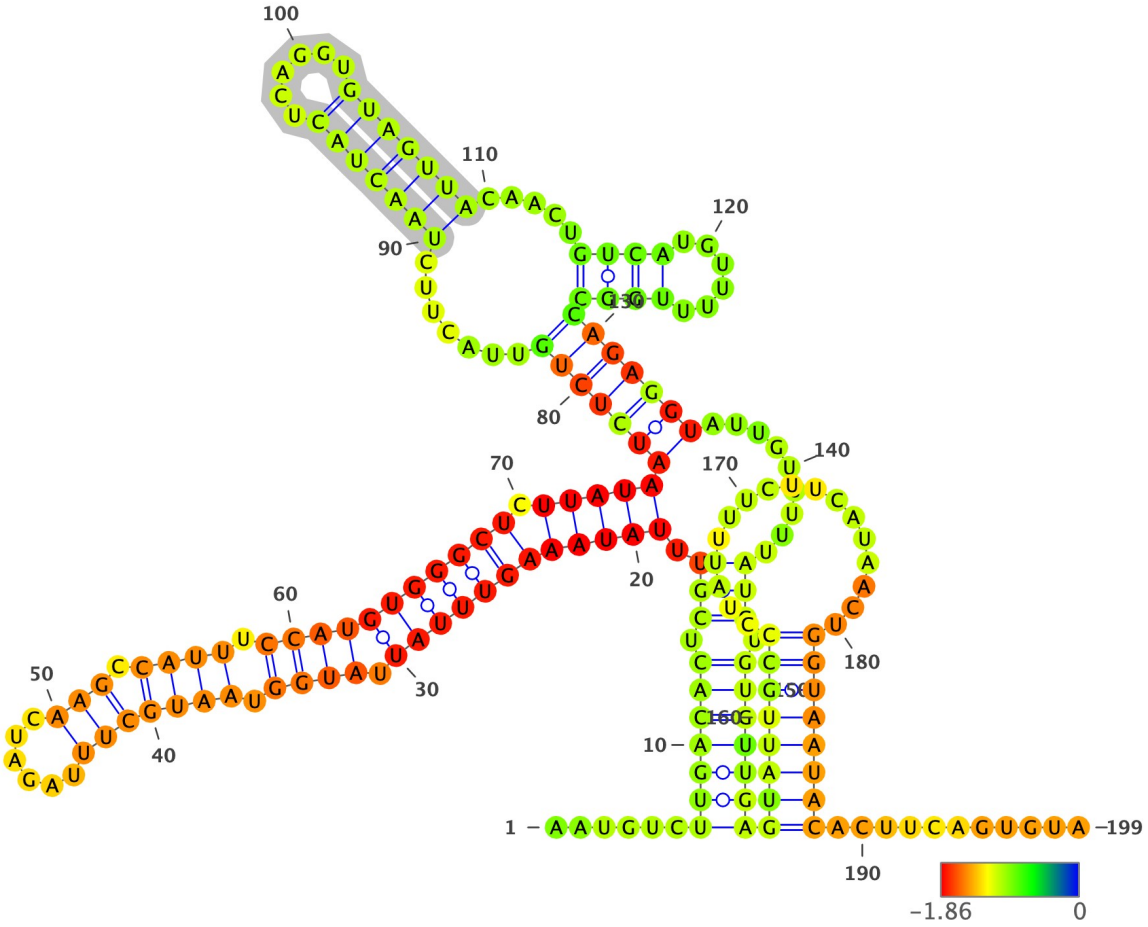
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 203 from nt 11491 to 11510 (nt 90 to 109)

```
5'-TAACTACTCAGGTGUAGUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.2; z-score = -4.52; 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 = -1.74; 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(+)

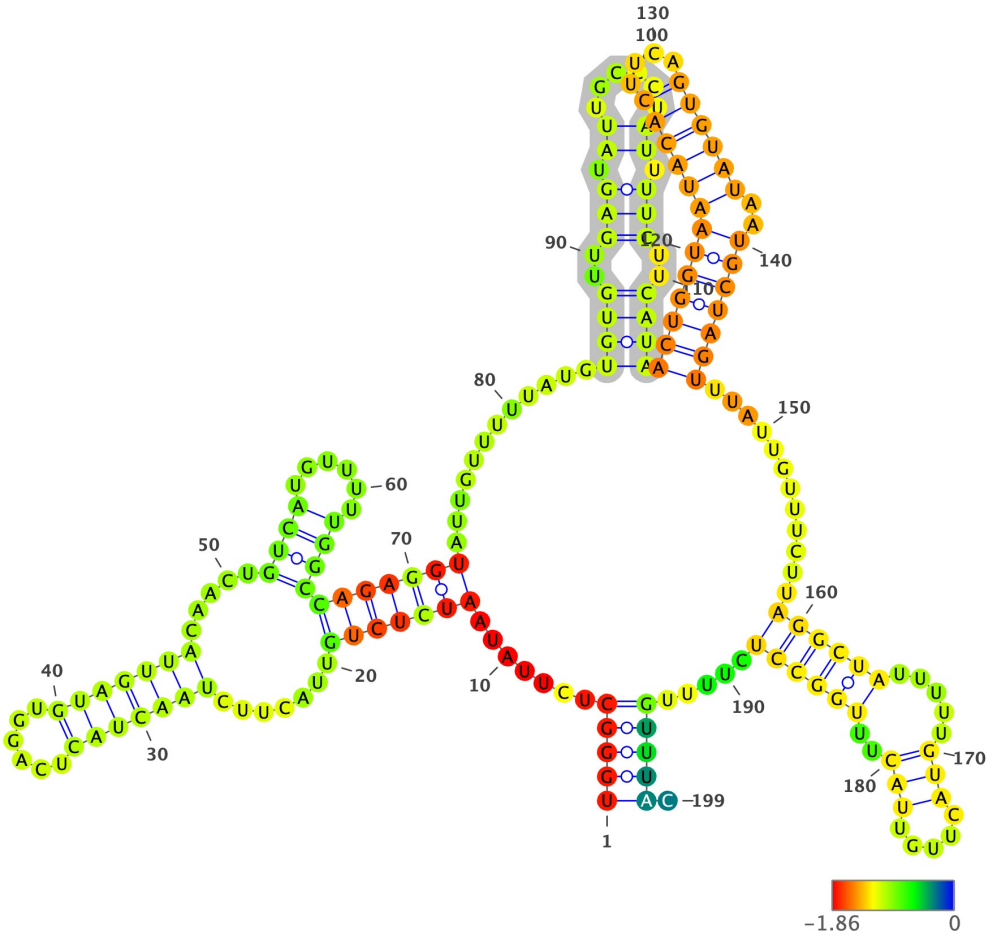
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 204 from nt 11549 to 11578 (nt 85 to 114)

```
5'-TGTGTTGAGTATTGCCCTAUTUUCTTCAUA-3'
5'-((((..(((.((......)).)))..))))-3'
Motif MFE = -2.6; z-score = -0.51; ED = 2.98
```



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 11465 to 11663 (motif highlighted in silver):

```
5'-UGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUC
AUAACUGGUAAUACACUUCAGUGUAUAAUGCUAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUAC-3
5'-(((((.......(((((((.......(((((((......)))))))).....((((......)))))))))))).............((((..(((.((......)).)))..)
)))(((((((((((((....))))))..)))))))............((((((.....(((.....)))..))))))).....))))).-3'
MFE = -38.5; z-score = -2.9; ED = 35.24
```

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(+)

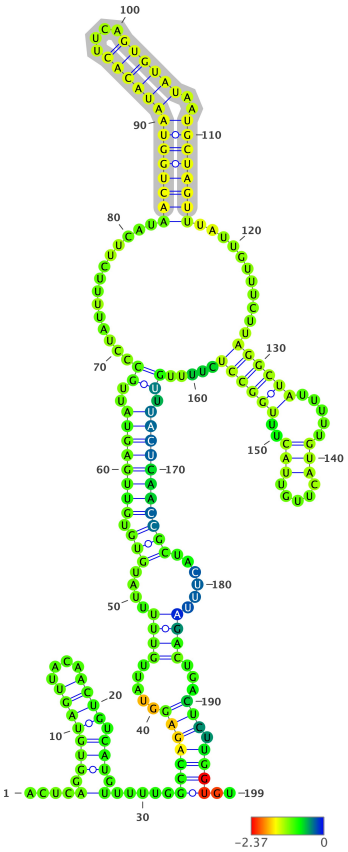
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 205 from nt 11579 to 11610 (nt 84 to 115)

```
5'-ACTGGTAATACACTTCAGUGUAUAAUGCUAGU-3'
5'-(((((((((((((....))))))..)))))))-3'
Motif MFE = -10.9; z-score = -4.01; 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 11496 to 11694 (motif highlighted in silver):

```
5'-ACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGC
UAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGU-3
5'-....(.(((((((....)))).))).).....(((((((.....((((....(((.((((((((..((..............((((((((((((((....))))))..)))
)))))..........((((((.....(((.....)))..))))))).....)).)))))))))))).....))))...))).))))..-3'
MFE = -42.0; z-score = -1.43; ED = 31.55
```

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(+)

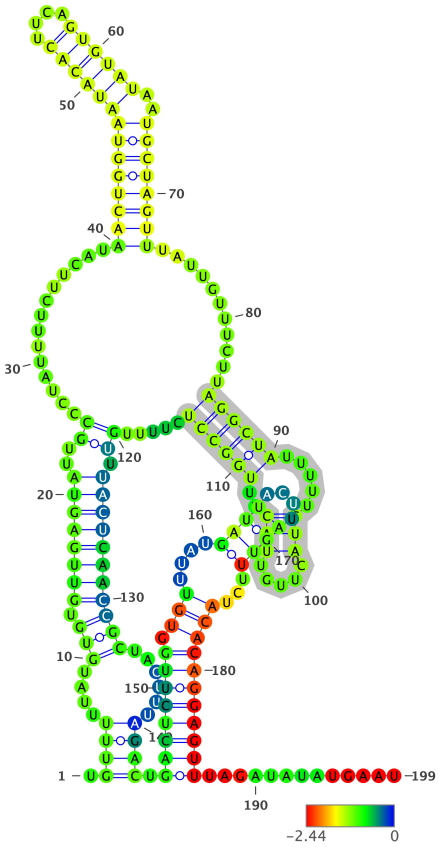
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 206 from nt 11623 to 11652 (nt 85 to 114)

```
5'-AGGCTATTTTTGTACTTGTUACTTUGGCCU-3'
5'-((((((.....(((.....)))..))))))-3'
Motif MFE = -6.0; z-score = -2.54; 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 11539 to 11737 (motif highlighted in silver):

```
5'-UGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGCUAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGG
CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAU-3
5'-.((((....(((.(((((((((..((..............((((((((((((((....))))))..))))))))).........((((((.....(((.....)))..)))
)))).....)).))))))))))).....)))).((((((((.(((....((((....))))...))))))))))).............-3'
MFE = -41.8; z-score = -2.44; ED = 23.52
```

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(+)

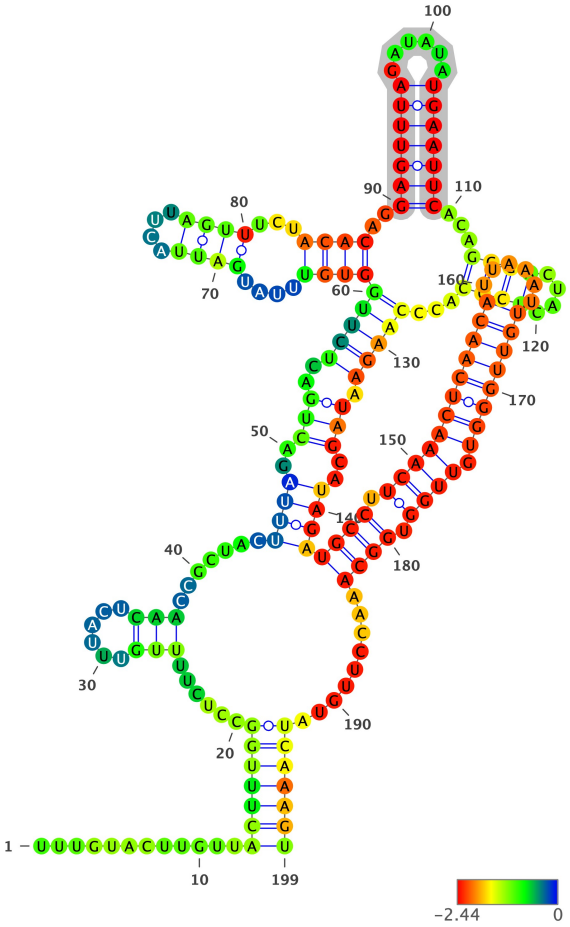
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 207 from nt 11720 to 11739 (nt 90 to 109)

```
5'-GAGTTTAGATATAUGAAUUC-3'
5'-(((((((......)))))))-3'
Motif MFE = -3.4; z-score = -2.78; 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(+)

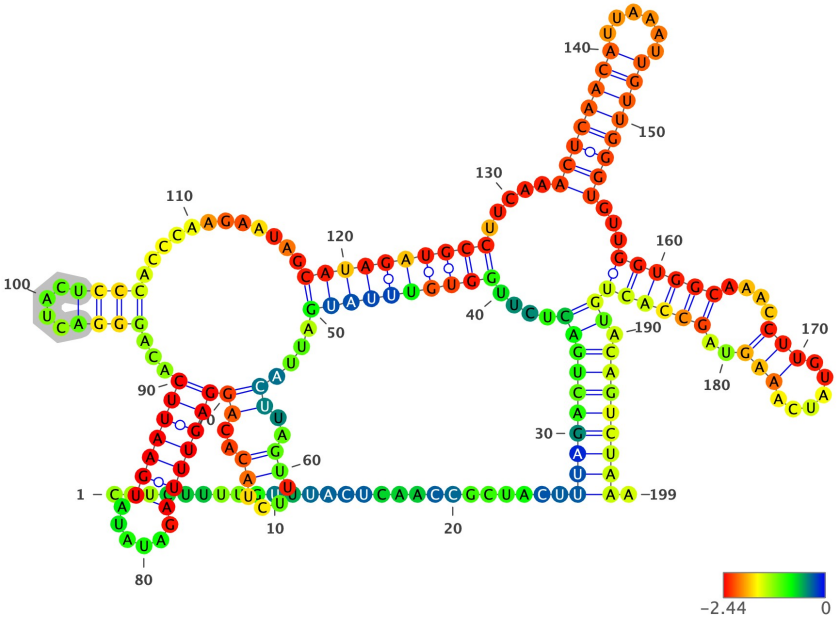
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 208 from nt 11746 to 11751 (nt 97 to 102)

```
5'-ACTACU-3'
5'-(....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.0
```



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 11650 to 11848 (motif highlighted in silver):

```
5'-CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAA
GAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAA-3
5'-.........................((((((((((....((((((((((....((..((....))..))(((((((.....)))))))...((((....)))).....
.....))))))))))).....(((((((.....)))))))...((((((....(((.....)))..)))))))).)))))))).-3'
MFE = -47.9; z-score = -2.53; ED = 38.66
```

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(+)

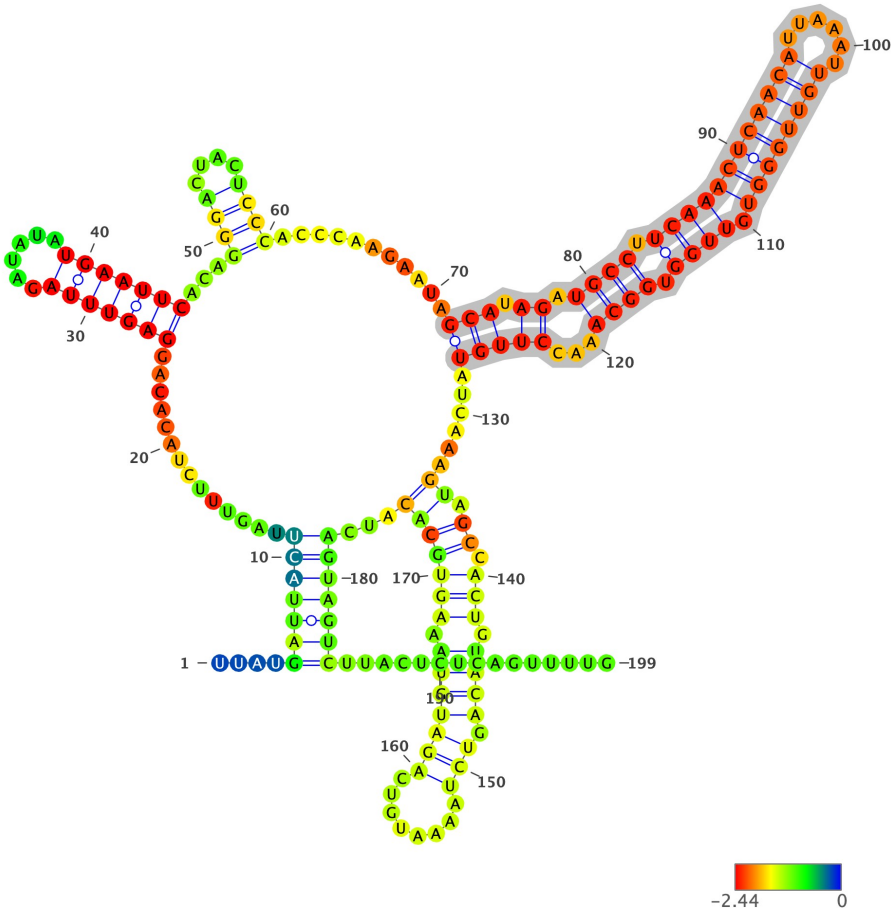
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 209 from nt 11766 to 11821 (nt 72 to 127)

```
5'-GCATAGATGCCTTCAAACTCAACATTAAATUGUUGGGUGUUGGTGGCAAACCUUGU-3'
5'-(((.((.((((.(((((((((((((.....))))))))).)))).))))...)))))-3'
Motif MFE = -18.5; z-score = -3.28; ED = 3.75
```



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 11695 to 11893 (motif highlighted in silver):

```
5'-UUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGU
UGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUG-3
5'-....(((((((.............(((((((.....)))))))...((((....))))...........(((.((.((((.(((((((((((((.....))))))))).)
))).))))...)))))......((.((.(((.((((.(((........)))))))).)))))))...)))))))................-3'
MFE = -44.2; z-score = -1.56; ED = 21.97
```

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(+)

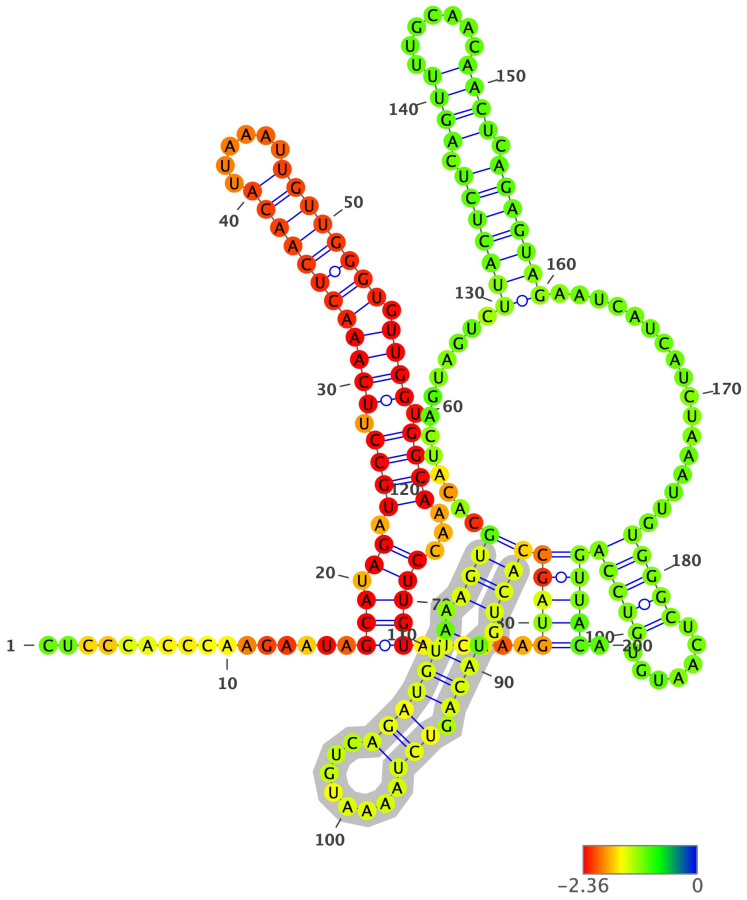
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 210 from nt 11834 to 11864 (nt 85 to 115)

```
5'-ACTGTACAGTCTAAAATGTCAGAUGUAAAGU-3'
5'-(((..(((..............))))..)))-3'
Motif MFE = -4.1; z-score = -0.89; ED = 6.29
```



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 11750 to 11949 (motif highlighted in silver):

```
5'-CUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUA
AAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACA-3
5'-.................(((.((.((((.((((((((((((.....)))))))).)))).)))).)))...)))))......(((((((((.((((.(((........)))))))
.))))).............(((((((.((((.......)))).))))))).................(((((.......)))))))))).-3'
MFE = -44.7; z-score = -1.53; ED = 28.19
```

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(+)

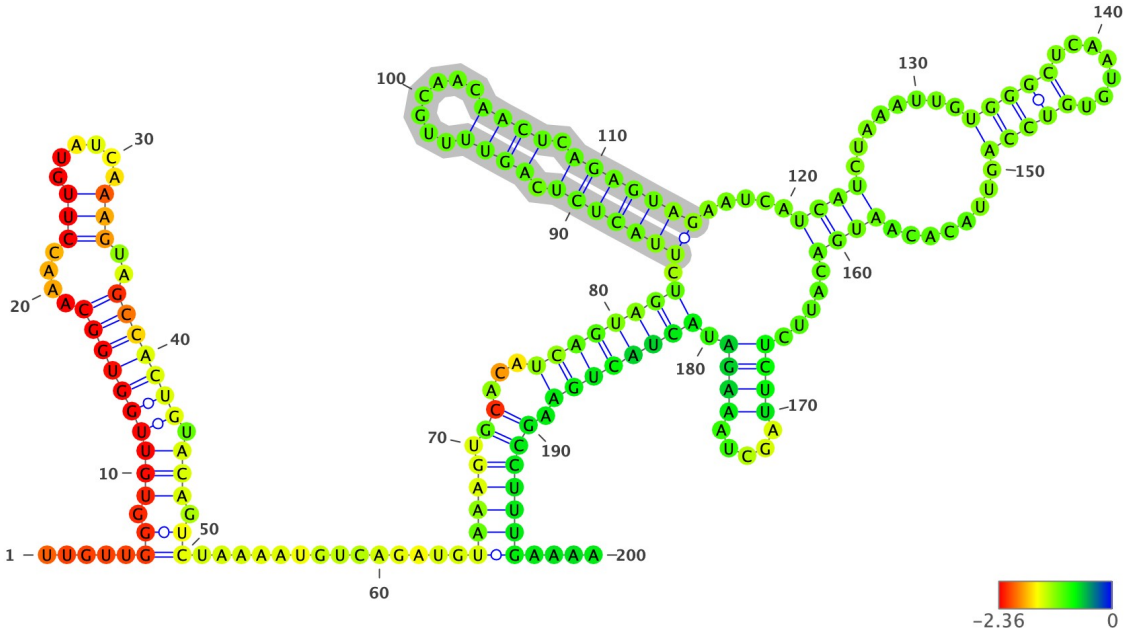
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 211 from nt 11879 to 11909 (nt 85 to 115)

```
5'-TTACTCTCAGTTTTGCAACAACUCAGAGUAG-3'
5'-(((((((.((((.......)))).)))))))-3'
Motif MFE = -8.0; z-score = -2.56; ED = 1.42
```



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 11795 to 11994 (motif highlighted in silver):

```
5'-UUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGA
GUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAA-3
5'-.....((.((((((((((....(((......)))..)))))))).))).))..............(((((.((...((((((((.(((((((.((((.......)))).)))
))))).....((((........(((((.......)))))........))))).....((((.....)))).))))))))).)))))))....-3'
MFE = -44.6; z-score = -1.33; ED = 35.41
```

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(+)

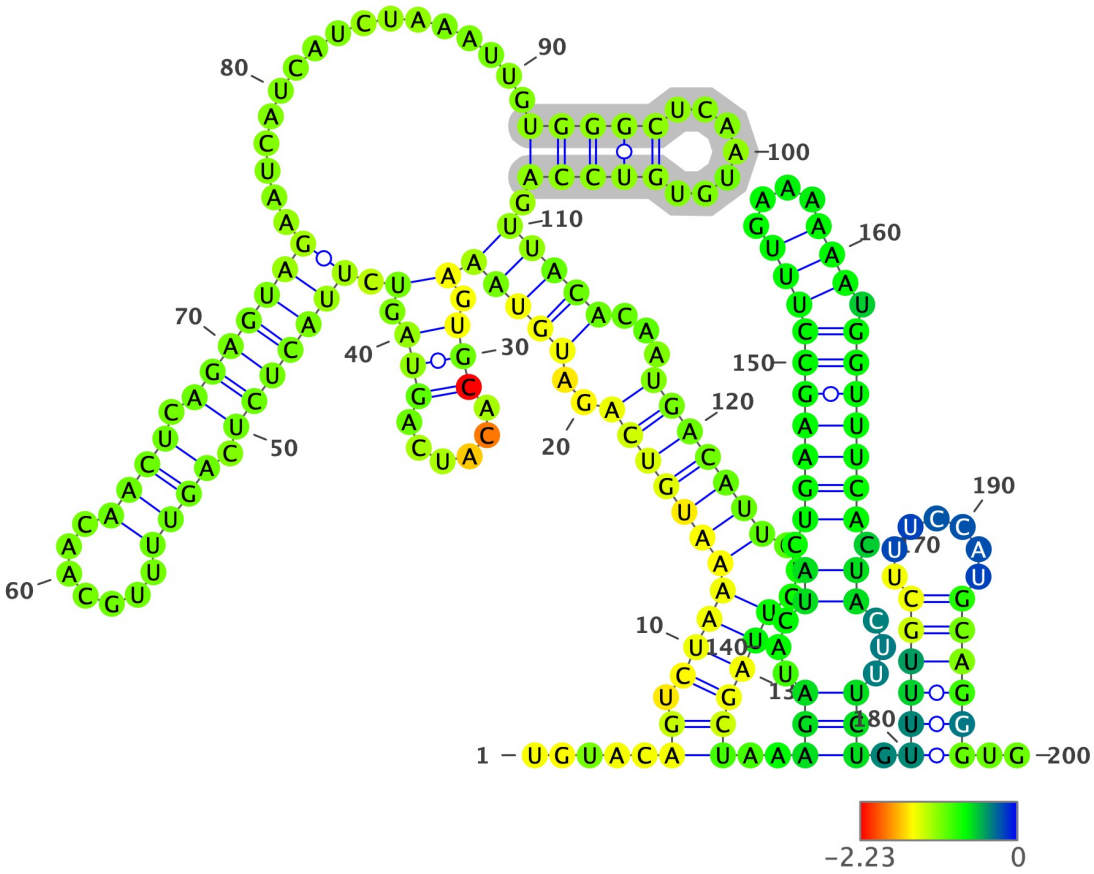
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 212 from nt 11927 to 11943 (nt 92 to 108)

```
5'-TGGGCTCAATGTGUCCA-3'
5'-(((((.......)))))-3'
Motif MFE = -5.0; z-score = -2.56; 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 11836 to 12035 (motif highlighted in silver):

```
5'-UGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAAUUGUGGGCUCAAUGUGUCCAGUU
ACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAAAAUGGUUUCACUACUUUCUGUUUUGCUUUCCAUGCAGGGUG-3
5'-.....((.(((((((((((..((((((.(((.....))).).(((((((.(((.....)))).)))))))).................(((((.....)))))).))
)))...)))))))...))))))..(((...((.((((((((((....)))).)))))))..))...))).((((((.....))))))..-3'
MFE = -38.8; z-score = -0.8; ED = 43.96
```

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(+)

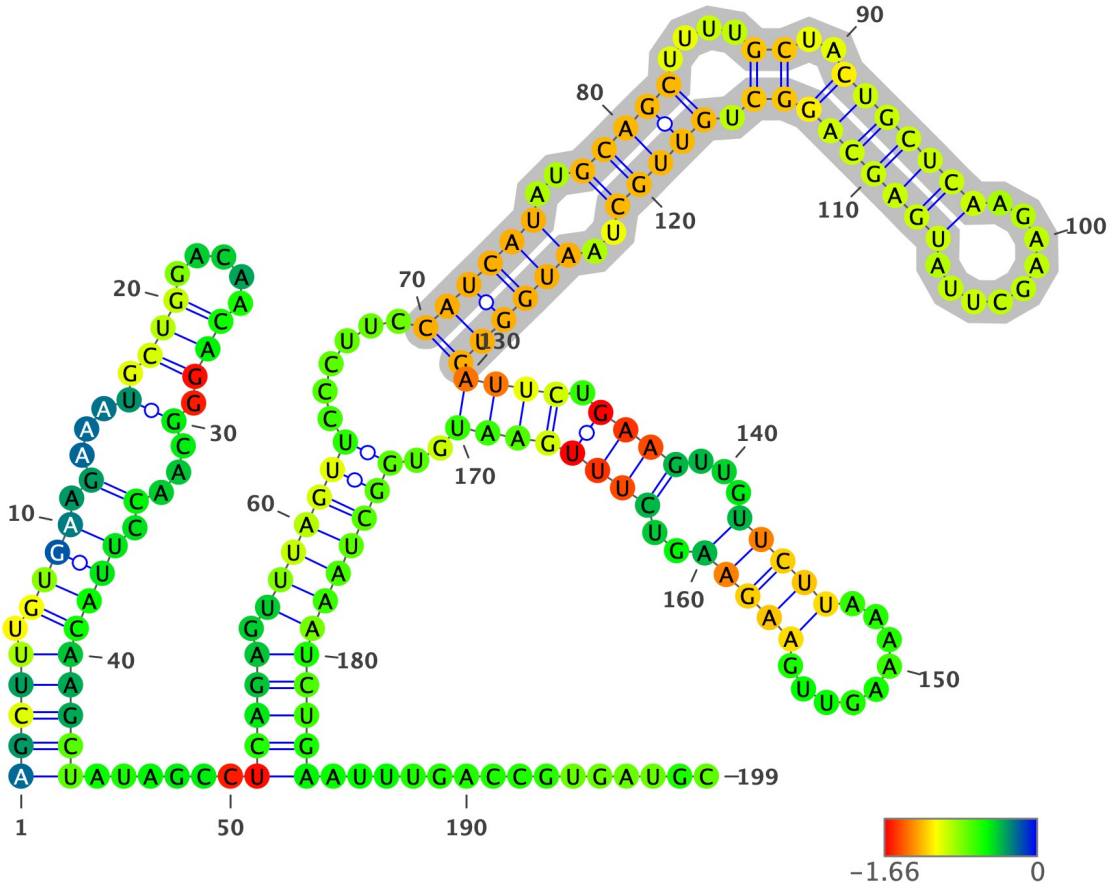
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 213 from nt 12120 to 12179 (nt 70 to 129)

```
5'-CATCATATGCAGCTTTTGCTACTGCTCAAGAAGCTTAUGAGCAGGCTGUUGCTAAUGGUG-3'
5'-((((((..(((((....((..(.....................))).))))))..)))))))-3'
Motif MFE = -19.9; z-score = -3.25; 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 12051 to 12249 (motif highlighted in silver):

```
5'-AGCUUUGUGAAGAAAUGCUGGACAACAGGGCAACCUUACAAGCUAUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUUAUGAGC
AGGCUGUUGCUAAUGGUGAUUCUGAAGUUGUUCUUAAAAAGUUGAAGAAGUCUUUGAAUGUGGCUAAAUCUGAAUUUGACCGUGAUGC-3
5'-(((((.(((((.(...(.(((.....))).).)...).)))))))))......(((((.(((((((.....((((((..((((((....((..(((((((.........)))))
))))).))))))..)))))))(((((.((((...(((((.........)))))..))))))))..)))))))))..............-3'
MFE = -44.9; z-score = 0.1; ED = 33.8
```

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(+)

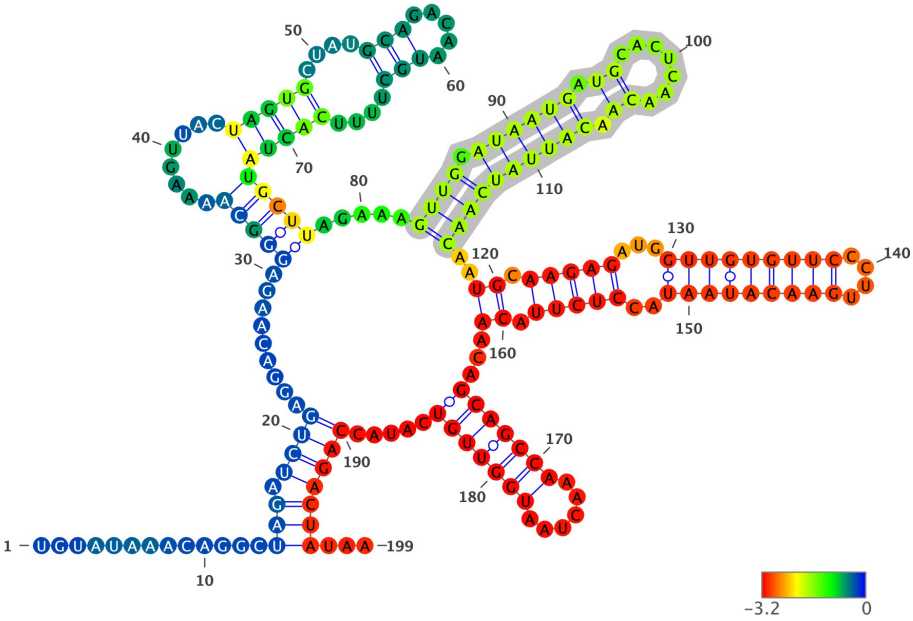
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 214 from nt 12382 to 12415 (nt 83 to 116)

```
5'-GTTGGATAATGATGCACTCAACAACAUUAUCAAC-3'
5'-((((.(((((((.((.......)).)))))))))))-3'
Motif MFE = -6.3; z-score = -2.6; 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 = -2.0; ED = 26.66
```

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(+)

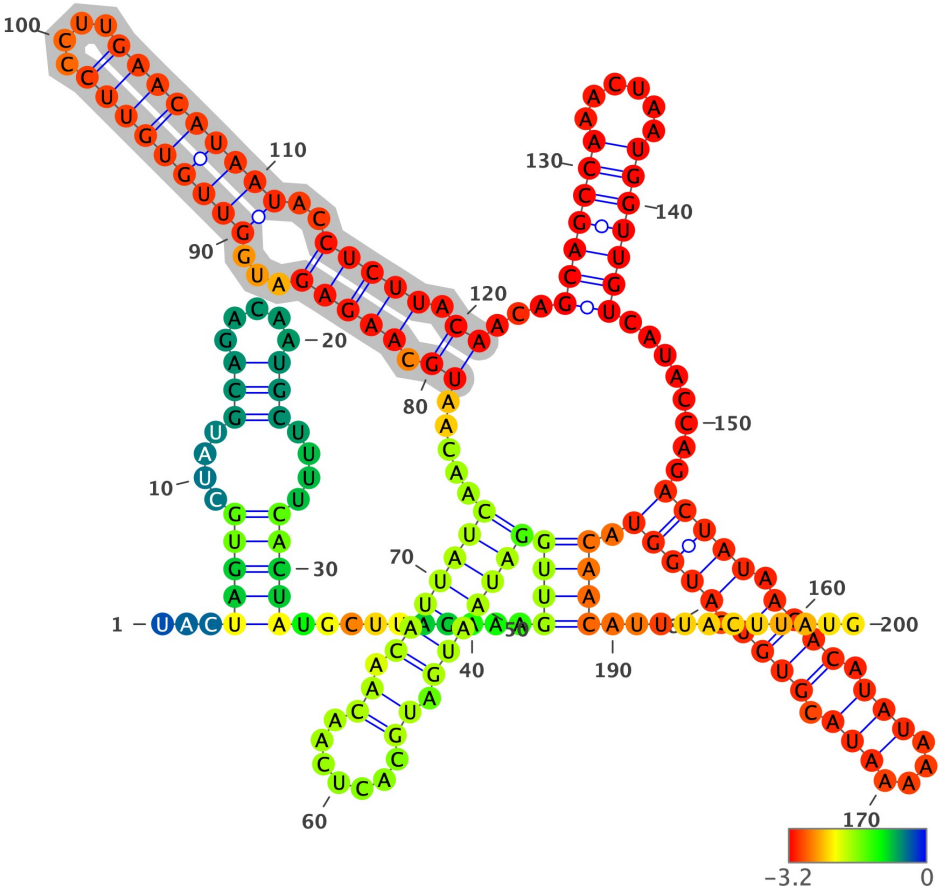
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 215 from nt 12418 to 12460 (nt 79 to 121)

```
5'-TGCAAGAGATGGTTGTGTTCCCTTGAACAUAAUACCUCUUACA-3'
5'-((.((((((...((((((((((....))))))))))..))))))..))-3'
Motif MFE = -12.6; z-score = -3.04; ED = 4.03
```



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 12340 to 12539 (motif highlighted in silver):

```
5'-UACUAGUGCUAUGCAGACAAUGCUUUUCACUAUGCUUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAU
ACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUG-3
5'-...((((((....(((.....)))....)))))).........((((((((((.((.......)).)))))))).....((.((((((...((((((((((....))))))))))
..))))))..))...(((((((.....)))))))........((((.((((.(((....))).)))).)))))..))))...........-3'
MFE = -46.4; z-score = -3.37; 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(+)

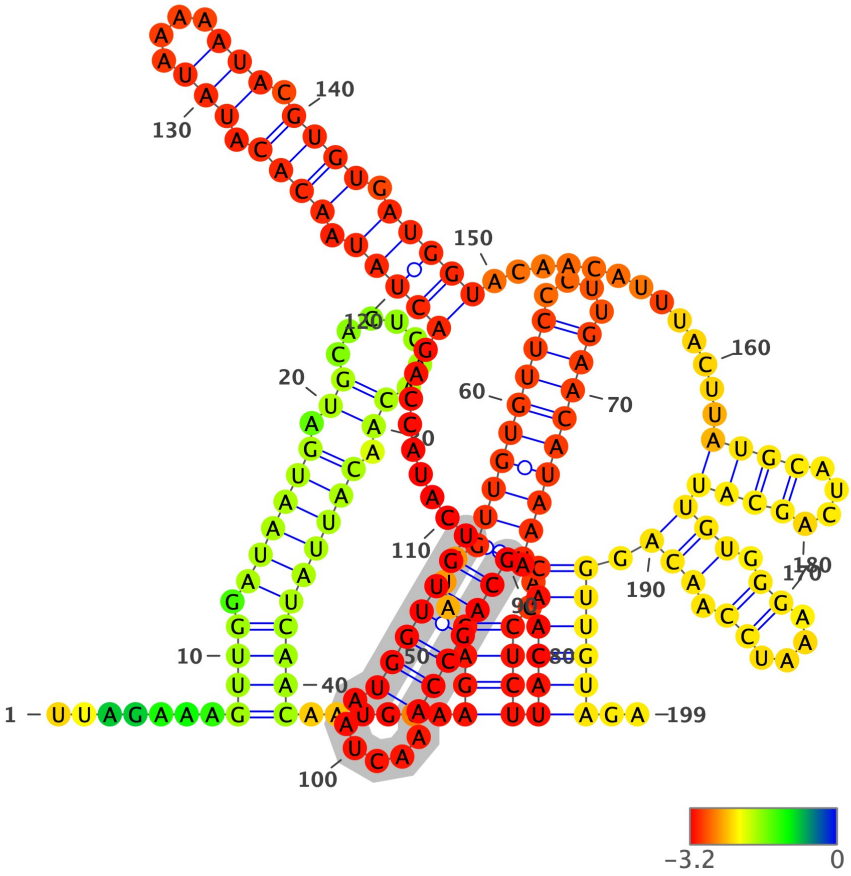
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 216 from nt 12464 to 12483 (nt 90 to 109)

```
5'-GCAGCCAAACTAAUGGUUGU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.5; z-score = -3.95; 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 = -2.62; 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(+)

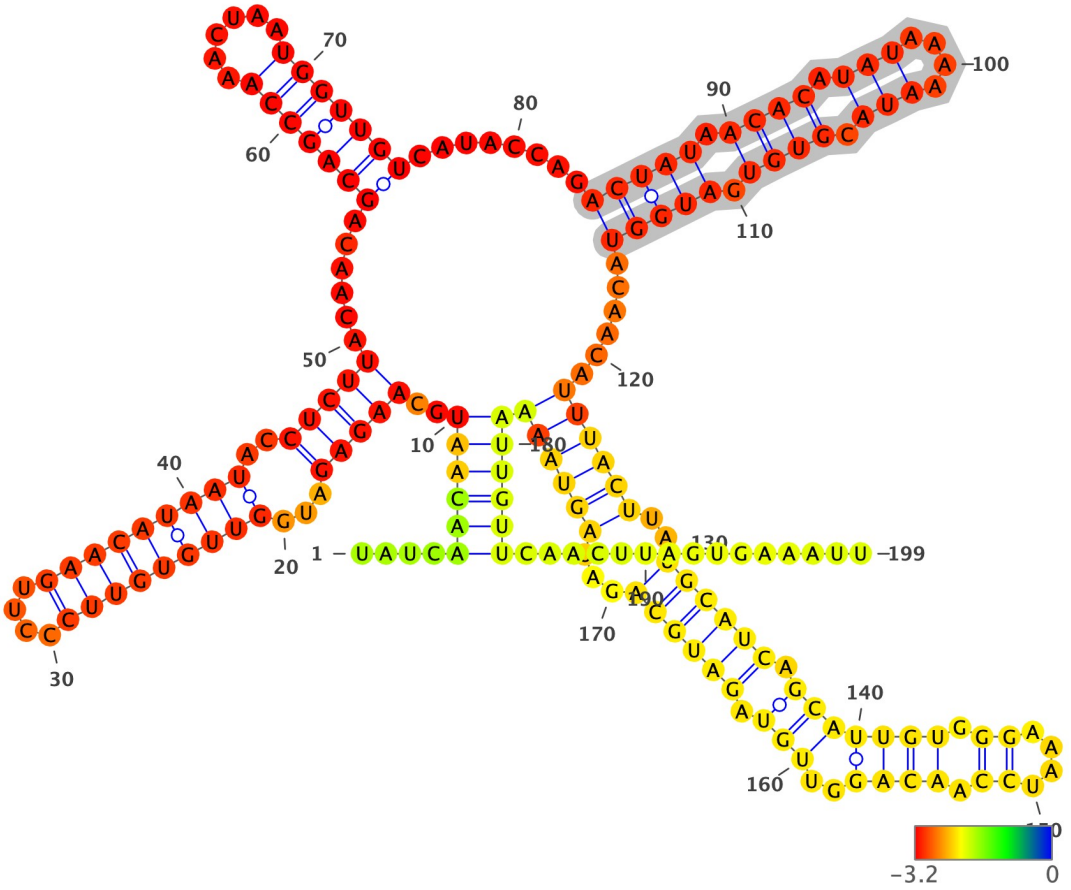
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 217 from nt 12492 to 12523 (nt 84 to 115)

```
5'-ACTATAACACATATAAAAAUACGUGUGAUGGU-3'
5'-(((((.((((.(((....))).)))).)))))-3'
Motif MFE = -6.6; z-score = -3.12; 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 = -3.98; 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, 266-13468(+)

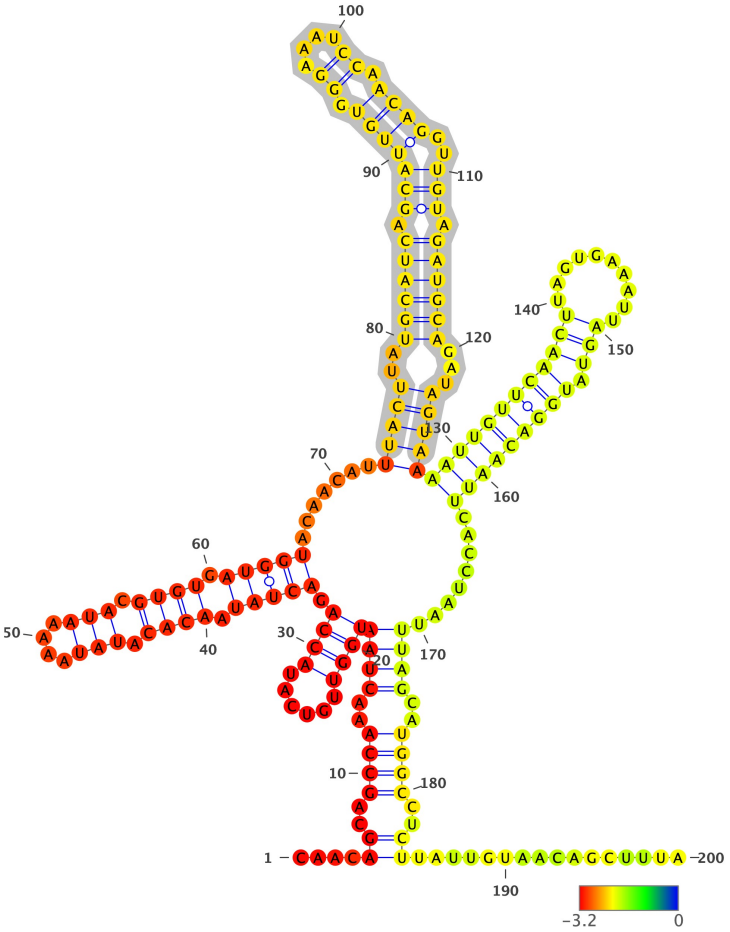
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 218 from nt 12532 to 12584 (nt 74 to 126)

```
5'-TACTTATGCATCAGCATTGTGGGAAATCCAACAGGTUGUAGAUGCAGATAGUA-3'
5'-((((..(((((((.(((((((.((....)).))))..))).))))))...))))-3'
Motif MFE = -15.1; z-score = -2.87; ED = 7.87
```



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 12459 to 12658 (motif highlighted in silver):

```
5'-CAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUG
UAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUA-3
5'-....((..((((..((((((((.....)))).(((((.((((.(((....))).)))).)))))).......(((((..(((((((.(((((((.((....)).))))..))
).))))))...)))))((((((((((((.........))).))))))))).........))))..))))..)).................-3'
MFE = -44.0; z-score = -2.43; ED = 25.26
```

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(+)

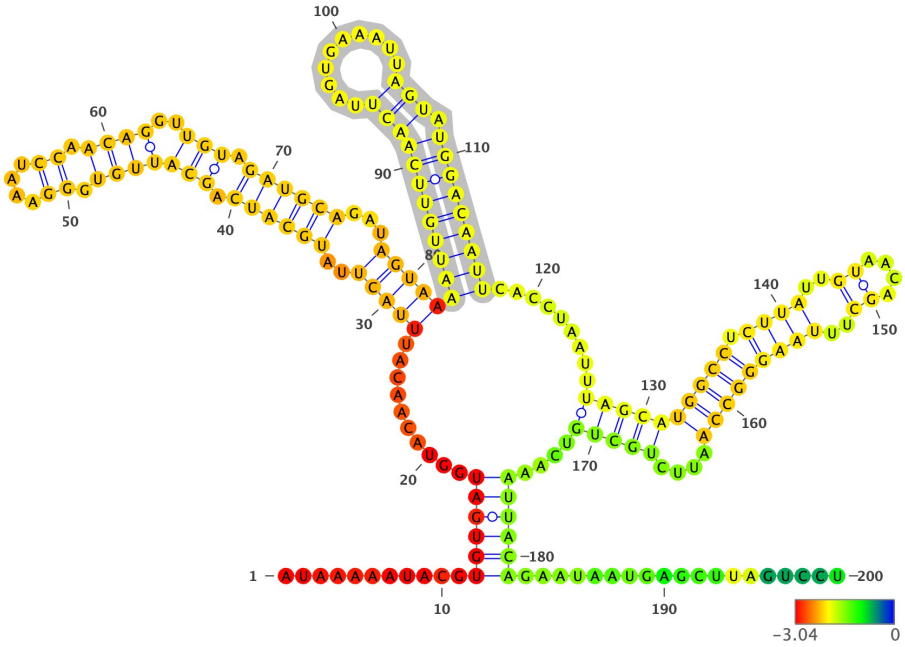
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 219 from nt 12586 to 12620 (nt 83 to 117)

```
5'-AATTGTTCAACTTAGTGAAATTAGUAUGGACAAUU-3'
5'-(((((((((((((..........))).)))))))))-3'
Motif MFE = -7.4; z-score = -2.91; 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 = -1.92; 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(+)

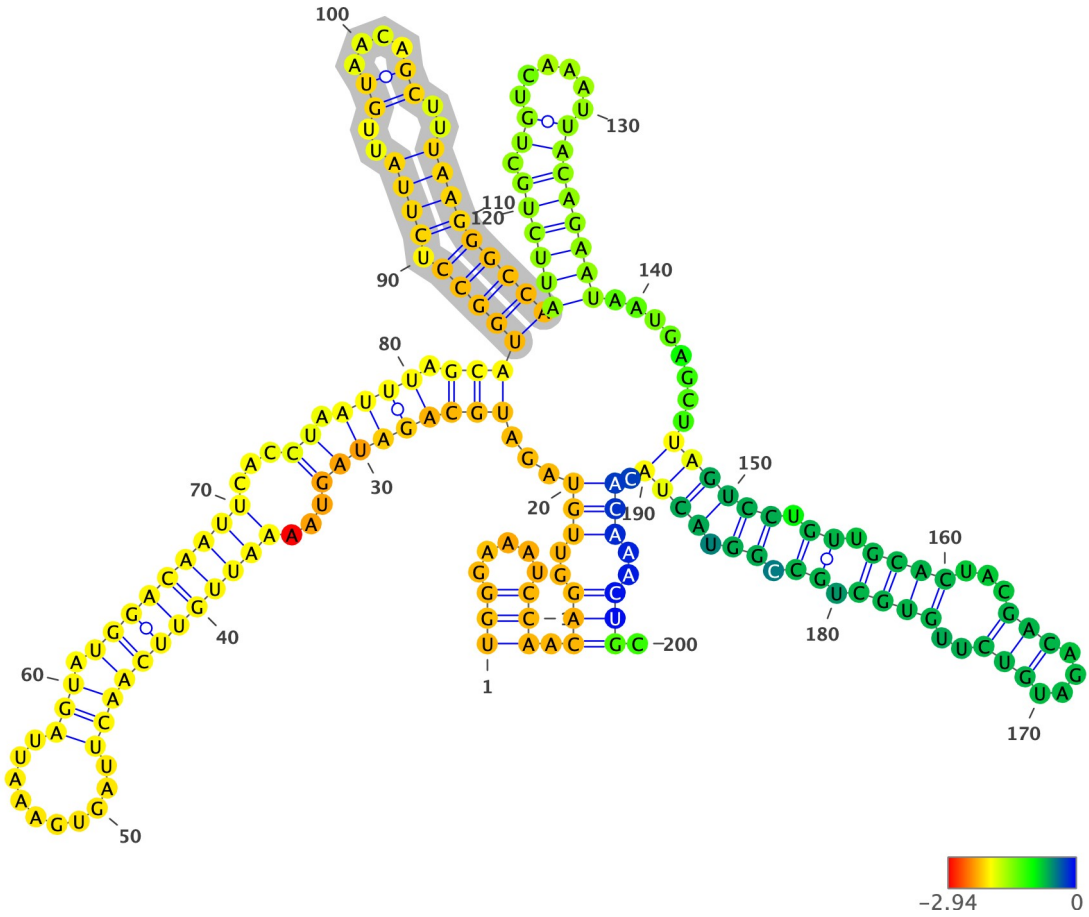
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 220 from nt 12635 to 12665 (nt 85 to 115)

```
5'-TGGCCTCTTATTGTAACAGCTTUAAGGGCCA-3'
5'-(((((.((((..((....))..)))))))))-3'
Motif MFE = -12.7; z-score = -4.56; 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 = -2.41; 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(+)

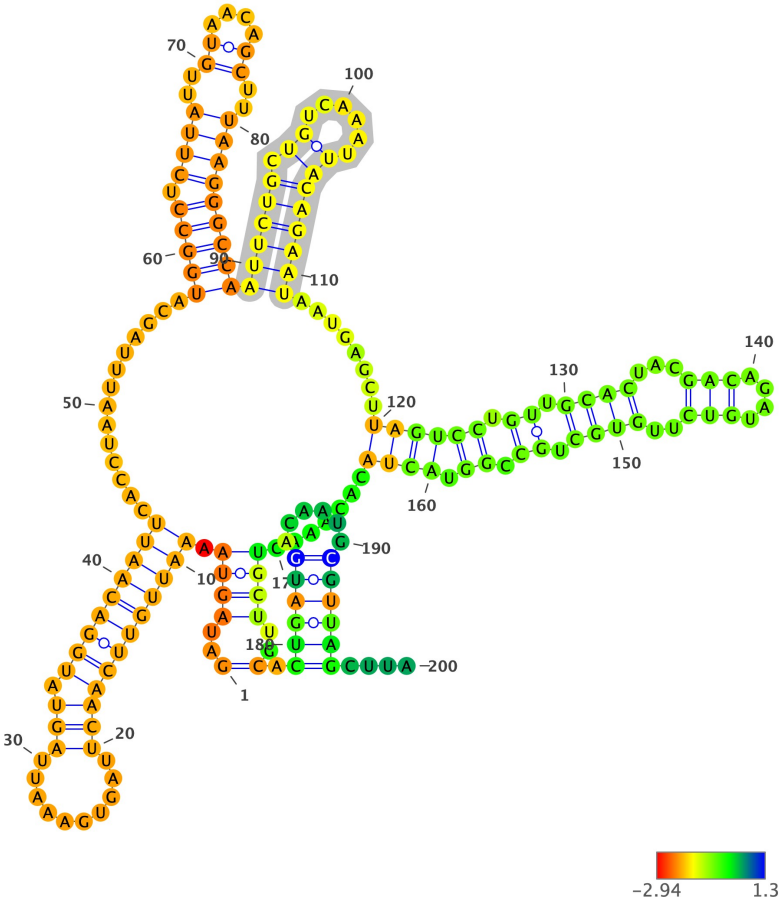
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 221 from nt 12666 to 12688 (nt 89 to 111)

```
5'-ATTCTGCTGTCAAATUACAGAAU-3'
5'-((((((.((......))))))))-3'
Motif MFE = -3.1; z-score = -2.08; 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 12578 to 12777 (motif highlighted in silver):

```
5'-GAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGCCAAUUCUGCUGUCAAAUUACAGAAU
AAUGAGCUUAGUCCUGUUGCACUACGACAGAUGUCUUGUGCUGCCGGUACUACACAAACUGCUUGCACUGAUGACAAUGCGUUAGCUUA-3
5'-(..((((.(((((((((((((..........))).)))))))))..............(((((.((((..((....))..)))))))))((((((.((......))))))))
........((((((.((.((((...(((....)))..)))).)).)).)))).......))))..).((((((......))))))....-3'
MFE = -47.5; z-score = -1.99; ED = 46.17
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

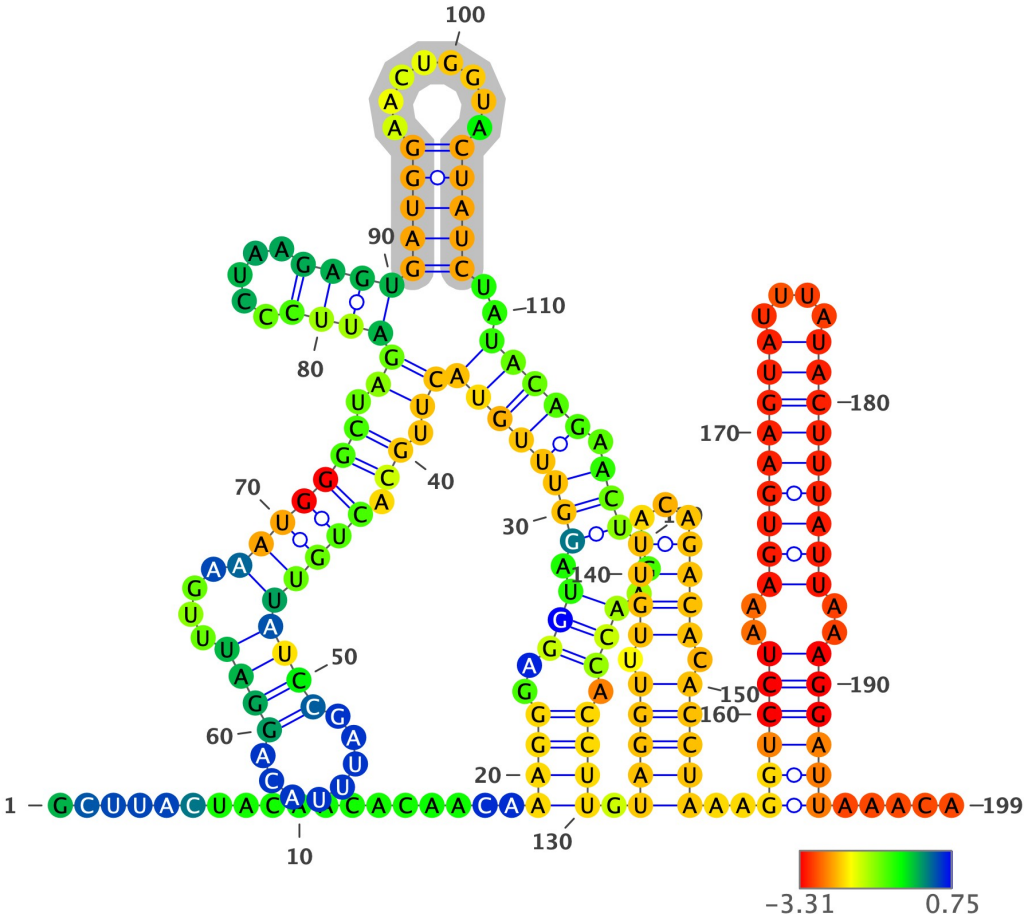
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 222 from nt 12863 to 12880 (nt 91 to 108)

```
5'-GATGGAACTGGTACUAUC-3'
5'-(((((........)))))-3'
Motif MFE = -2.2; z-score = -1.31; 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 12773 to 12971 (motif highlighted in silver):

```
5'-GCUUACUACAACACAACAAAGGGAGGUAGGUUUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAU
ACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACA-3
5'-..................(((((..(((.((((((((((.((.((((((((((........)))).....)))))))).))(((((.....)))))(((((........)))))).)
)))).)))...))).)))).((((((.((((...)))).)))))..((((((..((((((((((....))))))))))..))))))......-3'
MFE = -41.8; z-score = -1.65; ED = 42.57
```

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(+)

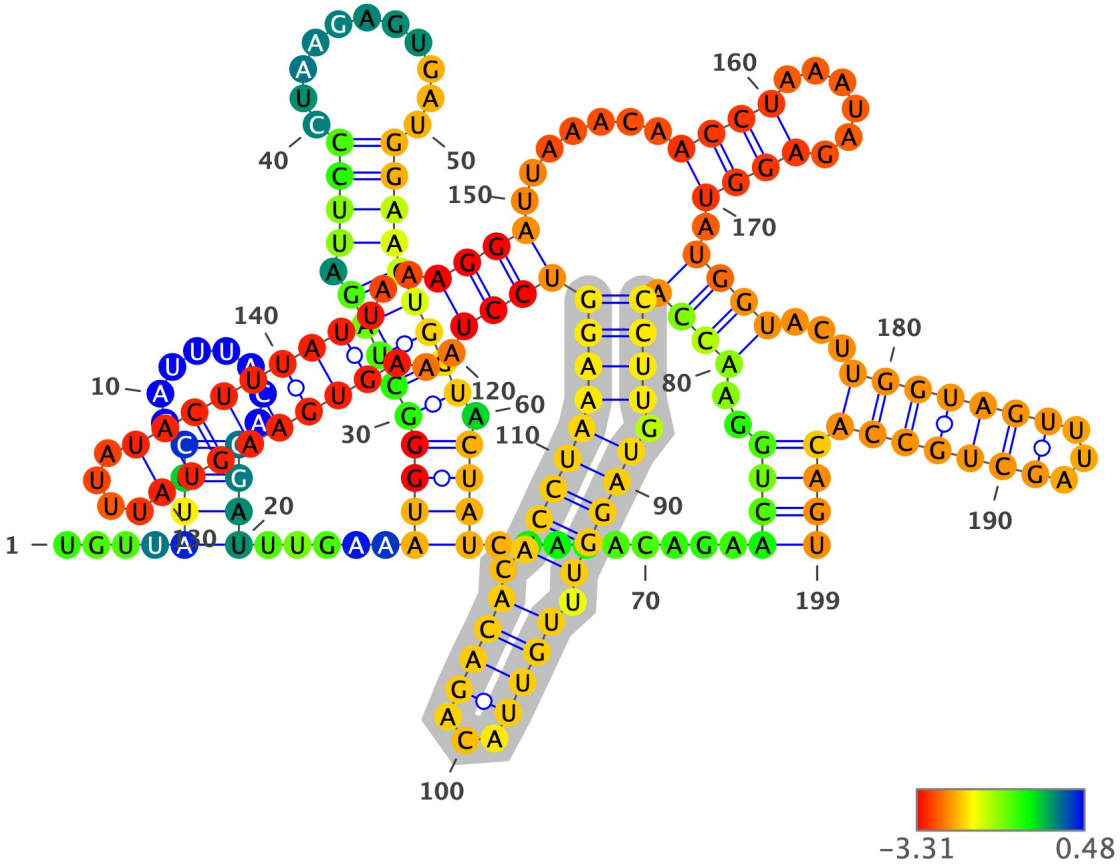
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 223 from nt 12899 to 12930 (nt 84 to 115)

```
5'-CCTTGTAGGTTTGTTACAGACACACCUAAAGG-3'
5'-((((.((((((.((((...)))).)))))))))-3'
Motif MFE = -10.1; z-score = -3.08; 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 12816 to 13014 (motif highlighted in silver):

```
5'-UGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUA
AAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGU-3
5'-....((((........))))....((((((((((.((((..........))))))))).))))).........((((..(((((((((.(((((.((((...)))).)))))
))))(((((..((((((((((....))))))))))..))))).......((((......)))).))))...(((((((...)))))))))))-3'
MFE = -48.9; z-score = -2.18; ED = 40.76
```

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(+)

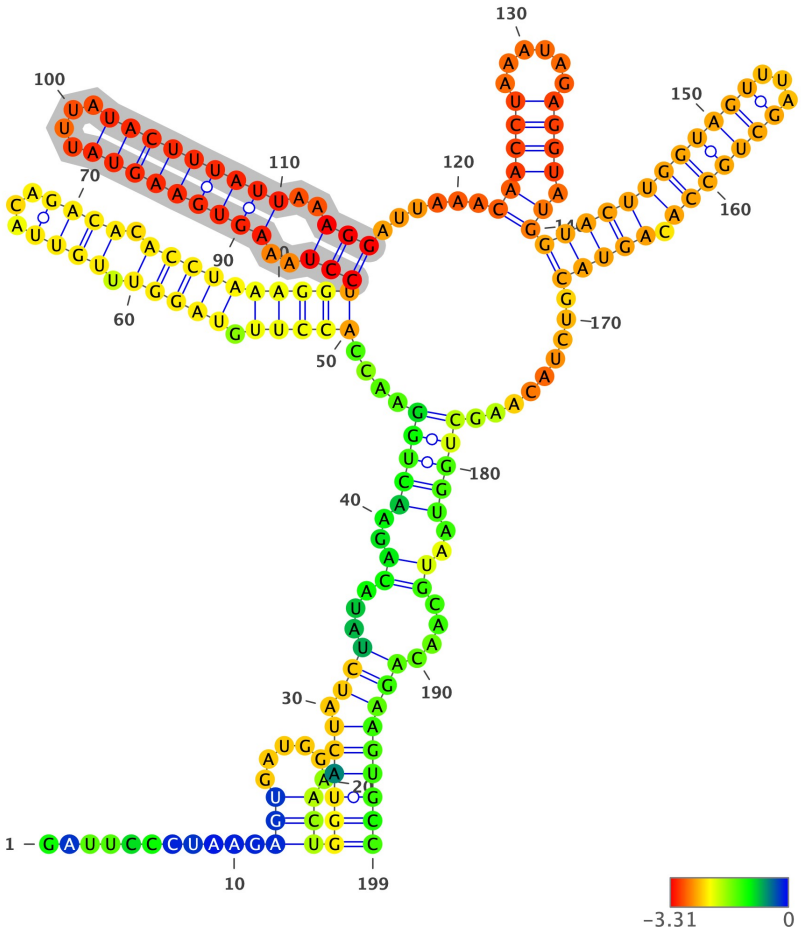
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 224 from nt 12932 to 12963 (nt 84 to 115)

```
5'-CCTAAAGTGAAGTATTTAUACUUUAUUAAAGG-3'
5'-(((..((((((((((....)))))))))..)))-3'
Motif MFE = -7.9; z-score = -3.36; 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 12849 to 13047 (motif highlighted in silver):

```
5'-GAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUA
AAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCC-3
5'-...........(((......)))((((((.(((...((..(((((....(((((.(((((.((((...)))).))))))))))(((..((((((((((....))))))))).
.)))......((((((......)))).))((((((((((((...)))))))).)))))........)))))..))....)))))))))-3'
MFE = -53.0; z-score = -2.93; ED = 31.84
```

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(+)

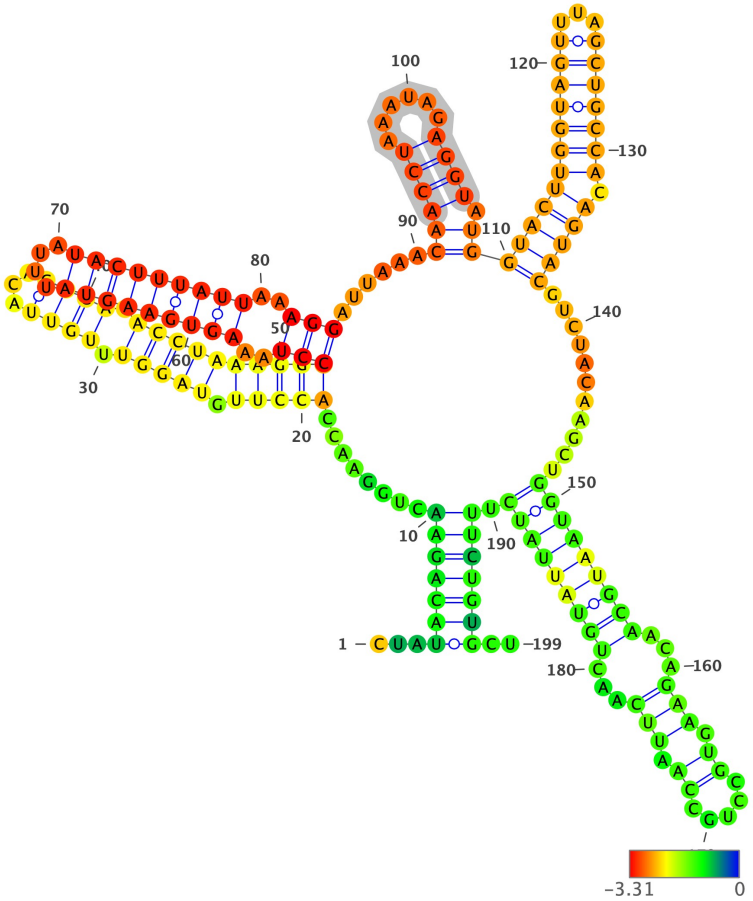
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 225 from nt 12972 to 12985 (nt 93 to 106)

```
5'-ACCTAAATAGAGGU-3'
5'-((((......))))-3'
Motif MFE = -2.2; z-score = -4.16; 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 12880 to 13078 (motif highlighted in silver):

```
5'-CUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGU
ACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCU-3
5'-...(((((((.........(((((.(((((.((((...)))).))))))))))(((..((((((((((....)))))))))..)))......((((((......)))).))((
((((((((((...)))))))).)))))...........((((((((...(((.((.....)).)))...))))))))).)))))))..-3'
MFE = -55.3; z-score = -3.86; ED = 29.18
```

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(+)

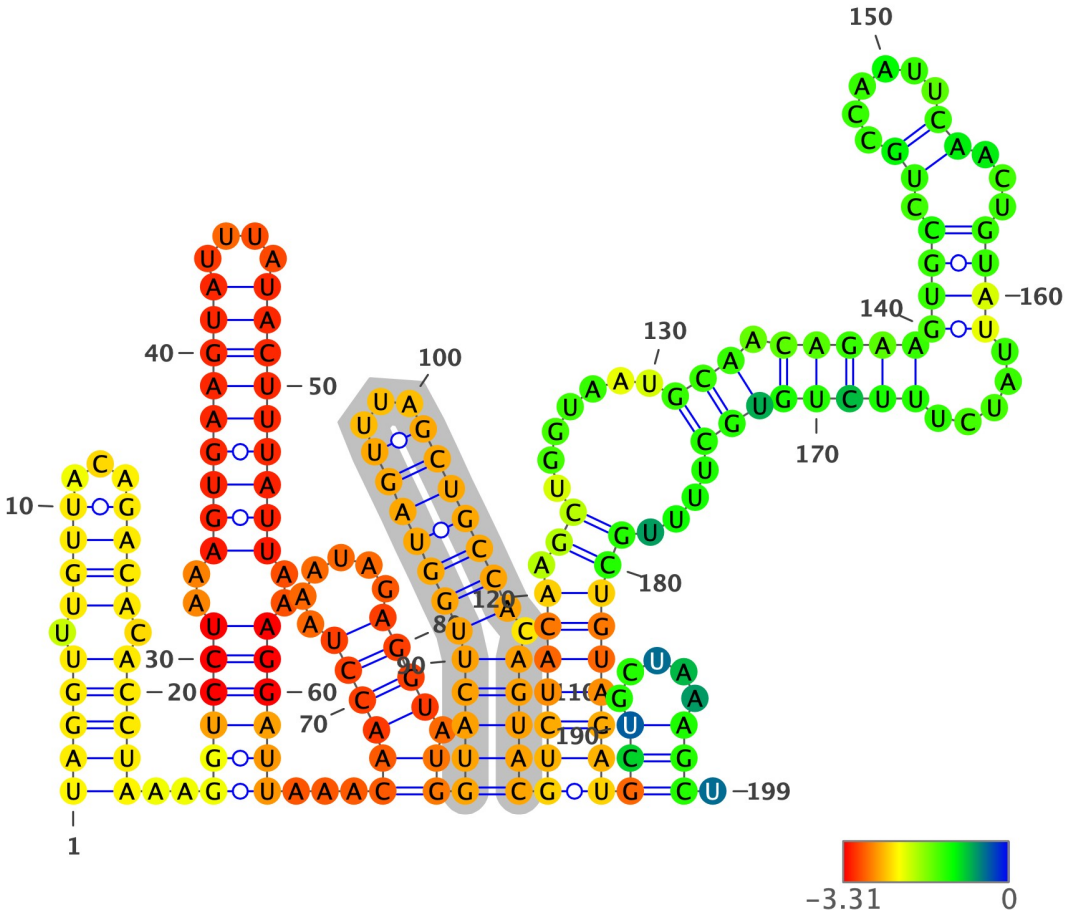
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 226 from nt 12989 to 13016 (nt 86 to 113)

```
5'-GTACTTGGTAGTTTAGCUGCCACAGUAC-3'
5'-(((((((((((...)))))))).)))))-3'
Motif MFE = -12.5; z-score = -3.45; 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 = -3.03; 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(+)

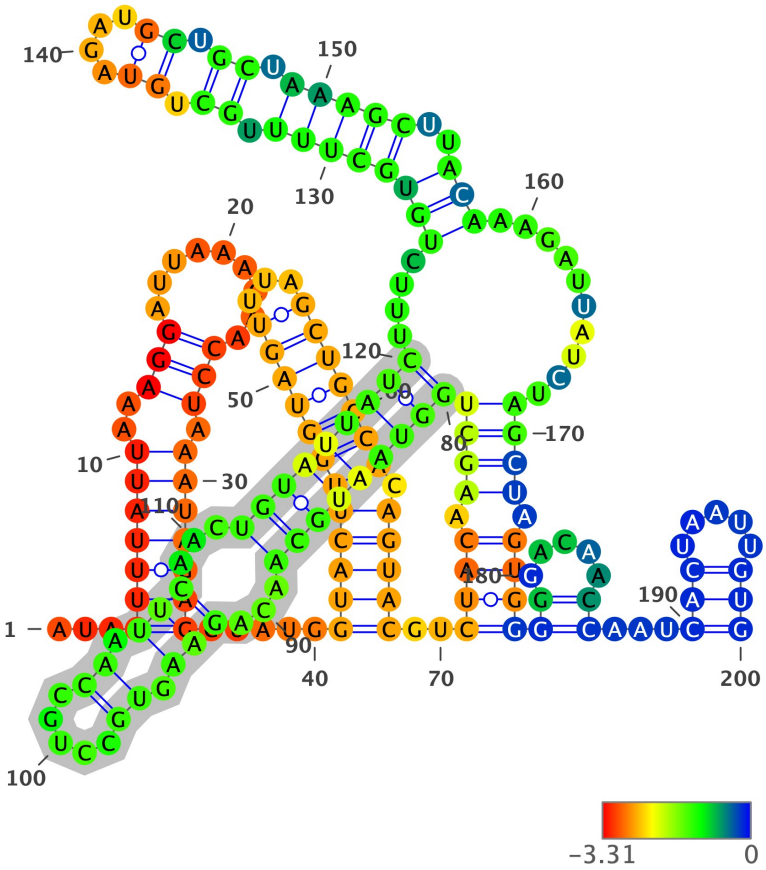
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 227 from nt 13028 to 13068 (nt 80 to 120)

```
5'-GGTAATGCAACAGAAGTGCCTGCCAAUTCAACUGUATUAUC-3'
5'-((((..(((...(.(.((.....)).).)...)))..))))-3'
Motif MFE = -7.6; z-score = -1.28; ED = 3.97
```



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 12949 to 13148 (motif highlighted in silver):

```
5'-AUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAAC
UGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCACUAAUUGUG-3
5'-...(((((((..(((.........))).)))))))).....((((((((((((...)))))))).)))))..((((.(((((((((((((...(((.((.....)).)))...
)))))))))....((((((((.((.((....)).)).)))))..)))..........)))).))))((.....))...(((.....)))-3'
MFE = -45.2; z-score = -1.37; ED = 42.29
```

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, 266-13468(+)

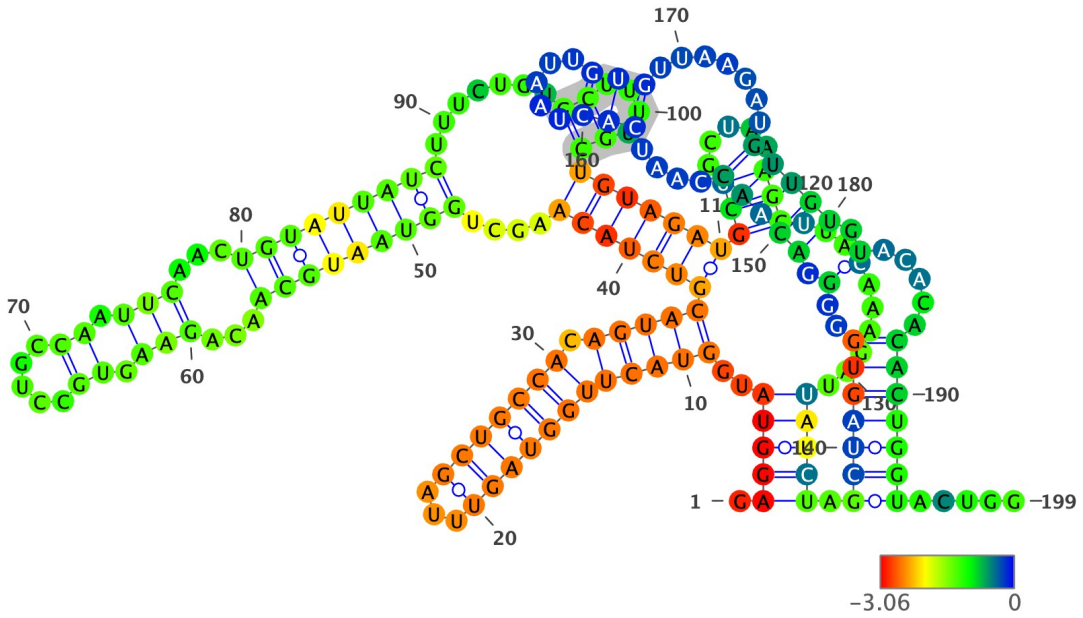
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 228 from nt 13076 to 13083 (nt 96 to 103)

```
5'-GCTTTTGC-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 12981 to 13179 (motif highlighted in silver):

```
5'-GAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUG
CUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAUGUUGUGUACACACACUGGUACUGG-3
5'-.(((((..((((((((((((...)))))))).)))))(((((((....((((((((((...(((.((.....)).)))...)))))))))).......((....)))))))))(
((.....)))..........))))).(((((((..(.(((((....(((.....)))).......))))).).....)))))))).....-3'
MFE = -48.4; z-score = -0.38; ED = 61.29
```

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(+)

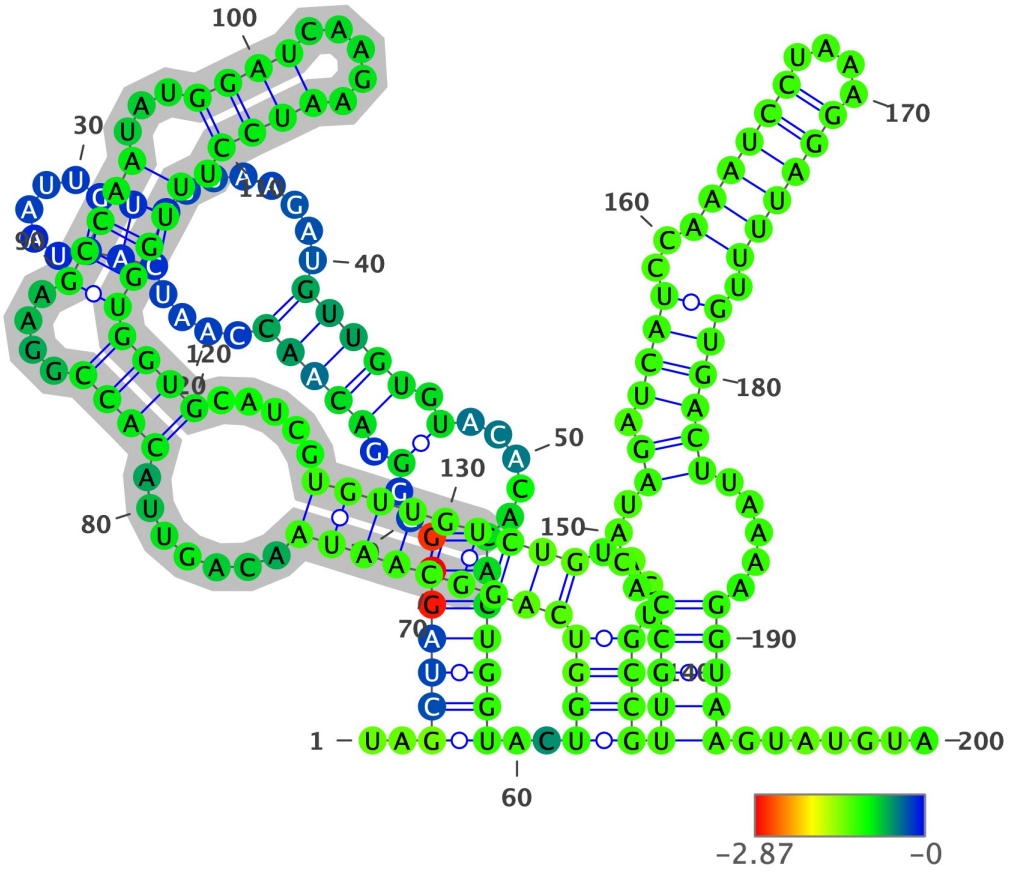
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 229 from nt 13184 to 13246 (nt 69 to 131)

```
5'-GCAATAACAGTTACACCGGAAGCCAATATGGATCAAGAAUCCTUUGGUGGUGCATCGUGUUGU-3'
5'-((((((.....................................................))))))-3'
Motif MFE = -15.3; z-score = -1.46; 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 = -0.81; 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(+)

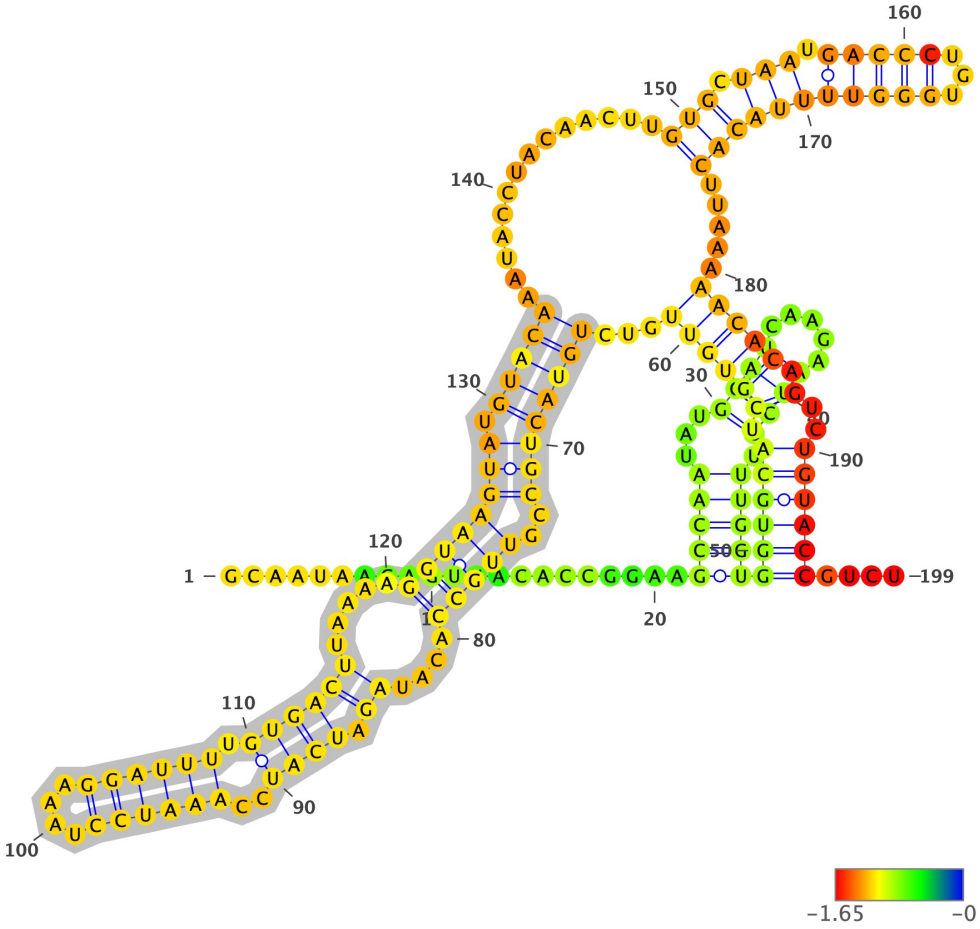
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 230 from nt 13248 to 13317 (nt 65 to 134)

```
5'-TGTACTGCCGTTGCCACATAGATCATCCAAATCCTAAAGGAUUUTGUGACUTAAAAGGUAAGTATGUACA-3'
5'-((.((.....(((((....((.((((..((((((....)))))).))))))).....)))))....)).))-3'
Motif MFE = -17.1; z-score = -2.58; ED = 6.32
```



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 13184 to 13382 (motif highlighted in silver):

```
5'-GCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGU
GACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCU-3
5'-.....................(((((...((((.....)))).)))))((((((.((((((...((((((((..(((((....((.((((..((((((....)))))).))
)))).....)))))))).)))))..............(((.(((.(((((...)))))))))))).....)))))).)..))))))....-3'
MFE = -43.2; z-score = -0.78; ED = 38.34
```

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(+)

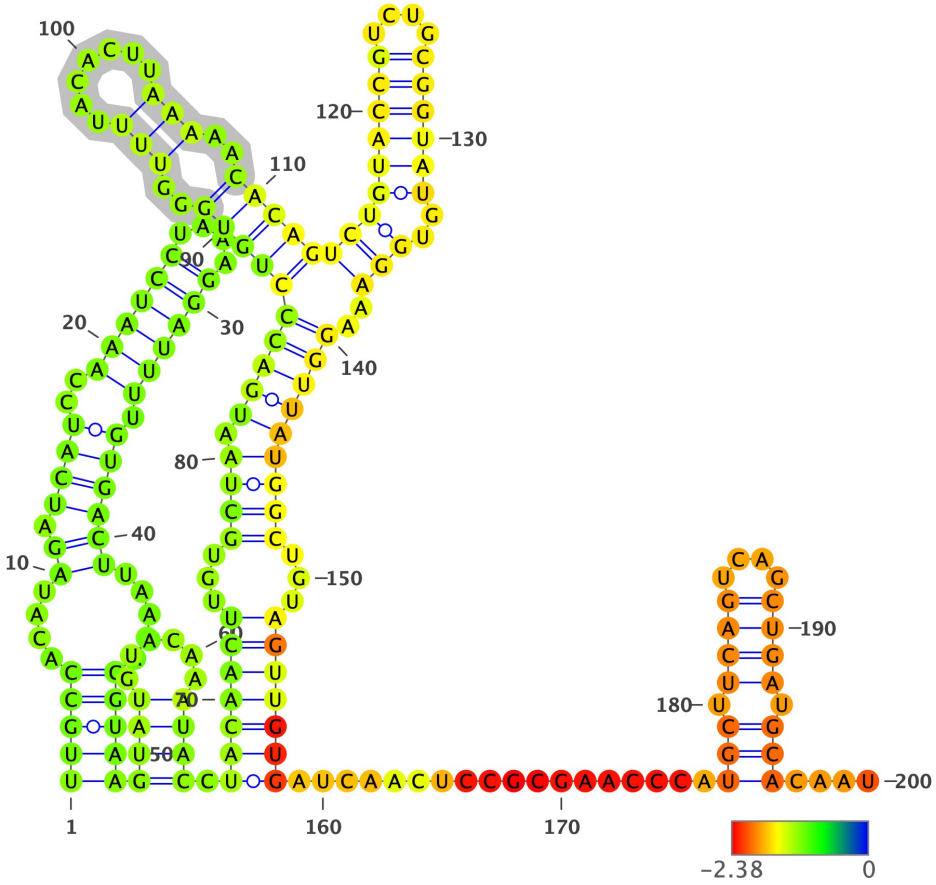
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 231 from nt 13348 to 13366 (nt 91 to 109)

```
5'-GGGTTTTACACTTAAAAAC-3'
5'-(.................)-3'
Motif MFE = 0.0; z-score = 0.58; 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 13258 to 13457 (motif highlighted in silver):

```
5'-UUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACAC
AGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAU-3
5'-(((((....((.((((..((((((....)))))).))))))....)))))(((.....))))..(((((((...((((.((((((((((..(((.......)))..)))
))(((((((((....))))))..))))..))))))))...)))))))..................(((.((((....)))).))).....-3'
MFE = -49.4; z-score = -1.66; ED = 56.88
```

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(+)

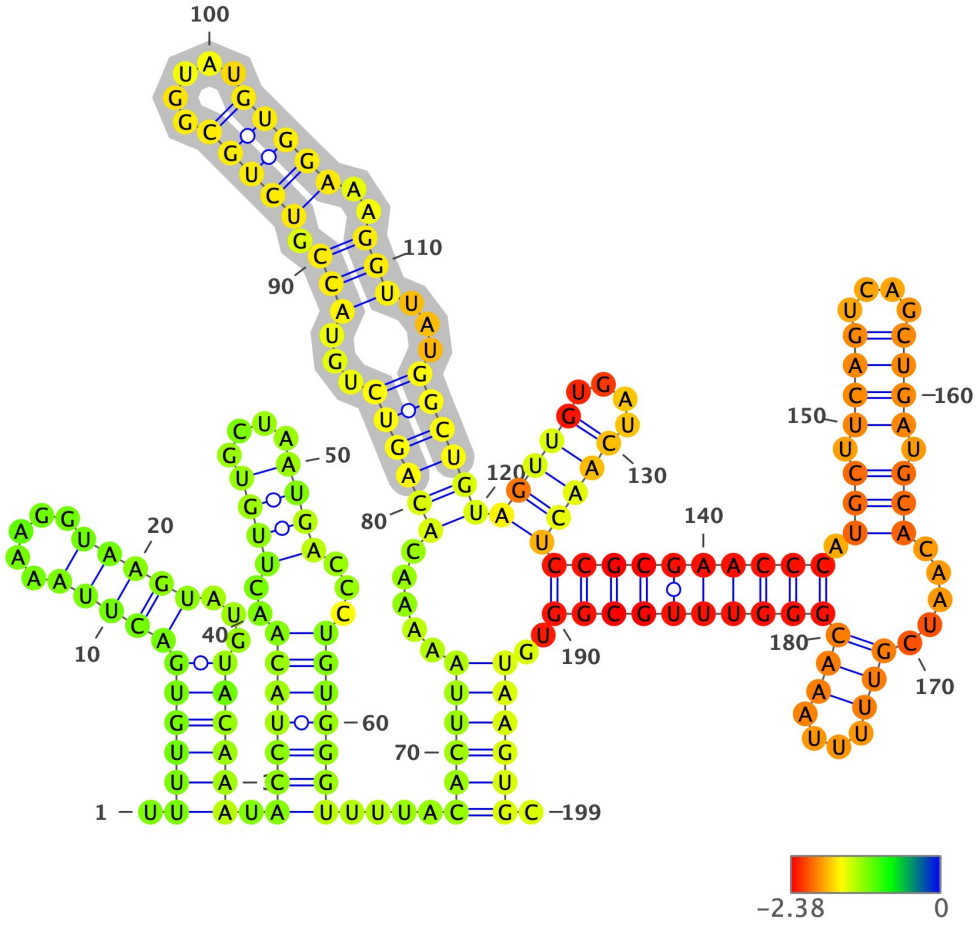
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 232 from nt 13369 to 13406 (nt 81 to 118)

```
5'-AGTCTGTACCGTCTGCGGTATGUGGAAAGGUTATGGCU-3'
5'-((((...(((.(((((.....)))))..)))...))))-3'
Motif MFE = -10.2; z-score = -1.46; 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 13289 to 13487 (motif highlighted in silver):

```
5'-UUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGU
UAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGC-3
5'-.(((((((((((.....)))))...)))))).(((((((..((((....))))...)))))))....((((((.....((((((...(((.(((((.....)))))..)))
...))))))(((((....)))))((((((((((.(((.((((....)))).)))).....(((....)))))))))))))..)))))).-3'
MFE = -57.6; z-score = -2.3; ED = 40.41
```

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(+)

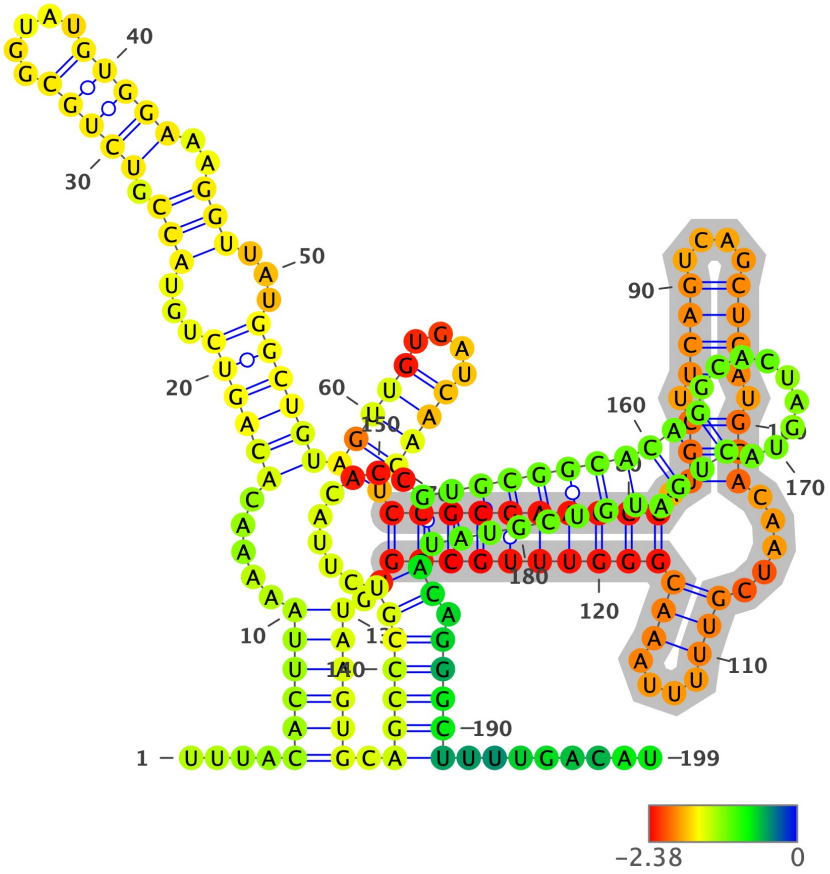
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 233 from nt 13423 to 13478 (nt 72 to 127)

```
5'-CCGCGAACCCATGCTTCAGTCAGCUGATGCACAATCGTTTTTAAACGGGUUUGCGG-3'
5'-((((((((((.(((.((((....)))).))).....(((....)))))))))))))-3'
Motif MFE = -22.5; z-score = -3.73; ED = 2.5
```



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 13352 to 13550 (motif highlighted in silver):

```
5'-UUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUU
UUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAU-3
5'-....((((((.....((((((...(((.(((((.....)))))..)))...)))))))(((((....)))))(((((((((.(((.((((....)))).))).....(((.
...)))))))))))))..)))))).(((((((........((((((((((.........))).)))))))))).)))))........-3'
MFE = -65.5; z-score = -2.99; ED = 15.22
```

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 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(+)

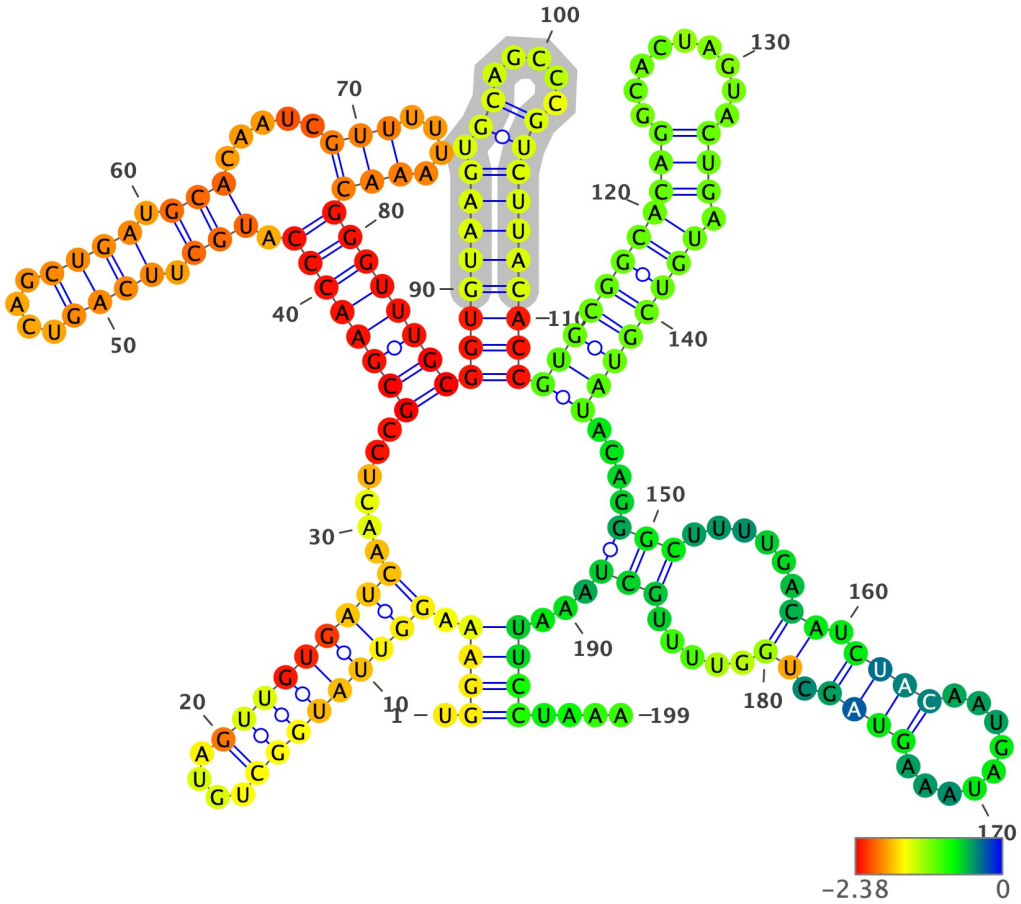
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 234 from nt 13480 to 13499 (nt 90 to 109)

```
5'-GTAAGTGCAGCCCGUCUUAC-3'
5'-(((((.((.....)))))))-3'
Motif MFE = -2.5; z-score = -0.3; 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 13391 to 13589 (motif highlighted in silver):

```
5'-UGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACAC
CGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAA-3
5'-.((((.((((((((((....)))))))))).....(((((((.(((.((((....)))).))).....(((....)))))))))))(((((((.((.....)))))))))
)((((((((((.........))).)))))))....(((......((.((((.........)))).))).....)))...))))....-3'
MFE = -58.8; z-score = -1.66; 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(+)

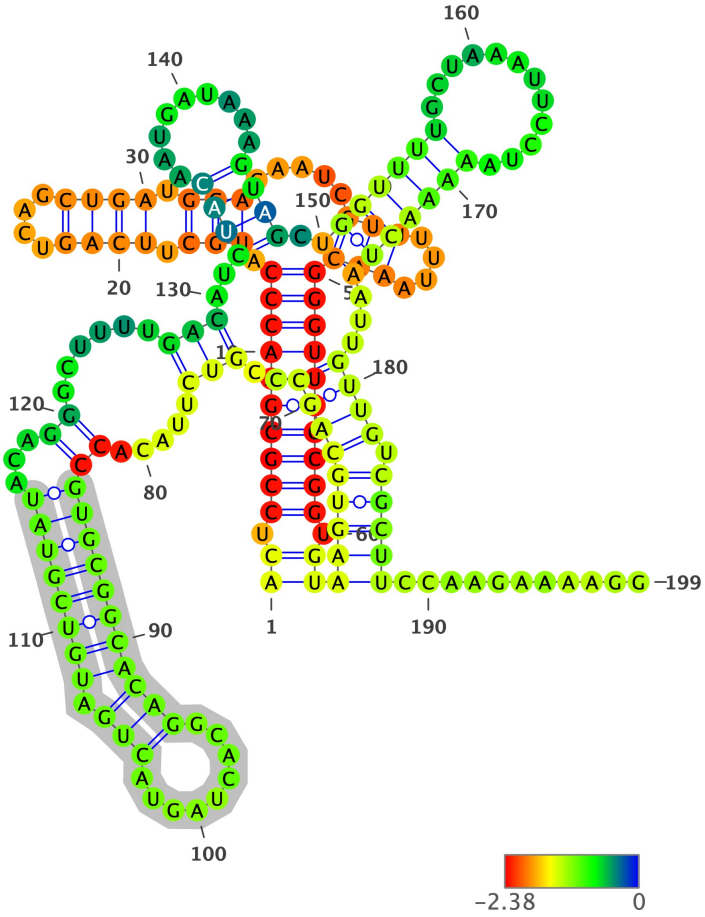
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 235 from nt 13503 to 13534 (nt 84 to 115)

```
5'-GTGCGGCACAGGCACTAGTACUGAUGUCGUAU-3'
5'-(((((((((((.........))).))))))))-3'
Motif MFE = -11.6; z-score = -2.02; 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 13420 to 13618 (motif highlighted in silver):

```
5'-ACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUC
GUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGG-3
5'-((.(((((((((((.(((.((((....)))).))).....(((....)))))))))))))).))(((((((((..(((.....(((((((((((((.........))).))))
))))...))......))).((((.........)))).(((((((.............)))))))...)))).)))))...........-3'
MFE = -52.5; z-score = -1.21; ED = 45.01
```

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_gp01, 266-21555(+)

Attributes: ['ID=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(+)

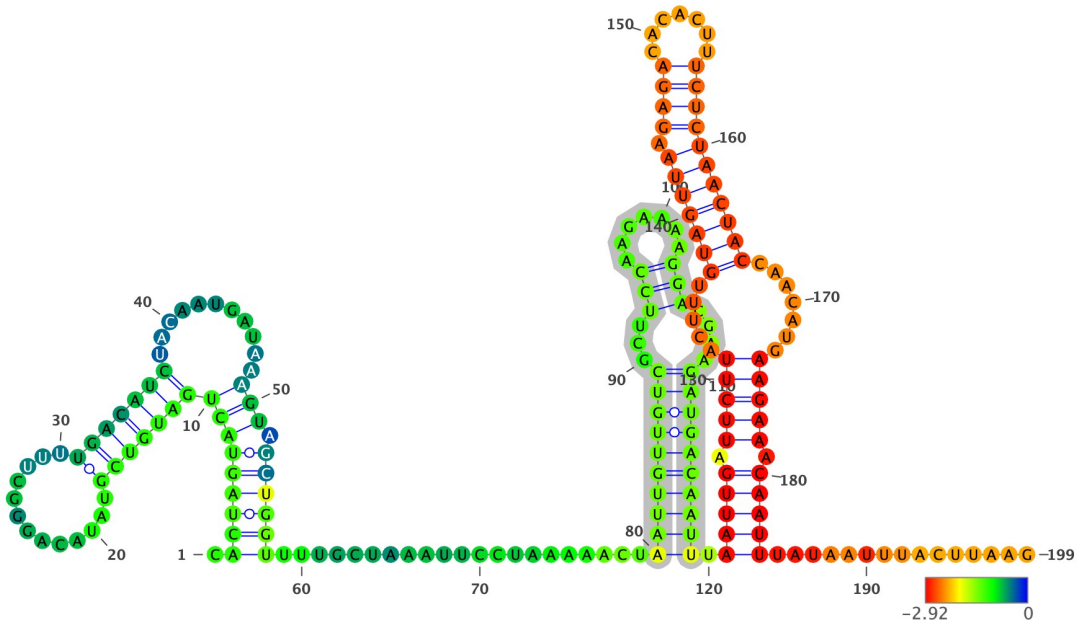
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 236 from nt 13594 to 13633 (nt 80 to 119)

```
5'-AATTGTTGTCGCTTCCAAGAAAAGGACGAAGAUGACAAUU-3'
5'-((((((((((...(((.......)))....)))))))))-3'
Motif MFE = -10.3; z-score = -2.84; 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 13515 to 13713 (motif highlighted in silver):

```
5'-CACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGA
UGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAG-3
5'-.(((((((((((((((.............)))))))...........))).))))))......................((((((((((...(((.......)))....))
))))))))).(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))................-3'
MFE = -38.3; z-score = -1.74; ED = 29.4
```

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(+)

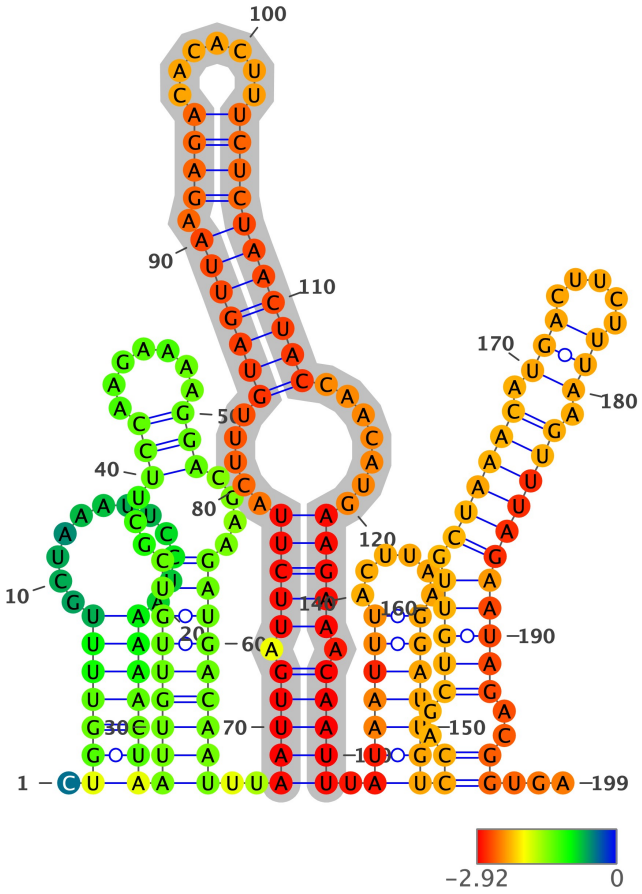
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 237 from nt 13635 to 13698 (nt 68 to 131)

```
5'-AATTGATTCTTACTTTGTAGTTAAGAGACACACTTUCUCUAACUACCAACATGAAGAAACAAUU-3'
5'-(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))-3'
Motif MFE = -15.2; z-score = -3.76; ED = 6.45
```



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 13568 to 13766 (motif highlighted in silver):

```
5'-CUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAUGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACU
ACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUGA-3
5'-.(((((((.............)))))))(((((((((...(((.......)))....)))))))))..(((((.(((((.....(((((((.((((.......)))))))))
))).......))))).))))).(((((((......)))))))((..(((((.((((((.(((.....))).)))))))))))..))...-3'
MFE = -41.1; z-score = -2.12; ED = 36.71
```

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(+)

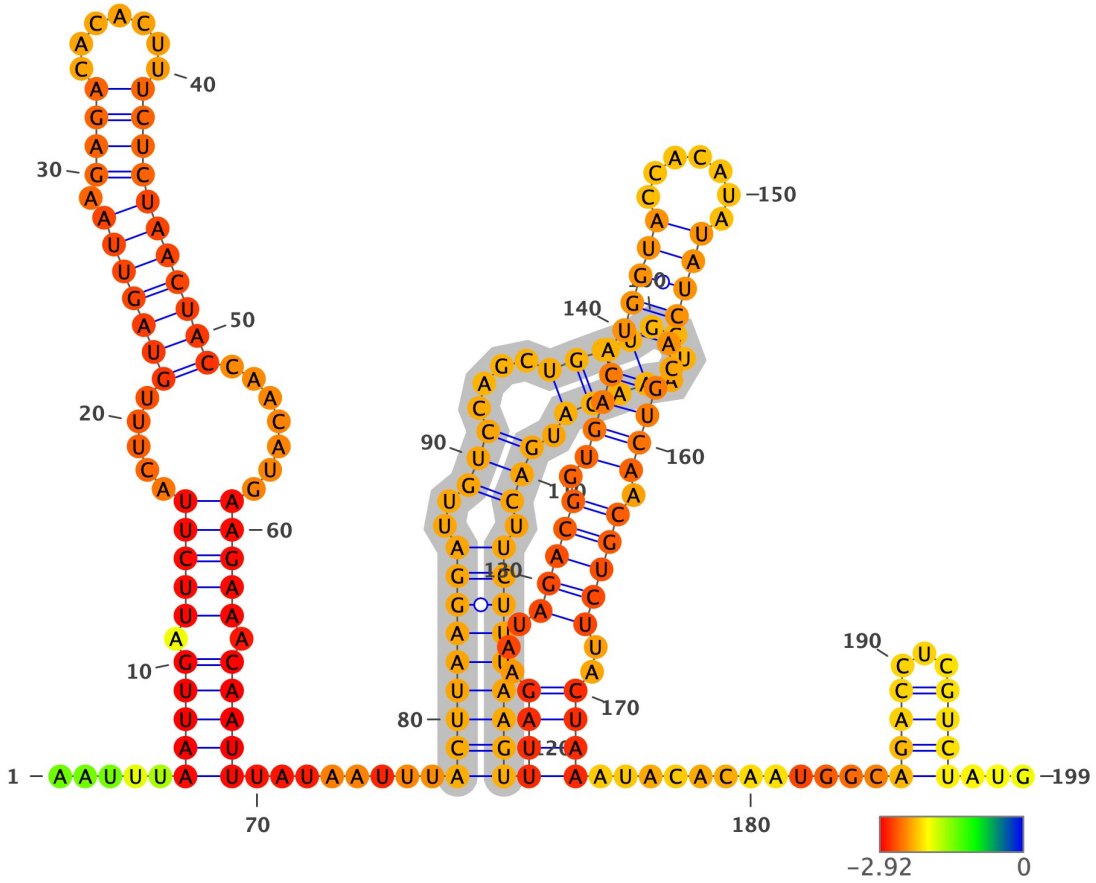
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 238 from nt 13707 to 13750 (nt 78 to 121)

```
5'-ACTTAAGGATTGTCCAGCTGTTGCTAAACATGACTUCUUUAAGU-3'
5'-(((((((((..(((....((((....)))).))).)))))))))-3'
Motif MFE = -11.0; z-score = -2.87; 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 = -3.6; 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(+)

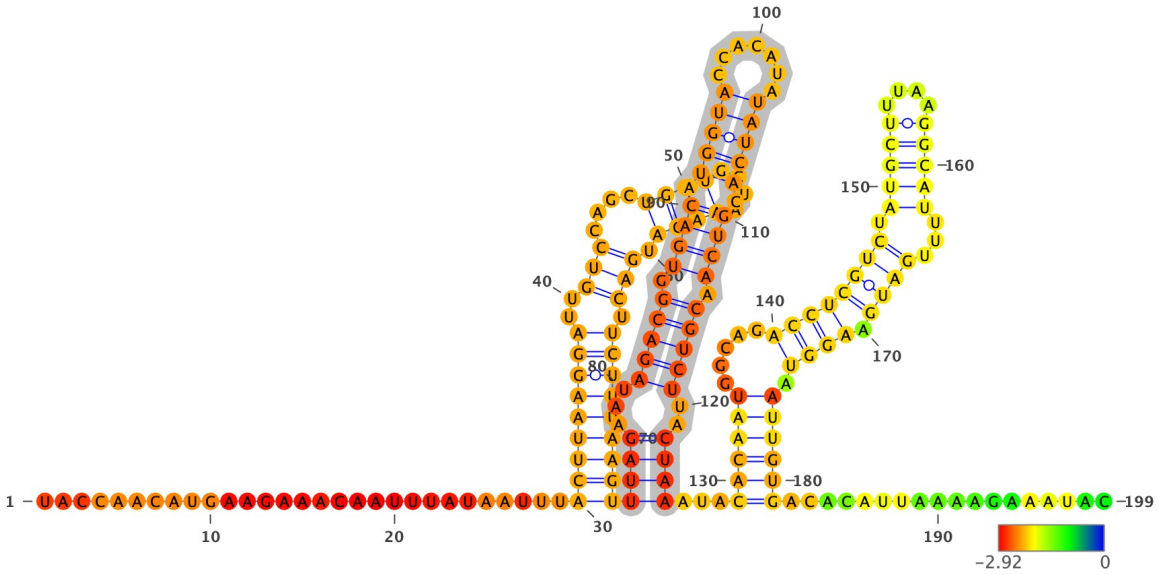
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 239 from nt 13751 to 13802 (nt 74 to 125)

```
5'-TTAGAATAGACGGTGACATGGTACCACATAUAUCACGUCAACGUCUTACUAA-3'
5'-((((...(((((.((((.(((((.......))))).)))).)))))..))))-3'
Motif MFE = -14.7; z-score = -4.2; 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 13678 to 13876 (motif highlighted in silver):

```
5'-UACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGU
CAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUGAAGGUAAUUGUGACACAUUAAAAGAAAUAC-3
5'-.............................(((((((((..(((....((((....)))).))).)))))))))((((...(((((.((((.(((((.......))))).))
)).)))))..))))...((((((.....((((((((.(((((....)))))...)))).)))).))))))...................-3'
MFE = -42.5; z-score = -2.49; ED = 31.37
```

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(+)

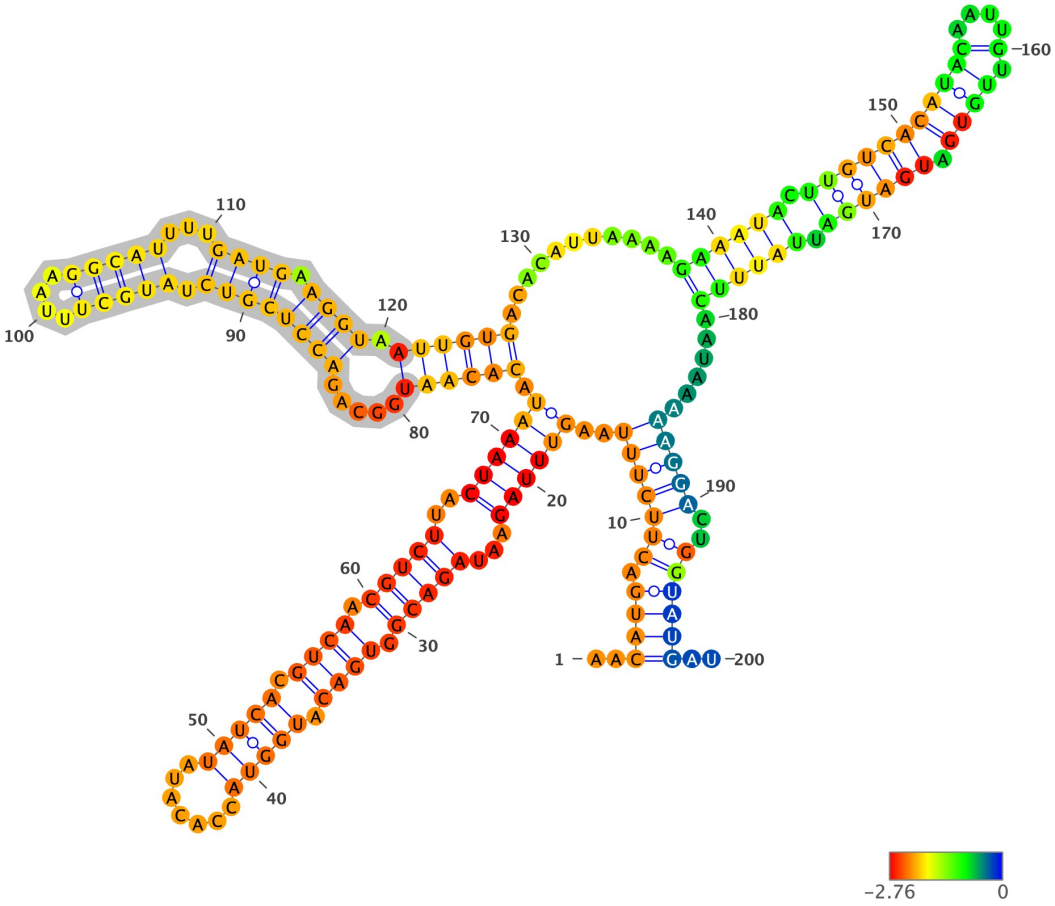
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 240 from nt 13811 to 13853 (nt 79 to 121)

```
5'-TGGCAGACCTCGTCTATGCTTTAAGGCAUTTTGAUGAAGGUAA-3'
5'-(.....((((((((.(((((....)))))...)))).)))).)-3'
Motif MFE = -12.3; z-score = -3.0; ED = 1.67
```



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 13733 to 13932 (motif highlighted in silver):

```
5'-AACAUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUG
AUGAAGGUAAUUGUGACACAUUAAAAGAAAUACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAU-3
5'-..((((.(((((((..((((((...(((((.((((.(((((.......))))).)))).))))).))))))..)))))).((((((.....((((((((.(((((....)))))...)
))).)))).))))))...........((((((.(((((((((((....).)))).))))))).))))))......)))))..))))))..-3'
MFE = -46.7; z-score = -2.57; ED = 30.77
```

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(+)

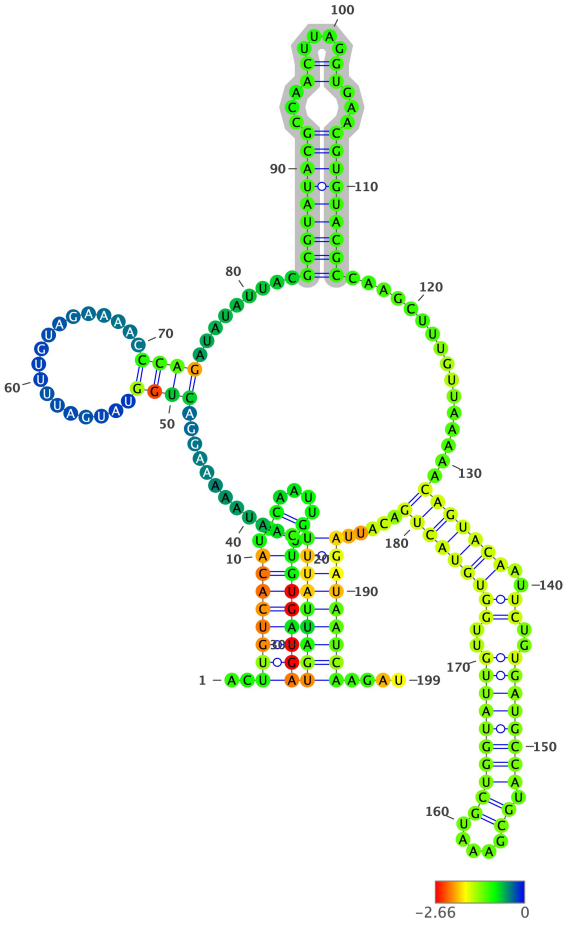
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 13958 to 13989 (nt 84 to 115)

```
5'-GCGTATACGCCAACTTAGGUGAACGUGUACGC-3'
5'-((((((((((...((....))...)))))))))-3'
Motif MFE = -13.3; z-score = -3.4; 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 = -1.8; 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(+)

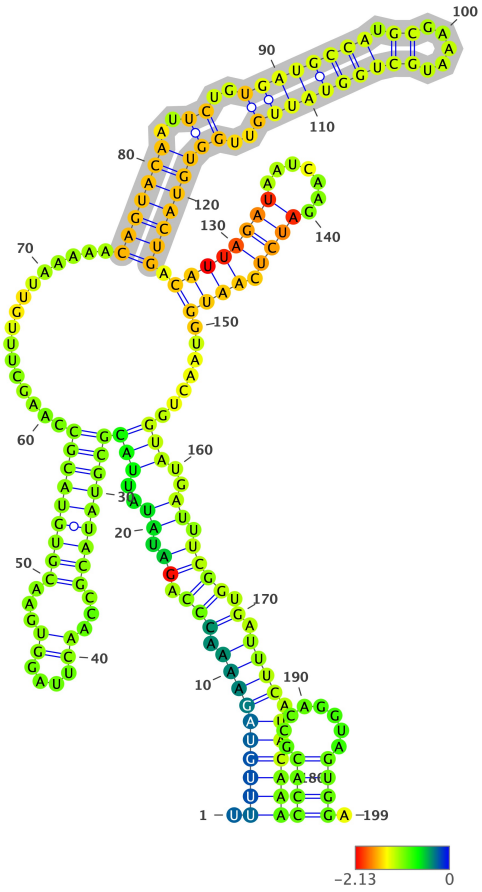
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 242 from nt 14006 to 14055 (nt 75 to 124)

```
5'-CAGTACAATTCTGTGATGCCATGCGAAATGCUGGUAUUGTTGGUGUACUG-3'
5'-(((((((..((..((((((((.((.....))))))))))..)))))))))-3'
Motif MFE = -16.7; z-score = -2.73; 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 = -2.45; ED = 23.42
```

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_gp01, 266-21555(+)

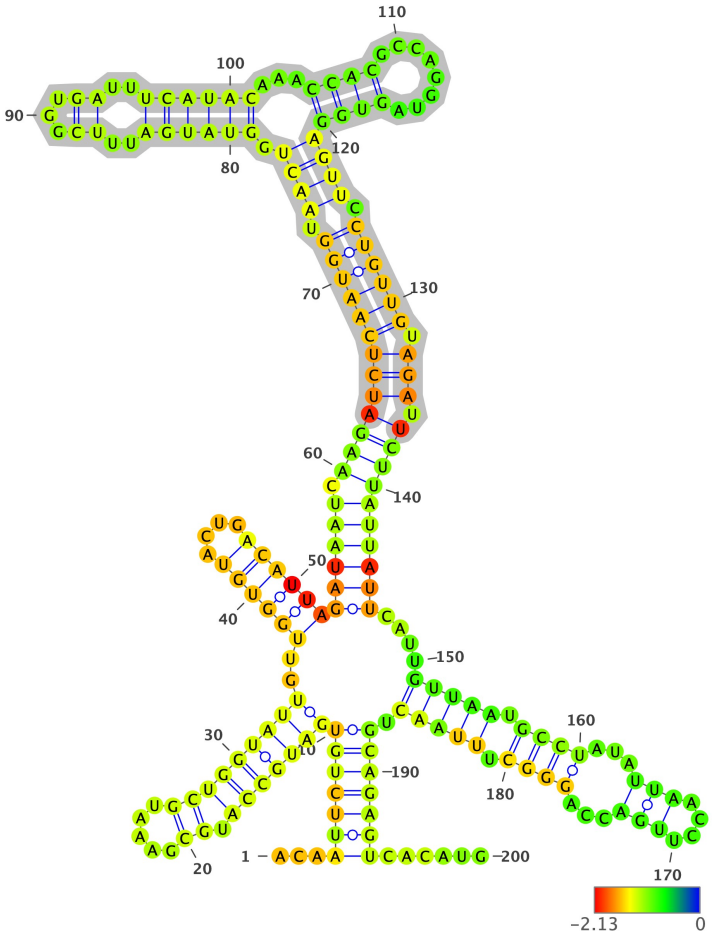
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 14072 to 14146 (nt 63 to 137)

```
5'-ATCTCAATGGTAACTGGTATGATTTCGGTGATTUCAUACAAACCACGCCAGGTAGUGGAGUUCCUGUUGTAGATU-3'
5'-((((((((((.((((.((((((..((...))..))))))..................)))).)))))).))).)-3'
Motif MFE = -20.5; z-score = -1.97; ED = 2.69
```



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 14010 to 14209 (motif highlighted in silver):

```
5'-ACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUGACAUUAGAUAAUCAAGAUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCC
AGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUG-3
5'-...(((((((((((((((.((.....)))))))))..((((((....))))))((((((.(((((((((((((.((((.((((((..((...))..))))))...((((...
.....))))))))).))))))).))).))))))))))....(((((.((((...(((....)))...)))).)))))).)))))))......-3'
MFE = -52.7; z-score = -2.45; ED = 36.88
```

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(+)

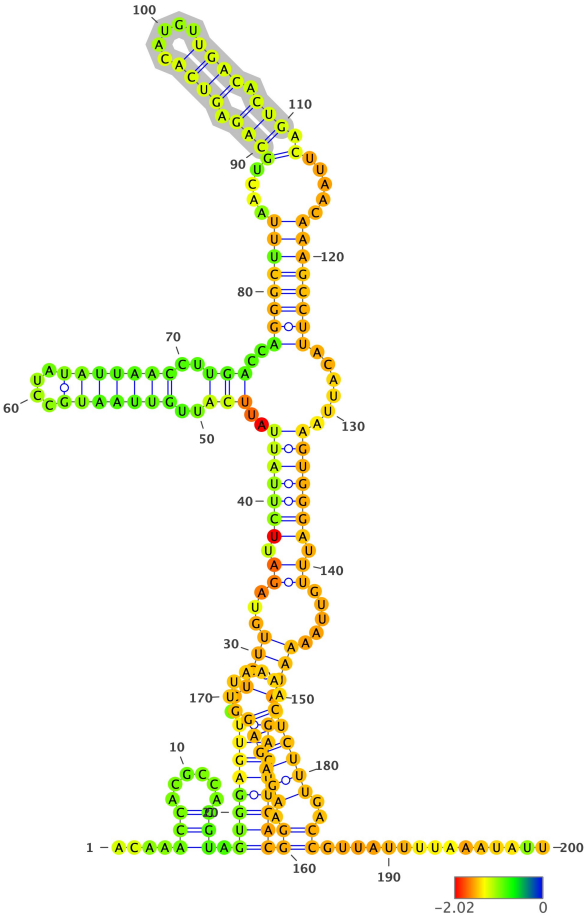
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 14198 to 14218 (nt 90 to 110)

```
5'-CAGAGTCACATGTUGACACUG-3'
5'-(((.((((.....)))).)))-3'
Motif MFE = -4.5; z-score = -1.58; 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 14109 to 14308 (motif highlighted in silver):

```
5'-ACAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGA
CUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUU-3
5'-....(((......))).(((((((((..((((...((.(((((((..(((..(((((((....)))))))..)))..(((((((((....(((((.((((.....)))))))))..
).....)))))))).....)))))))..))).....)))).)))))))))).(((((((.......)))))))..))..............-3'
MFE = -43.0; z-score = -1.2; ED = 56.95
```

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(+)

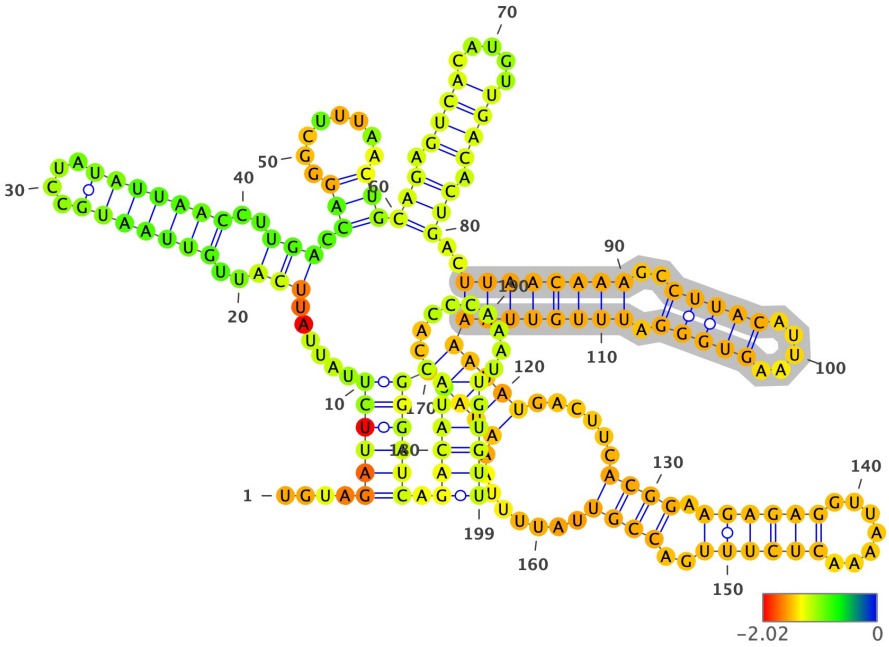
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 245 from nt 14221 to 14254 (nt 83 to 116)

```
5'-TTAACAAAGCCTTACATTAAGUGGGAUUUGUUAA-3'
5'-((((((((..(((((.....))))).))))))))-3'
Motif MFE = -8.5; z-score = -2.3; ED = 4.17
```



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 14139 to 14337 (motif highlighted in silver):

```
5'-UGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUU
GUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUU-3
5'-....((((((......(((..(((((((....)))))))..))).(((.........)))(((.((((.....)))).))).((((((((..(((((.....))))).)))
)))))(((((......((((.((((((.......))))))..))))........))))))))))).((((((..........))))))-3'
MFE = -41.7; z-score = -1.35; ED = 31.35
```

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_gp01, 266-21555(+)

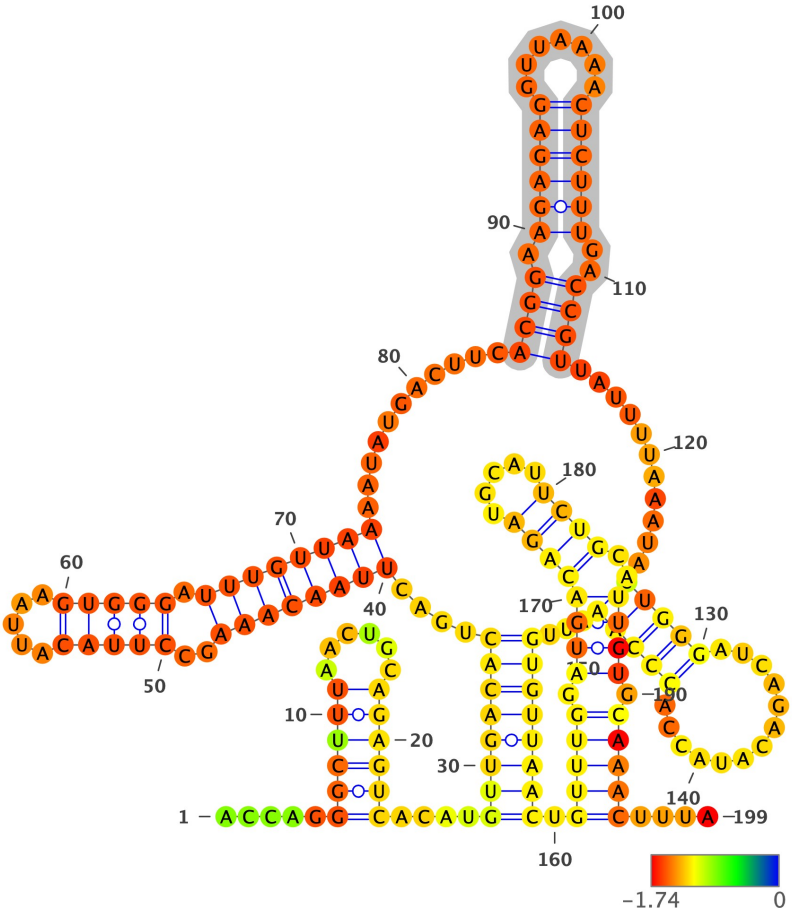
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 246 from nt 14266 to 14295 (nt 85 to 114)

```
5'-ACGGAAGAGAGGTTAAAACUCUUUGACCGU-3'
5'-((((.((((((.......))))))..))))-3'
Motif MFE = -10.5; z-score = -3.58; 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'-ACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGAC
CGUUAUUUUAAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUA-3
5'-.....((((((......))))))....(((((((((....(((((((((..(((((.....)))))).)))))))))...........((((.((((((.......))))))..)
)))).....((((((.............))))))...)))))))).((((((.(((((((((.....)))))..)))).)))))).....-3'
MFE = -47.5; z-score = -2.03; 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(+)

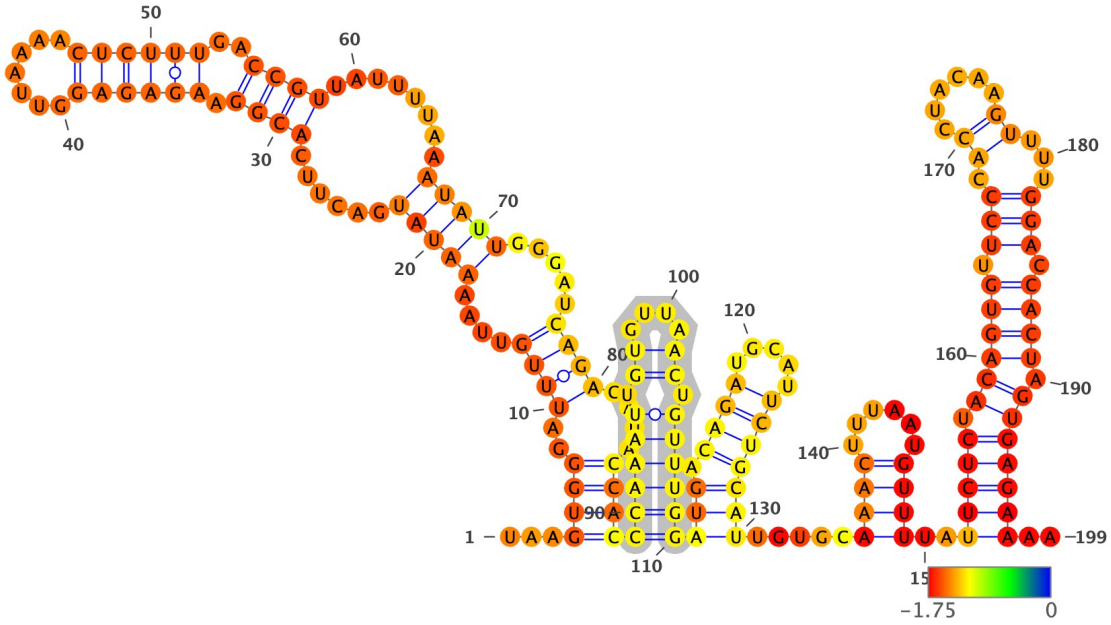
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 247 from nt 14326 to 14347 (nt 89 to 110)

```
5'-CCAAATTGTGTTAACTGUUUGG-3'
5'-((((((.((....)).))))))-3'
Motif MFE = -5.6; z-score = -2.86; 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 14238 to 14436 (motif highlighted in silver):

```
5'-UAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGA
UGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAA-3
5'-...((((..((((....(((((......((((.((((((.......))))))..))))........)))))).....))))....))))((((((.((....)).))))))(
((.((((.....)))))))).....((((......))))..(((((.((((((.(((.((......))...))).)))).)))))))..-3'
MFE = -44.1; z-score = -1.23; ED = 31.06
```

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(+)

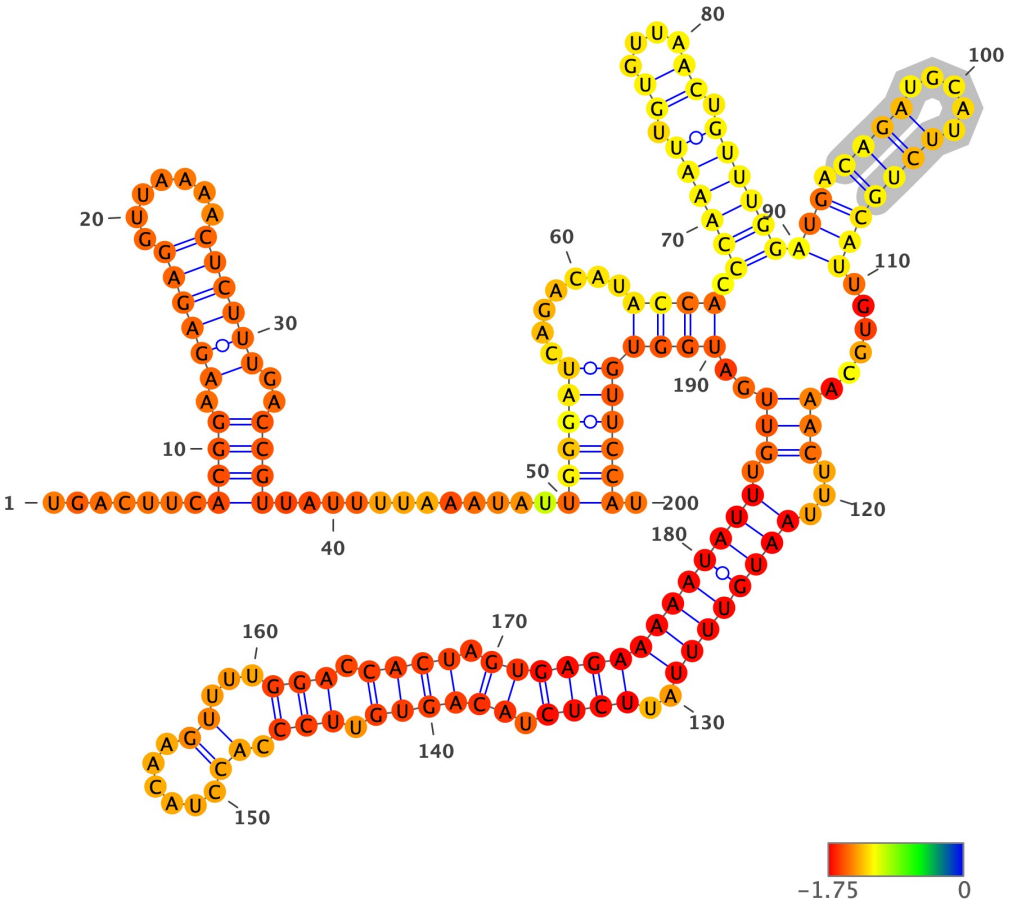
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14352 to 14364 (nt 94 to 106)

```
5'-CAGATGCATTCUG-3'
5'-((.........))-3'
Motif MFE = -2.1; z-score = -3.41; 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 14259 to 14458 (motif highlighted in silver):

```
5'-UGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUG
UGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAU-3
5'-.......((((.((((((.......))))))..))))............((((((.......((((.((((((.((....)).))))))(((.((((.....)))))))..
....(((...((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))).)))..)))))))))).-3'
MFE = -45.0; z-score = -1.42; ED = 35.64
```

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(+)

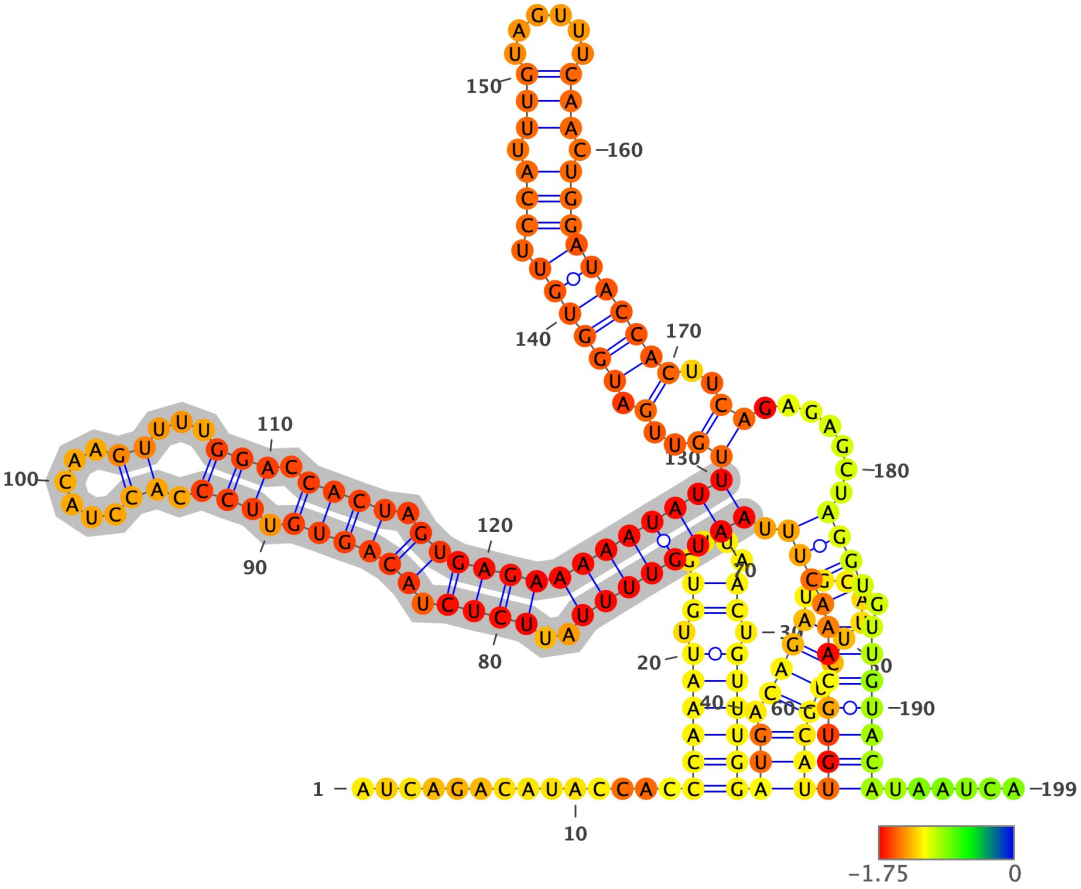
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 249 from nt 14380 to 14441 (nt 69 to 130)

```
5'-AATGTTTTATTCTCTACAGTGTTCCCACCTACAAGTTTTGGACCACUAGUGAGAAAAAUAUU-3'
5'-(((((((((..(((((.(((((((.(((..............))).)))).)))))))))))))))-3'
Motif MFE = -14.2; z-score = -2.95; ED = 5.47
```



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 14312 to 14510 (motif highlighted in silver):

```
5'-AUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGAC
CACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCA-3
5'-..............((((((.((....)).))))))(((.((((.....)))))))((((((((((((.(((((((((..((((.((((((.(((.((......))...))).
)))).))))))))))))))((..(.((((((.(((.(((......))).))))))))))..)).......)))).)))))))......-3'
MFE = -46.3; z-score = -1.81; ED = 30.74
```

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(+)

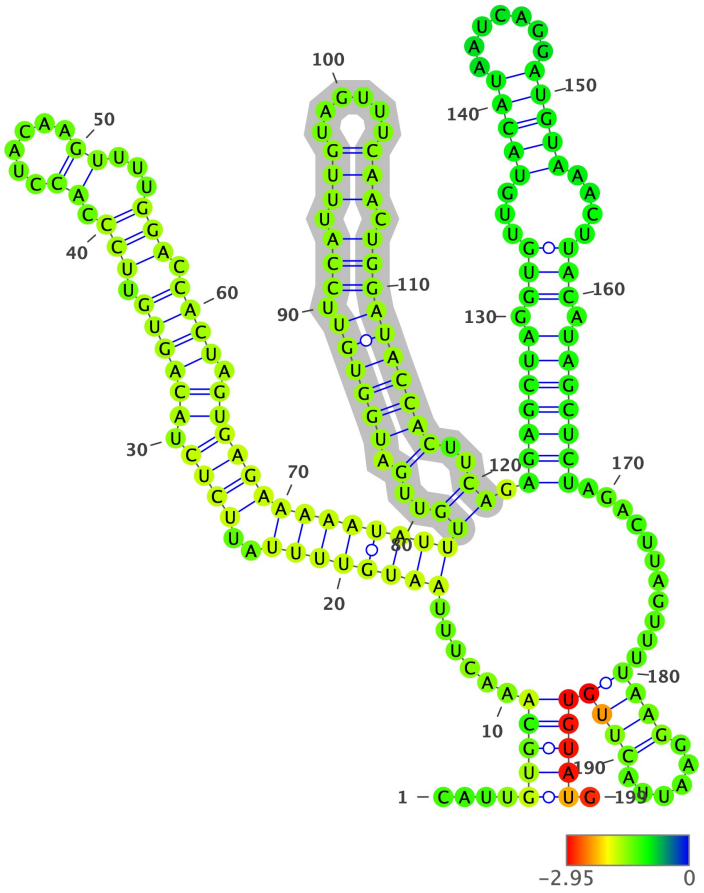
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14442 to 14485 (nt 78 to 121)

```
5'-TGTTGATGGTGTTCCATTTGTAGTTTCAACUGGAUACCACTTCA-3'
5'-((..(.(((((((.(((.(((......))).))))))))))..))-3'
Motif MFE = -11.9; z-score = -2.79; ED = 4.39
```



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 14365 to 14563 (motif highlighted in silver):

```
5'-CAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGA
UACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUG-3
5'-....(((((......((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))((..(.((((((.(((.(((......))).))))
))))))..)).(((((((.(((...(((((.......)))))....))).)))))))...........((((......)))))))).-3'
MFE = -46.1; z-score = -1.83; ED = 22.85
```

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(+)

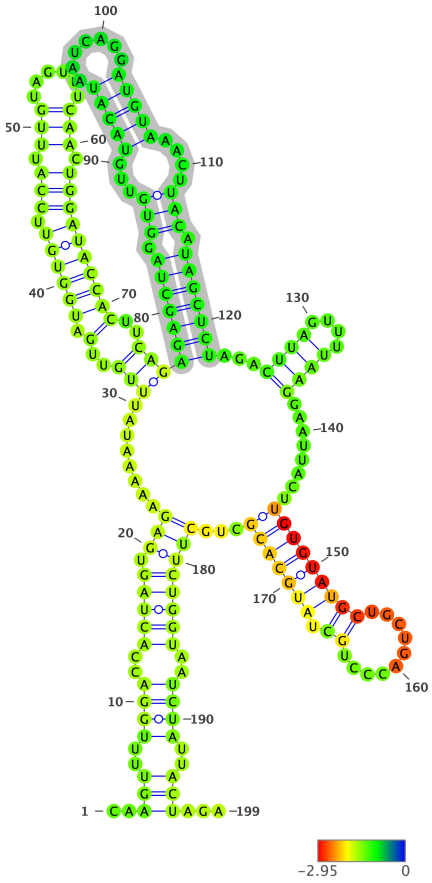
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14487 to 14532 (nt 77 to 122)

```
5'-AGAGCTAGGTGTTGTACATAATCAGGAUGUAAACTUACAUAGCUCU-3'
5'-(((((((.(((.......................))).)))))))-3'
Motif MFE = -13.4; z-score = -3.48; 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 14411 to 14609 (motif highlighted in silver):

```
5'-CAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACU
UACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGA-3
5'-..(((..((((..(((((.(((........(((..(.((((((.(((.(((......))).))))))))))..)))(((((((.(((...(((((.......)))))....
))).)))))))...((((....))))........(((((((((..........)).)))))))...)))))))))..))))..)))...-3'
MFE = -48.6; z-score = -1.71; ED = 46.14
```

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(+)

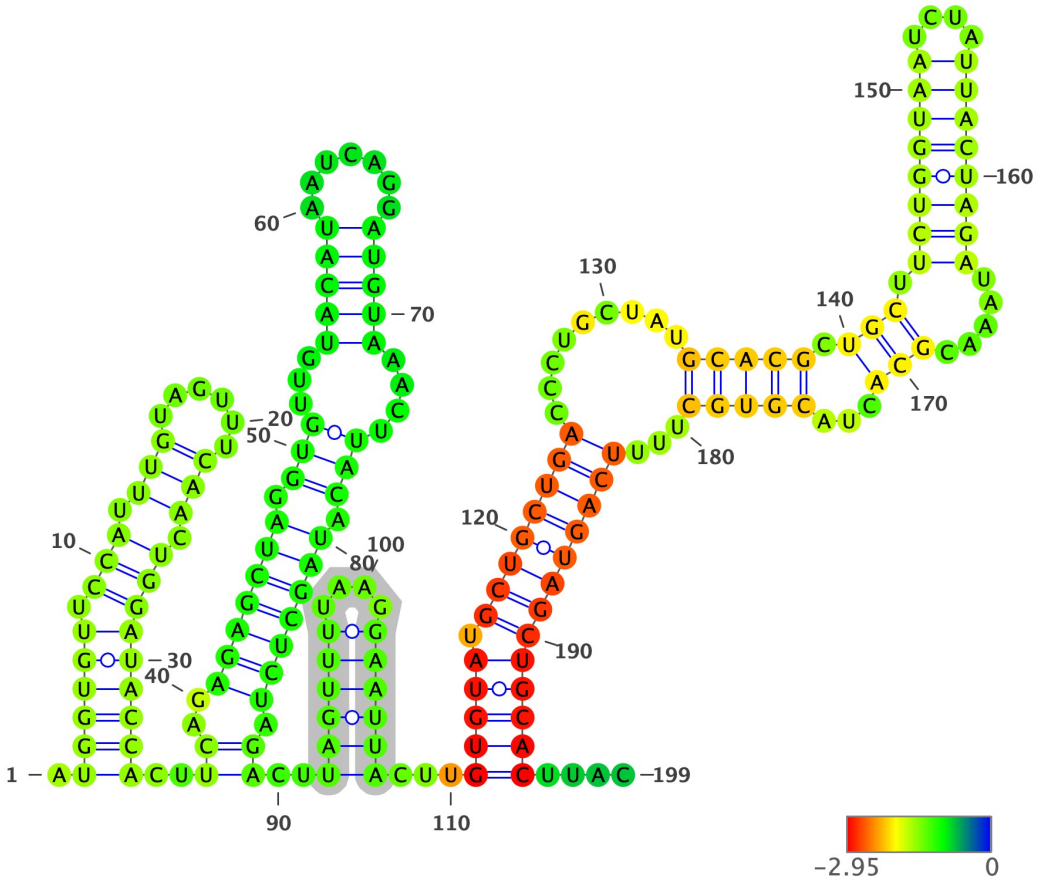
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 252 from nt 14538 to 14553 (nt 92 to 107)

```
5'-TAGTTTTAAGGAAUUA-3'
5'-((((((....))))))-3'
Motif MFE = 0.0; z-score = 0.17; 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 14447 to 14645 (motif highlighted in silver):

```
5'-AUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUG
UGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAUAAACGCACUACGUGCUUUUCAGUAGCUGCACUUAC-3
5'-.((((((.(((.(((.....))).)))))))))..((..(((((((.(((...(((((.......)))))....))).)))))))..))..((((((....))))))...(
((((.(((((((((.........(((((.(((.(((((((((....)))))))))).....)))...))))))...))))))))))))....-3'
MFE = -57.4; z-score = -4.05; ED = 13.52
```

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(+)

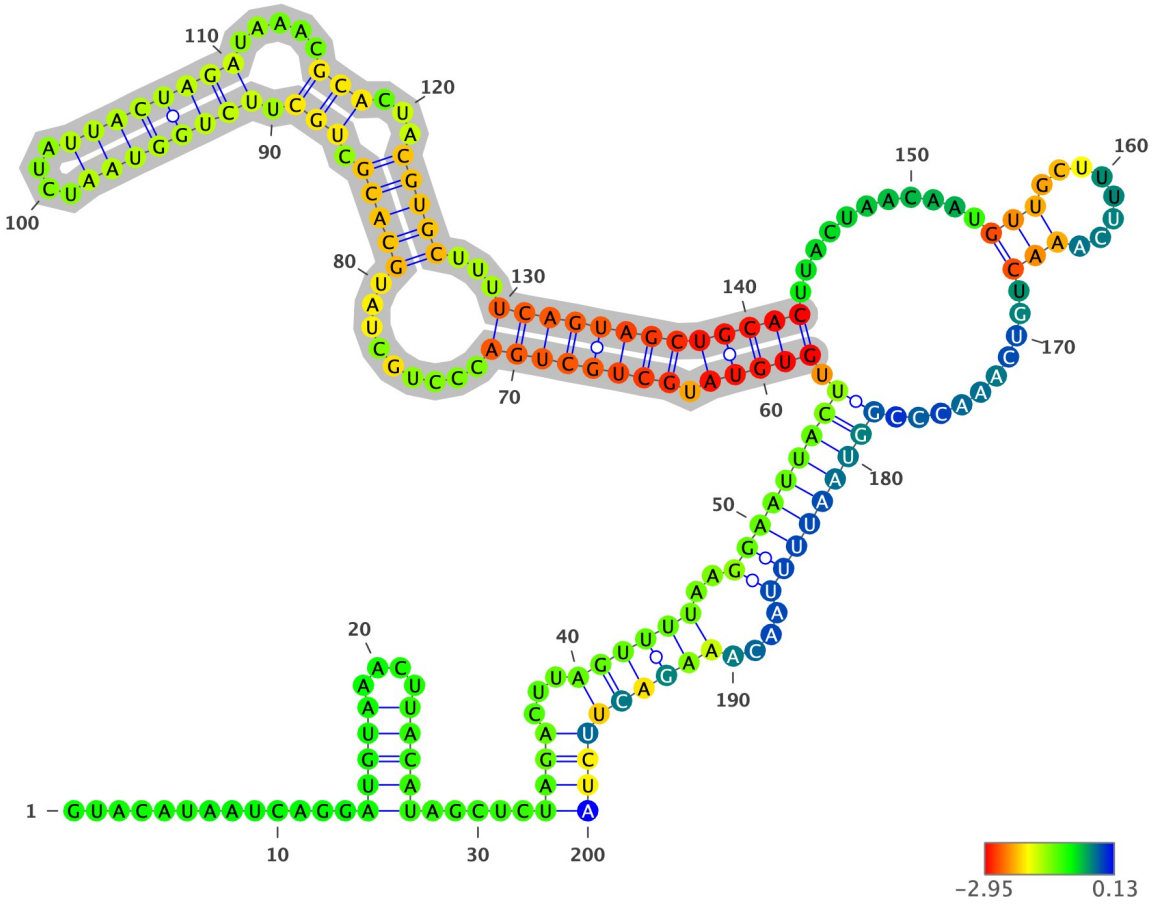
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 14557 to 14641 (nt 58 to 142)

```
5'-GTGTATGCTGCTGACCCTGCTATGCACGCTGCTTCTGGTAATCTAUUACUAGATAAACGCACTACGUGCTTTUCAGUAGCUGCAC-3'
5'-(((((.(((((((((.........(((((.(((.((((((((....))))))))).....)))...)))))...))))))))))))-3'
Motif MFE = -29.9; z-score = -4.01; 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 = -1.52; 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(+)

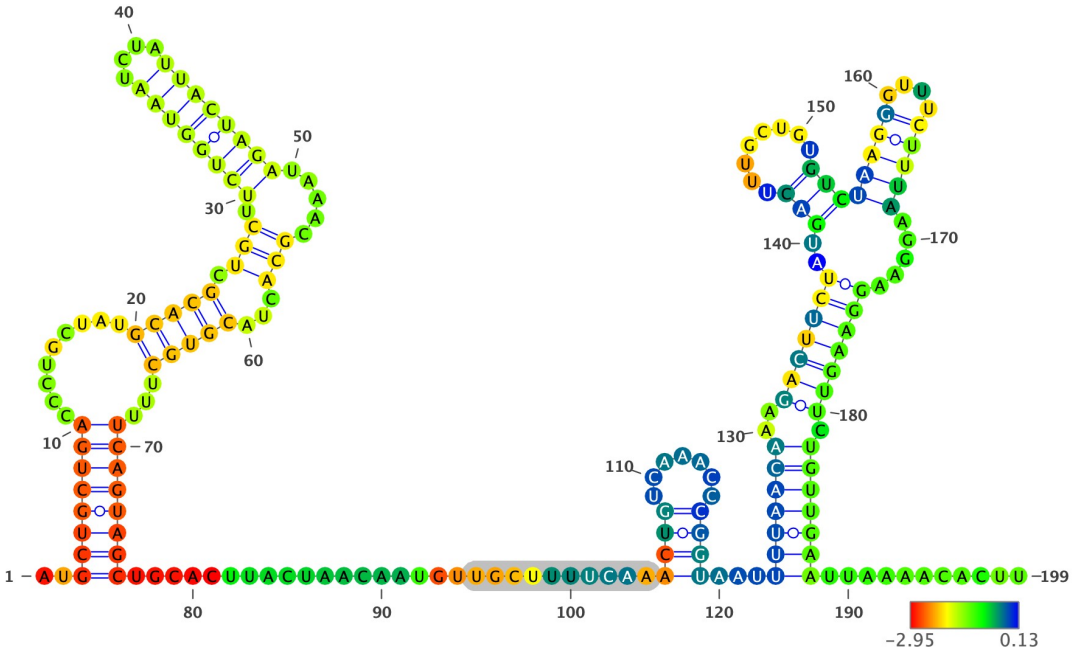
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 254 from nt 14655 to 14664 (nt 95 to 104)

```
5'-TGCTTTTCAA-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 14561 to 14759 (motif highlighted in silver):

```
5'-AUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAUAAACGCACUACGUGCUUUUCAGUAGCUGCACUUACUAACAAUGUUGCUUUUCAAACUGUCA
AACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUU-3
5'-..(((((((((.........(((((.(((.(((((((((....)))))))))).....)))...)))))...)))))))).........................((((....))))...(((((((..(((((((..(((........)))(((((....)))))).....)))))))..)))))))...........-3'
MFE = -39.8; z-score = -0.34; ED = 46.74
```

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(+)

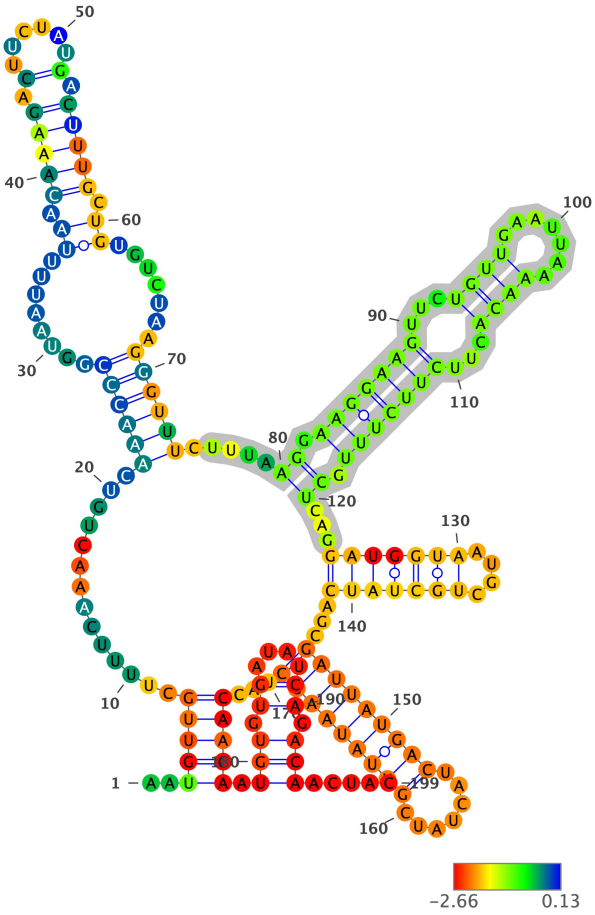
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14725 to 14772 (nt 76 to 123)

```
5'-TTTAAGGAAGGAAGTTCTGTTGAATTAAAACACTTCUUCUUUGCUCAG-3'
5'-(...((.(((((((...((((.......)))))...)))))))..))..)-3'
Motif MFE = -11.3; z-score = -2.89; ED = 7.55
```



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 14650 to 14848 (motif highlighted in silver):

```
5'-AAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUC
UUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUAC-3
5'-..(((((.............((((((........((.(((((.(......).)))))).))).......))))))).....((.(((((((...((((.......)))))...)
))))))).))...(((((((....)))))))...(((((((((.......)))))))))...)))))).(((.((....)).))).....-3'
MFE = -42.4; z-score = -1.27; ED = 31.66
```

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(+)

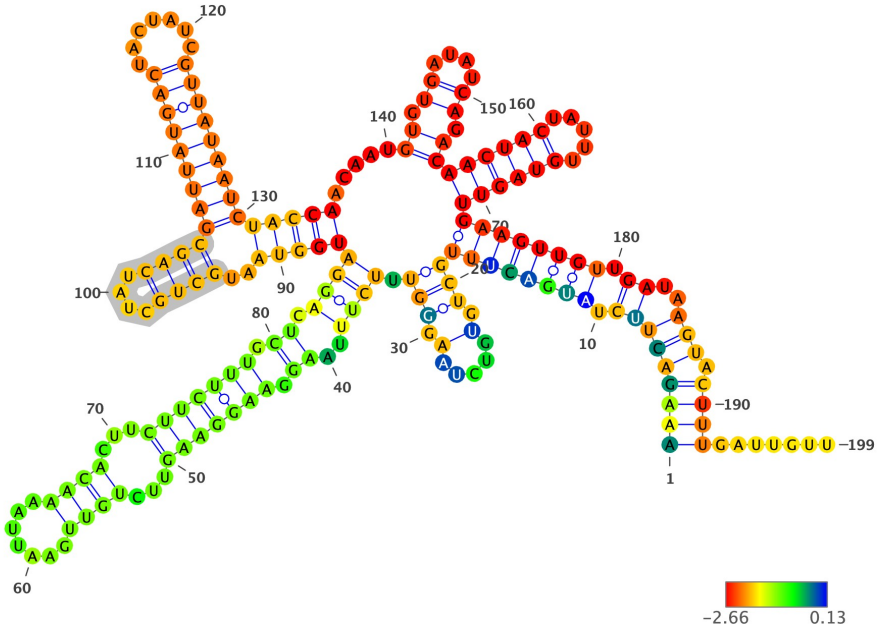
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 256 from nt 14782 to 14793 (nt 94 to 105)

```
5'-GCTGCTATCAGC-3'
5'-((((....))))-3'
Motif MFE = -2.5; z-score = -5.38; 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 14689 to 14887 (motif highlighted in silver):

```
5'-AAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAU
GACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUU-3
5'-(((((((((.((((((((((.(.....).))).((((..((.(((((((...((((.......))))...)))))))).)).))))((((((..((((....))))((((((
(((.......)))))))))))))).....((.((....)).))((((((.....))))))))))))))..))..))).))))).......-3'
MFE = -46.6; z-score = -2.33; ED = 46.56
```

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(+)

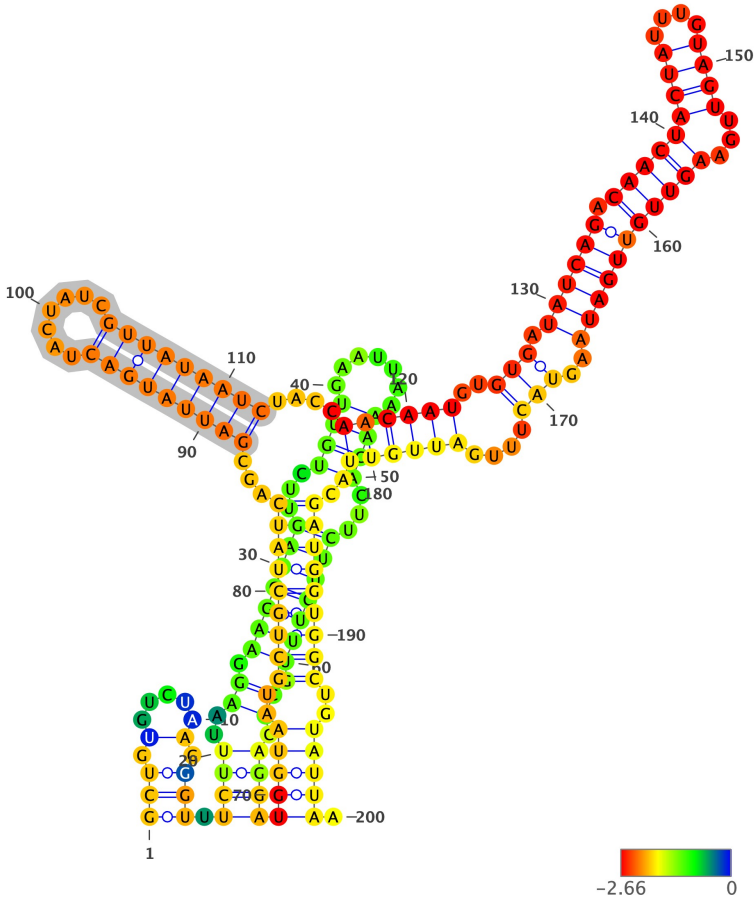
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14794 to 14818 (nt 88 to 112)

```
5'-GATTATGACTACTATCGUUAUAAUC-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.7; z-score = -4.38; 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 14707 to 14906 (motif highlighted in silver):

```
5'-GCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAU
CUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAA-3
5'-(((.(.....).))).((((..((.(((((((...((((.......))))...))))))).)).))))(((((..((((((((((...((((((((((.......))))))))
)....((((((..(((.((((((.((((((((((....))))...)))))))))))..)))....))))))..)))))))))..))))).-3'
MFE = -48.8; z-score = -2.16; ED = 61.93
```

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(+)

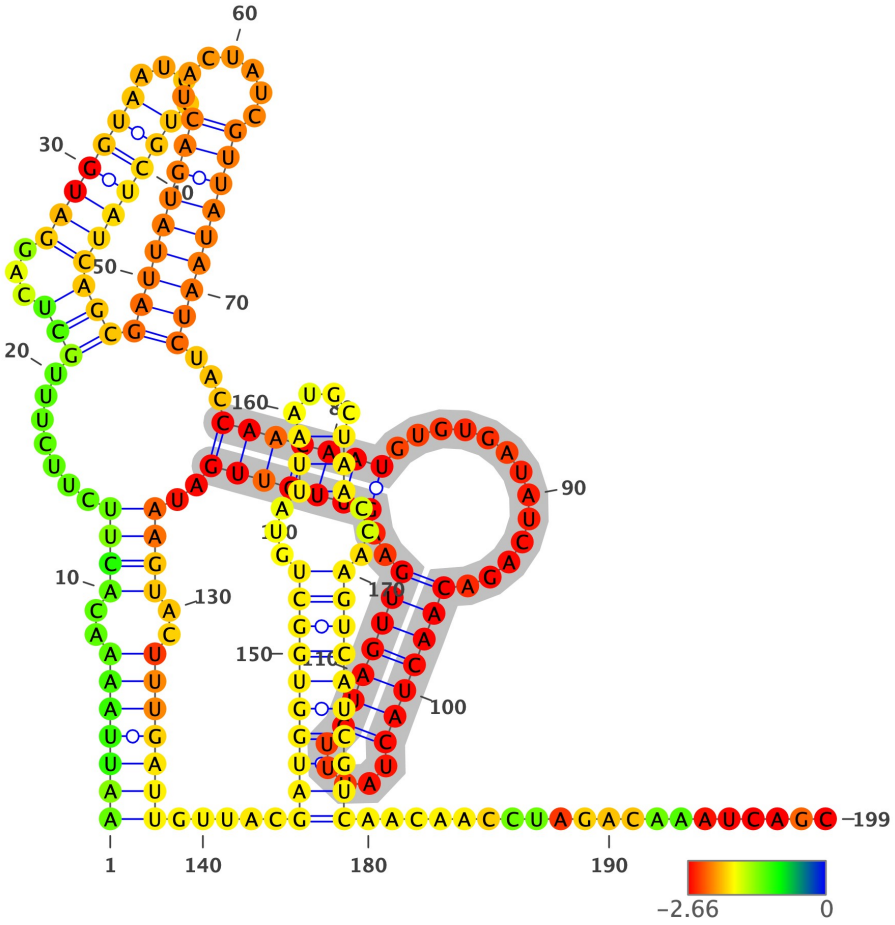
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 258 from nt 14822 to 14869 (nt 76 to 123)

```
5'-CAACAATGTGTGATATCAGACAACTACTATTTGUAGUUGAAGUUGTUG-3'
5'-((.((((.............(((((((.....)))))))..))))).))-3'
Motif MFE = -11.2; z-score = -2.22; ED = 4.52
```



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 14747 to 14945 (motif highlighted in silver):

```
5'-AAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAG
UUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGC-3
5'-(((((((..((((.......(((...(((((((((....)))))))))))(((((((((.......)))))))))...(((((((.............(((((((.....))))
)))..)))))))..))))..)))))))).....((((((((((...(((....)))...))))))))))...................-3'
MFE = -44.8; z-score = -3.16; ED = 36.93
```

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(+)

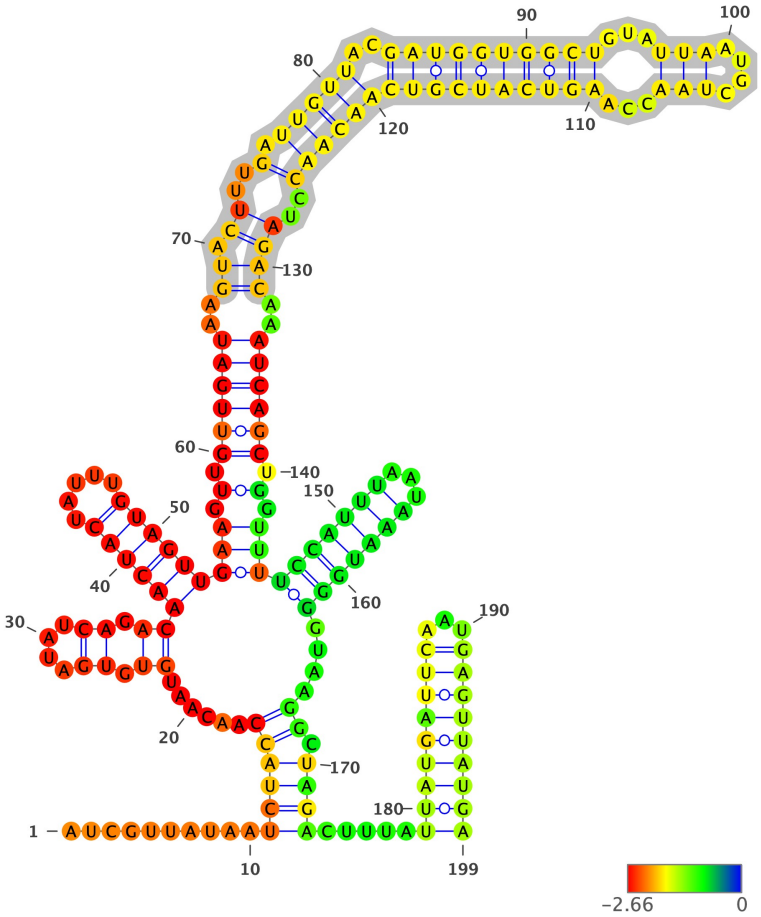
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14874 to 14937 (nt 68 to 131)

```
5'-GTACTTTGATTGTTACGATGGTGGCTGTATTAATGCUAACCAAGUCAUCGUCAACAACCTAGAC-3'
5'-((.(...(.((((((..((((((((((...(((....)))...))))))))))))))))...)))-3'
Motif MFE = -14.2; z-score = -1.76; ED = 12.59
```



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 14807 to 15005 (motif highlighted in silver):

```
5'-AUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAG
UCAUCGUCAACAACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGA-3
5'-..........((((((......((.((....)).))((((((.....))))))(((.(.(((((((..((.((..(.((((((..((((((((((...((((....))))...))
))))))))))))))..)))))..)))))))).).)))(((((((...)))))))....)).))))).....(((((((((...)))))))))-3'
MFE = -43.4; z-score = -1.51; ED = 35.46
```

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(+)

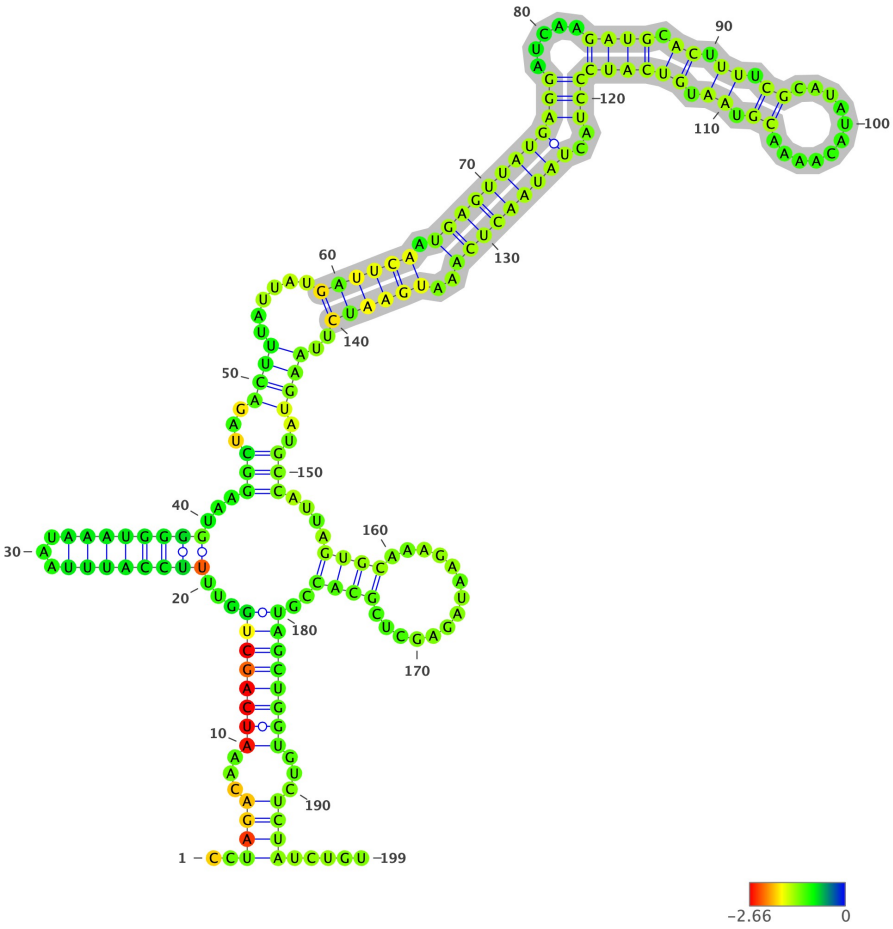
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 14989 to 15070 (nt 59 to 140)

```
5'-GATTCAATGAGTTATGAGGATCAAGATGCACTTTTCGCATATACAAAACGTAATGUCAUCCCUACUAUAACUCAAAUGAATC-3'
5'-(.((((..(((((((((((.....((((.((.((.((...........)).)).)))))))))..))))))))...)))).)-3'
Motif MFE = -18.4; z-score = -3.59; ED = 11.84
```



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 14931 to 15129 (motif highlighted in silver):

```
5'-CCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUAA
UGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGU-3
5'-..((((...((((((((...((((((((...))))))))...(((...((((......((((((.(((((((((((((.....((((.((.((.((...........)).))
.)))))))))..)))))))))..))))))..))))..)))....((((..............))))..))))))))...))))).....-3'
MFE = -44.5; z-score = -1.84; ED = 36.75
```

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(+)

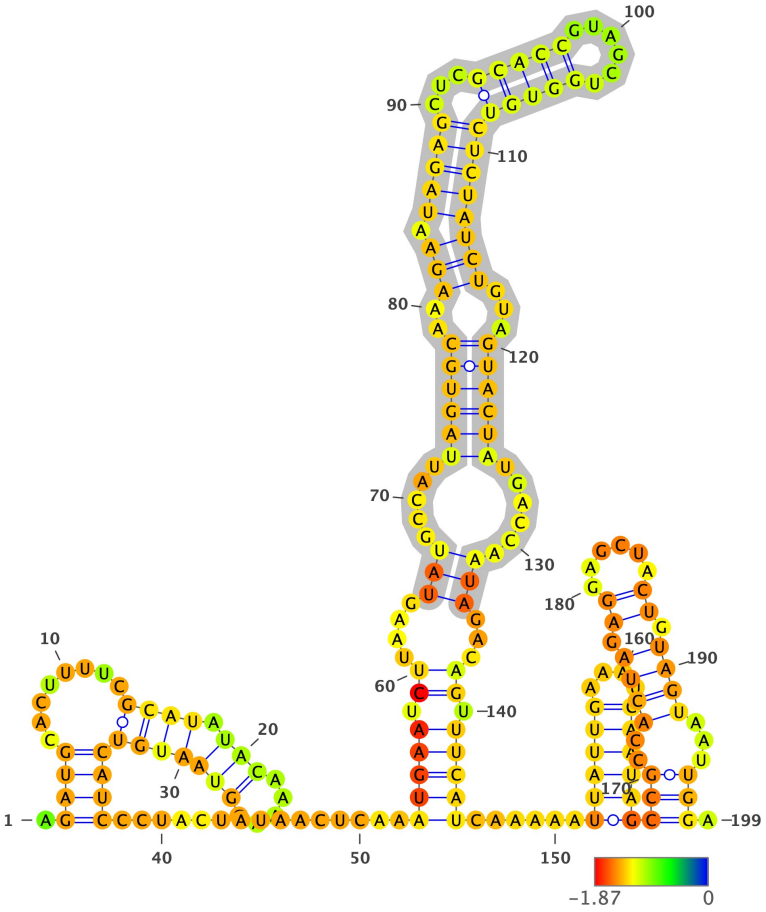
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 15076 to 15145 (nt 65 to 134)

```
5'-TATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGUGUCUCUAUCUGTAGUACUATGACCAAUA-3'
5'-((.......(((((..(((.(((((...(((((......)))))))))))))...)))))........))-3'
Motif MFE = -20.0; z-score = -2.36; 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 15012 to 15210 (motif highlighted in silver):

```
5'-AGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUC
UAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGA-3
5'-.((((........((((.(((.....)))))))))))...............(((((.((....(((.....((((((..(((.(((((...(((((......))))))))
)))))...))))))......)))...)).)))))......((((((....))))))(((..((((.((......)).))))...))).-3'
MFE = -36.4; z-score = -0.75; ED = 35.38
```

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(+)

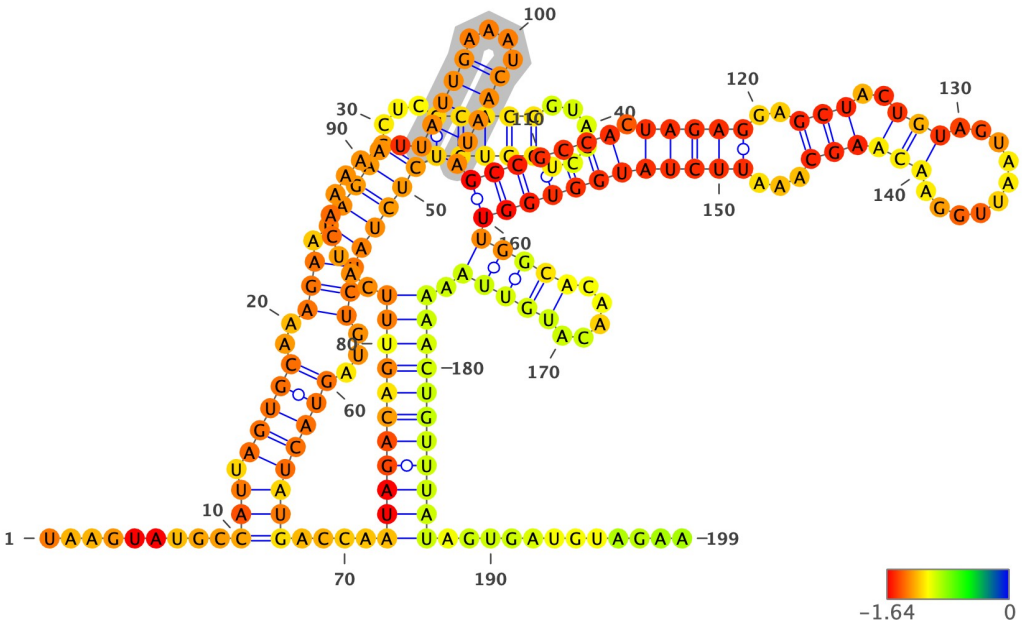
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 262 from nt 15164 to 15177 (nt 93 to 106)

```
5'-TATTGAAATCAAUA-3'
5'-(((((....)))))-3'
Motif MFE = -0.8; z-score = -9.8; 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 15072 to 15270 (motif highlighted in silver):

```
5'-UAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGC
CACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAA-3
5'-.........(((.(((((..(((.(((((...(((((......)))))))))))))...))))))))....((((((((((.........(((((....)))))(((((
((.(((((..(((..(((.........))))))...))))))))))))(((((.....))))).))))))))))).............-3'
MFE = -49.3; z-score = -2.52; ED = 30.9
```

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(+)

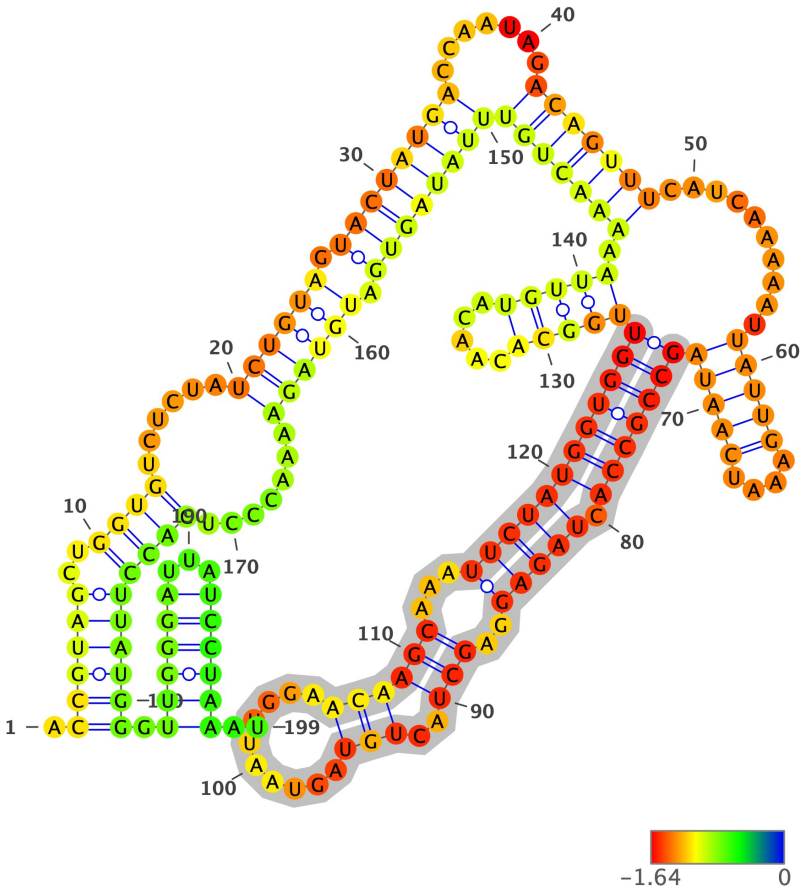
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 263 from nt 15178 to 15231 (nt 73 to 126)

```
5'-GCCGCCACTAGAGGAGCTACTGTAGTAATTGGAACAAGCAAAUUCUAUGGUGGU-3'
5'-(((((((.(((((..(((.................)))...)))))))))))-3'
Motif MFE = -16.1; z-score = -2.77; ED = 5.6
```



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 15106 to 15304 (motif highlighted in silver):

```
5'-ACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGC
AAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAU-3
5'-.((((((..((((......((((((.((((((((.......(((((((..........(((((....)))))(((((((.(((((..(((..(((..........))))))
...))))))))))))(((((.....))))).))))))))))))))).))))))).......))))))))))).((((((...))))))..-3'
MFE = -46.7; z-score = -1.78; ED = 19.97
```

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(+)

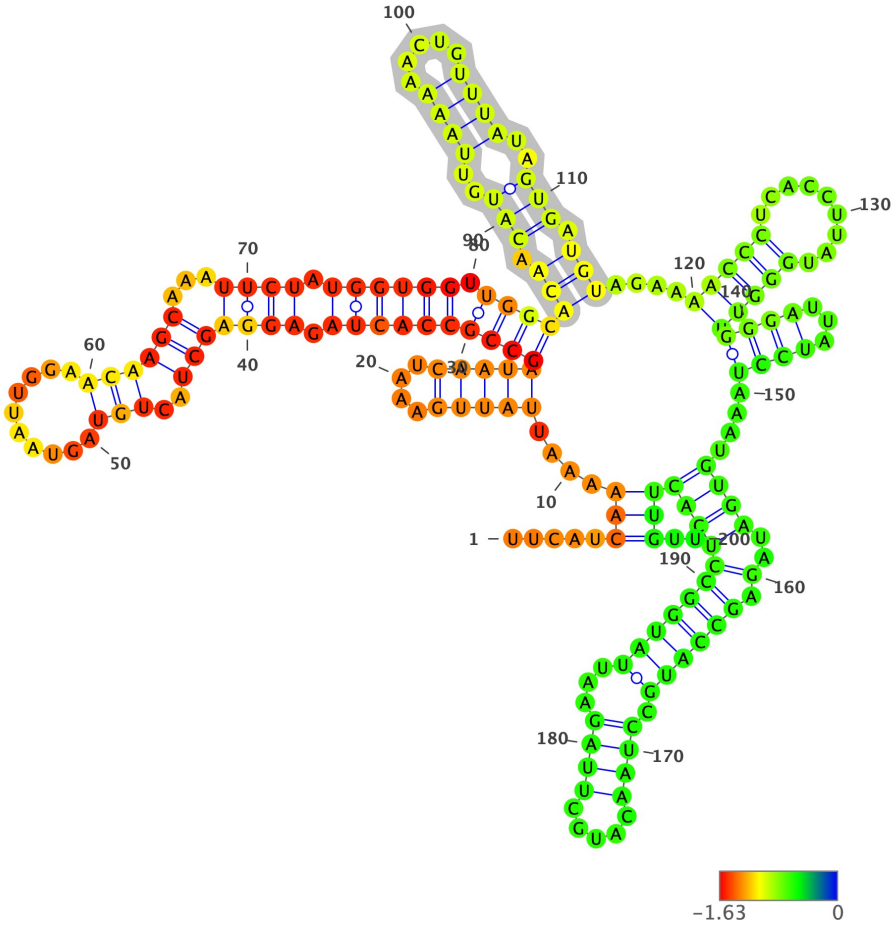
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 15236 to 15266 (nt 85 to 115)

```
5'-ACAACATGTTAAAAACTGUUUATAGUGAUGU-3'
5'-(((.........................)))-3'
Motif MFE = -3.5; z-score = -1.16; ED = 2.03
```



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 15152 to 15351 (motif highlighted in silver):

```
5'-UUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUG
AUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAUGUGAUAGAGCCAUGCCUAACAUGCUUAGAAUUAUGGCCUCACUUGUU-3
5'-.....(((....(((((....)))))((((((((((.(((((((..(((..........))))))...)))).)))))).))))(((.(((..((((.....))))..)))
.))).....(((((.........)))))((((...)))).....((((..(.((((((.((((.....))))...)))))))))))))..-3'
MFE = -44.6; z-score = -1.24; ED = 33.71
```

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(+)

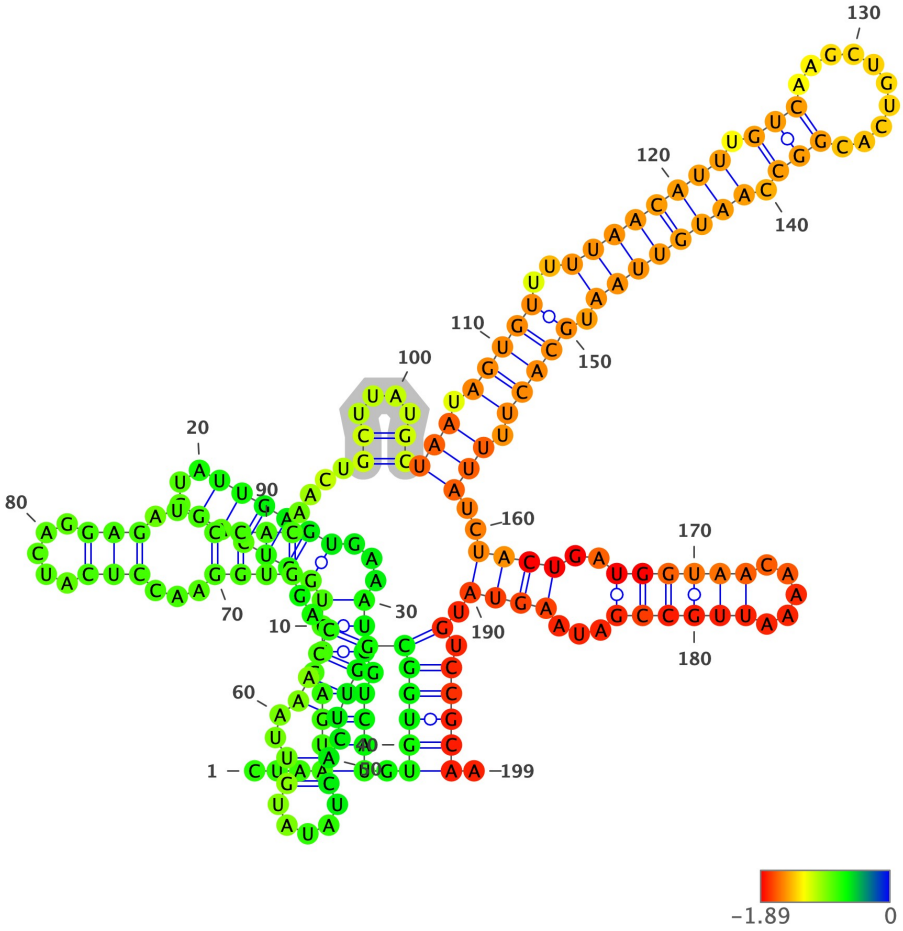
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 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 = -0.77; 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(+)

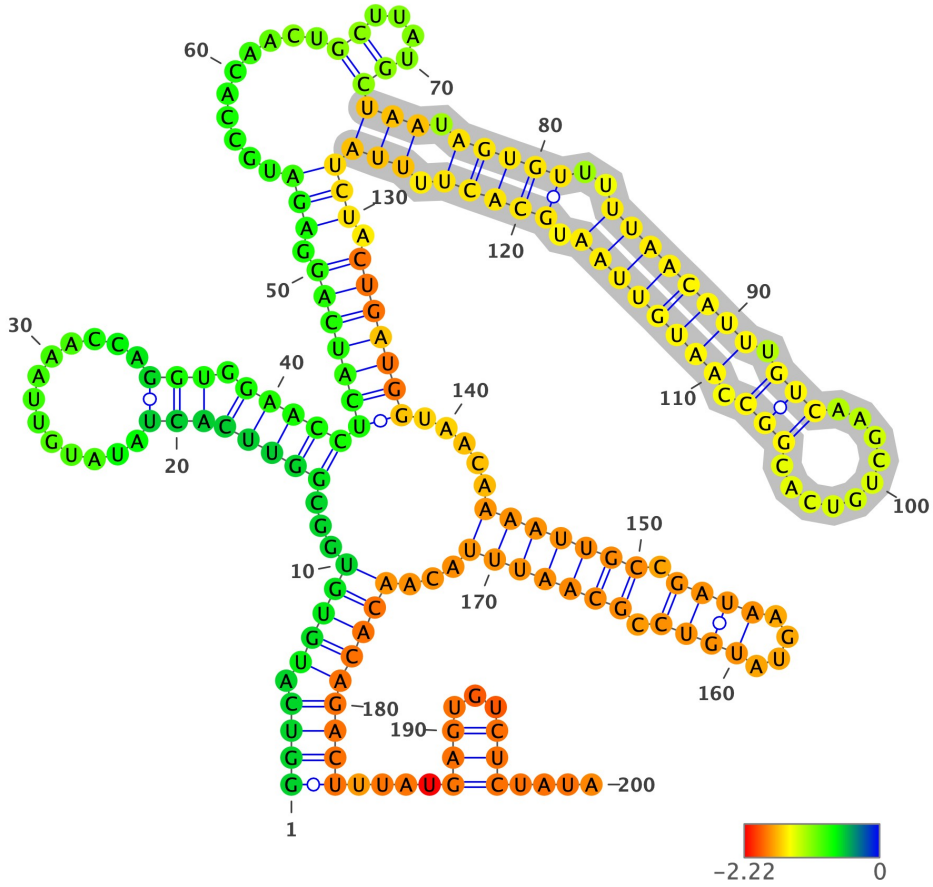
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 266 from nt 15510 to 15564 (nt 73 to 127)

```
5'-TAATAGTGTTTTTAACATTTGTCAAGCTGTCACGGCCAAUGUUAATGCACUTUUA-3'
5'-(((.((((((..(((((((((.(((.........))).))))))))).))))))...)))-3'
Motif MFE = -13.3; z-score = -2.69; 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 = -47.3; z-score = -1.61; ED = 19.7
```

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(+)

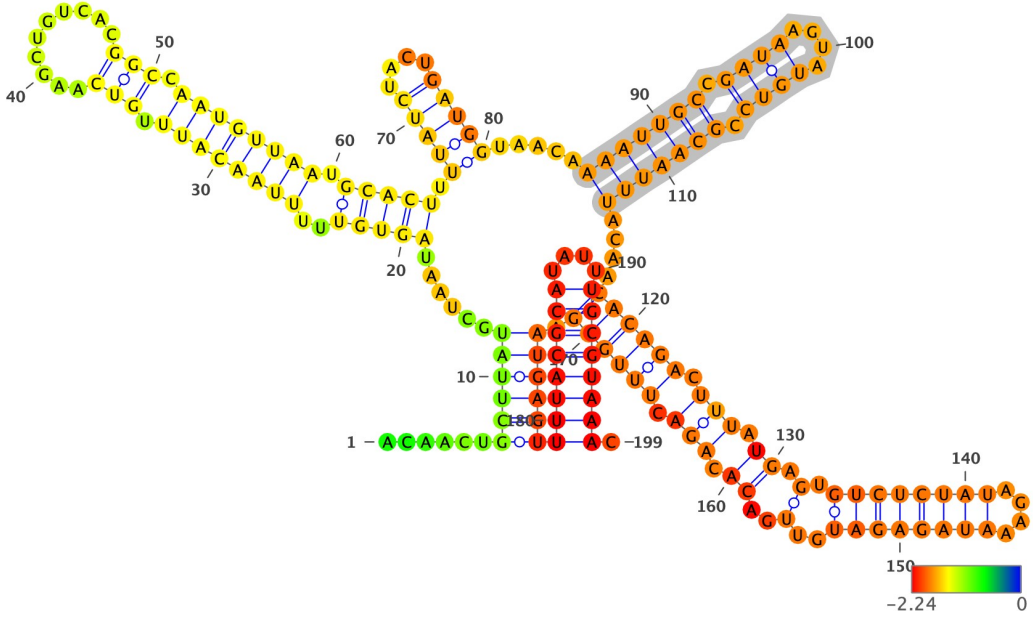
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 267 from nt 15581 to 15608 (nt 86 to 113)

```
5'-AAATTGCCGATAAGTAUGUCCGCAAUUU-3'
5'-(((((((.((((....)))).)))))))-3'
Motif MFE = -7.8; z-score = -3.26; 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 15496 to 15694 (motif highlighted in silver):

```
5'-ACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAU
UUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAAC-3
5'-......((((((......(((((..((((((((.(((..........))).)))))))).))))).(((((....))))).....(((((((.((((....)))).)))))
)).....((((((.(((.((.(.((((((((....))))))))..)..)).))).)))))).))))))((((((((....))))))))).-3'
MFE = -49.4; z-score = -2.97; ED = 33.11
```

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(+)

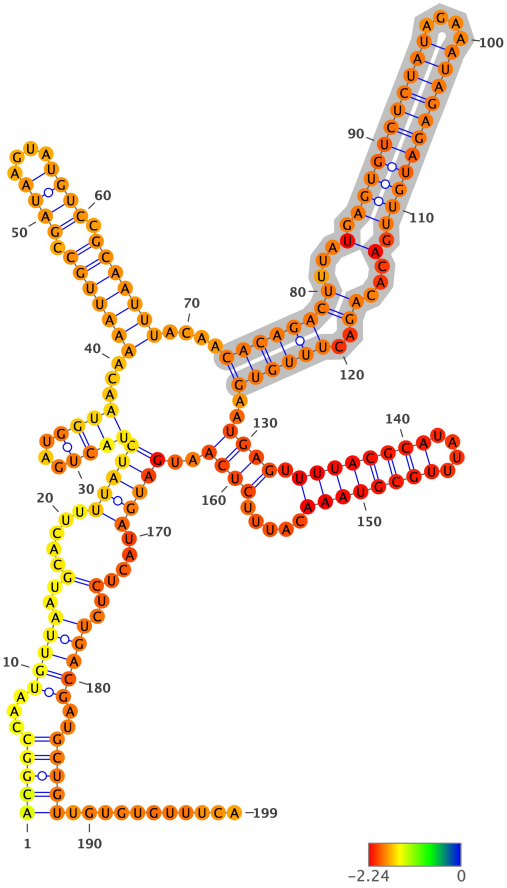
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 15613 to 15666 (nt 73 to 126)

```
5'-CACAGACTTTATGAGTGTCTCTATAGAAAUAGAGAUGUUGACACAGACUUUGUG-3'
5'-(((((((((.....((((((((((....))))))))))).....))..)))))))-3'
Motif MFE = -12.0; z-score = -1.81; ED = 6.7
```



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 15541 to 15739 (motif highlighted in silver):

```
5'-ACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUU
GACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCA-3
5'-(((((...((((((..(.....((((((((((...))))).....(((((((.(((((....))))).)))))))....(((((((((...(.((((((((((....))))))))))
.)...))..)))))))..((((.(((((((((....)))))))))..... ))))..))))))....)..))))))..))))).....-3'
MFE = -41.2; z-score = -1.55; ED = 38.59
```

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(+)

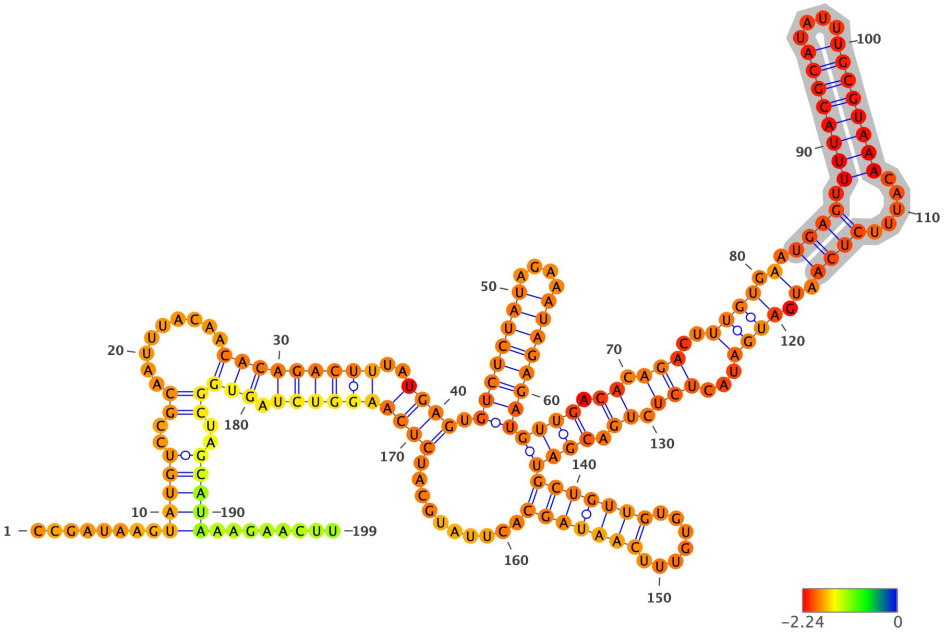
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 269 from nt 15669 to 15702 (nt 83 to 116)

```
5'-TGAGTTTTACGCATATTUGCGUAAACATTTCUCA-3'
5'-((((.((((((((....))))))))).....))))-3'
Motif MFE = -9.8; z-score = -4.2; 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 15587 to 15785 (motif highlighted in silver):

```
5'-CCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUU
UCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUU-3
5'-........(((((..((.........((((((((..((((.((((((((....))))))))((((.((.(((..((((.(.((((.((((((((....))))))))....
.)))).).))))...))).)).))))(((((((.......)))))))..........))))))))))).)))))..)))))........-3'
MFE = -45.7; z-score = -2.35; ED = 54.51
```

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(+)

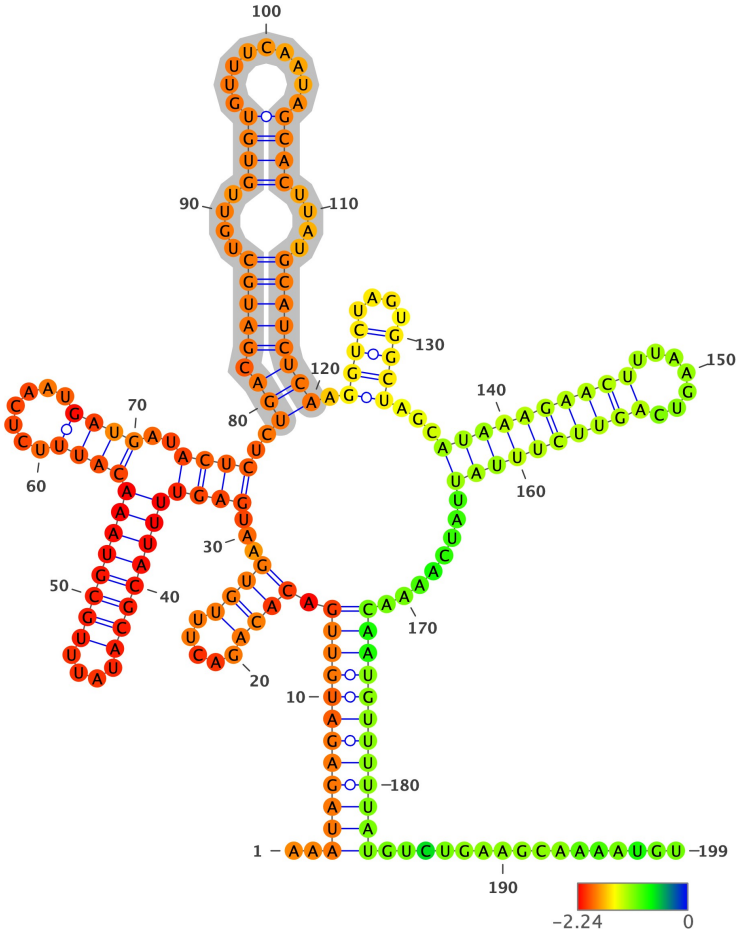
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 15717 to 15758 (nt 79 to 120)

```
5'-TGACGATGCTGTTGTGTGTTTCAATAGCACTTATGCAUCUCA-3'
5'-(((.(((((....((((.........))))....)))))))-3'
Motif MFE = -11.5; z-score = -2.9; 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 = -2.64; 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(+)

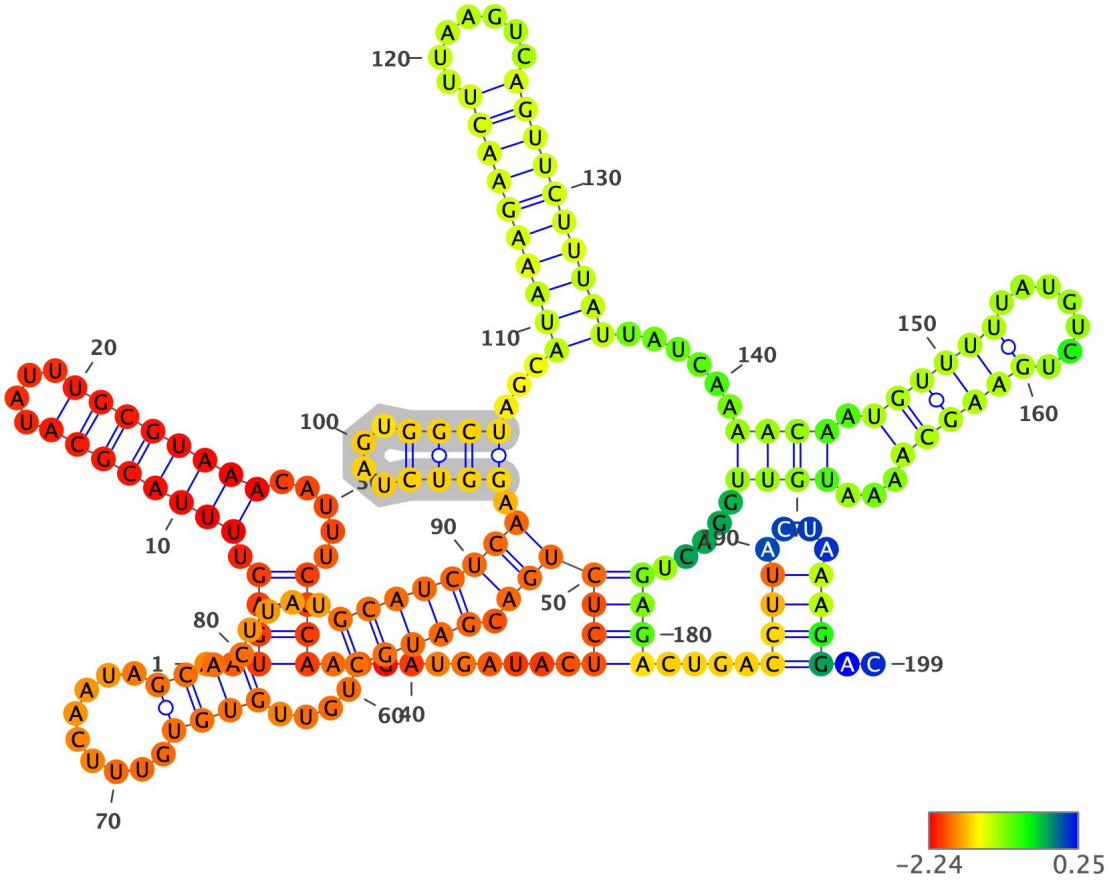
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 271 from nt 15760 to 15771 (nt 94 to 105)

```
5'-GGTCTAGTGGCU-3'
5'-((((....))))-3'
Motif MFE = -2.1; z-score = -3.15; ED = 0.58
```



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 15667 to 15865 (motif highlighted in silver):

```
5'-AAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUA
AAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGUUGGACUGAGACUGACCUUACUAAAGGAC-3
5'-..(((((.(((((((((....)))))))))).....)))).........(((((((.(((((....((((.........))))))....)))))))).((((....)))))...(((
(((((((.......)))))))))).....((((.((((((.......))))))...)))).....)))).....((((....)))))..-3'
MFE = -44.5; z-score = -1.74; ED = 48.8
```

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(+)

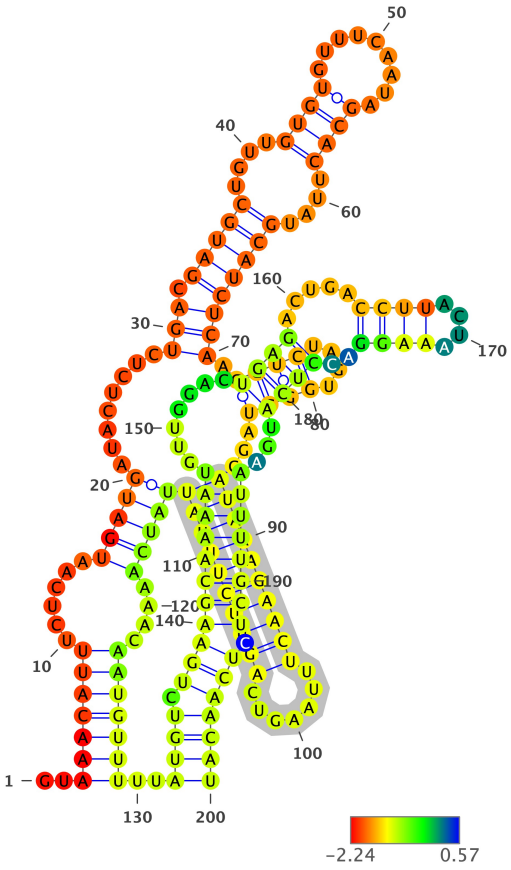
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 272 from nt 15775 to 15801 (nt 87 to 113)

```
5'-ATAAAGAACTTTAAGTCAGUUCUUUAU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -7.5; z-score = -5.0; 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 = -1.13; 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(+)

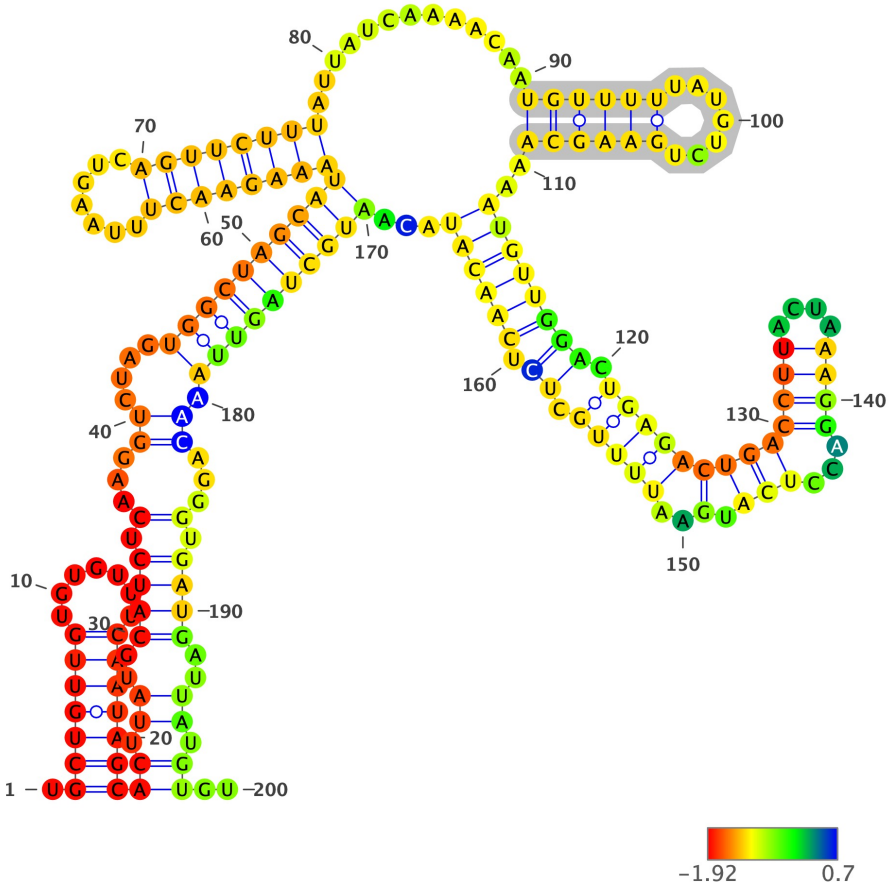
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 273 from nt 15813 to 15831 (nt 91 to 109)

```
5'-TGTTTTTATGTCTGAAGCA-3'
5'-((((((.......))))))-3'
Motif MFE = -1.8; z-score = -1.75; 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 15723 to 15922 (motif highlighted in silver):

```
5'-UGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAA
AUGUUGGACUGAGACUGACCUUACUAAAGGACCUCAUGAAUUUUGCUCUCAACAUACAAUGCUAGUUAAACAGGGUGAUGAUUAUGUGU-3
5'-.(((((((.......)))))))((.((..((((.(...((....((((((((((((((((((.......))))))))).............((((((.......))))))..
((((((((.((((((((((((....))))...))).)..))))).)).))))))...))))))))))).))...).))))..)).))..-3'
MFE = -41.8; z-score = -1.69; ED = 31.2
```

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(+)

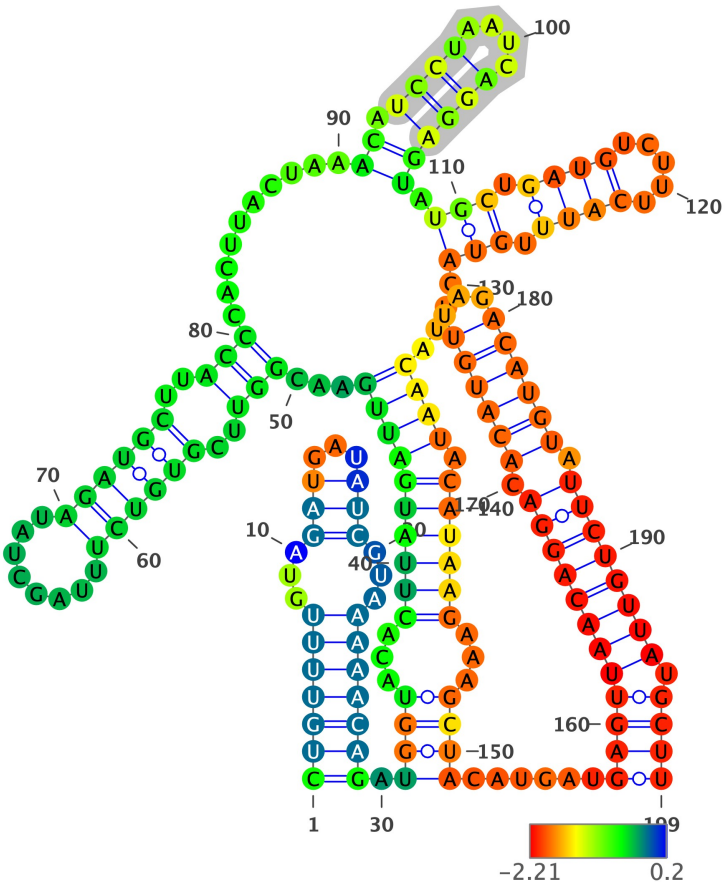
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 16056 to 16067 (nt 94 to 105)

```
5'-TCCTAATCAGGA-3'
5'-(.(......).)-3'
Motif MFE = -2.0; z-score = -6.33; 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 15963 to 16161 (motif highlighted in silver):

```
5'-CUGUUUUGUAGAUGAUAUCGUAAAAACAGAUGGUACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUGC
UGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUU-3
5'-(((((((...(((...))))...)))))))..(((((...((((((((((...(((..((((((........))))))..)))..........((.((((....)))))))..(((
.((((.....)))).)))....)))))..)))))))...))))......((((((((((((.((((((...))))))).)))))))).))))-3'
MFE = -46.7; z-score = -2.42; ED = 15.67
```

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, 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 16074 to 16118 (nt 78 to 122)

```
5'-TGATGTCTTTCATTTGTACTTACAAUACATAAGAAAGCTACAUGA-3'
5'-(.(((((((((...((((.......))))...)))))..)))).)-3'
Motif MFE = -6.7; z-score = -1.34; ED = 2.79
```



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 15997 to 16196 (motif highlighted in silver):

```
5'-ACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAGA
AAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGA-3
5'-................(((((((((((........))))))....(((..((((..........((((..((((.(((.(((((((((...((((.......))))...))
)))..)))).)....((((((((.((((((...))))))).))))))))).)).))))..))))..........)))).))))))))...-3'
MFE = -43.3; z-score = -1.45; ED = 29.21
```

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(+)

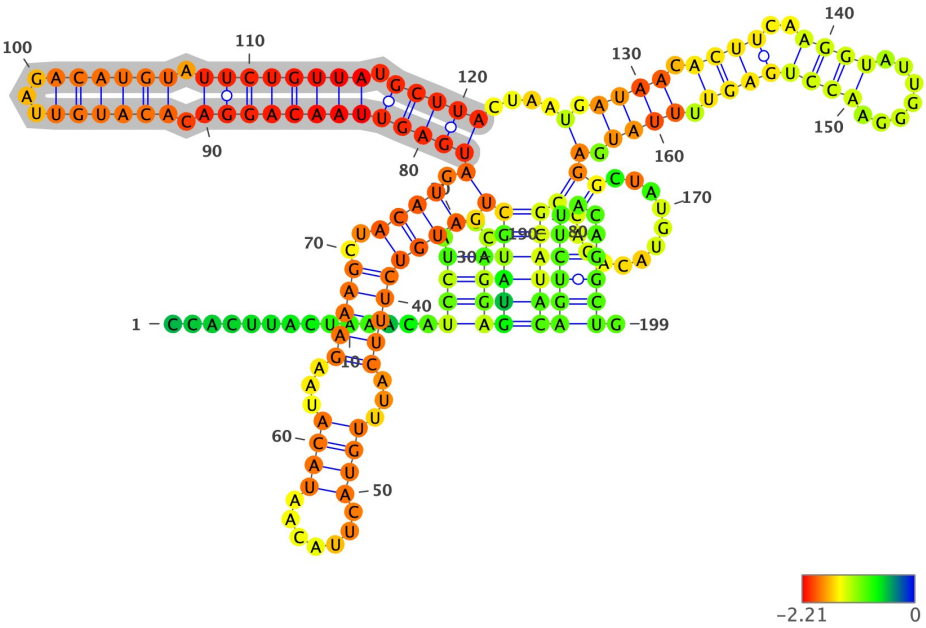
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 276 from nt 16119 to 16162 (nt 78 to 121)

```
5'-TGAGTTAACAGGACACATGTTAGACAUGUAUUCUGUUATGCUUA-3'
5'-(((((((((((((.((((((...)))))).)))))))).)))))-3'
Motif MFE = -16.5; z-score = -4.83; ED = 1.49
```



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 16042 to 16240 (motif highlighted in silver):

```
5'-CCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCU
GUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUG-3
5'-..............((((....))))(((((((.((((((((((...((((.......))))...))))))..))))).)((((((((((((.((((((...)))))).))))
))))).)))))....(.((((.((((..((((.......))))))))).))))).)((..........))))))))(((((...))))).-3'
MFE = -43.2; z-score = -1.25; ED = 46.98
```

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(+)

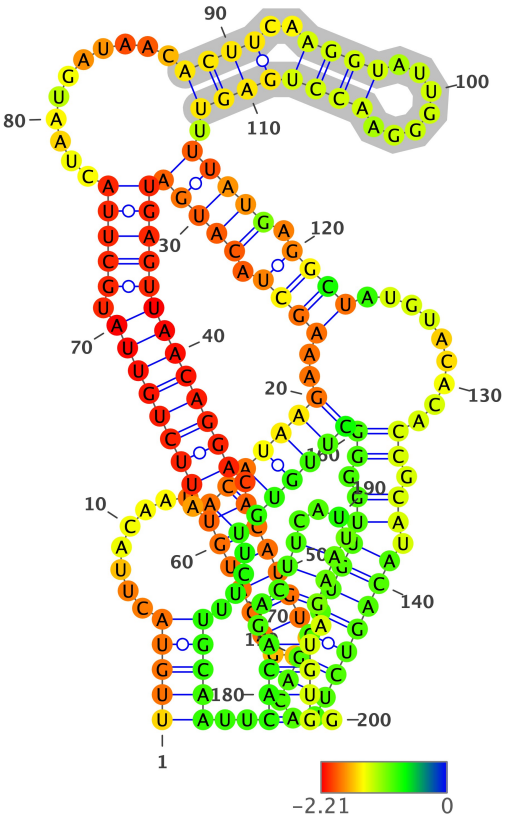
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 16174 to 16198 (nt 88 to 112)

```
5'-ACTTCAAGGTATTGGGAACCUGAGU-3'
5'-((((..((((.......))))))))-3'
Motif MFE = -3.7; z-score = -0.88; ED = 4.09
```



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 16087 to 16286 (motif highlighted in silver):

```
5'-UUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAG
UUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUUCACAGACUUCAUUAAGAUGUGG-3
5'-(((((........(((((((..((((.((((((((((((((((((.((((((...)))))).)))))))).)))))...........((((..((((.......)))))))
).)))))).))))........((.((.(((((((...)))))))))).))))))))....)))))..((((..(((....))).)))).-3'
MFE = -47.7; z-score = -1.29; ED = 36.92
```

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(+)

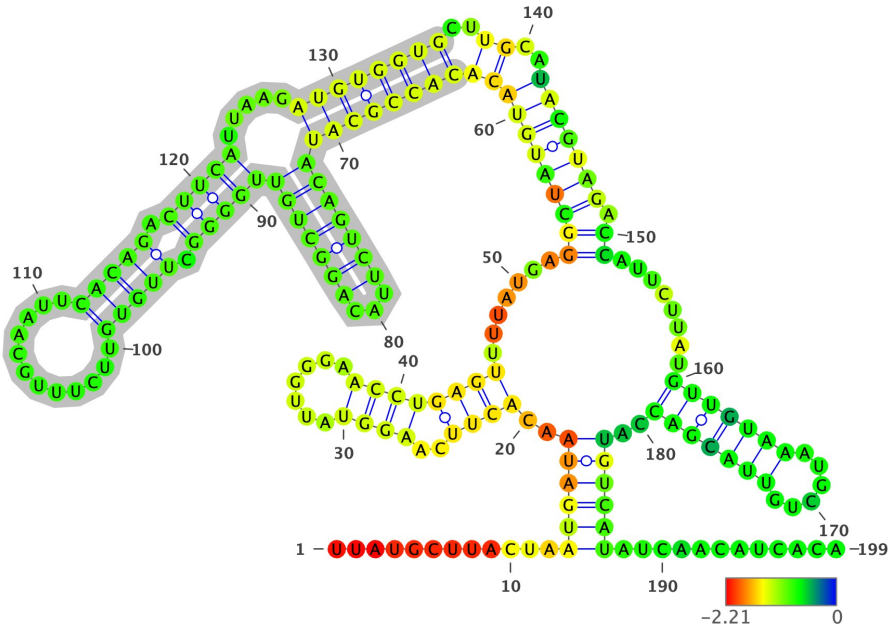
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 16217 to 16288 (nt 64 to 135)

```
5'-CACCGCATACAGTCTTACAGGCUGUTGGGGCTTGTGTTCTTTGCAATTCACAGACUUCATTAAGAUGUGGUG-3'
5'-(((((((((.....................................................)))))))))-3'
Motif MFE = -22.5; z-score = -2.34; ED = 3.6
```



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 16154 to 16352 (motif highlighted in silver):

```
5'-UUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUU
CACAGACUUCAUUAAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACA-3
5'-............((((((..((((..((((.......))))))))).......(((((((((((((((((((((((((...)))))))))))))))))))))))))))))(((((.(((((.............
)))))).))))).....)))))))))..))..)))))))..)).........(((((((.....)))))))..))))))............-3'
MFE = -44.2; z-score = -0.48; ED = 36.09
```

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(+)

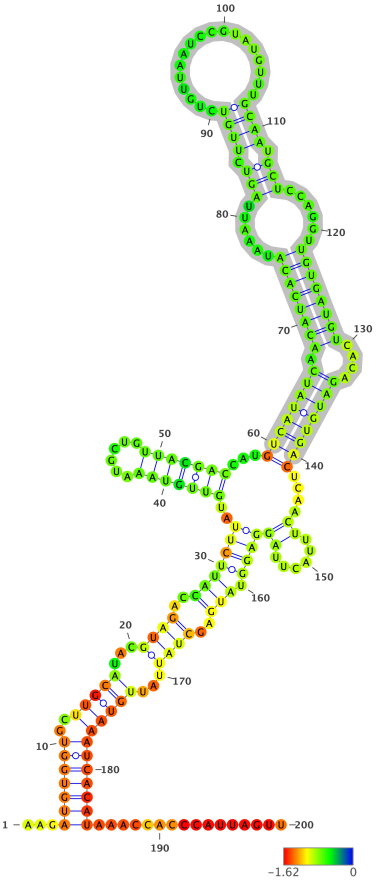
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 279 from nt 16337 to 16417 (nt 60 to 140)

```
5'-TCATATCAACATCACATAAATTAGTCTTGTCTGTTAATCCGTATGTTTGCAATGCUCCAGGTUGUGAUGUCACAGATGUGA-3'
5'-(.........................................................................)-3'
Motif MFE = -17.2; z-score = -1.52; ED = 5.36
```



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 16278 to 16477 (motif highlighted in silver):

```
5'-AAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACAUAAAUUAGUCUUGUCUGUUAAUCCGUAUGUUUGCAA
UGCUCCAGGUUGUGAUGUCACAGAUGUGACUCAACUUUACUUAGGAGGUAUGAGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUU-3
5'-...(((((((..(((((...((((..(((((((..(((((((......)))))))...((((((((.((((((((......(((.((((.................))))
.)))......))))))))....))))))))....((......)))))).)))..))))...)))))))))))).................-3'
MFE = -41.7; z-score = -0.75; ED = 25.77
```

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(+)

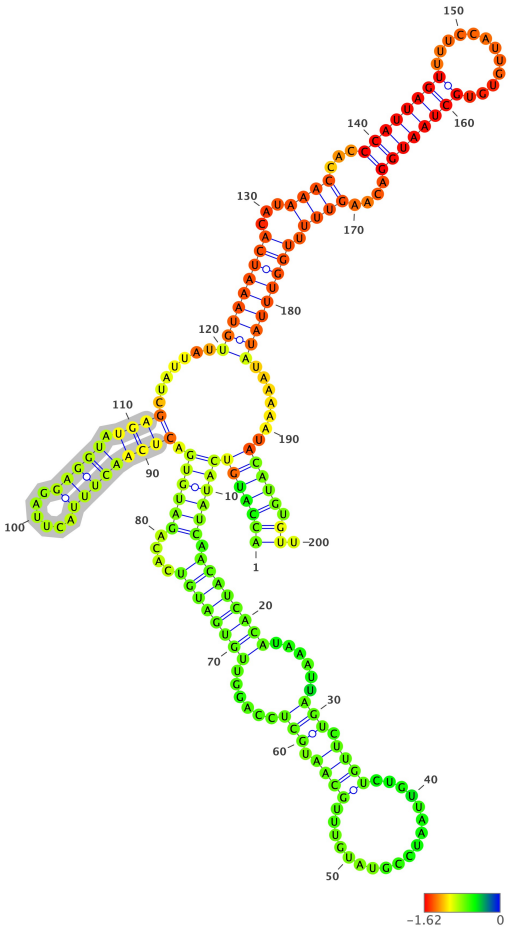
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 16419 to 16441 (nt 89 to 111)

```
5'-TCAACTTTACTTAGGAGGUAUGA-3'
5'-(((.................)))-3'
Motif MFE = -2.5; z-score = -0.75; ED = 3.2
```



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 16331 to 16530 (motif highlighted in silver):

```
5'-ACCAUGUCAUAUCAACAUCACAUAAAUUAGUCUUGUCUGUUAAUCCGUAUGUUUGCAAUGCUCCAGGUUGUGAUGUCACAGAUGUGACUCAACUUUACUUAGGAGGUAUGA
GCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUU-3
5'-(((((((((((((.((((((((.......(((.((((.................)))).)))......))))))))....)))))).((((((((((......))))).)))
).......((((((((...((((...((((((((.............)))))))).....)))).))))))))).......))))).)).-3'
MFE = -42.0; z-score = -1.45; ED = 16.89
```

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_gp01, 266-21555(+)

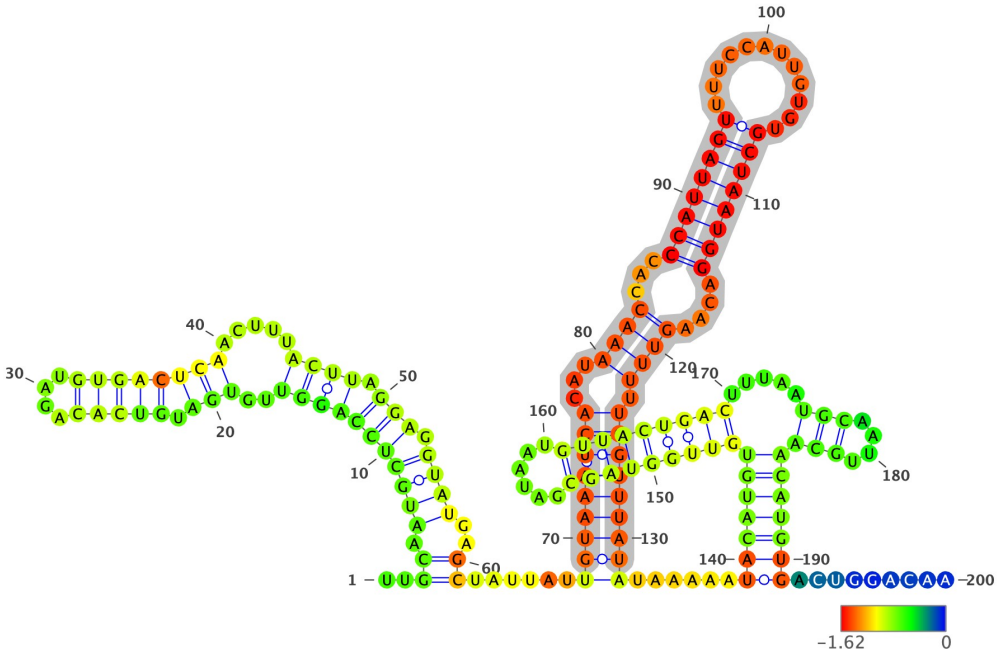
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 16451 to 16513 (nt 69 to 131)

```
5'-GTAAATCACATAAACCACCCATTAGTTTTCCATTGTGTGCUAAUGGACAAGUUUTUGGUUUAU-3'
5'-((((((((...((((...((((((((.............))))))))....)))).))))))))-3'
Motif MFE = -14.1; z-score = -2.35; ED = 8.83
```



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 16383 to 16582 (motif highlighted in silver):

```
5'-UUGCAAUGCUCCAGGUUGUGAUGUCACAGAUGUGACUCAACUUUACUUAGGAGGUAUGAGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAA
UGGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGACUUUAAUGCAAUUGCAACAUGUGACUGGACAA-3
5'-..((.(((((((((((..(((.(((((....))))))))).....)))).))).))))..)).....((((((((...((((...((((((((.............)))))
))).....)))).))))))))).....((((((((((((((((.....))))))))).....(((....))))))))))).........-3'
MFE = -49.5; z-score = -2.01; ED = 33.76
```

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(+)

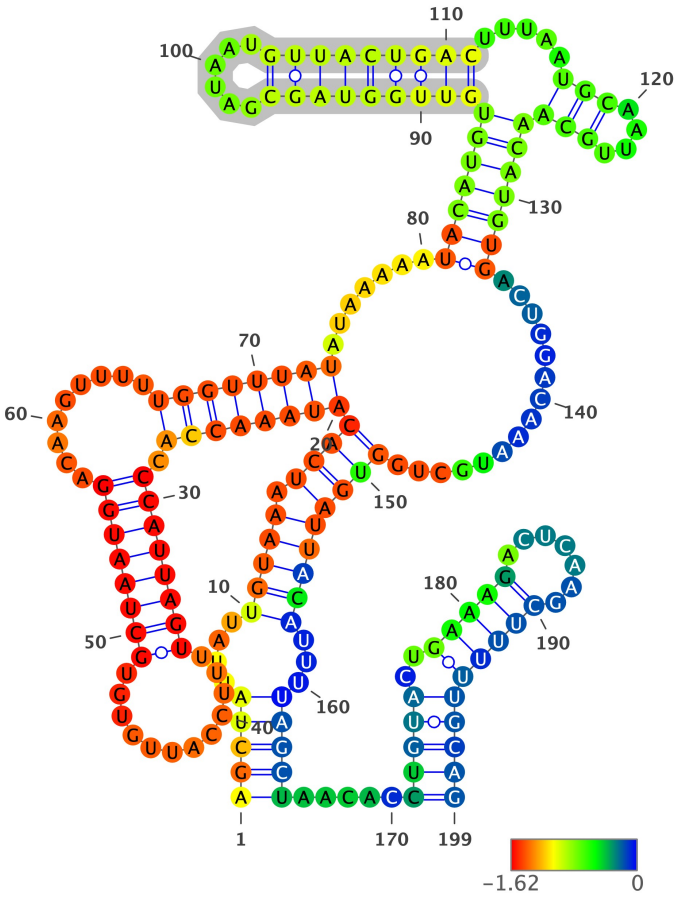
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 16528 to 16551 (nt 88 to 111)

```
5'-GTTGGTAGCGATAATGUUACUGAC-3'
5'-(((.................)))-3'
Motif MFE = -8.0; z-score = -3.02; 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(+)

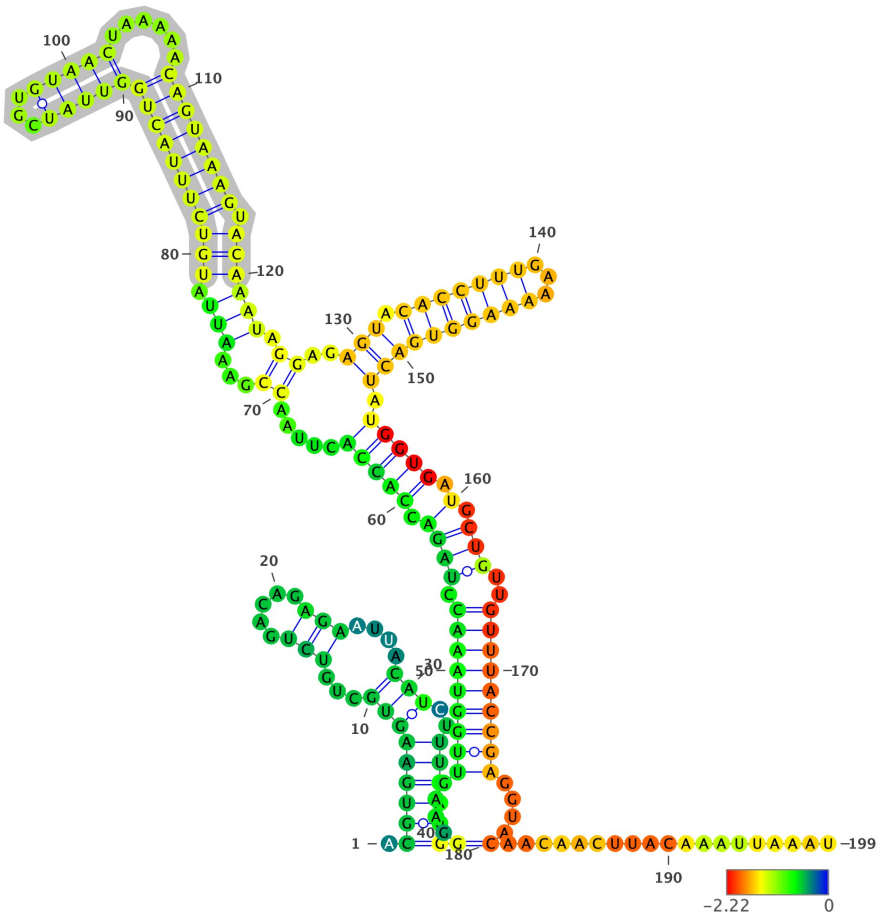
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 283 from nt 16776 to 16817 (nt 79 to 120)

```
5'-TGTCTTTACTGGTTATCGTGUAACTAAAAACAGUAAAGTACA-3'
5'-(((((((((((((((...)))))......)))))))).)))-3'
Motif MFE = -9.5; z-score = -2.78; 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 = -0.92; ED = 48.55
```

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(+)

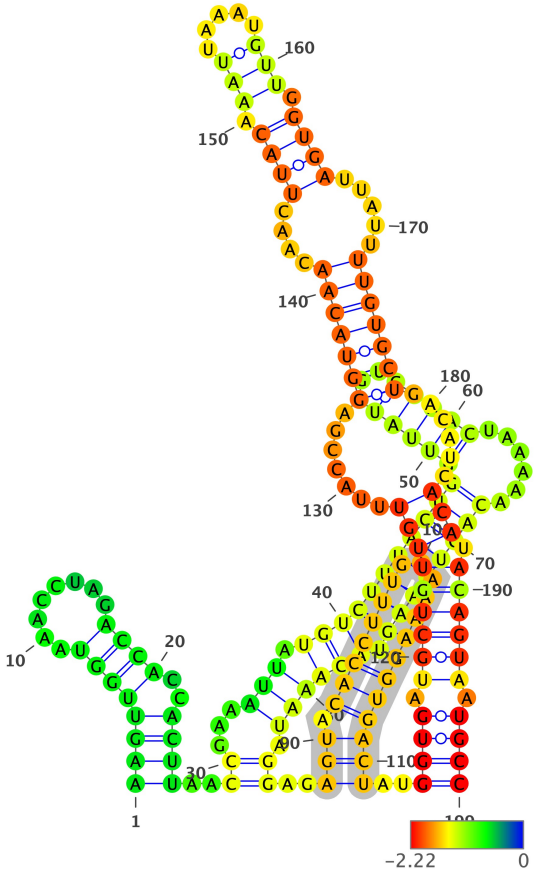
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 16826 to 16849 (nt 88 to 111)

```
5'-AGTACACCTTTGAAAAAGGUGACU-3'
5'-(((.(((((((...))))))))))-3'
Motif MFE = -8.0; z-score = -4.48; 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 = -1.25; ED = 47.6
```

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(+)

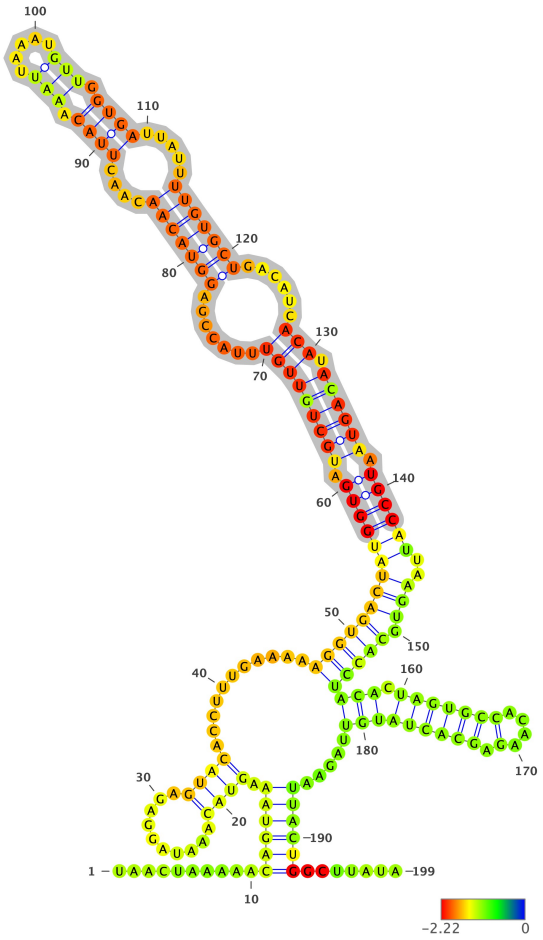
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 16852 to 16937 (nt 57 to 142)

```
5'-GGTGATGCTGTTGTTTACCGAGGTACAACAACTTACAAATTAAATGTTGGUGATTATTUUGUGCUGACATCACATACAGUAAUGCC-3'
5'-((((..(((.((((.......(((((((....((((.............))))).....)))))))......))).).)))..))))-3'
Motif MFE = -18.3; z-score = -1.46; ED = 10.57
```



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 16796 to 16994 (motif highlighted in silver):

```
5'-UAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUU
AUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUA-3
5'-..........((((((.((((..........))))...........(((((((((((((.(((((((((.......(((((((....((((.(((.....))).))))..
...)))))))......))).))))))).))))))..))).)))))(((.(((((((....).)))))))))).....))))))).......-3'
MFE = -45.9; z-score = -2.43; 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(+)

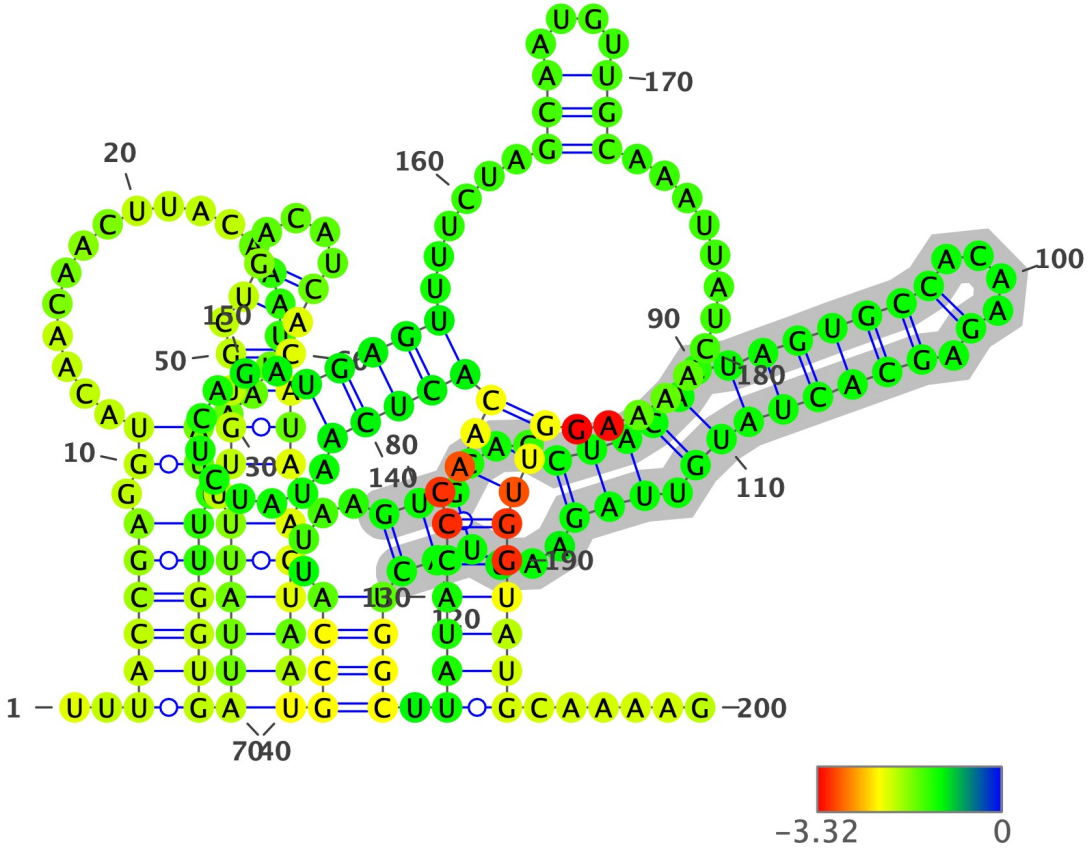
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 286 from nt 16943 to 16985 (nt 79 to 121)

```
5'-GTGCACCTACACTAGTGCCACAAGAGCACUAUGTUAGAATUAC-3'
5'-(((...(((((.(((((((....).))))))))).)))...)))-3'
Motif MFE = -9.2; z-score = -1.95; ED = 4.98
```



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 16865 to 17064 (motif highlighted in silver):

```
5'-UUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUG
UUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAG-3
5'-..((((((.((...................)).))))))((((((.((((.((....)))))).))))))((((....(((...(((((.(((((((....).))))))))
.)))...)))))))).((((((.((((((((..........)))))......(((....)))..............)))))))))......-3'
MFE = -34.1; z-score = -0.09; ED = 53.43
```

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(+)

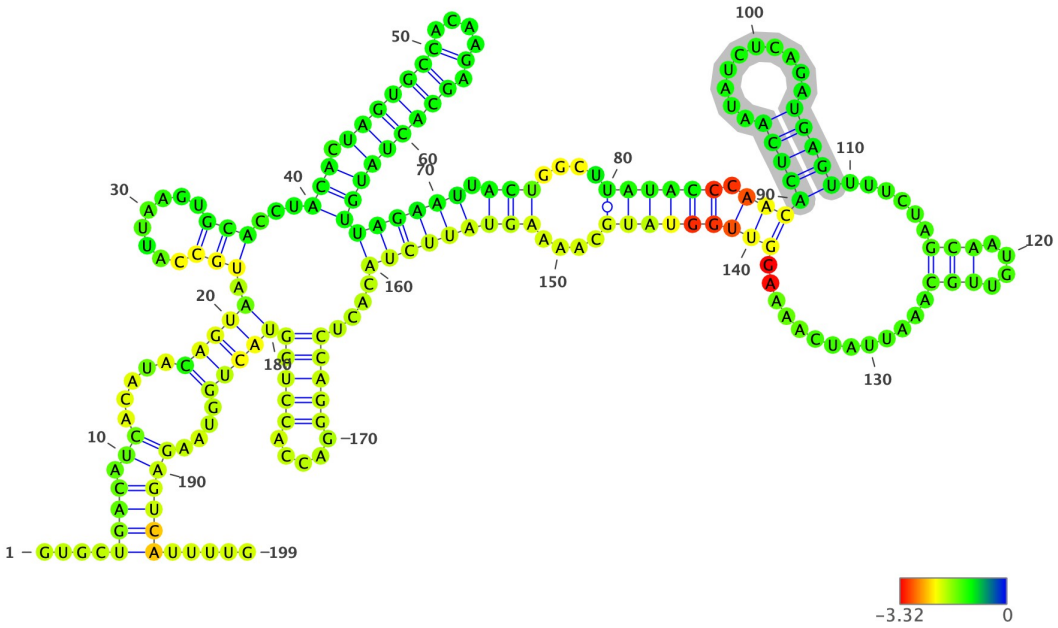
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17001 to 17020 (nt 90 to 109)

```
5'-ACTCAATATCTCAGAUGAGU-3'
5'-(((((..........)))))-3'
Motif MFE = -2.1; z-score = -1.9; 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 = -0.97; ED = 44.74
```

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(+)

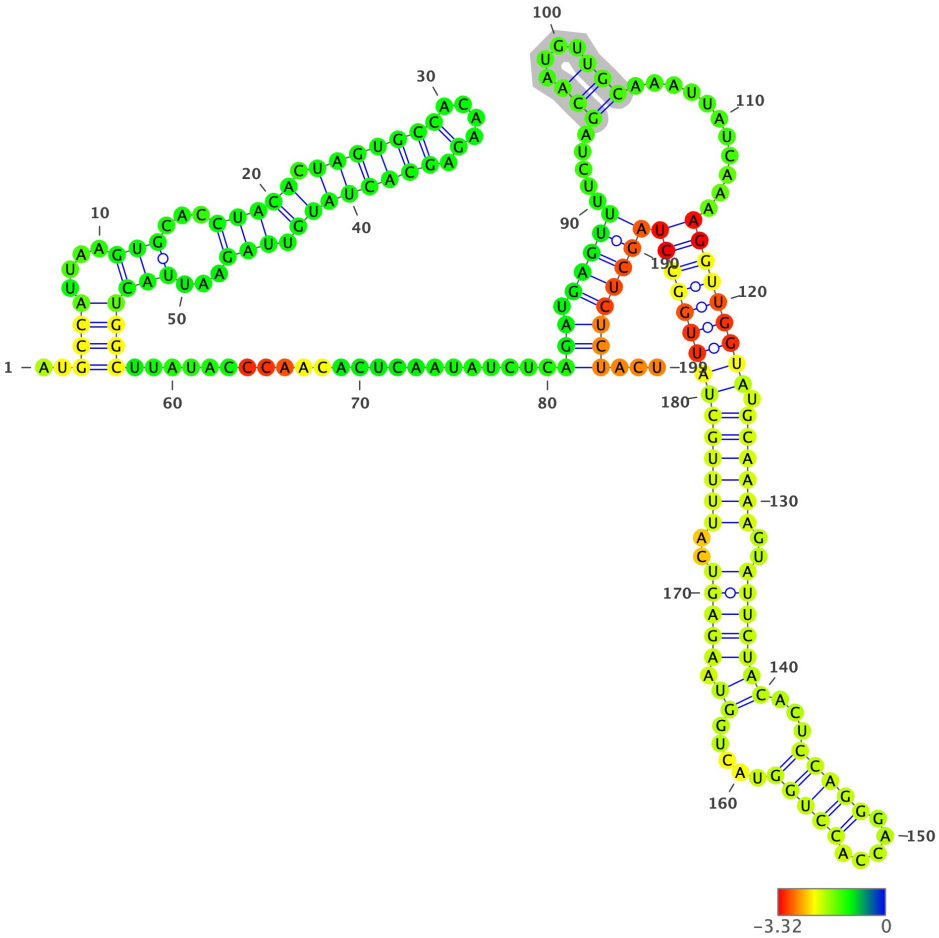
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 17027 to 17036 (nt 95 to 104)

```
5'-GCAATGTUGC-3'
5'-(((....)))-3'
Motif MFE = -0.4; z-score = -7.11; 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 = -2.42; ED = 34.47
```

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(+)

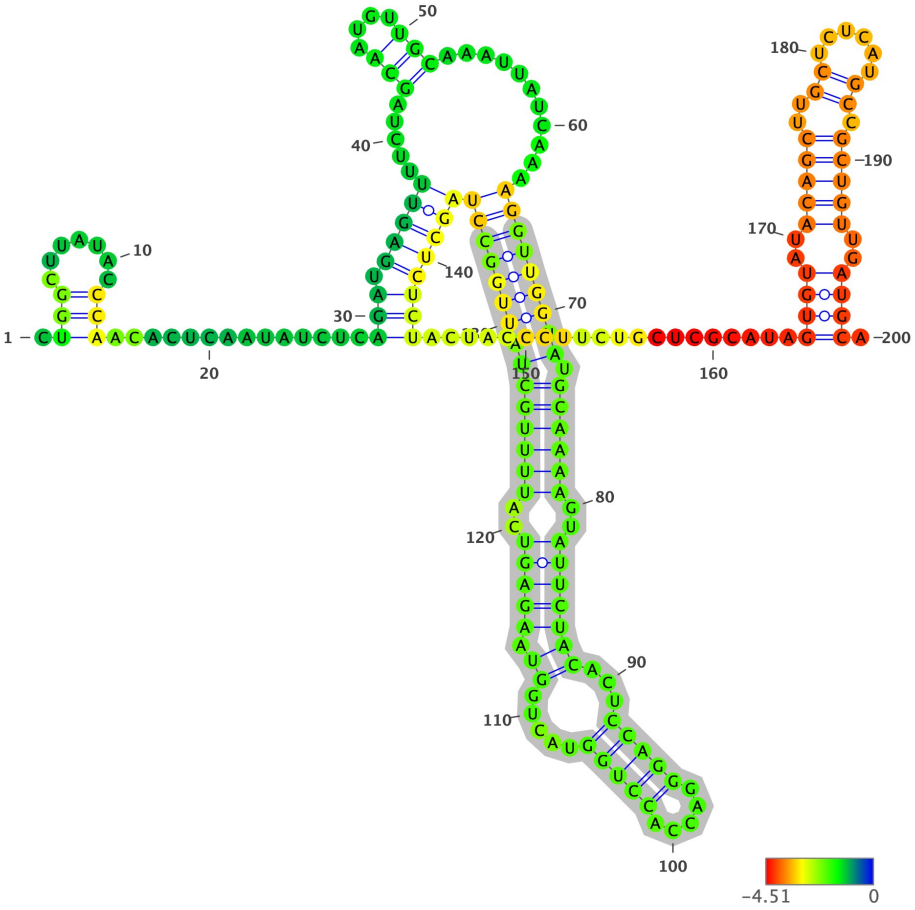
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 289 from nt 17050 to 17118 (nt 66 to 134)

```
5'-GTTGGTATGCAAAAGTATTCTACACTCCAGGGACCACCUGGTACTGGUAAGAGUCAUUUUGCTATTGGC-3'
5'-((...(..((((((..(((((((...(((((.....))))).....)).)))))..)))))).)...))-3'
Motif MFE = -22.3; z-score = -3.29; ED = 4.01
```



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 16985 to 17184 (motif highlighted in silver):

```
5'-CUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUG
GUAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCA-3
5'-.(((.......)))..............(((.(((((.....(((....))).........((((((((.((((((..(((((((...(((((.....)))))).....
)).)))))..))))))))))))))))))))))).....................((((..(((((..((......)).)))))..)))).-3'
MFE = -46.5; z-score = -1.13; ED = 28.11
```

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(+)

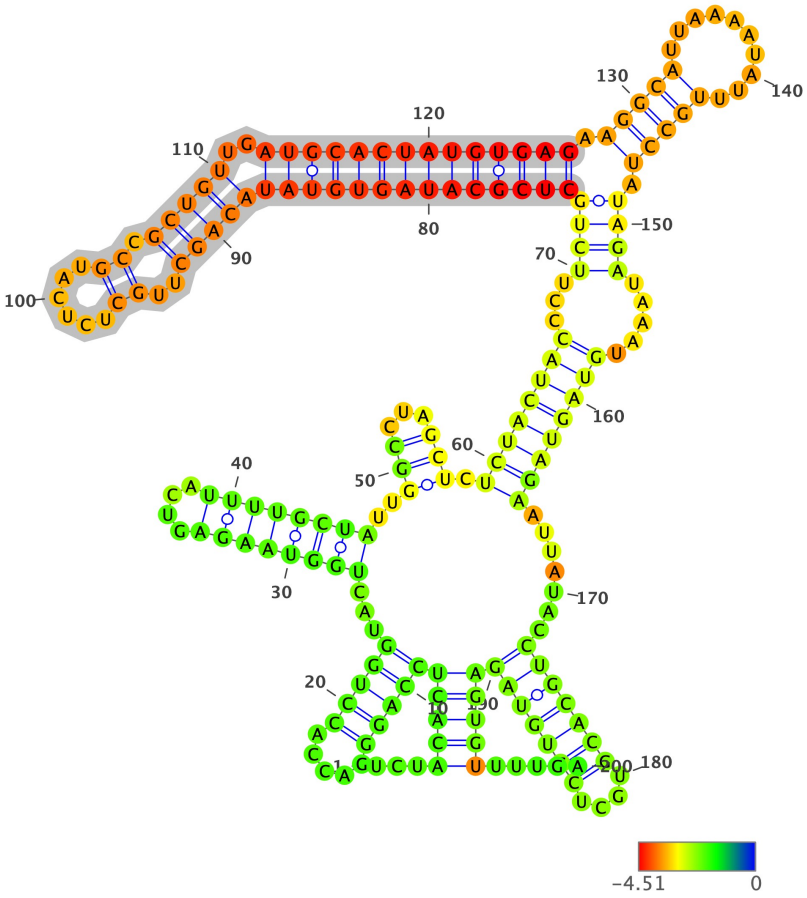
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17141 to 17193 (nt 74 to 126)

```
5'-CTCGCATAGTGTATACAGCTTGCTCTCATGCCGCUGUTGAUGCACUAUGUGAG-3'
5'-(((((((((((((((((((..((......)).)))))..))))))))))))))-3'
Motif MFE = -27.7; z-score = -5.78; 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 = -5.36; 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(+)

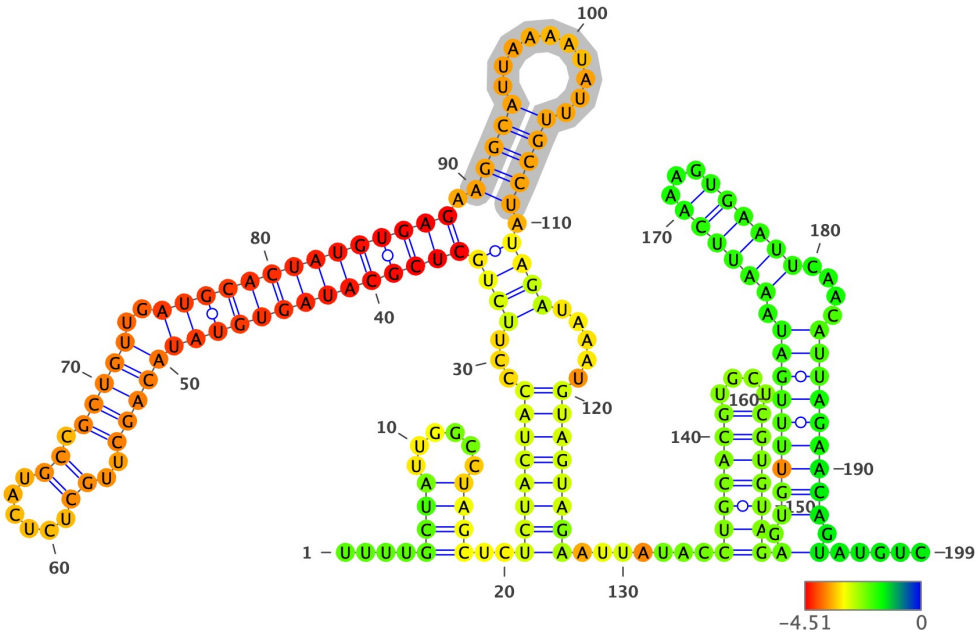
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 291 from nt 17195 to 17214 (nt 90 to 109)

```
5'-AGGCATTAAAATATTUGCCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.1; z-score = -5.15; 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 = -5.28; 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(+)

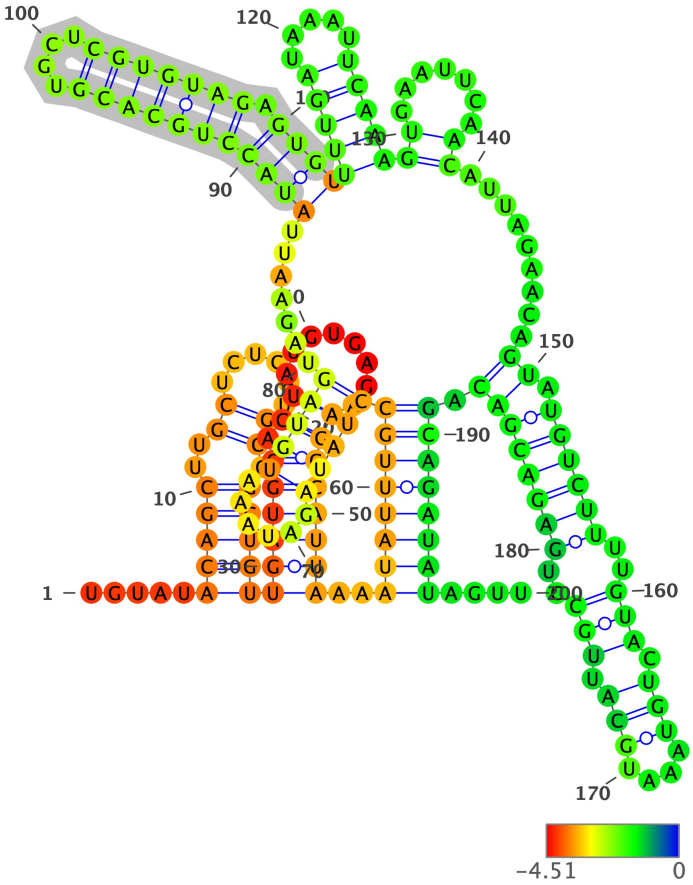
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 292 from nt 17237 to 17261 (nt 88 to 112)

```
5'-TACCTGCACGTGCTCGUGUAGAGUG-3'
5'-((((((((((....)))))))).)))-3'
Motif MFE = -10.5; z-score = -3.38; 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 17150 to 17349 (motif highlighted in silver):

```
5'-UGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGU
GUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUU-3
5'-.....((((((..((......)).))))))((((((.((........))))))))..((((((((((((((.....)))))).......((((((((((....))))))))).))
))))))(.....))))))((.......)).........((.((((((..(((.(((....))).))).))..)))))))).)))))))).....-3'
MFE = -48.0; z-score = -2.44; ED = 61.04
```

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(+)

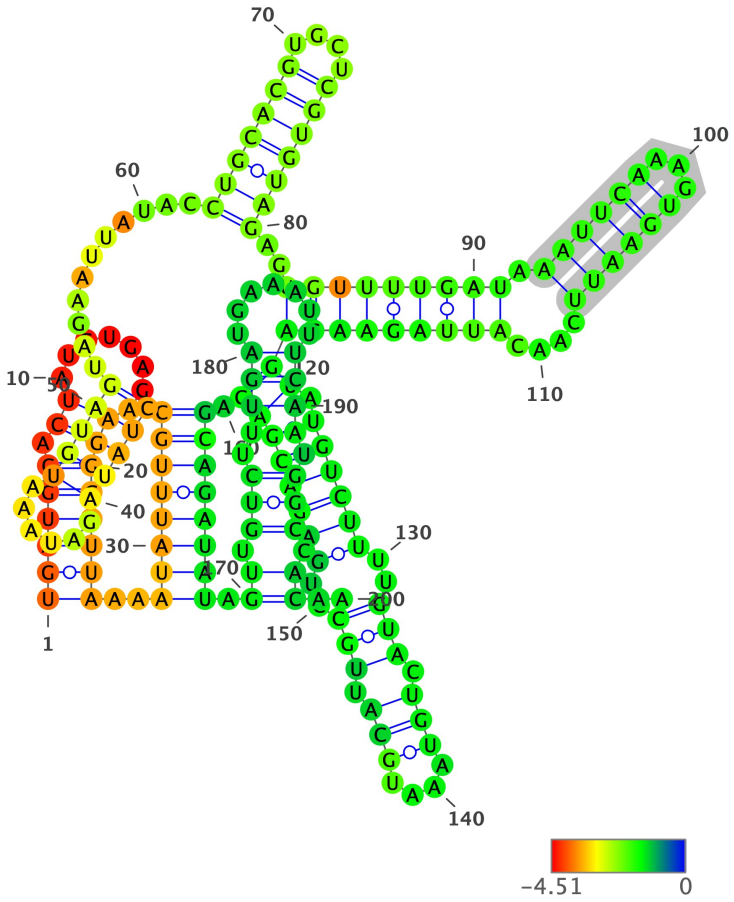
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 293 from nt 17270 to 17284 (nt 93 to 107)

```
5'-AATTCAAAGTGAAUU-3'
5'-(((((.....)))))-3'
Motif MFE = -1.0; z-score = -2.86; 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 17178 to 17377 (motif highlighted in silver):

```
5'-UGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAAC
AUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAA-3
5'-((((((.((........))))))))..(((((((((((((.....)))))..........(((((((....)))))))..(((((((((.((((((...))))))....
))))))))))((.((((((..(((.(((....))).))).))))))))).))))))))).((.(((.((((.......)))).))).))..-3'
MFE = -48.6; z-score = -2.48; ED = 43.79
```

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(+)

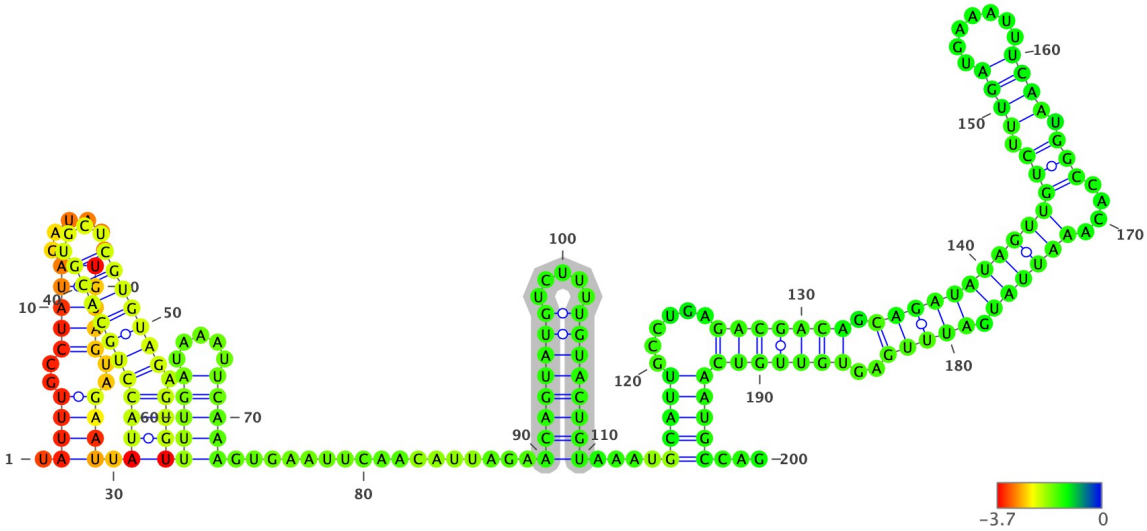
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 294 from nt 17295 to 17315 (nt 90 to 110)

```
5'-ACAGTATGTCTTTUGUACUGU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -5.8; z-score = -4.03; 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 = -1.84; ED = 31.2
```

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(+)

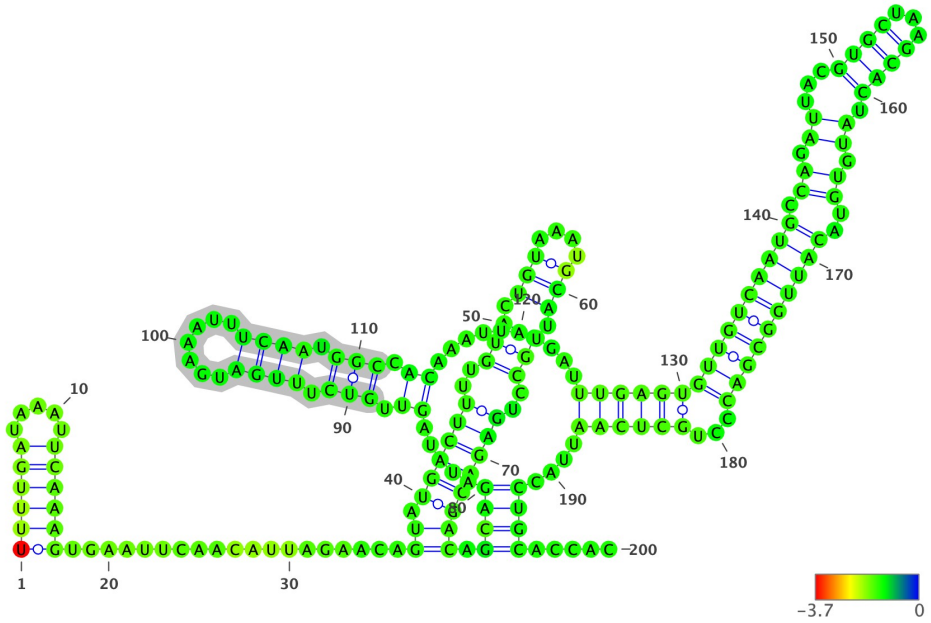
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17350 to 17372 (nt 89 to 111)

```
5'-GTCTTTGATGAAATTUCAATGGC-3'
5'-(((.((((.......)))).)))-3'
Motif MFE = -3.8; z-score = -1.56; 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 17262 to 17461 (motif highlighted in silver):

```
5'-UUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGC
CACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCAC-3
5'-((((((.....))))))...................((.((((((..(((.(((....))).)))..)))))))).((((.....((.(((.((((.......)))).)))
.)).........((((((((((((((((.((.((...((((...)))).)).)).)..))))))))))...))))))....))))).....-3'
MFE = -44.8; z-score = -1.22; ED = 34.07
```

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(+)

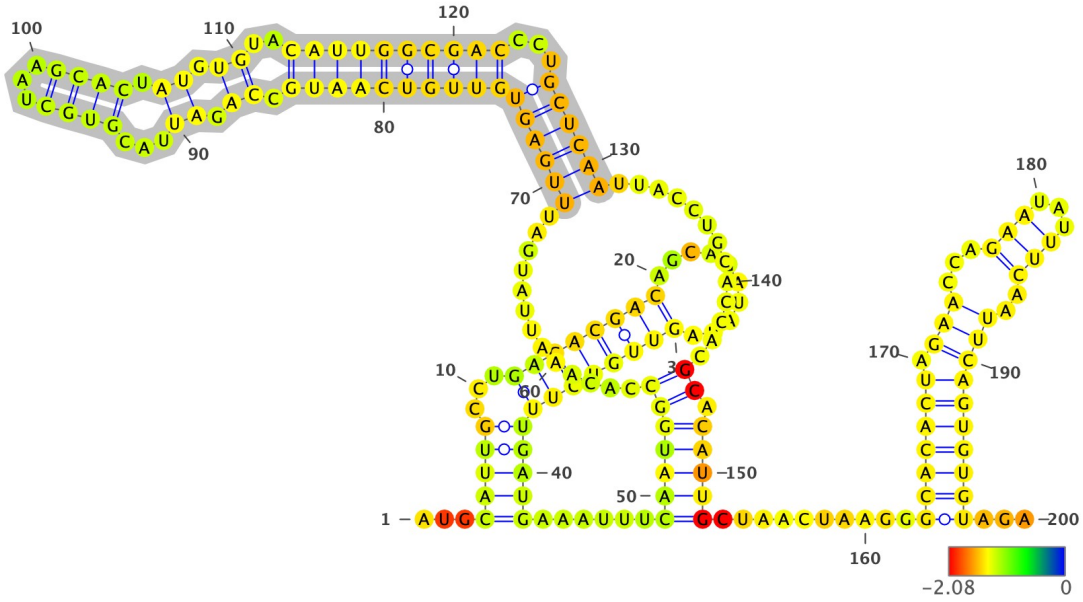
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 296 from nt 17386 to 17448 (nt 69 to 131)

```
5'-TTGAGTGTTGTCAATGCCAGATTACGTGCTAAGCACTAUGUGTACAUUGGCGACCCTGCUCAA-3'
5'-(((((((((((((((.((.((...((((...)))).)).)).)).)))))))))))...)))))))-3'
Motif MFE = -21.9; z-score = -3.56; 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 = -0.99; ED = 34.25
```

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(+)

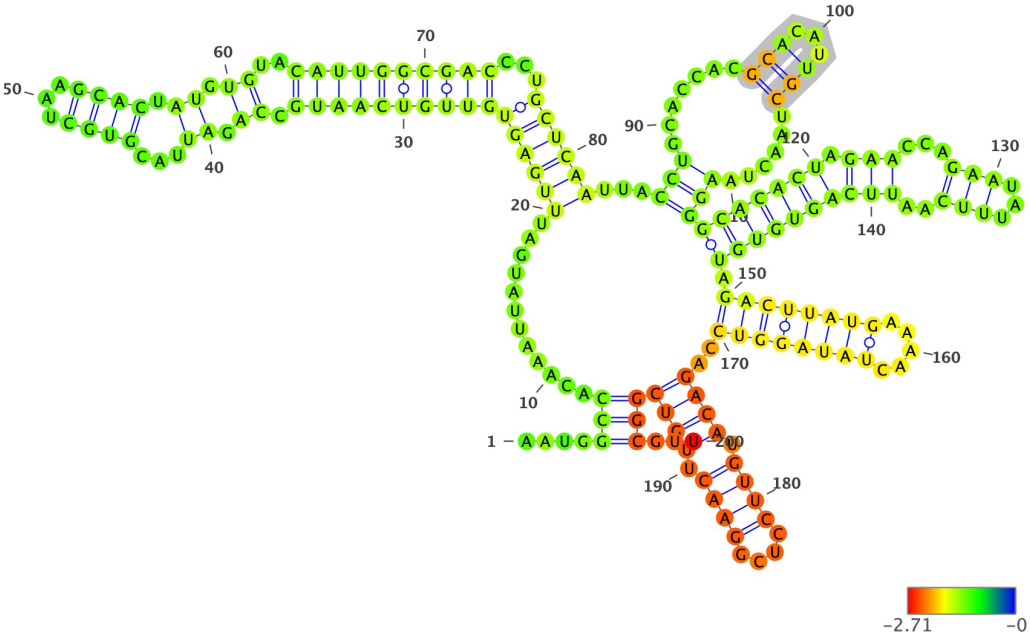
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17462 to 17470 (nt 96 to 104)

```
5'-GCACATTGC-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 = -3.2; 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(+)

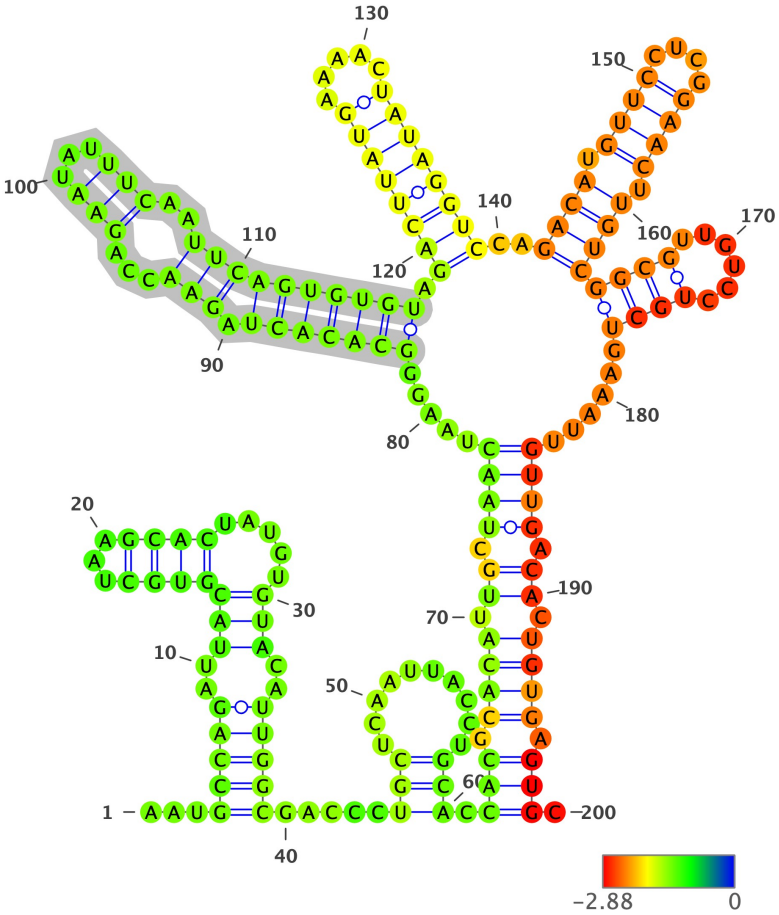
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 298 from nt 17480 to 17514 (nt 83 to 117)

```
5'-GCACACTAGAACCAGAATATUUCAAUUCAGUGUGU-3'
5'-(((((((.(((...(((...))).)))))))))-3'
Motif MFE = -8.4; z-score = -2.57; 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 = -0.95; ED = 40.77
```

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(+)

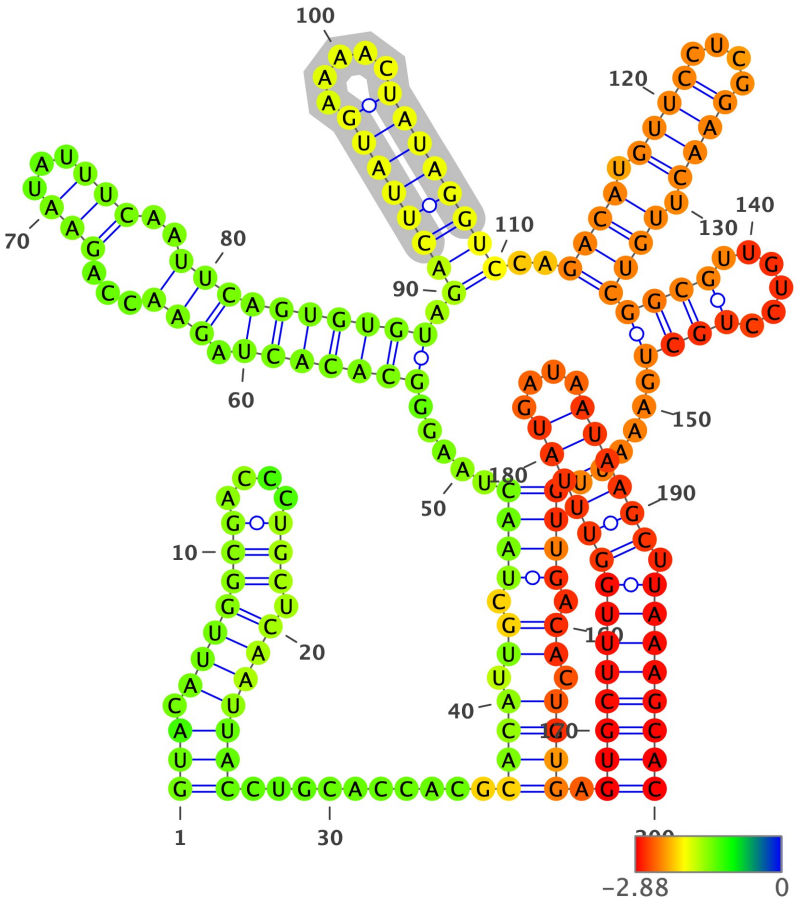
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17518 to 17534 (nt 92 to 108)

```
5'-CTTATGAAAACUAUAGG-3'
5'-((((((.....))))))-3'
Motif MFE = -0.9; z-score = -0.93; 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 17427 to 17626 (motif highlighted in silver):

```
5'-GUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCC
AGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCAC-3
5'-(((.(((((((....))).)))))))..........((((.((.((((.....(((((((.(((...(((...))).)))))))))).((((((((.....))))))))).
.((((.((((....)))).))))((((......))))......)))).)).)))).((((((((((((((....)))))).))))))))-3'
MFE = -53.7; z-score = -2.35; ED = 34.33
```

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(+)

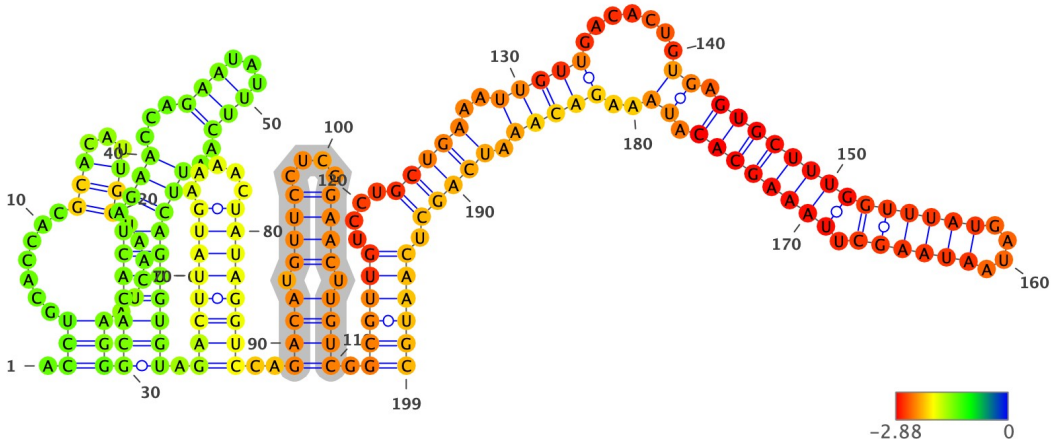
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 300 from nt 17539 to 17560 (nt 89 to 110)

```
5'-GACATGTTCCTCGGAACTUGUC-3'
5'-((((.((((....)))).))))-3'
Motif MFE = -8.9; z-score = -3.3; ED = 0.16
```



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 17451 to 17649 (motif highlighted in silver):

```
5'-ACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCG
GCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGC-3
5'-.(((.......(((...)))......)))(((((((.(((...(((...)))..)))))))))).((((((((.....))))))))..((((.((((....)))).)))).
((((((....(((((..(((((.......((.((((((((((((((....)))))).))))))))).))..))))).))))).))))))-3'
MFE = -56.6; z-score = -3.2; ED = 16.86
```

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(+)

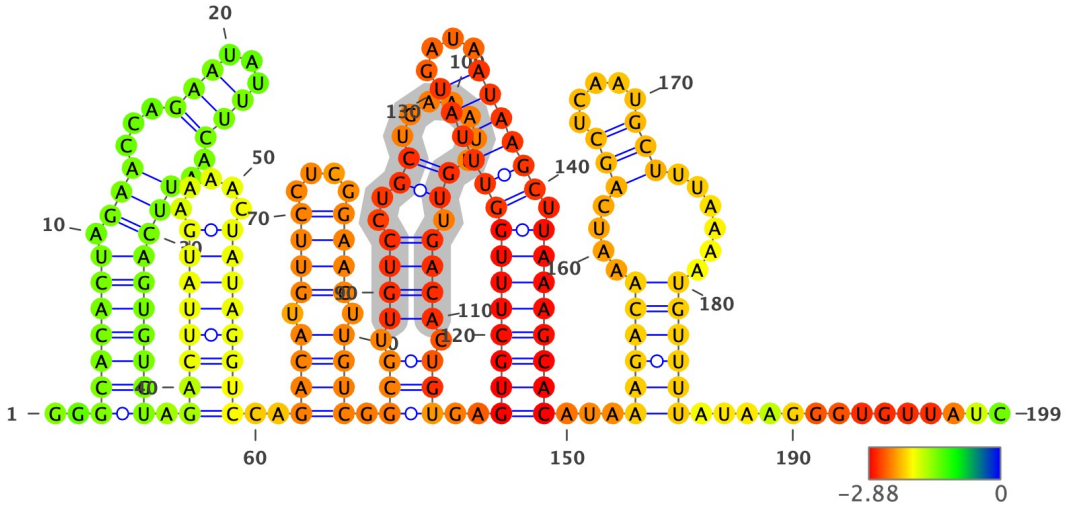
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 301 from nt 17566 to 17587 (nt 89 to 110)

```
5'-TGTCCTGCTGAAATTGUTGACA-3'
5'-((((..((.......)).))))-3'
Motif MFE = -2.6; z-score = -0.61; 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 = -2.73; 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(+)

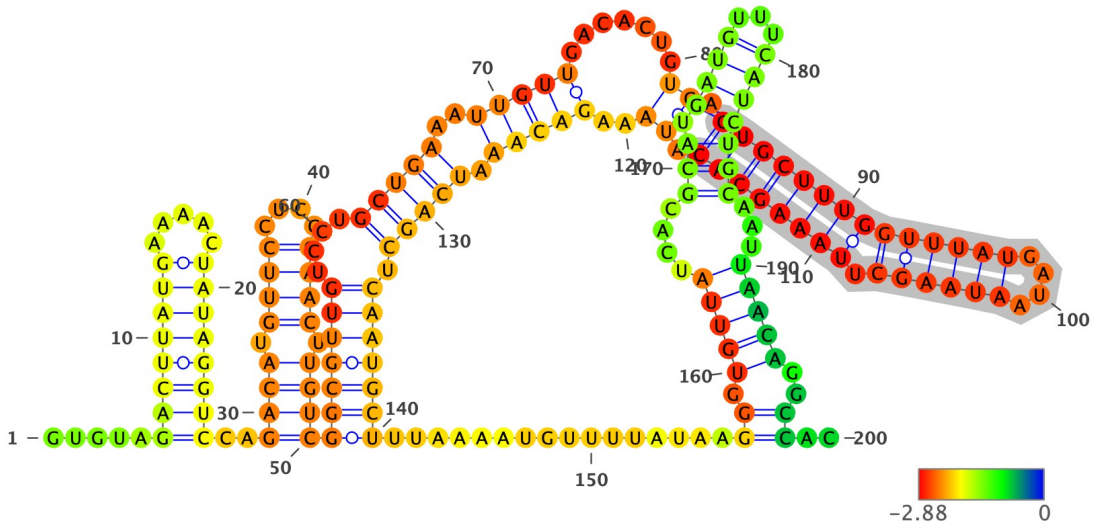
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 302 from nt 17594 to 17626 (nt 84 to 116)

```
5'-GTGCTTTGGTTTATGATAAUAAGCTUAAAGCAC-3'
5'-(((((((((((((((....)))))).))))))))-3'
Motif MFE = -13.2; z-score = -4.76; 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 = -3.05; ED = 24.06
```

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(+)

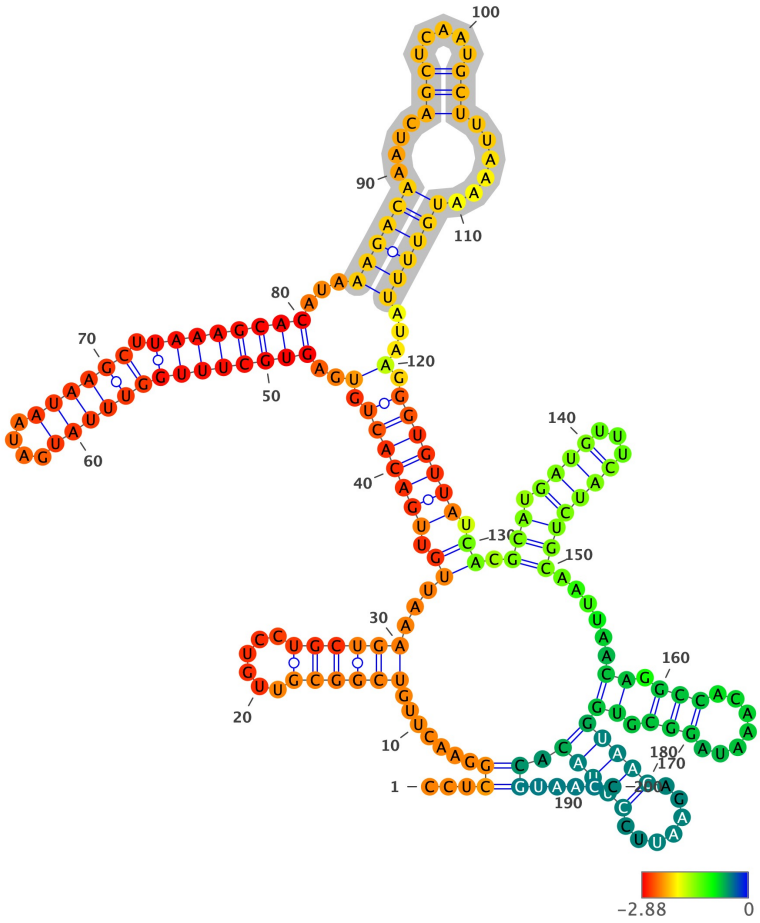
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17630 to 17662 (nt 84 to 116)

```
5'-AAGACAAATCAGCTCAATGCUTTAAAAUGUUUU-3'
5'-((((((....(((.....))).....))))))-3'
Motif MFE = -3.4; z-score = -1.29; 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 17547 to 17746 (motif highlighted in silver):

```
5'-CCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAU
GUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACC-3
5'-...((.......((((((.....))))))...((.(((((((.(..(((((((((((((((....)))))))).)))))))))...((((((....(((.....)))).....)
))))))...).)))))))..)).(((.(((((...)))))))......((.(((.......))).))(((((.......))))))..))......-3'
MFE = -49.1; z-score = -1.85; ED = 34.04
```

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(+)

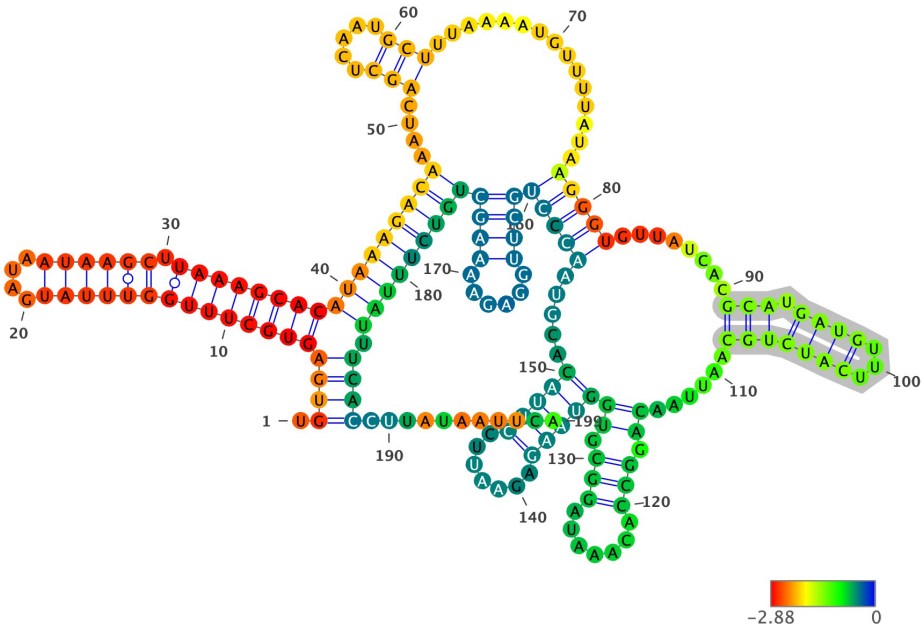
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 304 from nt 17679 to 17696 (nt 91 to 108)

```
5'-GCATGATGTTTCAUCUGC-3'
5'-(((.(((((...)))))))-3'
Motif MFE = -4.0; z-score = -2.49; ED = 1.3
```



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 17589 to 17787 (motif highlighted in silver):

```
5'-UGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAU
UAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCA-3
5'-.(((((((((((((((((....)))))).)))))))))(((((((((....(((.....)))).............(((((........(((.((((...)))))))...
...((.(((.......))).))(((((.......))))).....)))))(((((......)))))))))))).))))...........-3'
MFE = -52.3; z-score = -3.38; ED = 18.62
```

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(+)

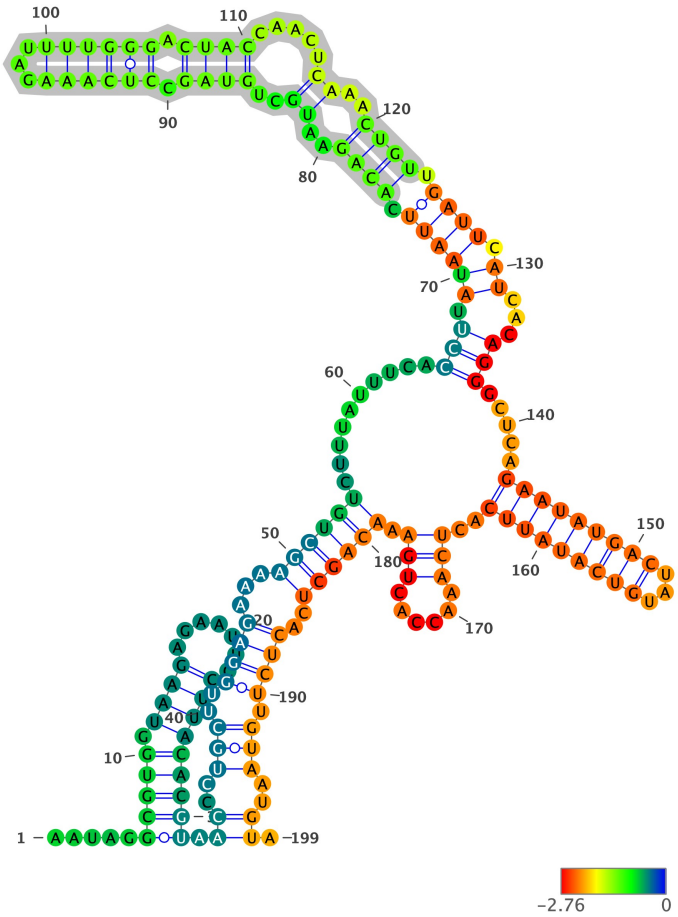
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 305 from nt 17787 to 17834 (nt 76 to 123)

```
5'-ACAGAATGCTGTAGCCTCAAAGATUUUGGGACUACCAACTCAAACUGU-3'
5'-((((......((((.(((((((...)))))).)))).........))))-3'
Motif MFE = -8.7; z-score = -1.43; 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 17712 to 17910 (motif highlighted in silver):

```
5'-AAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACC
AACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUA-3
5'-.....(((((.((((.......)))))))).((..(((..((((...((((((..........(((.((((((.((((..((..((((.((((((...)))))).)))).
....))..)))).)))).))...))).....((((((((...)))))))))..(((......))).))))))..)))).)))..)).-3'
MFE = -42.0; z-score = -1.65; 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(+)

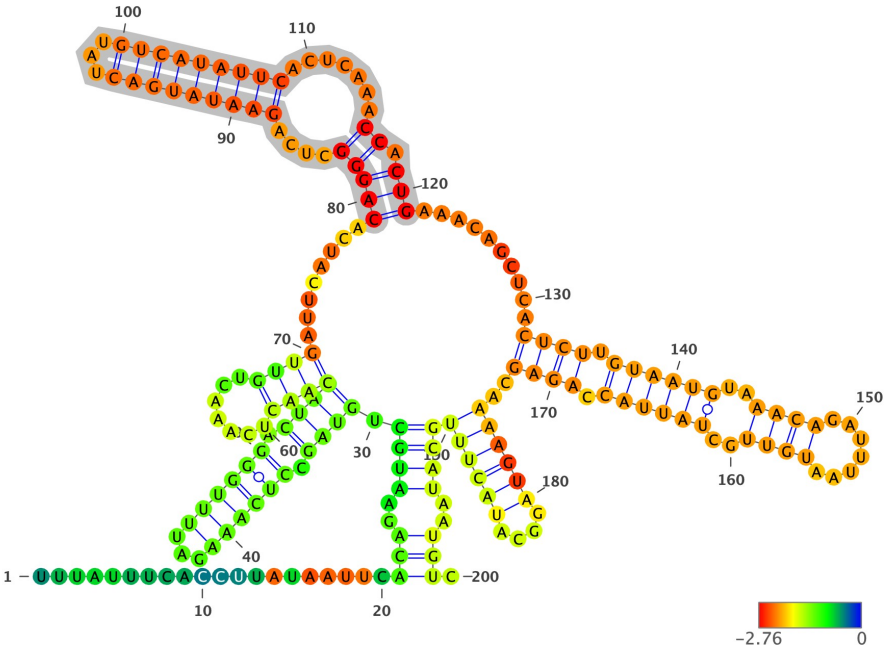
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 306 from nt 17845 to 17887 (nt 79 to 121)

```
5'-CAGGGCTCAGAATATGACTATGTCAUAUUCACTCAAACCACUG-3'
5'-(((((....((((((((((...))))))))))).......)).)))-3'
Motif MFE = -10.7; z-score = -3.07; ED = 3.93
```



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 17767 to 17966 (motif highlighted in silver):

```
5'-UUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACU
CAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUC-3
5'-.....(((..((((.((((.((((((...)))))).))))((((.......)))).....((((.....(((((((((...)))))))))...
....)).)))..........((((.((((((..((((.......))))..))))))).)))))..((((((....))))))))))..))).-3'
MFE = -43.3; z-score = -3.24; ED = 14.37
```

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(+)

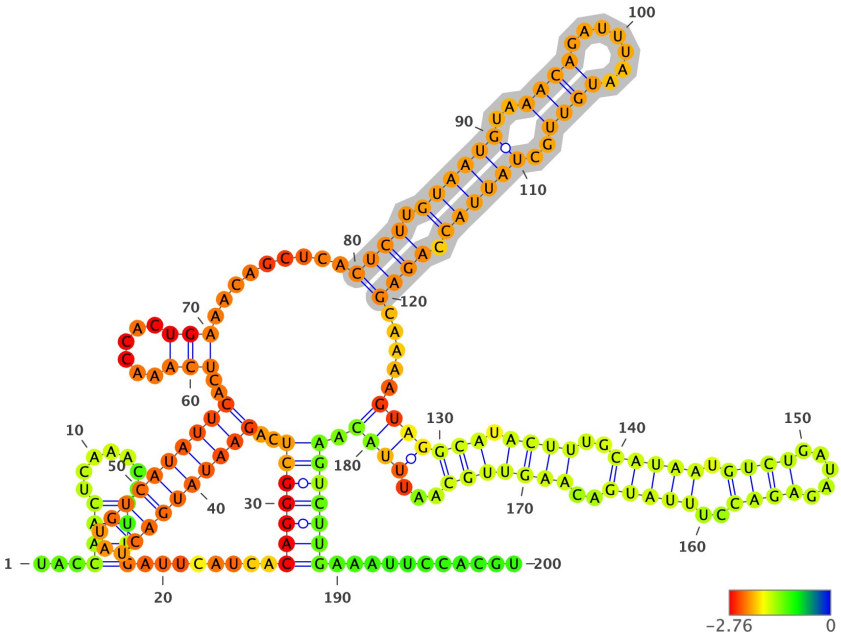
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17898 to 17938 (nt 80 to 120)

```
5'-CTCTTGTAATGTAAACAGATTTAAUGUUGCUAUUACCAGAG-3'
5'-((((.((((((..((((.......))))..)))))).))))-3'
Motif MFE = -9.7; z-score = -2.39; 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 = -44.8; z-score = -3.54; ED = 19.79
```

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(+)

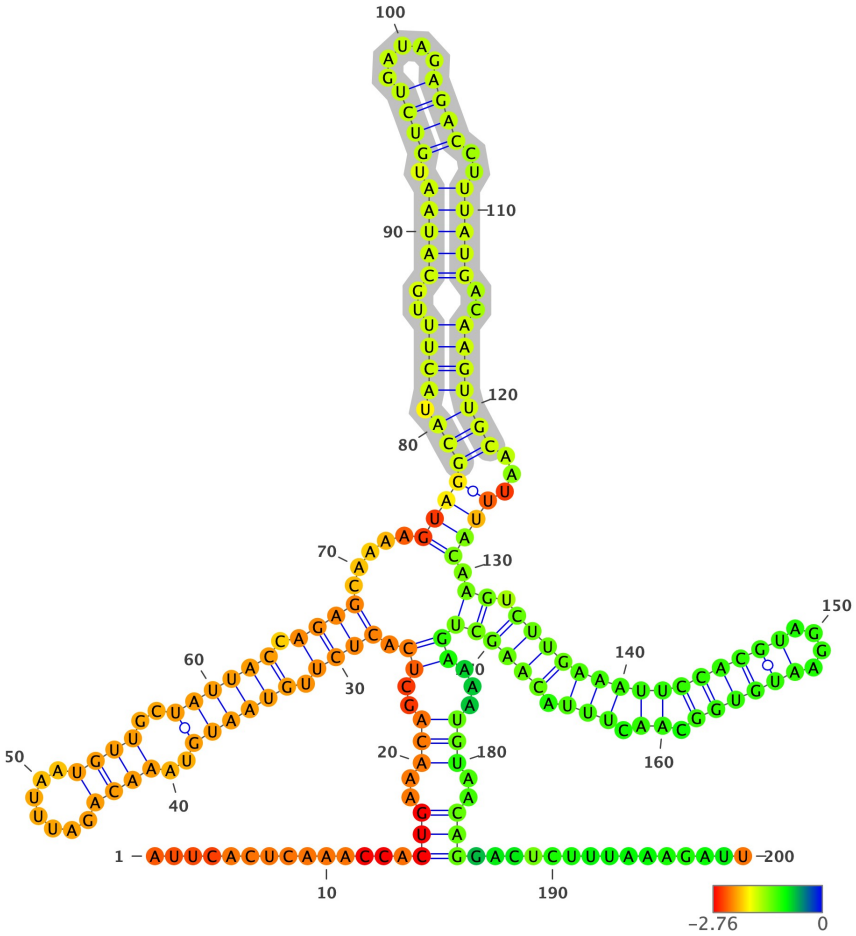
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 308 from nt 17948 to 17992 (nt 78 to 122)

```
5'-GCATACTTTGCATAATGTCTGATAGAGACCTUUAUGACAAGUUGC-3'
5'-(((.(((((..((((((.((((.....)))))..))))))..)))))))-3'
Motif MFE = -12.2; z-score = -2.59; 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 = -1.47; 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(+)

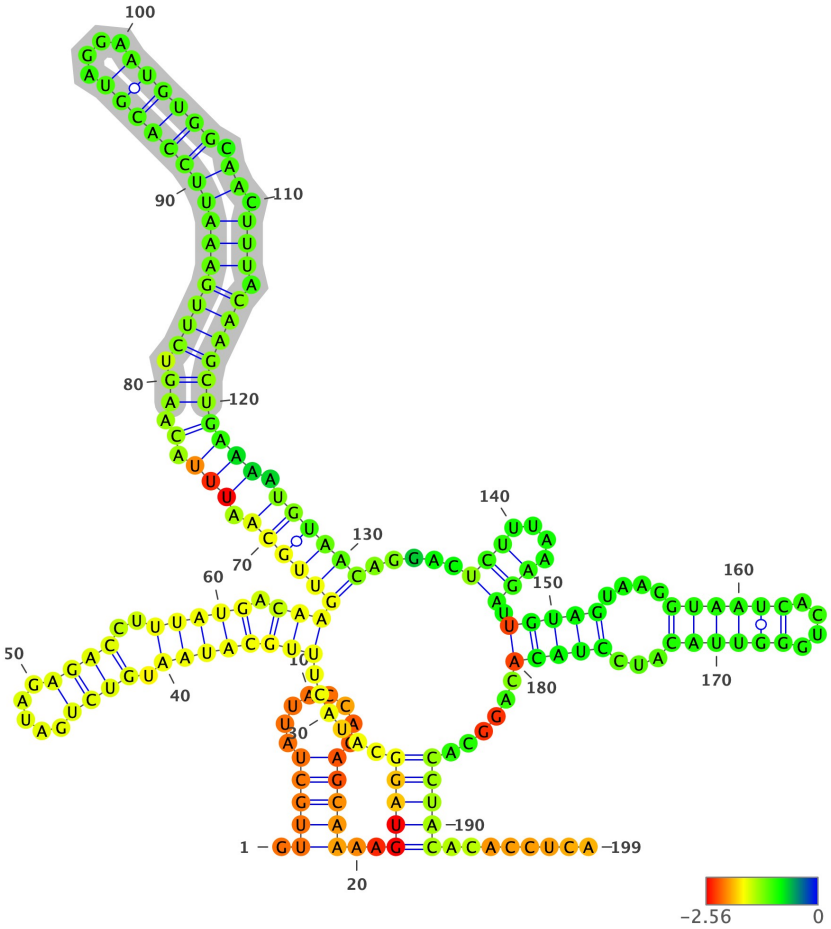
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 309 from nt 18001 to 18042 (nt 79 to 120)

```
5'-AGTCTTGAAATTCCACGTAGGAAUGUGGCAACTTTACAAGCU-3'
5'-((.((((.....((((((....))))))........))))))-3'
Motif MFE = -8.8; z-score = -1.49; ED = 4.59
```



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 17923 to 18121 (motif highlighted in silver):

```
5'-GUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACU
UUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCA-3
5'-.(((((........)))))..(((((......((((((((.((((.....))))..))))).)))((((((.(((.(.((.((((((((((((((....))))))).)).)
)).))))))))))).))))))).....(((....))).(((((....((((((....))))))...)))))......)))))........-3'
MFE = -44.1; z-score = -1.5; ED = 41.51
```

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(+)

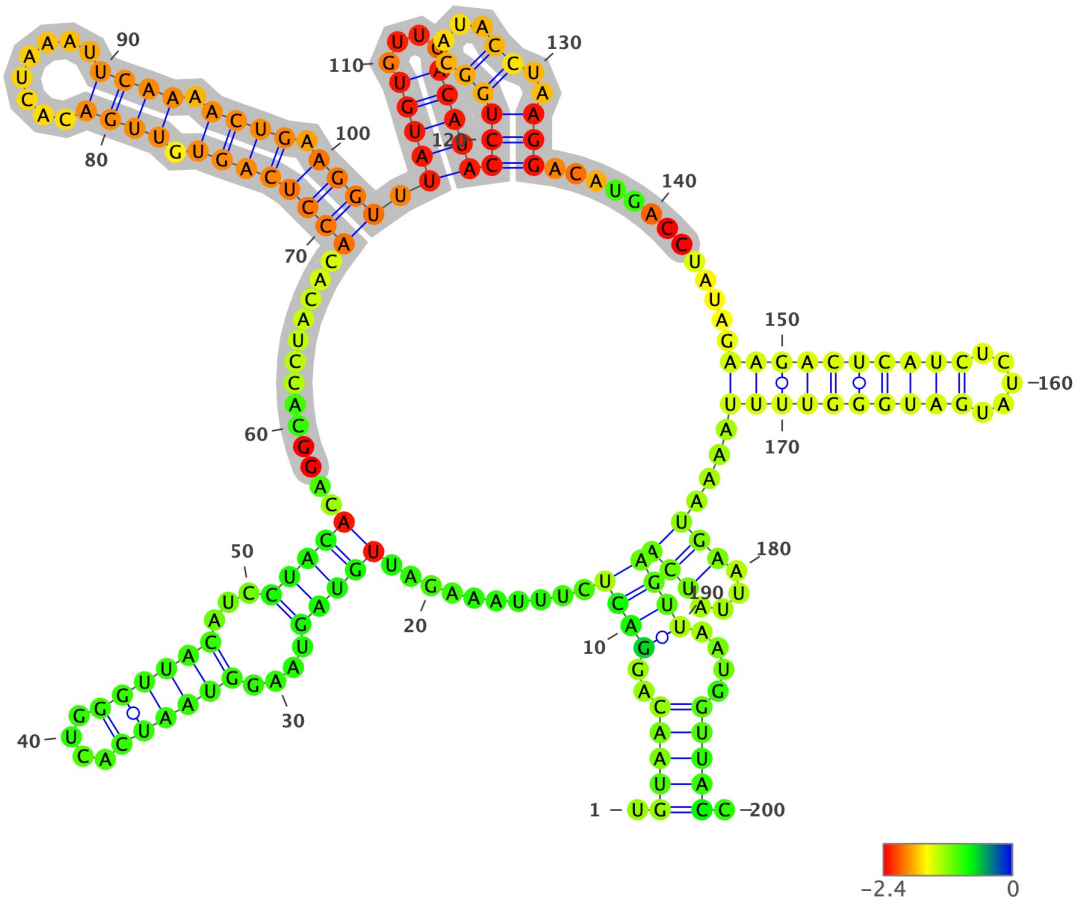
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 18105 to 18189 (nt 58 to 142)

```
5'-GGCACCTACACACCTCAGTGTTGACACTAAATUCAAAACUGAAGGUTTATGTGTTGACAUACCTGGCATACCTAAGGACATGACC-3'
5'-((.........(((((((.((((........)))).)))))).)))).(((((....)))))(((.........))).....))-3'
Motif MFE = -16.9; z-score = -1.01; ED = 17.67
```



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 18048 to 18247 (motif highlighted in silver):

```
5'-UGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGU
UGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACC-3
5'-.((((((..((((..........((((....((((((....))))))...))))).............(((((((.((((........)))).)))))).)))).((((((..
..)))))(((((....))..))).............((((((((((.....))))))))))....(((....)))))))....))))).-3'
MFE = -43.4; z-score = -2.66; ED = 13.96
```

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(+)

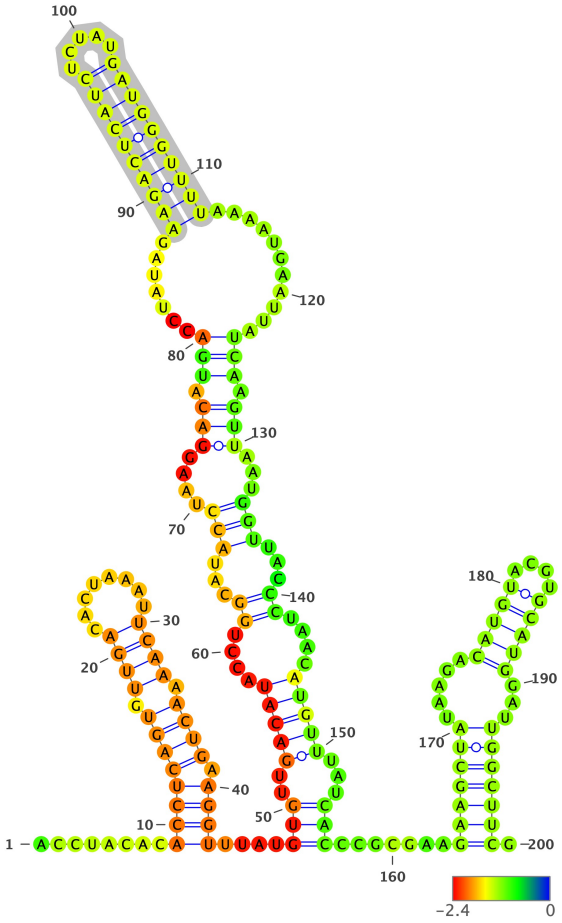
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 18195 to 18219 (nt 88 to 112)

```
5'-AAGACTCATCTCTATGAUGGGUUUU-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -10.1; z-score = -5.27; 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 = -2.02; 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(+)

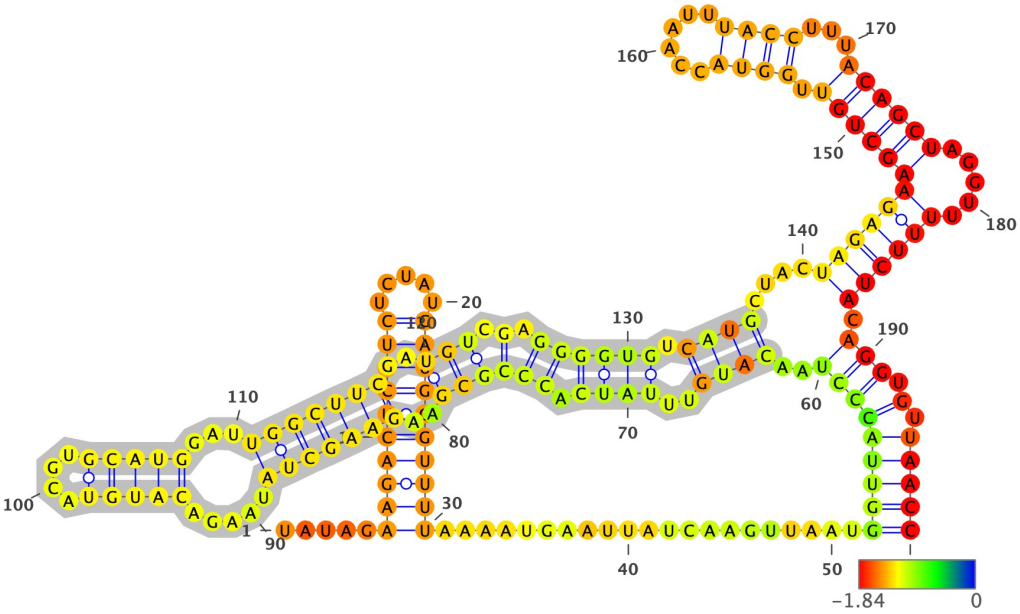
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 312 from nt 18252 to 18325 (nt 63 to 136)

```
5'-CATGTTTATCACCCGCGAAGAAGCTATAAGACATGTACGTGCAUGGATUGGCUUCGATGUCGAGGGGTGTCATG-3'
5'-(.(...(..(.((.(....(((((((.....(((((....)))))...)))))))....)...)))..)..).)-3'
Motif MFE = -23.1; z-score = -2.25; ED = 11.89
```



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 18190 to 18388 (motif highlighted in silver):

```
5'-UAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUU
GGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACC-3
5'-.....(((((((((((.....)))))))))).....................(((((((((..((((..((((.((((((..(((((((.....(((((....)))))...)
))))))..)))).).))))))).))))....((((((((((((.((((......))))...))))))).....))))))).))).).)))))-3'
MFE = -51.3; z-score = -2.16; ED = 16.56
```

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(+)

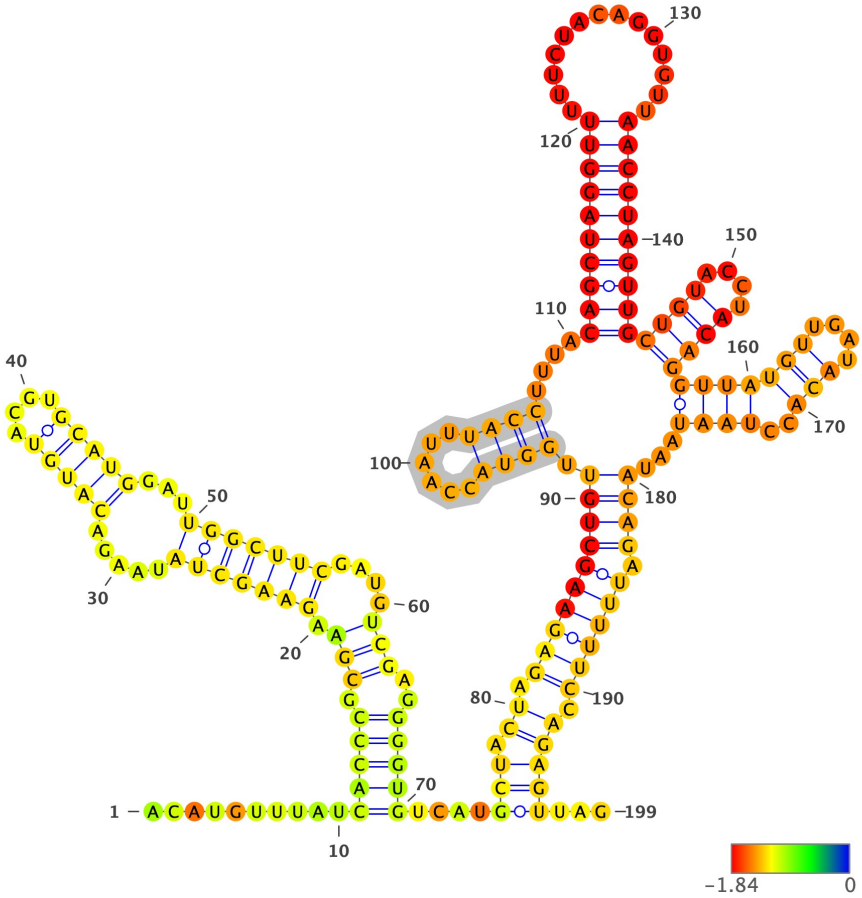
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 18343 to 18356 (nt 93 to 106)

```
5'-GGTACCAATTUACC-3'
5'-((((......))))-3'
Motif MFE = -1.6; z-score = -7.46; 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 18251 to 18449 (motif highlighted in silver):

```
5'-ACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUAC
AGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAG-3
5'-..........(((((.(((.(((((((.....(((((....)))))...)))))))....)))..)))))....(((.((.((((((((((.((((......))))....(
((((((((.............))))))))))((((....))))(((((((....)))..))))...)))).))))))).)))))...-3'
MFE = -50.6; z-score = -1.18; ED = 40.18
```

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(+)

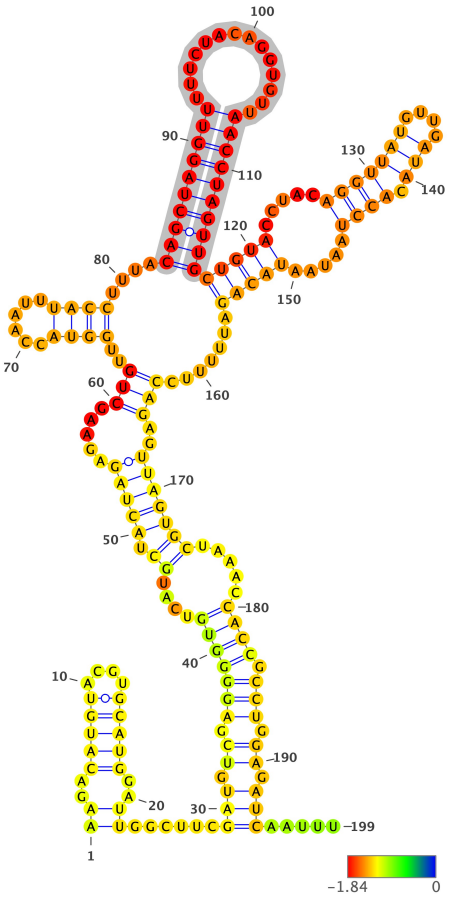
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 18361 to 18394 (nt 83 to 116)

```
5'-CAGCTAGGTTTTTCTACAGGTGTTAACCUAGUUG-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -11.1; z-score = -3.56; 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 18279 to 18477 (motif highlighted in silver):

```
5'-AAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCU
AGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUU-3
5'-((..(((((....)))))..)).....(((.((.(((((((....((.(((((.....(((..((((......))))....((((((((((.............)))))
)))))(((((.....(((((((....))).))))).....)))))).......)))..)))))))).....)))).))).)).)))).....-3'
MFE = -51.8; z-score = -1.32; 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(+)

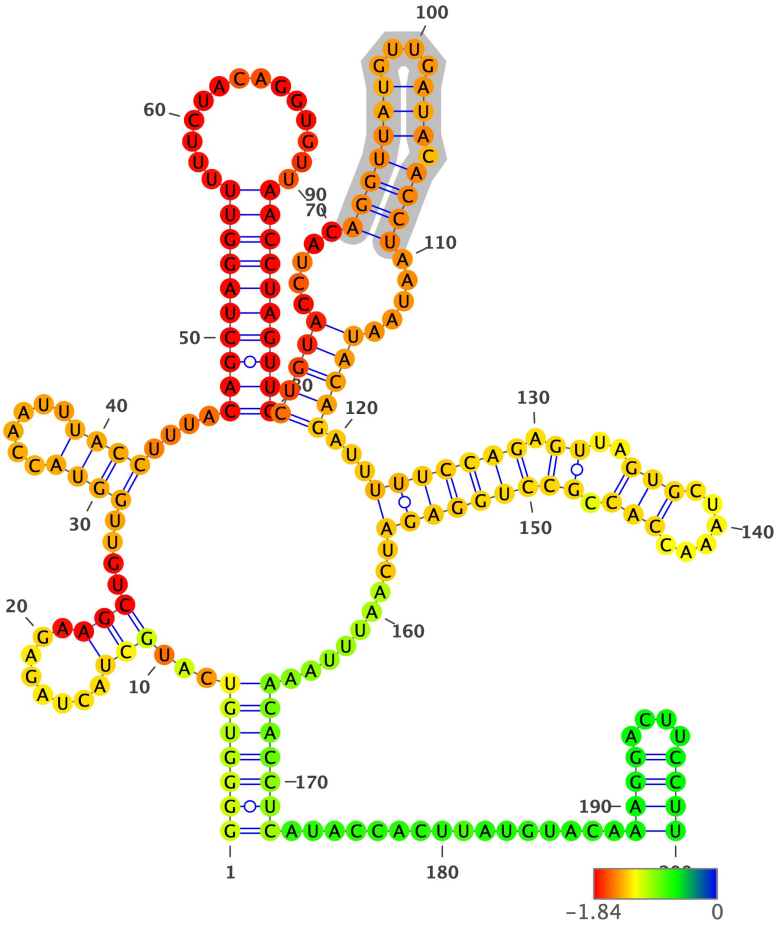
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 315 from nt 18405 to 18423 (nt 91 to 109)

```
5'-AGGTTATGTTGATACACCU-3'
5'-(((((........).))))-3'
Motif MFE = -2.5; z-score = -1.45; 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 18315 to 18514 (motif highlighted in silver):

```
5'-GGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAA
UAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUU-3
5'-(((((((...(((........))))....((((......))))....((((((((((.............))))))))))(((((.....(((((((....))).)))))..
...))))))...(((((((.((..(((......))).)))))))))........)))))))..............((((....))))-3'
MFE = -48.9; z-score = -2.3; ED = 21.28
```

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(+)

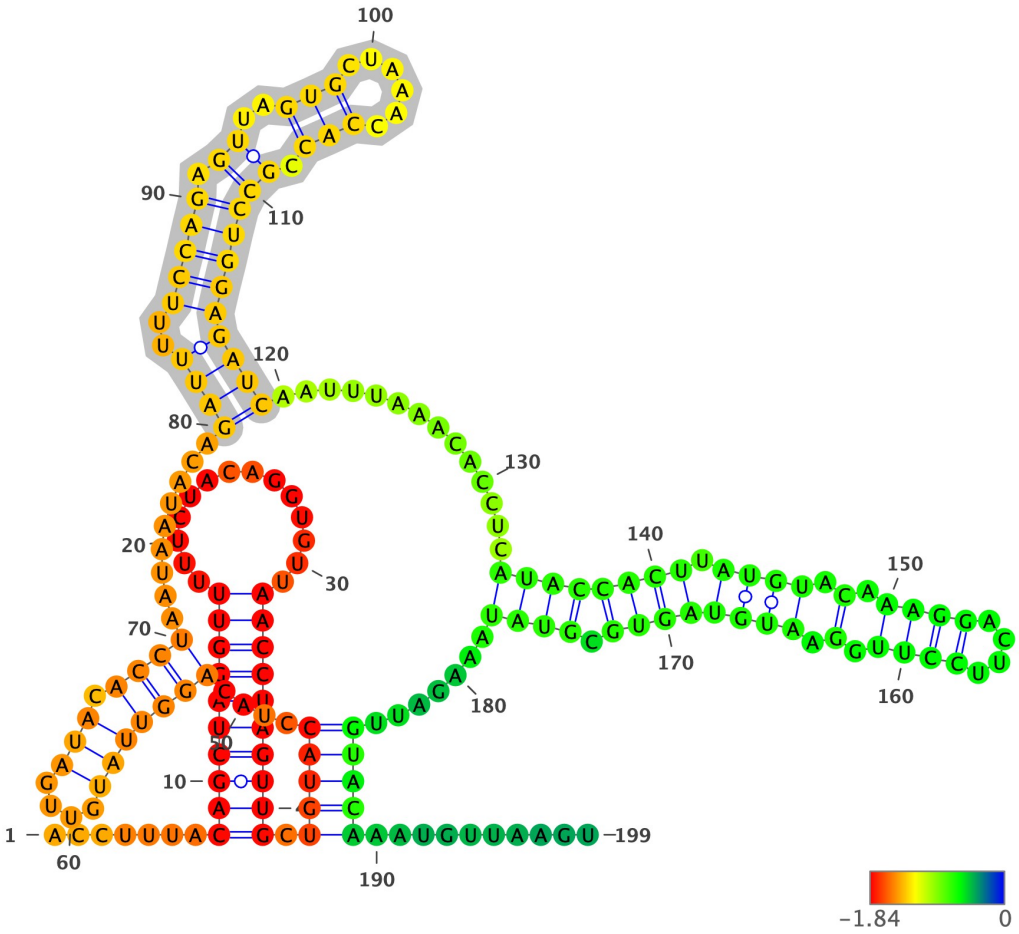
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 18433 to 18472 (nt 80 to 119)

```
5'-GATTTTTCCAGAGTTAGTGCTAAACCACCGCCUGGAGAUC-3'
5'-(((((..((((((.((..(((.....))).))))))))))))-3'
Motif MFE = -10.7; z-score = -2.06; 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 18354 to 18552 (motif highlighted in silver):

```
5'-ACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCC
UGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUUGGAAUGUAGUGCGUAUAAAGAUUGUACAAAUGUUAAGU-3
5'-.......((((((((((.............))))))))))..(((((....(((((((....))).))))).........((((..((((((.((..(((.....))).)))
))))))))).............(((((((((.((((.(.((((....)))).).)))))))))..))))......)))))..........-3'
MFE = -40.5; z-score = -1.38; ED = 31.24
```

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(+)

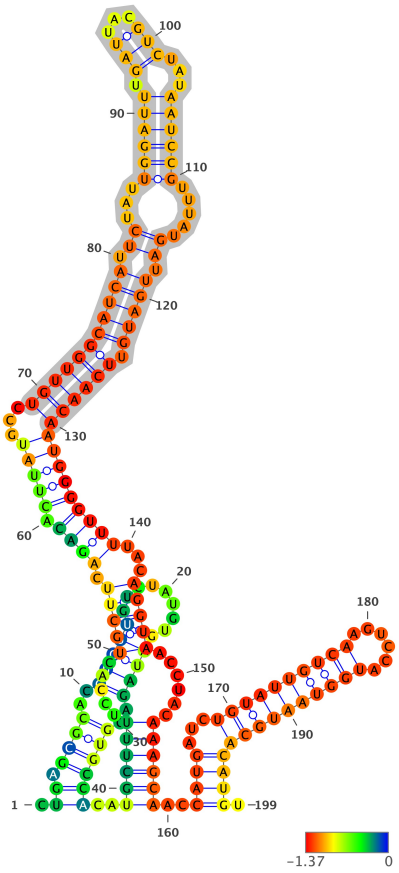
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 18715 to 18776 (nt 69 to 130)

```
5'-TGTTGGCATCATTCTATTGGATTTGATTACGUCTATAAUCCGTTTATGATUGAUGTUCAACA-3'
5'-(((((((((((.((...((((((.(((...)))...)))))).....)).)))))).))))))-3'
Motif MFE = -16.9; z-score = -3.8; ED = 5.44
```



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 18647 to 18845 (motif highlighted in silver):

```
5'-CUGAGCGCACCUGUUGUCUAUGUGAUAGACGUGCCACAUGCUUUUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGU
UUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGU-3
5'-.((.((((..(((((.........)))))..))))))..((((((.....(((((.((((.(((((...((((((((((((.((...((((((.(((...)))...)))))).
....)).)))))).))))))))))))))...)))))).....))))))..((((...((((((((((.....))))))))))))))).-3'
MFE = -46.7; z-score = -0.99; ED = 51.13
```

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(+)

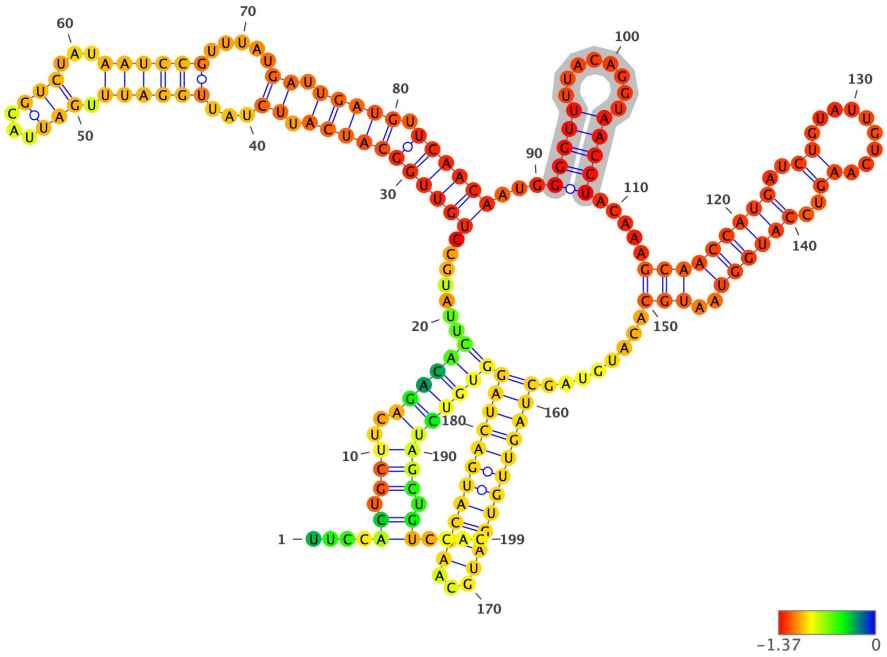
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 18780 to 18797 (nt 91 to 108)

```
5'-GGGTTTTACAGGTAACCU-3'
5'-(((((........)))))-3'
Motif MFE = -3.4; z-score = -2.17; 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 18690 to 18888 (motif highlighted in silver):

```
5'-UUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACA
AAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCAC-3
5'-....((.(((..((((((.......((((((((((.((...((((((.(((...)))...))))))).....)).)))))).))))))...(((((........)))))...
..((((((((..((.........))..))))))..)))........((((((((((...)))))))))))))))))))).))....-3'
MFE = -55.4; z-score = -3.11; ED = 16.59
```

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(+)

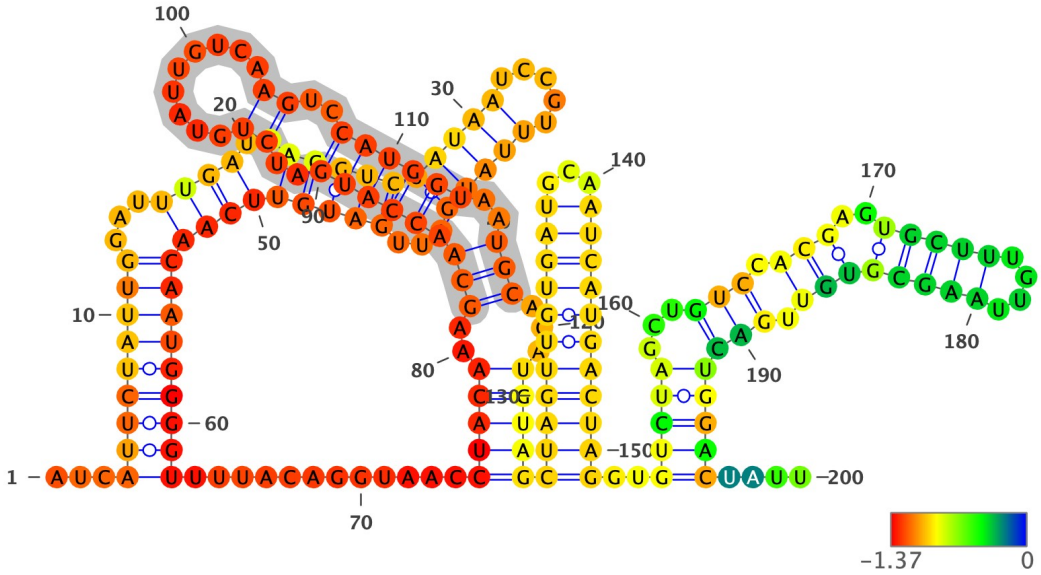
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 18803 to 18839 (nt 82 to 118)

```
5'-GCAACCATGATCTGTATTGTCAAGTCCAUGGUAAUGC-3'
5'-((((((((((..((.........))..)))))))..)))-3'
Motif MFE = -9.5; z-score = -1.81; 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 = -1.24; 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(+)

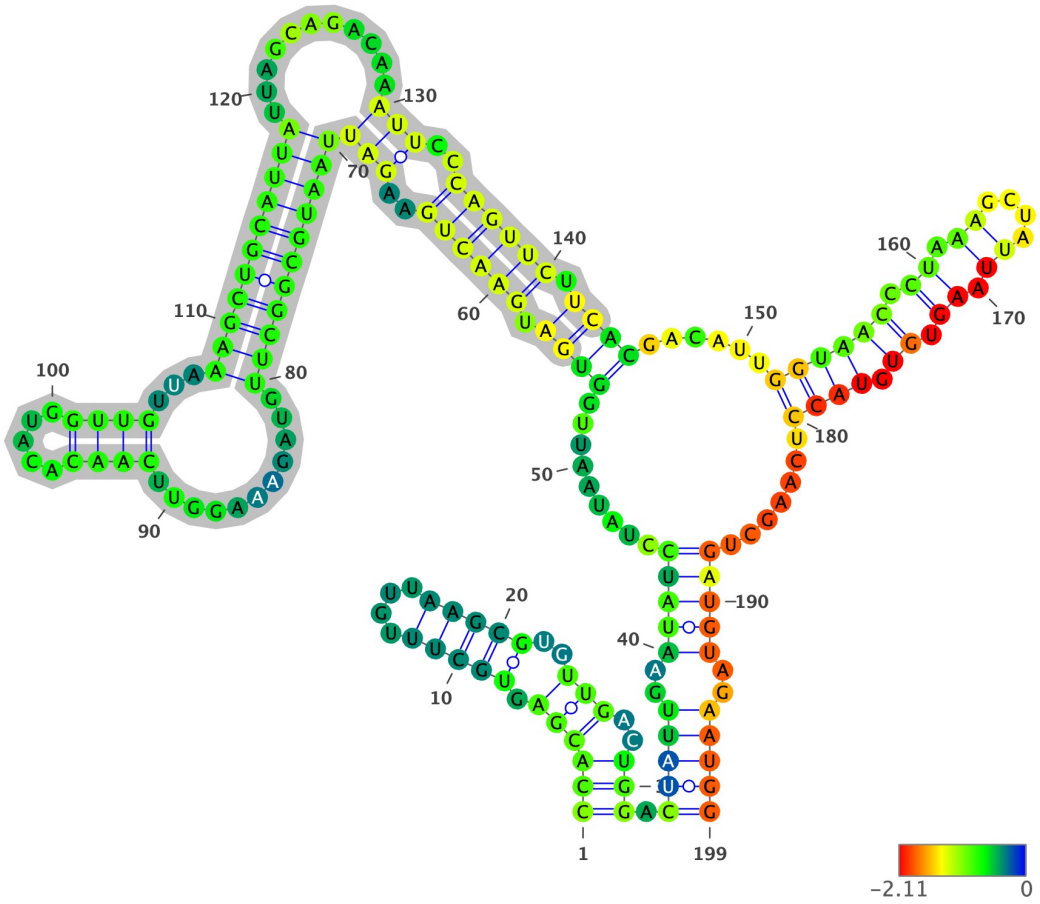
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 320 from nt 18940 to 19027 (nt 56 to 143)

```
5'-GATGAACTGAAGATTAATGCGGCTTGTAGAAAGGTTCAACACATGGUUGTTAAAGCUGCAUUATTAGCAGACAAAUUCCCAGUUCTUC-3'
5'-((.((((((..((((.............................................)...........)))..)))))).))-3'
Motif MFE = -20.5; z-score = -1.7; 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 = 0.82; ED = 32.67
```

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(+)

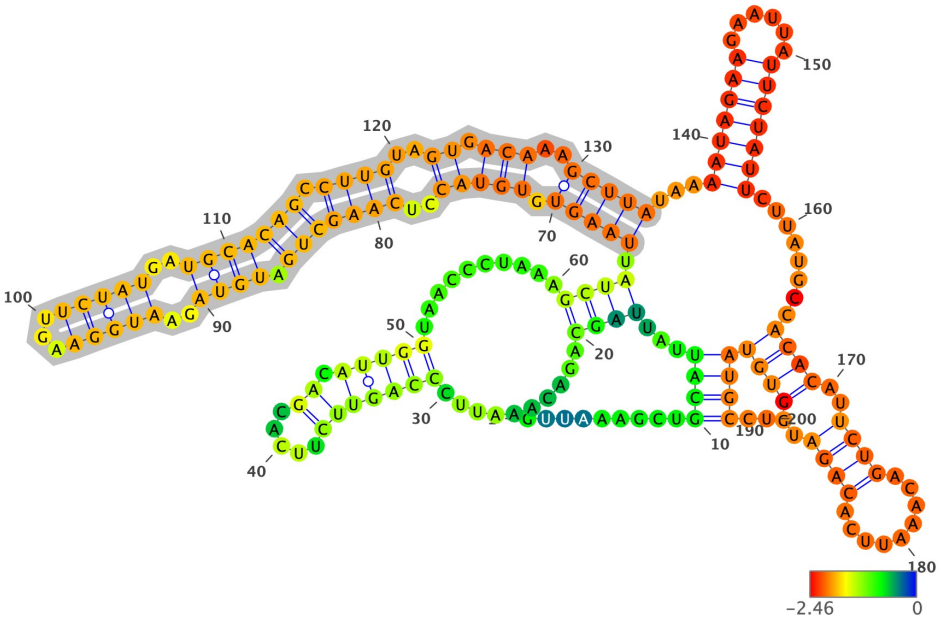
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 19053 to 19121 (nt 66 to 134)

```
5'-TAAGTGTGTACCTCAAGCTGATGTAGAATGGAAGTUCUAUGAUGCACAGCCUUGTAGUGACAAAGCUUA-3'
5'-(((((.(((((..(((((((.((((..((((((...))))))..)))))))).)))))..))).))).))))-3'
Motif MFE = -21.0; z-score = -3.41; 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 18988 to 19187 (motif highlighted in silver):

```
5'-GUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCA
CAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCU-3
5'-.........((((...((((..........(((((((.....)).)))))..........)))).(((((.((((((..(((((((.((((..((((((...))))))..))))
))).)))))..)).)))..))))))...(((((((.....)))))))........((((..((((.........))))..))))))))..-3'
MFE = -43.6; z-score = -1.61; ED = 23.18
```

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(+)

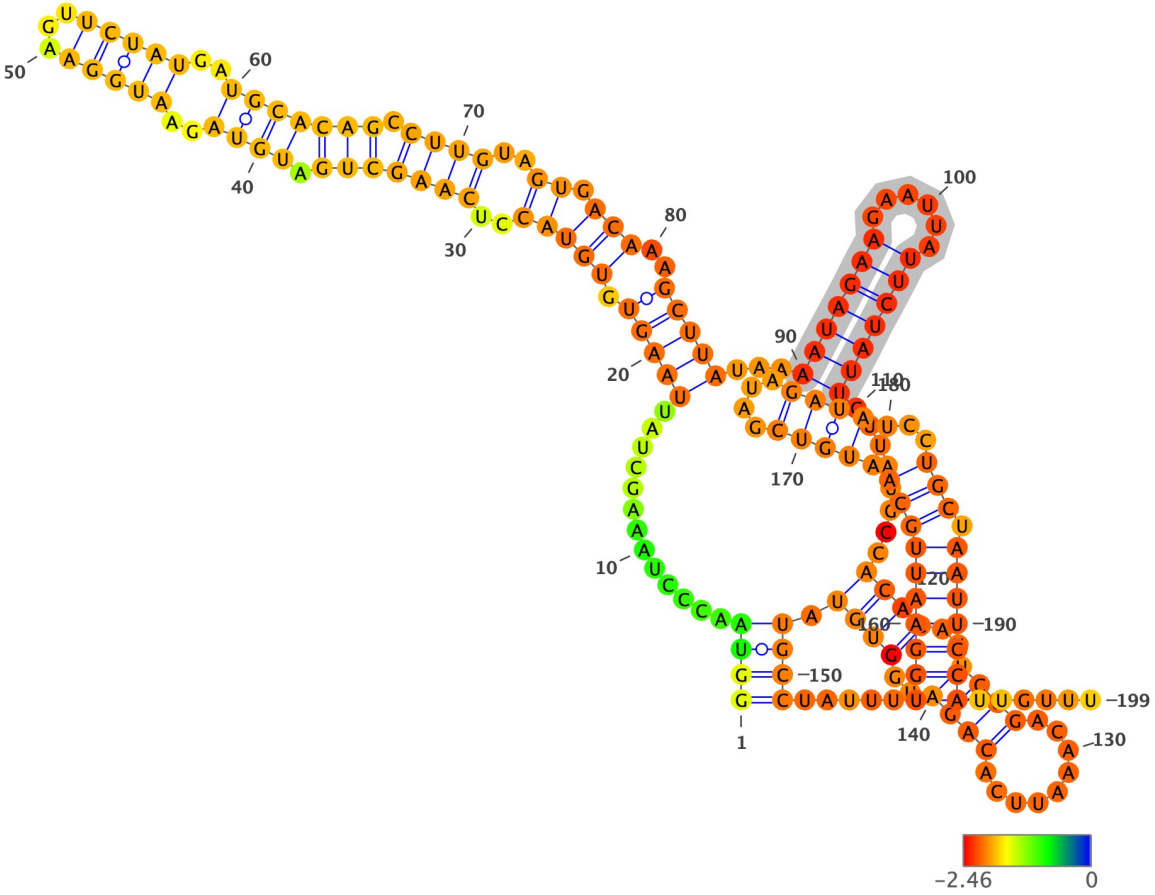
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 19125 to 19144 (nt 90 to 109)

```
5'-AATAGAAGAATTAUUCUAUU-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.0; z-score = -5.72; 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 19036 to 19234 (motif highlighted in silver):

```
5'-GGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCU
UAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUU-3
5'-((((.............((((((.((((((..(((((((.((((..((((((...))))))..))))))).))))..)).))))..))))))...(((((((......)))))))..
......((((..((((.........))))..)))).))))).....((((((((((((((....))))))..))).)))))))......-3'
MFE = -50.8; z-score = -2.86; ED = 21.65
```

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(+)

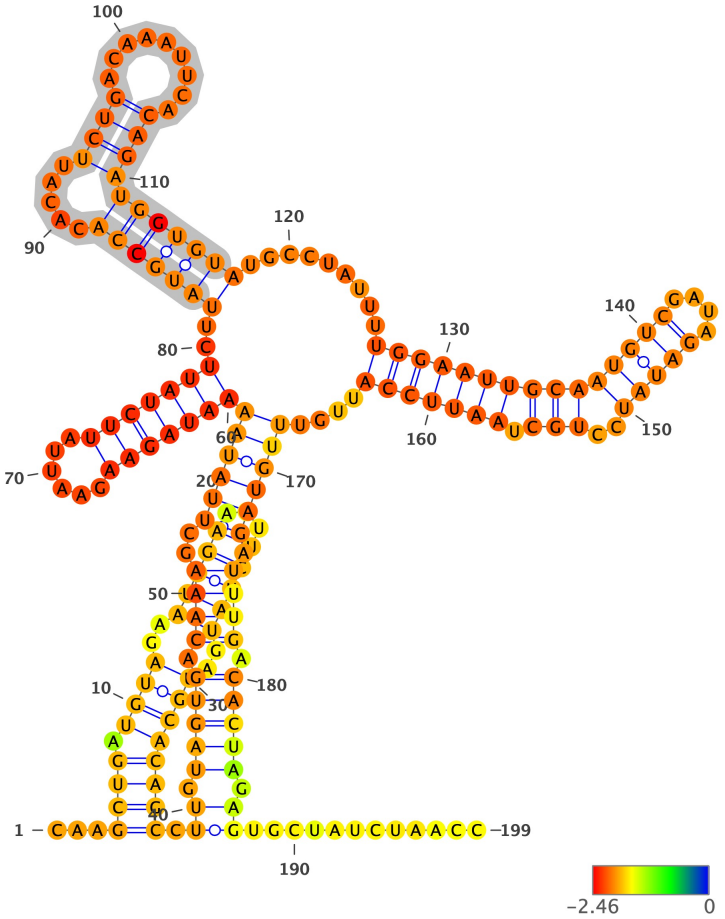
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 19148 to 19181 (nt 83 to 116)

```
5'-ATGCCACACATTCTGACAAATTCACAGAUGGUGU-3'
5'-(((.((.....((((.........))))))).)))-3'
Motif MFE = -7.6; z-score = -2.49; ED = 2.03
```



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 19066 to 19264 (motif highlighted in silver):

```
5'-CAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAU
GGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACC-3
5'-...((((.((((..(((((...)))))..)))))))).((.(((((.((((..(((((((((((((.....)))))))..(((((((.....((((.........)))))
))))))).........((((((((((((((....)))))..))).)))))))....)))))).)))).)))))).))............-3'
MFE = -47.8; z-score = -2.73; ED = 19.42
```

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_gp01, 266-21555(+)

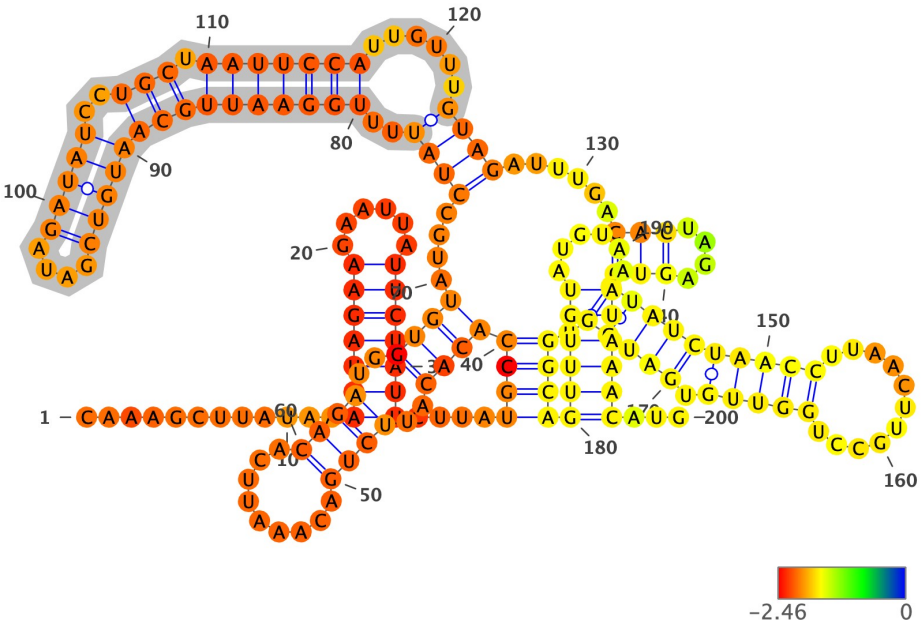
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 324 from nt 19189 to 19235 (nt 77 to 123)

```
5'-TTTTGGAATTGCAATGTCGATAGAUAUCCUGCTAAUUCCATTGTTTG-3'
5'-(..((((((((((((((....)))))..))).)))))))......)-3'
Motif MFE = -13.6; z-score = -3.7; ED = 1.2
```



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 19113 to 19312 (motif highlighted in silver):

```
5'-CAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAA
UUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUG-3
5'-............(((((((......)))))))....((((((((..((((.........))))..))))....((((..((((((((((((((....)))))..))).))
)))))......))))......(((....)))((((((((((...........)))))).)))))).))))((((((......))))))...-3'
MFE = -46.0; z-score = -2.81; ED = 36.34
```

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(+)

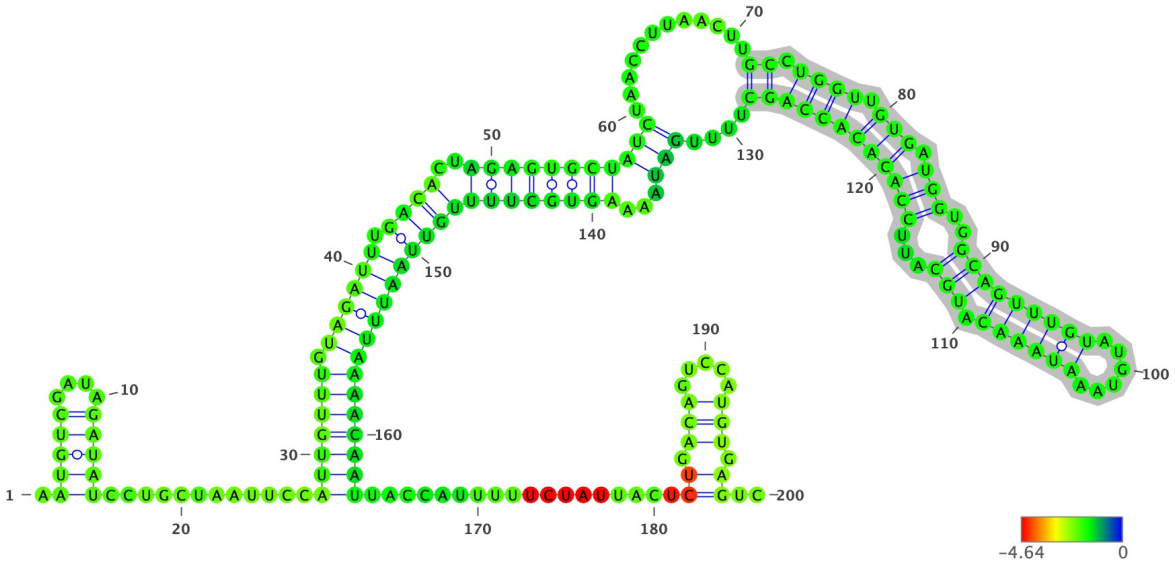
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 325 from nt 19272 to 19328 (nt 72 to 128)

```
5'-GCCTGGTTGTGATGGTGGCAGTTTGTATGTAAAUAAACAUGCATTCCACACACCAGC-3'
5'-((.((((.(((.(((..((((((((((.....))))))).)))...)))))))))))))-3'
Motif MFE = -20.3; z-score = -3.18; 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 = -1.0; ED = 27.24
```

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(+)

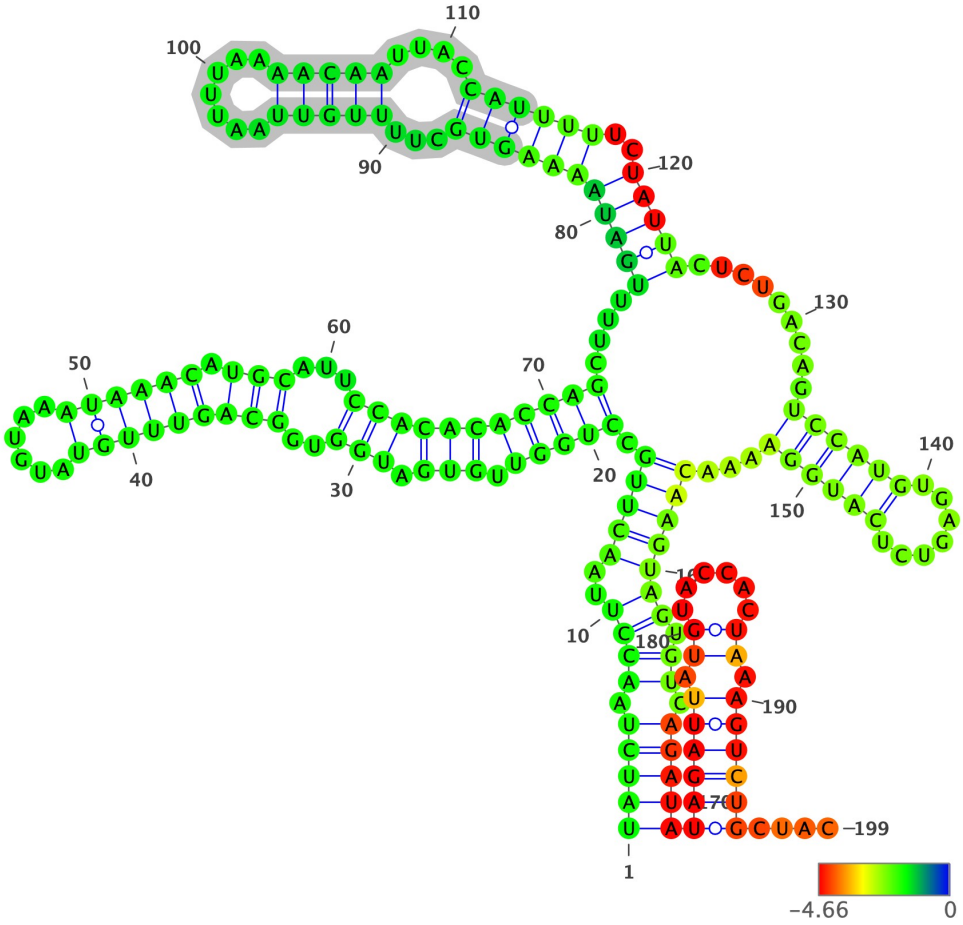
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 326 from nt 19340 to 19369 (nt 85 to 114)

```
5'-GTGCTTTTGTTAATTTAAAACAATTACCAU-3'
5'-(((...(((((.......)))))....)))-3'
Motif MFE = -0.9; z-score = 0.12; ED = 6.5
```



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 19256 to 19454 (motif highlighted in silver):

```
5'-UAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUAC
CAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUAC-3
5'-(((((.(((((..(((((.(((((.(((.(((..(((((((((.....))))))).)))...))))))))))))....(((((((((((...(((((.......)))))....
))))))..)))))).........((((((.......))))))...)))))))).)).)))))((((((.((......)).))))))....-3'
MFE = -41.4; z-score = -1.66; ED = 47.8
```

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(+)

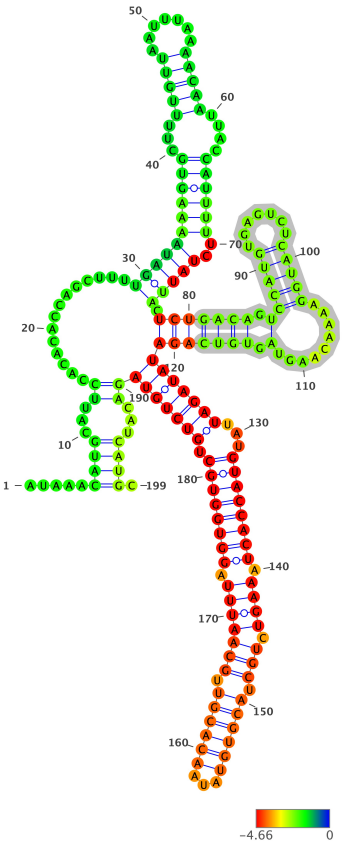
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 327 from nt 19384 to 19421 (nt 81 to 118)

```
5'-GACAGTCCATGTGAGTCTCAUGGAAAACAAGTAGUGUC-3'
5'-((((.((((((.......)))))).........).))))-3'
Motif MFE = -6.9; z-score = -0.84; ED = 5.79
```



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 19304 to 19502 (motif highlighted in silver):

```
5'-AUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAG
UAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGC-3
5'-.....((((...((..............((((((((((...(((((.......)))))....))))))..))))).(((((((.((((((.......)))))........
.).)))))))(((((((...((((((((.((((.(((.((((((...)))))).)))))))).)))))))).))))))))...)))).-3'
MFE = -49.3; z-score = -3.84; ED = 35.77
```

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(+)

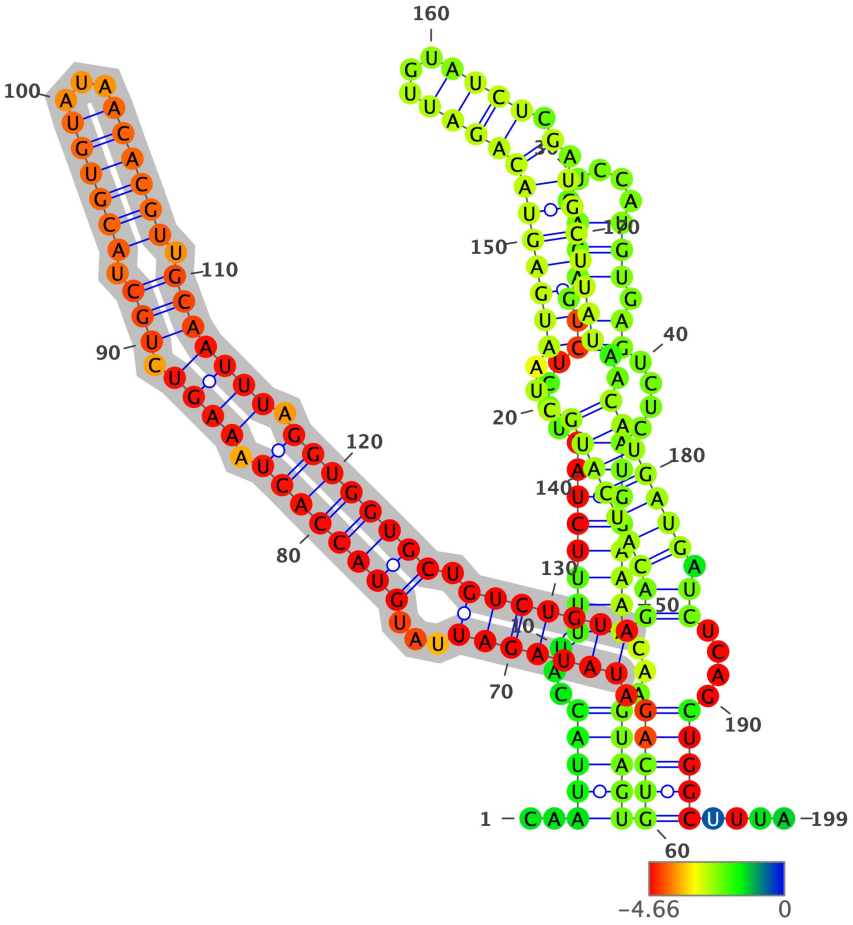
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 19425 to 19492 (nt 66 to 133)

```
5'-TATAGATTATGTACCACTAAAGTCTGCTACGTGTATAACACGUTGCAAUUUAGGUGGUGCTGUCUGUA-3'
5'-(((((((...((((((((.((((.(((.((((((...)))))).)))))))).)))))))).)))))))-3'
Motif MFE = -29.1; z-score = -5.03; ED = 2.99
```



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 19360 to 19558 (motif highlighted in silver):

```
5'-CAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGC
AAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUGAUCUCAGCUGGCUUUA-3
5'-..(((((...((((((((....((.(((.....))).)).....))))))))...)))))(((((.(((((((...((((((((.((((.(((.((((((...)))))).))
))))).))))))))).)))))))(((((((((...((((((((((((...)))).).)))))))..)))))))).)).....)))))....-3'
MFE = -61.7; z-score = -4.53; ED = 15.64
```

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(+)

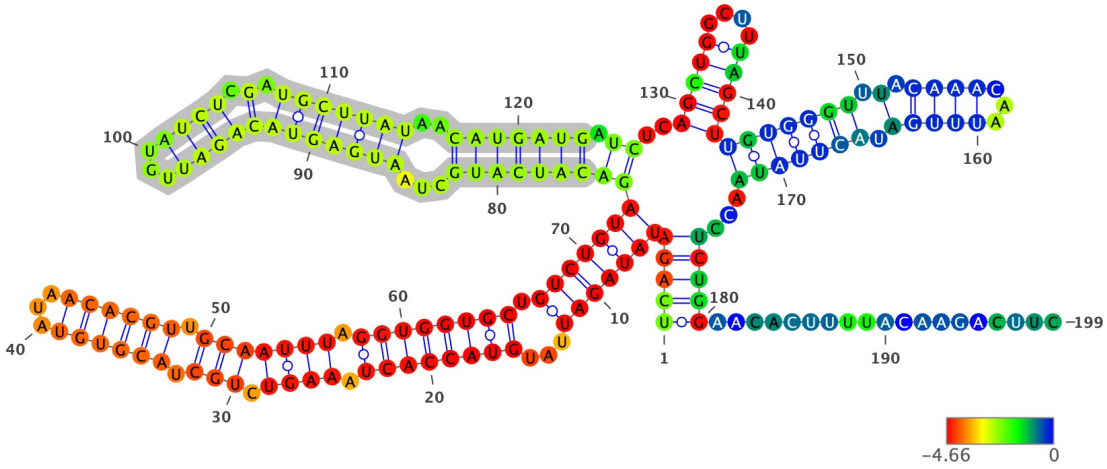
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 19495 to 19542 (nt 76 to 123)

```
5'-CATCATGCTAATGAGTACAGATTGTAUCUCGAUGCUUAUAACAUGAUG-3'
5'-(((((((...((((((((((.....))).).)))))))..)))))))-3'
Motif MFE = -13.0; z-score = -3.09; ED = 4.62
```



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 19420 to 19618 (motif highlighted in silver):

```
5'-UCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCU
UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUC-3
5'-(((((((((((...((((((((.((((.((((.((((((...)))))).)))))))).))))))))).)))))))(((((((((...((((((((((((...)))).).))))
)))..)))))))).))..(((((....)))))(((((((.(.((((...)))))).)))))))...)))))).....................-3'
MFE = -56.0; z-score = -3.93; ED = 13.27
```

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_gp01, 266-21555(+)

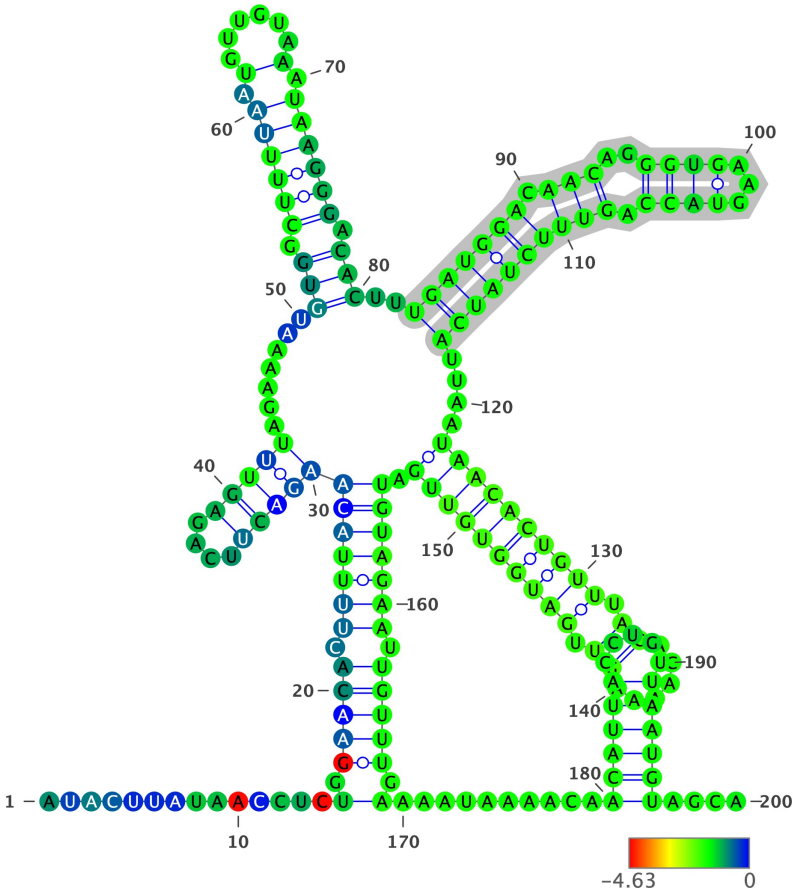
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 19665 to 19699 (nt 83 to 117)

```
5'-TGATGGACAACAGGGTGAAGUACCAGUUUCUATCA-3'
5'-((.((((.(((..((.(...).)).)))))))).))-3'
Motif MFE = -10.3; z-score = -3.03; ED = 3.6
```



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 19583 to 19782 (motif highlighted in silver):

```
5'-AUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUU
CUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCA-3
5'-..............(.(((((.((((((((((((....)))))).......(((.((((((.(......).))))))..))).((((((((.(((..((((...))))).))))
))))))....((((((((((.((......)).)))))))))).)))))))..)))))).)..........((((((.....))))))....-3'
MFE = -38.4; z-score = -1.25; ED = 48.32
```

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(+)

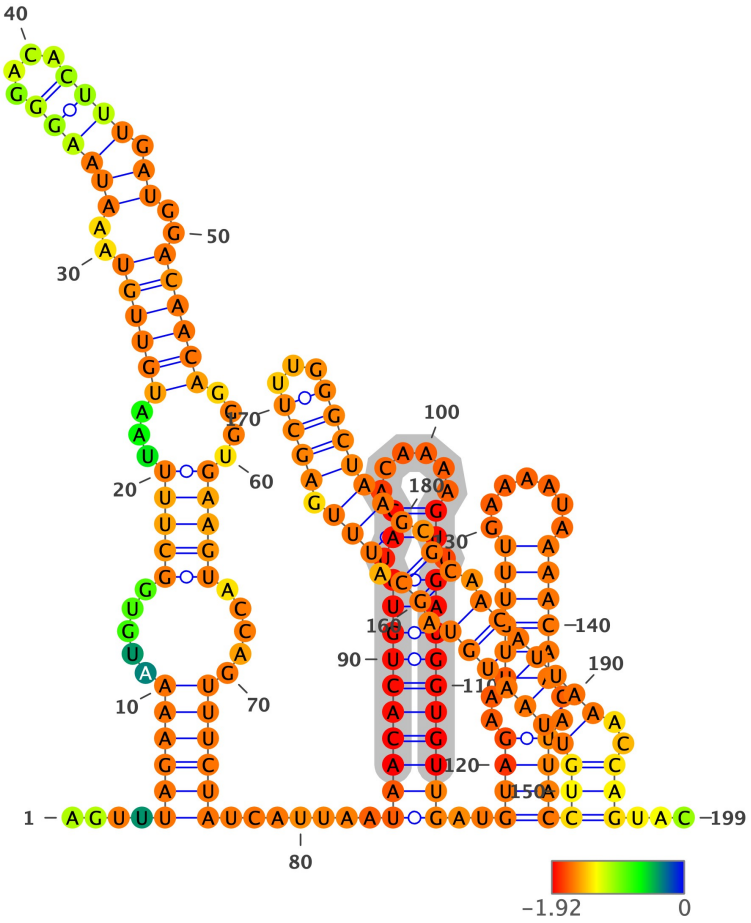
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 331 from nt 19706 to 19733 (nt 86 to 113)

```
5'-ACACTGTTTACACAAAAGUTGAUGGUGU-3'
5'-((((((((.((......)).))))))))-3'
Motif MFE = -6.9; z-score = -3.2; 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 = -1.61; 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(+)

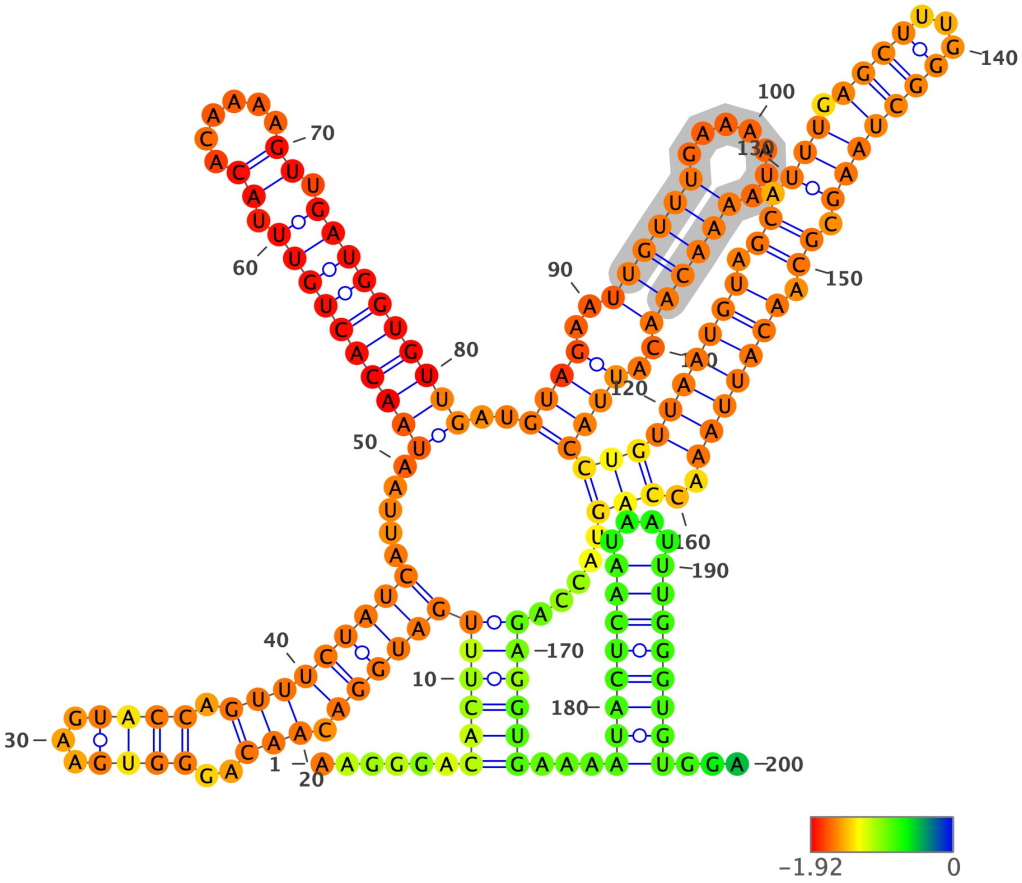
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 332 from nt 19745 to 19761 (nt 92 to 108)

```
5'-TGTTTGAAAATAAAACA-3'
5'-(((((.......)))))-3'
Motif MFE = -1.1; z-score = -3.42; 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 19654 to 19853 (motif highlighted in silver):

```
5'-AAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACA
UUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGA-3
5'-......((((((((((((.((((..(((((...)))))..)))))))))).....((((((((((.((......)).))))))))))..((((..((((((.......))))))..
))))((((((((((.((.(((.(((((...)))))))).)).)))))))..)))).....))))))...(((((((((....)))))))))...-3'
MFE = -48.3; z-score = -3.14; ED = 35.02
```

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_gp01, 266-21555(+)

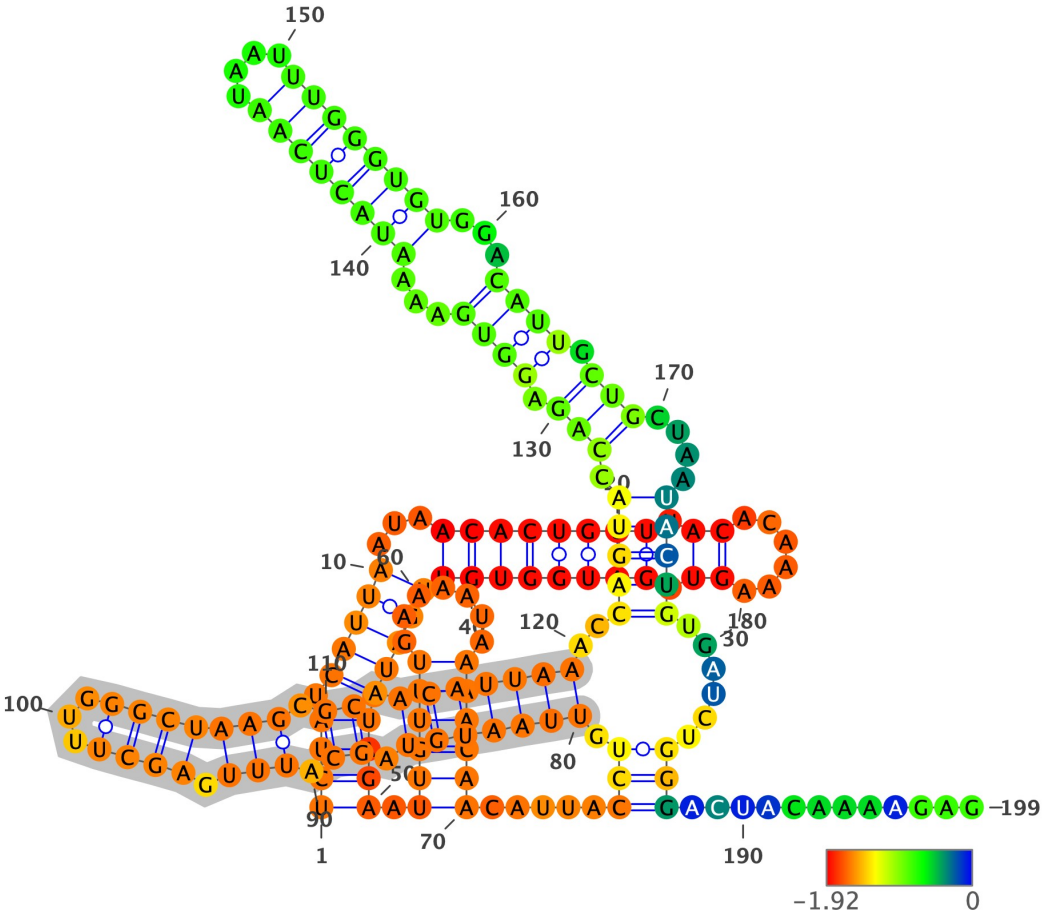
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 333 from nt 19772 to 19811 (nt 80 to 119)

```
5'-TTAATGTAGCATTTGAGCTTTGGGCUAAGCGCAACAUUAA-3'
5'-(((((((.((.(((.((((...)))))))).)).)))))))-3'
Motif MFE = -10.5; z-score = -2.53; ED = 2.75
```



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 19693 to 19891 (motif highlighted in silver):

```
5'-UCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGC
AACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAG-3
5'-((((.((((((...(((((((((.((......)).)))))))))))))))))).((((((.......)))))).....(((.(((((((.((.(((.((((...)))))))).)).
.)))))))..((((((.(((.((((((...(((((((((....)))))))))...)))))).))).....))))).....))).............-3'
MFE = -43.7; z-score = -1.79; ED = 25.96
```

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(+)

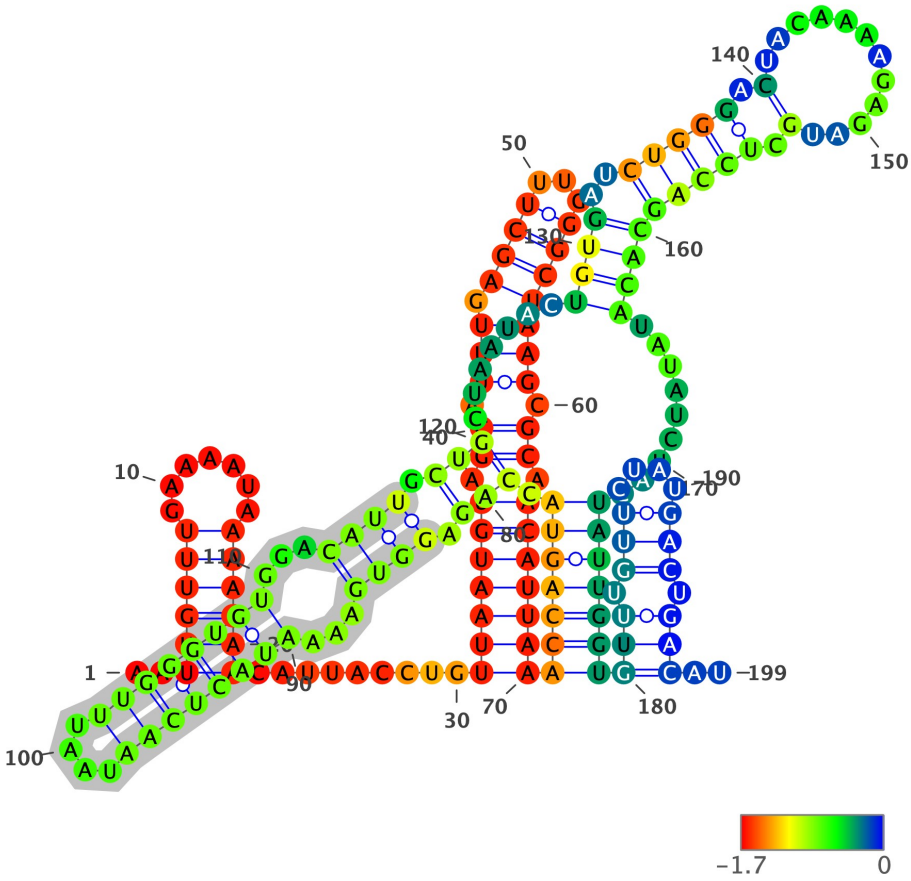
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 334 from nt 19824 to 19857 (nt 83 to 116)

```
5'-GGTGAAAATACTCAATAATUUGGGUGUGGACAUU-3'
5'-(.............................)-3'
Motif MFE = -8.8; z-score = -3.21; 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
ACAUUGCUGCUAAUACUGUGAUCUGGGACUACACAAAGAGAUGCUCCAGCACAUAUAUCUACUAUUGGUGUUUGUUCUAUGACUGACAU-3
5'-..((((((.......))))))........(((((((.((.(((.((((...)))))))).)).)))))))(((((((.(((.(((((...(((((((((....)))))))))..
.))))).)))......((((..((((((.(...........).)))))))))........)))))))(((.(((....))).))).)..-3'
MFE = -40.8; z-score = -0.35; 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(+)

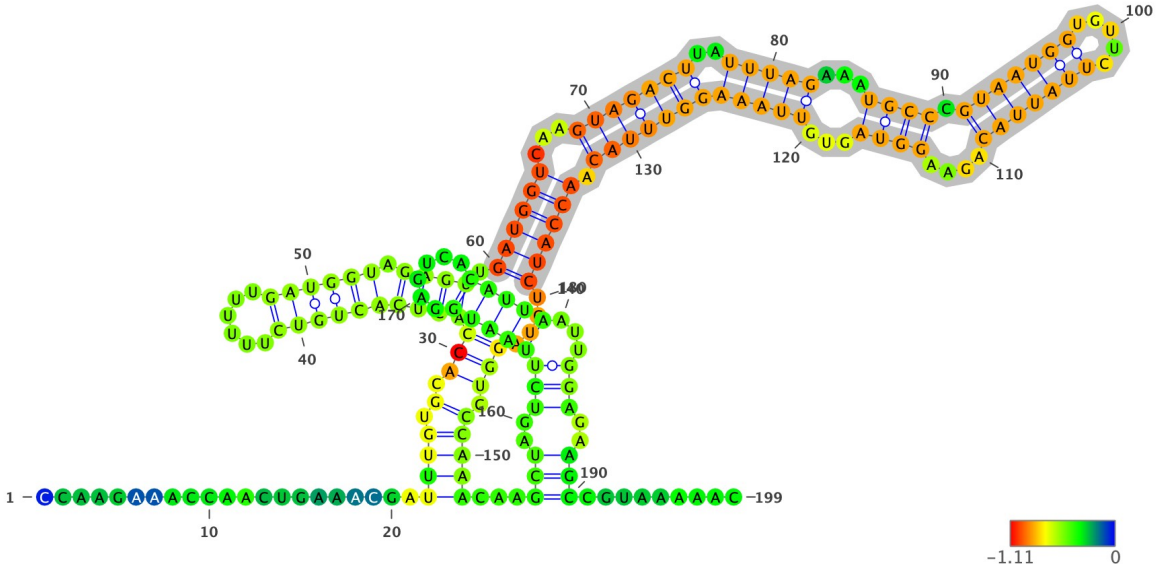
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 335 from nt 20002 to 20081 (nt 60 to 139)

```
5'-GATGGTCAAGTAGACTTATTTAGAAATGCCCGTAATGGTGTTCUUAUUACAGAAGGUAGTGUUAAAGGUUUACAACCAUC-3'
5'-((((((.....................................................................))))))-3'
Motif MFE = -20.7; z-score = -2.13; 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 = -42.5; z-score = -0.48; ED = 20.98
```

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(+)

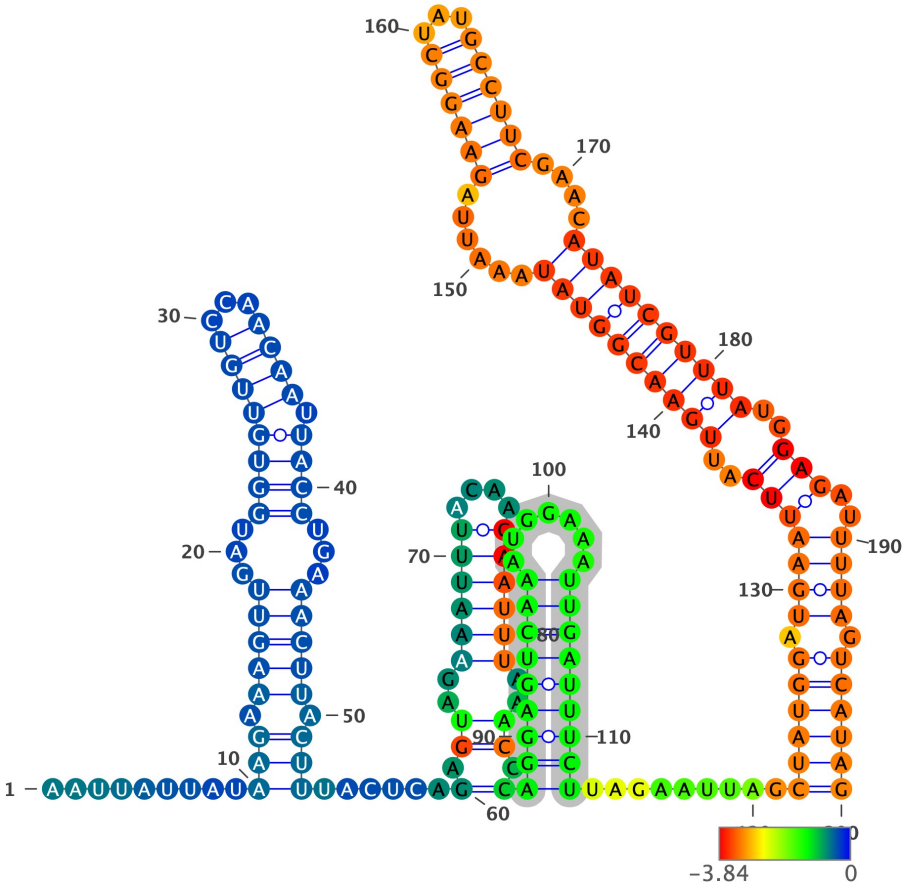
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 336 from nt 20236 to 20260 (nt 88 to 112)

```
5'-AGGAGTCAAATGGAAAUUGAUUUCU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -6.1; z-score = -3.56; 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 = -2.09; 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(+)

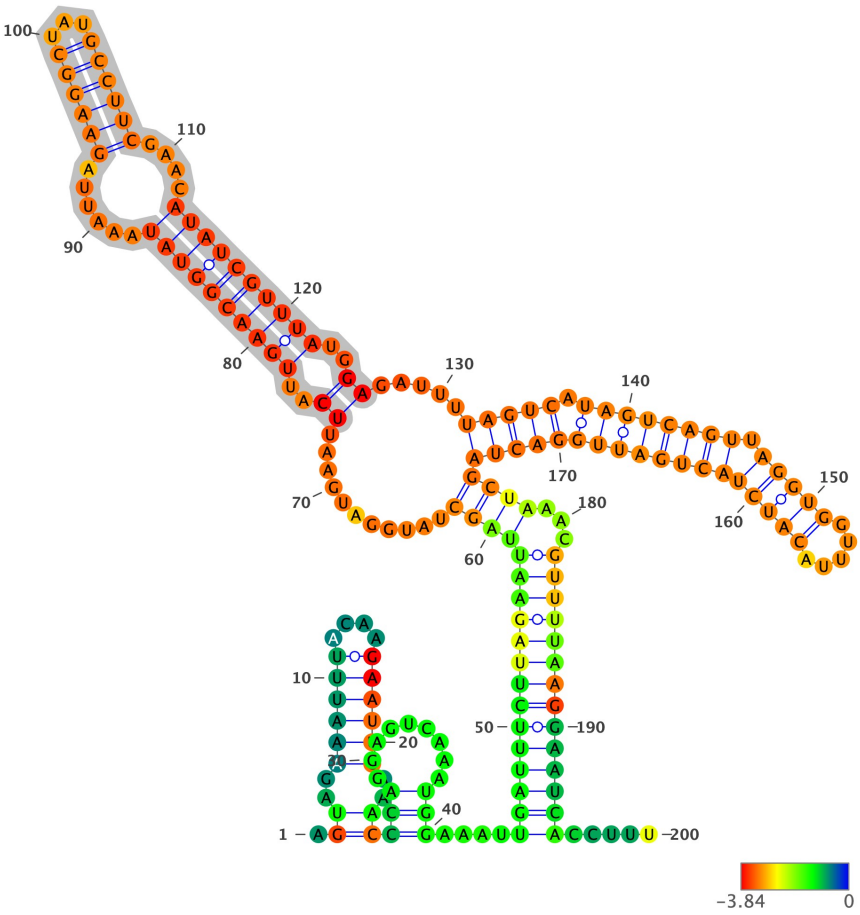
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 337 from nt 20282 to 20334 (nt 74 to 126)

```
5'-TCATTGAACGGTATAAATTAGAAGGCTATGCCUUCGAACAUAUCGUUUATGGA-3'
5'-((..(((((((((((......((((((...)))))).....)))))))))))..))-3'
Motif MFE = -18.3; z-score = -4.29; ED = 4.25
```



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 20209 to 20408 (motif highlighted in silver):

```
5'-AGUAGAAAUUUACAAGAAUUUAAACCCAGGAGUCAAAUGGAAAUUGAUUUCUUAGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAA
CAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUU-3
5'-.((..((((((....))))))..))(((.........))).....(((((((((((((((((((.............((..((((((((((......((((((...))))))...
.))))))))))..)).....(((((.((((((((.(((((.....)))))))))))))))))))))))...))))))))))))))).....-3'
MFE = -57.4; z-score = -4.21; ED = 17.27
```

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(+)

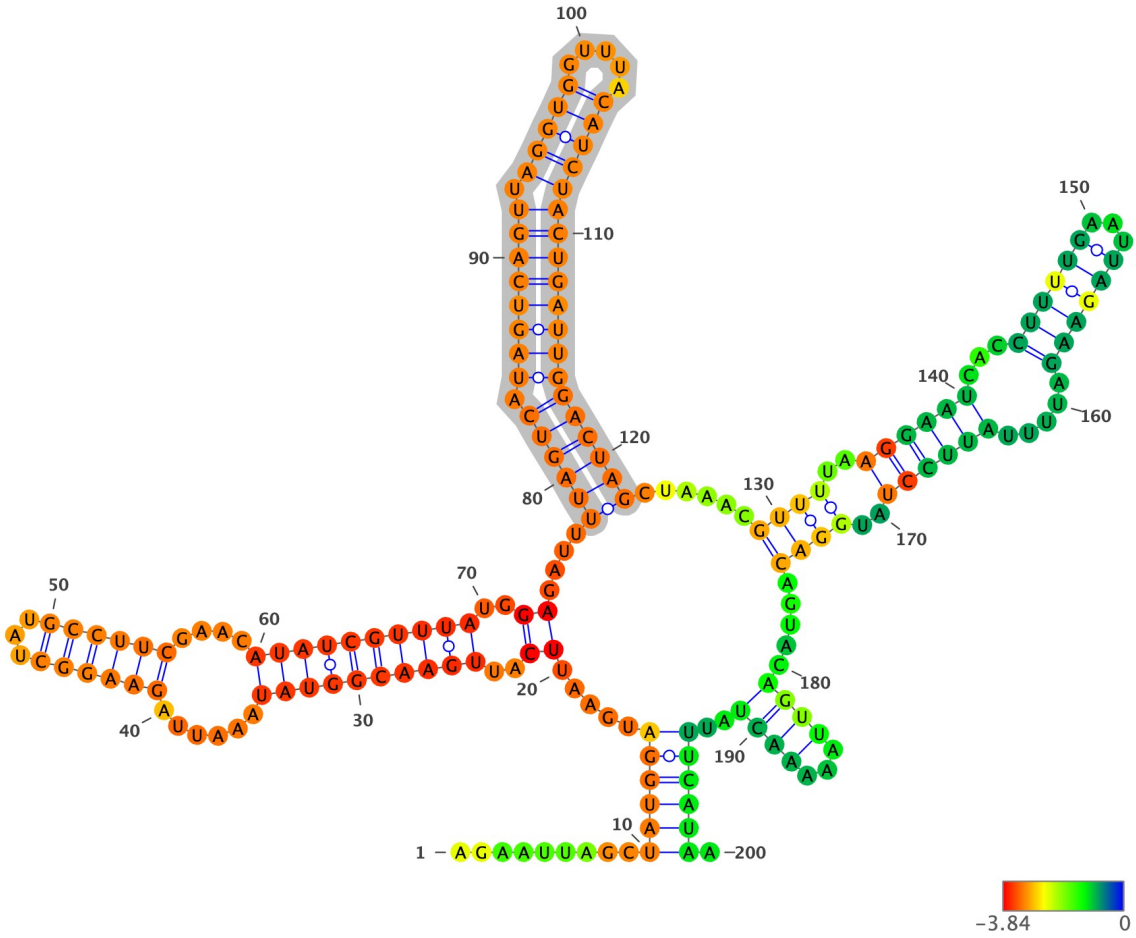
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 338 from nt 20339 to 20383 (nt 78 to 122)

```
5'-TTAGTCATAGTCAGTTAGGTGGTTTACAUCUACUGAUUGGACUAG-3'
5'-((((((.(((((((((.(((((.....)))))))))))))))))))-3'
Motif MFE = -20.0; z-score = -5.33; 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 20262 to 20461 (motif highlighted in silver):

```
5'-AGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACU
GAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAA-3
5'-.........((((((.....((..((((((((((.....((((((...))))))....))))))))))..)).....((((((.(((((((((.(((((.....)))))))))
))))))))))).....((((..((((((...((((((...))))))).....))))))..))))....((((...))))..))))))).-3'
MFE = -50.2; z-score = -3.3; ED = 30.2
```

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(+)

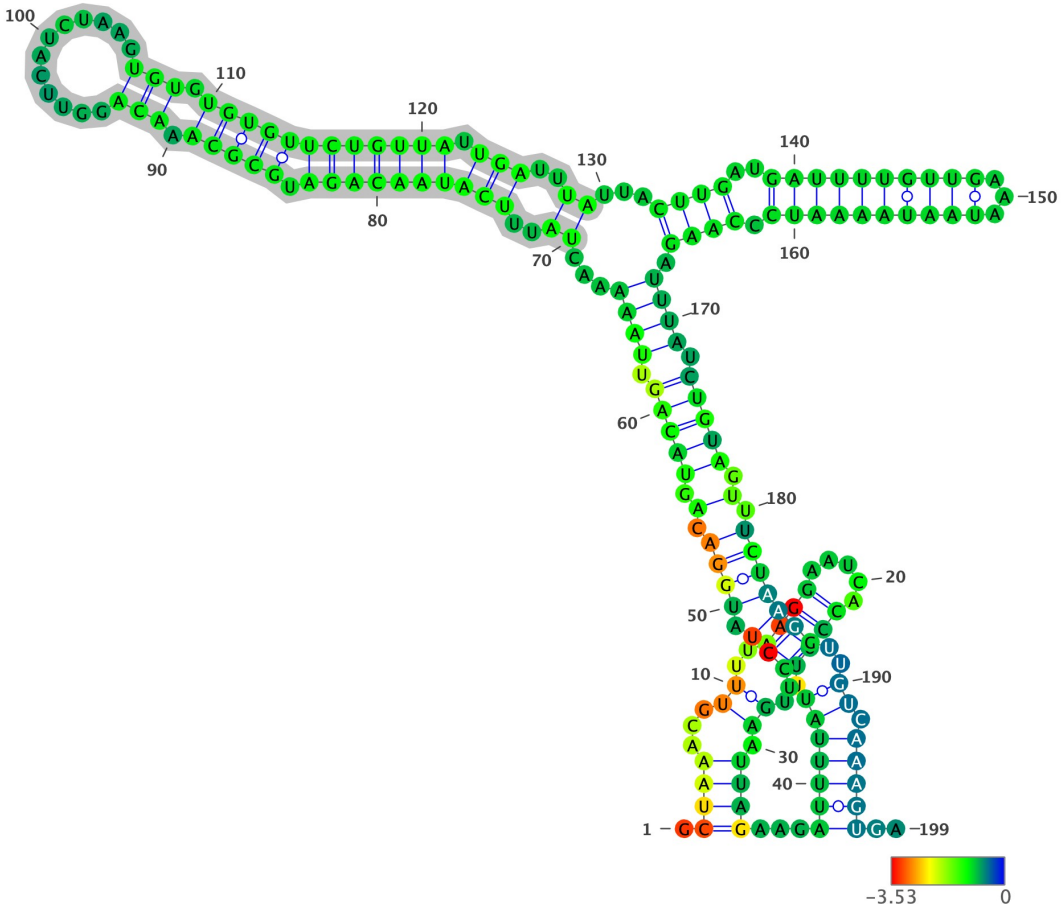
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 339 from nt 20452 to 20511 (nt 70 to 129)

```
5'-TATTTCATAACAGATGCGCAAACAGGTTCATCTAAGUGUGUGUGUUCUGUUATUGATTUA-3'
5'-((..((((((((((.(((((.(((.............))).))))))))))))).)))..))-3'
Motif MFE = -15.2; z-score = -2.61; 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 = -0.82; ED = 49.26
```

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(+)

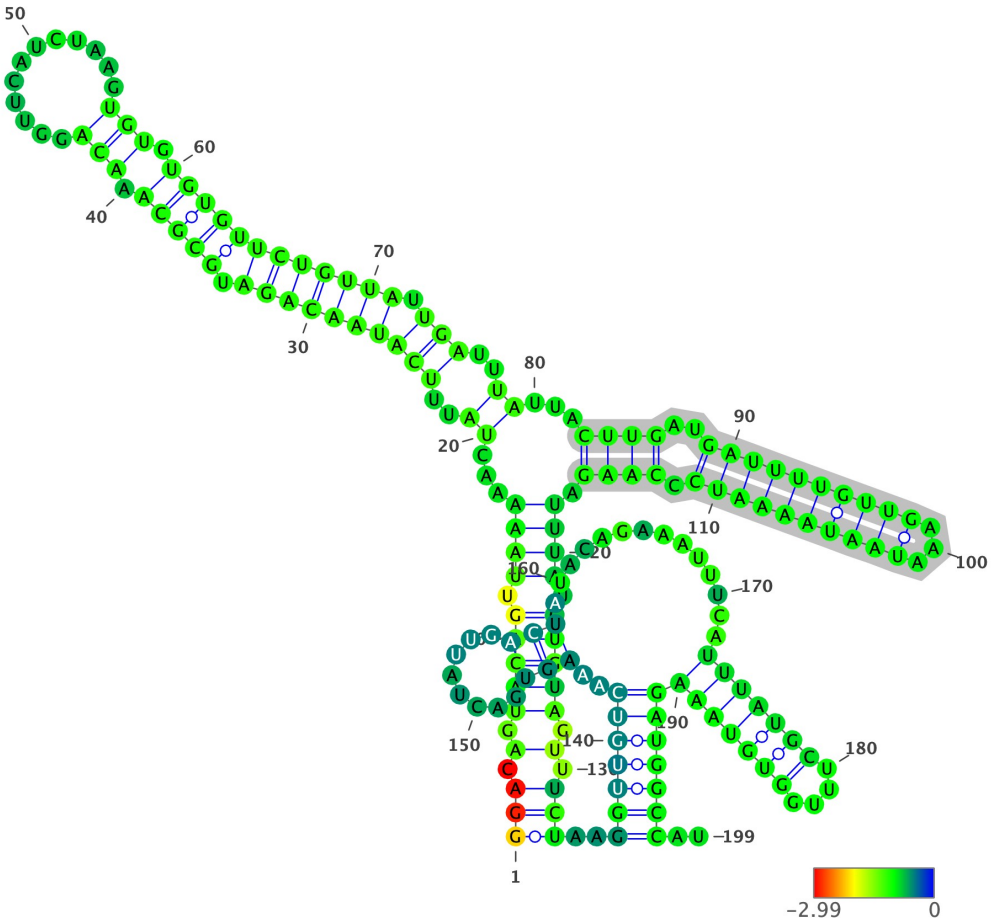
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 340 from nt 20515 to 20548 (nt 83 to 116)

```
5'-CTTGATGATTTTGTTGAAAUAAUAAAAUCCCAAG-3'
5'-((((..((((((((((...)))))))))).))))-3'
Motif MFE = -7.4; z-score = -2.81; 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 20433 to 20631 (motif highlighted in silver):

```
5'-GGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUC
CCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAU-3
5'-(((.(.(((((.((((...((..((((((((((.(((((.(((............))).))))))))))).)))..))...((((..((((((((((...))))))))))
.)))).)))).))))).).)))..(((((((..(((........)))..............(((((((....)))))))))))))..-3'
MFE = -41.9; z-score = -1.52; ED = 46.54
```

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(+)

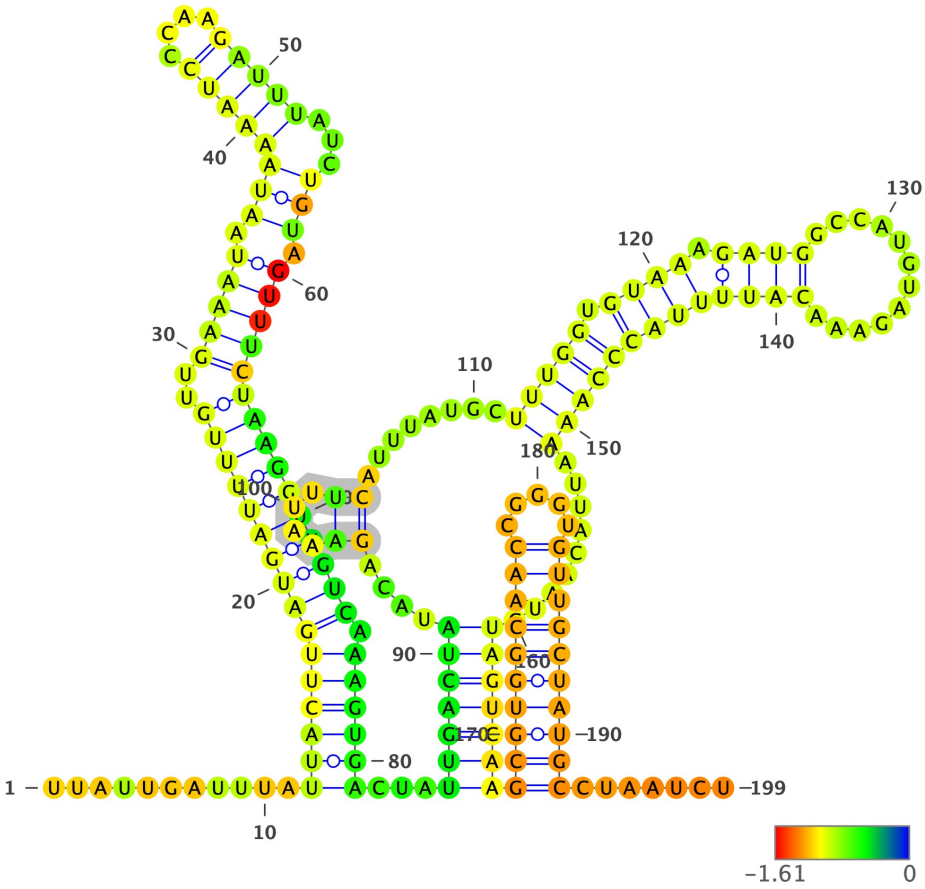
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 341 from nt 20596 to 20603 (nt 96 to 103)

```
5'-GAAATTTC-3'
5'-(......)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 20501 to 20699 (motif highlighted in silver):

```
5'-UUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGC
UUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCU-3
5'-...........(((((((((((((((..(((((.(((((((((....)))))...)))).)))))))))))))).))))))...(((((((....((....)).......
(((((.((((.((((...........))))))))))).........)))))))((((((((((.....))))))))))........-3'
MFE = -40.9; z-score = -1.82; ED = 59.4
```

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(+)

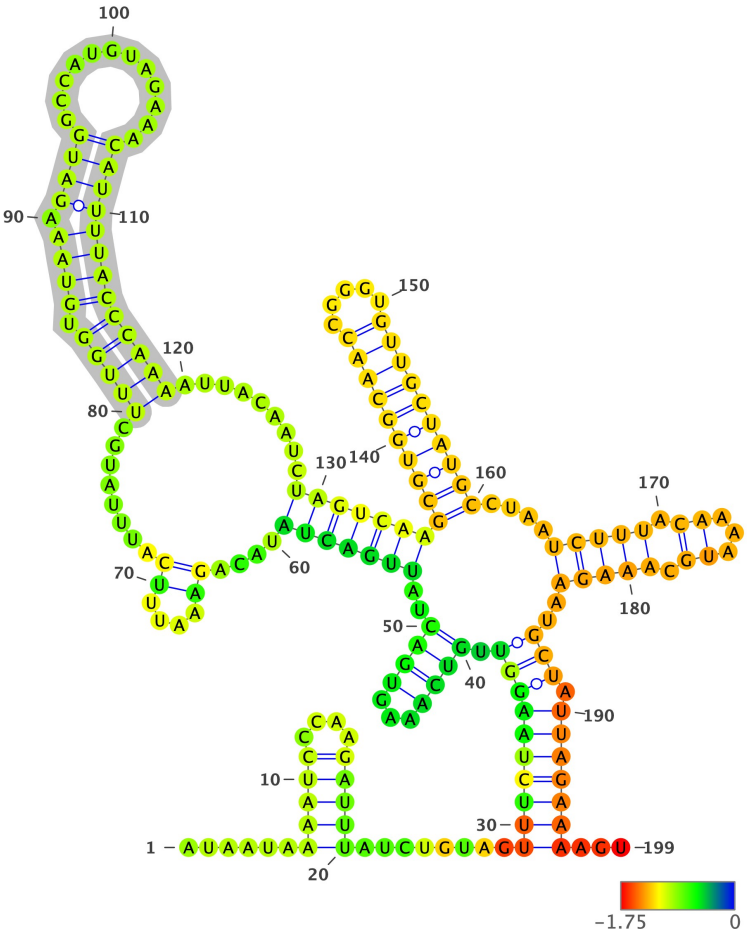
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 342 from nt 20612 to 20651 (nt 80 to 119)

```
5'-TTTGGTGTAAAGATGGCCATGTAGAAACAUUUUACCCAAA-3'
5'-((.....................................))-3'
Motif MFE = -7.8; z-score = -1.4; ED = 4.57
```



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 20533 to 20731 (motif highlighted in silver):

```
5'-AUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUU
UACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGU-3
5'-......(((((....)))))........(((((((((.((((...)))).((((((((....((....)).........(((((.((((.((((.............)))))
))))))))).........)))))))((((((((((.....)))))))))....(((((.((...)).)))))..))).)))))))...-3'
MFE = -36.7; z-score = -1.12; ED = 55.99
```

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(+)

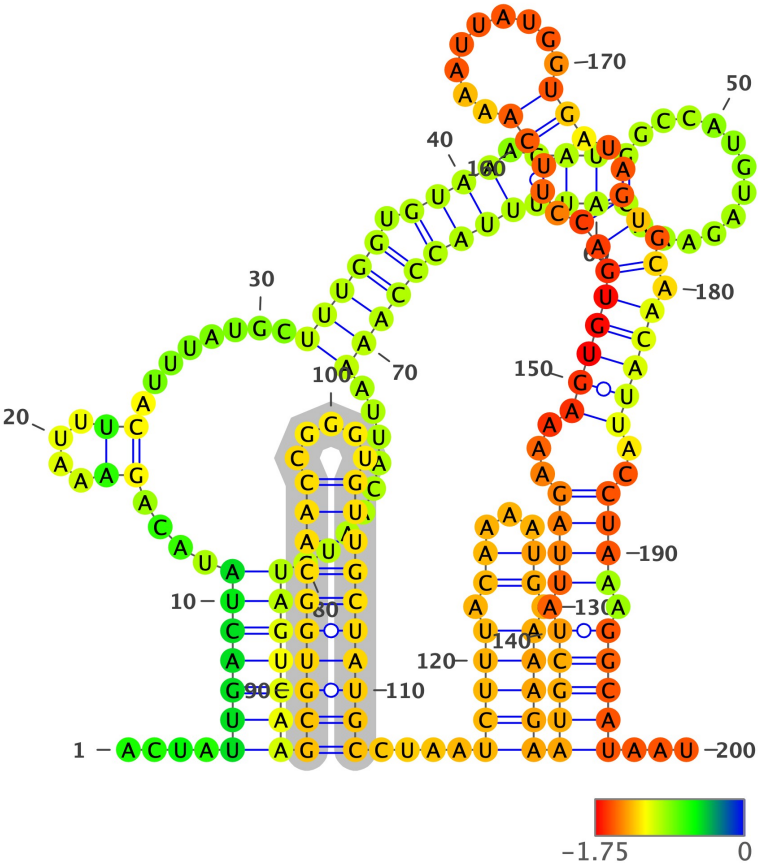
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 343 from nt 20668 to 20692 (nt 88 to 112)

```
5'-GCGTGGCAACCGGGTGUUGCUAUGC-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -13.0; z-score = -3.43; 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 = -1.1; 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(+)

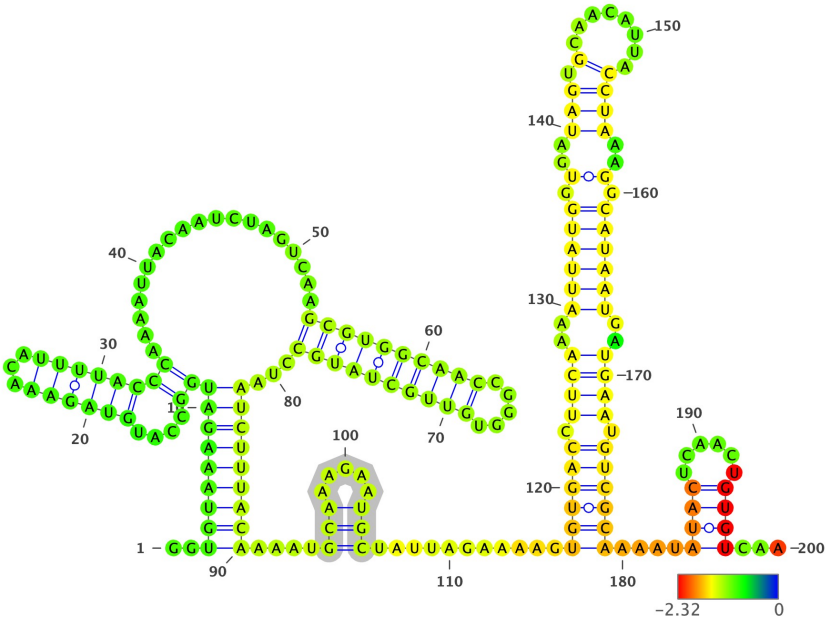
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 344 from nt 20709 to 20719 (nt 95 to 105)

```
5'-GCAAAGAAUGC-3'
5'-(((.....)))-3'
Motif MFE = -0.1; z-score = -0.39; ED = 1.48
```



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 20615 to 20814 (motif highlighted in silver):

```
5'-GGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAG
AAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAA-3
5'-..((((((((((....((((((...))))))))).....................((((((((((.....))))))))))...))))))))....(((.....))).....
.....((((((.((((..((((((.(..(((.(........)))))..).)))))))..)))))..))))))....((((......))))...-3'
MFE = -43.9; z-score = -1.99; ED = 25.99
```

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(+)

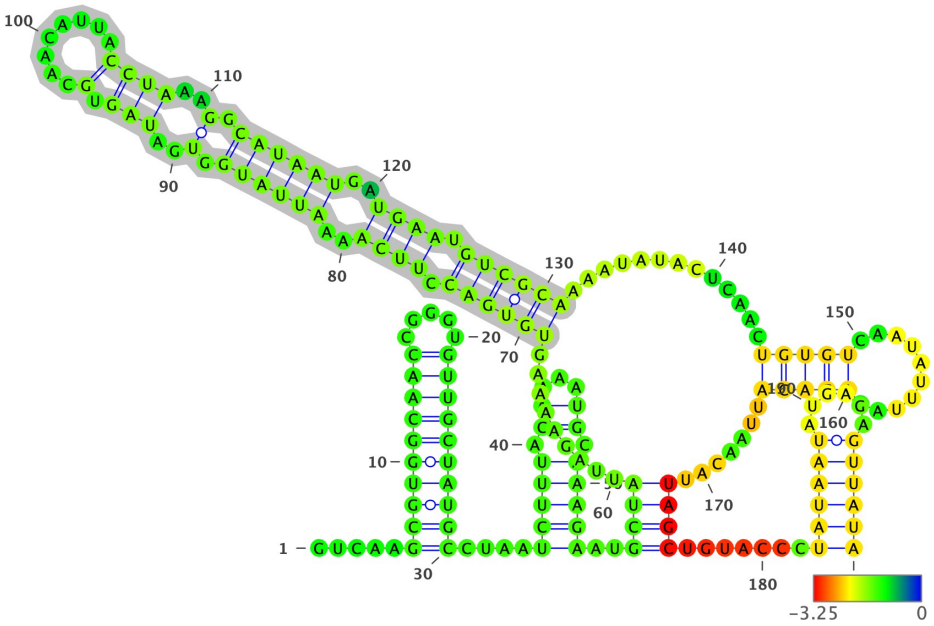
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 345 from nt 20731 to 20793 (nt 69 to 131)

```
5'-TGTGACCTTCAAAATTATGGTGATAGTGCAACATTACCUAAAGGCAUAAUGAUGAATGUCGCA-3'
5'-((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))-3'
Motif MFE = -17.6; z-score = -3.1; 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 = -1.46; 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(+)

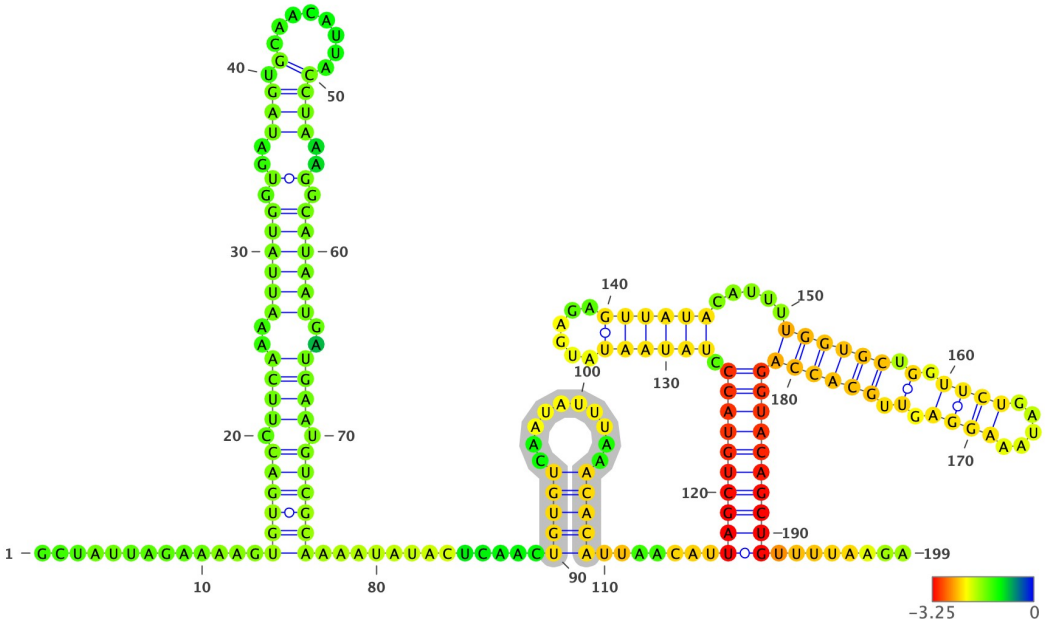
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 346 from nt 20807 to 20826 (nt 90 to 109)

```
5'-TGTGTCAATATTTAAACACA-3'
5'-(((((..........)))))-3'
Motif MFE = -1.8; z-score = -2.8; 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 20718 to 20916 (motif highlighted in silver):

```
5'-GCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUU
AACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGA-3
5'-.............((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))............(((((..........)))))..
.....((((((((((.((((((......))))))).....((((((.(.((((.....)))).).))))))))))))))))........-3'
MFE = -50.4; z-score = -2.74; ED = 15.52
```

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(+)

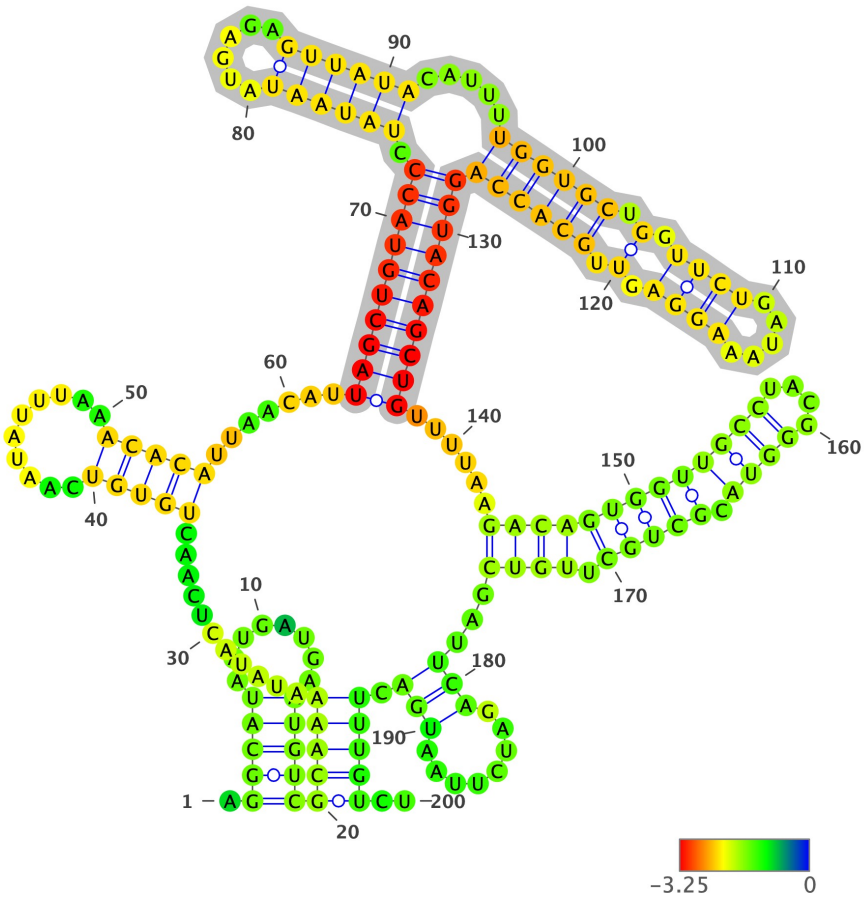
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 347 from nt 20834 to 20908 (nt 63 to 137)

```
5'-TAGCTGTACCCTATAATATGAGAGUUAUACATTTTGGTGCTGGTTCTGATAAAGGAGUTGCACCAGGUACAGCUG-3'
5'-((((((((((.((((((......))))))).....((((((.(.((((.....)))).).))))))))))))))))-3'
Motif MFE = -28.8; z-score = -4.62; 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 = -2.56; ED = 36.82
```

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(+)

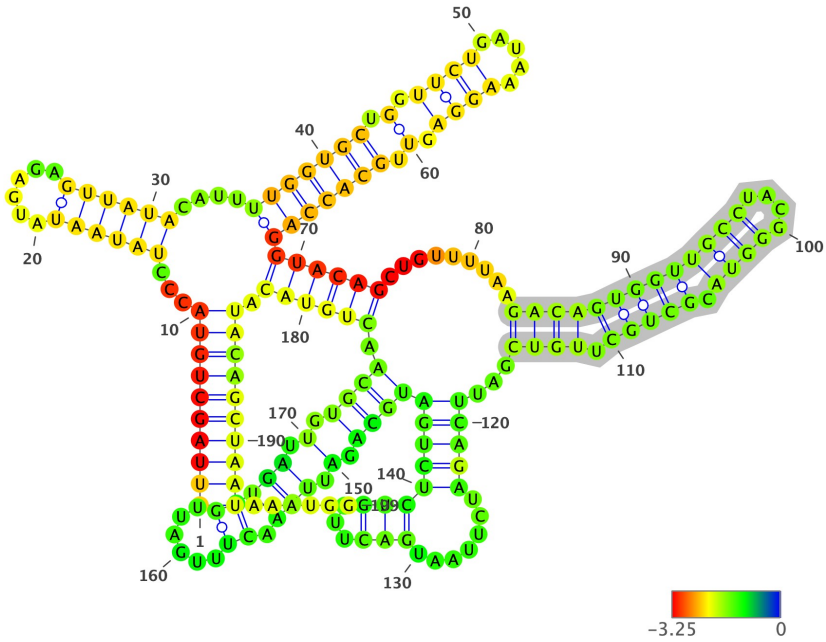
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 348 from nt 20915 to 20946 (nt 84 to 115)

```
5'-GACAGTGGTTGCCTACGGGUACGCUGCTUGUC-3'
5'-(((((((((((((....)))).))))).))))-3'
Motif MFE = -12.6; z-score = -2.09; 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 = -3.17; 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(+)

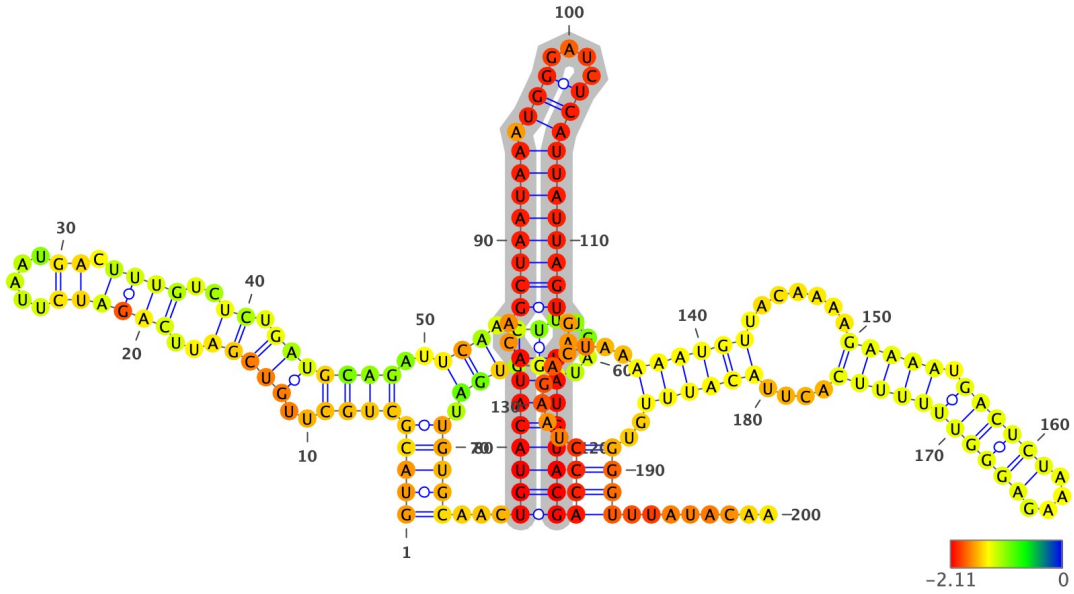
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 349 from nt 21009 to 21055 (nt 77 to 123)

```
5'-TGTACATACAGCTAATAAATGGGATCUCAUUAUUAGUGAUAUGUACG-3'
5'-((((((((..((((((((.(((....)))))))))))..))))))))-3'
Motif MFE = -16.4; z-score = -4.48; 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 20933 to 21132 (motif highlighted in silver):

```
5'-GUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUA
GUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAA-3
5'-(((((((((..(((((..((((((.....)).))))..)).)))))))..(((.((.....))))).)))))...((((((((..((((((((.(((....)))))))))
))..)))))))))((((.........((((((.......(((((.((((((....)))))))))))....))))))..))))........-3'
MFE = -42.6; z-score = -1.19; ED = 44.15
```

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(+)

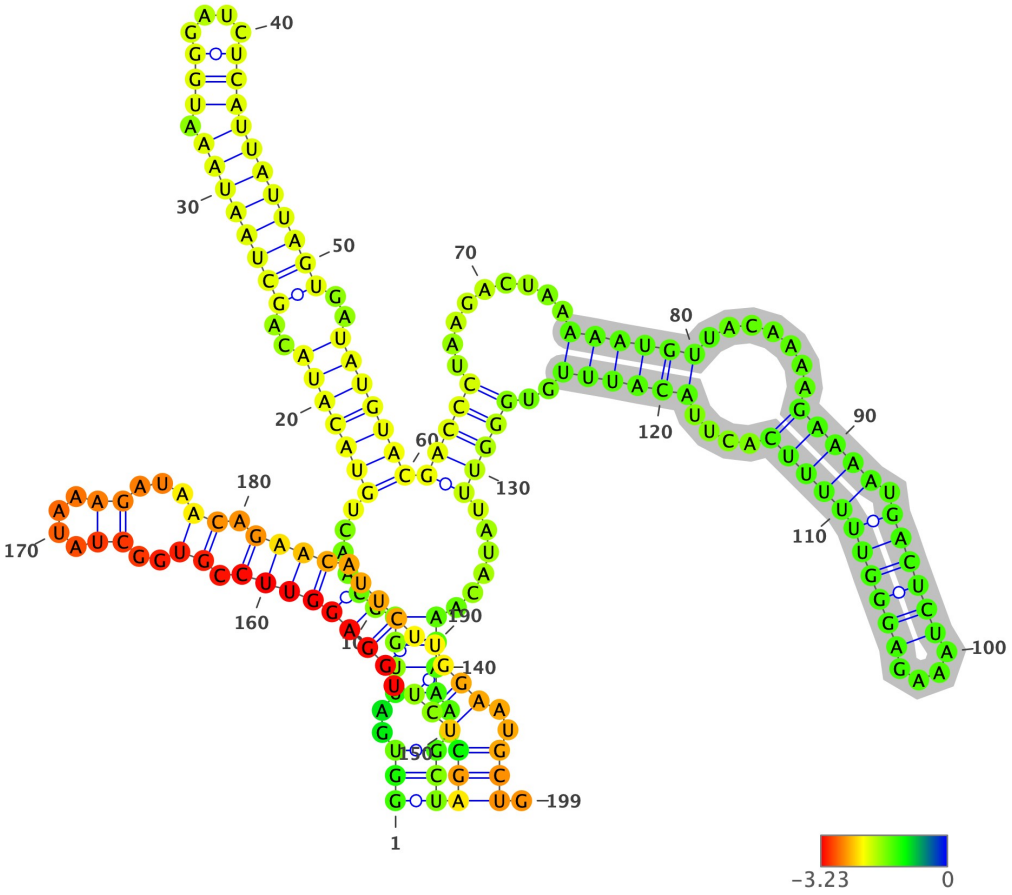
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 350 from nt 21069 to 21118 (nt 75 to 124)

```
5'-AAATGTTACAAAAGAAAATGACTCTAAAGAGGGUUUUUUCACTTACAUUU-3'
5'-((((((.......(((((.((((((....)))))))))))....))))))-3'
Motif MFE = -8.2; z-score = -1.84; ED = 6.51
```



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 20995 to 21193 (motif highlighted in silver):

```
5'-GGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUU
UUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUG-3
5'-(((..((((......(((((((..((((((((.(((....)))))))))))..)))))))(((((.........((((((.......(((((.((((((....))))))))
)))....))))))..)))))......))))..)))((((((.((((((((.((..((....))...)).)))).)))).)))..))).-3'
MFE = -43.7; z-score = -1.43; ED = 31.37
```

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(+)

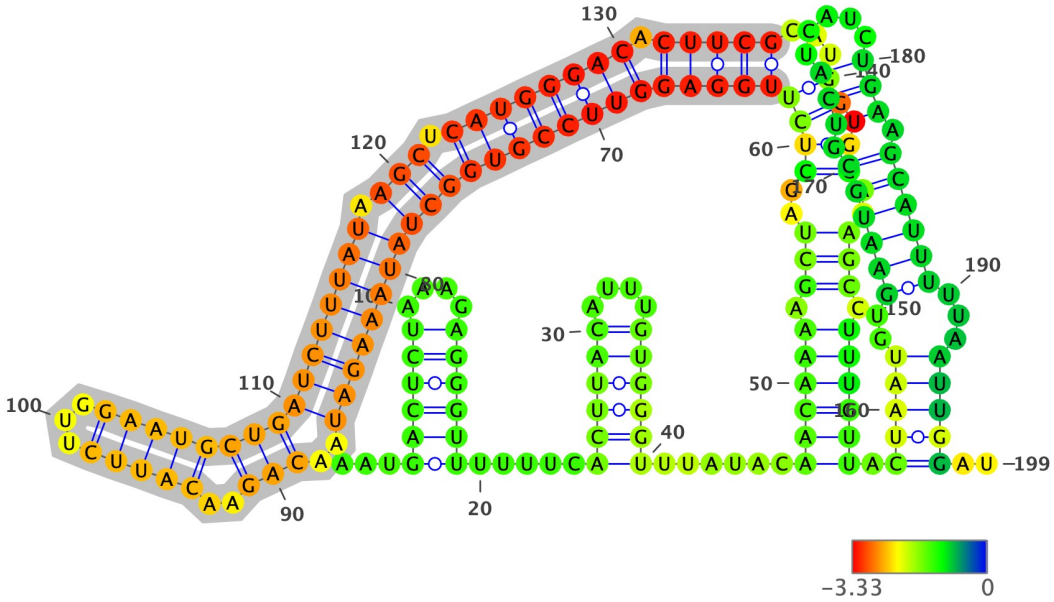
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 351 from nt 21147 to 21220 (nt 63 to 136)

```
5'-TGGAGGTTCCGTGGCTATAAAGATAACAGAACATTCTTGGAAUGCUGAUCUUUAUAAGCTCAUGGGACACUUCG-3'
5'-(((((((((((((((((((((((..(((..(((((...))))))))))))))).))).)))))))).)))))-3'
Motif MFE = -30.6; z-score = -5.71; 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 21085 to 21283 (motif highlighted in silver):

```
5'-AAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU
CUUUAUAAGCUCAUGGGACACUUCGCAUGGUGGACAGCCUUUGUUACUAAUGUGAAUGCGUCAUCAUCUGAAGCAUUUUUAAUUGGAU-3
5'-...((((((....))))))).....((((((....))))))......((((((.(((..((((((((((((((((((((((((((((..(((..(((((...)))))))))))
))))))).))).)))))))).)))))...)).))..))).)))))).(((((..((((((.(((.....))).))))))...)))))..-3'
MFE = -57.5; z-score = -3.22; ED = 14.21
```

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(+)

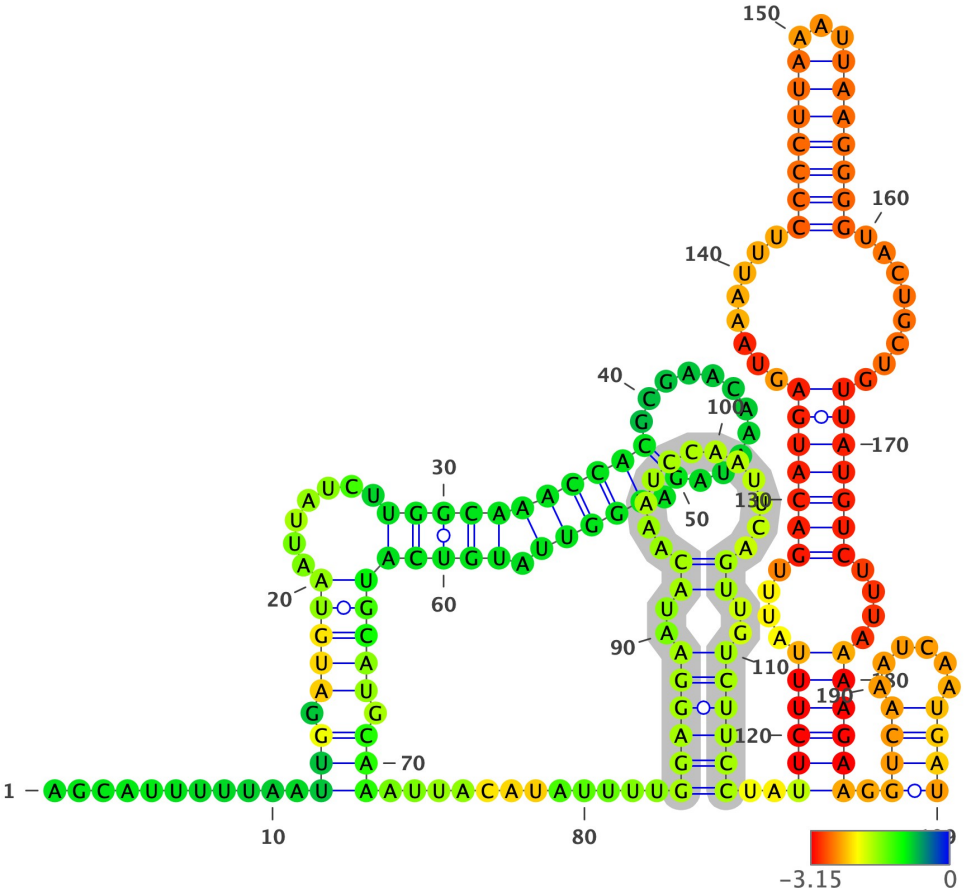
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 352 from nt 21350 to 21381 (nt 84 to 115)

```
5'-GGAGGAATACAAATCCAATTCAGUTGUCUUCC-3'
5'-((((((..((............))..))))))-3'
Motif MFE = -6.4; z-score = -2.02; ED = 2.14
```



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 21267 to 21465 (motif highlighted in silver):

```
5'-AGCAUUUUUAAUUGGAUGUAAUUAUCUUGGCAAACCACGCGAACAAAUAGAUGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUUCAGUUGUC
UUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAU-3
5'-...........(((.(((((.......((((((((((...........).)))))..)))))))))).)))............((((((..((............))..))
))))..((((((....(((((((........(((((((...)))))))).......)))))))....))))))..((((......))))-3'
MFE = -43.4; z-score = -1.96; ED = 35.56
```

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(+)

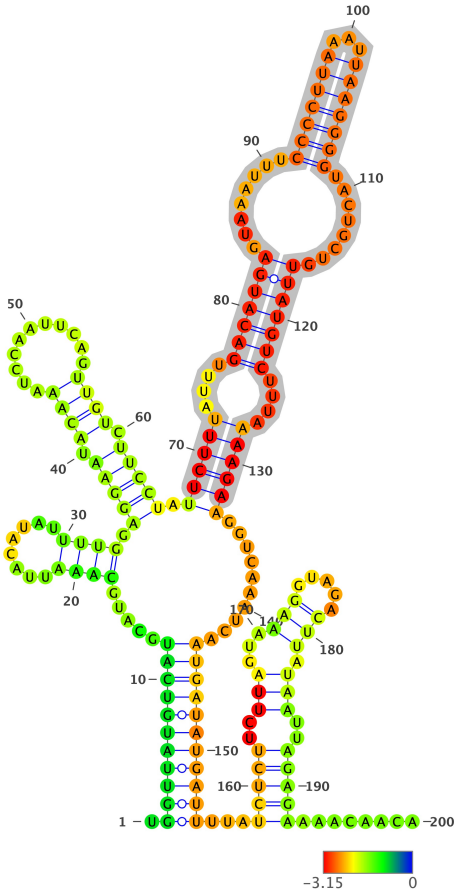
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 353 from nt 21385 to 21449 (nt 68 to 132)

```
5'-TCTTTATTTGACATGAGTAAATTTCCCCTTAAATUAAGGGGTACTGCTGUUAUGUCTTTAAAAGA-3'
5'-((((.....(((((((.........(((((((...)))))))........)))))))).....))))-3'
Motif MFE = -19.7; z-score = -4.38; ED = 4.28
```



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 21318 to 21517 (motif highlighted in silver):

```
5'-UGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUAC
UGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACA-3
5'-.(((((((((((.....((((.........)))).(((((.((((...........)))).))))).((((((....(((((((.........(((((((...)))))))...
.....)))))))....))))))..........))))))))))...(((((..(((...(((.....))).)))..)))))........-3'
MFE = -42.8; z-score = -1.96; ED = 39.55
```

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(+)

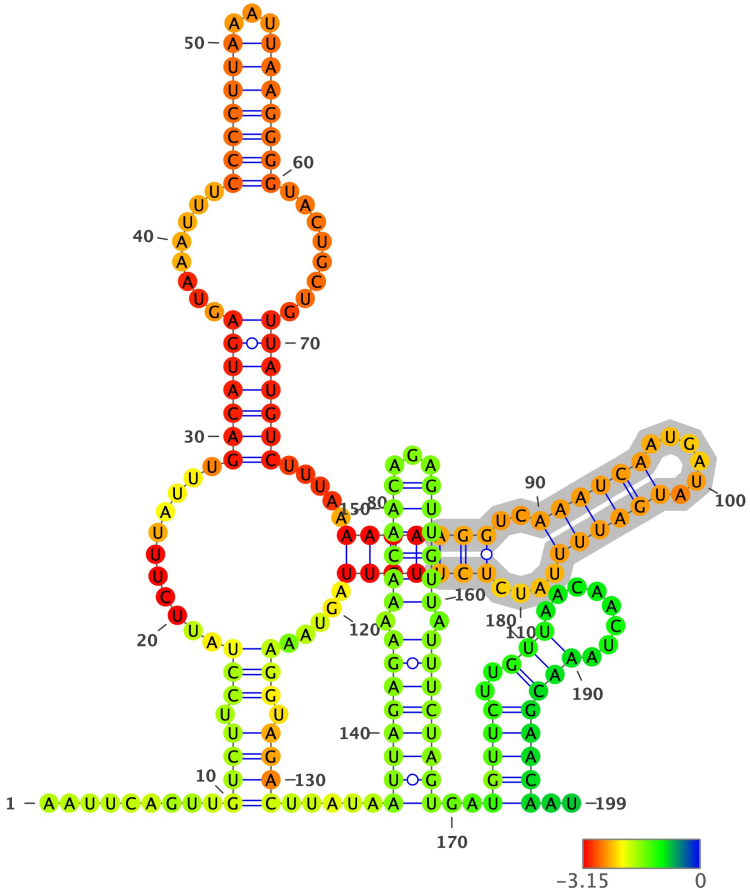
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 354 from nt 21450 to 21479 (nt 85 to 114)

```
5'-AGGTCAAATCAATGATAUGAUUUTATCUCU-3'
5'-(((..((((((.....))))))....)))-3'
Motif MFE = -5.0; z-score = -1.89; ED = 2.54
```



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 21366 to 21564 (motif highlighted in silver):

```
5'-AAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUC
UCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAAU-3
5'-.........((((.(((...........(((((((........(((((((...)))))))........)))))))).....(((((((..((((((.....))))))....
)))))))).....))).))))....((((((((.((((((...))))))..)))))))..((((..(((........)))))))..-3'
MFE = -46.1; z-score = -3.01; ED = 26.06
```

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 190--gene, gene-GU280_gp01, 266-21555(+)

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

3-- nt 1 to 190--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 198 to 199--gene, gene-GU280_gp02, 21563-25384(+)

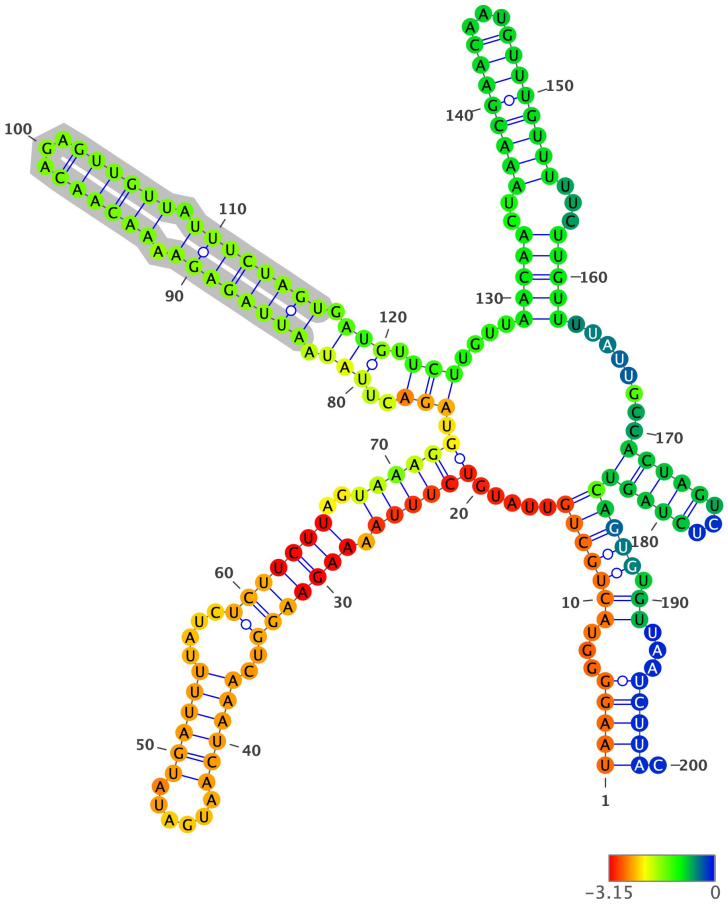
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 198 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 355 from nt 21502 to 21534 (nt 84 to 116)

```
5'-ATTAGAGAAAACAACAGAGUUGUUAUUUCUAGU-3'
5'-(((((((((.((((((...)))))).)))))))))-3'
Motif MFE = -10.2; z-score = -4.52; 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 21419 to 21618 (motif highlighted in silver):

```
5'-UAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUU
CUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUCUUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUAC-3
5'-(((((...(((((((.....((((((.(((((((..((((((......))))))....)))))))..))))))).(((..(((.(((((((((.((((((...)))))))))))))))))))))))))))))).)))....(((((..(((((((((...)))))))))...)))))........((((...))))))))))).))...))))).-3'
MFE = -39.1; z-score = -1.18; ED = 41.57
```

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 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(+)

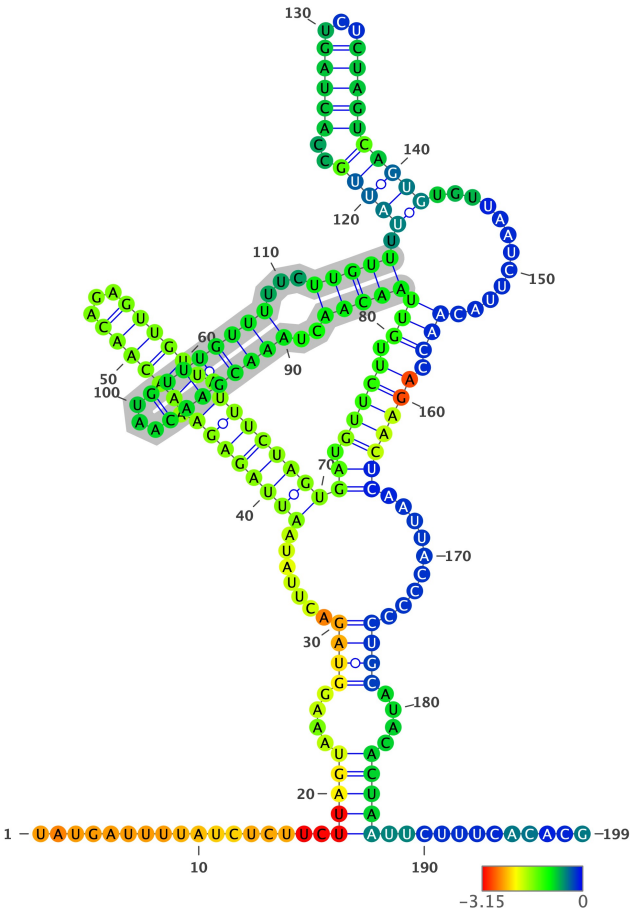
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 356 from nt 21547 to 21580 (nt 83 to 116)

```
5'-AACAACTAAACGAACAATGUUUGUUUTTCUUGUU-3'
5'-(..............................)-3'
Motif MFE = -6.3; z-score = -3.39; ED = 2.24
```



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 21465 to 21663 (motif highlighted in silver):

```
5'-UAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUC
UUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACG-3
5'-.................(((((....((((.......((((((((.((((((...)))))).))))))))((.(((((.((((((((..((((((((...))))))))...
))))).(((((..(((((...))))))))))............))).)))))))).........))))....)))))............-3'
MFE = -32.8; z-score = -1.22; ED = 31.56
```

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 91--gene, gene-GU280_gp01, 266-21555(+)

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

3-- nt 1 to 91--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 99 to 199--gene, gene-GU280_gp02, 21563-25384(+)

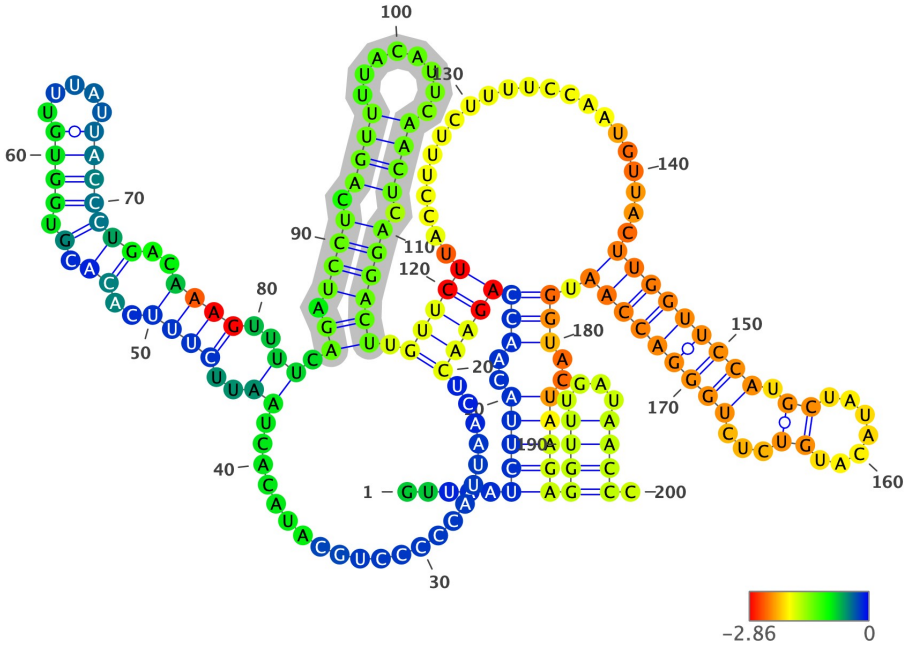
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 99 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 21692 to 21722 (nt 85 to 115)

```
5'-AGATCCTCAGTTTTACATTCAACUCAGGACU-3'
5'-((.((((.((((........)))).))))))-3'
Motif MFE = -5.8; z-score = -3.05; 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 = -1.23; 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(+)

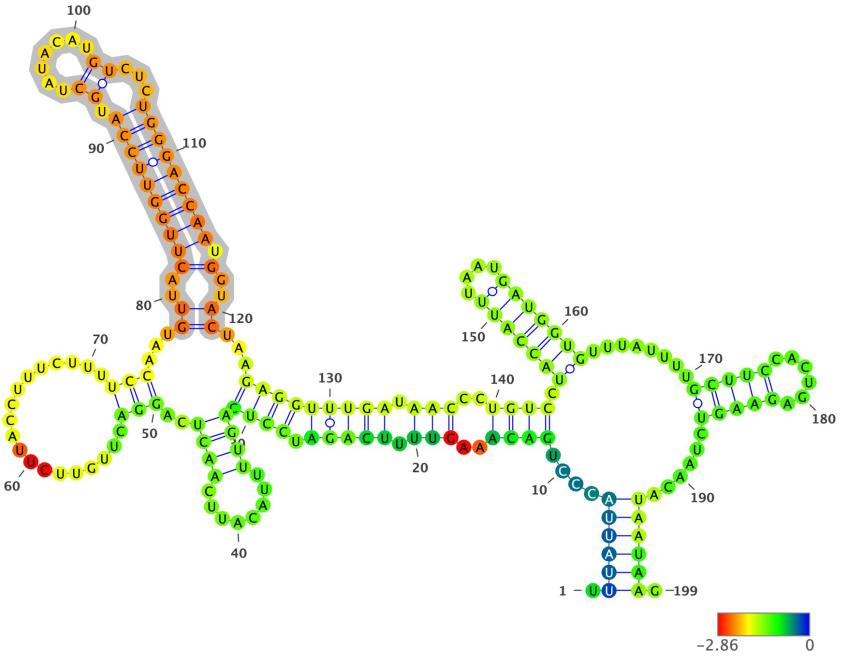
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 358 from nt 21746 to 21789 (nt 78 to 121)

```
5'-GTTACTTGGTTCCATGCTATACATGUCTCUGGGACCAATGGTAC-3'
5'-((..((((((((((.((.......))...)))))))))).)..))-3'
Motif MFE = -12.8; z-score = -2.25; 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 = -2.31; 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(+)

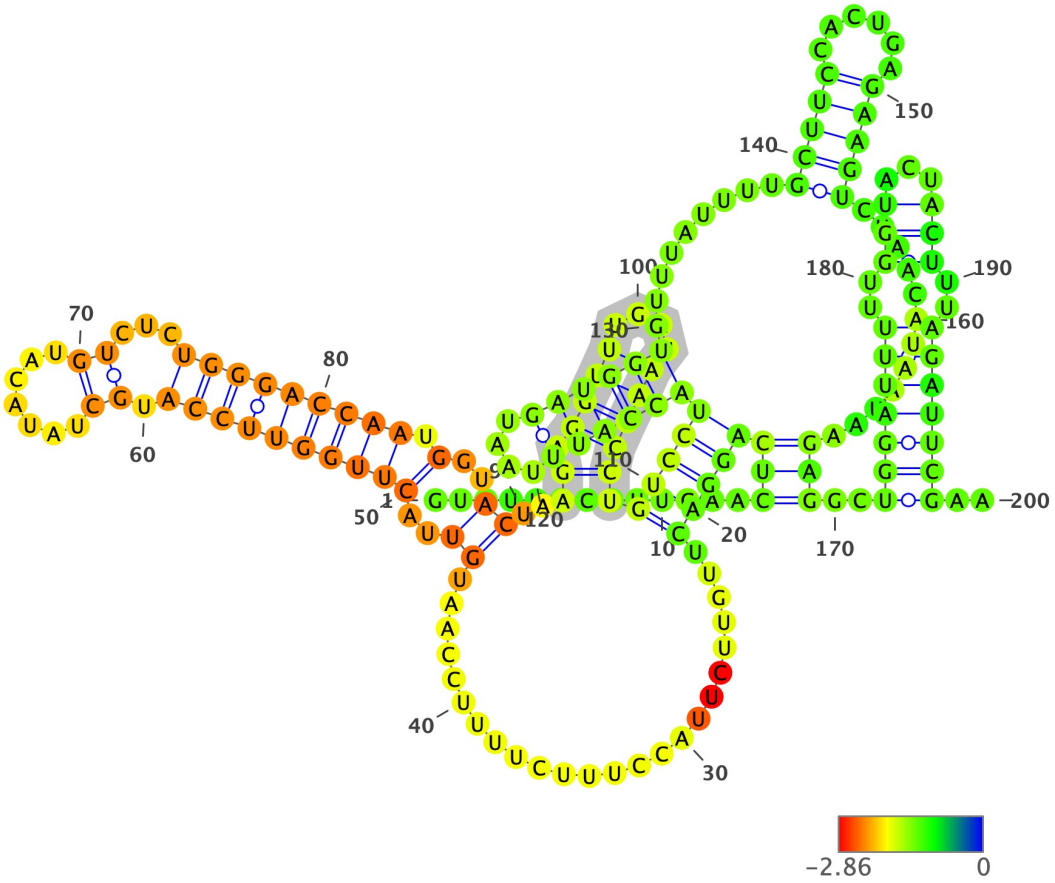
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 359 from nt 21792 to 21808 (nt 92 to 108)

```
5'-AGAGGTTTGATAACCCU-3'
5'-((.((((....))))))-3'
Motif MFE = -2.8; z-score = -2.18; 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 = -0.82; 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(+)

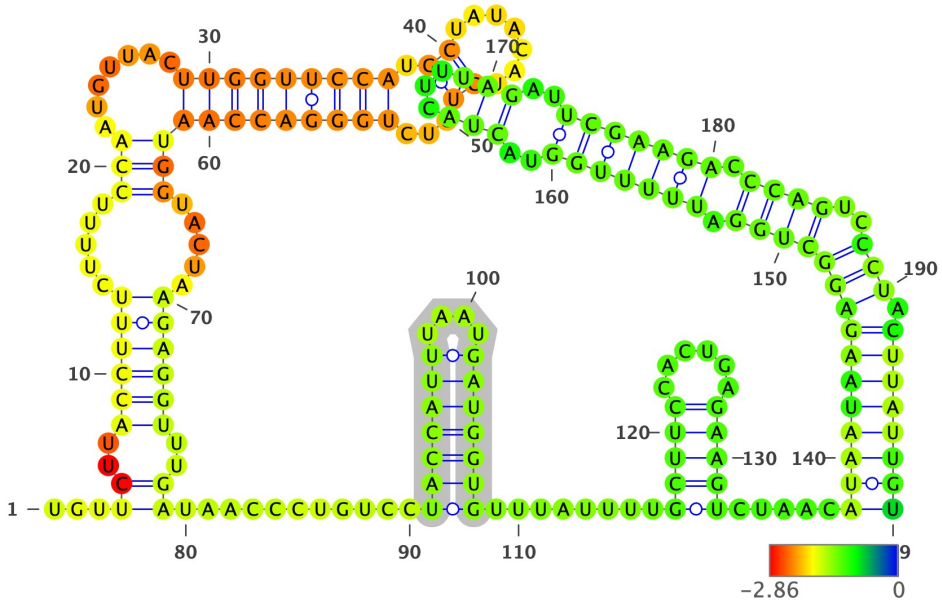
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 360 from nt 21813 to 21830 (nt 91 to 108)

```
5'-TACCATTTAATGAUGGUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.8; z-score = -4.75; 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 = -2.45; 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(+)

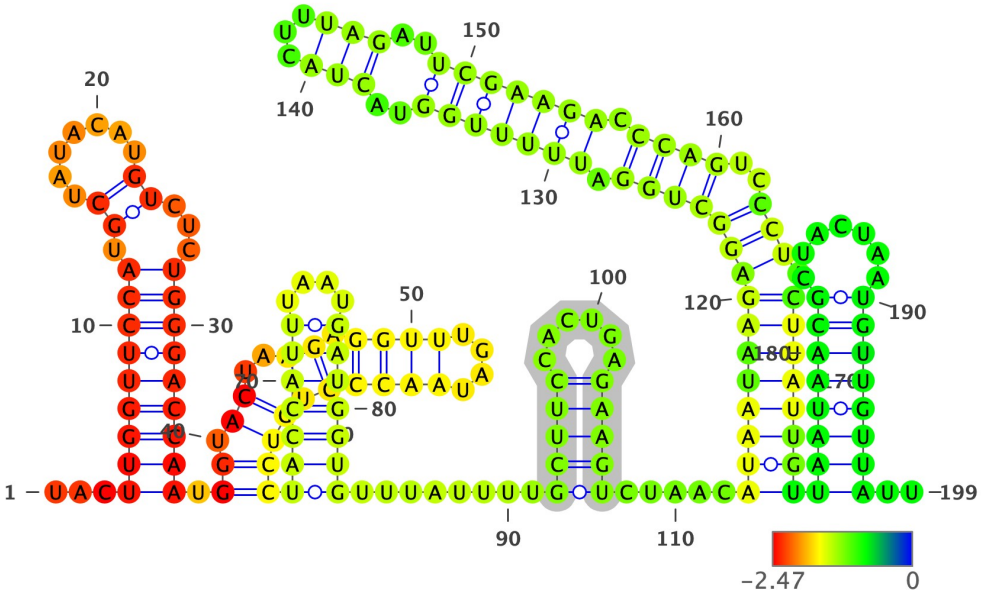
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 361 from nt 21839 to 21854 (nt 92 to 107)

```
5'-GCTTCCACTGAGAAGU-3'
5'-(((((......)))))-3'
Motif MFE = -3.0; z-score = -1.92; 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 = -1.98; 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(+)

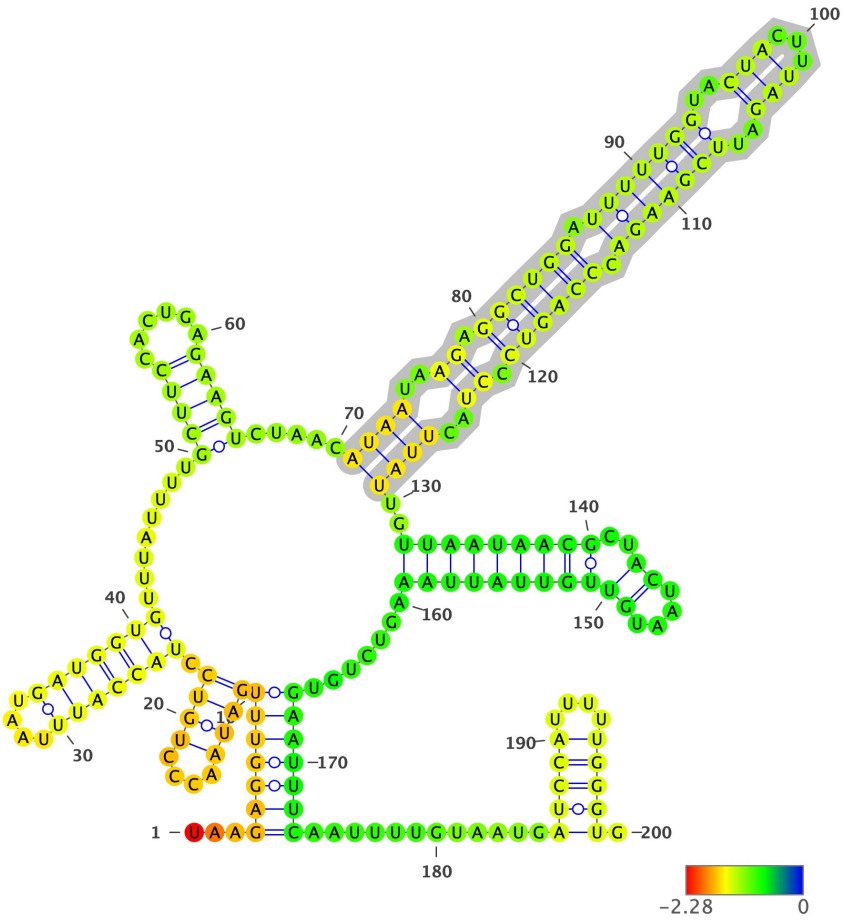
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 362 from nt 21860 to 21918 (nt 71 to 129)

```
5'-ATAATAAGAGGCTGGATTTTTGGTACTACTTUAGATUCGAAGACCCAGUCCCUACUUAU-3'
5'-((((..((.(((((((.(((((((..(((...))))..)))))))).)))))))..))))-3'
Motif MFE = -14.2; z-score = -2.39; ED = 10.15
```



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 21790 to 21989 (motif highlighted in silver):

```
5'-UAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAA
GACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUG-3
5'-...((((((((((....)))).(((((((....)))))))).......((((......)))))).....((((..((.((((((.(((((((..(((...))).))))))
)).)))))).))..)))).((((((((((..((....))))))))))).......)))))).....((((((....)))))).-3'
MFE = -39.8; z-score = -1.13; ED = 34.49
```

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_gp02, 21563-25384(+)

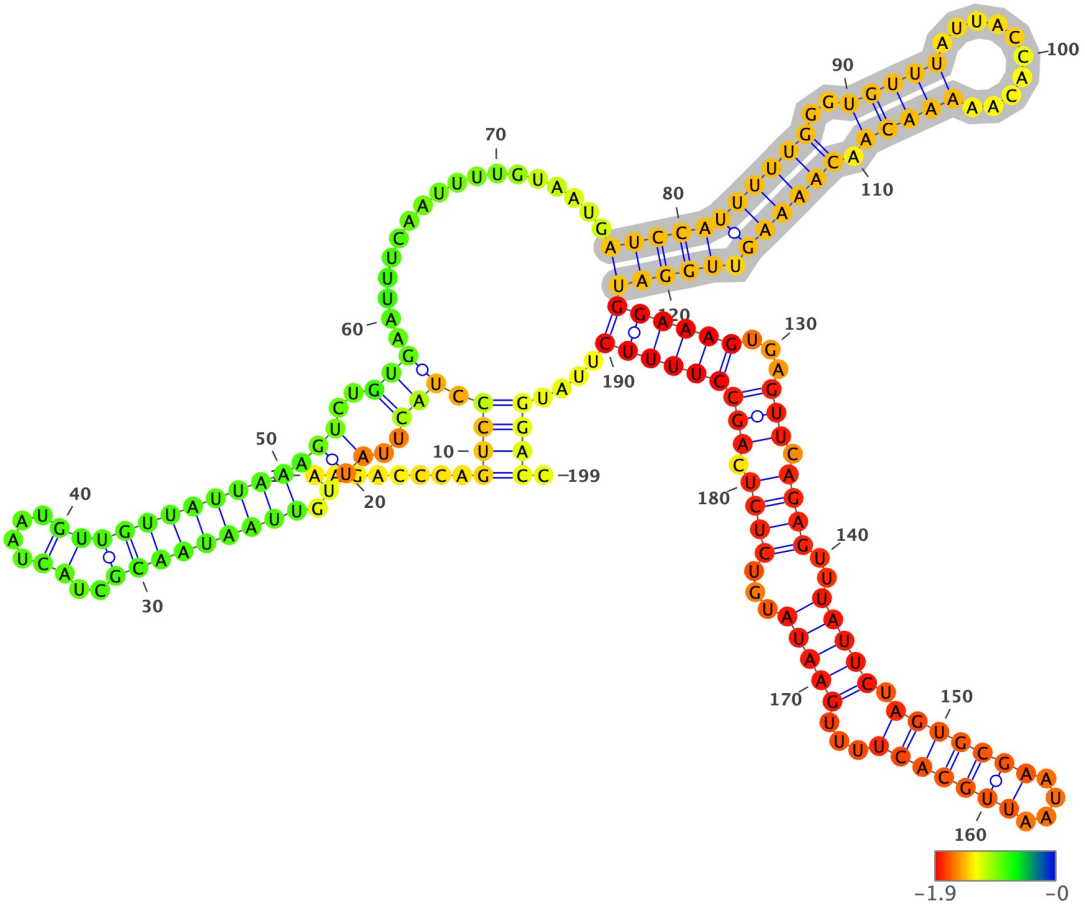
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 363 from nt 21975 to 22020 (nt 77 to 122)

```
5'-ATCCATTTTTGGGTGTTTATTACCACAAAAACAACAAAAGTUGGAU-3'
5'-(((((((((((..(((((..........))))).))))))).)))))-3'
Motif MFE = -9.8; z-score = -2.2; ED = 15.02
```



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 21899 to 22097 (motif highlighted in silver):

```
5'-AAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAAC
AAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACC-3
5'-........((((.(((..(((.(((((((((..((....))))))))))))))..))).................(((((((((((..(((((..........))))).)
))))).)))))((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))....)))).-3'
MFE = -41.3; z-score = -1.78; ED = 31.78
```

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(+)

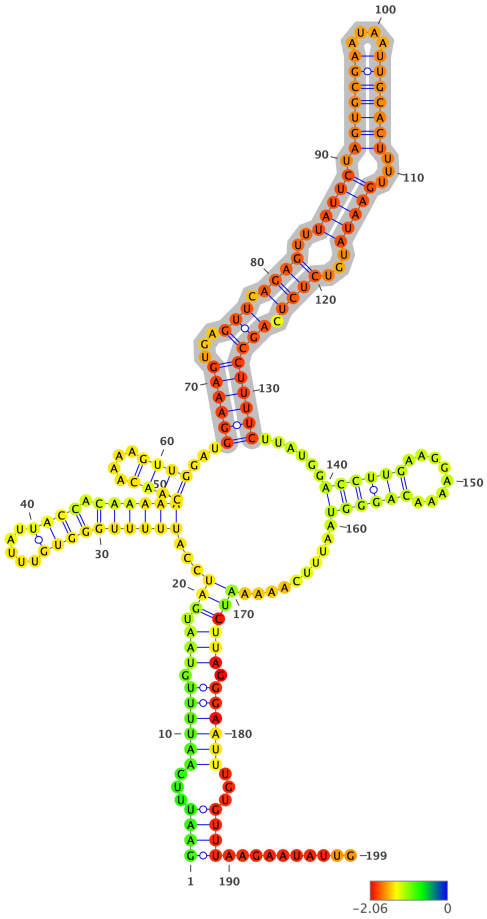
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 364 from nt 22021 to 22088 (nt 66 to 133)

```
5'-GGAAAGTGAGTTCAGAGTTTATTCTAGTGCGAATAAUUGCACUTTTGAAUATGTCUCUCAGCCUUUUC-3'
5'-((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).)))))))))-3'
Motif MFE = -18.5; z-score = -2.7; ED = 9.7
```



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 21956 to 22154 (motif highlighted in silver):

```
5'-GAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUU
GAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUG-3
5'-((((...((((((.(((.(((...(((((((((((.....)))).))))))((((....))))...((((((...(((.((((..(((((.(((((((....)))))))...
)))))...)))).))))))))).....((((((.........))))))..........))))))).))))))...))))..........-3'
MFE = -41.8; z-score = -1.31; ED = 38.87
```

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(+)

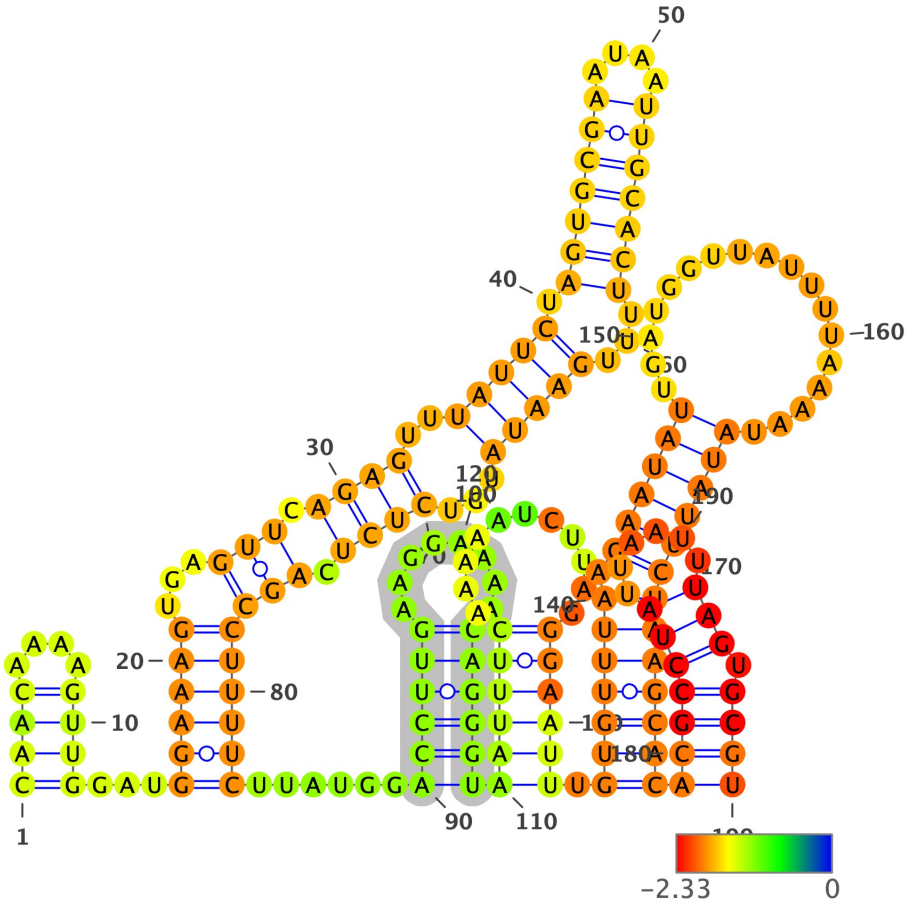
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 365 from nt 22095 to 22114 (nt 90 to 109)

```
5'-ACCTTGAAGGAAAACAGGGU-3'
5'-((((((........))))))-3'
Motif MFE = -5.4; z-score = -4.52; 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 = -2.27; 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(+)

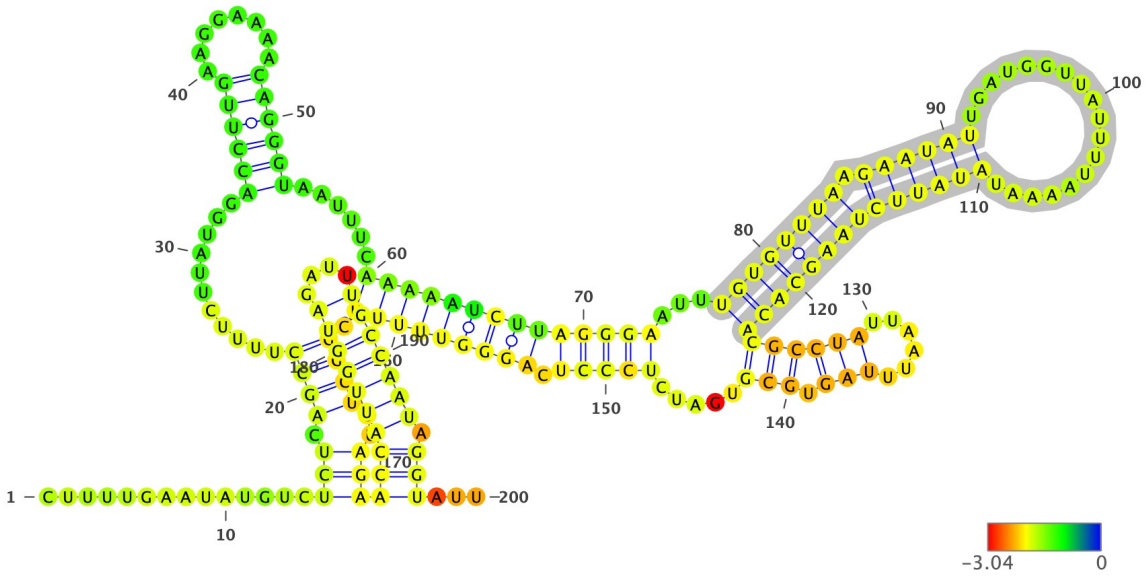
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 366 from nt 22138 to 22184 (nt 77 to 123)

```
5'-TGTGTTTAAGAATATTGATGGTTATTTTAAAATAUAUUCUAAGCACA-3'
5'-(((((((((.((((((.................))))))))))))))-3'
Motif MFE = -10.1; z-score = -2.77; ED = 5.42
```



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 22062 to 22261 (motif highlighted in silver):

```
5'-CUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAU
AUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUU-3
5'-..............(((.((((...........((((((........))))))......((((((((((((((...((((((((.((((((.................))
))))))))))))((((((......))).))).....)))))).))))))))).))))..)))((((((((((....)))))))).)))...-3'
MFE = -49.7; z-score = -3.16; ED = 12.8
```

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(+)

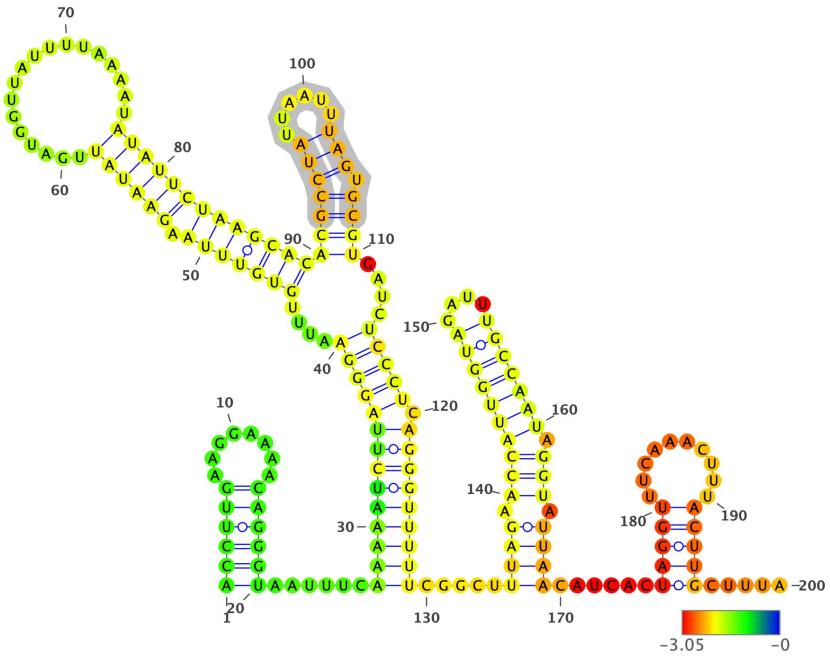
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 367 from nt 22186 to 22202 (nt 92 to 108)

```
5'-GCCTATTAATTUAGTGC-3'
5'-(((((......))).))-3'
Motif MFE = -2.1; z-score = -1.72; 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 = -2.29; 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 200--gene, gene-GU280_gp02, 21563-25384(+)

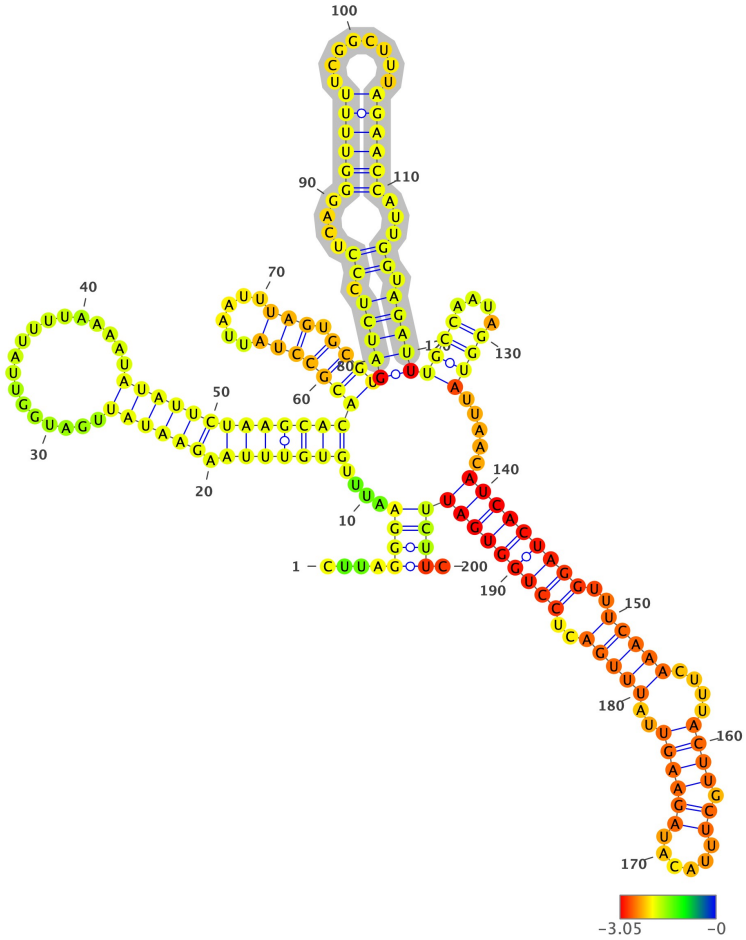
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 368 from nt 22206 to 22246 (nt 80 to 120)

```
5'-ATCTCCCTCAGGGTTTTTCGGCTTTAGAACCATTGGTAGAU-3'
5'-((((.((....((((((........))))))...)).))))-3'
Motif MFE = -9.6; z-score = -1.95; ED = 2.29
```



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 22127 to 22326 (motif highlighted in silver):

```
5'-CUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCA
UUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUC-3
5'-....((((....(((((((.((((((.................))))))))))))))(((((((......))).))))(((((.((....((((((........))))))).
..)).)))))((((....)))).....(((((((((..(((((....((((.((......))))))..)))))..))))))))))))).-3'
MFE = -52.4; z-score = -3.37; 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_gp02, 21563-25384(+)

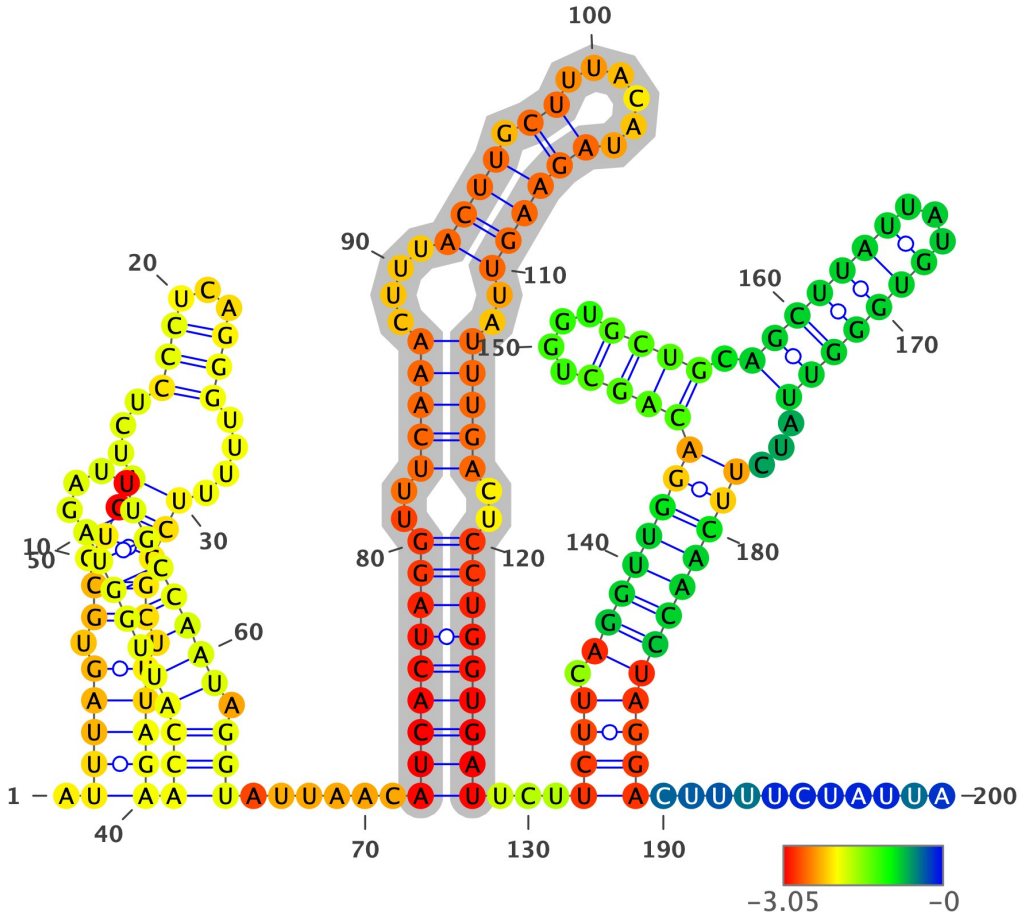
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 369 from nt 22265 to 22321 (nt 72 to 128)

```
5'-ATCACTAGGTTTCAAACTTTACTTGCTTTACATAGAAGUTAUUUGACTCCUGGUGAU-3'
5'-((((((((((..(((((....((((.((......))))))..)))))..)))))))))-3'
Motif MFE = -18.6; z-score = -4.31; 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 = -3.06; 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(+)

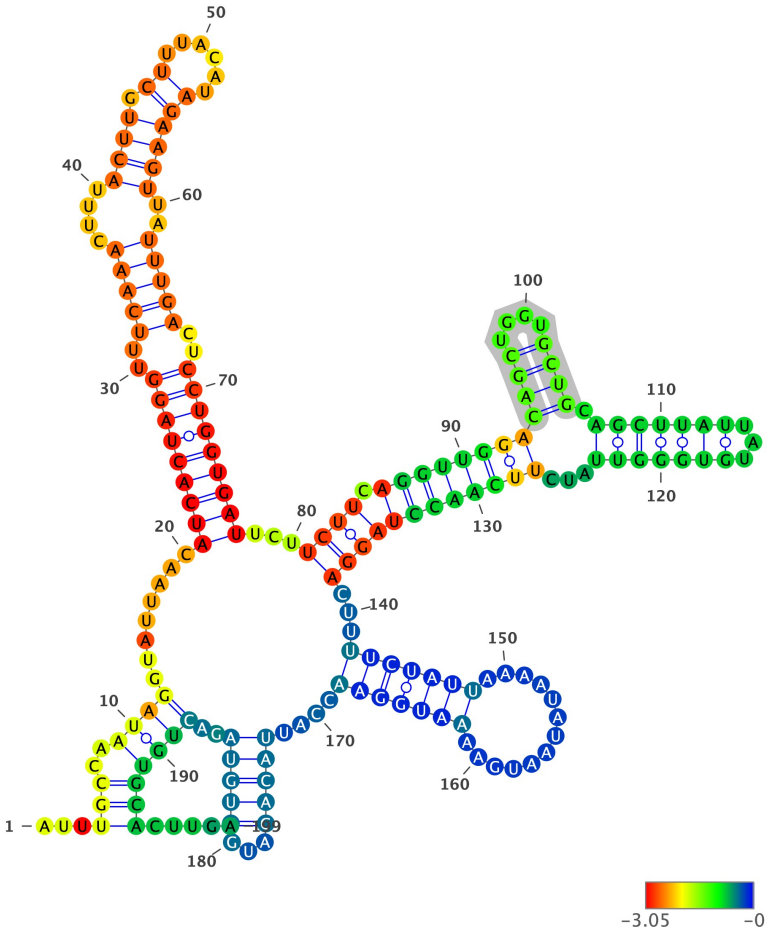
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 370 from nt 22338 to 22349 (nt 94 to 105)

```
5'-CAGCTGGTGCUG-3'
5'-((((....))))-3'
Motif MFE = -4.1; z-score = -4.06; 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 22245 to 22443 (motif highlighted in silver):

```
5'-AUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUGCUGCAGCUU
AUUAUGUGGGUUAUCUUCAACCUAGGACUUUUCUAUUAAAAUAUAAUGAAAAUGGAACCAUUACAGAUGCUGUAGACUGUGCACUUGA-3
5'-...(((..((((........(((((((((..(((((....((((.((......))))))..))))))..))))))))))...((((.((((((((((....)))))).(((((
((...)))))))...))))))))))...(((((((.............)))))))....((((((...))))))..)))))))......-3'
MFE = -45.5; z-score = -2.06; ED = 34.22
```

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_gp02, 21563-25384(+)

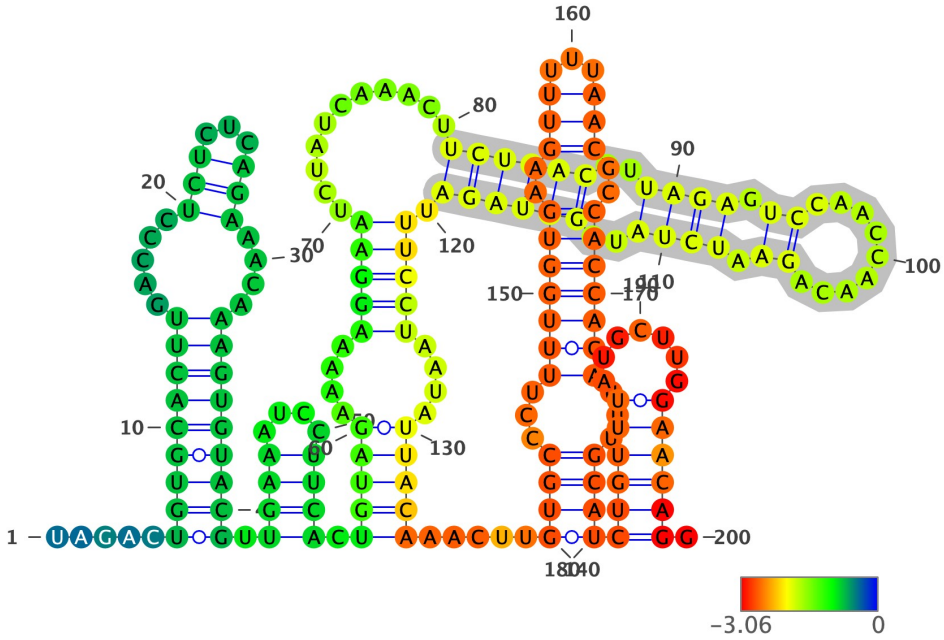
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22508 to 22546 (nt 81 to 119)

```
5'-TCTAACTTTAGAGTCCAACCAACAGAATCUATTGUUAGA-3'
5'-((((((..(((((.((.........)).)))))..)))))))-3'
Motif MFE = -9.2; z-score = -3.76; 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 = -1.71; 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(+)

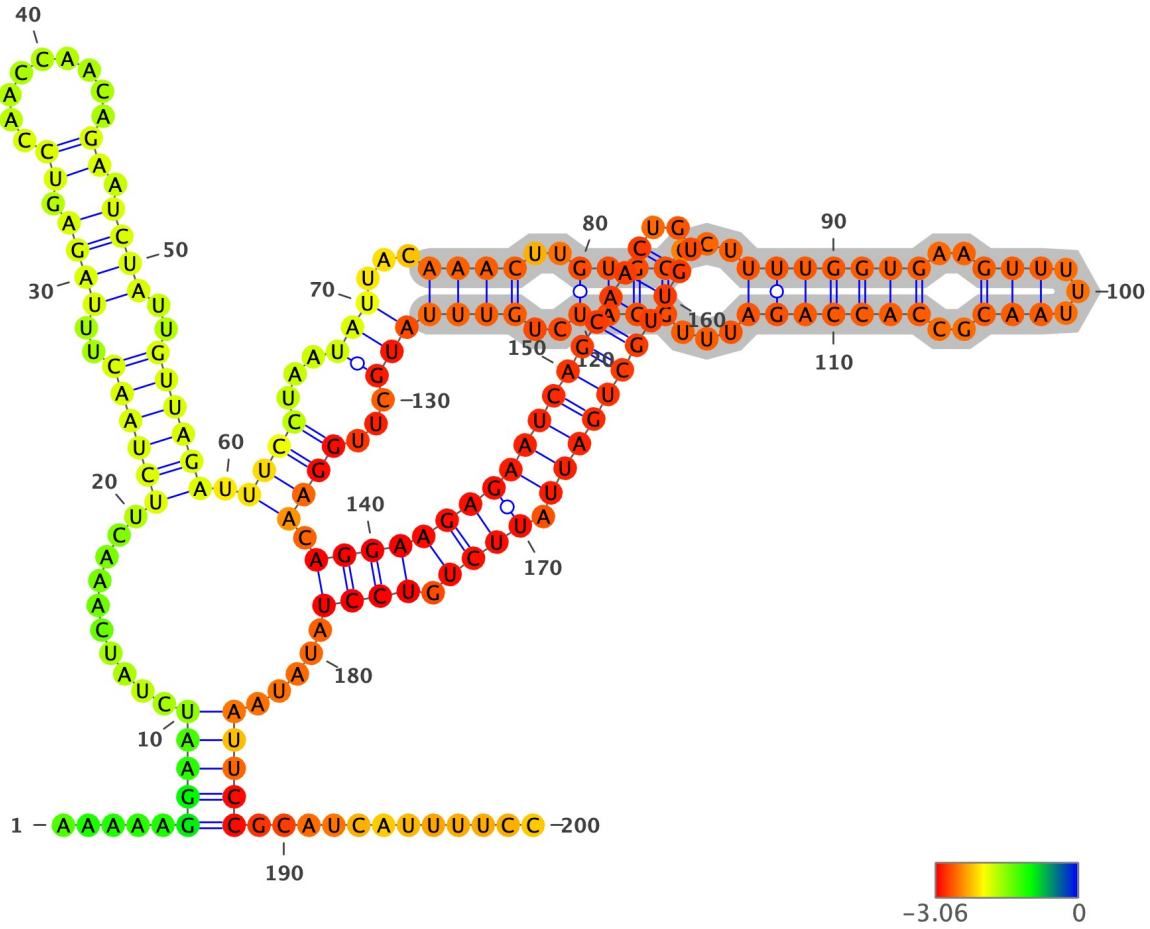
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 372 from nt 22561 to 22613 (nt 74 to 126)

```
5'-AAACTTGTGCCCTTTTGGTGAAGTTTTTAACGCCACCAGATTTGCAUCTGUUU-3'
5'-((((..((((...(((((((..(((...)))..)))))))...))))..))))-3'
Motif MFE = -15.2; z-score = -3.3; 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 = -3.88; ED = 20.83
```

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_gp02, 21563-25384(+)

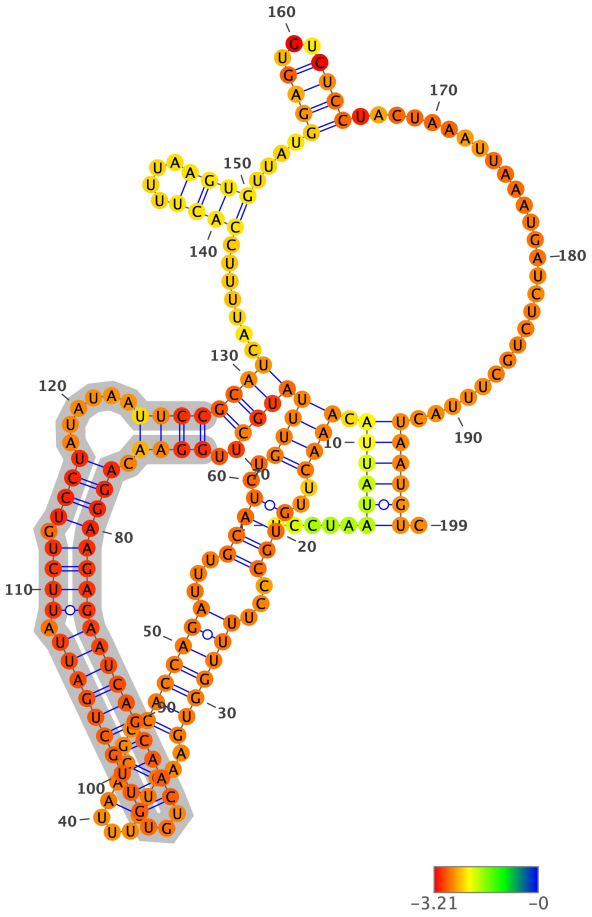
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22620 to 22675 (nt 72 to 127)

```
5'-GGAACAGGAAGAGAATCAGCAACTGTGUUGCUGAUUAUUCUGUCCUATATAATTCC-3'
5'-((...(((((((((((((((((...)))))))))).)))).))))........))-3'
Motif MFE = -19.6; z-score = -4.2; ED = 9.64
```



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 22549 to 22747 (motif highlighted in silver):

```
5'-UCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUC
UGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUC-3
5'-.....((((((.((((..((((...(((((((..(((...)))..)))))))...))))..))))((((..((((.((((((((((((((((((...)))))))))).)))
).))))......))))))))).......((((....))))....((((...))))..........................)))))).-3'
MFE = -46.1; z-score = -2.88; ED = 23.92
```

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_gp02, 21563-25384(+)

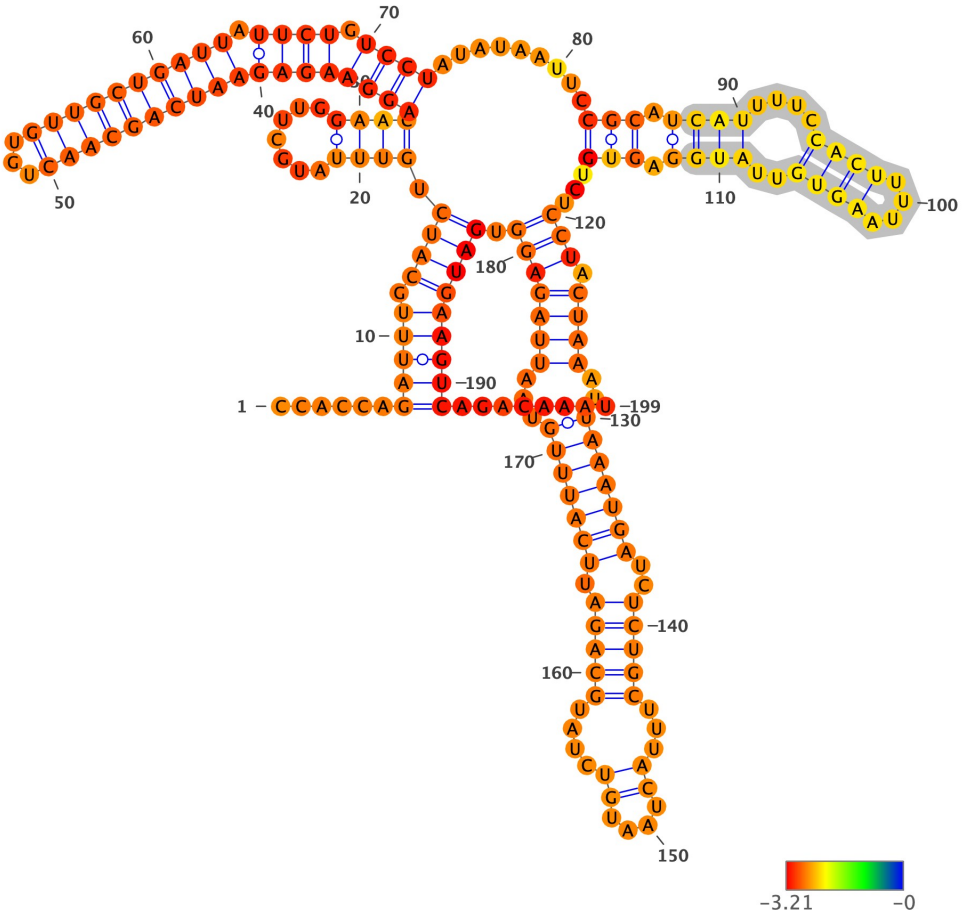
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22680 to 22703 (nt 88 to 111)

```
5'-CATTTTCCACTTTTAAGUGTTATG-3'
5'-(......((((....))))....)-3'
Motif MFE = -2.0; z-score = -1.38; ED = 1.85
```



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 22593 to 22791 (motif highlighted in silver):

```
5'-CCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUG
GAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAU-3
5'-......(((((.((((.((((.......))))((((((((((((((((((...)))))))))).)))).))))..........(((.((((....((((....))))..)))
).)))...(((.((((..(((((((..(((((...((....))....)))))).)))))))...)))))))).))))))))).........-3'
MFE = -50.8; z-score = -3.06; ED = 31.39
```

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_gp02, 21563-25384(+)

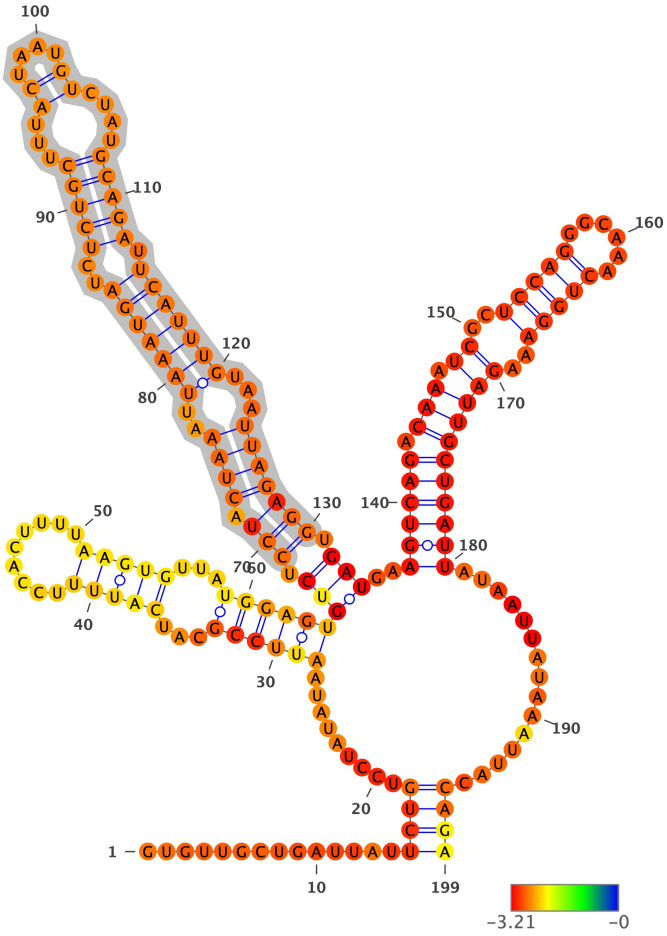
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22712 to 22773 (nt 69 to 130)

```
5'-CCTACTAAATTAAATGATCTCTGCTTTACTAATGTCTATGCAGATCAUUUGTAAUUAGAGG-3'
5'-((..(((((..(((((((..(((((.............)))))).)))))))...))))).))-3'
Motif MFE = -15.9; z-score = -3.95; ED = 3.42
```



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 22644 to 22842 (motif highlighted in silver):

```
5'-GUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAG
AUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGA-3
5'-..............((((.........((((((...(((((.........)))))...))))))))(((.(((.(((((..(((((((..((((((...((....)).....))))
).)))))))...)))))))..)))..((((((.(((.((..(((((......)))))..))))))))))).............))))-3'
MFE = -46.3; z-score = -2.41; ED = 30.23
```

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(+)

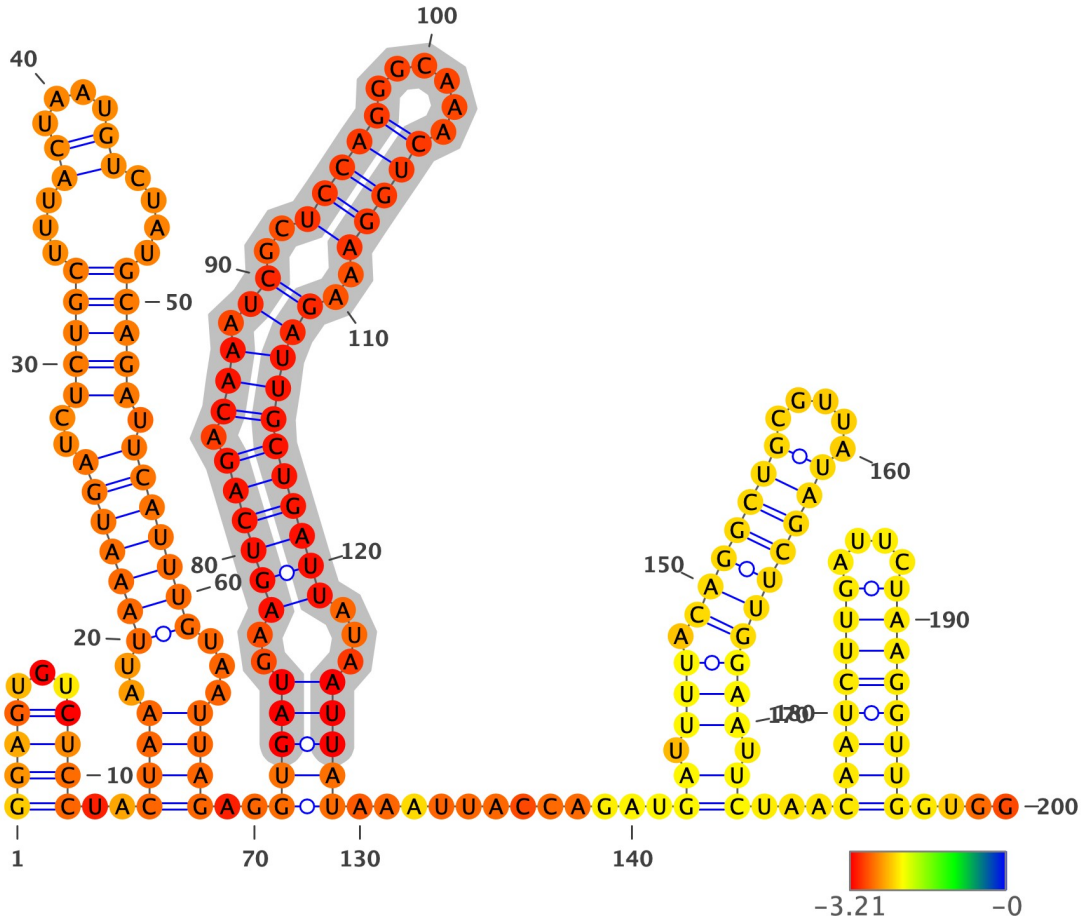
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 376 from nt 22775 to 22829 (nt 73 to 127)

```
5'-GATGAAGTCAGACAAATCGCTCCAGGGCAAACUGGAAAGAUUGCUGAUUATAAUU-3'
5'-(((..(((((((.(((.((..(((((.....)))))..)))))))))))...)))-3'
Motif MFE = -17.5; z-score = -4.12; ED = 3.69
```



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 22703 to 22902 (motif highlighted in silver):

```
5'-GGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAG
AUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUGG-3
5'-(((((...)))))..(((((..(((((((..((((((...((....))....))))).)))))))...)))))..((((((..((((((.(((.((..(((((.....)))))..)
))))))))))...)))))).....((.(((.(((((((.....))))))))))).))...(((((((((....)))))))))....-3'
MFE = -50.5; z-score = -3.47; ED = 28.1
```

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_gp02, 21563-25384(+)

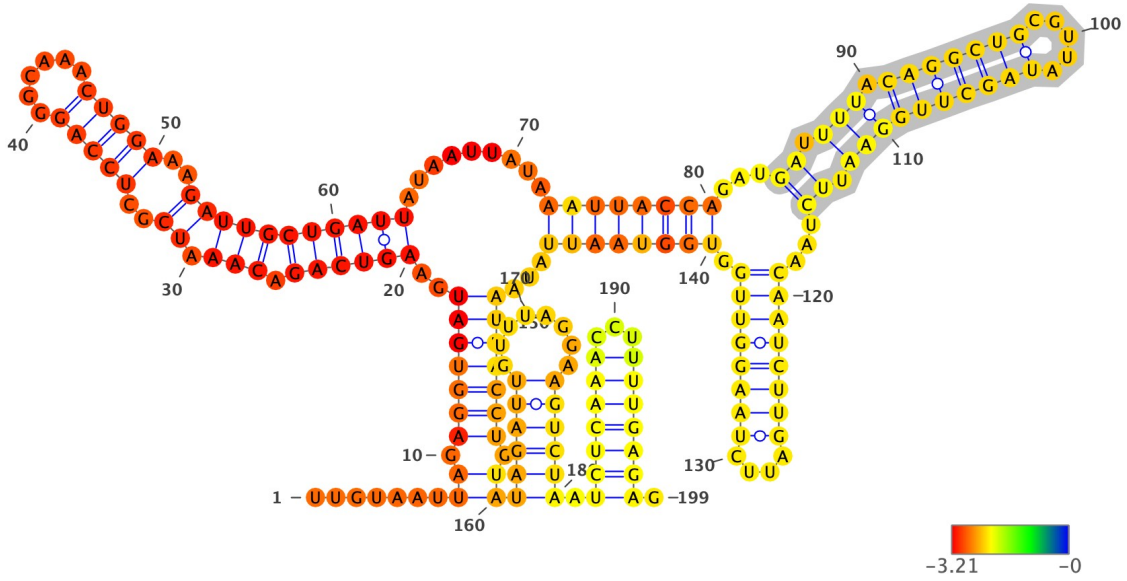
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22844 to 22875 (nt 84 to 115)

```
5'-GATTTTACAGGCTGCGTTAUAGCUUGGAATUC-3'
5'-((.(((.(((((((.....)))))))))).))-3'
Motif MFE = -7.3; z-score = -1.94; ED = 4.2
```



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 22761 to 22959 (motif highlighted in silver):

```
5'-UUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGA
AUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAG-3
5'-.......((.(((((((..((((((.(((.((..(((((......)))))..))))))))))).........((((((((...((.(((.(((((((.....)))))))))
).))...((((((((....)))))))).))))))))...)))))))).))((((((........)))))).(((((((...))))))).-3'
MFE = -54.5; z-score = -4.13; ED = 14.44
```

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_gp02, 21563-25384(+)

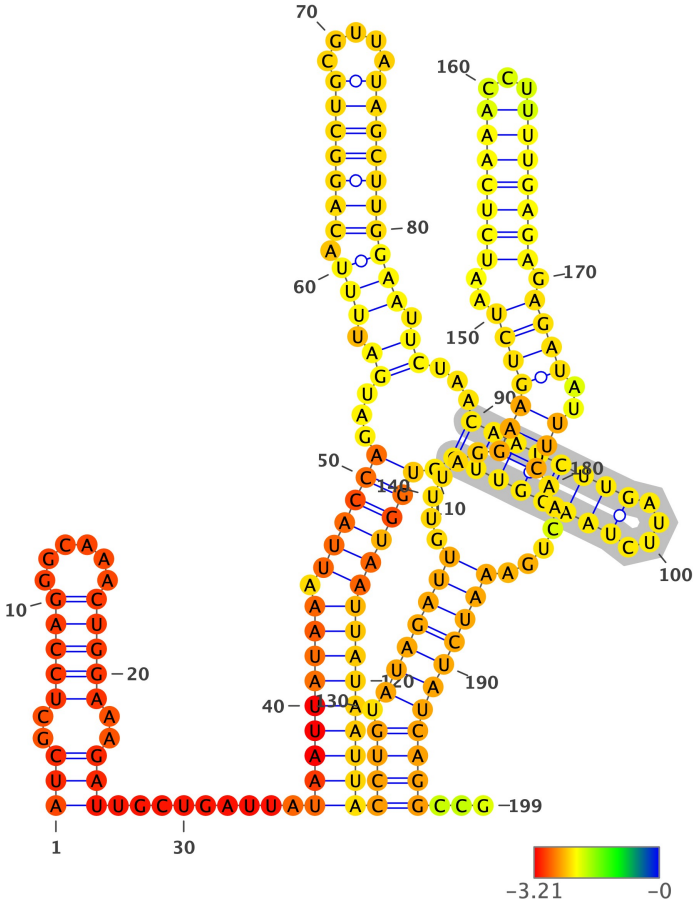
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 378 from nt 22879 to 22898 (nt 90 to 109)

```
5'-CAATCTTGATTCUAAGGUUG-3'
5'-((((((((....))))))))-3'
Motif MFE = -4.8; z-score = -3.4; 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 = -3.82; ED = 20.61
```

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_gp02, 21563-25384(+)

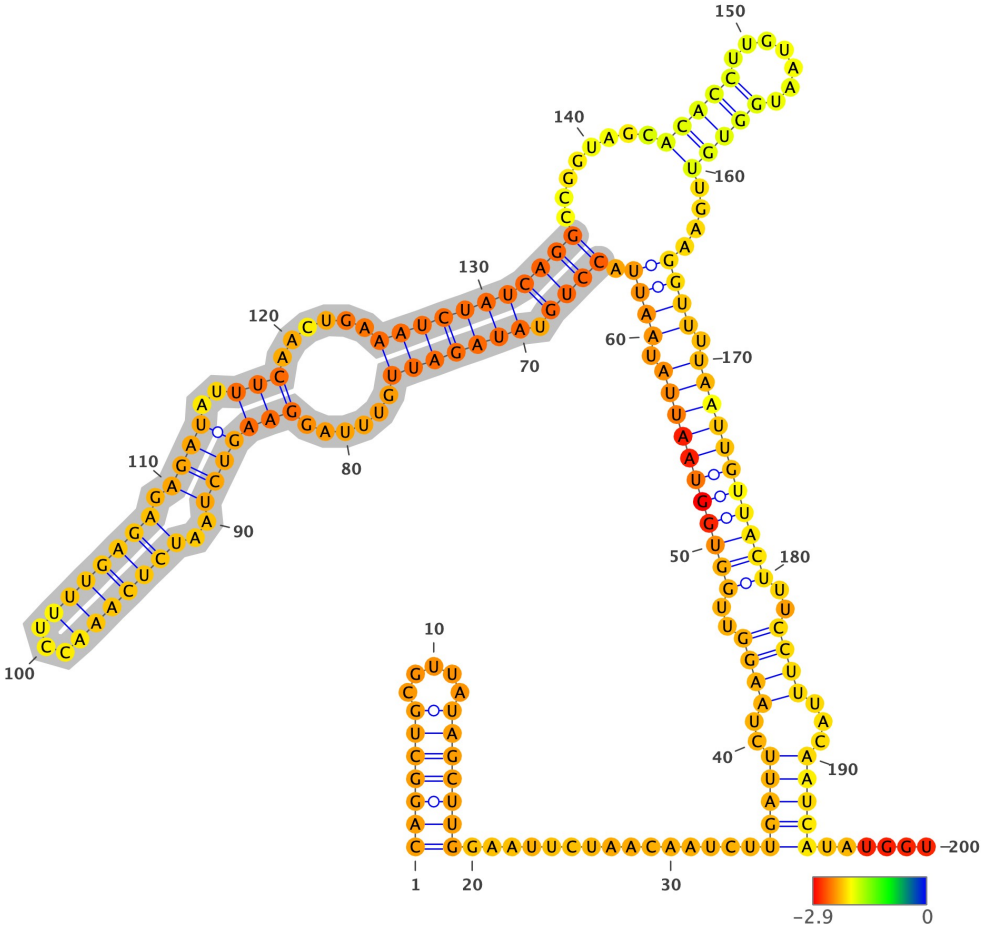
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 379 from nt 22915 to 22985 (nt 65 to 135)

```
5'-CCTGTATAGATTGTTTAGGAAGTCTAATCTCAAACCTTUUGAGAGAGAUATUUCAACTGAAAUCUAUCAGG-3'
5'-((((.(((((((.....(((((((..((((((.....)))))).))))..)))......)))))))))))-3'
Motif MFE = -21.1; z-score = -4.22; 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 = -3.13; ED = 32.65
```

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_gp02, 21563-25384(+)

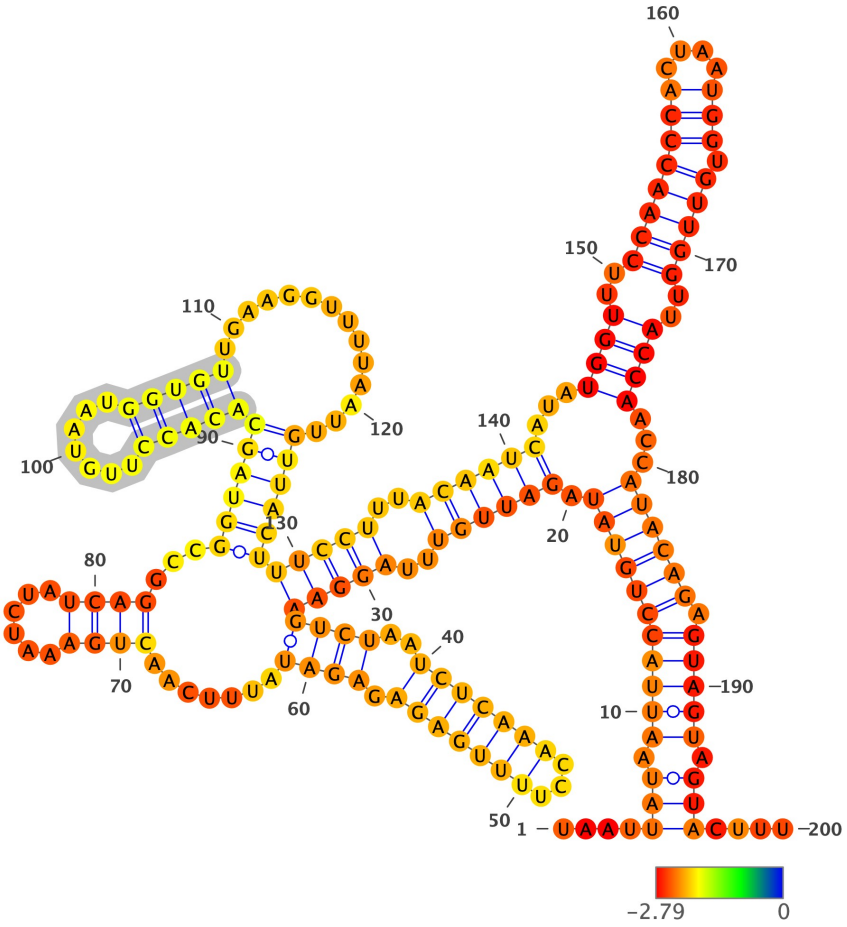
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 380 from nt 22994 to 23010 (nt 92 to 108)

```
5'-ACACCTTGTAATGGUGU-3'
5'-(((((.......)))))-3'
Motif MFE = -5.4; z-score = -3.59; 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 = -3.98; 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(+)

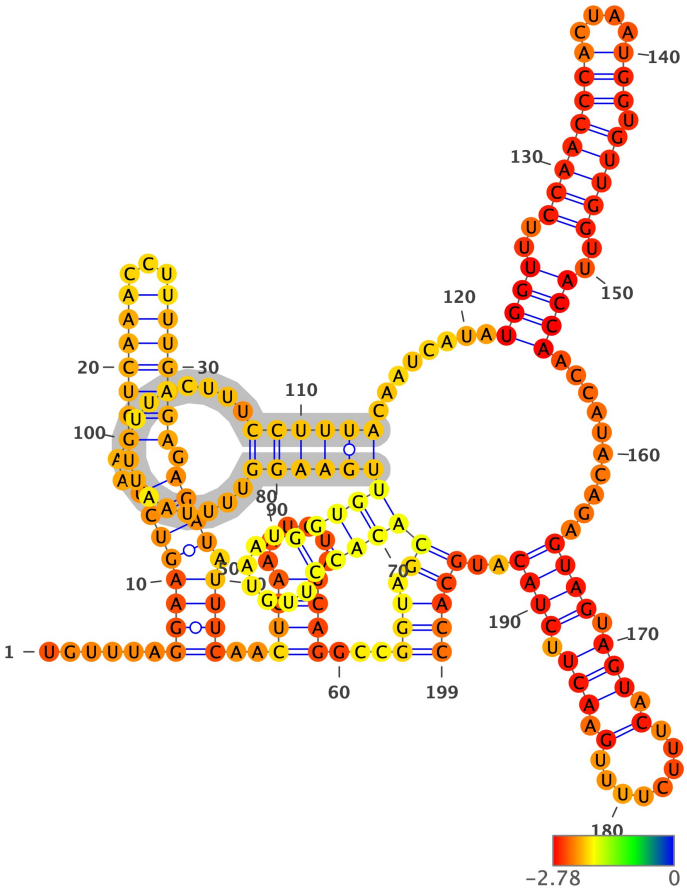
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 381 from nt 23011 to 23038 (nt 86 to 113)

```
5'-TGAAGGTTTTAATTGTTACTTTCCUUUA-3'
5'-((((((................))))))-3'
Motif MFE = -3.4; z-score = -1.54; ED = 6.44
```



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 22926 to 23124 (motif highlighted in silver):

```
5'-UGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUU
UACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACC-3
5'-......((((((((..(((((((...)))))))).)))).))))..((((......))))...(((.(((((((.......)))))((((((................))))
))........((((..((((((((....))).)))))..))))..........((((.(((.(........).))).)))))..)))))-3'
MFE = -48.0; z-score = -3.21; ED = 44.0
```

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_gp02, 21563-25384(+)

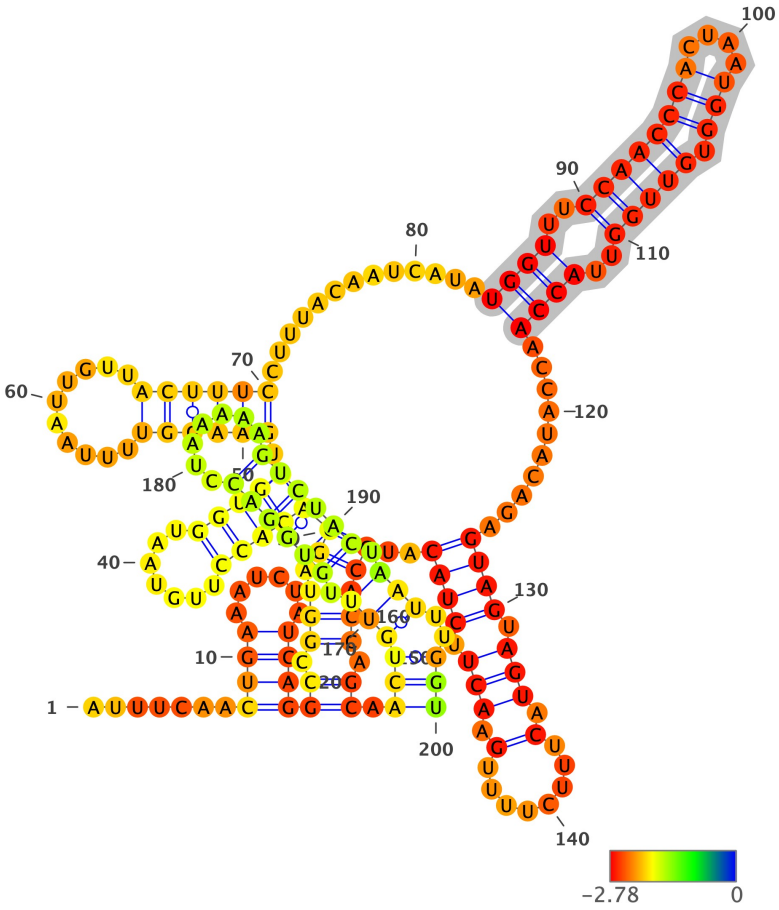
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 382 from nt 23047 to 23079 (nt 84 to 116)

```
5'-TGGTTTCCAACCCACTAATGGTGUUGGTTACCA-3'
5'-((((..(((((((......)).)))))..))))-3'
Motif MFE = -14.7; z-score = -4.38; 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 22964 to 23163 (motif highlighted in silver):

```
5'-AUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGU
UACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGU-3
5'-.......((((......))))((.(((.(((((((.......))))).((((((..........))))))..............((((..((((((((....))).)))))).
.))))..........((((.(((.(........).))).))))..)))))).)).((((((.((((((.......)))))).)))..)))-3'
MFE = -48.1; z-score = -2.03; ED = 55.51
```

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_gp02, 21563-25384(+)

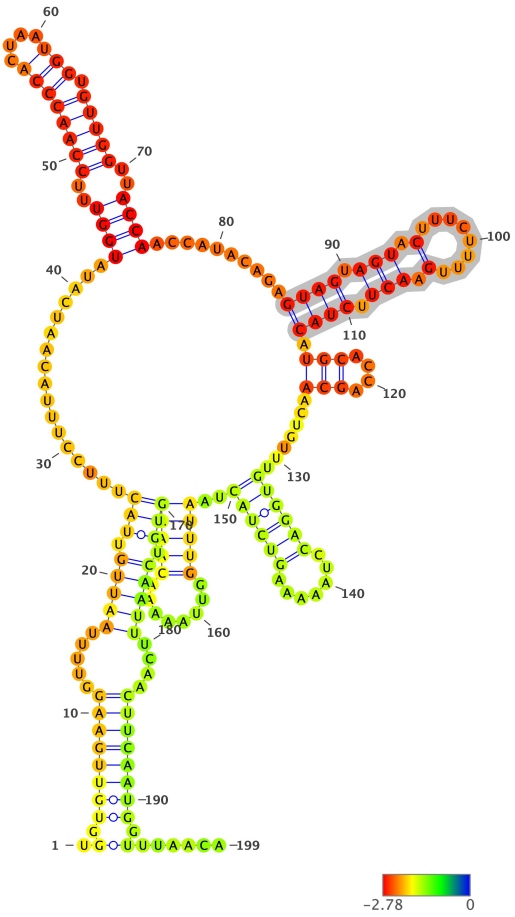
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23090 to 23117 (nt 86 to 113)

```
5'-GTAGTAGTACTTTCTTTTGAACUTCUAC-3'
5'-((((.(((.(........).))).))))-3'
Motif MFE = -4.1; z-score = -1.9; 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 = -2.45; 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(+)

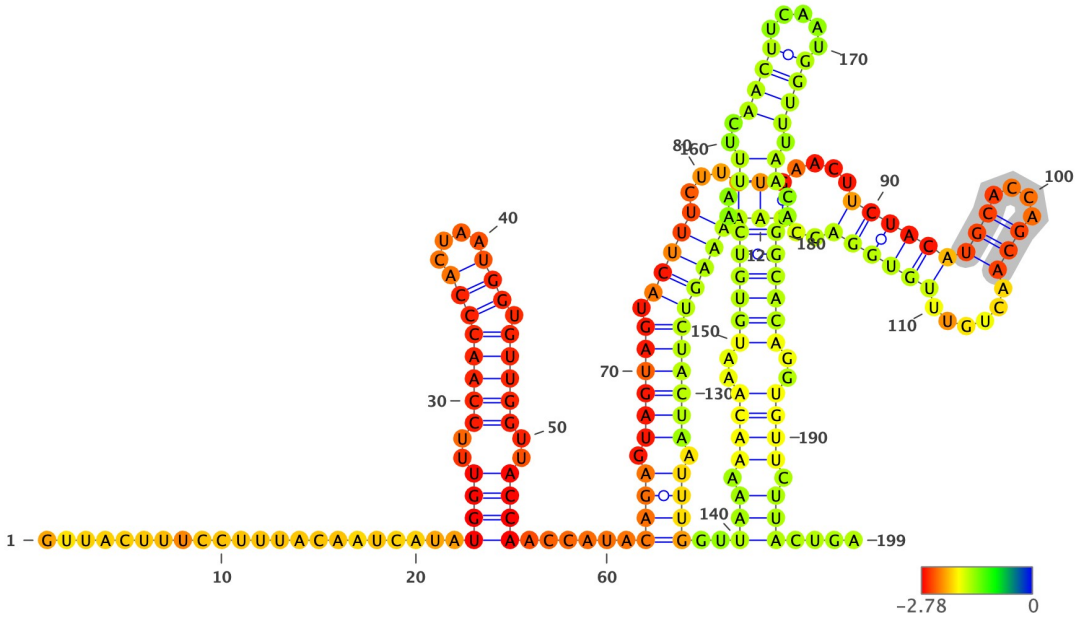
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 384 from nt 23119 to 23128 (nt 95 to 104)

```
5'-TGCACCAGCA-3'
5'-(((....)))-3'
Motif MFE = -0.9; z-score = -7.39; 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 = -2.68; 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(+)

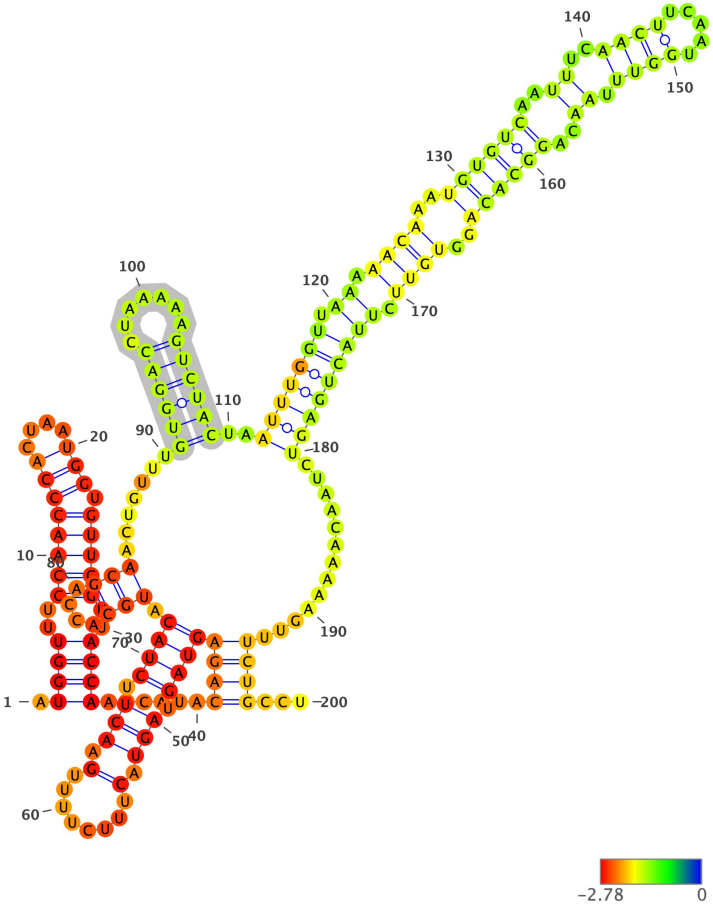
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 385 from nt 23136 to 23154 (nt 91 to 109)

```
5'-GTGGACCTAAAAAGUCUAC-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -3.13; 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 = -2.44; 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(+)

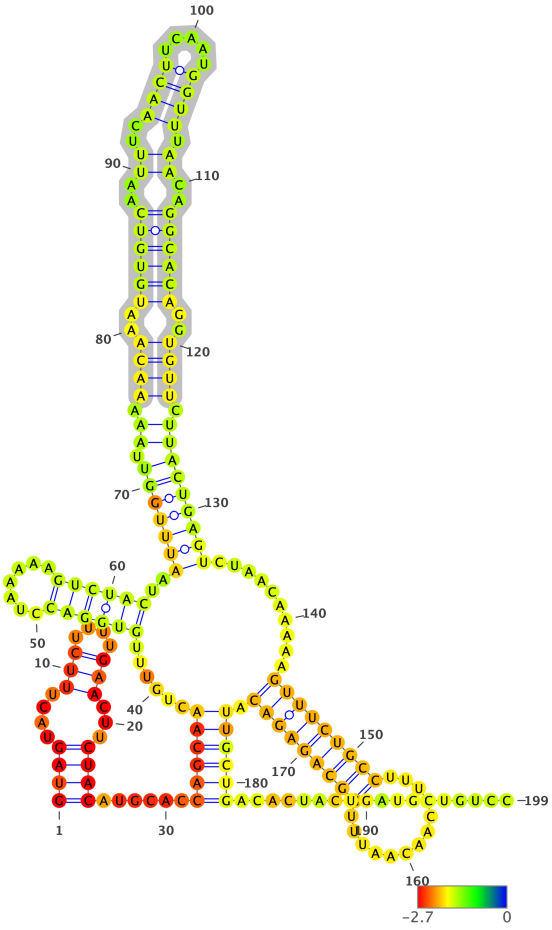
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 386 from nt 23168 to 23215 (nt 76 to 123)

```
5'-AACAAATGTGTCAATTTCAACTTCAATGGUUTAACAGGCACAGGUGUU-3'
5'-((((..(((((((..((..((((.....)))).))..)))))))..))))-3'
Motif MFE = -10.7; z-score = -1.86; ED = 3.01
```



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 23093 to 23291 (motif highlighted in silver):

```
5'-GUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACA
GGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCC-3
5'-((((....(((....)))...)))).....((((((......((((((.......))))))..(((((((.((.((((..((((((..((..((((.....)))).)).. ))))))..)))).))))))))).........(((((((((.............)))))))))).))))))..................-3'
MFE = -46.3; z-score = -2.21; ED = 25.4
```

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_gp02, 21563-25384(+)

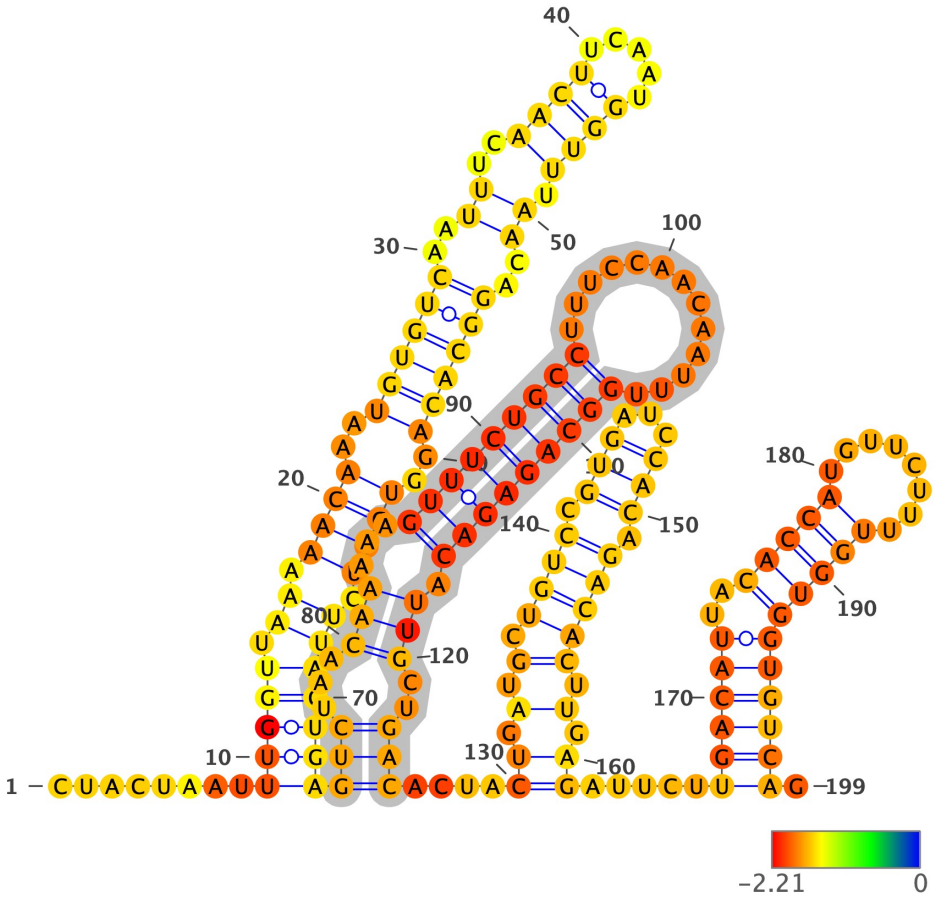
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 387 from nt 23224 to 23275 (nt 74 to 125)

```
5'-GTCTAACAAAAAGTTTCTGCCTTTCCAACAATTTGGCAGAGACATTGCTGAC-3'
5'-(((.........((((((((((.............)))))))))).....)))-3'
Motif MFE = -15.0; z-score = -3.85; 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 = -3.16; ED = 39.01
```

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(+)

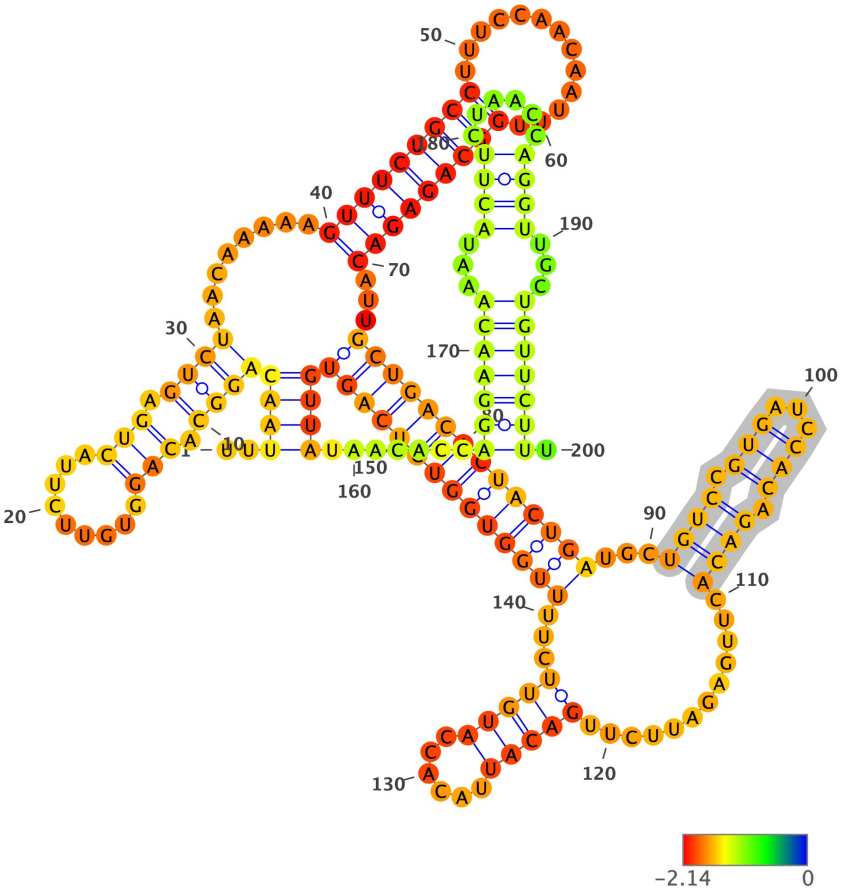
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 388 from nt 23287 to 23305 (nt 91 to 109)

```
5'-TGTCCGTGATCCACAGACA-3'
5'-((((.(((...))).))))-3'
Motif MFE = -4.6; z-score = -3.37; 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 23197 to 23396 (motif highlighted in silver):

```
5'-UUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACU
UGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUU-3
5'-..(((((((((.(((.........))).)))).........(((((((((.............)))))))))...((((((((((((...((((.(((...))).)))))..
.........(((((......)))))...)))))))))))))))).......(((((((...((((......))))...)))))))).-3'
MFE = -52.4; z-score = -2.73; ED = 34.13
```

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(+)

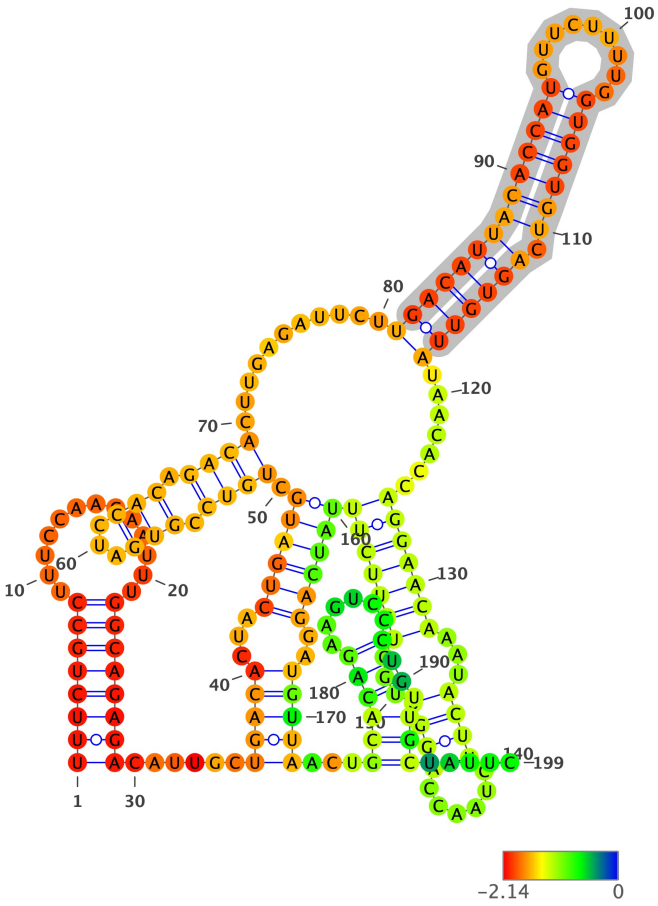
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 389 from nt 23318 to 23353 (nt 82 to 117)

```
5'-GACATTACACCATGTTCTTTTGGUGGUGTCAGUGUU-3'
5'-(((((...(((((.........)))))....)))))-3'
Motif MFE = -12.6; z-score = -3.47; ED = 7.87
```



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 23237 to 23435 (motif highlighted in silver):

```
5'-UUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUC
AGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUC-3
5'-((((((((.............))))))))......(((((...((((((.((((.(((...))).))))...........((((((((((((((.........)))))))).
)))))))).......(((((((...((((......))))...))))))))))))))..)))))...((((((......))).)))......-3'
MFE = -51.0; z-score = -2.54; ED = 17.6
```

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(+)

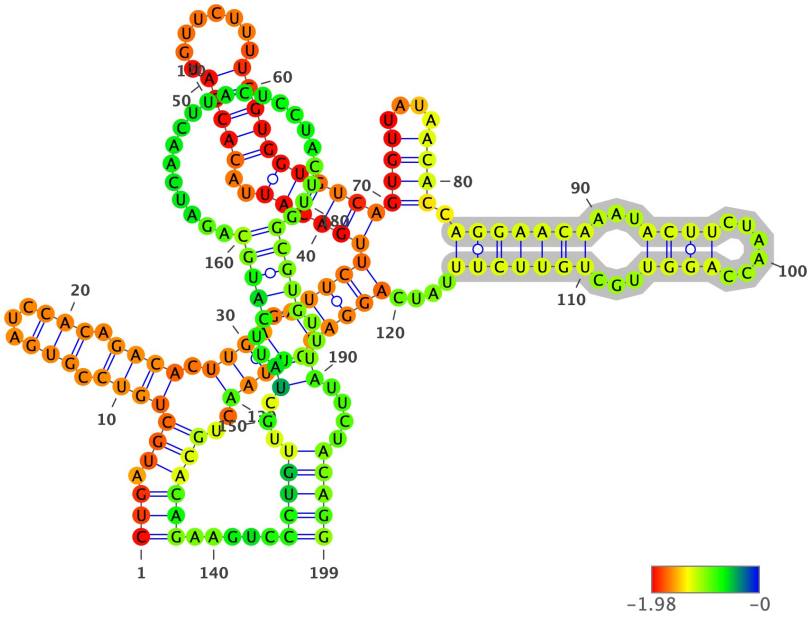
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23362 to 23395 (nt 83 to 116)

```
5'-AGGAACAAATACTTCTAACCAGGUTGCUGUUCUU-3'
5'-(((((((...((((......))))...)))))))-3'
Motif MFE = -6.7; z-score = -1.48; 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 23280 to 23478 (motif highlighted in silver):

```
5'-CUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUG
UUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGG-3
5'-(((.(((((((.(((...))).)))).((((.(((((((((((..(((((........)))))))))))((((....)))).(((((((...((((......))))...))
)))))....))))).))))..))))))).....(((((...((..(((((.....................)))))..))....)))))-3'
MFE = -45.9; z-score = -1.26; ED = 45.05
```

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(+)

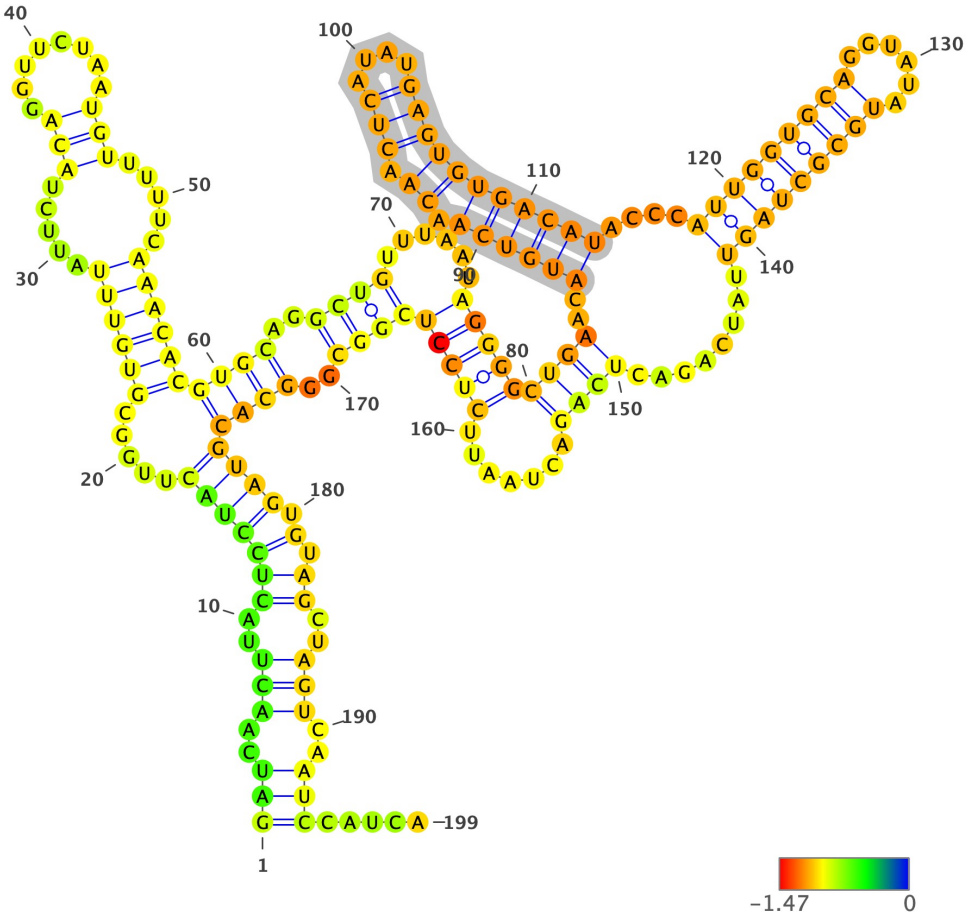
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 391 from nt 23526 to 23553 (nt 86 to 113)

```
5'-ATGTCAACAACTCATATGAGUGUGACAU-3'
5'-((((((.((.(((....)))))))))))-3'
Motif MFE = -8.7; z-score = -4.21; 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(+)

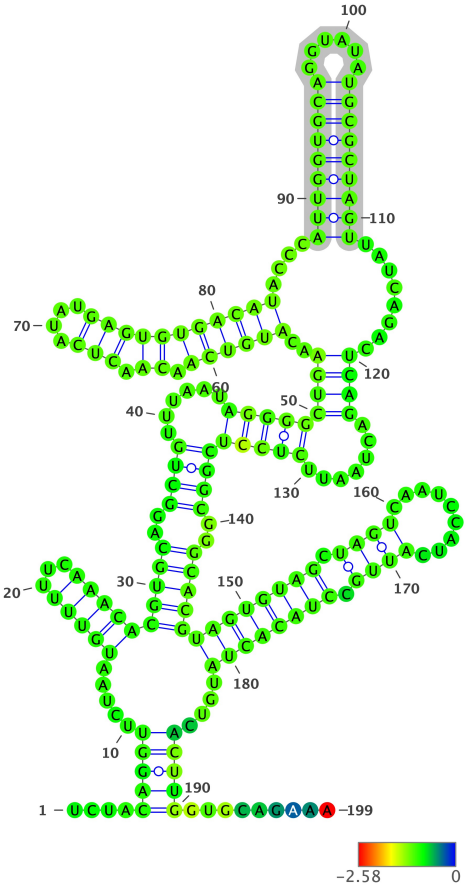
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 392 from nt 23558 to 23581 (nt 88 to 111)

```
5'-ATTGGTGCAGGTATAUGCGCUAGU-3'
5'-((((((((((......))))))))))-3'
Motif MFE = -9.8; z-score = -3.76; 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 23471 to 23669 (motif highlighted in silver):

```
5'-UCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGU
UAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACUUGGUGCAGAAA-3
5'-....(((((.....(((((...)))))(((((..((((......(((((((((..((((((.((.(((....)))))))))))....((((((((((......)))))))))
........))))).......))))))))).))))((((((((.((((.........)))).))))))))....)))))..........-3'
MFE = -50.2; z-score = -0.91; ED = 46.08
```

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_gp02, 21563-25384(+)

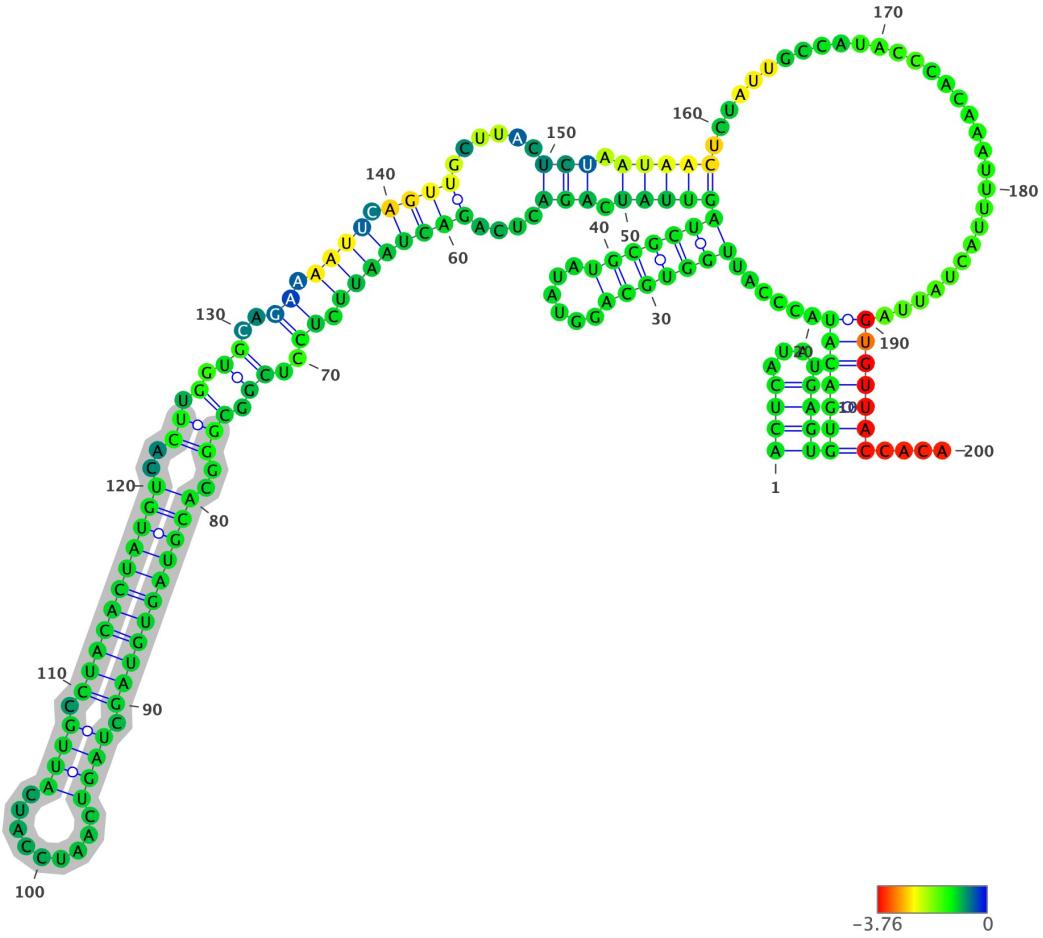
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23610 to 23658 (nt 76 to 124)

```
5'-GGGCACGTAGTGTAGCTAGTCAATCCATCAUUGCCUACACUAUGUCACU-3'
5'-((..(((((((((((.((((.........)))).))))))))))..))-3'
Motif MFE = -14.7; z-score = -2.68; ED = 6.66
```



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 23535 to 23734 (motif highlighted in silver):

```
5'-ACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCU
ACACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACA-3
5'-((((....))))(((((((.....(((((((.....)))))))(((((.(((....((((((((.((..((.(((..((((((((((((.((((.........)))).))
))))))))).))).)).))..)).)))).))))......))).)))))..............................))))))).....-3'
MFE = -42.5; z-score = -1.72; ED = 42.06
```

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_gp02, 21563-25384(+)

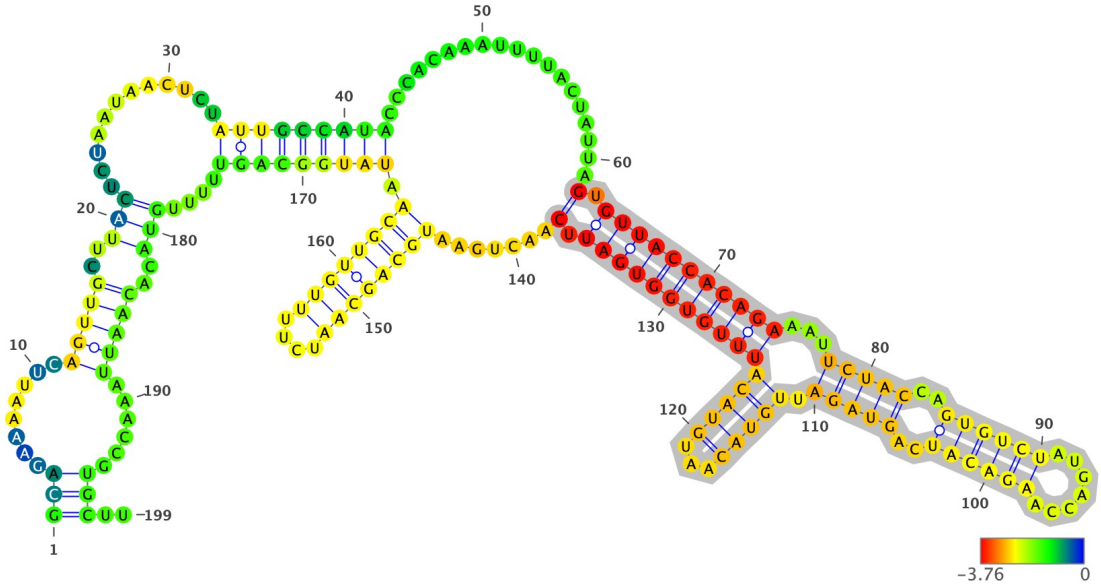
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 394 from nt 23724 to 23799 (nt 62 to 137)

```
5'-GTGTTACCACAGAAATTCTACCAGTGTCTATGACCAAGACATCAGTAGATTGTACAATGTACATTTGTGGTGAUTC-3'
5'-(.((((((((((...((((((..((((((.......))))))..))))))..((((...)))).)))))))))).)-3'
Motif MFE = -25.0; z-score = -3.89; 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 = -4.38; 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(+)

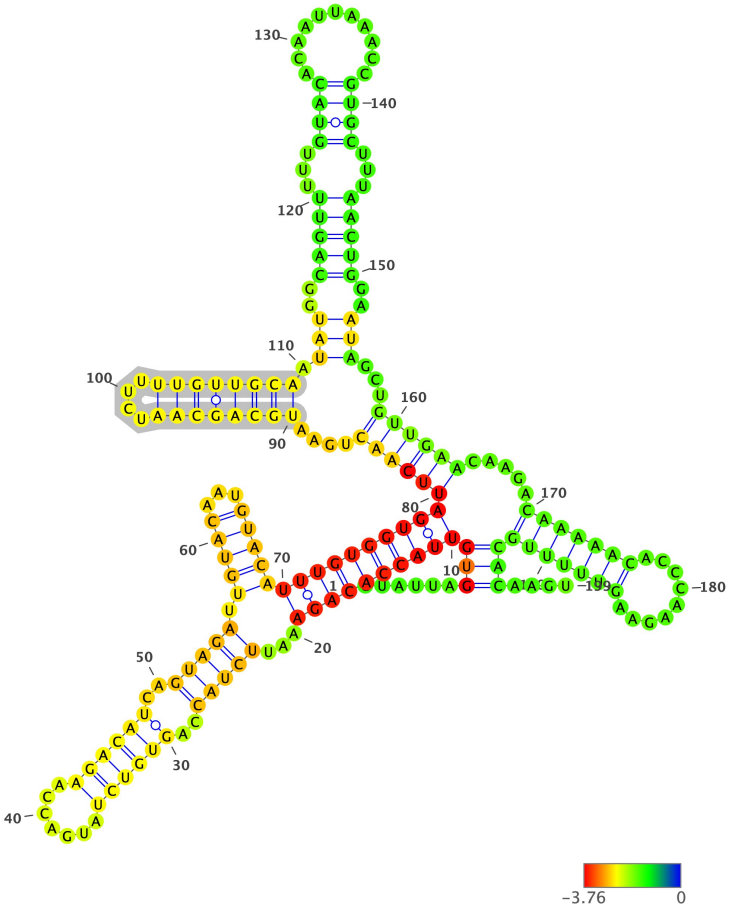
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 395 from nt 23807 to 23826 (nt 90 to 109)

```
5'-TGCAGCAATCTTUUGUUGCA-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -8.8; z-score = -5.92; 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 = -3.54; 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(+)

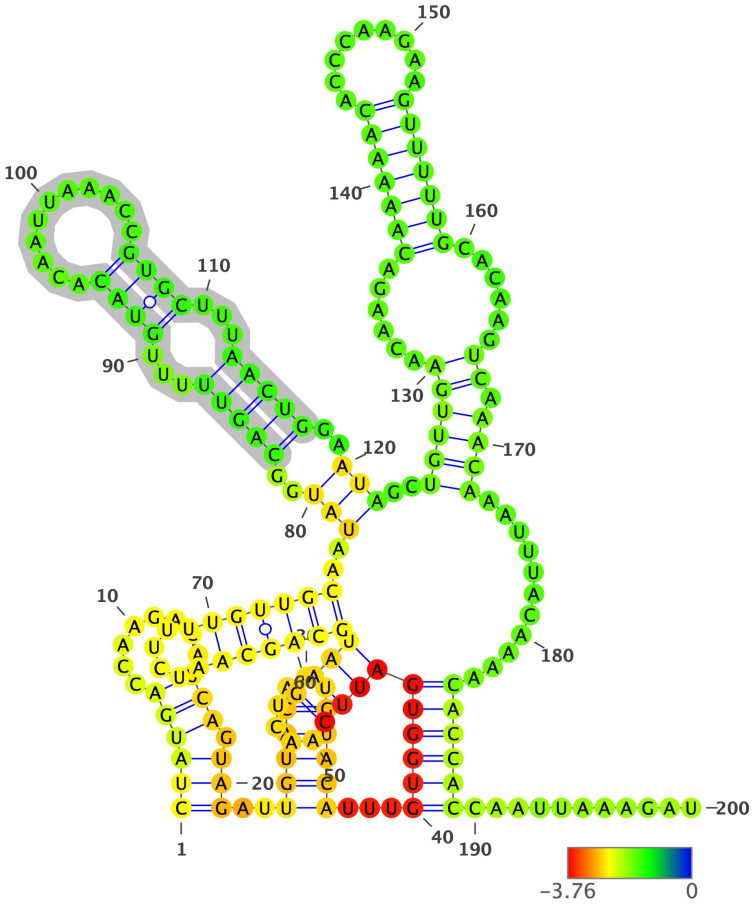
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 396 from nt 23833 to 23867 (nt 83 to 117)

```
5'-CAGTTTTTGTACACAATTAAACCGUGCTTTAACUG-3'
5'-((((((...((((..........))))...))))))-3'
Motif MFE = -6.4; z-score = -1.96; 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 23751 to 23950 (motif highlighted in silver):

```
5'-CUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUU
UAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGUCAAACAAAUUUACAAAACACCACCAAUUAAAGAU-3
5'-((((((........)))).))))..((((((...))))))...((((((((((....))))))))))....))))))).((((..((((((...((((..........))))..
.))))))..))))..((((((......(((((((.........)))))))......)).))))..........))))))..........-3'
MFE = -37.5; z-score = -2.06; ED = 23.85
```

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(+)

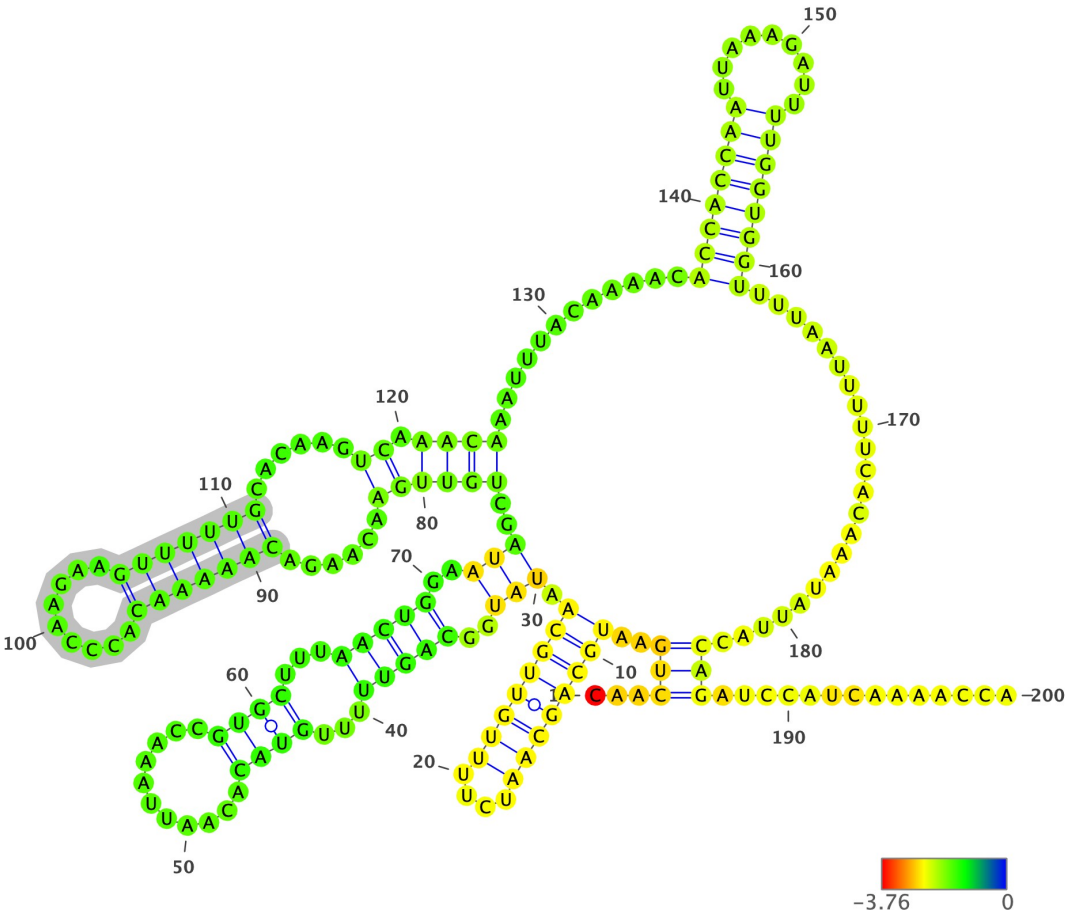
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 397 from nt 23887 to 23909 (nt 89 to 111)

```
5'-CAAAAACACCCAAGAAGUUUUUG-3'
5'-(((((((.........)))))))-3'
Motif MFE = -3.0; z-score = -2.39; 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 = -2.51; 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(+)

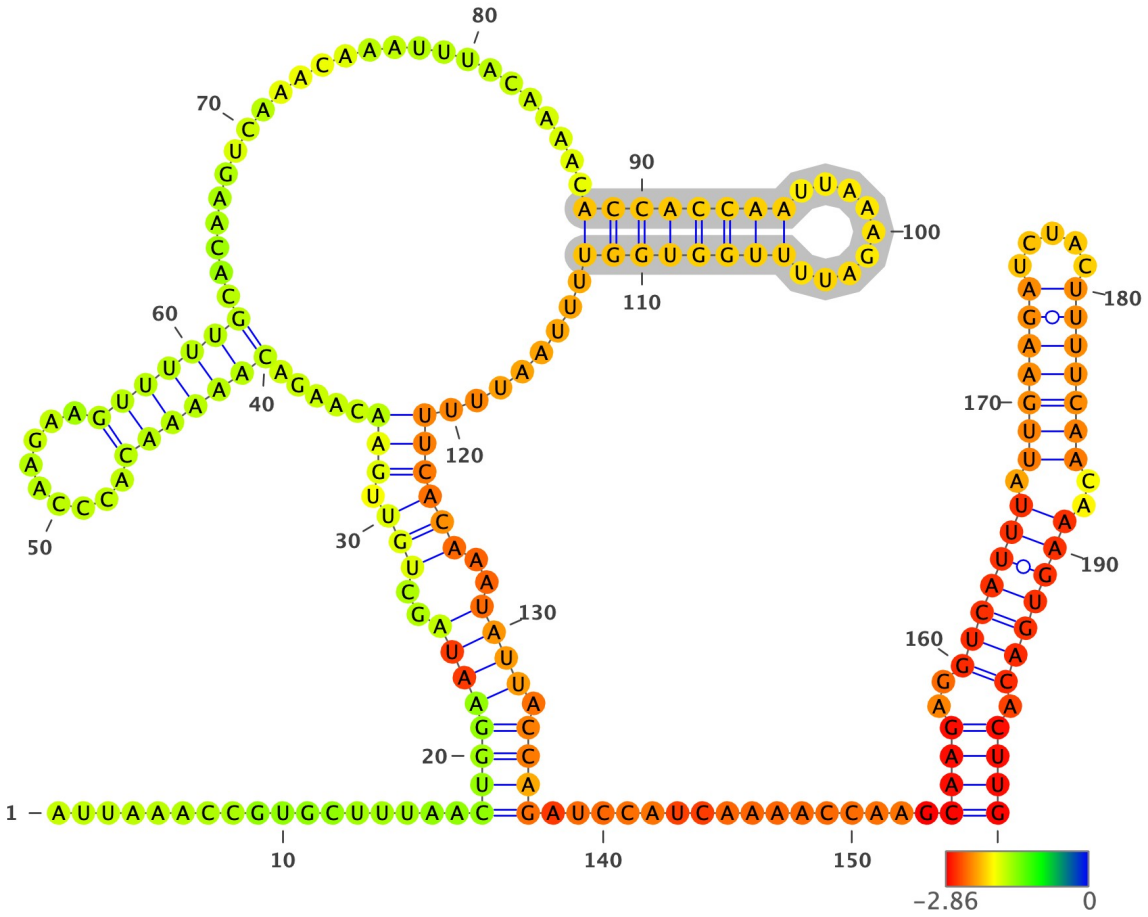
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 398 from nt 23935 to 23959 (nt 88 to 112)

```
5'-ACCACCAATTAAAGATTUUGGUGGU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -10.4; z-score = -4.42; 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 = -2.58; 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(+)

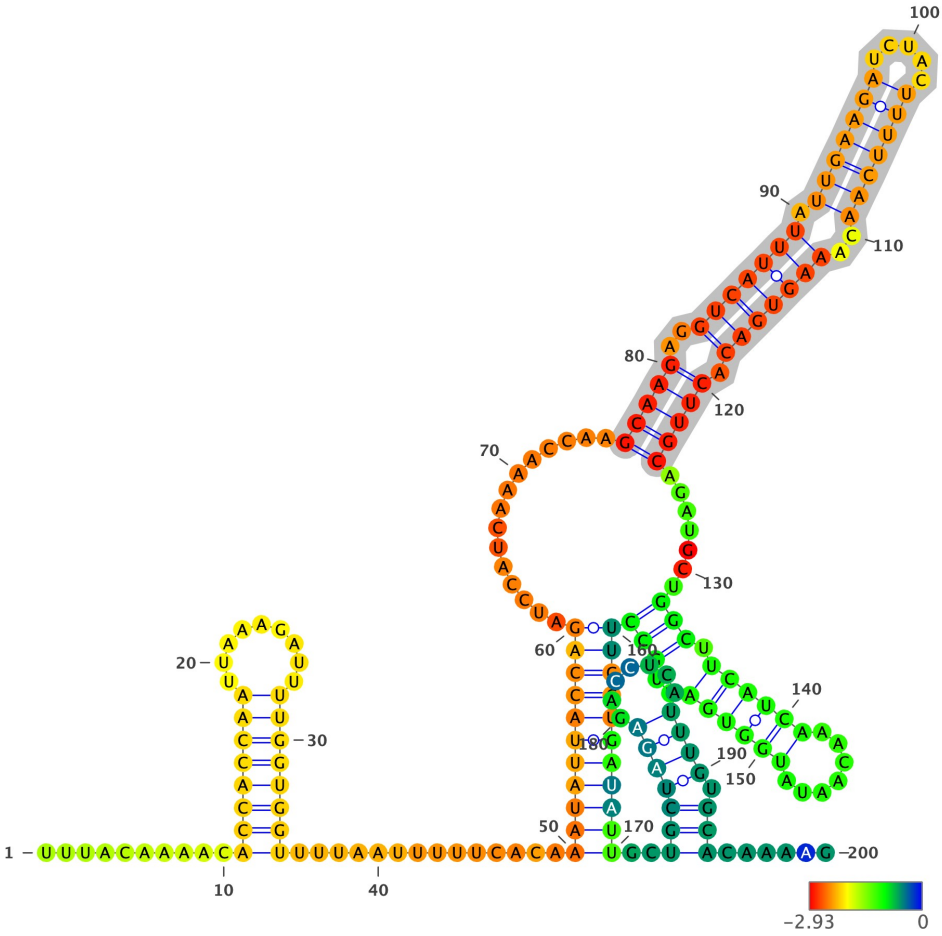
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 399 from nt 24000 to 24048 (nt 76 to 124)

```
5'-GCAAGAGGTCATTTATTGAAGATCTACUUUUCAACAAAGUGACACUUGC-3'
5'-((((((..(((((((.(((((((.....)))))))..)))))))..))))))-3'
Motif MFE = -16.1; z-score = -3.77; 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 = -4.23; ED = 18.82
```

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_gp02, 21563-25384(+)

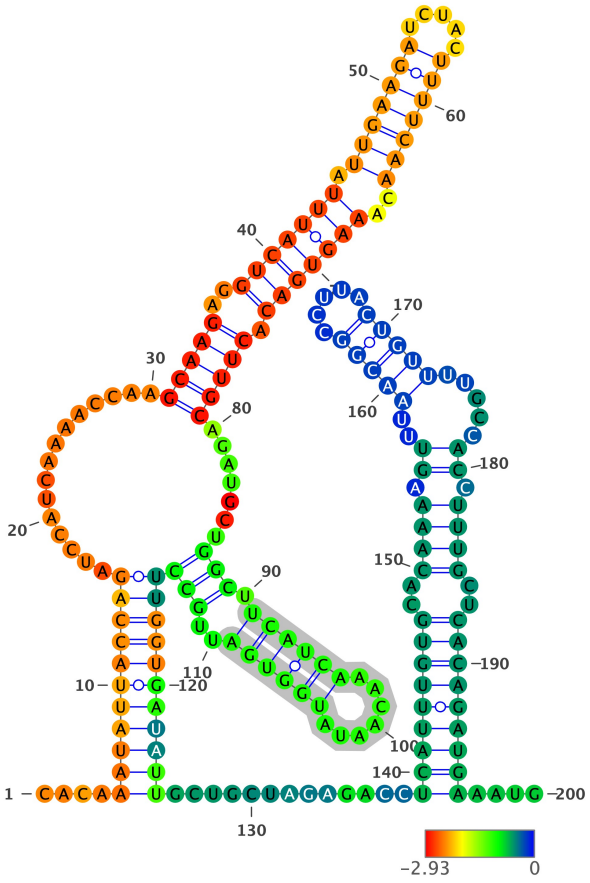
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 400 from nt 24060 to 24078 (nt 91 to 109)

```
5'-TCATCAAACAATAUGGUGA-3'
5'-((((((.......))))))-3'
Motif MFE = -3.3; z-score = -3.15; 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 23970 to 24169 (motif highlighted in silver):

```
5'-CACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUGCAGAUGCUGGCUUCAUCAAACAAUAUGGUGAUU
GCCUUGGUGAUAUUGCUGCUAGAGACCUCAUUUGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUG-3
5'-....((((((((((.............(((((..(((((((.(((((((.....)))))))..)))))))).)))))).......(((.((((((.......)))))))..
))))))))))))).............((((((((((..((((.((..(((((.....)))))).....)).)))))..)))))))))....-3'
MFE = -52.1; z-score = -3.53; ED = 13.36
```

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_gp02, 21563-25384(+)

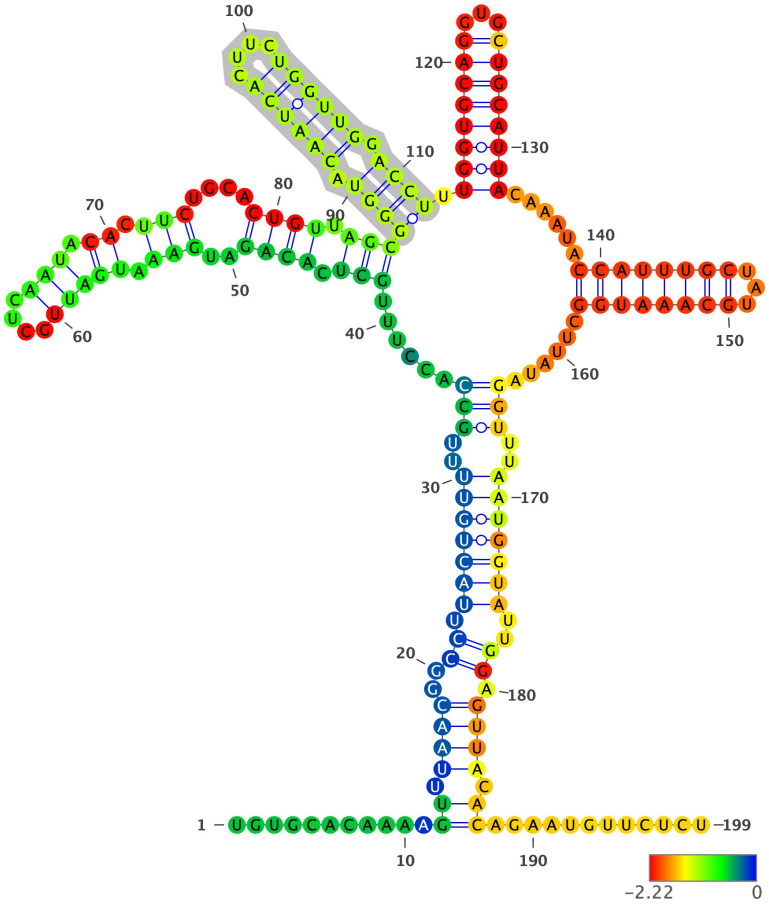
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 401 from nt 24199 to 24224 (nt 87 to 112)

```
5'-GGGTACAATCACTTCUGGUUGGACCU-3'
5'-((((.((((((....)))))).))))-3'
Motif MFE = -8.5; z-score = -3.02; ED = 1.59
```



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 24113 to 24311 (motif highlighted in silver):

```
5'-UGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACC
UUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCU-3
5'-...........((.((((..((.(((((((..(((.......(((.((((..(((.(((((....))).)).)))....)))).)))((((.((((((....)))))).)))
).((((((((...))))))))......((((((((...))))))))......)))..)))))))..)).)))).)).............-3'
MFE = -48.1; z-score = -0.99; ED = 36.46
```

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_gp02, 21563-25384(+)

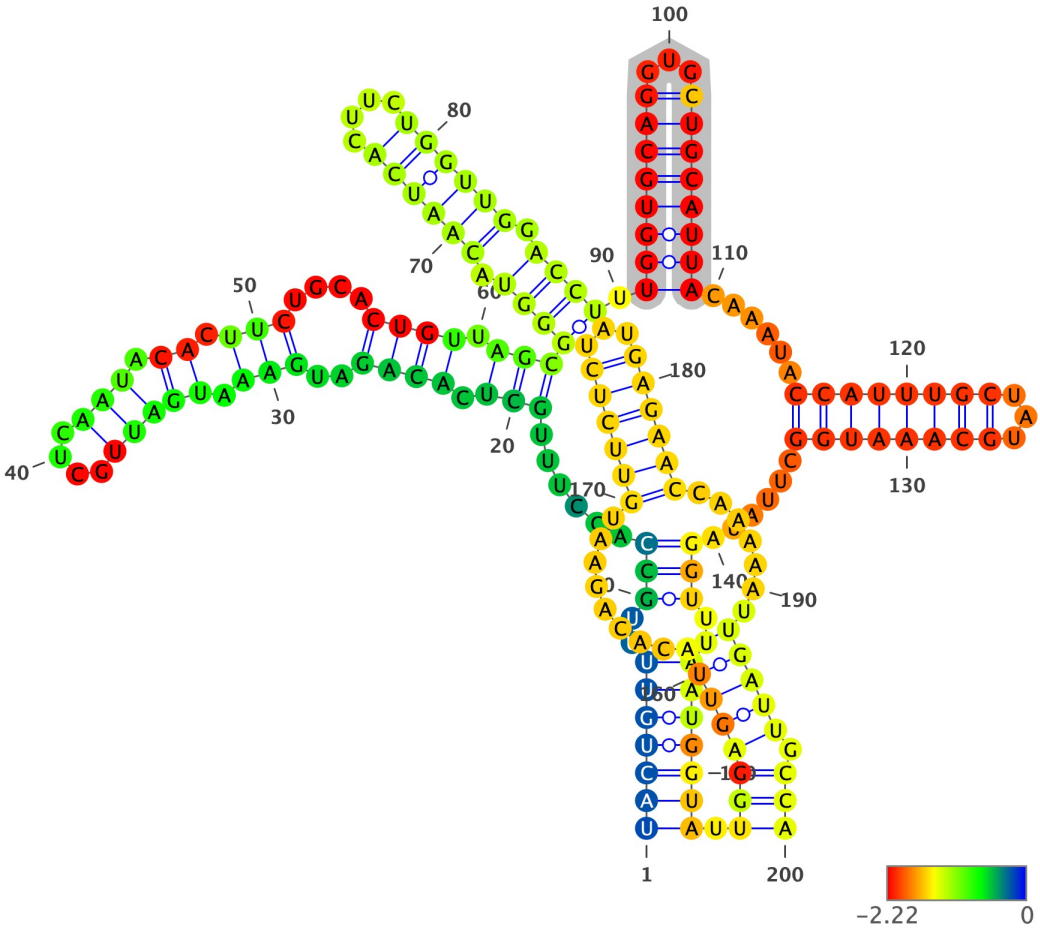
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 402 from nt 24226 to 24244 (nt 91 to 109)

```
5'-TGGTGCAGGTGCUGCAUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.7; z-score = -2.92; 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 24136 to 24335 (motif highlighted in silver):

```
5'-UACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACA
AAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCA-3
5'-(((((((..(((......(((.((((..(((.(((((....))).)).)))....)))).)))((((.((((((....)))))).)))).((((((((...))))))))..
....((((((((...))))))))......)))..)))))))).((((((((........((((((...))))))).......))))).)))-3'
MFE = -50.4; z-score = -1.68; ED = 16.95
```

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_gp02, 21563-25384(+)

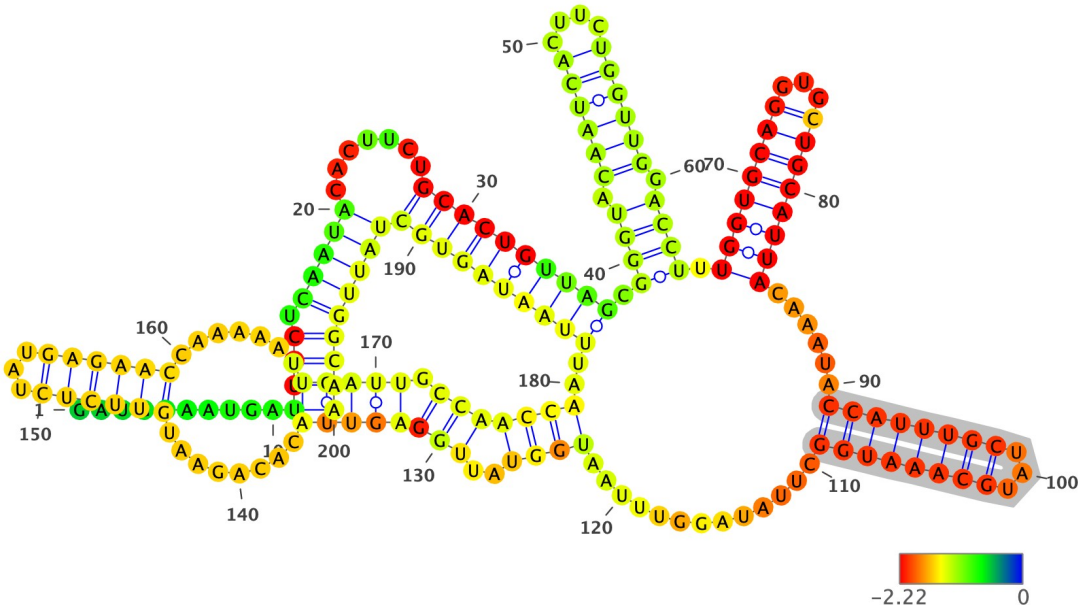
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 403 from nt 24251 to 24269 (nt 91 to 109)

```
5'-CCATTTGCTATGCAAAUGG-3'
5'-((((((((...))))))))-3'
Motif MFE = -8.4; z-score = -6.07; 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 = -2.98; 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(+)

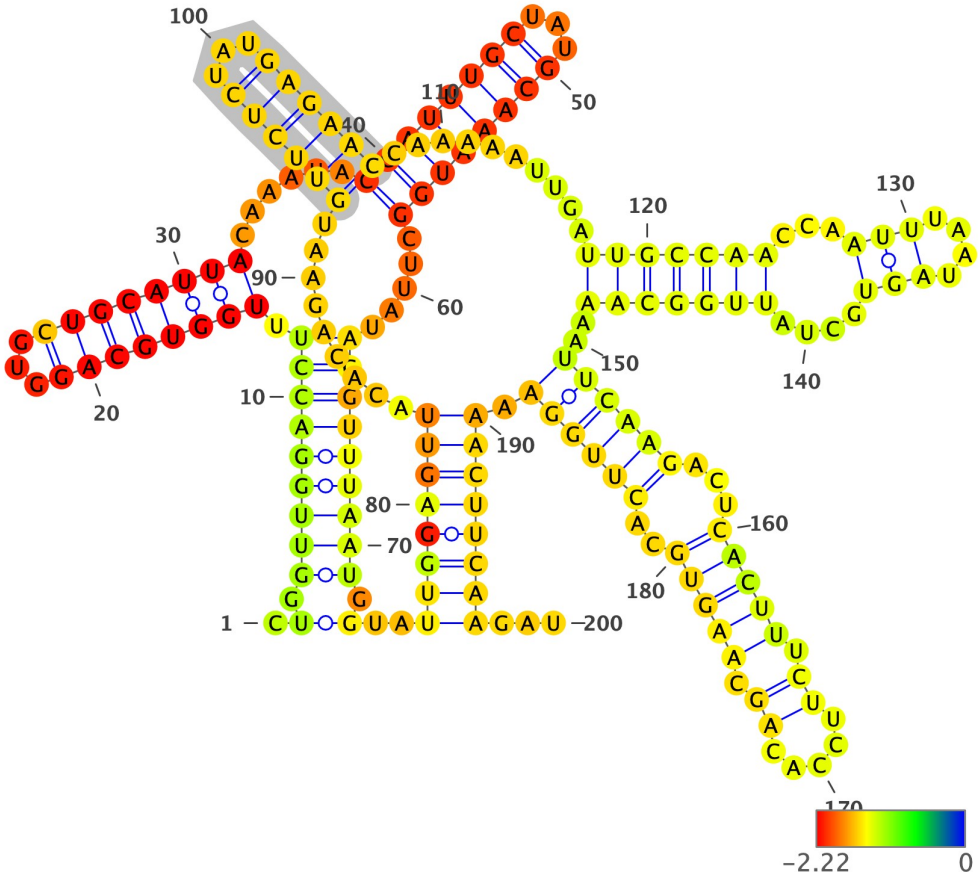
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 404 from nt 24305 to 24319 (nt 93 to 107)

```
5'-GTTCTCTATGAGAAC-3'
5'-((((((...))))))-3'
Motif MFE = -4.6; z-score = -4.78; 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 = -2.4; 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(+)

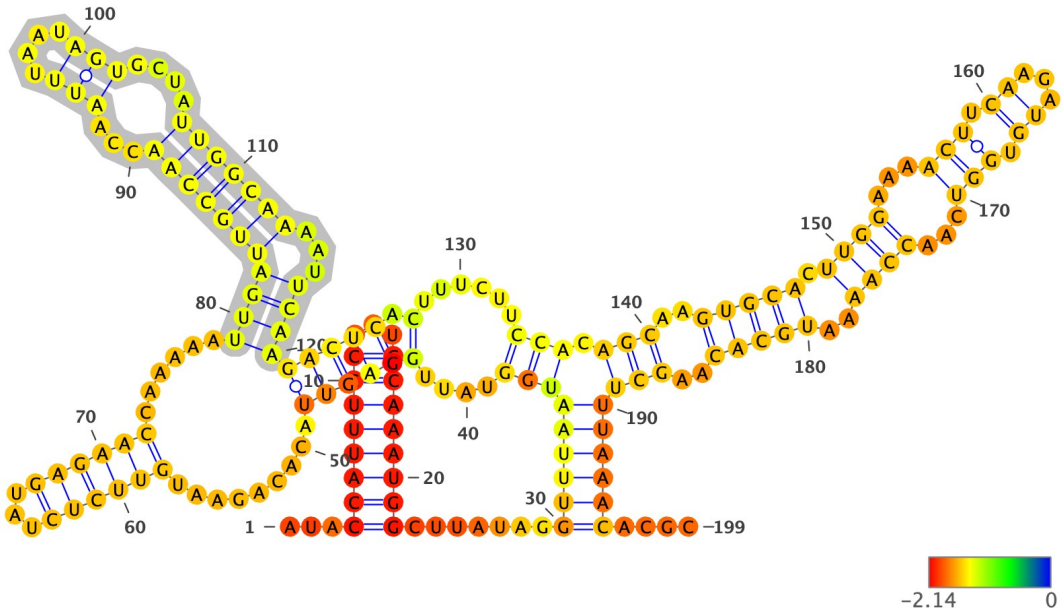
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 405 from nt 24326 to 24367 (nt 79 to 120)

```
5'-TTGATTGCCAACCAATTTAATAGUGCTAUUGGCAAAATUCAA-3'
5'-((((((((((...(((....)))....)))))))...))))-3'
Motif MFE = -7.7; z-score = -2.17; 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 24248 to 24446 (motif highlighted in silver):

```
5'-AUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGC
AAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGC-3
5'-...(((((((((...)))))))).......((((((((((....((((((.........((((((...))))))......((((((((((...(((....)))....)))))
))...))))))))).).......))).(((..((((((.((((...(((.((...)).))))...)))))..))))))..)))))))))....-3'
MFE = -42.9; z-score = -2.09; ED = 28.19
```

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_gp02, 21563-25384(+)

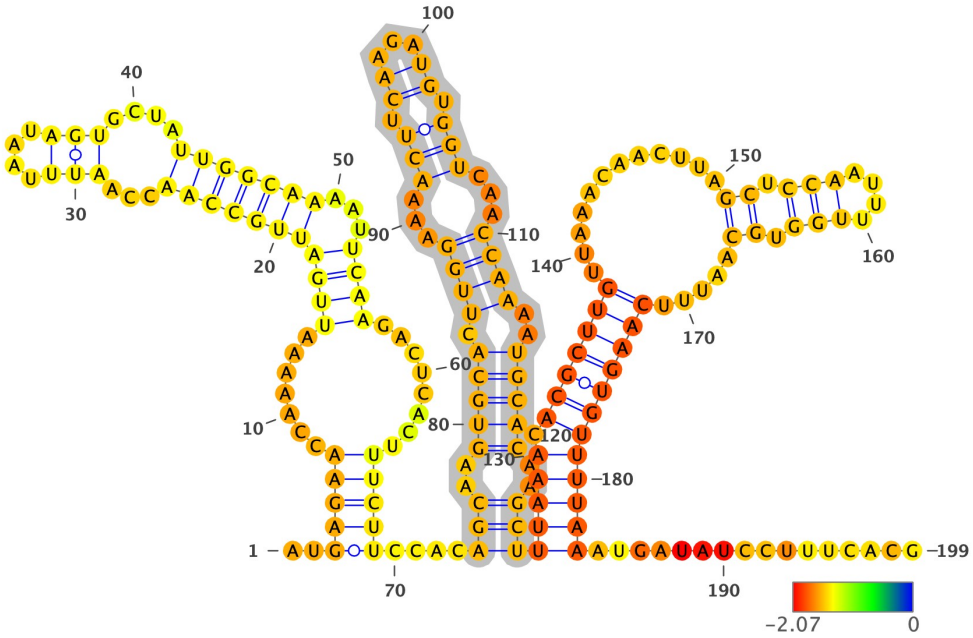
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 406 from nt 24385 to 24436 (nt 74 to 125)

```
5'-AGCAAGTGCACTTGGAAAACTTCAAGAUGTGGUCAACCAAAAUGCACAAGCU-3'
5'-(((..(((((.((((...(((.((...)).)))...)))))..)))))..)))-3'
Motif MFE = -13.3; z-score = -2.76; 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 = -1.68; ED = 24.52
```

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(+)

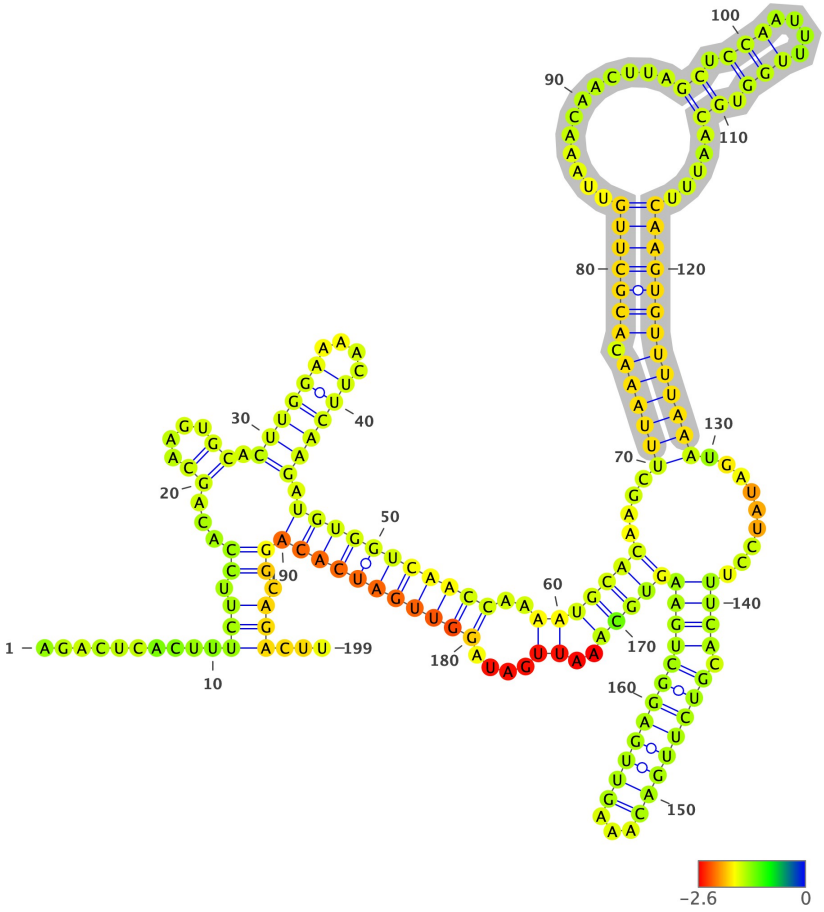
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 407 from nt 24437 to 24494 (nt 71 to 128)

```
5'-TTAAACACGCTTGTTAAACAACTTAGCTCCAATTTUGGTGCAATTTCAAGUGUUUUAA-3'
5'-(((((.(((((((.............((.(((....))).)).....)))))))))))))-3'
Motif MFE = -10.2; z-score = -1.6; ED = 6.67
```



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 24367 to 24565 (motif highlighted in silver):

```
5'-AGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGC
AAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUU-3
5'-..........(((.((...((....)).((((((....)))))).((((((((((..(((((((....((((((.(((((((.............((.(((....))).))
.....)))))))))))))).........((((.((((((((...)))))))))))))))))..))....)))))))))))))).)))...-3'
MFE = -47.9; z-score = -2.16; ED = 18.51
```

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(+)

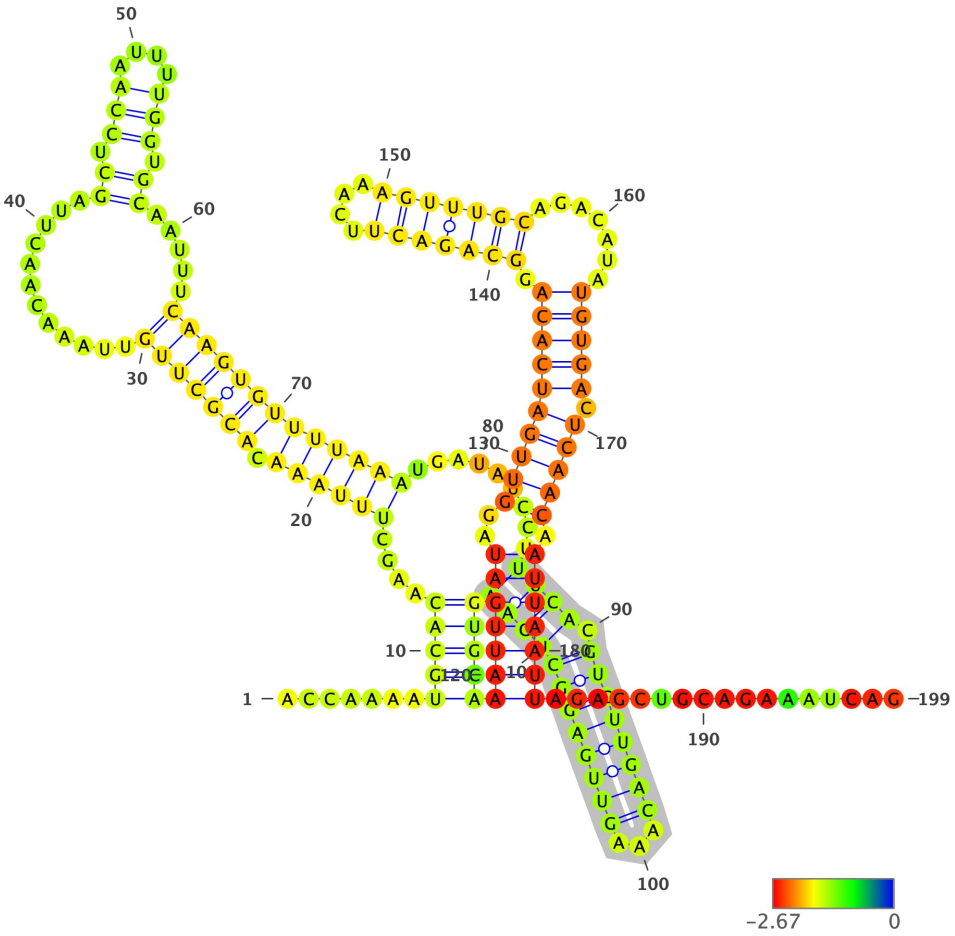
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 408 from nt 24505 to 24532 (nt 86 to 113)

```
5'-TTCACGTCTTGACAAAGUUGAGGCUGAA-3'
5'-((((.(((((((((...))))))))))))-3'
Motif MFE = -8.5; z-score = -2.64; 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 = -2.56; 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(+)

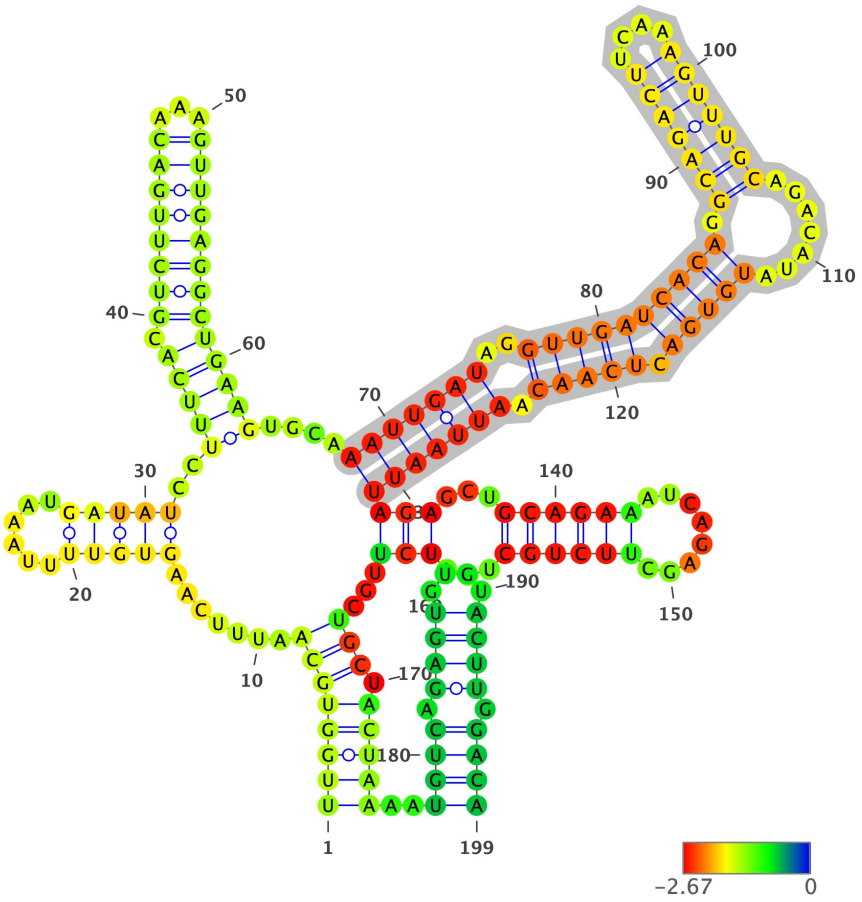
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 409 from nt 24538 to 24601 (nt 68 to 131)

```
5'-AATTGATAGGTTGATCACAGGCAGACTTCAAAGUUUGCAGACATAUGUGACUCAACAAUUAAUU-3'
5'-(((((((..((((((((((.(((((((....)))))))).......))))).)))))).)))))))-3'
Motif MFE = -17.9; z-score = -3.44; 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 24471 to 24669 (motif highlighted in silver):

```
5'-UUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAU
AUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACA-3
5'-((((((((.......(((((......)))))..(((((.((((((((...)))))))))))))....(((((((..((((((((((.(((((((....)))))))).......
.))))).))))).)))))))(((...((((((........))))))...)))...))).)))))..((((.((((....)))).))))-3'
MFE = -50.4; z-score = -2.27; ED = 31.33
```

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_gp02, 21563-25384(+)

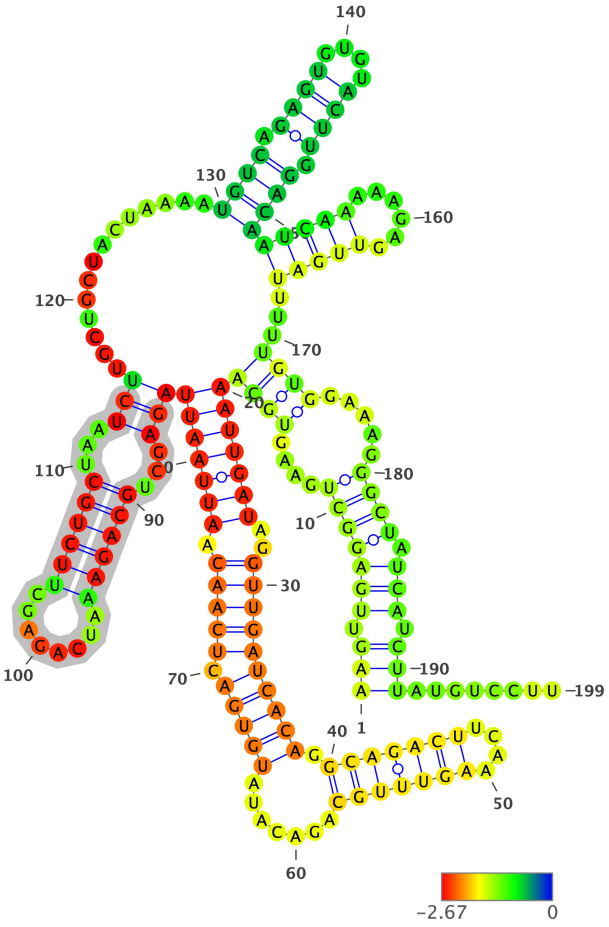
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 410 from nt 24603 to 24632 (nt 85 to 114)

```
5'-GAGCTGCAGAAATCAGAGCTUCUGCTAATC-3'
5'-(....(((((..........)))))....)-3'
Motif MFE = -7.2; z-score = -1.66; 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 = -1.22; 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(+)

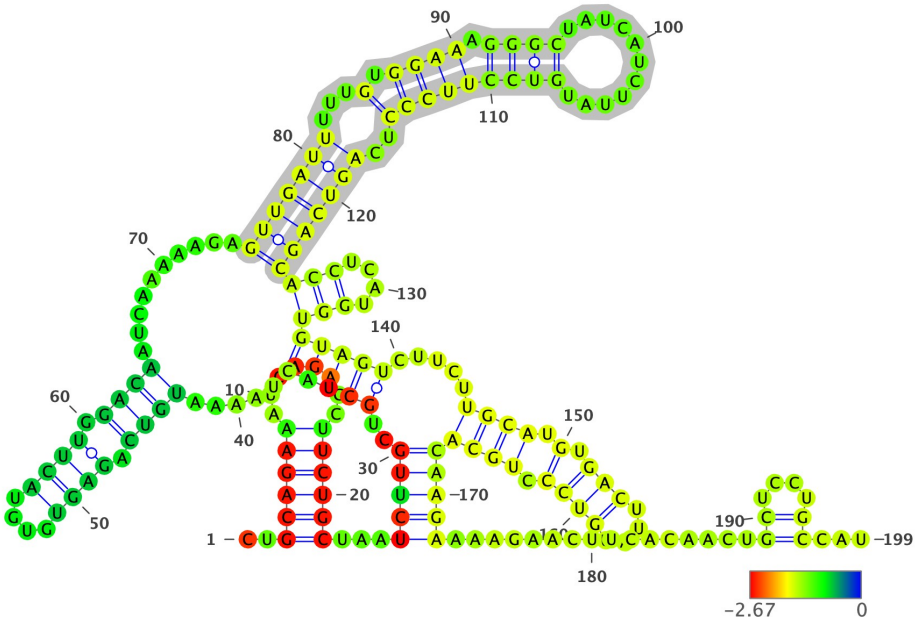
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 411 from nt 24680 to 24729 (nt 75 to 124)

```
5'-GTTGATTTTTGTGGAAAGGGCTATCATCTTATGUCCUUCCCTCAGUCAGC-3'
5'-(((((((...(.((((.((((...........)))))))))..)))))))-3'
Motif MFE = -14.9; z-score = -2.77; ED = 6.93
```



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 24606 to 24804 (motif highlighted in silver):

```
5'-CUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCU
UCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAU-3
5'-..((((((........))))))...(((((..(((((.....((((.((((....)))).))))..........(((((((...(.((((.((((...........)))))
))))..)))))))(((....))))))))).....((((.(.(((....)))).)))))))))................((....))...-3'
MFE = -44.6; z-score = -0.79; ED = 39.51
```

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(+)

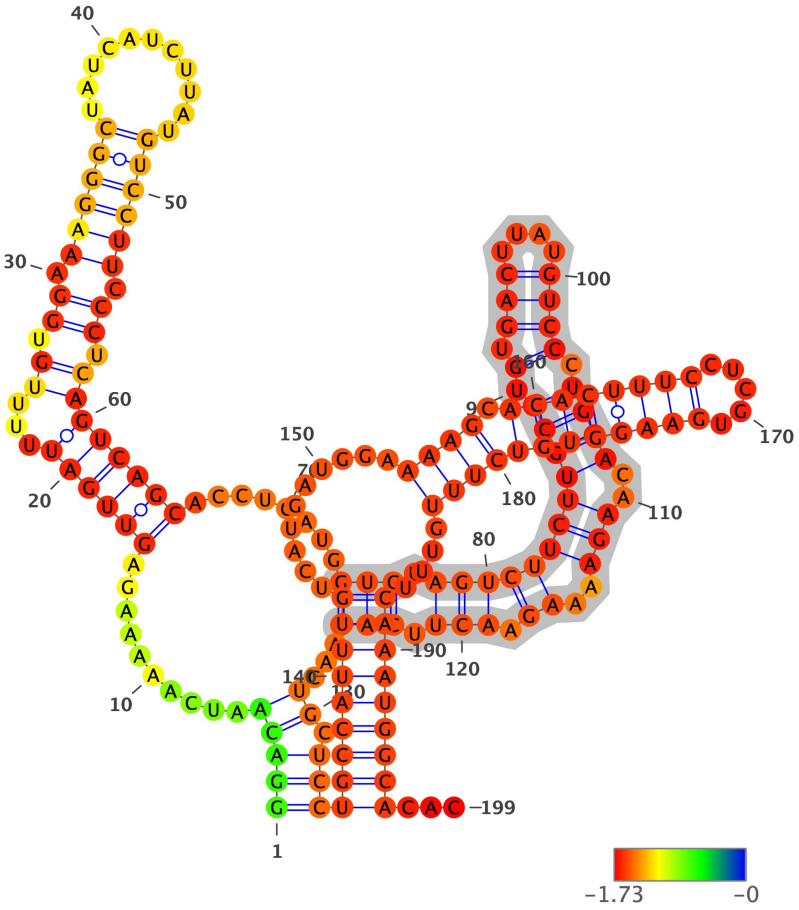
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 412 from nt 24738 to 24789 (nt 74 to 125)

```
5'-GTGTAGTCTTCTTGCATGTGACTTATGUCCCUGCACAAGAAAAGAACUTCAC-3'
5'-(((.(((((((((((.(.(((....)))).)))))..))))..)).))).)))-3'
Motif MFE = -12.0; z-score = -2.04; ED = 6.31
```



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 24665 to 24863 (motif highlighted in silver):

```
5'-GGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAA
GAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACAC-3
5'-(((((.........((((((...((.((.((((((..........))))))..)).)))))))).......(((.((((((((((((.(.(((....)))).)))))..)
))..)).))).)))...)).)))((((((((((.........((((.(((((((((.....)))))))))))))....))))))))).-3'
MFE = -52.3; z-score = -2.15; ED = 25.36
```

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(+)

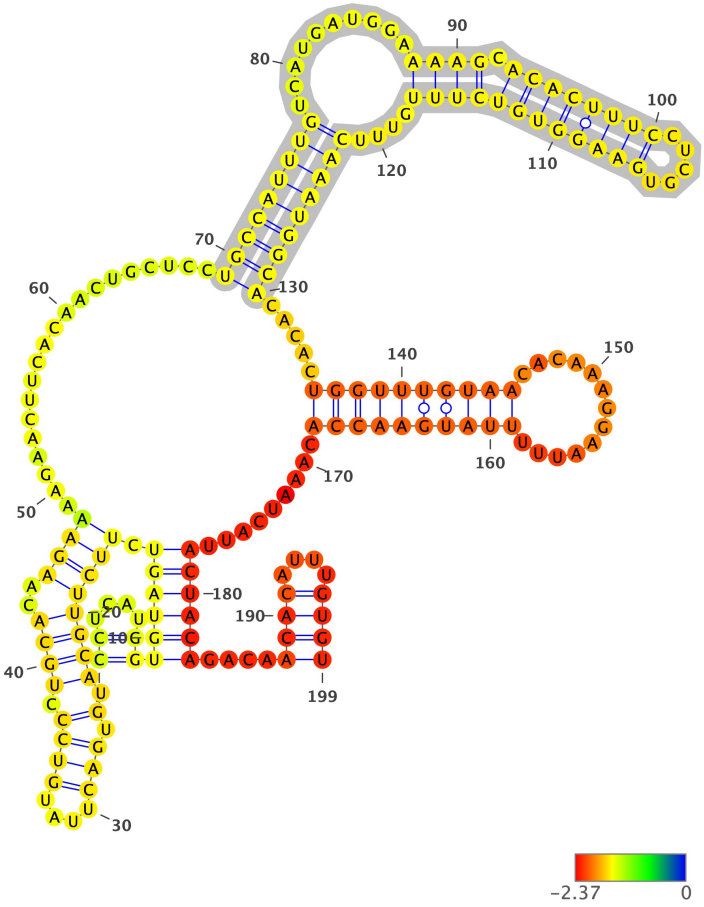
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 413 from nt 24799 to 24860 (nt 69 to 130)

```
5'-TGCCATTTGTCATGATGGAAAAGCACACTTTCCTCGTGAAGGUGUCUUUGTTTCAAAUGGCA-3'
5'-(((((((((.........((((.((((((((.....))))))))))))....)))))))))-3'
Motif MFE = -20.5; z-score = -3.29; ED = 10.87
```



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 24731 to 24929 (motif highlighted in silver):

```
5'-CCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGU
GUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGU-3
5'-((....))((((((.((((((((.(.(((....)))).))))..))))....................(((((((((.........((((.((((((((.....))))))
))))))....)))))))))).....((((((((((.............))))))))))).........))))))....((((....))))-3'
MFE = -44.1; z-score = -1.53; ED = 32.65
```

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(+)

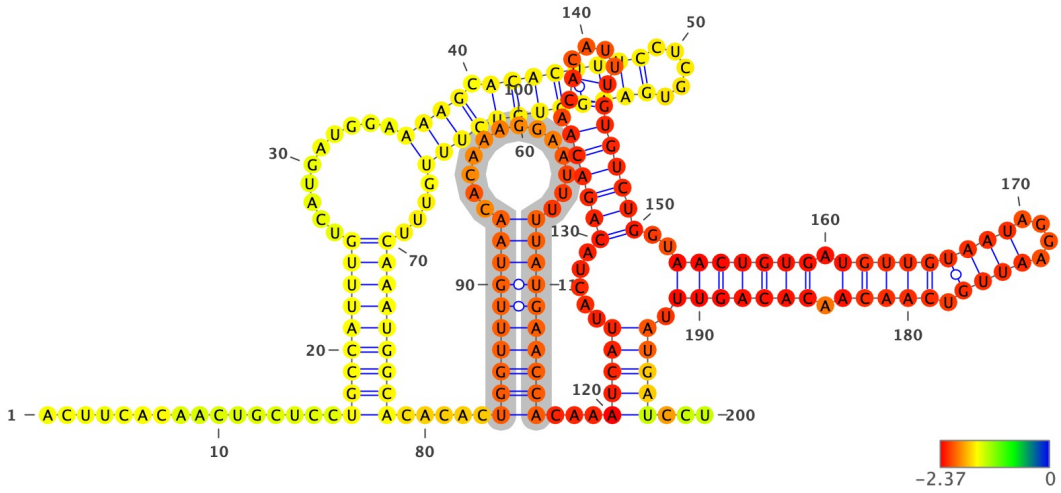
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 414 from nt 24866 to 24898 (nt 84 to 116)

```
5'-TGGTTTGTAACACAAAGGAATTTUUAUGAACCA-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -6.0; z-score = -1.95; 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 24783 to 24982 (motif highlighted in silver):

```
5'-ACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUG
AACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCU-3
5'-................(((((((((..........((((.((((((((.....)))))))))))....)))))))))).....((((((((((.............)))))
)))))...(((((.....((((((.((....))))))))..(((((((.((((((((((....)))).))))).)))))))).)))))...-3'
MFE = -50.1; z-score = -2.8; ED = 31.17
```

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(+)

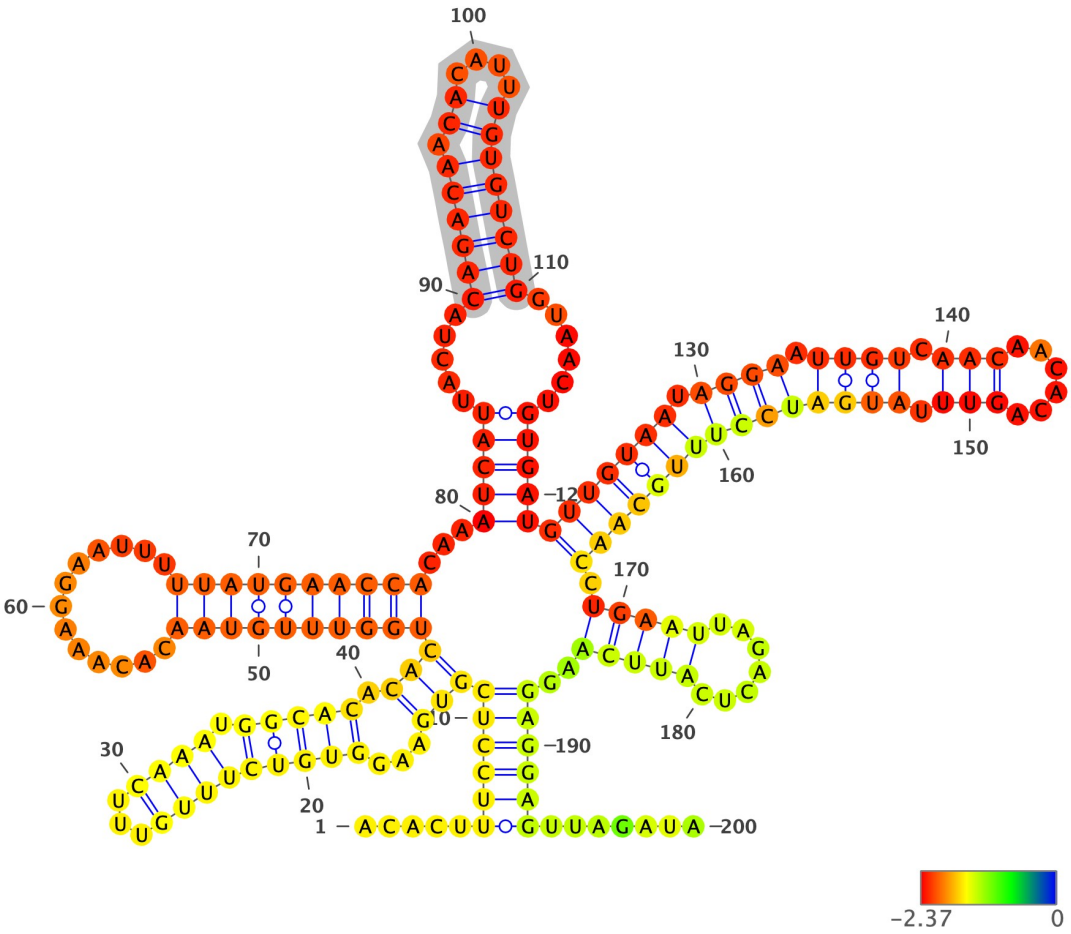
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 415 from nt 24912 to 24932 (nt 90 to 110)

```
5'-CAGACAACACATTUGUGUCUG-3'
5'-((((((.((....)))))))))-3'
Motif MFE = -6.0; z-score = -3.57; 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 24823 to 25022 (motif highlighted in silver):

```
5'-ACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGG
UAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUA-3
5'-.....(((((((((...(((((((((...)))))).)))))).)))((((((((((.............))))))))))...((((((.....((((((.((....)))))))).
.....)))))(((((((.((((.((((.(((.......))).)))))))))))))))).(((((.......))))))..))))))........-3'
MFE = -48.5; z-score = -2.69; ED = 58.34
```

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(+)

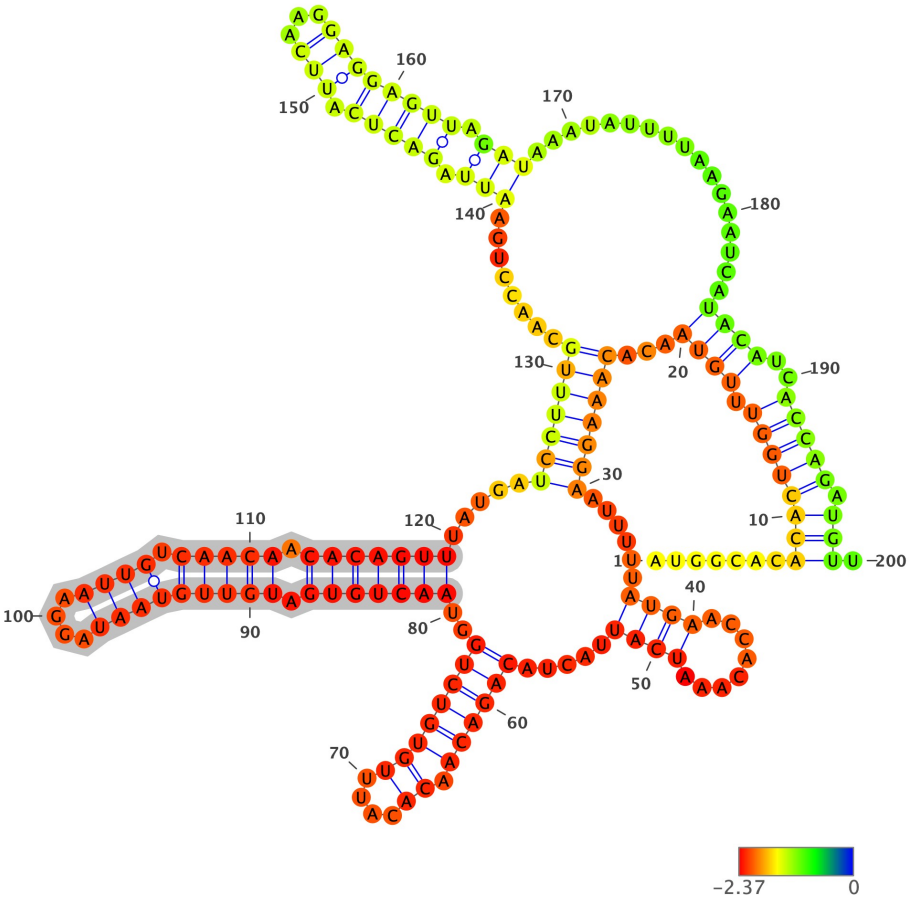
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 416 from nt 24935 to 24973 (nt 81 to 119)

```
5'-AACTGTGATGTTGTAATAGGAAUUGTCAACAACACAGUU-3'
5'-(((((((.(((((((((....)))).))))).)))))))-3'
Motif MFE = -13.8; z-score = -4.9; 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 24855 to 25054 (motif highlighted in silver):

```
5'-AUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACA
ACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUU-3
5'-.......((((((((.((((...(((((((......((((........))))).....((((((.((....))))))))..(((((((.(((((((((....)))).)))))
.)))))))).....)))))))........(((.(((((.(((...))))))))).)))................))))..))))).))).-3'
MFE = -43.4; z-score = -2.27; ED = 27.72
```

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(+)

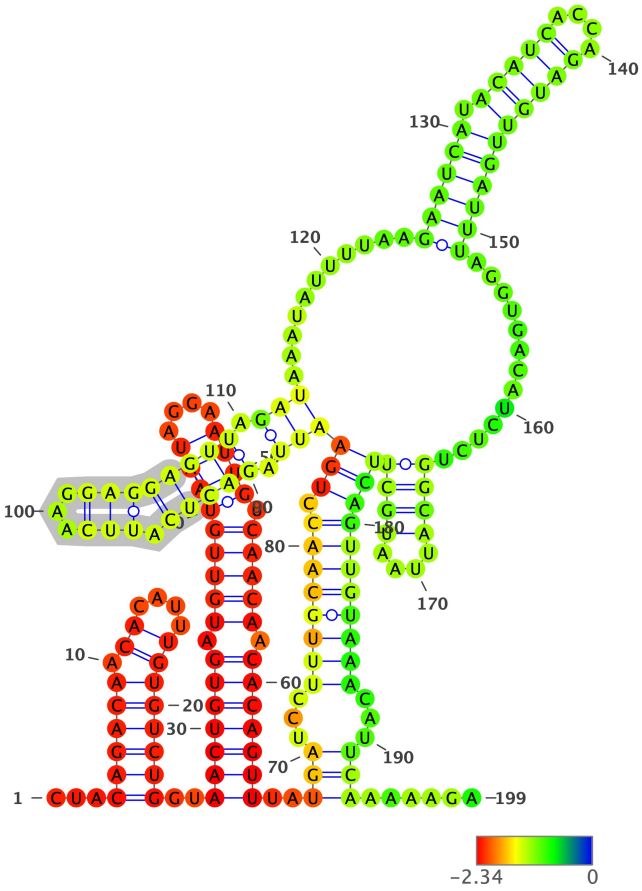
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 417 from nt 25001 to 25014 (nt 93 to 106)

```
5'-TCATTCAAGGAGGA-3'
5'-((.(((...))))))-3'
Motif MFE = 0.0; z-score = 0.34; ED = 1.39
```



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 24909 to 25107 (motif highlighted in silver):

```
5'-CUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAG
AUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGA-3
5'-...((((((.((....))))))))..(((((((.((((((((((....)))).)))))).)))))))..(((...(((((((((.((((((.(((((.(((...)))))))))))))))))))))))))
))...........((((((.((((((....))))))))))).............((((....))))))))))))))...)))).....-3'
MFE = -48.1; z-score = -2.93; ED = 20.72
```

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(+)

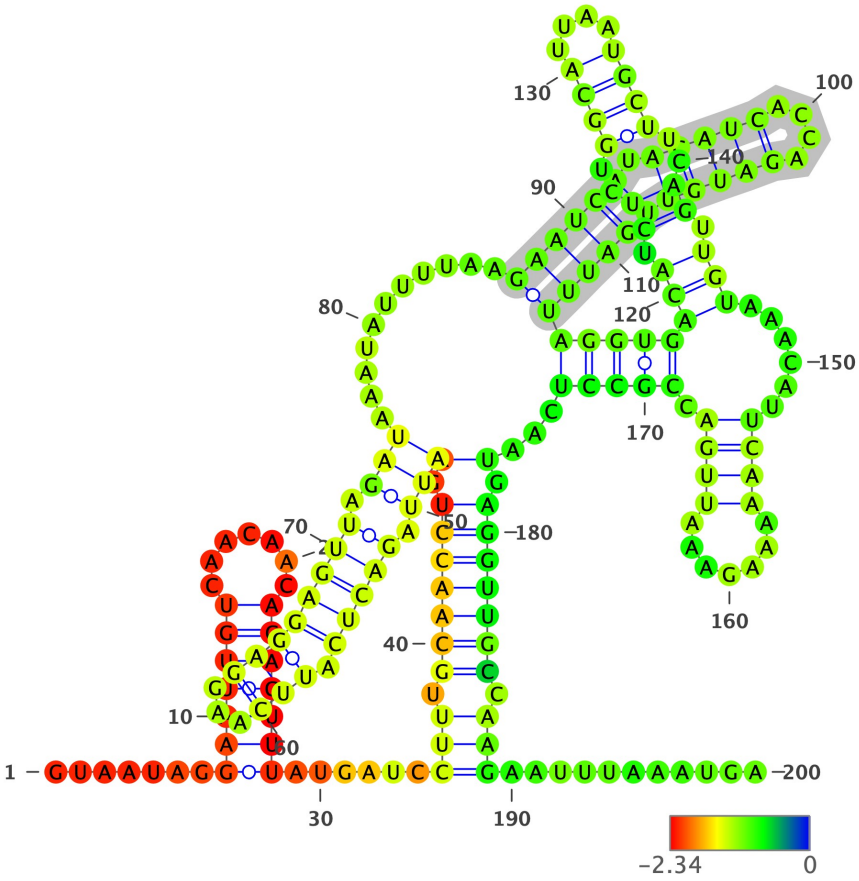
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 418 from nt 25033 to 25059 (nt 87 to 113)

```
5'-GAATCATACATCACCAGAUGUUGAUUU-3'
5'-((((((.((((((....))))))))))))-3'
Motif MFE = -8.1; z-score = -4.4; 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 24947 to 25146 (motif highlighted in silver):

```
5'-GUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAU
UUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGA-3
5'-.......(((((((.......)))))))......(((.(((((((.((((.(((((.(((...)))))))).))))...........((((((.(((((....)))))))))
))(((((((((.((..((((....))))..)).)))......((((.......)))).))))))...).)))))).)))...........-3'
MFE = -39.4; z-score = -1.17; ED = 40.83
```

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_gp02, 21563-25384(+)

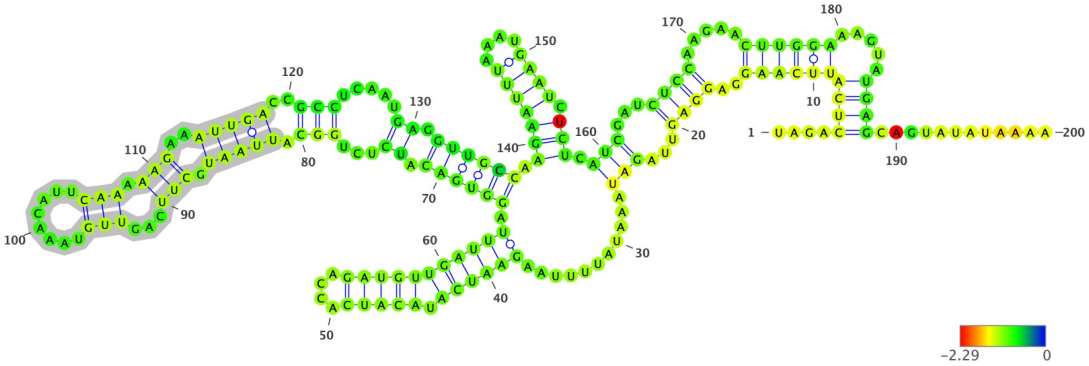
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 419 from nt 25077 to 25113 (nt 82 to 118)

```
5'-TTAATGCTTCAGTTGTAAACATTCAAAAAGAAAUUGA-3'
5'-(((((.(((...(((........))).)))..)))))-3'
Motif MFE = -1.5; z-score = 0.11; 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 24996 to 25195 (motif highlighted in silver):

```
5'-UAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAG
AAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAA-3
5'-....((((((((((..((((...(((...........((((((.(((((....)))))))))))).((((((.((...(((.(((((.(((...(((........))).)))
..)))))..)))).....)).)))))).(((((((....)))).))).)))...)))).....))))))).....))))............-3'
MFE = -36.0; z-score = -0.75; ED = 51.93
```

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(+)

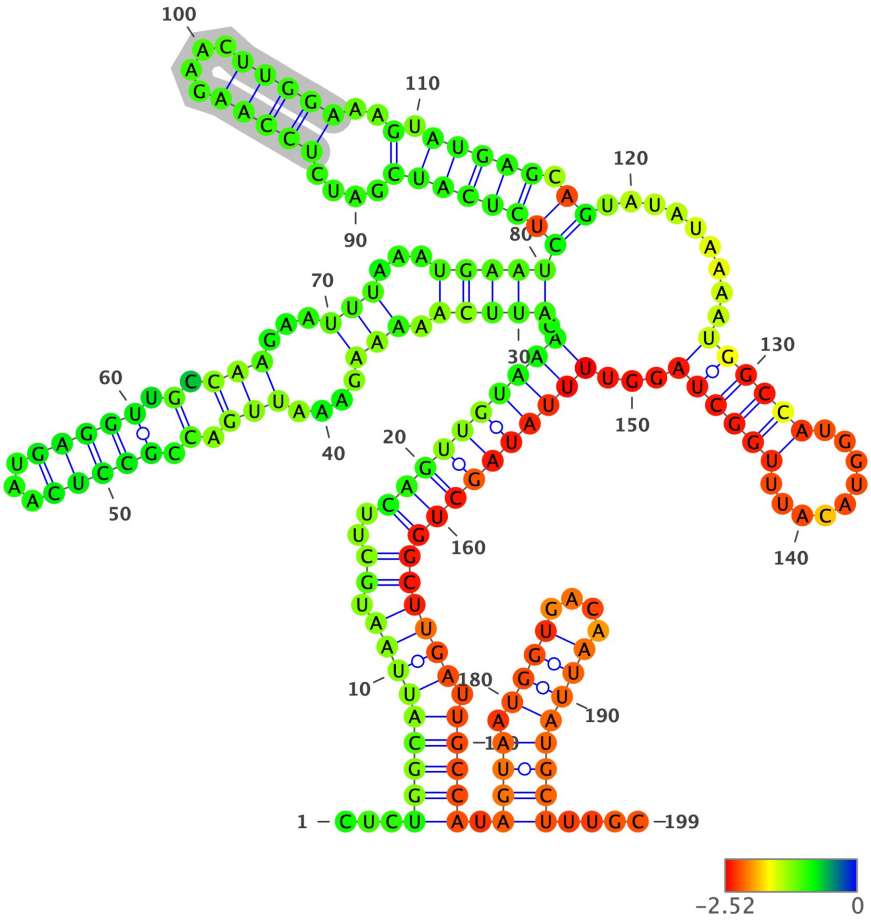
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 420 from nt 25161 to 25174 (nt 93 to 106)

```
5'-TCCAAGAACUUGGA-3'
5'-(((((....)))))-3'
Motif MFE = -3.1; z-score = -3.42; 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 = -0.67; 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(+)

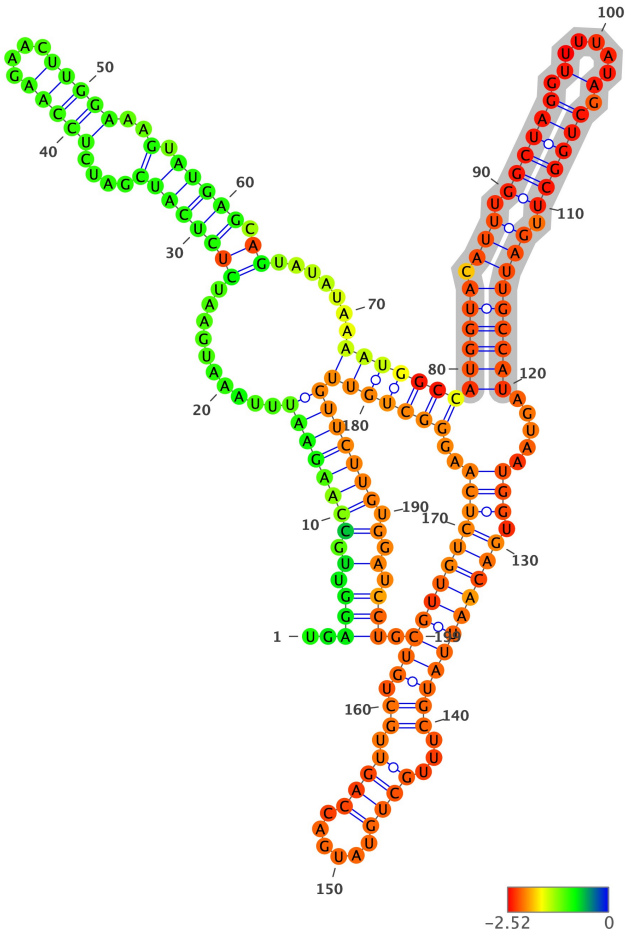
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 421 from nt 25201 to 25242 (nt 79 to 120)

```
5'-ATGGTACATTTGGCTAGGTTTTATAGCUGGCUTGAUUGCCAU-3'
5'-((((((.(((.((((((.(.....).)))))).)))))))))-3'
Motif MFE = -14.4; z-score = -3.08; ED = 2.51
```



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 25123 to 25321 (motif highlighted in silver):

```
5'-UGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUU
GAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGC-3
5'-..(((.(.((((((((..........((((((((....(((((....))))).).))))).))......((((((((((((.(((.((((((.(.....).)))))).
)))))))))).....(((.((((((((((...((((.....)))).)).))))))))))))..)))))))))))))).).).)))..-3'
MFE = -54.0; z-score = -1.4; ED = 18.85
```

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_gp02, 21563-25384(+)

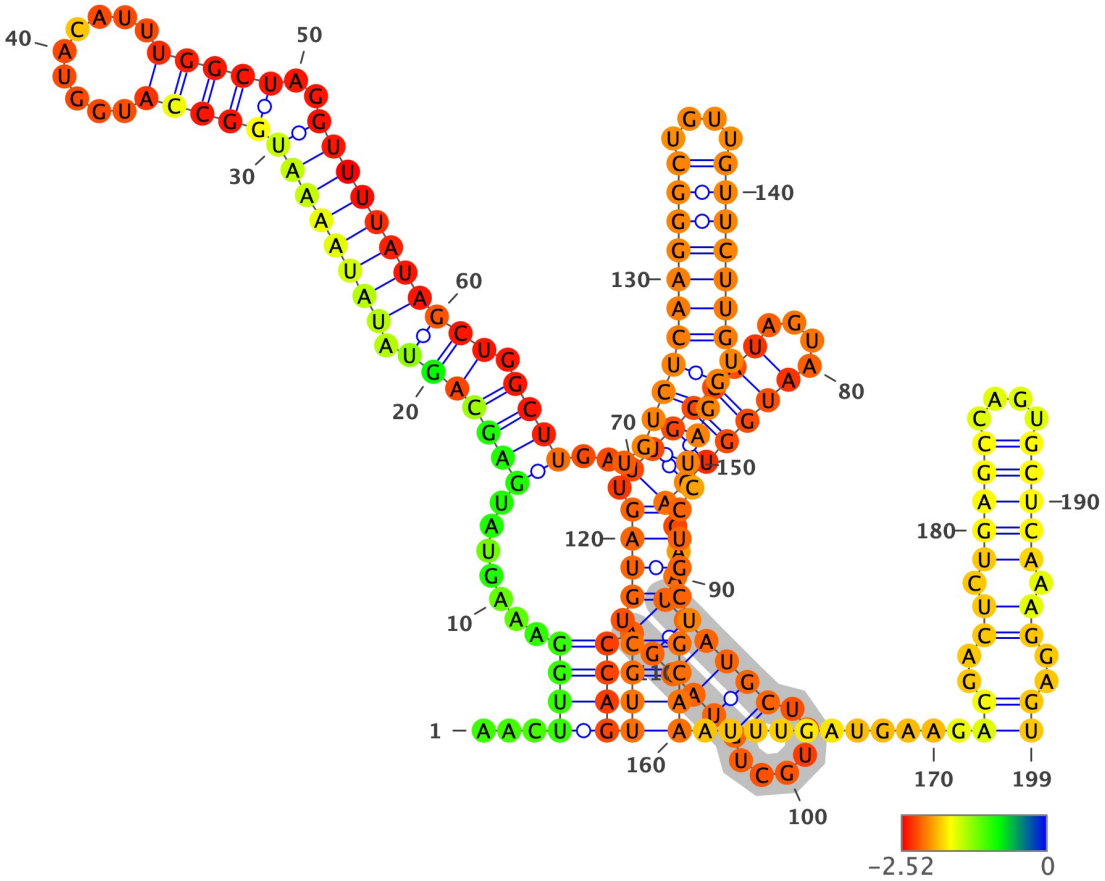
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 422 from nt 25257 to 25274 (nt 91 to 108)

```
5'-TTATGCTTTGCTGUAUGA-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -2.66; 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 25167 to 25365 (motif highlighted in silver):

```
5'-AACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCA
GUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGU-3
5'-...((((.......(((((((.((((((((((((((.........)))))..))))))))))).))))..(((((((....)))))))...((((((......)))))))))
)((((.((((..((((((((((((....)))))))).)))).)))).))))...........((..((.(((((....))))).))..))-3'
MFE = -54.7; z-score = -2.03; ED = 42.2
```

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_gp02, 21563-25384(+)

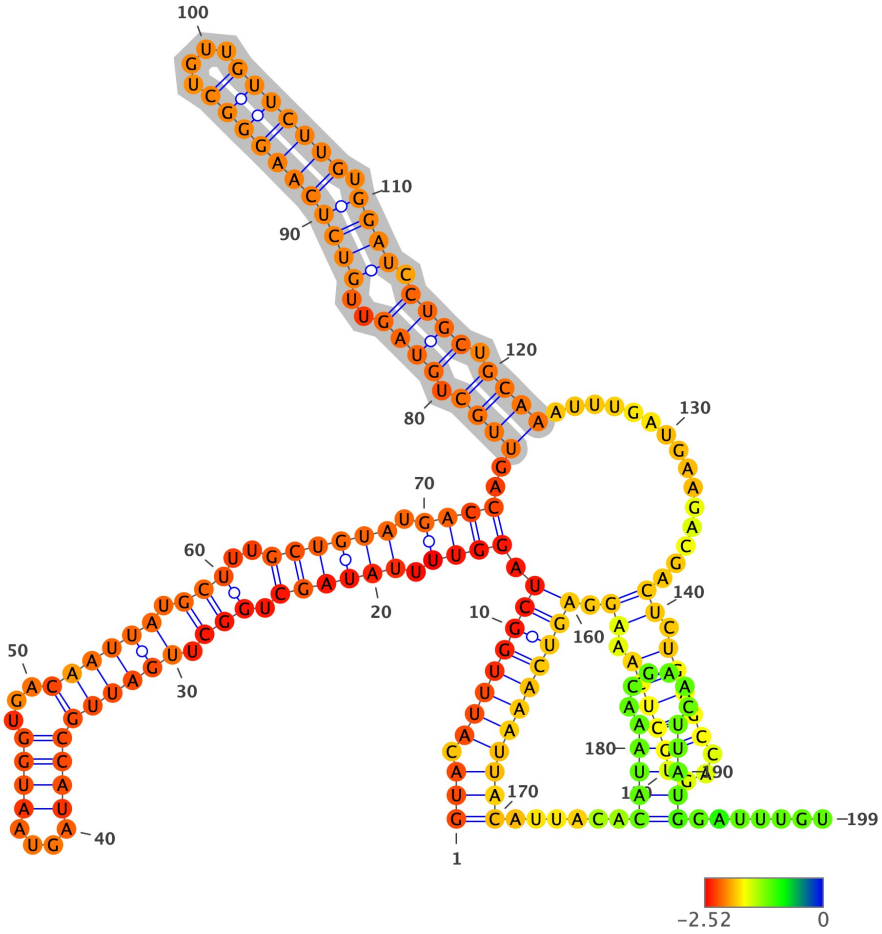
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 423 from nt 25279 to 25326 (nt 76 to 123)

```
5'-TTGCTGTAGTTGTCTCAAGGGCTGTTGUUCUUGTGGAUCCUGCTGCAA-3'
5'-((((.((((..(((((((((((....)))))))).)))).)))).))))-3'
Motif MFE = -17.9; z-score = -3.46; ED = 4.27
```



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 25204 to 25402 (motif highlighted in silver):

```
5'-GUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGG
AUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGU-3
5'-(((.((((((((.((((.((((((.(((.(((((((((((....))))...))))))).)))..))))))).))))..((((.((((..(((((((((((....)))))))).))
)).)))).))))...............((.(((((....))))).)).))))))))))).....(((((......)))))........-3'
MFE = -59.0; z-score = -3.25; ED = 26.86
```

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 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(+)

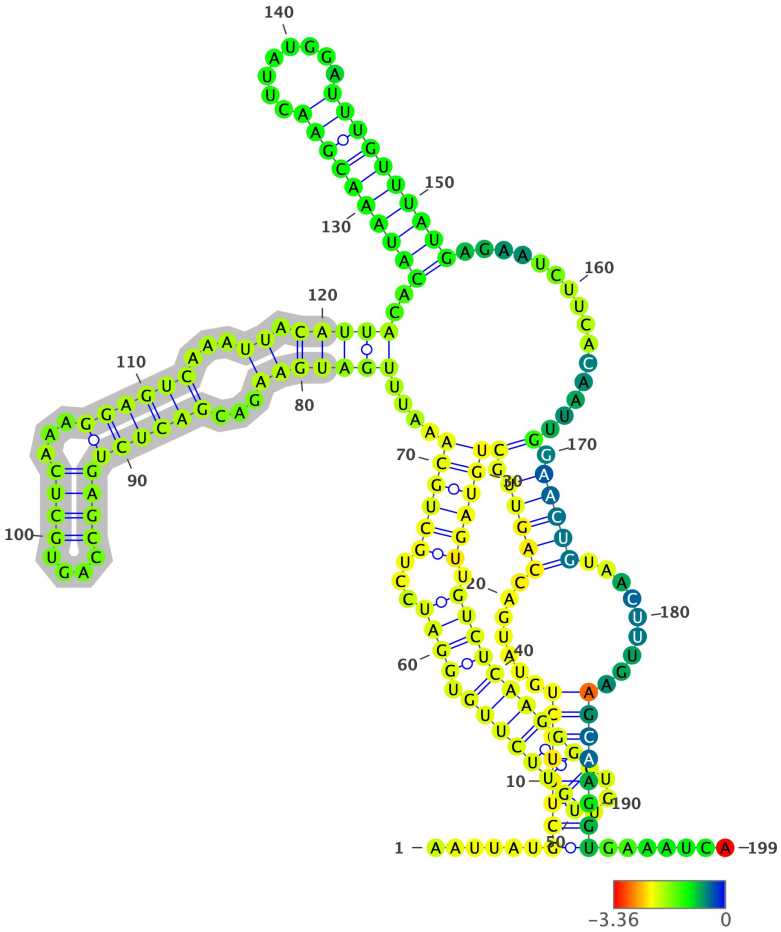
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 424 from nt 25333 to 25374 (nt 79 to 120)

```
5'-TGAAGACGACTCTGAGCCAGTGCUCAAAGGAGUCAAAUUACA-3'
5'-((((...(((((((((((....))))...))))))...)).))-3'
Motif MFE = -13.2; z-score = -3.45; ED = 4.88
```



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 25255 to 25453 (motif highlighted in silver):

```
5'-AAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGU
CAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUAUGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCA-3
5'-......((((((((.......(((((.(((((((.(((((((((((....)))))))).))))...))))))....(((((((...((((((((((....))))...)))))
)...)).)))))..((((((((((........))))))))))...............).)))))........))))))))........-3'
MFE = -52.9; z-score = -2.58; ED = 26.45
```

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 130--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 130--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 139 to 199--gene, gene-GU280_gp03, 25393-26220(+)

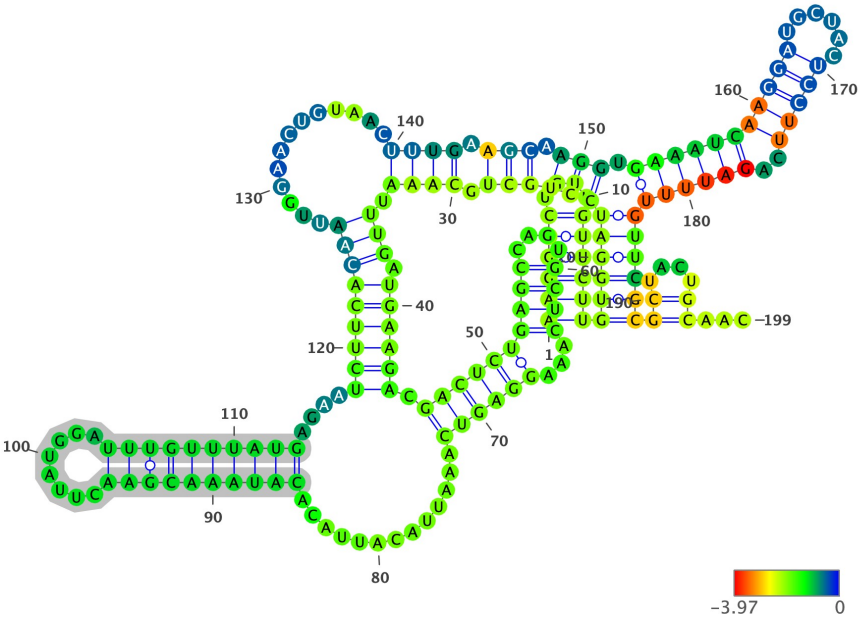
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 139 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 425 from nt 25380 to 25407 (nt 86 to 113)

```
5'-CATAAACGAACTTATGGAUUUGUUUAUG-3'
5'-((((((((((........))))))))))-3'
Motif MFE = -6.7; z-score = -2.76; 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 25295 to 25493 (motif highlighted in silver):

```
5'-AAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUA
UGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAAC-3
5'-((((((....))))))((((((((((((.((((.(((.((((((.((((((((((....)))))...))))))).............((((((((((........))))))))))
))....))))))))).............))))).))).))).(((((((((((.....))))))..)))))))))))((....))...-3'
MFE = -45.8; z-score = -0.46; ED = 48.79
```

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']

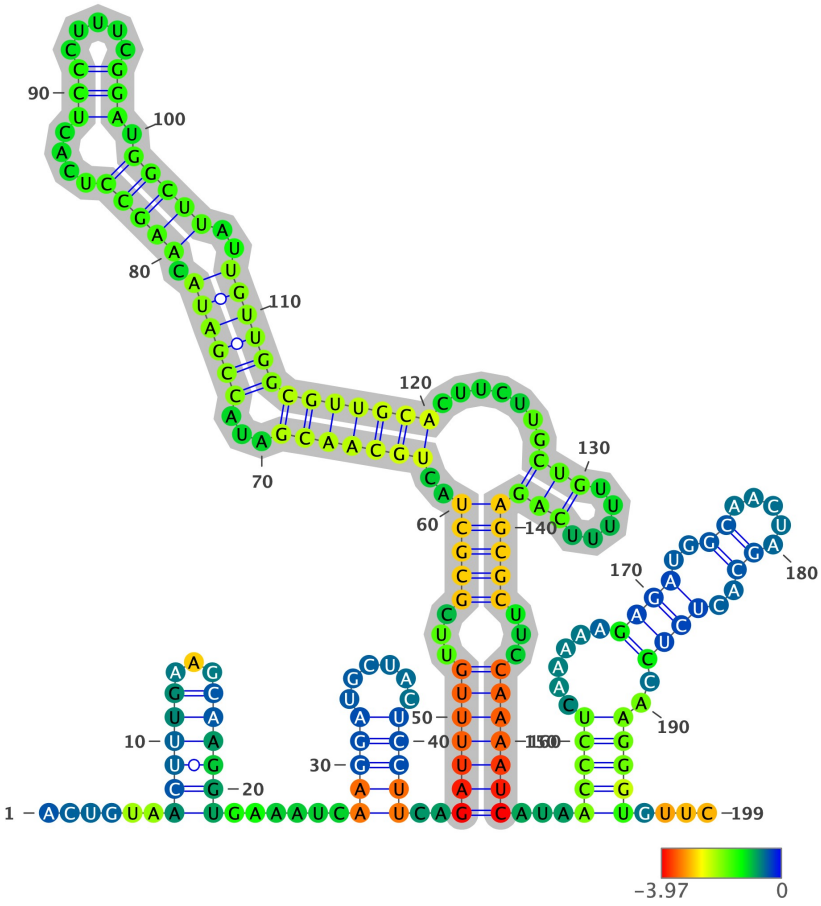
5-- nt 99 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

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 426 from nt 25471 to 25578 (nt 46 to 153)

```
5'-GATTTTGTTCGCGCTACTGCAACGATACCGATACAAGCCTCACTCCCTTTCGGATGGCUUATUGUUGGCGUUGCACTTCTTGCTGTTTTTCAGAGCGCTTCCAAAAUC-3'

5'-(((((((...(((((..(((((((...((((((.(((((....(((.....))).)))))..))))))))))))).......(((.....))))))))...)))))))-3'
Motif MFE = -34.1; z-score = -3.56; 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 = -2.84; ED = 25.82
```

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_gp03, 25393-26220(+)

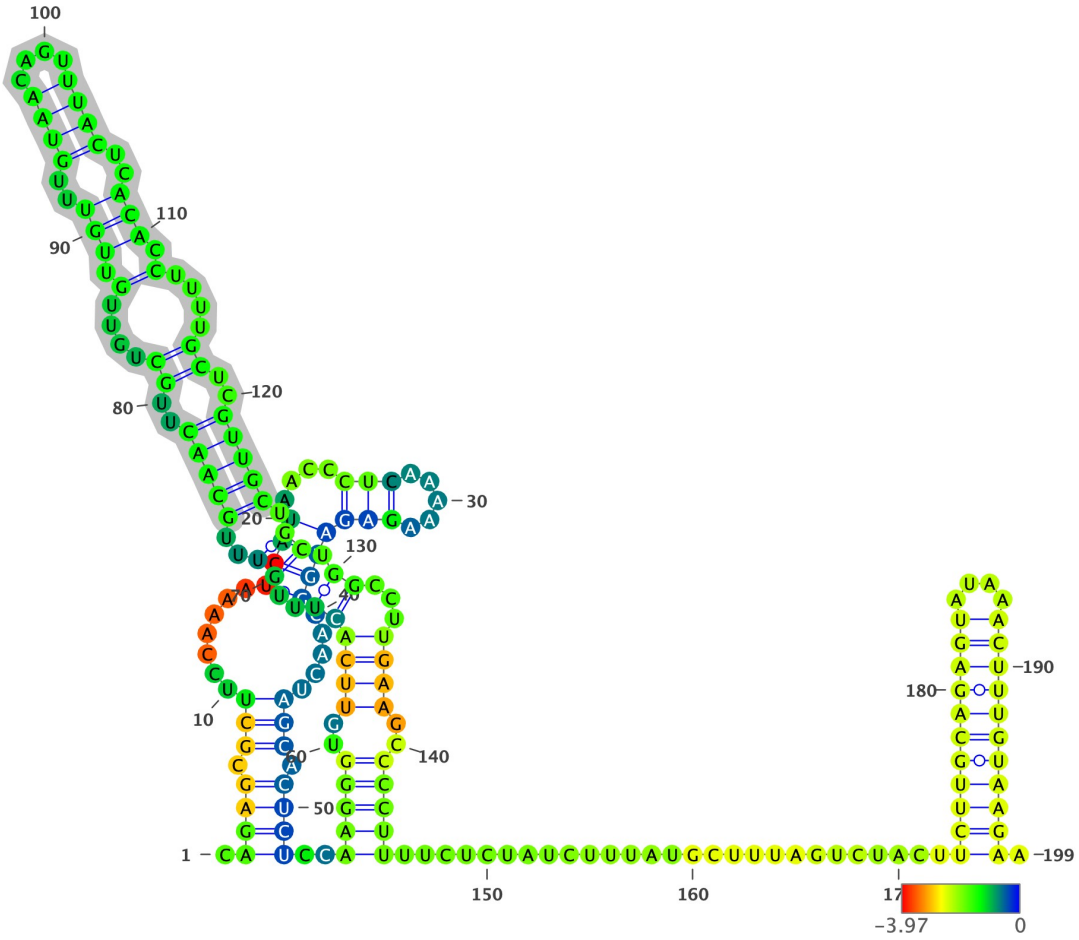
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 427 from nt 25634 to 25685 (nt 74 to 125)

```
5'-GCAACTTGCTGTTGTTGTTTGTAACAGTUUACTCACACCTTTTGCTCGUUGC-3'
5'-(((((..((....(.(((..((((....)))))..))).)....))..)))))-3'
Motif MFE = -11.3; z-score = -2.07; 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 = -2.16; 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(+)

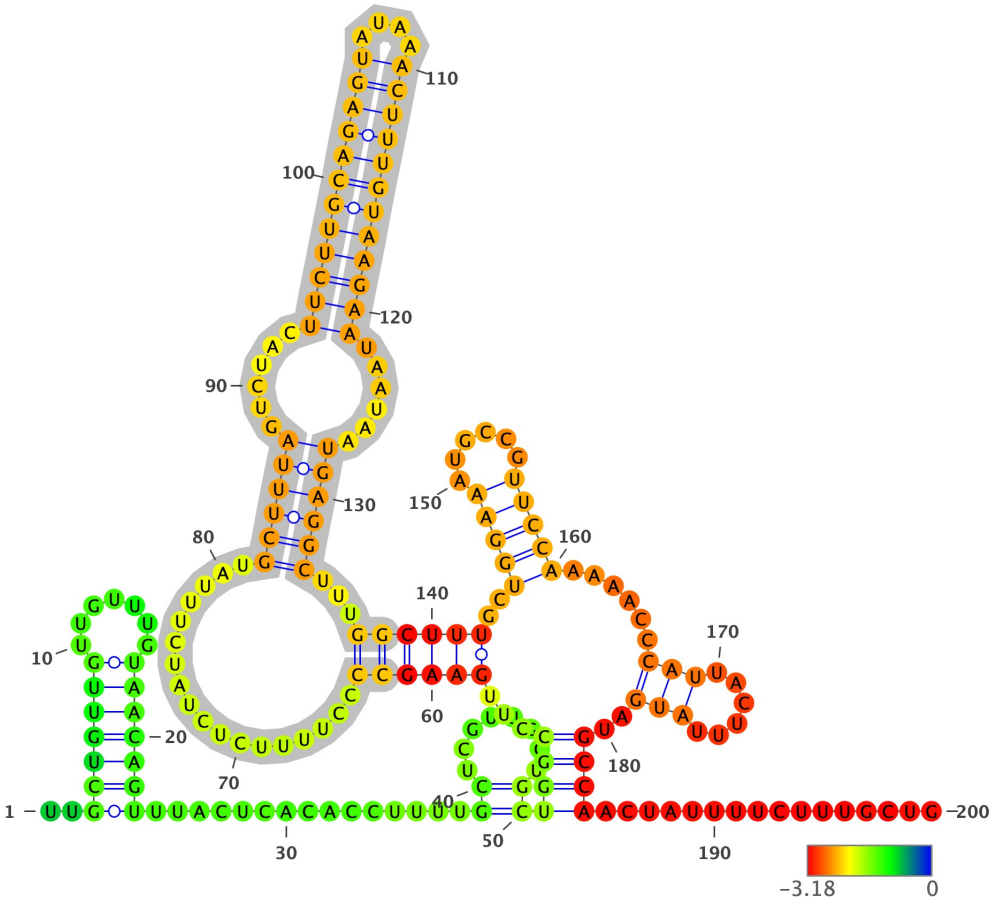
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 428 from nt 25700 to 25776 (nt 62 to 138)

```
5'-CCCCTTTTCTCTATCTTTATGCTTTAGTCTACTTCTTGCAGAGTATAAACUUUGUAAGAATAATAAUGAGGCTTTGG-3'
5'-((.................((((((......((((((((((((....))))))))))))......))))))...))-3'
Motif MFE = -19.5; z-score = -3.66; ED = 2.32
```



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 25639 to 25838 (motif highlighted in silver):

```
5'-UUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAAC
UUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUG-3
5'-..(((((((.......)))))))..............((........))(((((...((((((.................((((((......((((((((((((....))
))))))))))).....))))))...))))))..(((((.....)))))).....(((.....)))..))))................-3'
MFE = -38.7; z-score = -0.87; ED = 23.19
```

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_gp03, 25393-26220(+)

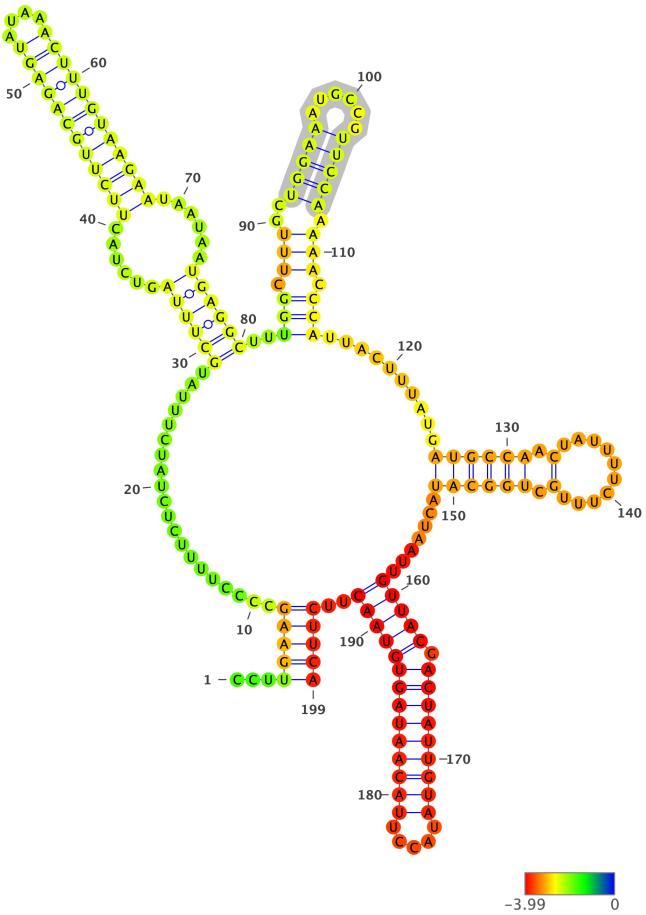
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 429 from nt 25783 to 25798 (nt 92 to 107)

```
5'-TGGAAATGCCGUUCCA-3'
5'-(((((......)))))-3'
Motif MFE = -3.1; z-score = -2.56; 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 25692 to 25890 (motif highlighted in silver):

```
5'-CCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAA
CCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCA-3
5'-...(((((.....................((((((.....((((((((((((....))))))))))))).....))))))..(((.(((..(((((.....)))))).)))
.))).........((((((.(.........).))))))......(((((.((((((((.....))))))))))))))..))))-3'
MFE = -51.5; z-score = -4.44; ED = 15.64
```

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_gp03, 25393-26220(+)

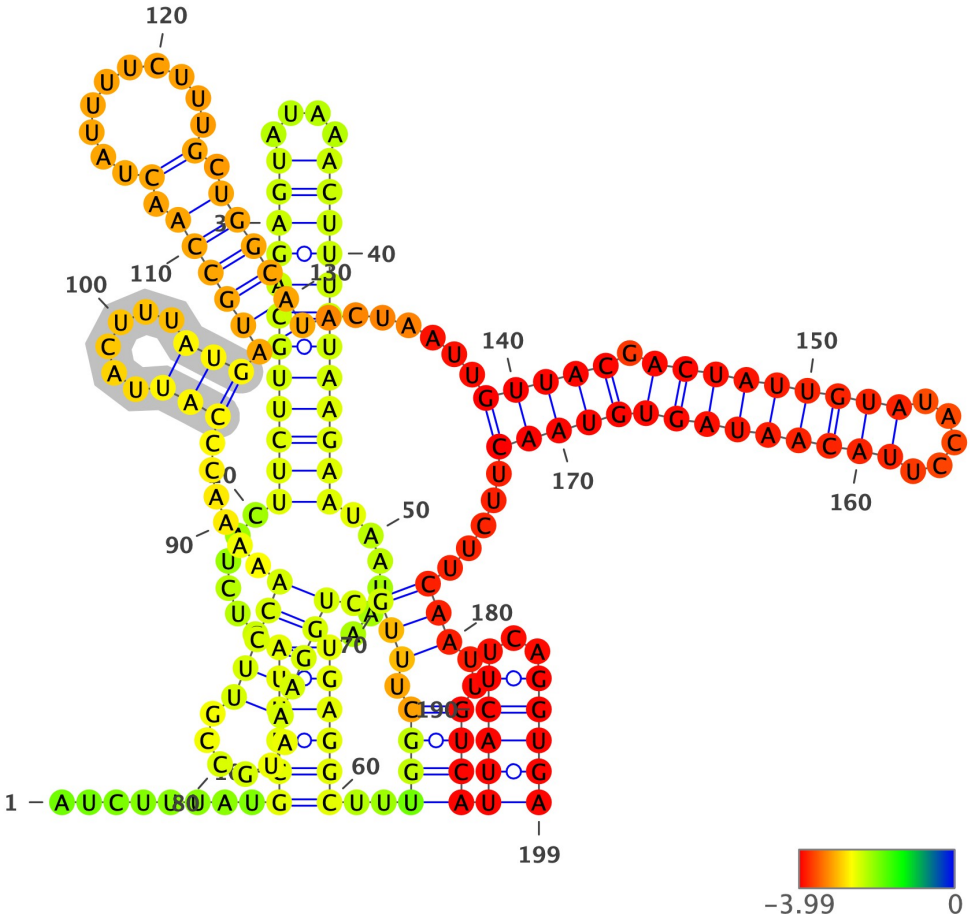
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 430 from nt 25805 to 25816 (nt 94 to 105)

```
5'-CATTACTTTAUG-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.63
```



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 25712 to 25910 (motif highlighted in silver):

```
5'-AUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCA
ACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGA-3
5'-........((((((......(((((((((((....)))))))))))).....))))))..((((.(((.(((((......)))))......(((......)))((((((
.(..........).))))))).......(((((.((((((((.....)))))))))))))).....)))..))))(((((...)))))-3'
MFE = -49.0; z-score = -3.86; ED = 25.7
```

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(+)

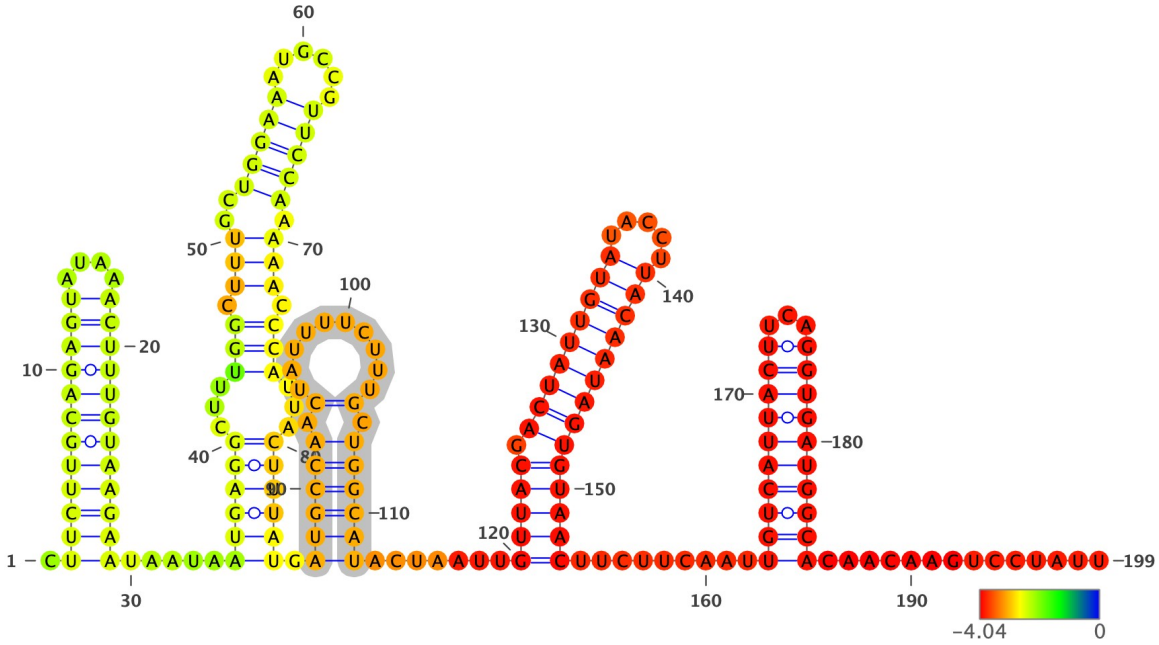
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 431 from nt 25817 to 25842 (nt 87 to 112)

```
5'-ATGCCAACTATTTTCTTTGCUGGCAU-3'
5'-((((((.(.........).)))))))-3'
Motif MFE = -5.9; z-score = -4.32; ED = 1.59
```



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 25731 to 25929 (motif highlighted in silver):

```
5'-CUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCA
UACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUU-3
5'-.(((((((((((....)))))))))))).....((((((...(((.(((..(((((.....)))))).))).)))...))))))).((((((.(.........).))))))
).......(((((.(((((((((.....)))))))))))))).........((((((((((...))))))))))..............-3'
MFE = -56.9; z-score = -5.09; ED = 21.94
```

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_gp03, 25393-26220(+)

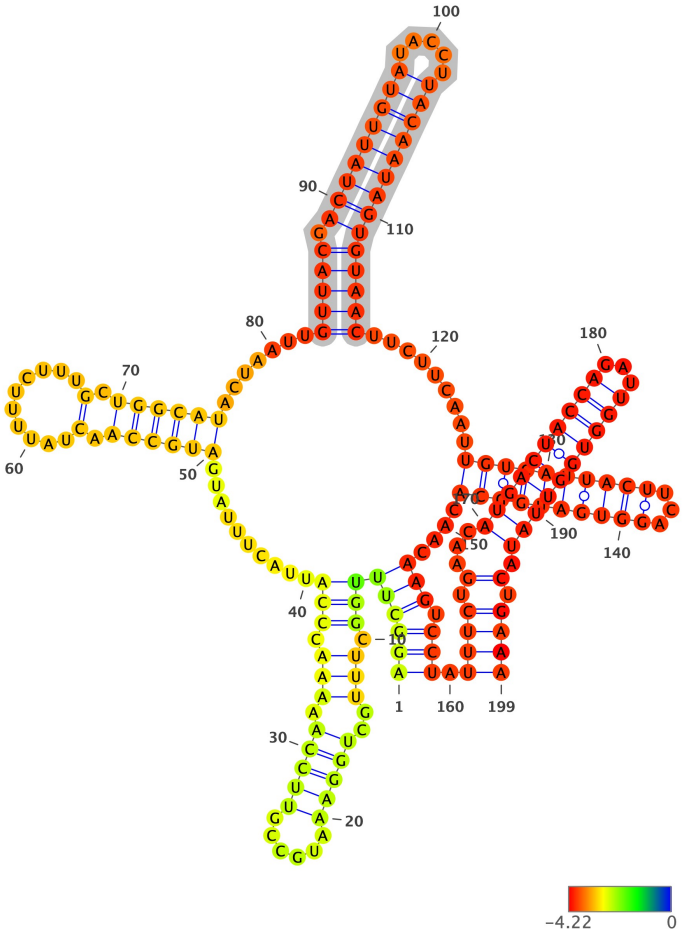
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 432 from nt 25850 to 25883 (nt 83 to 116)

```
5'-GTTACGACTATTGTATACCTUACAAUAGUGUAAC-3'
5'-(((((.((((((((((.....))))))))))))))-3'
Motif MFE = -13.6; z-score = -5.4; 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 = -4.02; 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(+)

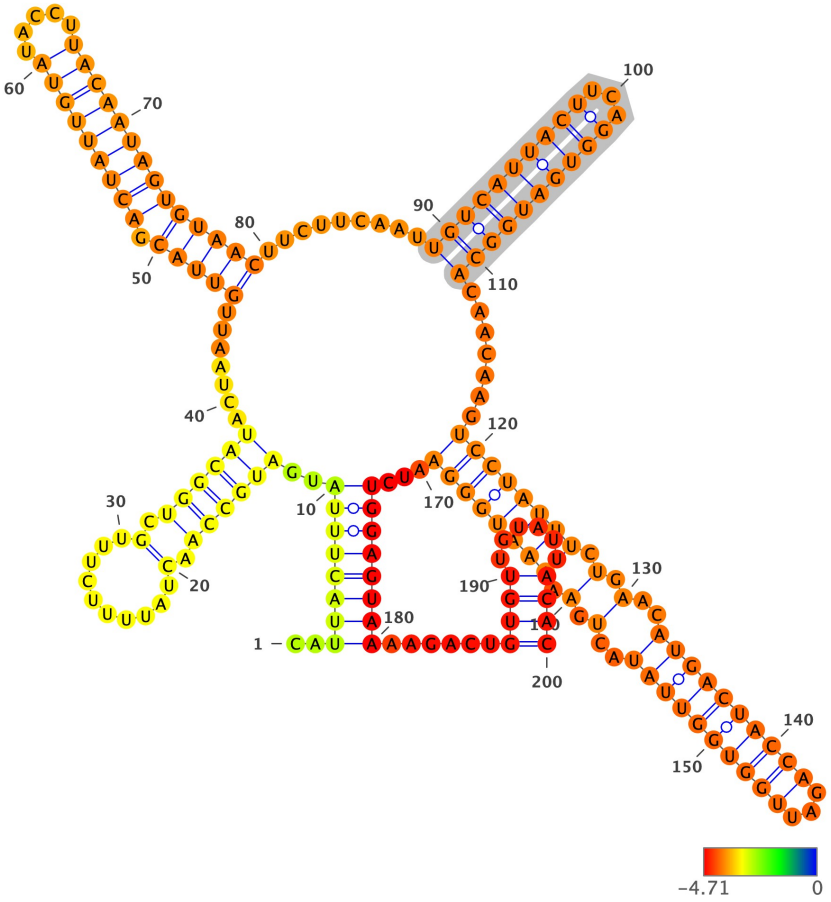
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 433 from nt 25893 to 25915 (nt 89 to 111)

```
5'-TGTCATTACTTCAGGUGAUGGCA-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -9.5; z-score = -4.47; ED = 0.82
```



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 25805 to 26004 (motif highlighted in silver):

```
5'-CAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCA
CAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACAC-3
5'-..(((((((((..((((((.(..........).))))))).......(((((.(((((((((.....)))))))))))))))).........((((((((((...))))))))))
.......(((((((((.(.(..((((((((((...))))))))))..).).)))))))))...)))))))).....((((......))))-3'
MFE = -57.7; z-score = -4.53; ED = 14.43
```

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_gp03, 25393-26220(+)

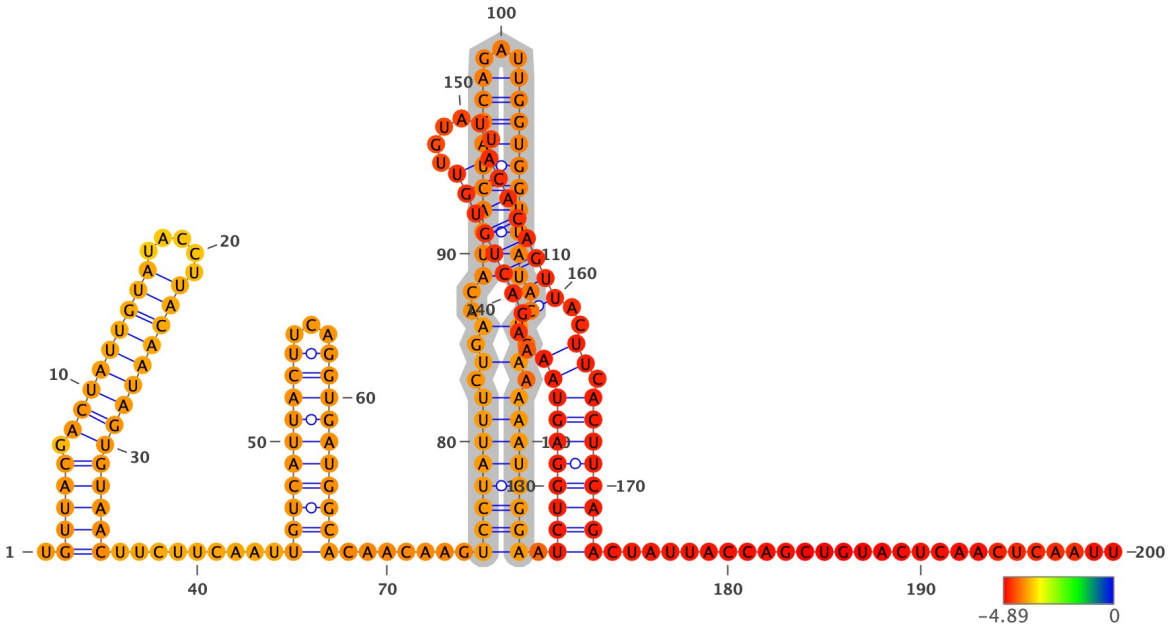
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 434 from nt 25923 to 25973 (nt 75 to 125)

```
5'-TCCTATTTCTGAACATGACTACCAGATTGGUGGUUAUACUGAAAAAUGGGA-3'
5'-(((((((((.(.(..((((((((((.....))))))))))..).).)))))))))-3'
Motif MFE = -17.8; z-score = -4.3; ED = 3.46
```



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 25849 to 26048 (motif highlighted in silver):

```
5'-UGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAU
ACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUU-3
5'-.(((((.((((((((((.....))))))))))))))).........((((((((((...))))))))))).......(((((((((.(.(..((((((((((...))))))))))
..).).)))))))).((((((((((..(((((((((.....)))))))))..)).)))))))).............................-3'
MFE = -63.2; z-score = -5.29; ED = 16.82
```

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_gp03, 25393-26220(+)

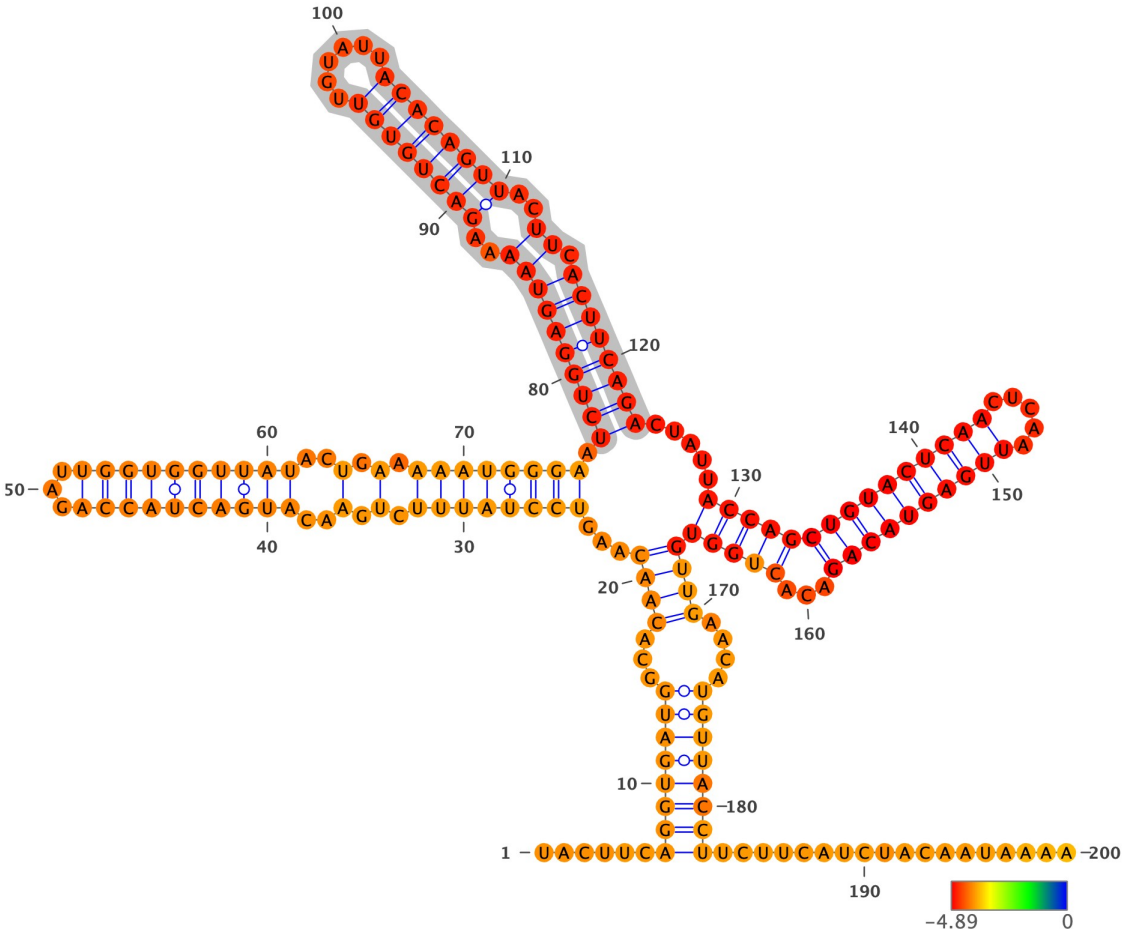
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 435 from nt 25975 to 26021 (nt 77 to 123)

```
5'-TCTGGAGTAAAAGACTGTGTTGTATTACACAGUUACUUCACUUCAGA-3'
5'-((((((((((..(((((((((.....)))))))))..)).)))))))))-3'
Motif MFE = -19.0; z-score = -5.0; ED = 2.84
```



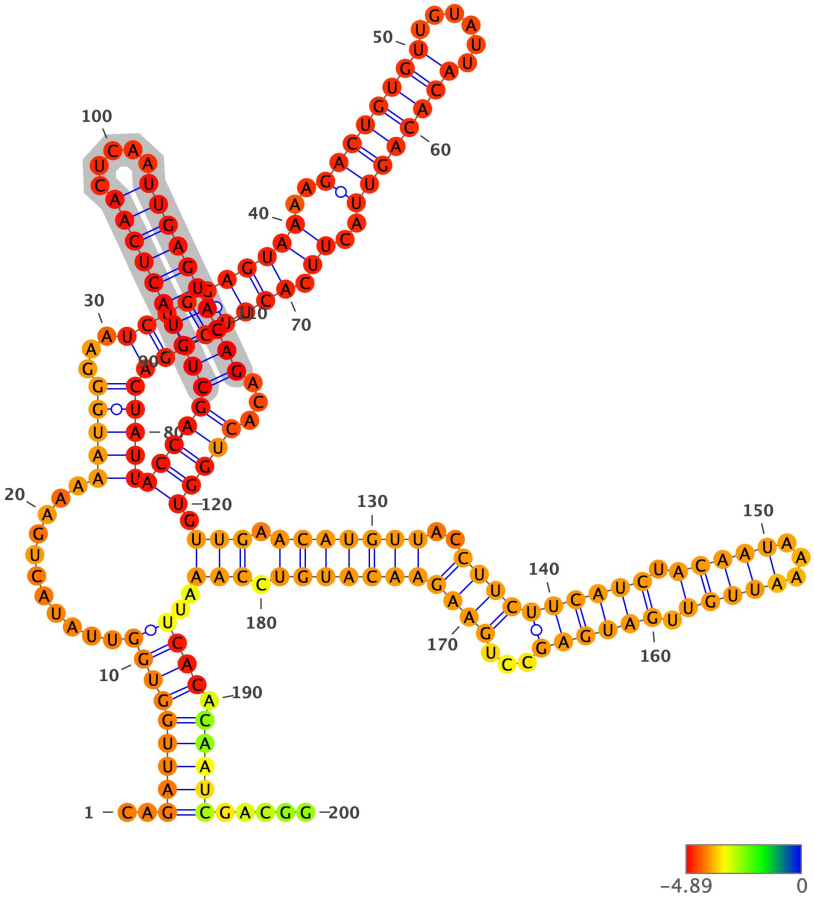
Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25899 to 26098 (motif highlighted in silver):

```
5'-UACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUA
CUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAA-3
5'-......(((((((((...(((((...(((((((((.(.(..((((((((((...)))))))))).)).).)))))))).((((((((((..(((((((((.....)))))))))..)).)))))))))).....(((((((((((((((.....)))))))))).)))))))))).....(((((((((((((((.....)))))))))).)))))))))).....(((((((((((((((.....)))))))))
```

NC_045512.2 (forward strand): Structure number 436 from nt 26032 to 26056 (nt 88 to 112)

```
5'-CTGTACTCAACTCAAUUGAGUACAG-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -11.8; z-score = -5.37; 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 = -5.9; 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(+)

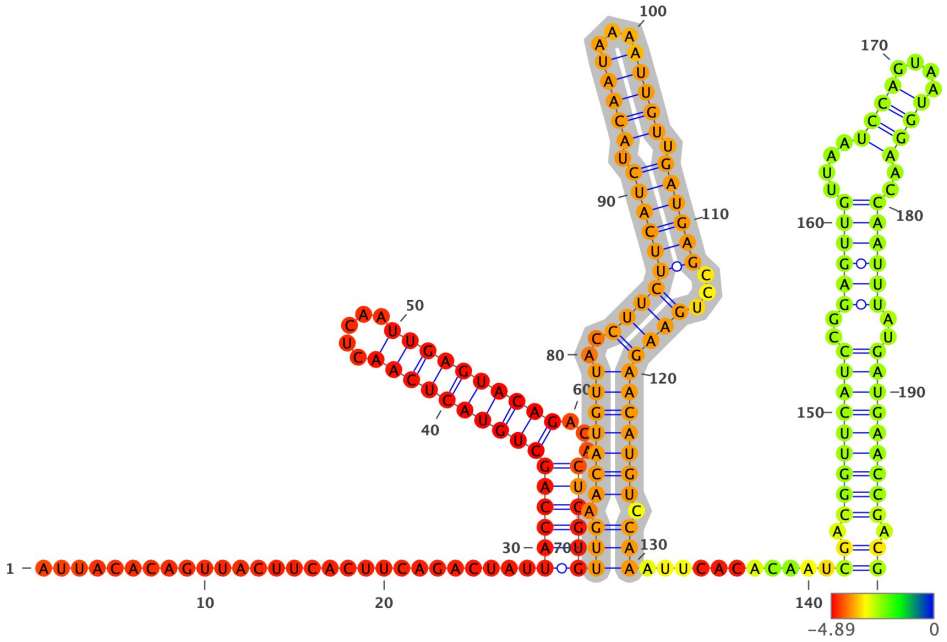
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 437 from nt 26066 to 26127 (nt 69 to 130)

```
5'-TTGAACATGTTACCTTCTTCATCTACAATAAAAUUGUTGAUGAGCCTGAAGAACAUGUCCAA-3'
5'-(((.(((((((..((((((((((.((((.....)))).))))))...))))))))))).)))-3'
Motif MFE = -18.2; z-score = -3.98; 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 = -5.37; 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(+)

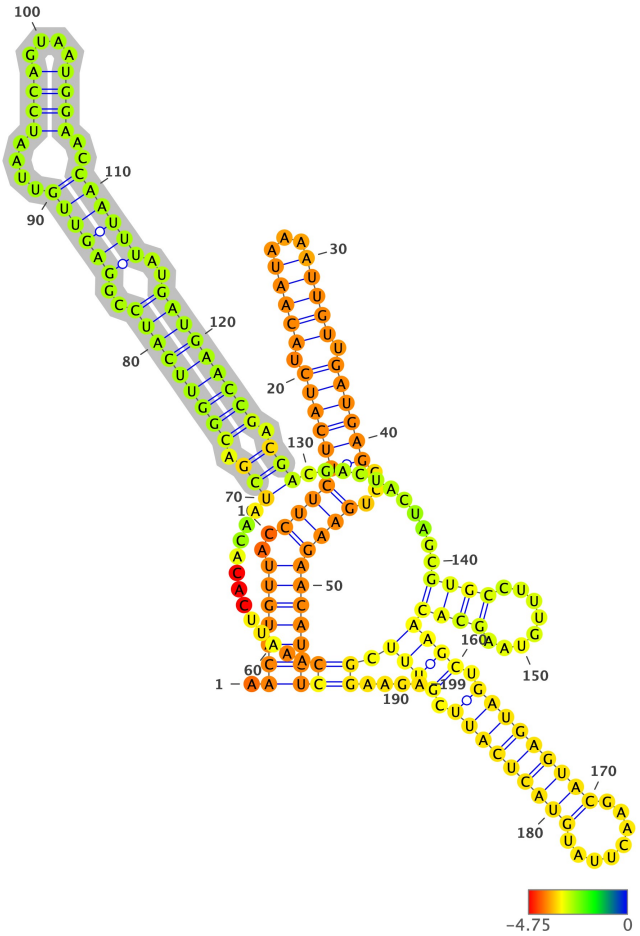
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 438 from nt 26139 to 26196 (nt 71 to 128)

```
5'-CGACGGTTCATCCGGAGTTGTTAATCCAGTAAUGGAACCAAUUUATGAUGAACCGACG-3'
5'-(..(((((((((..((((((....((((....))))..))))))..))))))))))..)-3'
Motif MFE = -21.2; z-score = -3.37; 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 26069 to 26267 (motif highlighted in silver):

```
5'-AACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAA
UUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGA-3
5'-.(((((((..(((((((((((.(((((...))))).))))))...))))))))))))((.............(((.(((((((((..((((((....((((....))))..)))
)))..)))))))))).))).........((((........))))((((.(((((((((........))))))))).)))).))....-3'
MFE = -59.6; z-score = -4.87; ED = 14.04
```

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 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(+)

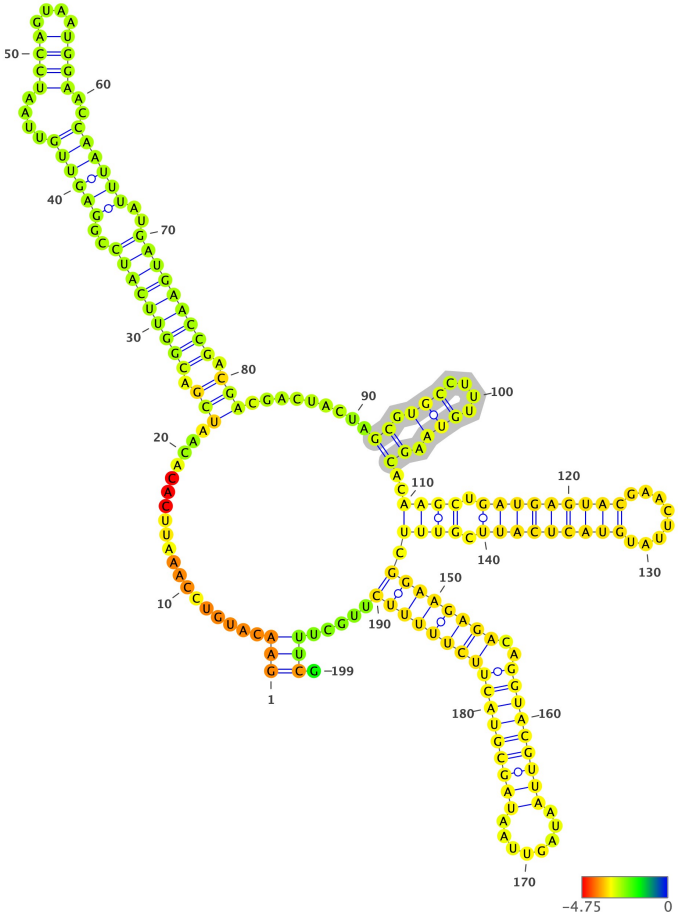
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 439 from nt 26207 to 26222 (nt 92 to 107)

```
5'-GCGTGCCTTTGTAAGC-3'
5'-(..............)-3'
Motif MFE = -0.9; z-score = 0.1; ED = 2.76
```



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 26116 to 26314 (motif highlighted in silver):

```
5'-GAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAA
GCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCG-3
5'-(((.................(((.((((((((((..((((((....((((....))))..))))))..))))))))).))).........((.(((....))).))..((
((.((((((((((........))))))))).)))).(((((((((..((((((((((........))))))))))))))))))).....))).-3'
MFE = -57.2; z-score = -3.79; ED = 16.44
```

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 105--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 105--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 130 to 199--gene, gene-GU280_gp04, 26245-26472(+)

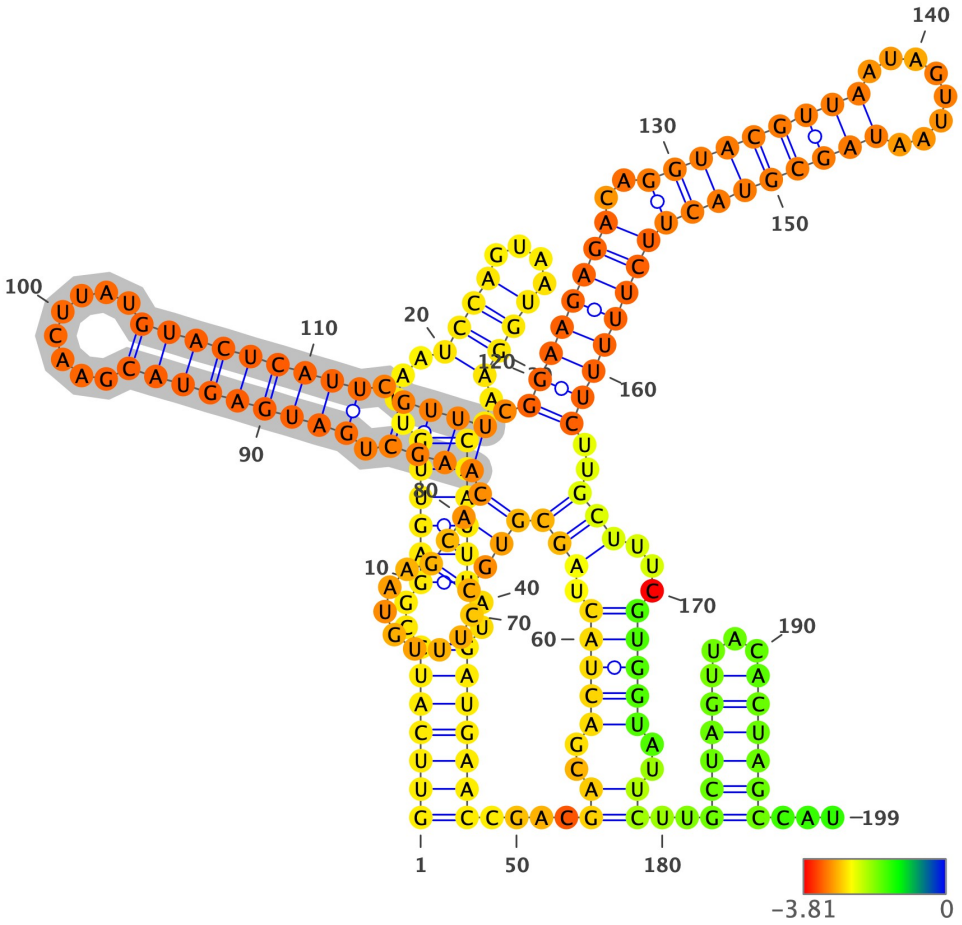
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 130 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 440 from nt 26225 to 26260 (nt 82 to 117)

```
5'-AAGCTGATGAGTACGAACTTATGUACUCAUUCGUUU-3'
5'-((((.((((((((((........)))))))))).))))-3'
Motif MFE = -13.0; z-score = -4.41; 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 = -3.98; 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(+)

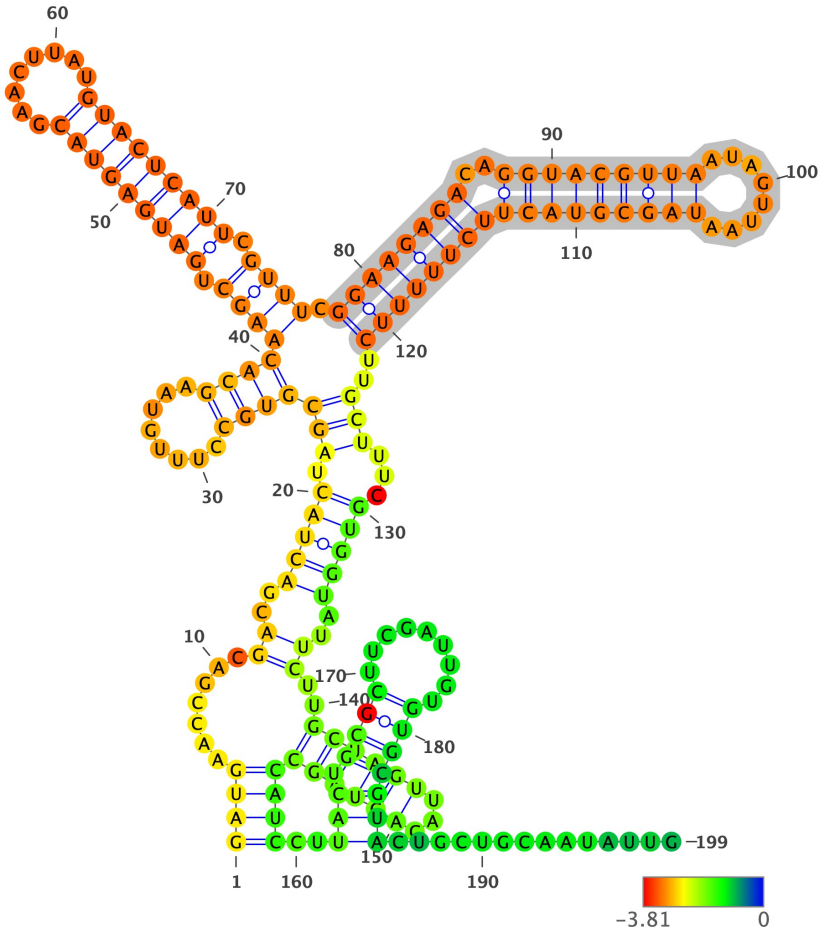
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 441 from nt 26262 to 26305 (nt 78 to 121)

```
5'-GGAAGAGACAGGTACGTTAATAGTTAATAGCGUACUUCUUUUUC-3'
5'-(((((((((..((((((((((........))))))))))))))))))-3'
Motif MFE = -15.7; z-score = -3.85; 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 26185 to 26383 (motif highlighted in silver):

```
5'-GAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUA
CUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUG-3
5'-((((.......((..((((((.(((((((........)))))(((((.(((((((((........)))))))))))))))))))))))))))))))))))..)))...))))))..))..((((((...))))))))))..(((.(((.........)))))))..............-3'
MFE = -55.4; z-score = -1.99; ED = 37.91
```

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 36--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 36--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 61 to 199--gene, gene-GU280_gp04, 26245-26472(+)

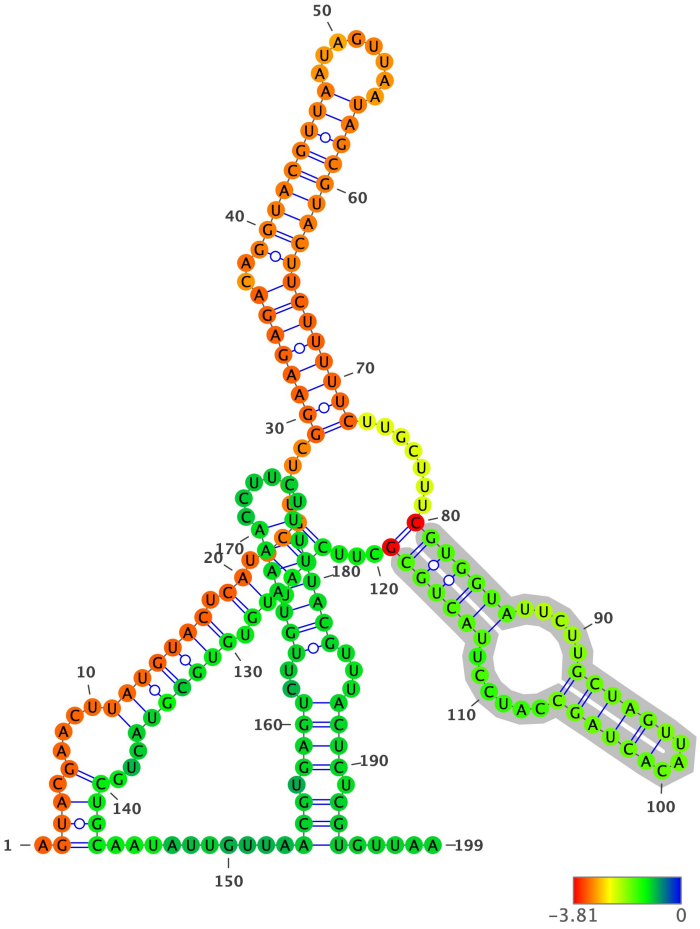
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 61 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 442 from nt 26314 to 26351 (nt 81 to 118)

```
5'-GTGGTATTCTTGCTAGTTACACUAGCCATCCTUACUGC-3'
5'-((((((.....(((((.....)))))).....)))))-3'
Motif MFE = -9.7; z-score = -2.5; ED = 1.75
```



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 26234 to 26432 (motif highlighted in silver):

```
5'-AGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCC
UUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAA-3
5'-.(((.(....(((((((.((.(((....(((((((..(((((((((........)))))))))))))))))).....(((((((.....((((((...)))))).....
.)))))))...))).)).)))))))...))))..........(((.(((((..(((((((.....)))))))...)))))..))).....-3'
MFE = -50.8; z-score = -3.3; ED = 27.05
```

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 12 to 199--gene, gene-GU280_gp04, 26245-26472(+)

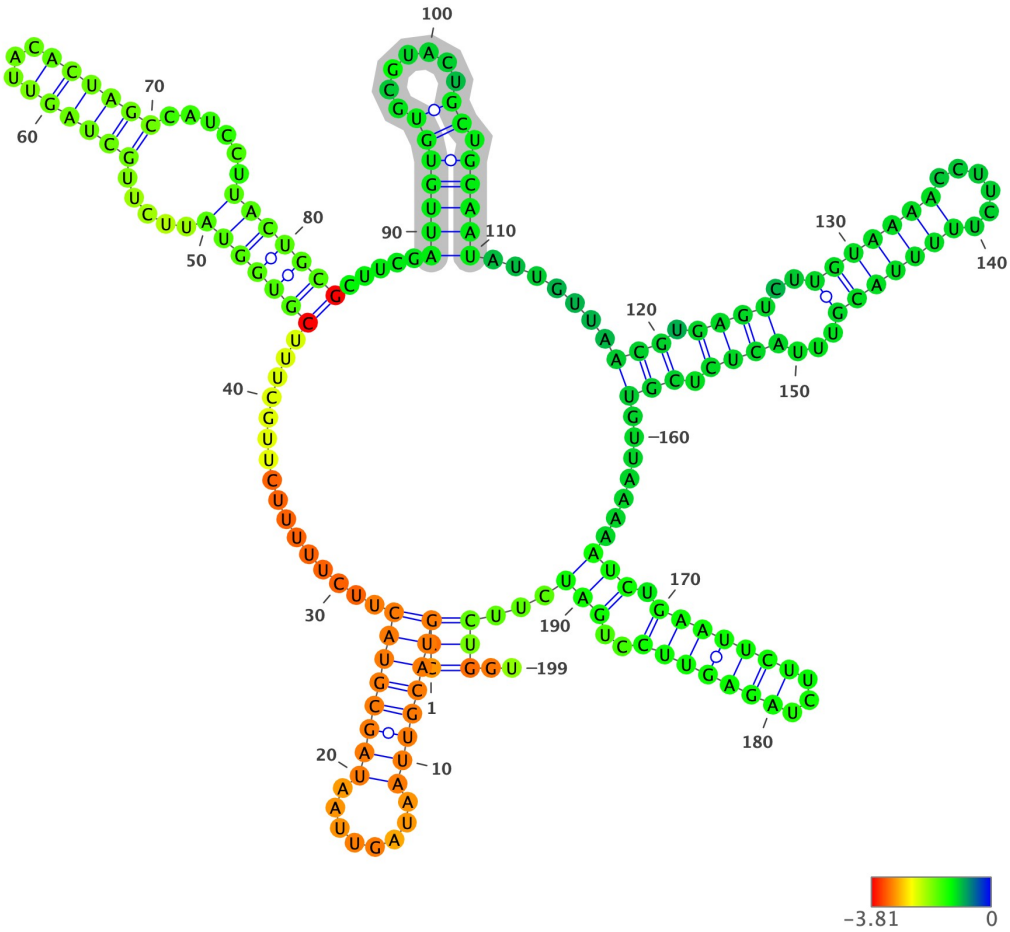
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 443 from nt 26358 to 26379 (nt 89 to 110)

```
5'-ATTGTGTGCGTACTGCTGCAAU-3'
5'-(((((((.......)).)))))-3'
Motif MFE = -3.3; z-score = -0.78; 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 26270 to 26468 (motif highlighted in silver):

```
5'-CAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUA
UUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGU-3
5'-((((((((((((........))))))))).................(((((((.....(((((((...)))))))......)))))))).....(((((((.......)).)))))).
......(((.(((((..(((((((.....)))))))...)))))..))).))).......(((.(((((((...)))))))..)))...))))..-3'
MFE = -42.4; z-score = -2.31; ED = 19.42
```

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_gp04, 26245-26472(+)

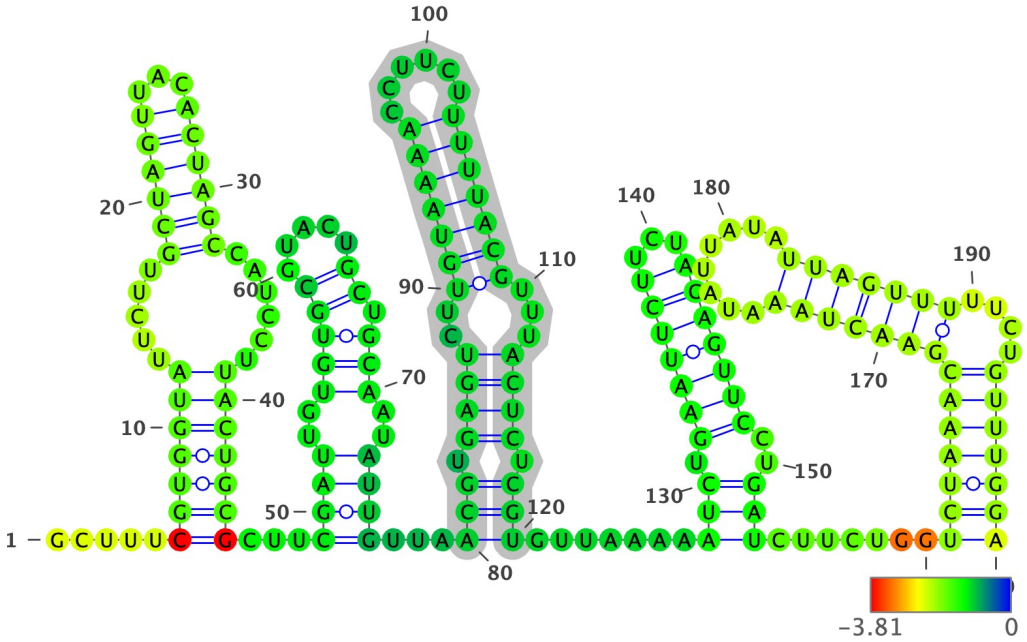
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 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 444 from nt 26387 to 26427 (nt 80 to 120)

```
5'-ACGTGAGTCTTGTAAAACCTTCTUUUUACGTTTACUCTCGU-3'
5'-(((.((((..(((((((.....)))))))...)))).)))-3'
Motif MFE = -9.6; z-score = -3.84; ED = 1.39
```



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 26308 to 26507 (motif highlighted in silver):

```
5'-GCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUU
UACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGA-3
5'-.....(((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..))))...(((.((((..(((((((.....)))))))..
.)))).)))......(((.(((((((...)))))))..)))......((((((((((((((.......)))))))....)))))))-3'
MFE = -42.5; z-score = -1.74; ED = 20.96
```

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 165--gene, gene-GU280_gp04, 26245-26472(+)

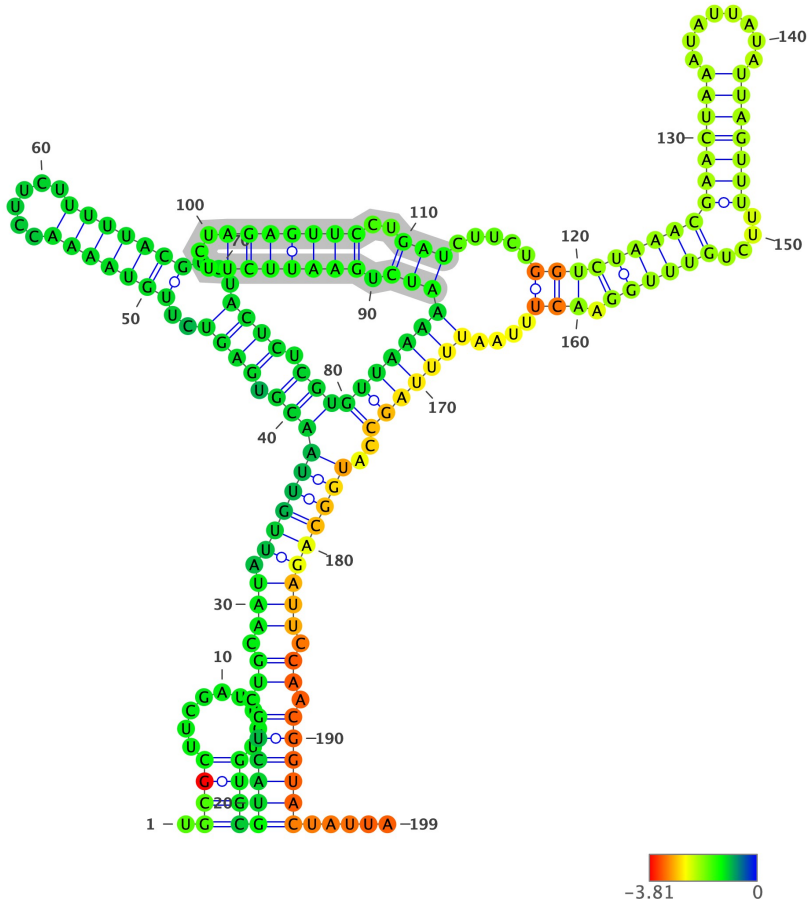
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 445 from nt 26435 to 26460 (nt 87 to 112)

```
5'-ATCTGAATTCTTCTAGAGUUCCTGAU-3'
5'-(((.(((((((...)))))))..)))-3'
Motif MFE = -5.4; z-score = -2.79; ED = 1.53
```



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 26349 to 26547 (motif highlighted in silver):

```
5'-UGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGA
UCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUA-3
5'-.((((.........))))((((((.((.(((.(((((((((.((((..(((((((.......)))))))...)))).)))((((((((((.(((((((...)))))))..))
).....((((((((((((((((.........)))))))....)))))).)))....)))))))..))))))))).)).))))))).....-3'
MFE = -42.5; z-score = -1.97; ED = 20.78
```

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 124--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 124--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 175 to 199--gene, gene-GU280_gp05, 26523-27191(+)

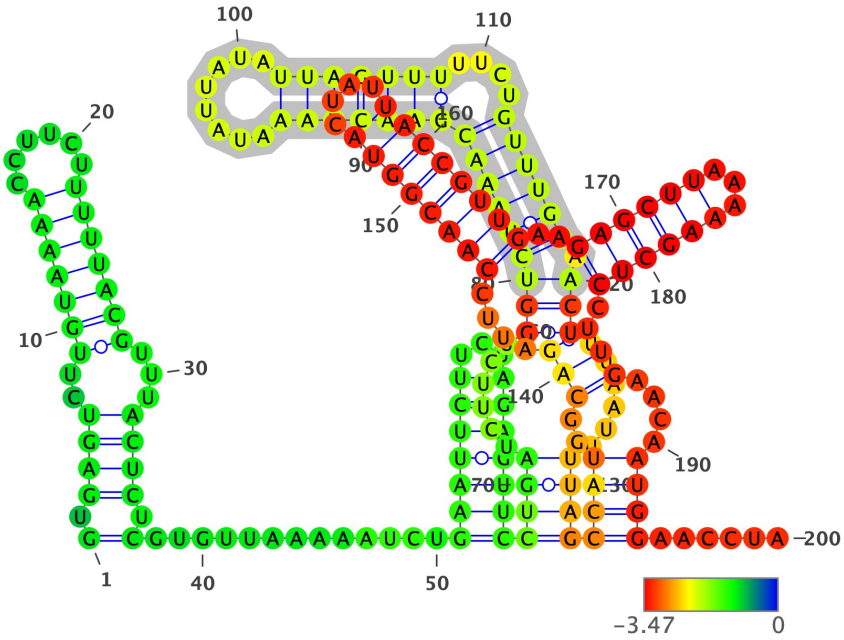
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 175 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 446 from nt 26468 to 26508 (nt 80 to 120)

```
5'-TCTAAACGAACTAAATATTATAUUAGUUUTTCTGUUUGGAA-3'
5'-(((((((((((((.........)))))))....)))))).)-3'
Motif MFE = -9.2; z-score = -3.6; 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 26389 to 26588 (motif highlighted in silver):

```
5'-GUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUC
UGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUA-3
5'-(.((((..(((((((......)))))))...)))).).............(((((((...)))))))((((......((((((((((((((((.........)))))))...
.)))))).)))......))))((((..(((....((((((((....))))))))..((((((...)))))).)))....))))......-3'
MFE = -42.3; z-score = -2.87; ED = 34.57
```

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 84--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 84--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 135 to 200--gene, gene-GU280_gp05, 26523-27191(+)

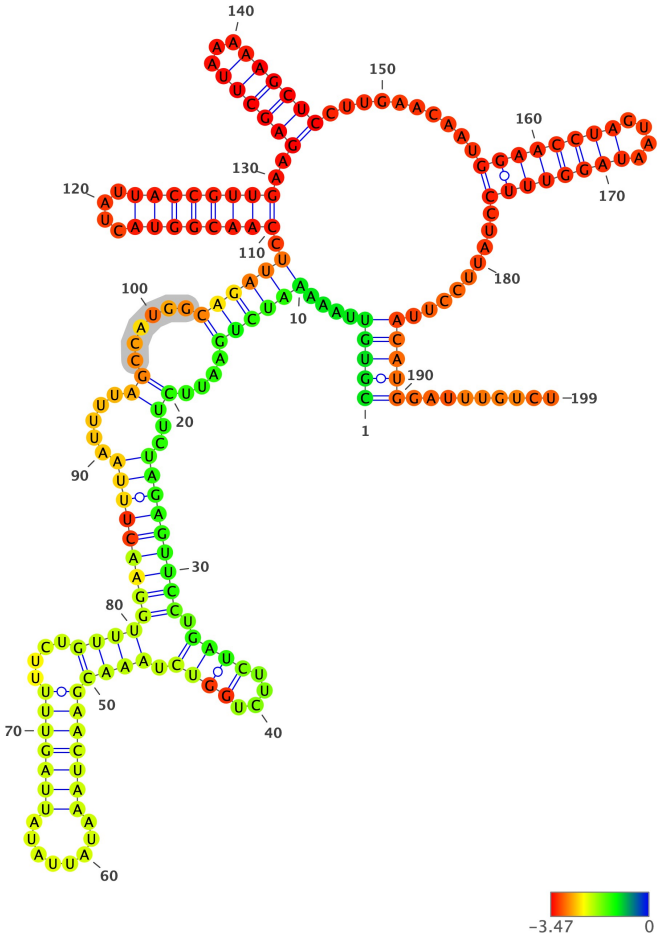
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 135 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 447 from nt 26521 to 26526 (nt 97 to 102)

```
5'-CCATGG-3'
5'-(....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.0
```



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 26425 to 26623 (motif highlighted in silver):

```
5'-CGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCA
ACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCU-3
5'-(((((....((((((....((..((((((((((.((((....)))).(((((((((((........)))))))....))))))))))))).....))......)))))).((
((((((....))))))))..(((((((...)))))))..........(((((((((....)))))))))........)))))..........-3'
MFE = -47.8; z-score = -3.88; ED = 42.91
```

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 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(+)

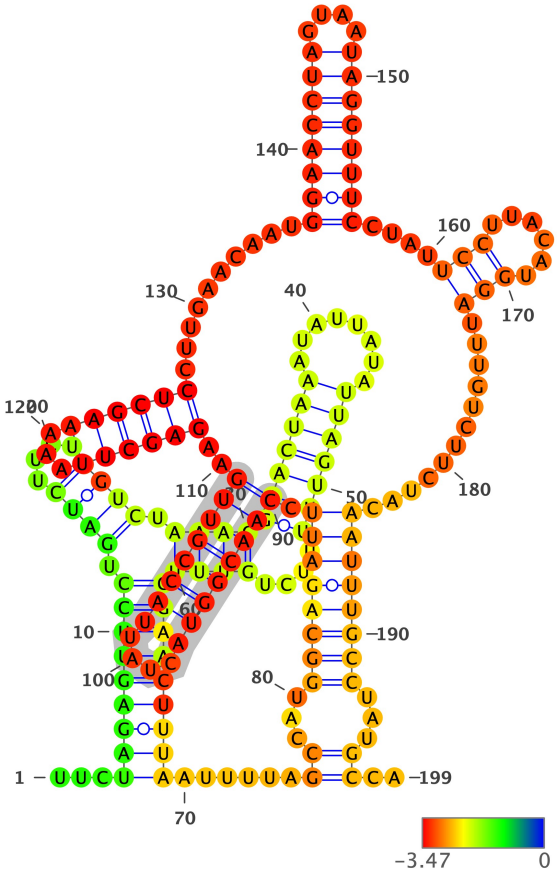
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 448 from nt 26534 to 26553 (nt 90 to 109)

```
5'-CAACGGTACTATUACCGUUG-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -9.0; z-score = -4.97; 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 = -4.44; 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(+)

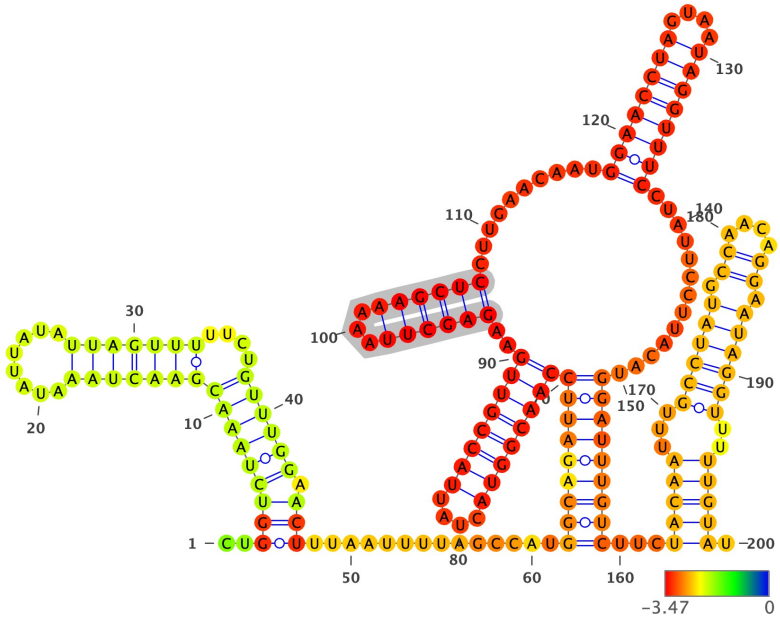
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 449 from nt 26556 to 26570 (nt 93 to 107)

```
5'-GAGCTTAAAAAGCUC-3'
5'-(((((.....)))))-3'
Motif MFE = -5.0; z-score = -6.41; 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 = -4.21; 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 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(+)

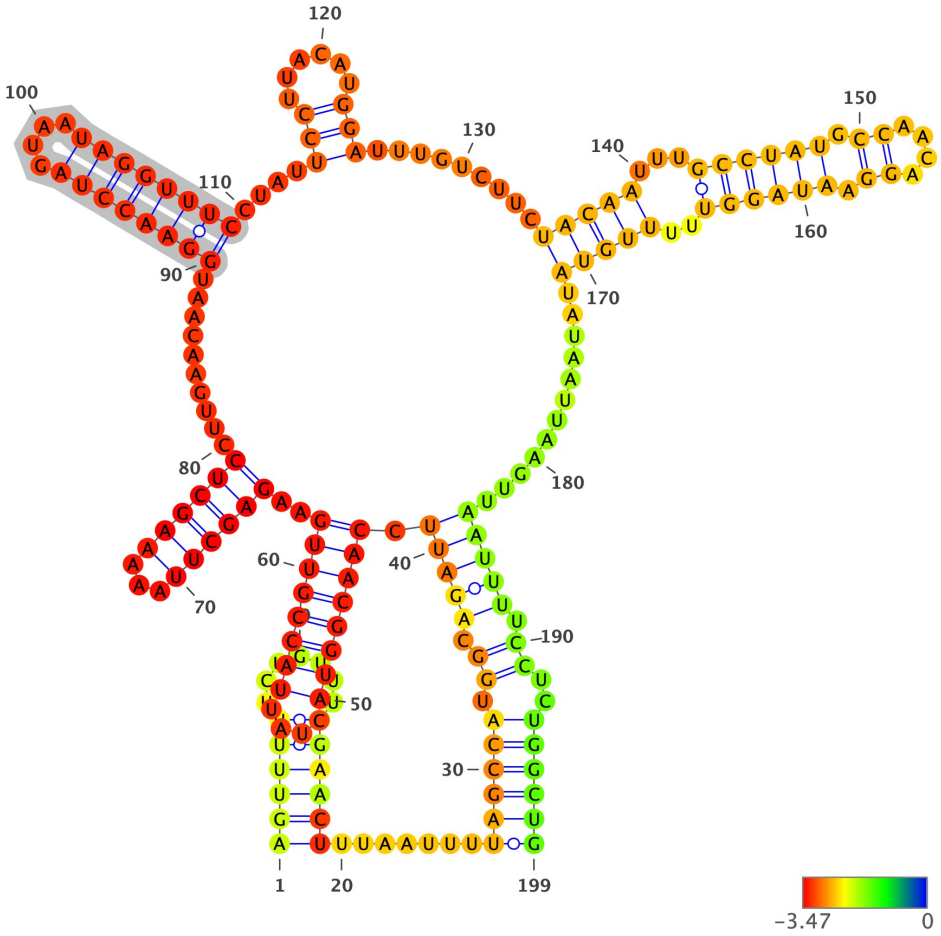
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 450 from nt 26581 to 26600 (nt 90 to 109)

```
5'-GGAACCTAGTAAUAGGUUUC-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.2; z-score = -4.74; 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 = -4.5; 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(+)

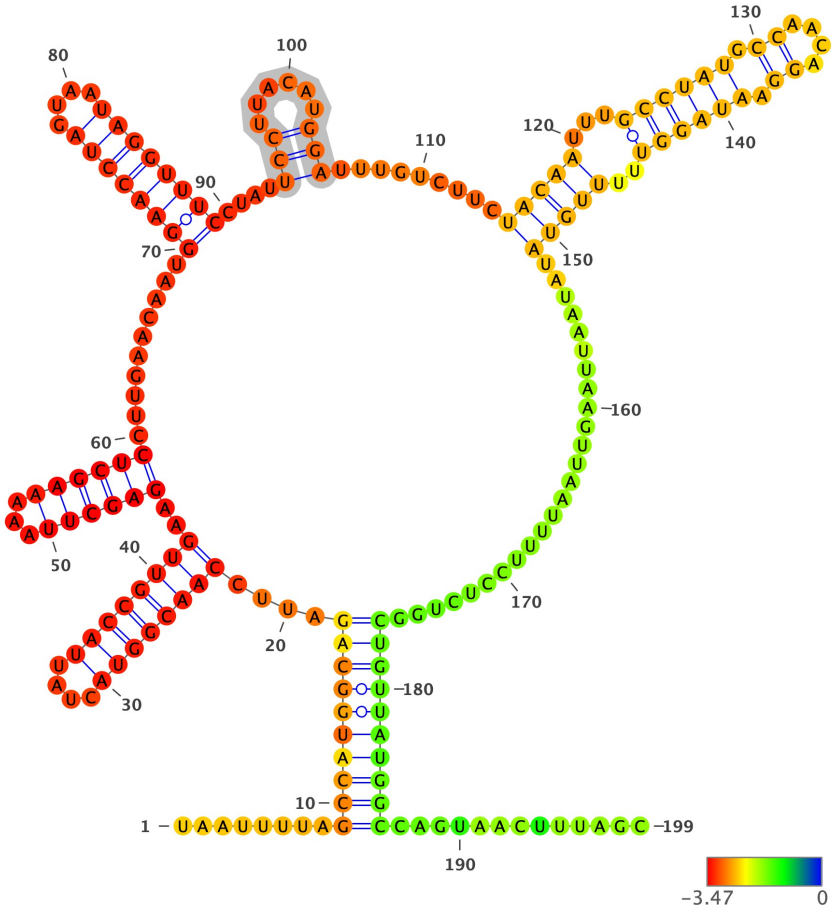
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 451 from nt 26605 to 26616 (nt 94 to 105)

```
5'-TCCTTACATGGA-3'
5'-(((......)))-3'
Motif MFE = -1.9; z-score = -6.52; 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 26512 to 26710 (motif highlighted in silver):

```
5'-UAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUC
UUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGC-3
5'-.........((((((((((....(((((((((....)))))))))..((((((...))))))..........(((((((((....)))))))))....(((......)))).....
...(((((...(((((((.((....)).)))))))..)))))).........................)))))))))............-3'
MFE = -56.4; z-score = -3.57; ED = 19.14
```

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(+)

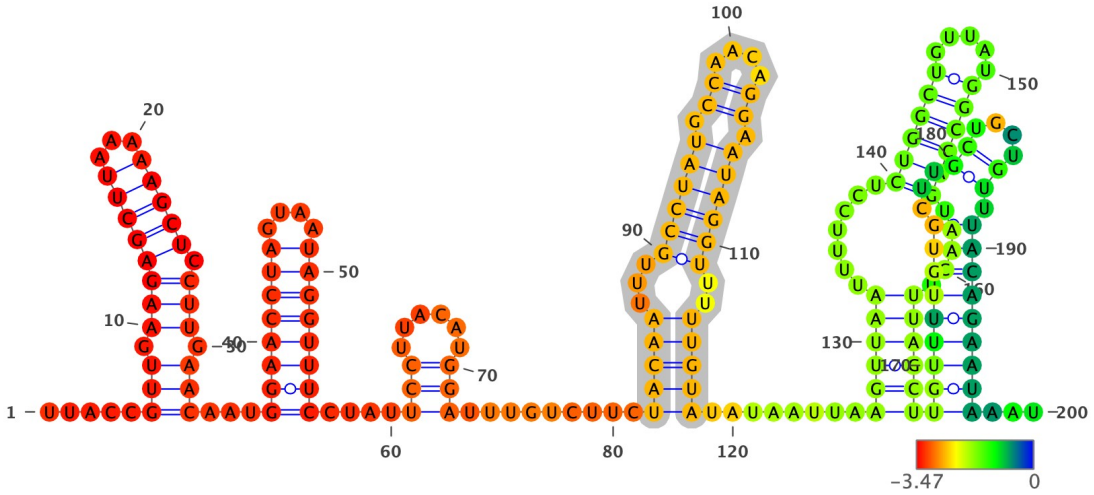
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 452 from nt 26626 to 26662 (nt 82 to 118)

```
5'-TACAATTTGCCTATGCCAACAGGAAUAGGUTTUUGUA-3'
5'-(((((...((((((.((....)).))))))..)))))-3'
Motif MFE = -10.9; z-score = -3.54; 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 = -3.27; 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(+)

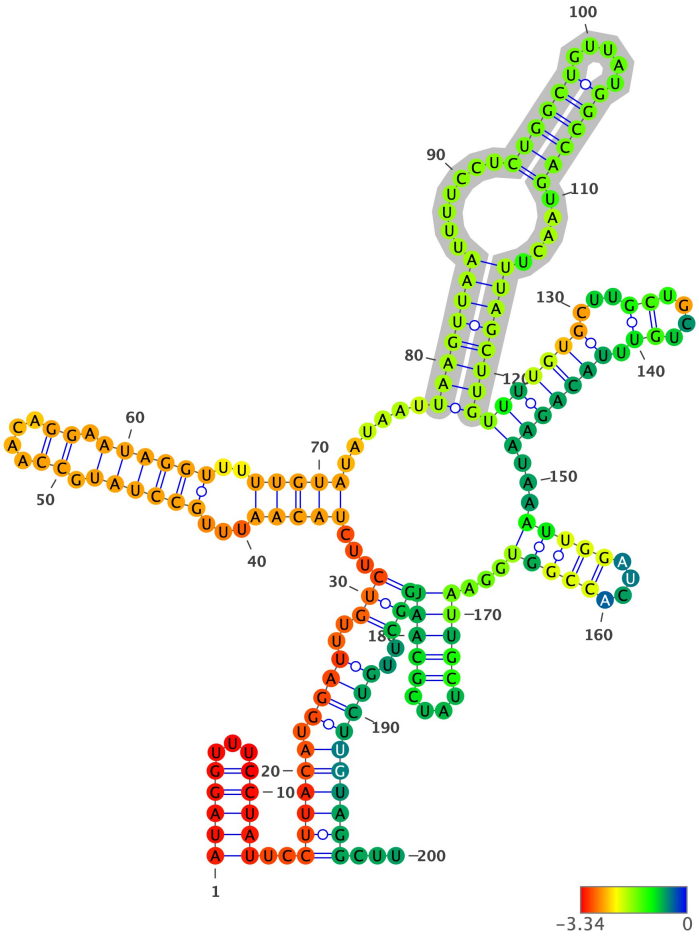
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 453 from nt 26669 to 26713 (nt 78 to 122)

```
5'-TAAGTTAATTTTCCTCTGGCTGTTATGGCCAGTAACTUUAGCUUG-3'
5'-(((((((((.......((((((.....))))))).....)))))))))-3'
Motif MFE = -13.0; z-score = -3.41; 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 26592 to 26791 (motif highlighted in silver):

```
5'-AUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUA
ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUU-3
5'-(((((...)))))..((((((.((((..(((...((((((...((((((.((....)).))))))..)))))).....((((((((.......((((((.....)))))))..
...))))))))))(((((((...((....)).)))))))...(((((....)))))...(((((....)))))))).)))))))))...-3'
MFE = -49.2; z-score = -2.02; ED = 47.22
```

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_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']

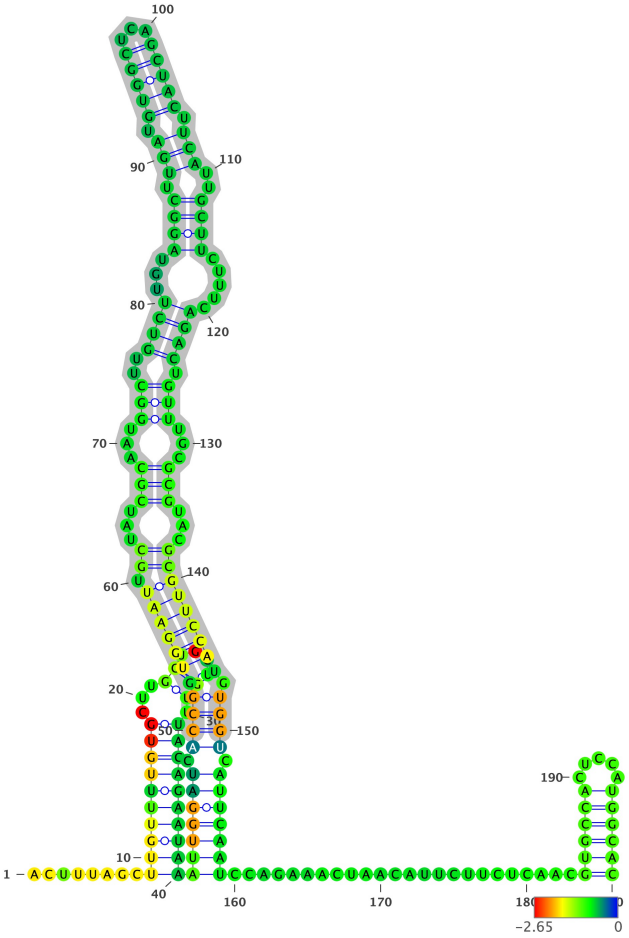
3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

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 454 from nt 26752 to 26852 (nt 50 to 150)

```
5'-CCGGTGGAATTGCTATCGCAATGGCTTGTCTTGTAGGCTTGATGTGGCTCAGCUACTUCATTGCUUCTTTCAGACTGUUTGCGCGTACGCGUUCCATGUGG-3'

5'-(((.(((((((.((...(.....................................................................)...)))))))))..)))-3'
Motif MFE = -31.3; z-score = -1.71; ED = 12.18
```



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 26703 to 26902 (motif highlighted in silver):

```
5'-ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUU
GCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCAC-3
5'-........((((((((((...((....)).)))))))))).(((((((.(((((((((((.((...(((...(((..(((((...((((.(((.((((((...)))))).)))).
))))).....)))))...))).)))...))).)))))))))).)))).)))))))).....................((((((.....))))))-3'
MFE = -53.9; z-score = -2.22; ED = 16.78
```

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_gp05, 26523-27191(+)

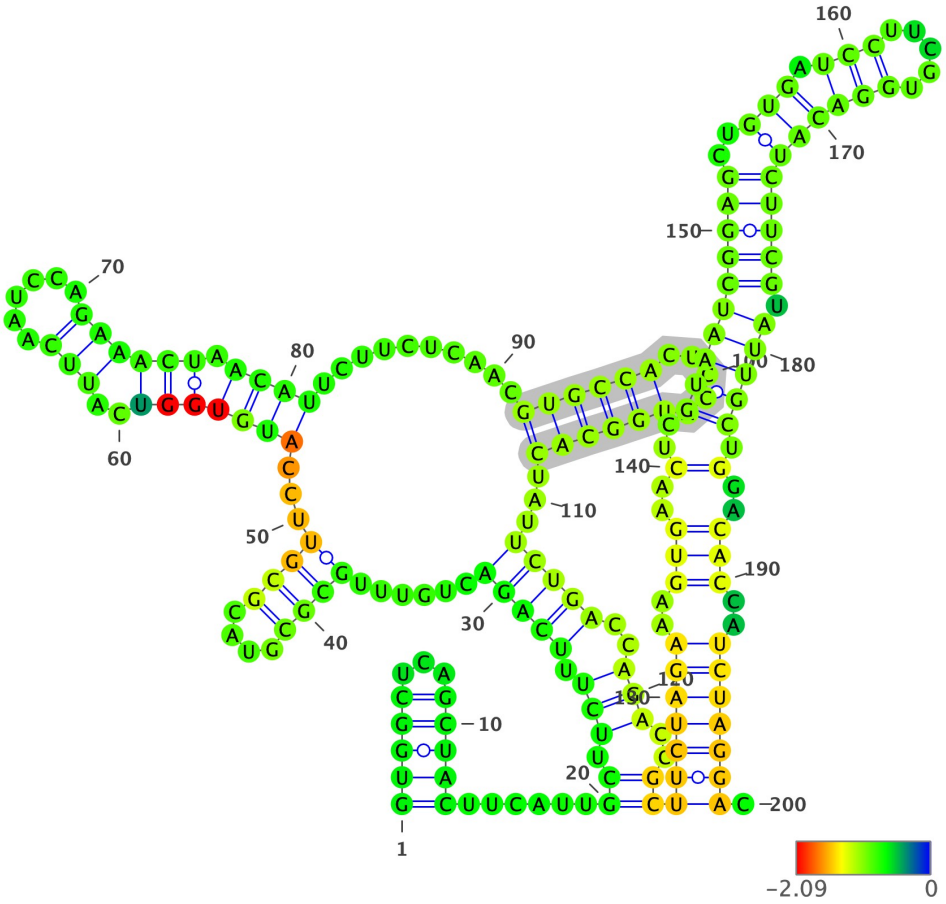
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 455 from nt 26886 to 26902 (nt 92 to 108)

```
5'-GTGCCACTCCAUGGCAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.5; z-score = -3.8; 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 = -0.89; 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(+)

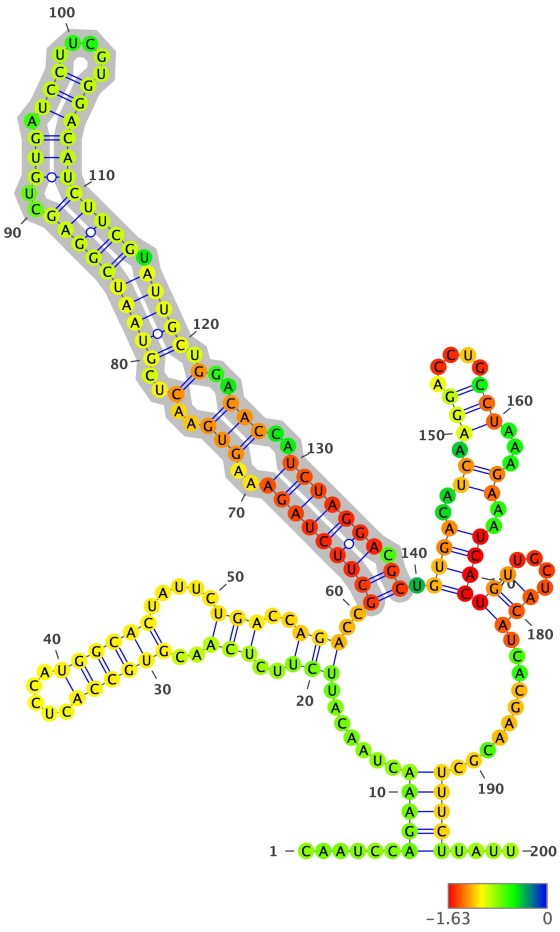
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 456 from nt 26918 to 26996 (nt 61 to 139)

```
5'-GCTTCTAGAAAGTGAACTCGTAATCGGAGCTGTGATCCTTCGTGGACAUCUUCGTAUUGCTGGACACCAUCUAGGACGC-3'
5'-(((((((((..(((..(..(((((.............................)))))).)..)))..)))))))).))-3'
Motif MFE = -25.9; z-score = -2.64; 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 = -44.3; z-score = -1.16; ED = 23.27
```

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_gp05, 26523-27191(+)

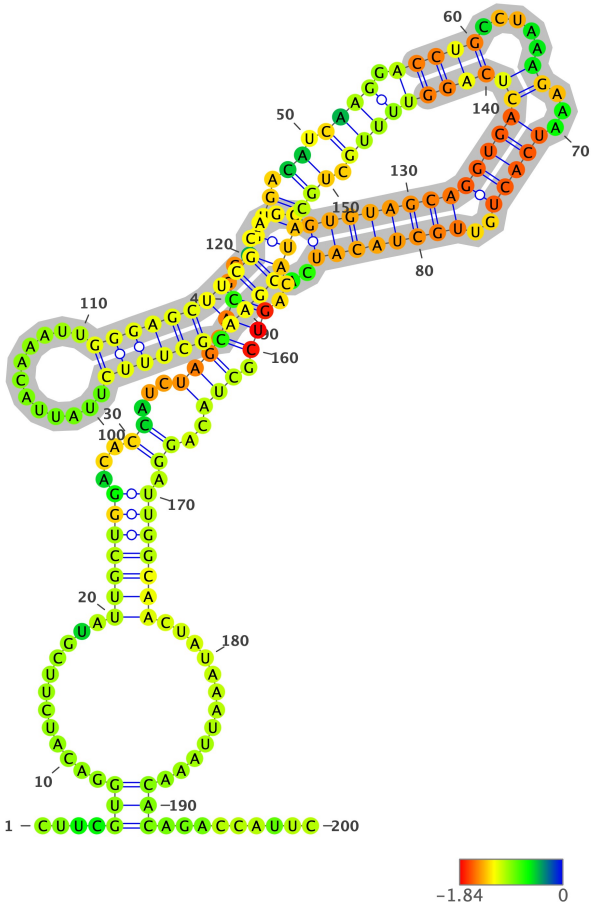
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 457 from nt 27011 to 27097 (nt 57 to 143)

```
5'-CCTGCCTAAAGAAATCACTGTTGCTACATCACGAACGCTTTCTTATTACAAATTGGGAGCUUCGCAGCGUGUAGCAGGUGACTCAGG-3'
5'-((.(..........(((((..(((((((((..((((.((((((...........))))))))))....)))))))))))))..).))-3'
Motif MFE = -25.3; z-score = -1.94; ED = 7.86
```



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 26955 to 27154 (motif highlighted in silver):

```
5'-CUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUG
GGAGCUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUC-3
5'-....(((............(((((((...((...((((((..((((.((.((((.(((((.....((...(((((..((((((((..((((.((((((.............)
))))))))....))))))))))))))))))))))).))))))..))).)))..)).)))))))............)))..........-3'
MFE = -48.0; z-score = -0.68; ED = 29.16
```

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(+)

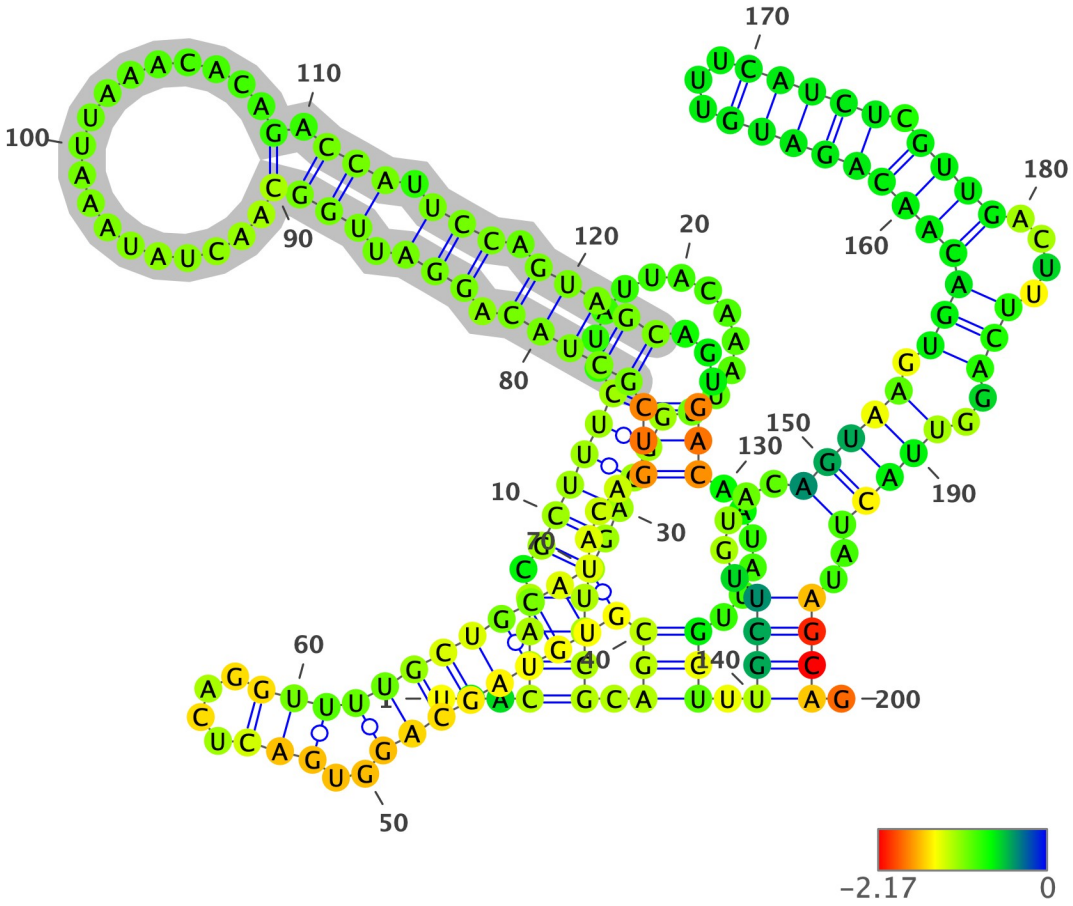
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 458 from nt 27115 to 27161 (nt 77 to 123)

```
5'-GCTACAGGATTGGCAACTATAAATTAAACACAGACCATUCCAGUAGC-3'
5'-(((((.(((.(((.....................))).))).)))))-3'
Motif MFE = -12.0; z-score = -3.96; 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 = -1.1; 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(+)

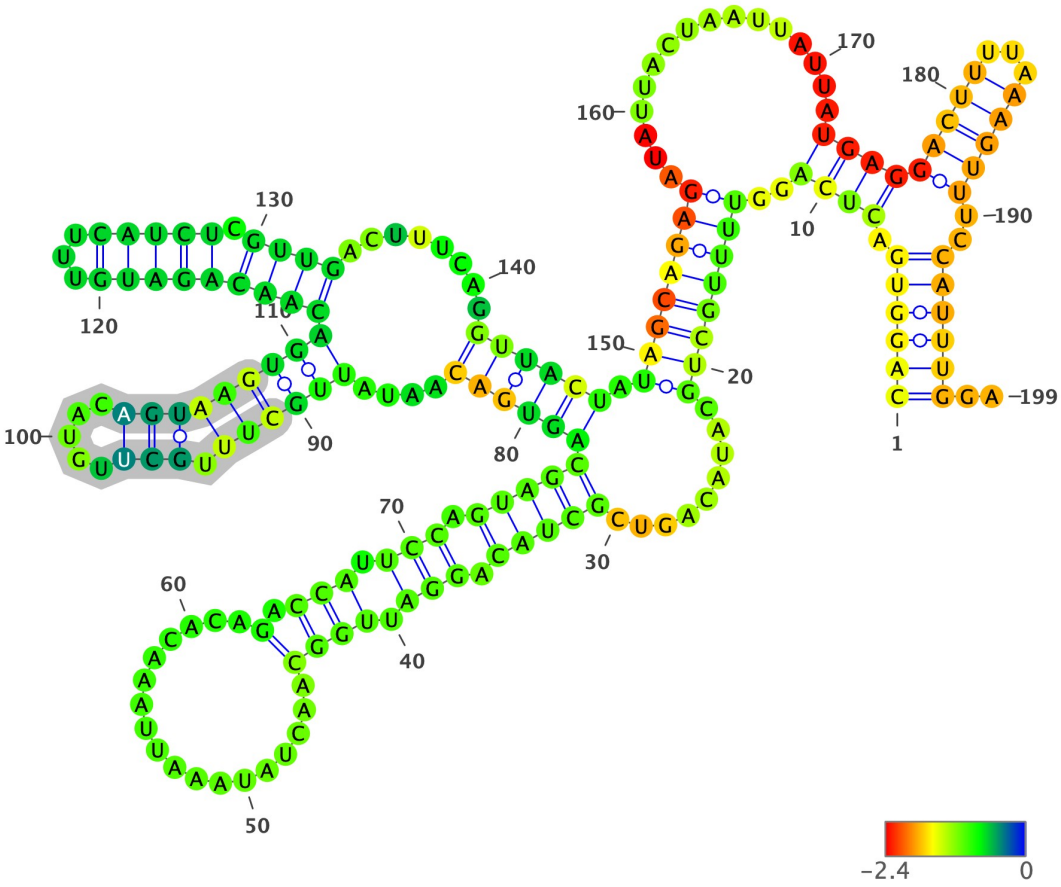
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

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 459 from nt 27175 to 27192 (nt 91 to 108)

```
5'-CTTTGCTTGTACAGTAAG-3'
5'-(.(............).)-3'
Motif MFE = -1.4; z-score = -0.68; 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 27085 to 27283 (motif highlighted in silver):

```
5'-CAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUAGCAGUGACAAUAUUGCUUUGCUUGUACAGUAAGUGA
CAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAGAGAUAUUACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGA-3
5'-((((((.((((..((((((((.........(((((.(((.((((.................).))).))).)))))((((((....((((((.(((.....)))))))))
(((((((((...))))).)))).......))))))).))))))))................))))(((((...)))))..))))))..-3'
MFE = -37.9; z-score = -0.52; ED = 39.07
```

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 107--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 107--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 118 to 199--gene, gene-GU280_gp06, 27202-27387(+)

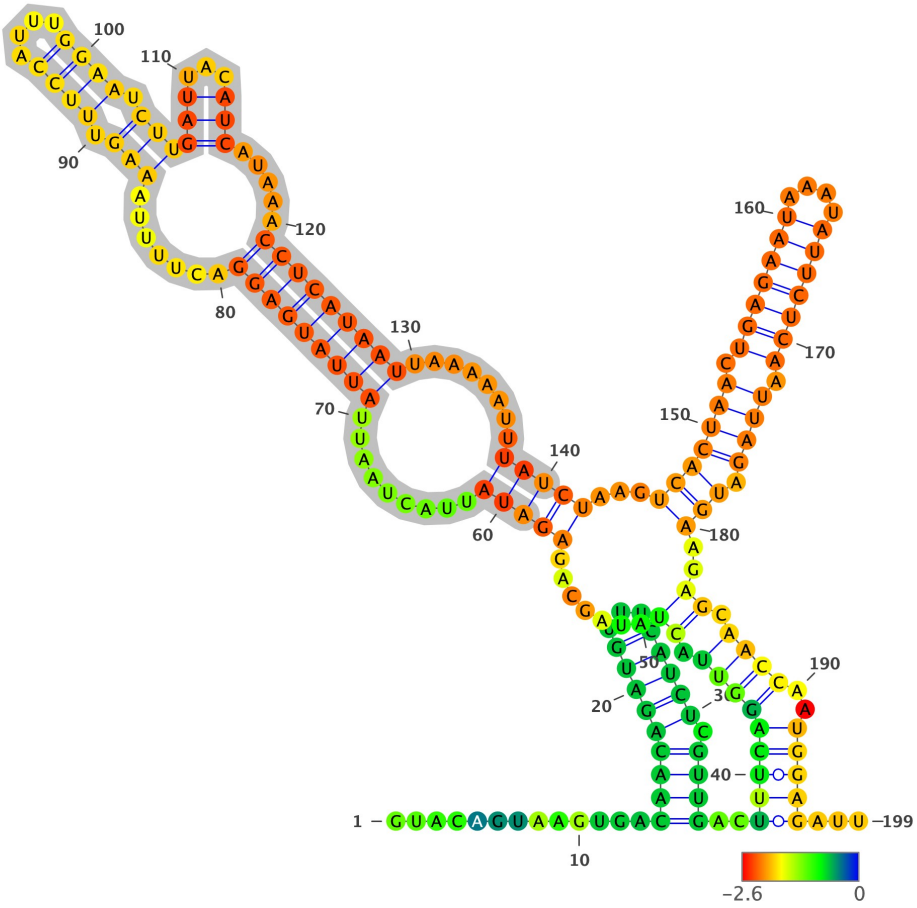
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 118 to 199--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 460 from nt 27241 to 27322 (nt 59 to 140)

```
5'-ATATTACTAATTATTATGAGGACTTTTAAAGTTTCCATTTGGAATCUUGATTACAUCATAAACCUCAUAAUTAAAAATTTAU-3'
5'-(...........(((((((((.......(((.((((....)))).)))(((...))).....)))))))))..........)-3'
Motif MFE = -13.2; z-score = -2.56; ED = 8.73
```



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 27183 to 27381 (motif highlighted in silver):

```
5'-GUACAGUAAGUGACAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAGAGAUAUUACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUA
CAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUU-3
5'-.............(((((((((...))))).))))..(((((((((.((.......(((((.........(((((((((.......(((.((((....)))).)))(((..
.)))).....))))))))).......))))).....(((((((.(((((((....)))))))).)))).)))..)).)))).))))))...-3'
MFE = -39.0; z-score = -2.37; 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 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 199--gene, gene-GU280_gp06, 27202-27387(+)

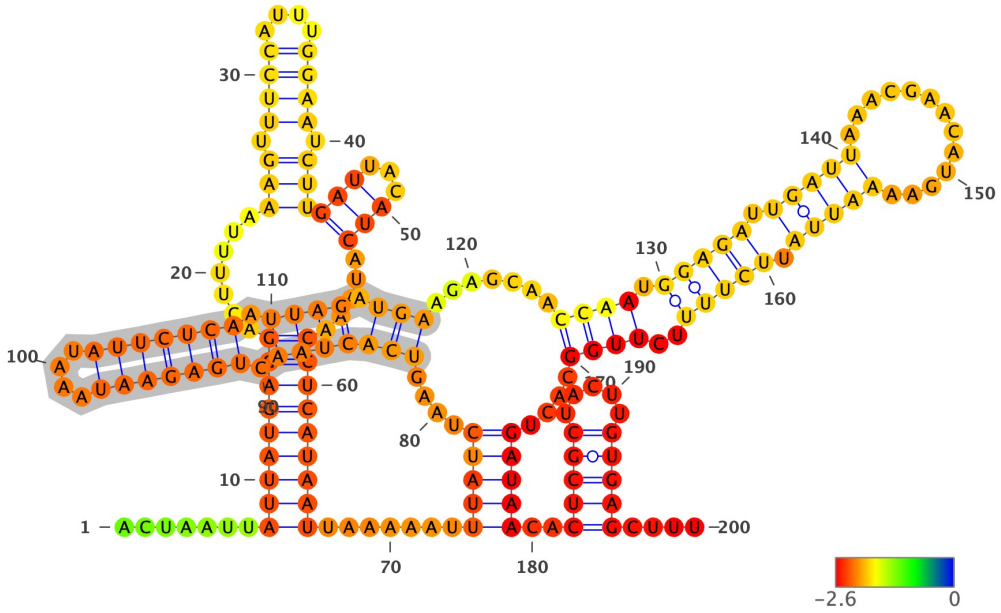
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 20 to 199--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 461 from nt 27328 to 27362 (nt 83 to 117)

```
5'-TCACTAACTGAGAATAAATAUUCUCAAUUAGAUGA-3'
5'-(((((((.(((((((....)))))))).)))).)))-3'
Motif MFE = -10.5; z-score = -4.82; 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 = -2.7; 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(+)

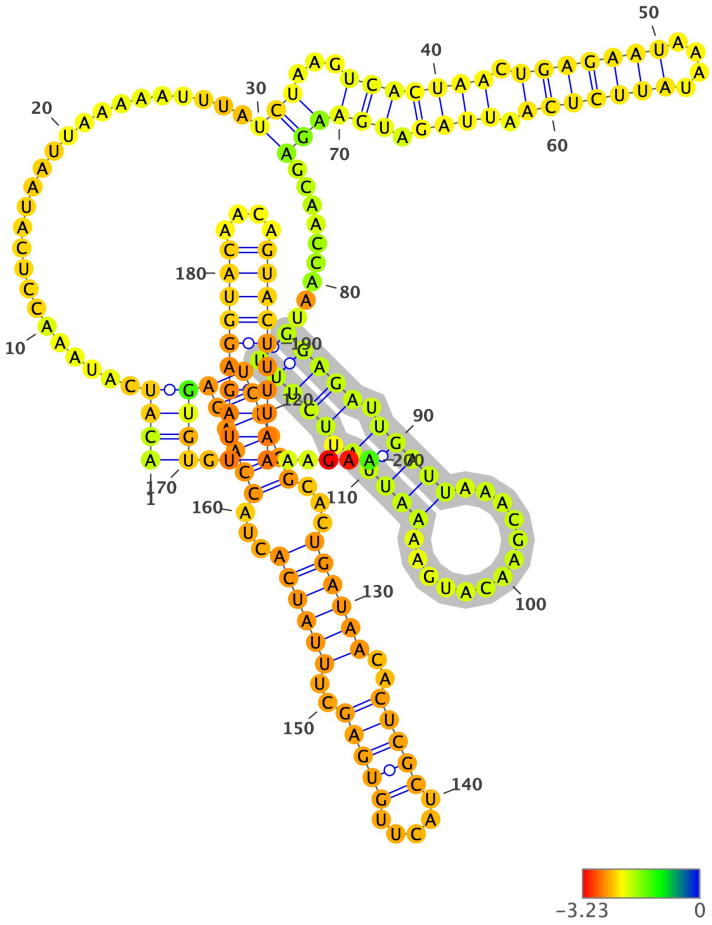
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 462 from nt 27375 to 27409 (nt 83 to 117)

```
5'-GGAGATTGATTAAACGAACATGAAAAUUATUCUUU-3'
5'-(((((.(((((.............))))).))))))-3'
Motif MFE = -2.8; z-score = -0.44; 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 27293 to 27492 (motif highlighted in silver):

```
5'-ACAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUA
UUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAA-3
5'-((((.........................(((...(((((((.(((((((....)))))))).)))).))))))).........(((((.(((((.............)))))
.)))))((((((...((((((..(((((.....))))))..))))))...))))))))).((((((((((....))))))))))).....-3'
MFE = -43.3; z-score = -3.9; ED = 18.13
```

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 95--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 95--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 102 to 200--gene, gene-GU280_gp07, 27394-27759(+)

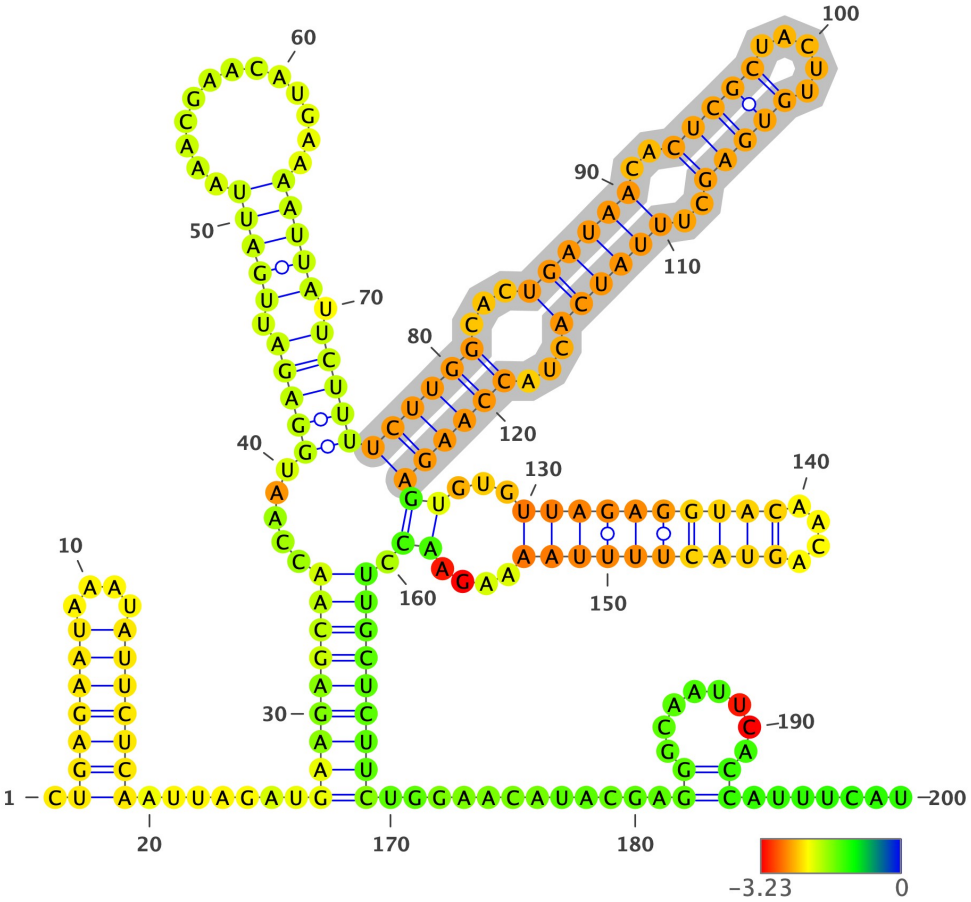
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 102 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 463 from nt 27410 to 27458 (nt 76 to 124)

```
5'-TCTTGGCACTGATAACACTCGCTACTTGUGAGCTUUAUCACTACCAAGA-3'
5'-((((((...((((((..(((((.....)))))..))))))...))))))-3'
Motif MFE = -18.5; z-score = -5.32; ED = 1.14
```



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 27335 to 27534 (motif highlighted in silver):

```
5'-CUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUU
AUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAU-3
5'-.(((((((....)))))))).......(((((((((.....(((((.(((((.............))))).)))))((((((...((((((..(((((.....)))))..))
))))...))))))((...((((((((((....)))))))))....)).))))))))).............((........)).......-3'
MFE = -51.9; z-score = -3.92; ED = 18.75
```

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 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(+)

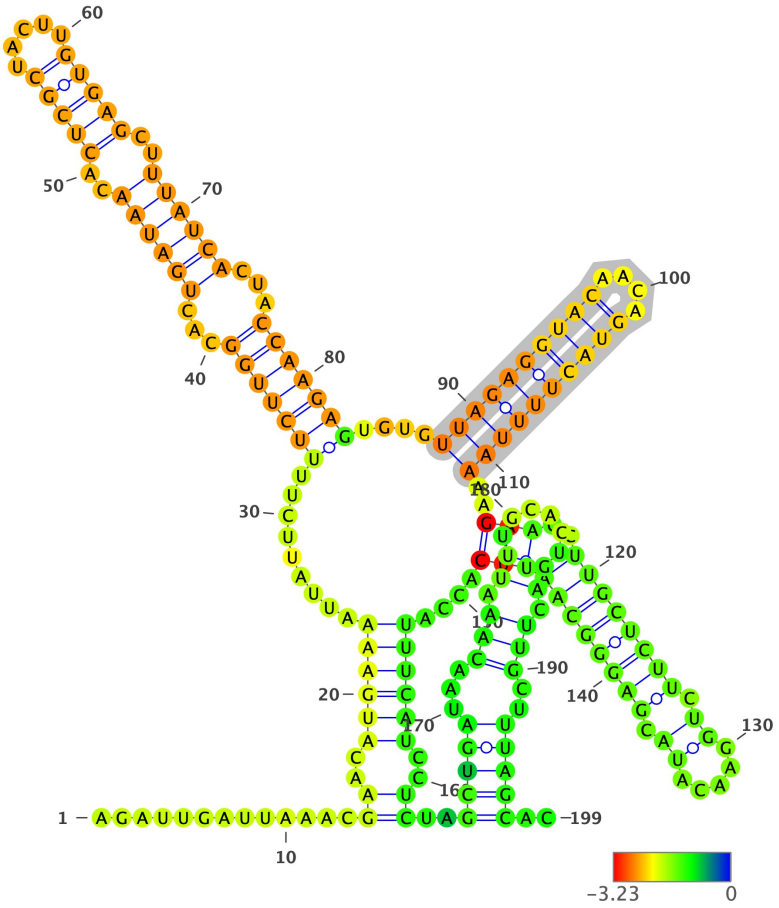
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 464 from nt 27464 to 27487 (nt 88 to 111)

```
5'-TTAGAGGTACAACAGUACUUUUAA-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -8.0; z-score = -4.83; 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 27377 to 27575 (motif highlighted in silver):

```
5'-AGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAA
AAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCAC-3
5'-............((..((((((.........(((((((...((((((..(((((.....)))))..))))))...)))))))....((((((((((....))))))))))
..(((..(((((((((.((.....)).)))))))))))....))))))..))..((((((...(((.((......)).))))..))))))..-3'
MFE = -44.6; z-score = -2.35; ED = 21.66
```

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 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(+)

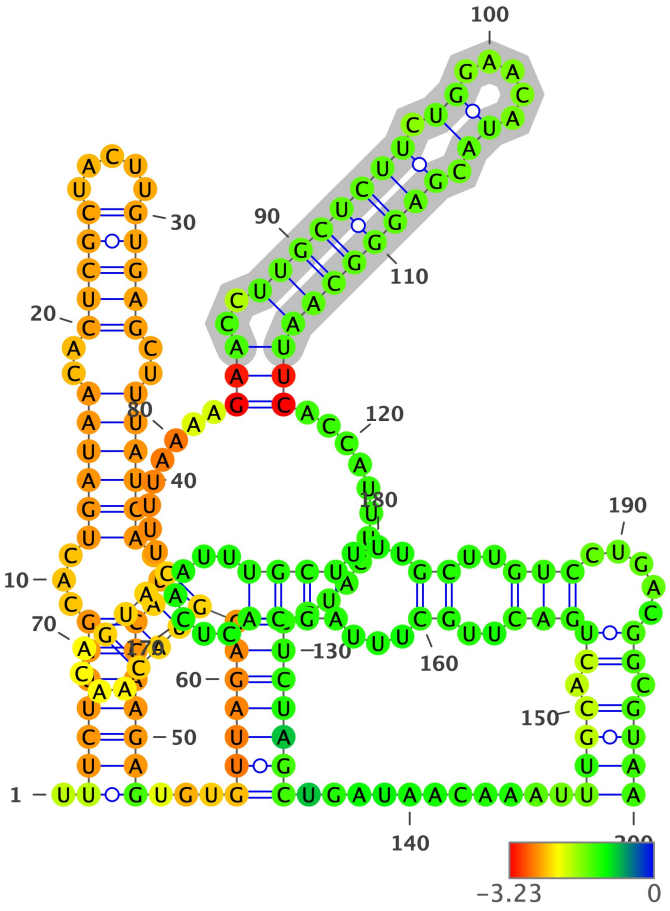
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 465 from nt 27492 to 27522 (nt 85 to 115)

```
5'-ACCTTGCTCTTCTGGAACAUACGAGGGCAAU-3'
5'-(..(((((((((.((.....)).)))))))))-3'
Motif MFE = -8.1; z-score = -2.08; 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 27408 to 27607 (motif highlighted in silver):

```
5'-UUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGG
CAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAA-3
5'-.(((((((...((((((..(((((.....)))))..))))))...)))))))...((((((((((....))))).......(((..(((((((.((.....)).)))))
))))))).....)))))))..........((((.(((((..((...((((.......))))...))..)))).....)).))))-3'
MFE = -49.0; z-score = -2.4; 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_gp07, 27394-27759(+)

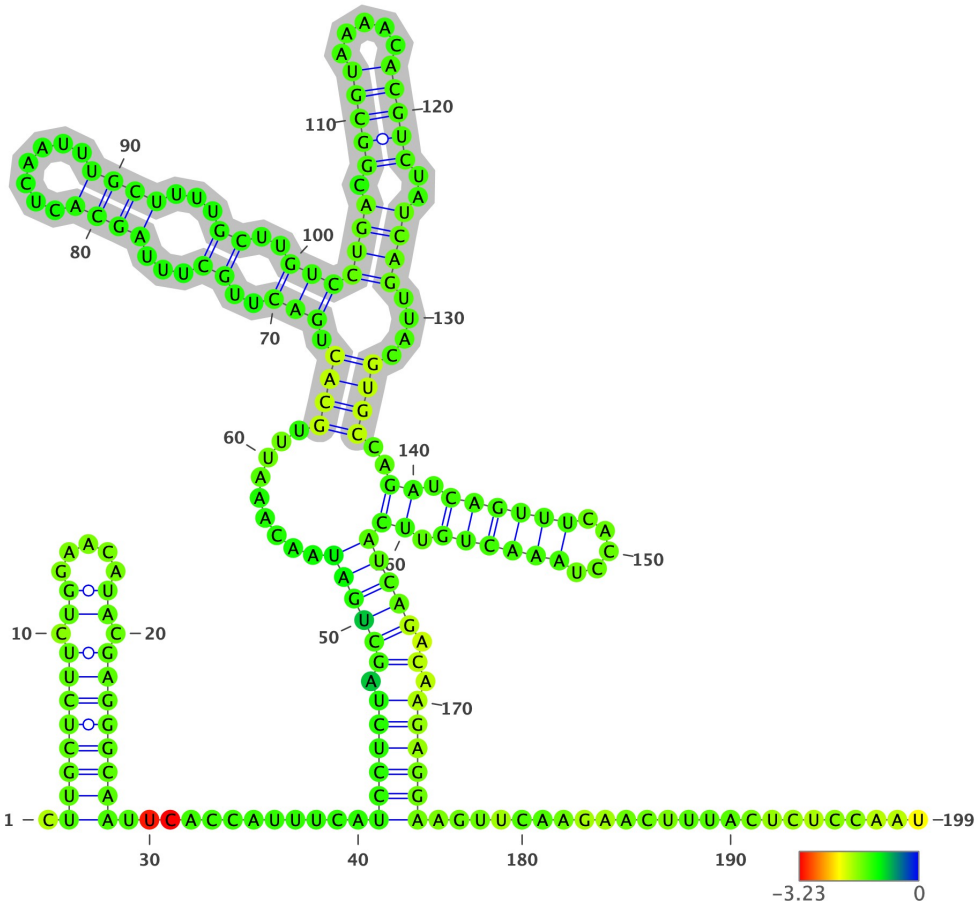
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 466 from nt 27556 to 27629 (nt 63 to 136)

```
5'-GCACTGACTTGCTTTAGCACTCAATTUGCUTTTGCTTGUCCTGACGGCGTAAAACACGUCTAUCAGTTACGUGC-3'
5'-((((.(((..((...((((.......))))...))..)))((((.(((((.....)))))..))))....))))-3'
Motif MFE = -19.8; z-score = -2.24; 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 = -3.13; ED = 13.61
```

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_gp07, 27394-27759(+)

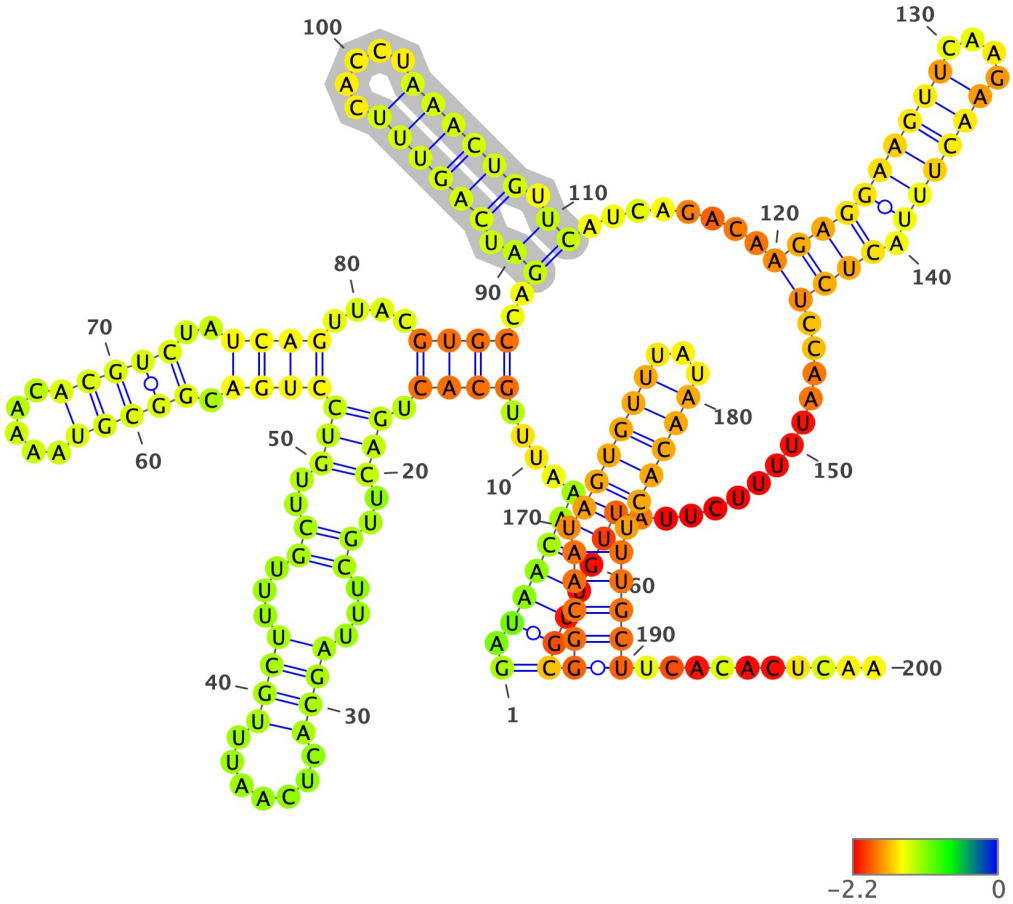
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 467 from nt 27632 to 27654 (nt 89 to 111)

```
5'-GATCAGTTTCACCTAAACUGTUC-3'
5'-((.((((((.....)))))).))-3'
Motif MFE = -4.1; z-score = -2.59; 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 = -2.4; 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(+)

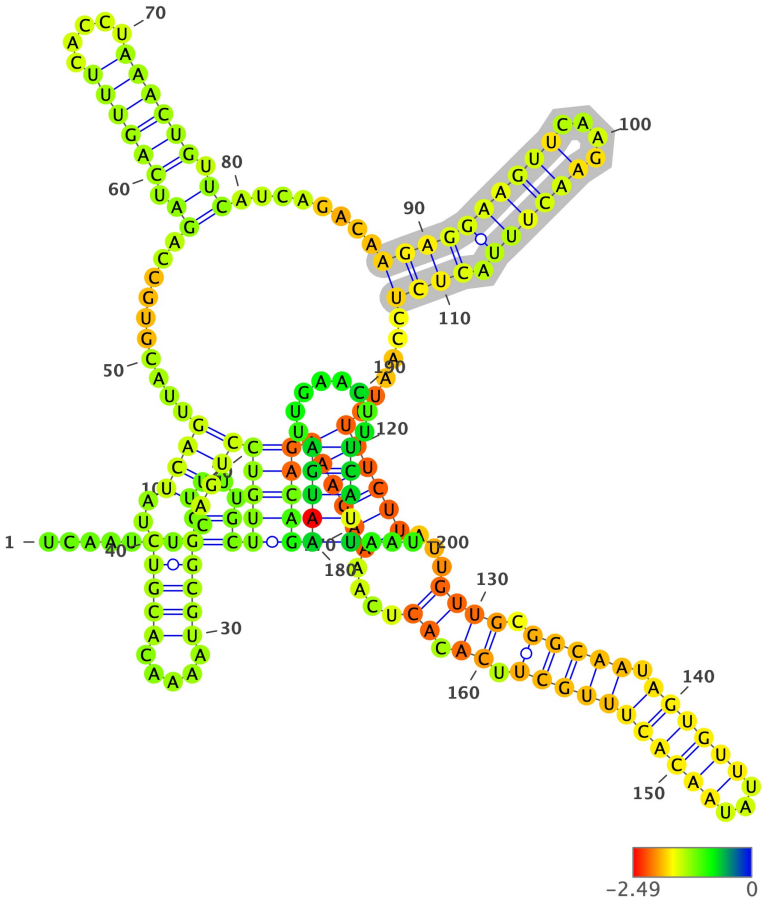
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 468 from nt 27663 to 27687 (nt 88 to 112)

```
5'-AGAGGAAGTTCAAGAACTTTACTCU-3'
5'-(.......................)-3'
Motif MFE = -5.8; z-score = -2.3; 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 = 34.73
```

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 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(+)

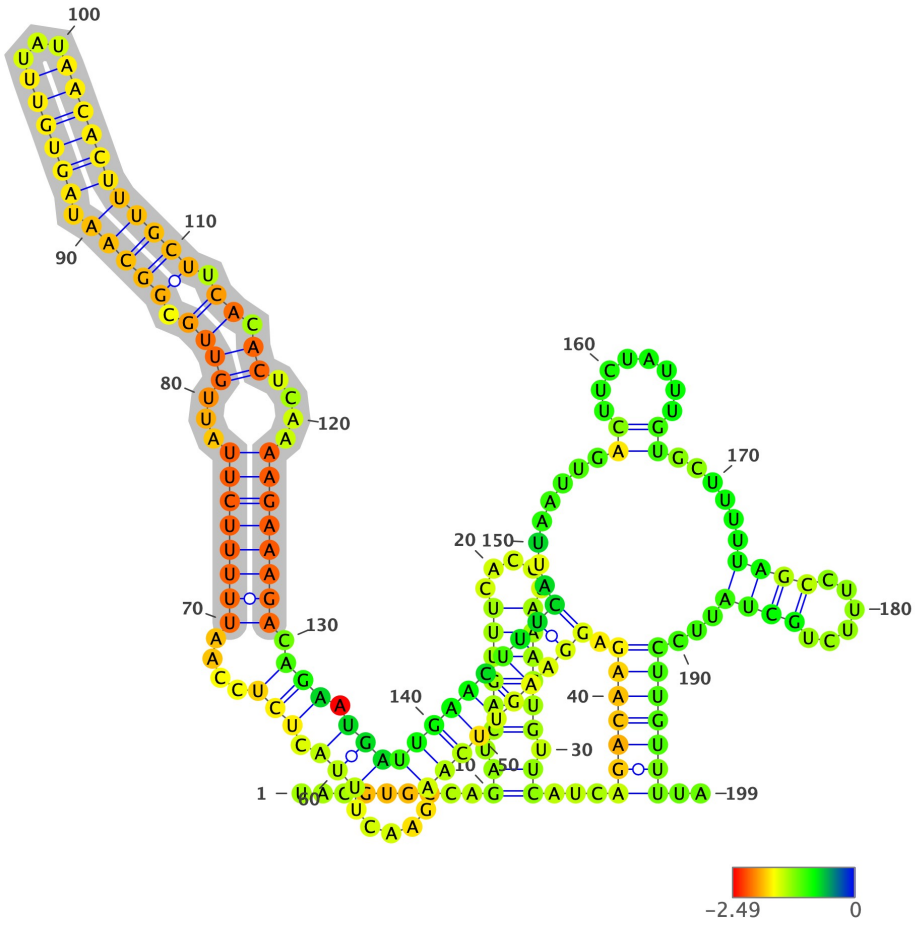
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 469 from nt 27692 to 27751 (nt 70 to 129)

```
5'-TTTTTCTTATTGTTGCGGCAATAGTGTTTATAACACUUUGCUTCACACTCAAAAGAAAGA-3'
5'-((((((((...((((.(((((.((((((...)))))))))))).)).)).....))))))))-3'
Motif MFE = -15.2; z-score = -3.38; ED = 7.13
```



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 27623 to 27821 (motif highlighted in silver):

```
5'-UACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCU
UCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUA-3
5'-.........((.((((((.....)))))).))...(((((((.((((((((((.....(((.(((....((((((((...((((.(((((.((((((...)))))))))))
.)).)).....))))))))).))).))))))))))))).........((........)).....((((......))))...)))))))..-3'
MFE = -38.9; z-score = -1.95; ED = 28.92
```

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 137--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 137--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 134 to 199--gene, gene-GU280_gp08, 27756-27887(+)

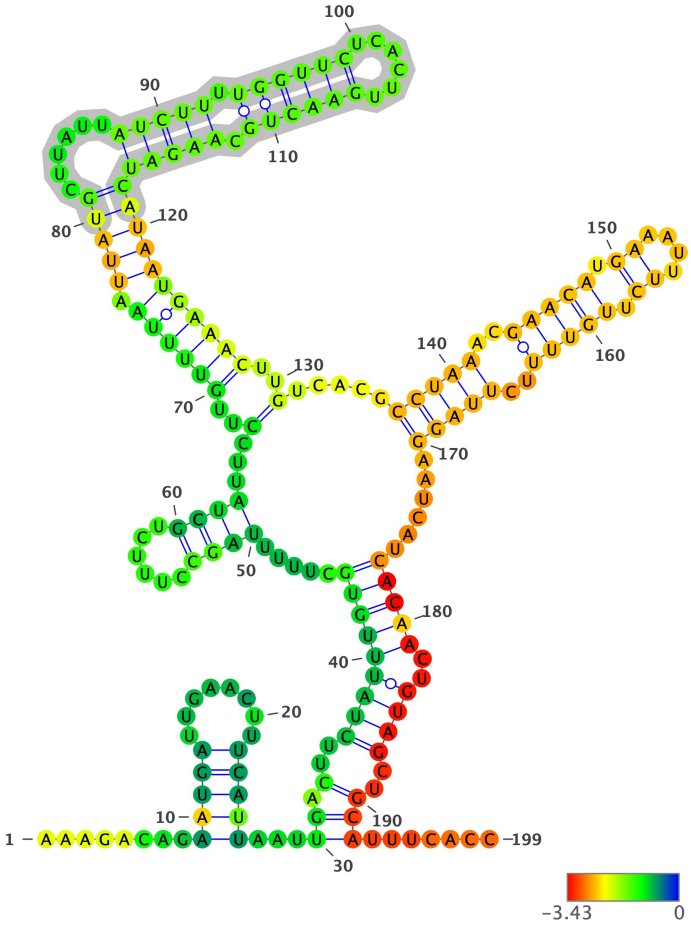
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 134 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 470 from nt 27826 to 27865 (nt 80 to 119)

```
5'-TGCTTATTATCTTTTGGTTCTCACTTGAACUGCAAGAUCA-3'
5'-(.......(((((.((((((......)))))).)))))).)-3'
Motif MFE = -8.6; z-score = -2.86; 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 27747 to 27945 (motif highlighted in silver):

```
5'-AAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUG
CAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACC-3
5'-........(((((........)))))...((.(..(((((((((.....((((......))))...(..((((((.(((((......(((((.((((((......))))))
.))))))))))))))))..).....(((((..(((((.((....)).)))))..)))))......)))))..))))..)))........-3'
MFE = -33.5; z-score = -1.11; ED = 25.85
```

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 13--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 13--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 10 to 141--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 10 to 141--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 148 to 199--gene, gene-GU280_gp09, 27894-28259(+)

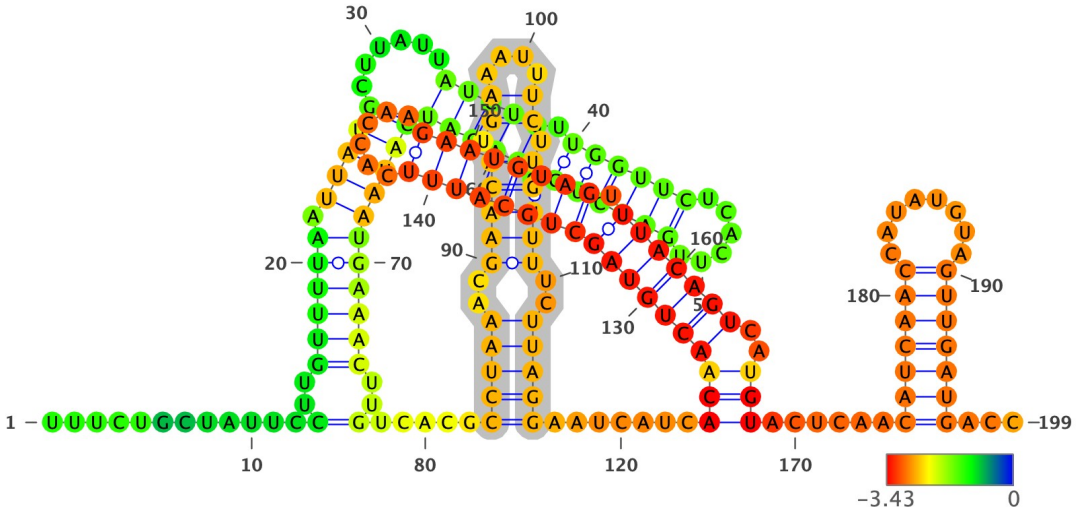
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 148 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 471 from nt 27883 to 27916 (nt 83 to 116)

```
5'-CCTAAACGAACATGAAATTUCTUGUUUTCUUAGG-3'
5'-(((((..(((((.((....)).)))))..)))))-3'
Motif MFE = -8.0; z-score = -2.86; 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 27801 to 27999 (motif highlighted in silver):

```
5'-UUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUC
UUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACC-3
5'-............(..((((((.(((((......(((((.((((((......))))))).))))))))))))))))..).....(((((..(((((.((....)).)))))..
)))))).......((((((((((((((((((.....)))))))).)))))))..))).....(((((((........)))))))...-3'
MFE = -46.6; z-score = -4.1; ED = 12.85
```

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 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(+)

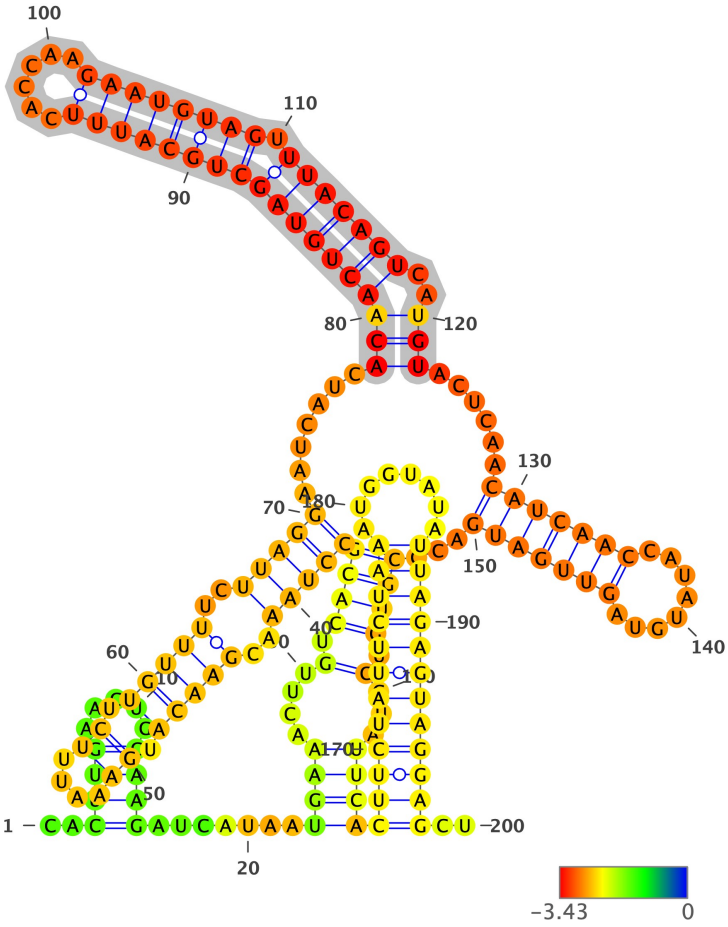
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 472 from nt 27924 to 27968 (nt 78 to 122)

```
5'-ACAACTGTAGCTGCATTTCACCAAGAAUGUAGTUUACAGUCATGU-3'
5'-((.((((((((((((((.....)))))))).)))))))...))-3'
Motif MFE = -15.2; z-score = -4.2; ED = 4.71
```



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 27847 to 28046 (motif highlighted in silver):

```
5'-CACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUU
UACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCU-3
5'-..((((.....))))......((((....(.((((((((..(((((.((....)).)))))..)))))).....((((((((((((((((.....))))))))).)
))))))..)))......(((((((........)))))))...)))))...)...))))((((((((((((........))))))))))))..-3'
MFE = -51.6; z-score = -4.35; ED = 15.84
```

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 41--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 41--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 48 to 200--gene, gene-GU280_gp09, 27894-28259(+)

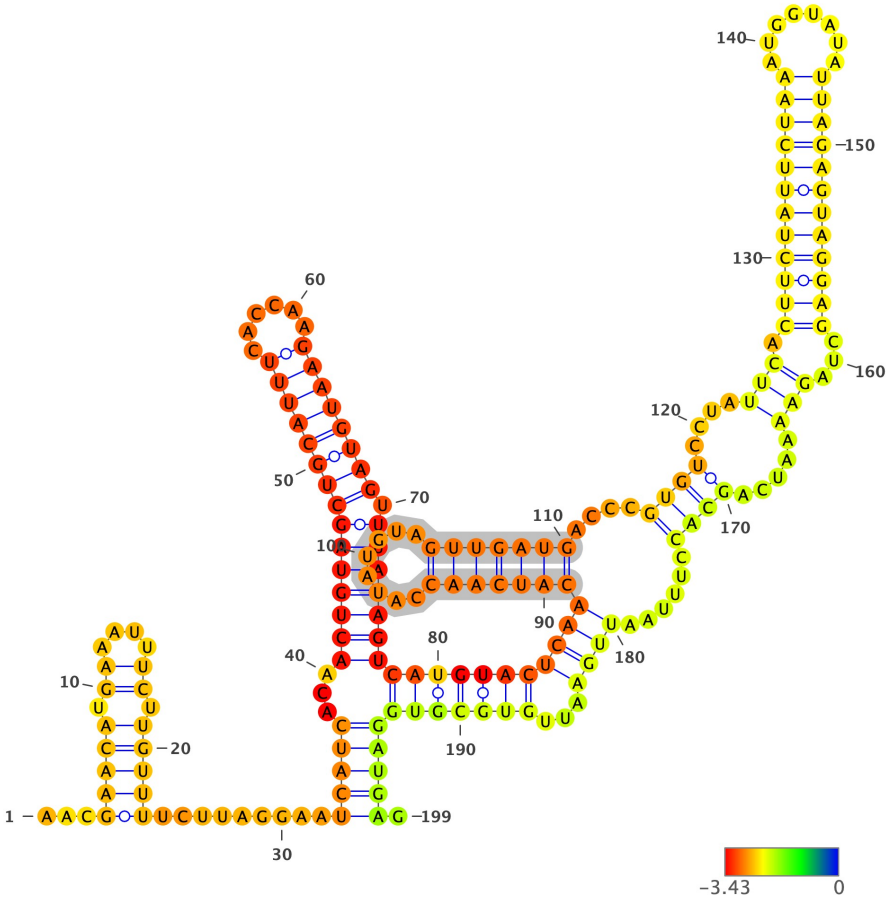
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 48 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 473 from nt 27975 to 27996 (nt 89 to 110)

```
5'-CATCAACCATATGTAGUUGAUG-3'
5'-(((((((........)))))))-3'
Motif MFE = -6.3; z-score = -4.2; 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 27887 to 28085 (motif highlighted in silver):

```
5'-AACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGA
CCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAG-3
5'-...(((((.((....)).))))).........(((((...(((((((((((((((.....)))))))).)))))))(((((((((((((((.......)))))))).
...((((....(((.(((((((((((.......))))))))))))...)))).....))))......))))...)))))))))))).-3'
MFE = -52.4; z-score = -3.16; 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(+)

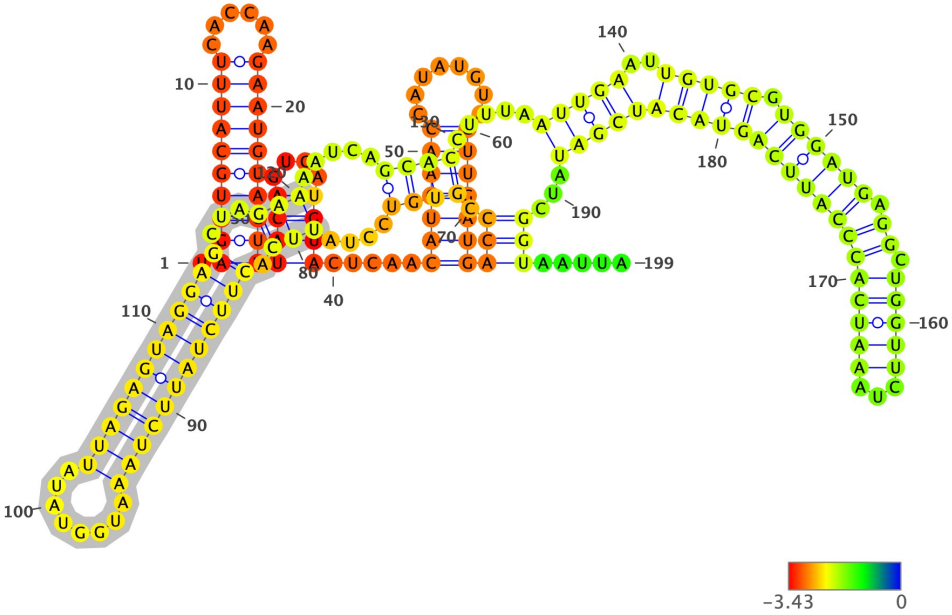
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 474 from nt 28009 to 28050 (nt 79 to 120)

```
5'-TTCACTTCTATTCTAAATGGTATAUUAGAGUAGGAGCTAGAA-3'
5'-(((.(((((((((((((.........)))))))))))))...)))-3'
Motif MFE = -12.9; z-score = -4.07; 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 = -3.29; ED = 22.85
```

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_gp09, 27894-28259(+)

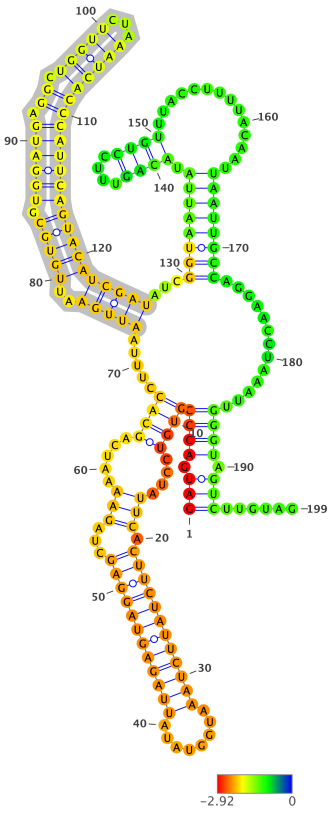
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 475 from nt 28065 to 28118 (nt 73 to 126)

```
5'-ATTGAATTGTGCGTGGATGAGGCTGGTTCTAAAUCACCCAUUCAGUACAUCGAU-3'
5'-((((((..((((((.(((((((.((.((((((...))))))))))))))))))))))))))-3'
Motif MFE = -17.3; z-score = -2.87; 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 27993 to 28191 (motif highlighted in silver):

```
5'-GAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCC
AUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAG-3
5'-(((.(((((((((....(((.(((((((((((((........)))))))))))))...))))).....))))).....((((((..((((((.(((((((.((.((((((...))))))))))))))))))))))))))
))))))))))))))...(((((((((.((((....)))).............)))))))).............)))).)))......-3'
MFE = -49.3; z-score = -2.07; ED = 30.55
```

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_gp09, 27894-28259(+)

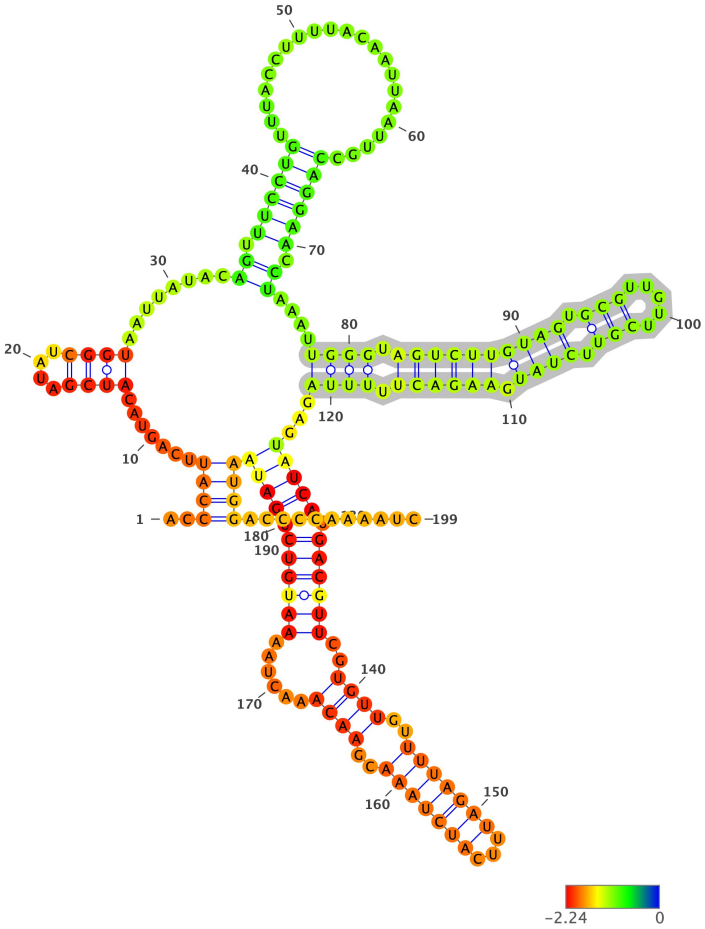
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 476 from nt 28177 to 28220 (nt 78 to 121)

```
5'-TGGGTAGTCTTGTAGTGCGTTGTTCGUTCUAUGAAGACUTUUUA-3'
5'-((((.((((((((((.(((.....))).)))))..)))))))..))))-3'
Motif MFE = -11.8; z-score = -2.86; ED = 3.97
```



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 28100 to 28298 (motif highlighted in silver):

```
5'-ACCCAUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGA
AGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUC-3
5'-..((((.......((((....)))).........((.((((((.....................))))))..)).....((((.((((((((((.(((.....))).)))))..)
))))))..))))...((((((.(((((((..(((((..(((((((...)))))))..))))).....))))))))))))))).....-3'
MFE = -38.8; z-score = -2.06; ED = 39.4
```

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 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(+)

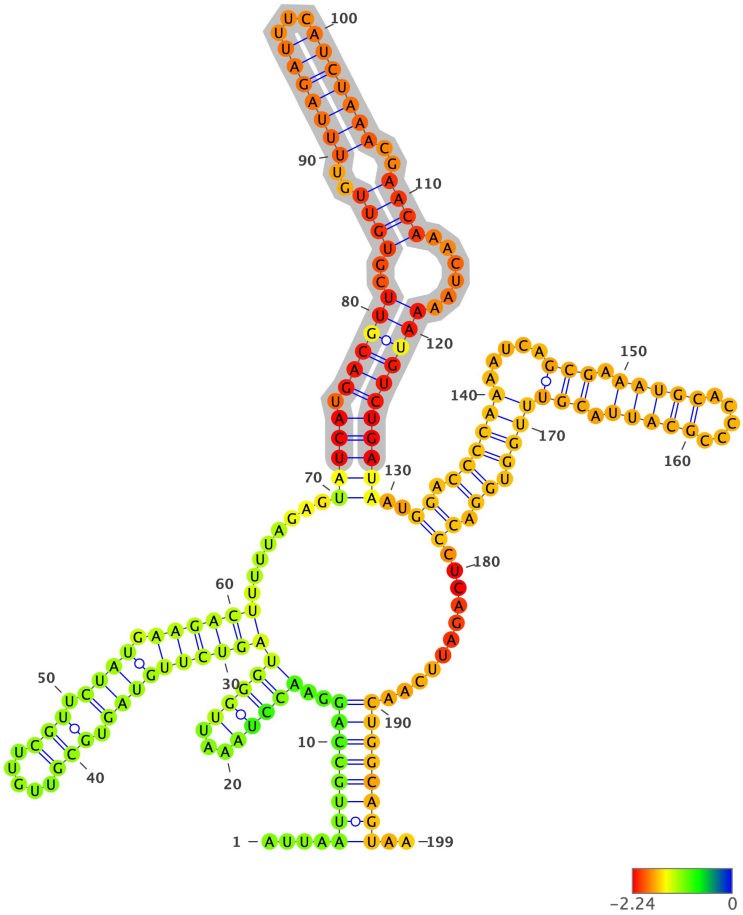
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 477 from nt 28226 to 28281 (nt 72 to 127)

```
5'-TCATGACGTTCGTGTTGTTTTAGATTTCAUCUAAACGAACAAACTAAAATGUCUGA-3'
5'-(((.(((.((..(((((..(((((((...)))))))..))))).....)).)))))-3'
Motif MFE = -12.3; z-score = -2.44; ED = 9.58
```



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 28155 to 28353 (motif highlighted in silver):

```
5'-AUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAAC
AAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAA-3
5'-....(((((((((..((((((...))))))((((((((((.(((.....))).)))))..))))))........(((((.((((((..((((..(((((((...)))))))..)))
).....))))))))))))..((.((((((.....(((.(((((.....)))))).)))))))..)).))..........)))))))..-3'
MFE = -57.2; z-score = -3.55; 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 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(+)

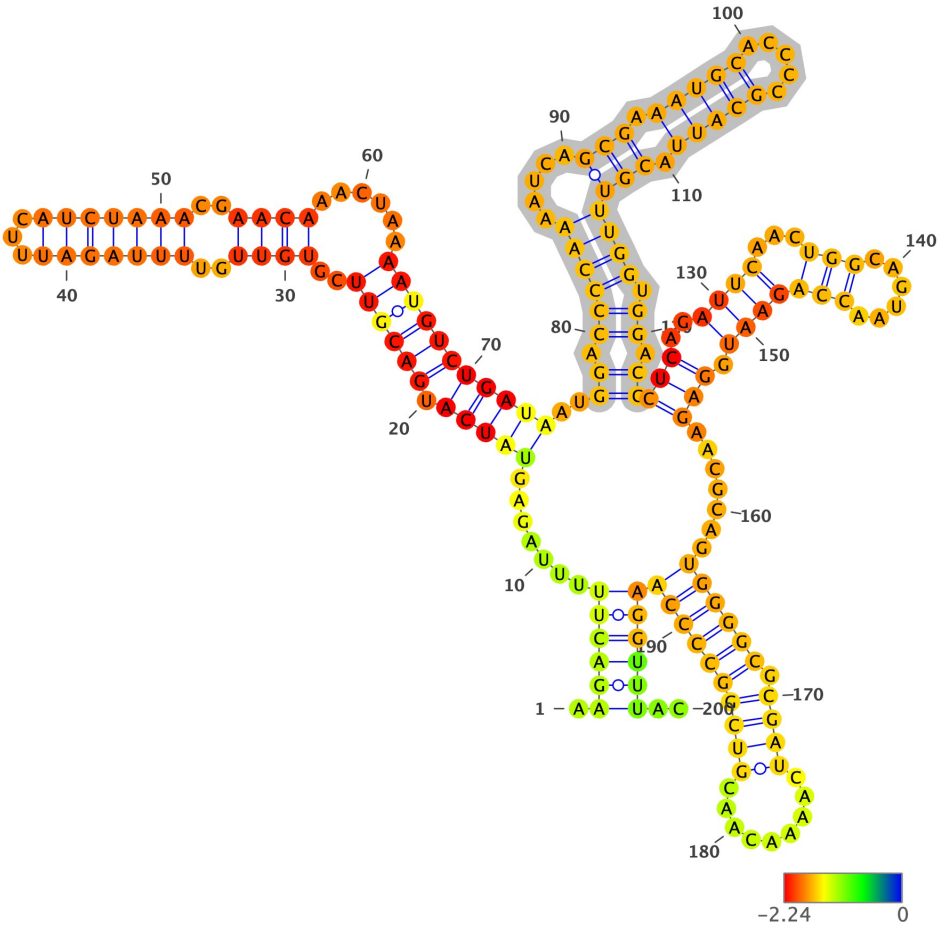
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 478 from nt 28286 to 28332 (nt 77 to 123)

```
5'-GGACCCCAAAATCAGCGAAATGCACCCCGCAUUACGUUUGGTGGACC-3'
5'-((.((((((.....(((.(((((.....))))).)))))))).)).))-3'
Motif MFE = -13.6; z-score = -2.03; 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 28210 to 28409 (motif highlighted in silver):

```
5'-AAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUAC
GUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUAC-3
5'-.((((((.......(((((.((((((..((((..(((((((...)))))))..))))......)))))))))))..((.((((((.....(((.(((((.....))))).)
))))))).)).))(((..((((...(((.....)))))))).))).......((((((.((((.........)))))))))))))))..-3'
MFE = -53.6; z-score = -2.22; ED = 31.94
```

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 50--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 50--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 65 to 200--gene, gene-GU280_gp10, 28274-29533(+)

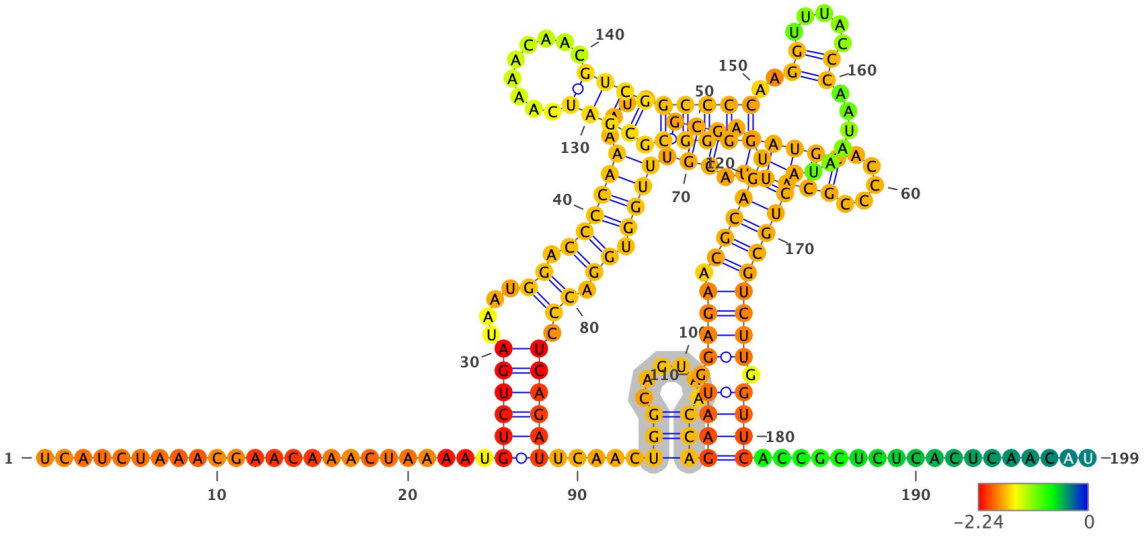
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 65 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 479 from nt 28345 to 28356 (nt 94 to 105)

```
5'-TGGCAGTAACCA-3'
5'-(((......)))-3'
Motif MFE = -0.6; z-score = -0.72; 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(+)

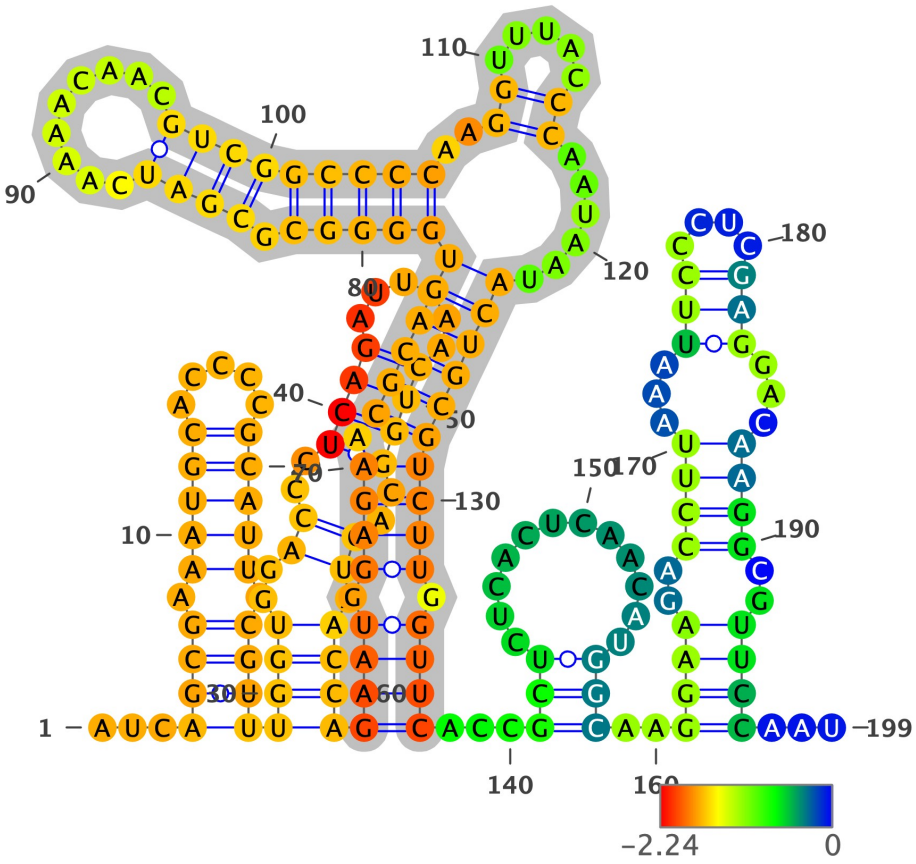
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 480 from nt 28357 to 28432 (nt 62 to 137)

```
5'-GAATGGAGAACGCAGTGGGGCGCGATCAAAACAACGUCGGCCCCAAGGTTTACCCAATAATACUGCGUCUUGGUUC-3'
5'-((((.((((.(((((((((((.((((.........)))))))))..((.....)).....))))))))))).))))-3'
Motif MFE = -29.8; z-score = -3.81; 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 28296 to 28494 (motif highlighted in silver):

```
5'-AUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUU
UACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAU-3
5'-...((((.(((((.....))))).))))((((..((..((((......))))..)).))))((((.((((.(((((((((((.((((.........)))))))))..((..
...)).....))))))))))).))))...(((............)))..((((..((((...(((....)))...))))..))))...-3'
MFE = -56.6; z-score = -2.09; ED = 16.4
```

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_gp10, 28274-29533(+)

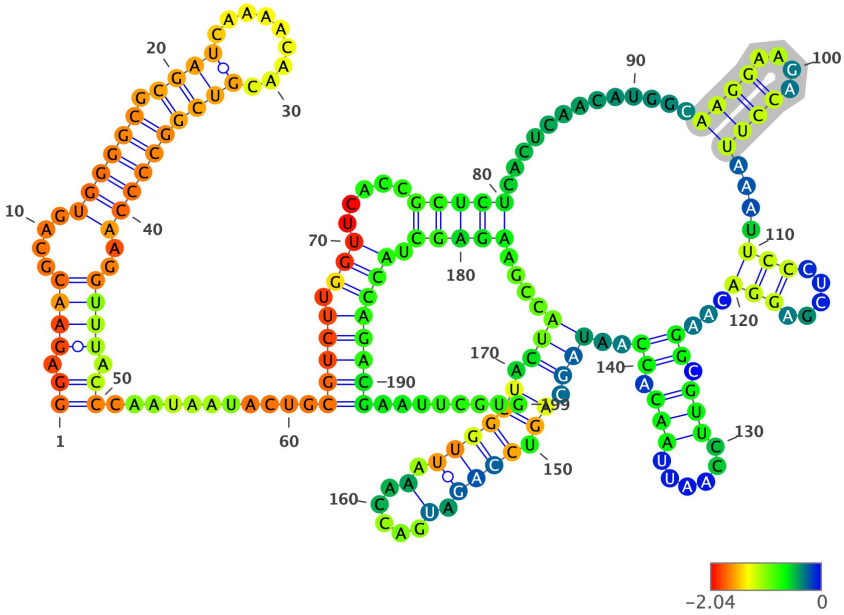
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 481 from nt 28454 to 28465 (nt 94 to 105)

```
5'-AAGGAAGACCUU-3'
5'-((((....))))-3'
Motif MFE = -1.3; z-score = -5.49; 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 28361 to 28559 (motif highlighted in silver):

```
5'-GGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUC
CCUCGAGGACAAGGCGUUCCAAUUAACACCAAUAGCAGUCCAGAUGACCAAAUUGGCUACUACCGAAGAGCUACCAGACGAAUUCGUG-3
5'-((.((((....((((((.((((.........))))))))))..)))))..))...........((((((.(((.....(((((.............((((....)))).....((
(.....))))...((.(((......))).))..(((.((.((((.(.....).)))))).))).....)))))).)))))))).........-3'
MFE = -44.2; z-score = -0.35; ED = 40.41
```

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(+)

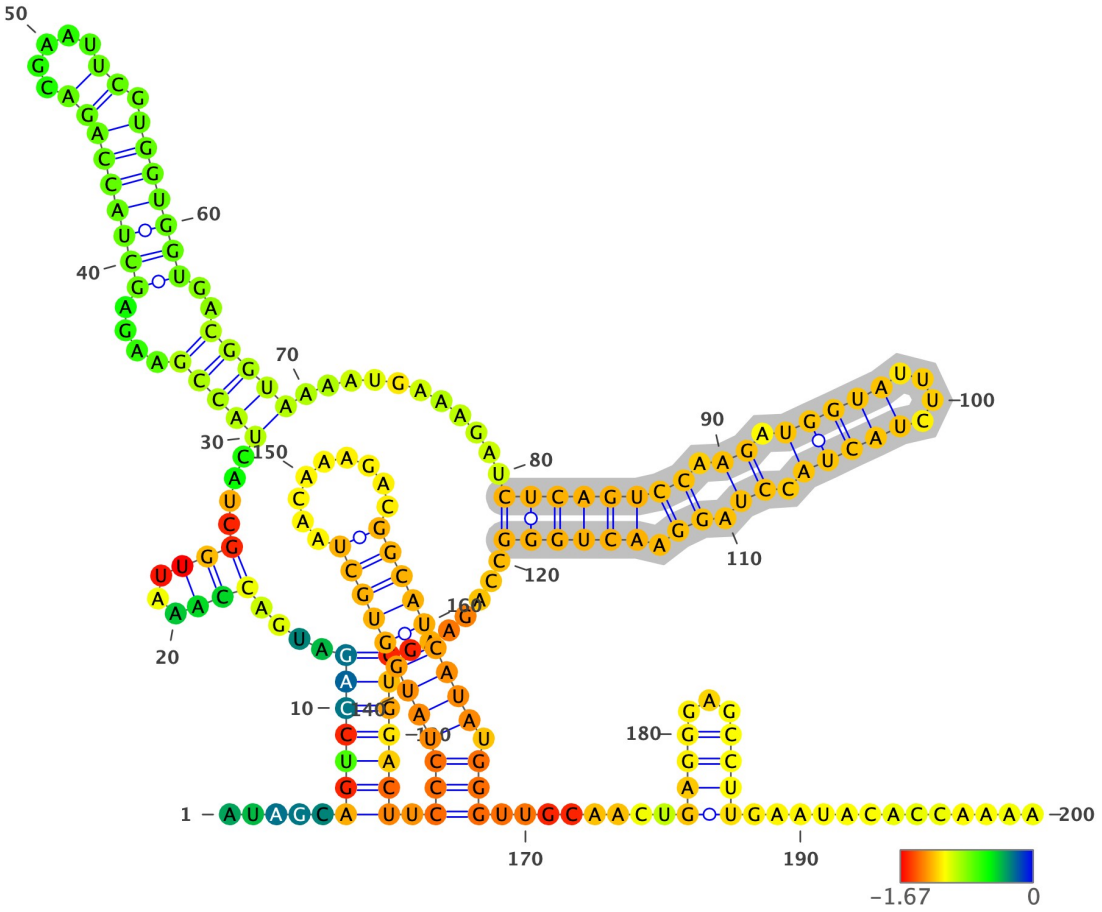
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 482 from nt 28583 to 28621 (nt 81 to 119)

```
5'-CTCAGTCCAAGATGGTATTTCUACUACCUAGGAACUGGG-3'
5'-((((((((.((.(((((....))))).)).)).))))))-3'
Motif MFE = -12.9; z-score = -3.02; 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 = -55.2; z-score = -1.73; ED = 20.17
```

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_gp10, 28274-29533(+)

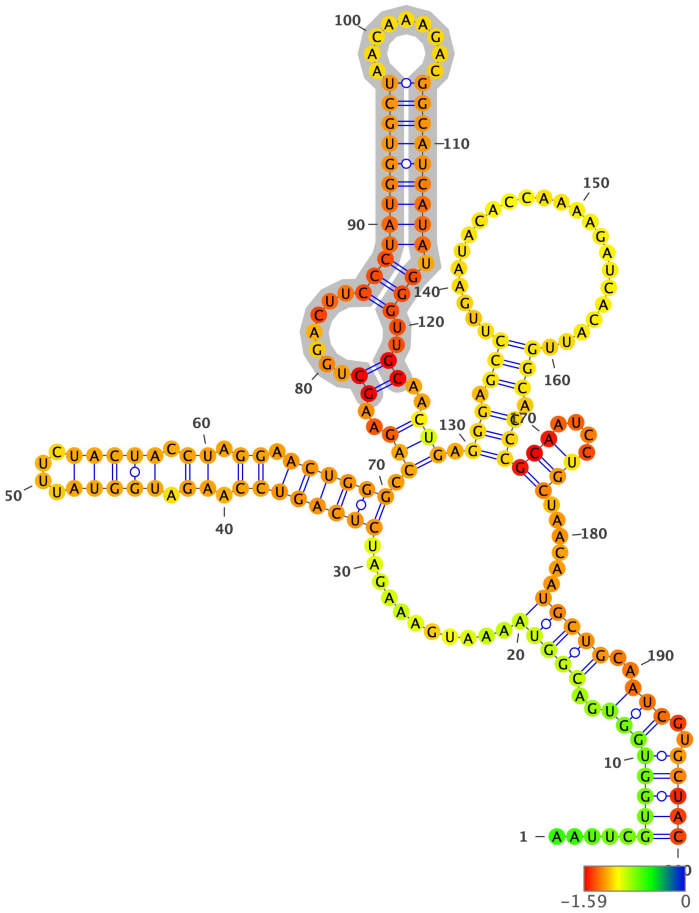
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 483 from nt 28628 to 28674 (nt 77 to 123)

```
5'-GCTGGACTTCCCTATGGTGCTAACAAAGACGGCAUCAUATGGGTTGC-3'
5'-((.......((((((((((((.........)))))))))).)))..))-3'
Motif MFE = -15.5; z-score = -2.29; 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 28552 to 28751 (motif highlighted in silver):

```
5'-AAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAU
CAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUAC-3
5'-.....((((((((..(((((...........((((((((.((.(((((....))))).)).)).)))))).(((..((.......((((((((((((.........)))))
)))).)))..))..))).(((.(((.......................))).)))(((....)))......)))))..)))..)))))-3'
MFE = -50.5; z-score = -1.12; ED = 19.7
```

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_gp10, 28274-29533(+)

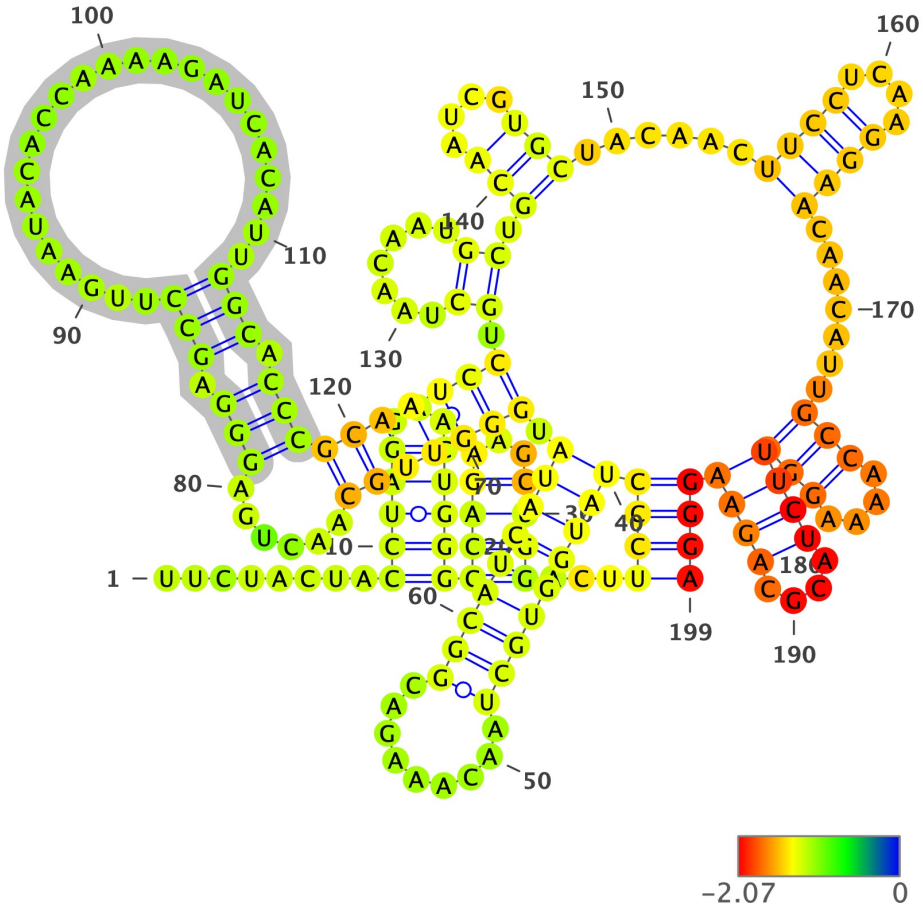
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 484 from nt 28681 to 28718 (nt 81 to 118)

```
5'-GGGAGCCTTGAATACACCAAAAGATCACATTGGCACCC-3'
5'-(((.(((.....................))).)))-3'
Motif MFE = -7.1; z-score = -1.26; ED = 2.46
```



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 28601 to 28799 (motif highlighted in silver):

```
5'-UUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUU
GGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAGGGA-3
5'-........(((((...)))))(((((...))))).((((((((((((.........)))))))))).(((((((.....(((.(((.....................
))).)))))))))).((.......)).(((....))).....((((....)))).....(((....)))(((((....)))))))-3'
MFE = -49.6; z-score = -1.21; ED = 27.65
```

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(+)

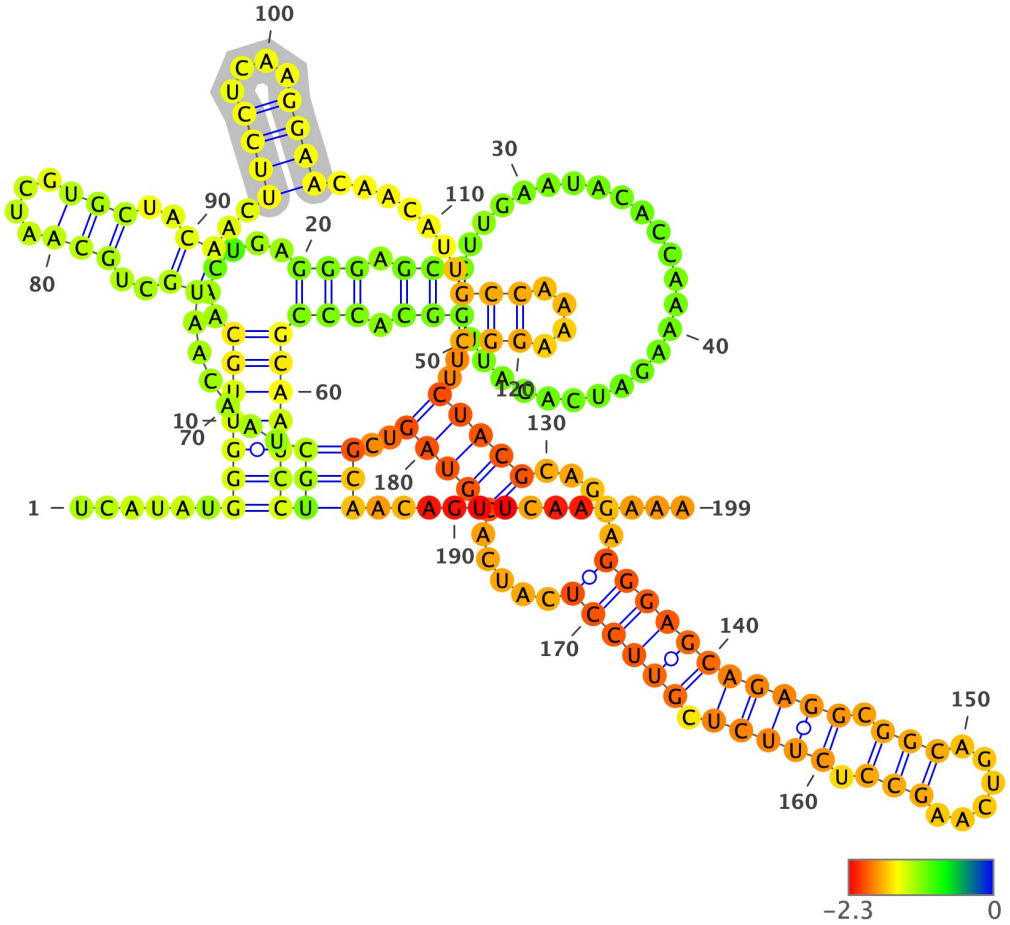
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 485 from nt 28755 to 28766 (nt 94 to 105)

```
5'-TTCCTCAAGGAA-3'
5'-((((....))))-3'
Motif MFE = -1.6; z-score = -5.91; 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 = -1.39; 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(+)

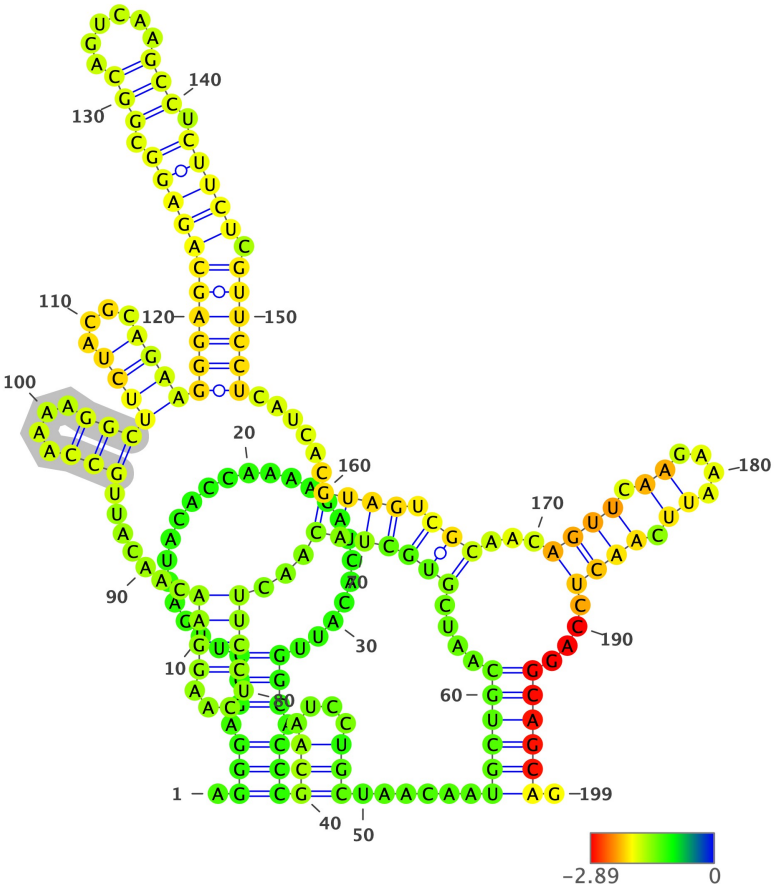
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 486 from nt 28774 to 28783 (nt 95 to 104)

```
5'-GCCAAAAGGC-3'
5'-(((....)))-3'
Motif MFE = -2.6; z-score = -9.92; 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 = -2.11; 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(+)

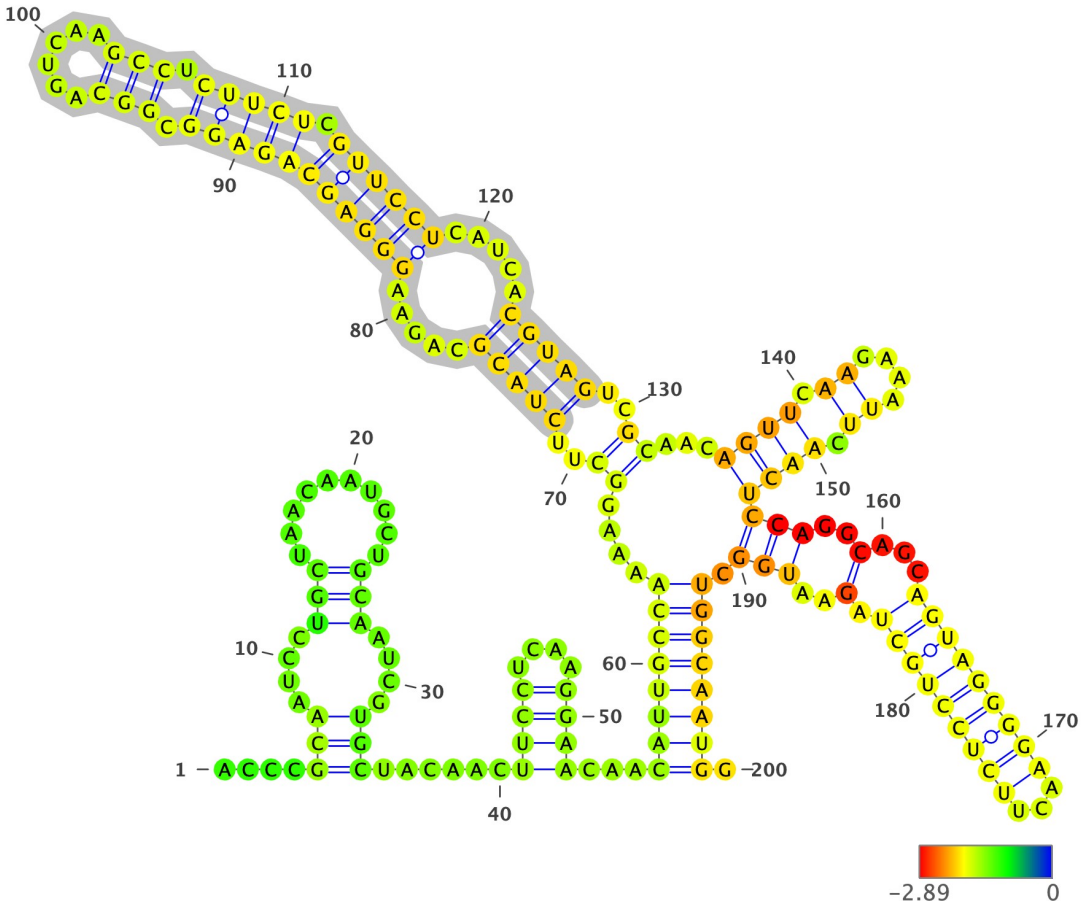
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 487 from nt 28786 to 28842 (nt 72 to 128)

```
5'-CTACGCAGAAGGGAGCAGAGGCGGCAGTCAAGCCTCUUCUCGUUCCUCATCACGUAG-3'
5'-(((((.....(((((((((((.(((......))).))))).))))))).....)))))-3'
Motif MFE = -24.0; z-score = -3.15; 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 = -3.05; 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(+)

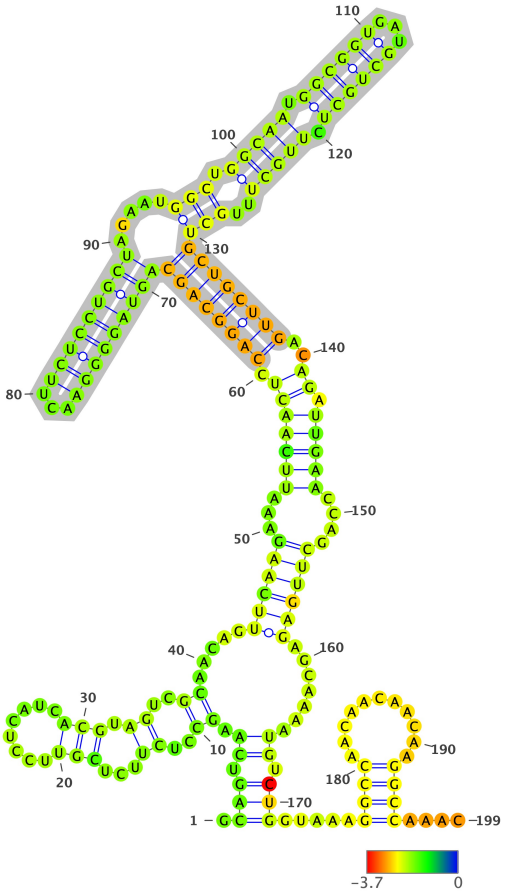
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 488 from nt 28869 to 28946 (nt 61 to 138)

```
5'-CAGGCAGCAGTAGGGGAACTUCUCCUGCUAGAATGGCTGGCAATGGCGGTGATGCUGCUCUUGCUTTGCUGCUGCUUG-3'
5'-((((((((((((((((...))))))))).....(((.(((((.(((((((...))))))).))))))..)))))))))))-3'
Motif MFE = -37.9; z-score = -5.66; 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 = -1.77; 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(+)

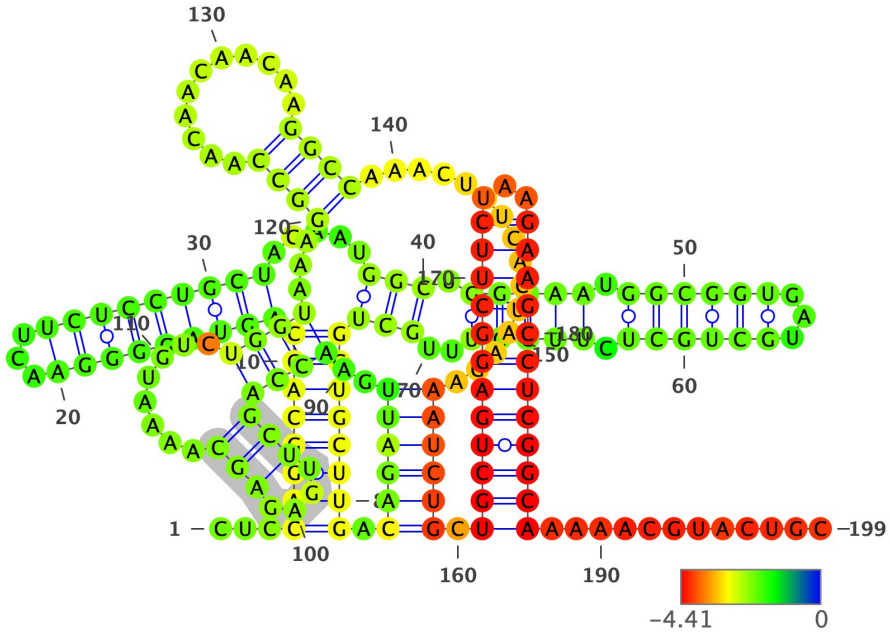
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 489 from nt 28960 to 28969 (nt 95 to 104)

```
5'-GCTTGAGAGC-3'
5'-(((....)))-3'
Motif MFE = -0.1; z-score = -0.1; ED = 1.48
```



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 28866 to 29064 (motif highlighted in silver):

```
5'-CUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGU
CUGGUAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGC-3
5'-...((((((((((((((((...))))))))).....(((.(((((.((((((...)))))).)))))..))))))))))).((((((..(((((((....))).......
.))))...((((..........))))..............))))))..((((((((((...))))))))))).............-3'
MFE = -73.2; z-score = -4.34; ED = 25.27
```

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_gp10, 28274-29533(+)

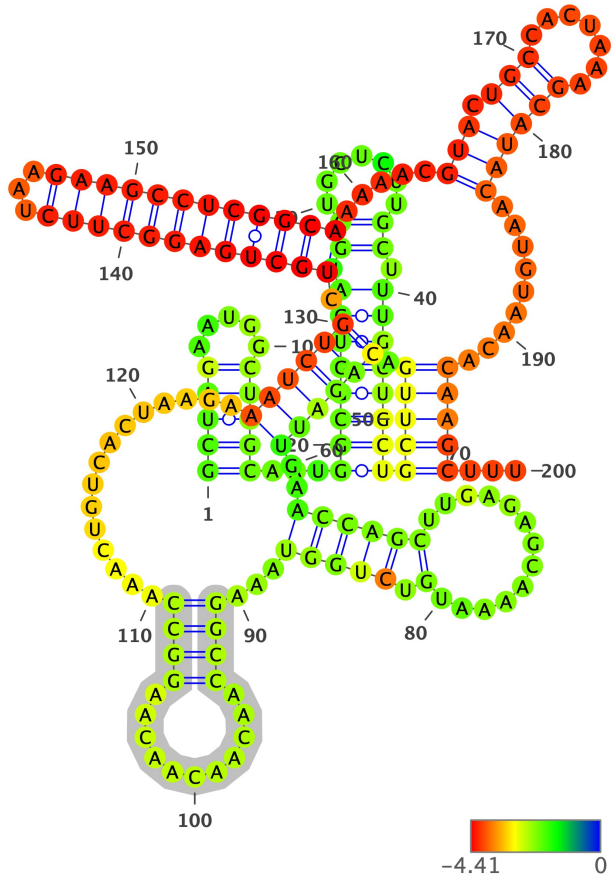
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 490 from nt 28985 to 29003 (nt 91 to 109)

```
5'-GGCCAACAACAACAAGGCC-3'
5'-((((...........))))-3'
Motif MFE = -4.9; z-score = -3.78; 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 = -2.89; 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(+)

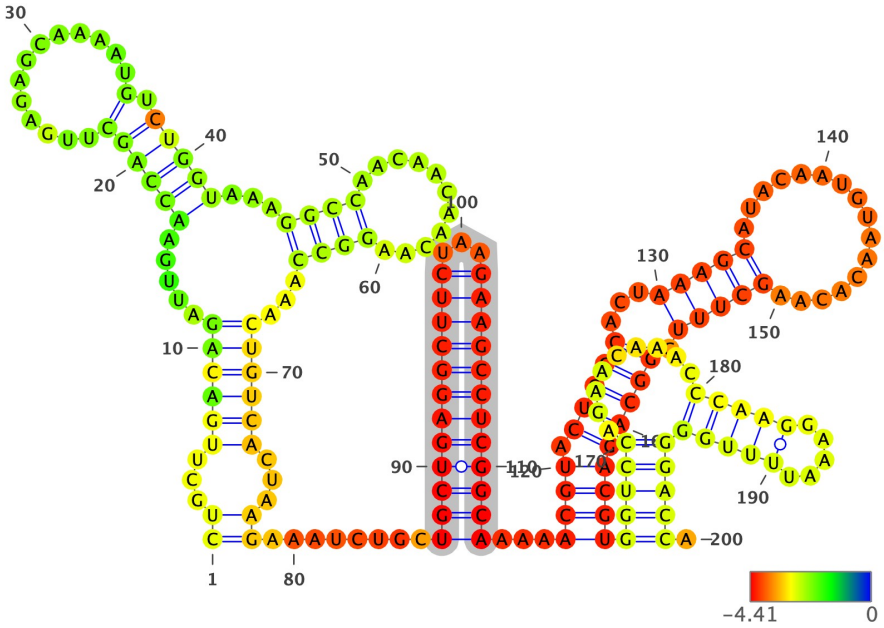
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 491 from nt 29026 to 29052 (nt 87 to 113)

```
5'-TGCTGAGGCTTCTAAGAAGCCUCGGCA-3'
5'-(((((((((((...)))))))))))-3'
Motif MFE = -19.7; z-score = -5.75; 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 = -4.85; 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(+)

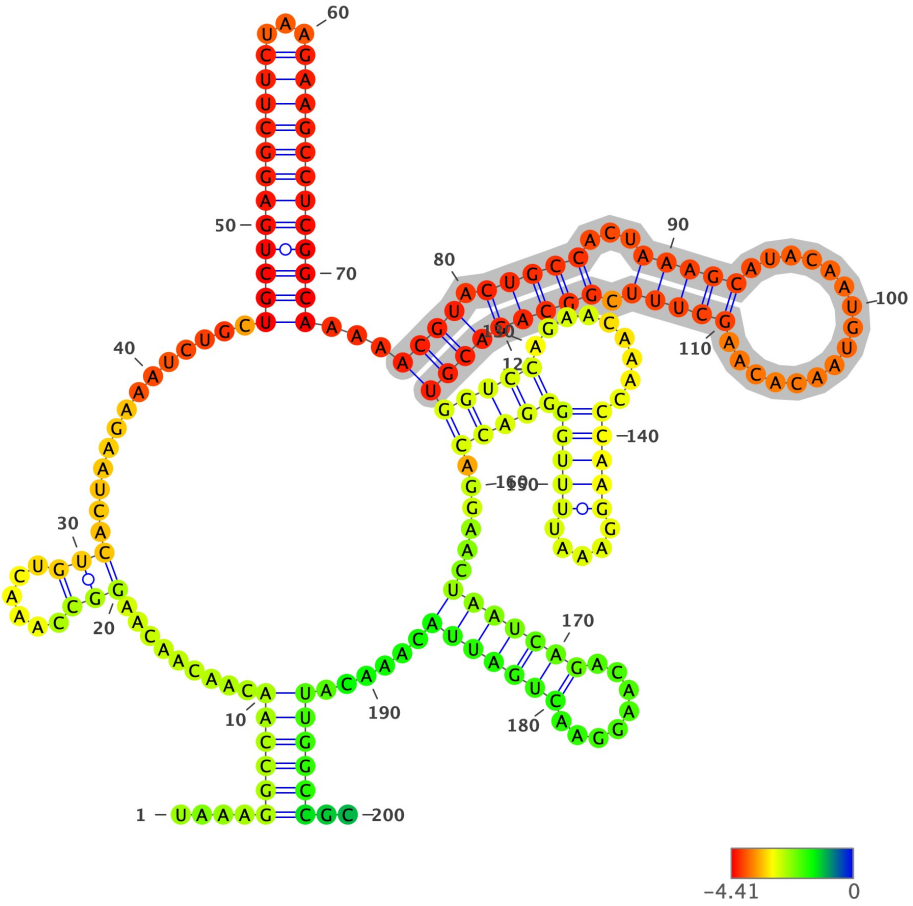
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 492 from nt 29056 to 29104 (nt 76 to 124)

```
5'-ACGTACTGCCACTAAAGCATACAATGTAACACAAGCUUUCGGCAGACGU-3'
5'-((((.(((((...(((((.................))))).)))))))))-3'
Motif MFE = -14.6; z-score = -3.19; 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 = -5.01; 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(+)

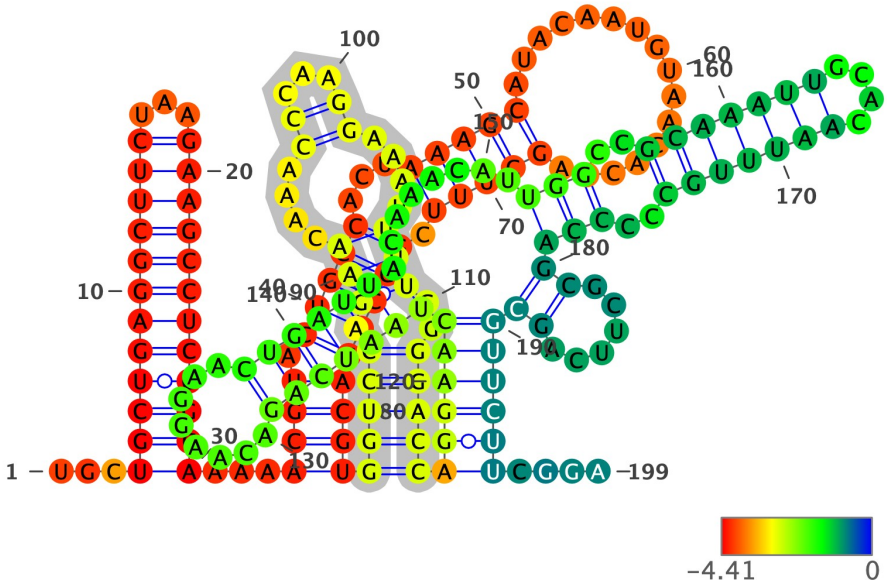
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 493 from nt 29105 to 29138 (nt 83 to 116)

```
5'-GGTCCAGAACAAACCCAAGGAAATUUUGGGGACC-3'
5'-(((((.(((....((...)).....)))..)))))-3'
Motif MFE = -8.1; z-score = -1.91; 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 = -64.3; z-score = -4.6; ED = 12.65
```

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(+)

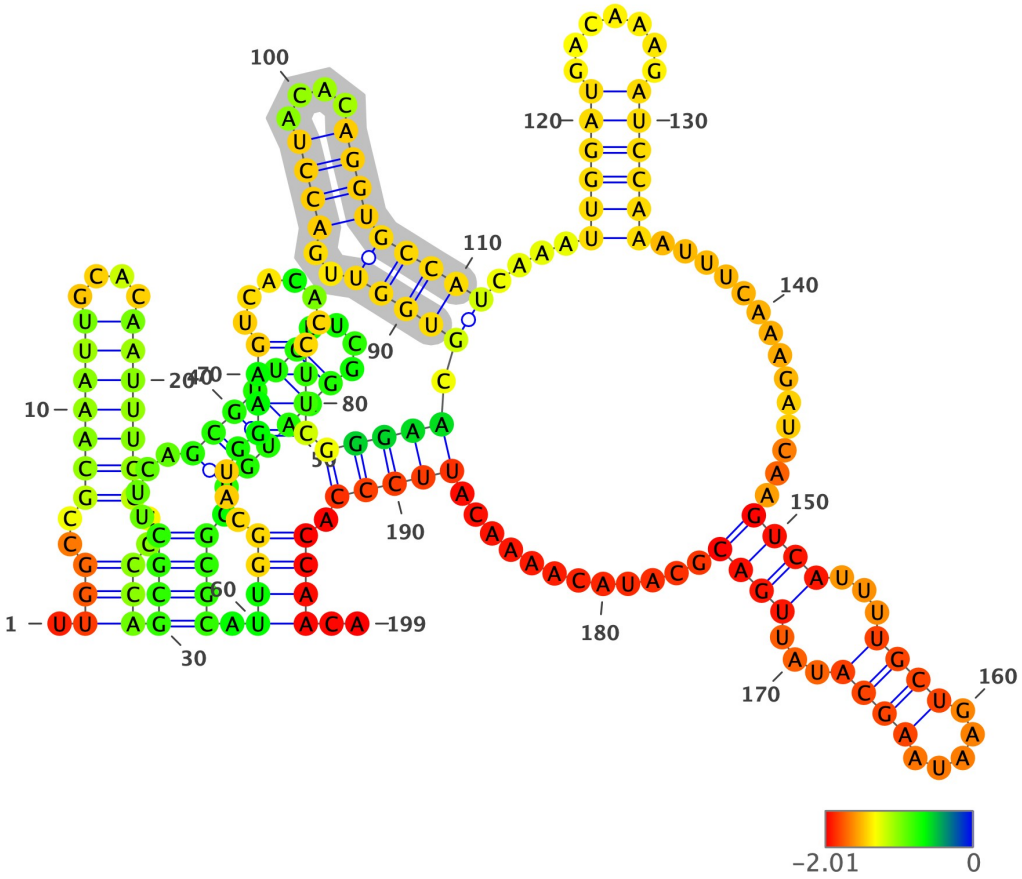
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 494 from nt 29261 to 29282 (nt 89 to 110)

```
5'-TGGTTGACCTACACAGGUGCCA-3'
5'-(((((..((((....))))))))-3'
Motif MFE = -5.9; z-score = -1.78; 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 = -2.34; ED = 21.65
```

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(+)

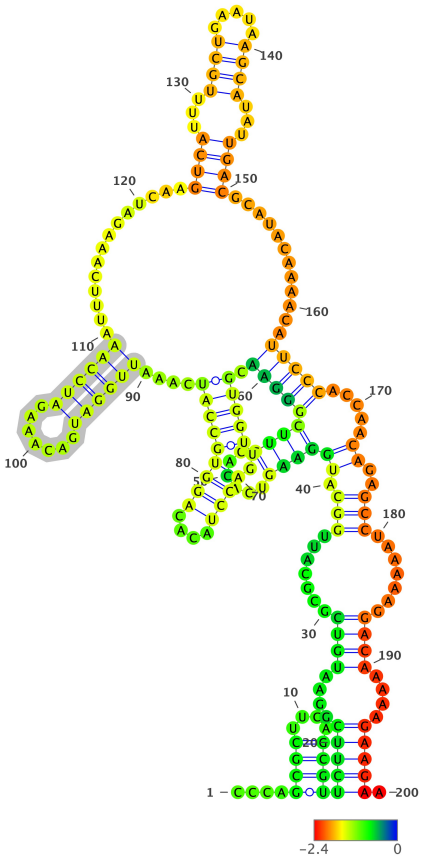
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 495 from nt 29288 to 29306 (nt 91 to 109)

```
5'-TTGGATGACAAAGAUCCAA-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -3.06; 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 = -2.4; 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(+)

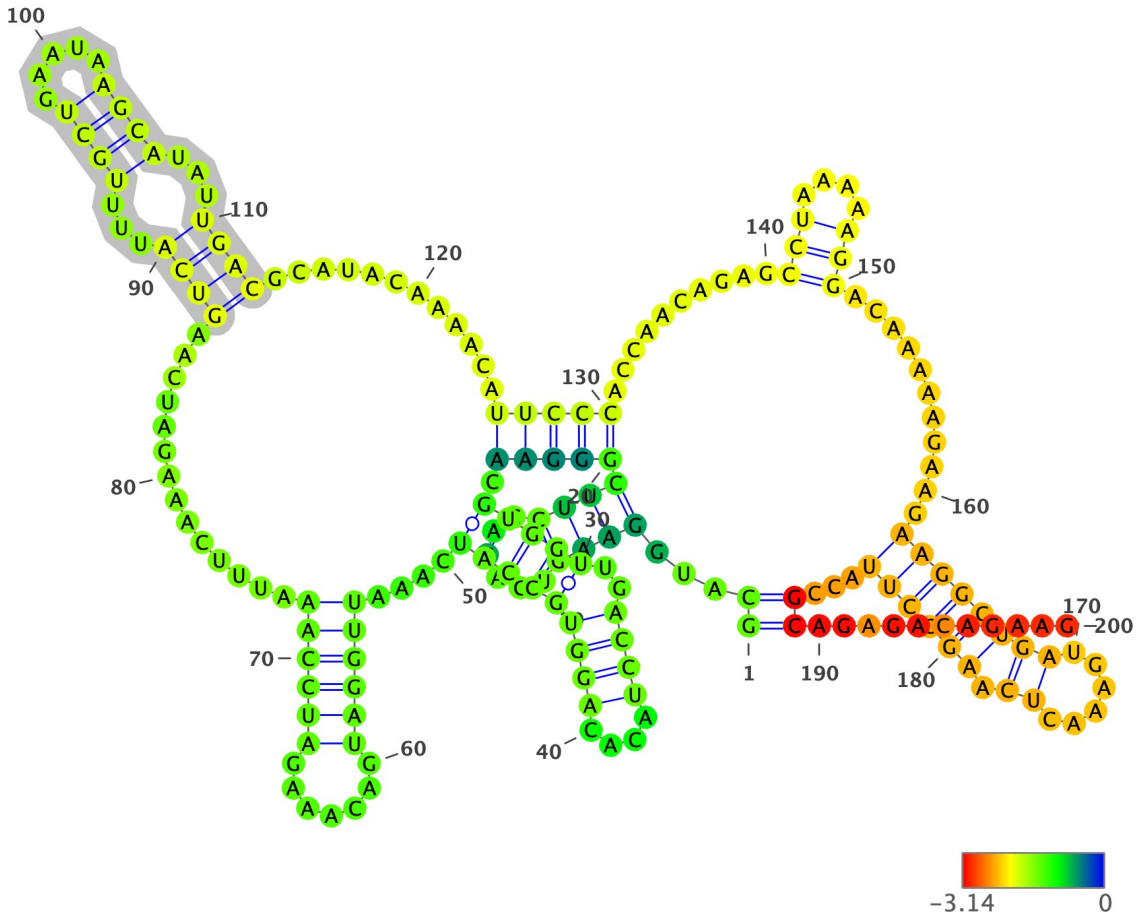
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 496 from nt 29321 to 29347 (nt 87 to 113)

```
5'-GTCATTTTGCTGAATAAGCATATUGAC-3'
5'-((((...((((.....))))...))))-3'
Motif MFE = -7.9; z-score = -3.42; 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 = -2.21; ED = 18.54
```

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_gp10, 28274-29533(+)

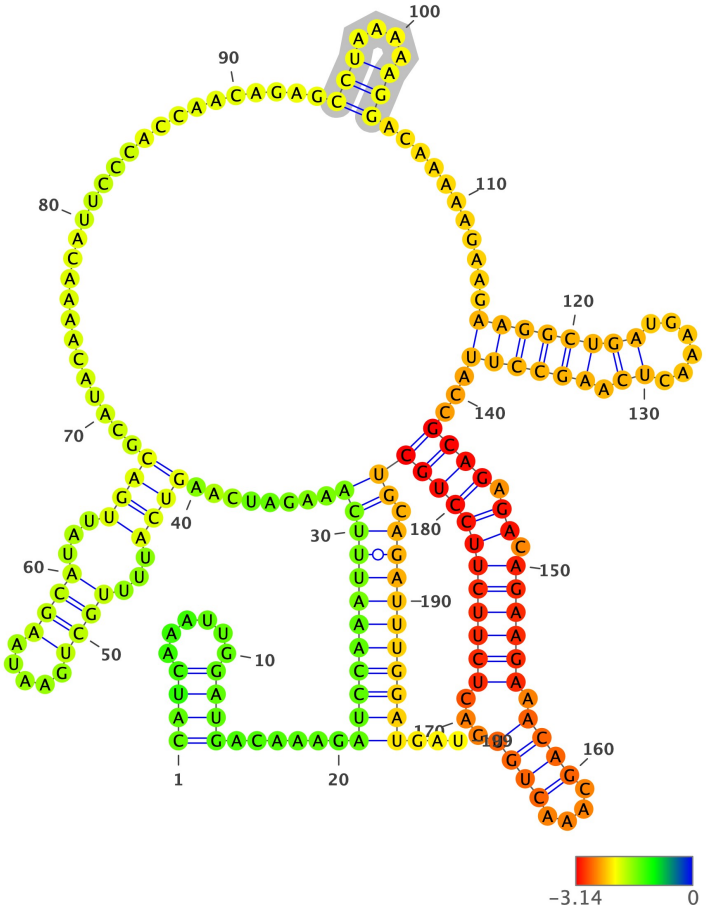
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 497 from nt 29375 to 29384 (nt 95 to 104)

```
5'-CCTAAAAAGG-3'
5'-(((....)))-3'
Motif MFE = -0.3; z-score = -7.11; 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 = -4.44; ED = 15.27
```

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_gp10, 28274-29533(+)

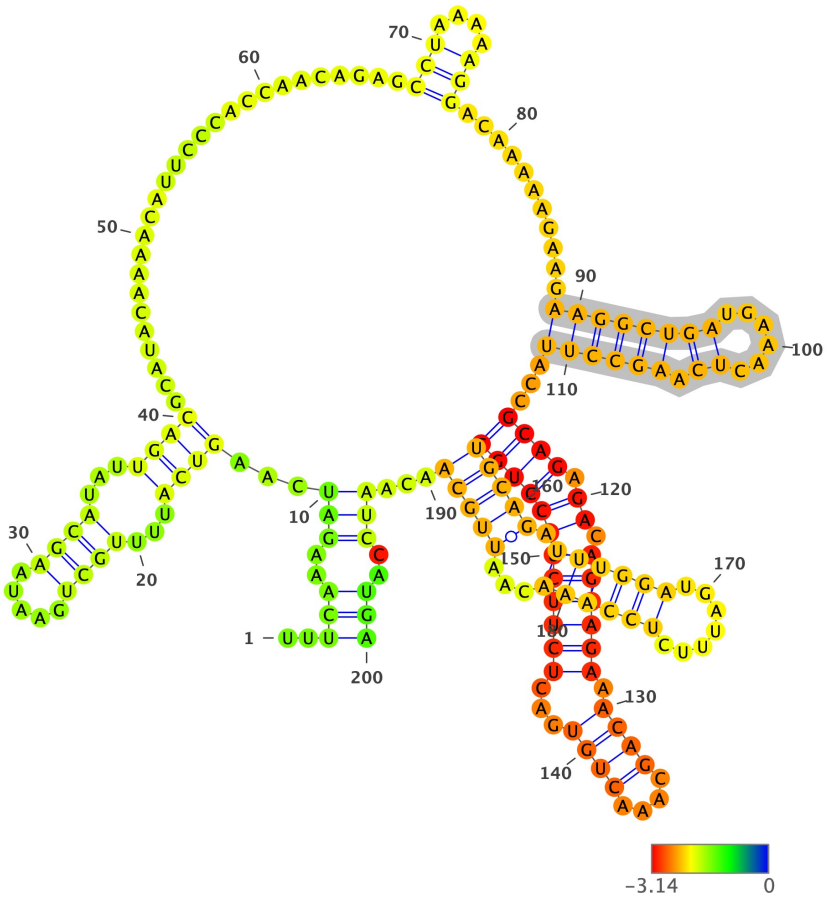
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 498 from nt 29396 to 29418 (nt 89 to 111)

```
5'-AAGGCTGATGAAACUCAAGCCUU-3'
5'-((((((((......)).))))))-3'
Motif MFE = -6.9; z-score = -3.28; 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 = -3.76; 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(+)

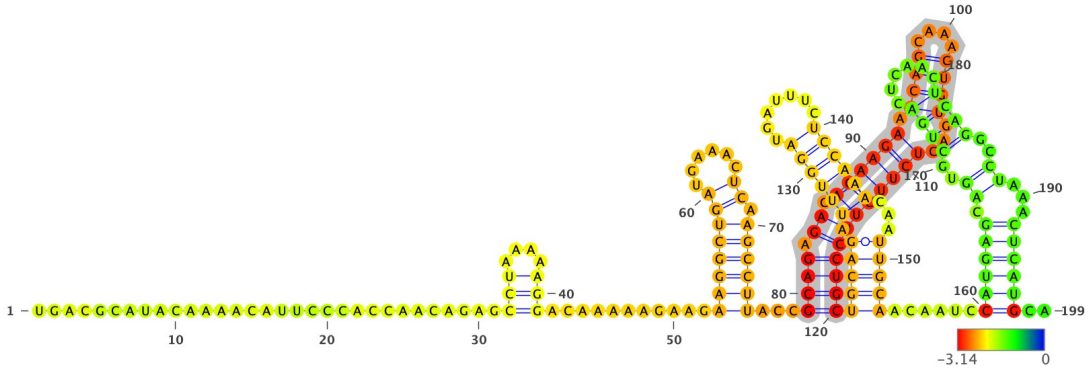
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 499 from nt 29422 to 29463 (nt 79 to 120)

```
5'-GCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGC-3'
5'-((((.((.(((((((.((((....))))...))))))))))))-3'
Motif MFE = -14.7; z-score = -3.97; 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 = -3.39; 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(+)

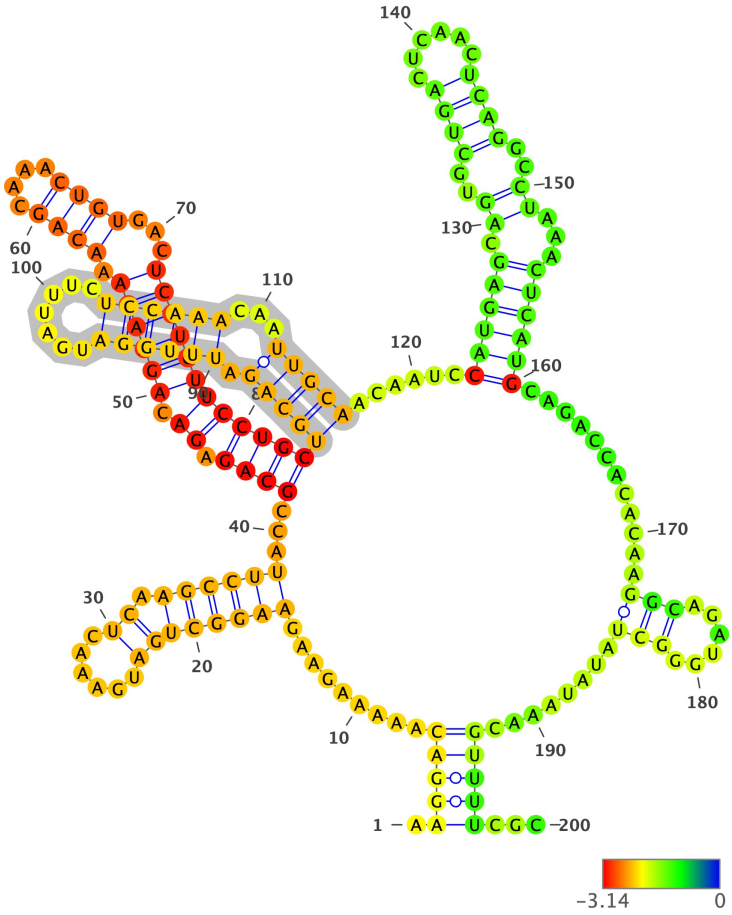
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 500 from nt 29464 to 29496 (nt 84 to 116)

```
5'-TGCAGATTTGGATGATTTCUCCAAACAAUUGCA-3'
5'-(((((.((((((.......))))))...)))))-3'
Motif MFE = -7.9; z-score = -2.07; ED = 1.78
```



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 29381 to 29580 (motif highlighted in silver):

```
5'-AAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAA
UUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGC-3
5'-.(((((.........((((((((......)).))))))...((((.((.((((((.((((....))))...))))))))))))(((((.((((((.......))))))...
)))))......((((((.((..((((......))))..))...))))))............(((......)))........)))))...-3'
MFE = -48.8; z-score = -2.82; ED = 28.94
```

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 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(+)

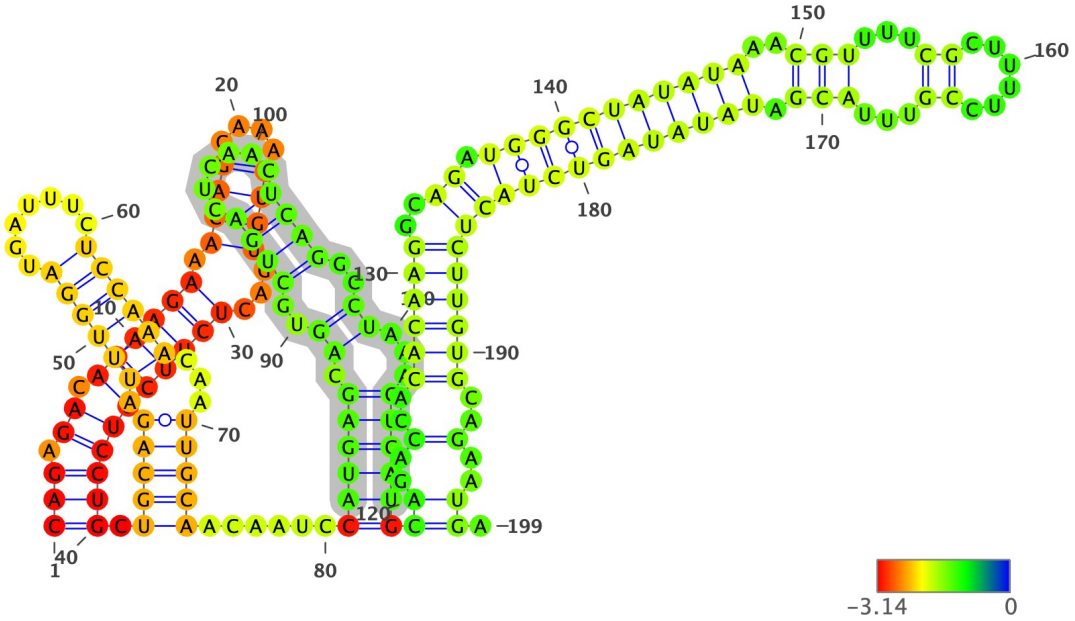
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

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 501 from nt 29504 to 29539 (nt 82 to 117)

```
5'-ATGAGCAGTGCTGACTCAACUCAGGCCUAAACUCAU-3'
5'-(((((.((..((((.....)))))..))...)))))-3'
Motif MFE = -8.1; z-score = -1.87; 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 = -3.04; 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(+)

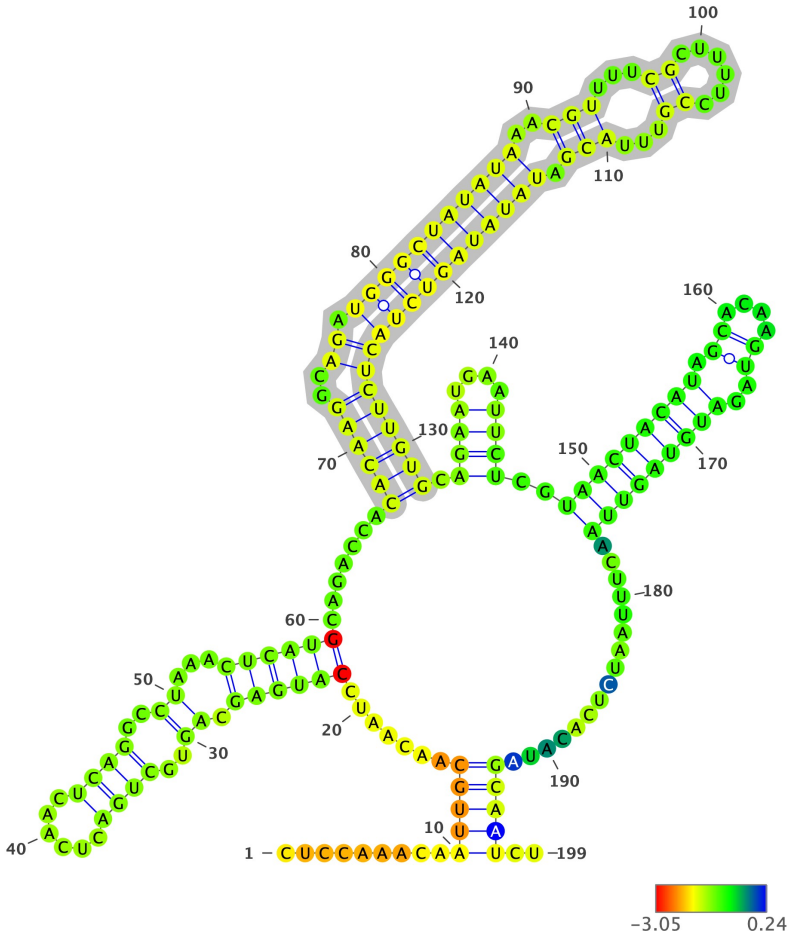
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

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 502 from nt 29548 to 29613 (nt 67 to 132)

```
5'-CACAAGGCAGATGGGCTATATAAACGTTTTCGCTTTTCCGTTTACGAUAUAUAGUCUACUCUUGUG-3'
5'-((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))-3'
Motif MFE = -19.7; z-score = -3.8; 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 = -45.9; z-score = -3.0; ED = 11.06
```

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 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(+)

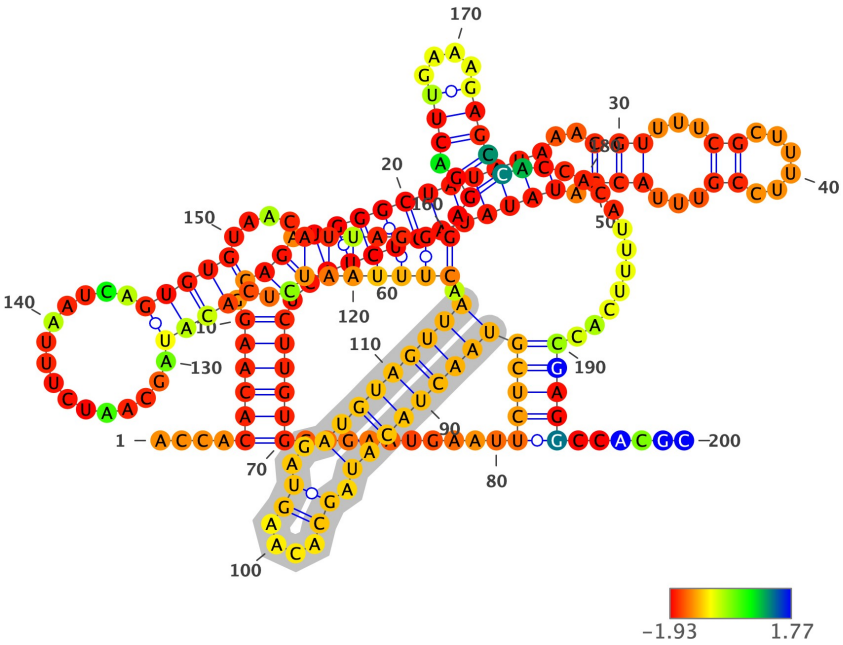
Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

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 503 from nt 29629 to 29657 (nt 86 to 114)

```
5'-TAACTACATAGCACAAGUAGAUGUAGUUA-3'
5'-(((((...................)))))-3'
Motif MFE = -8.5; z-score = -4.34; 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 = -1.3; 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"]