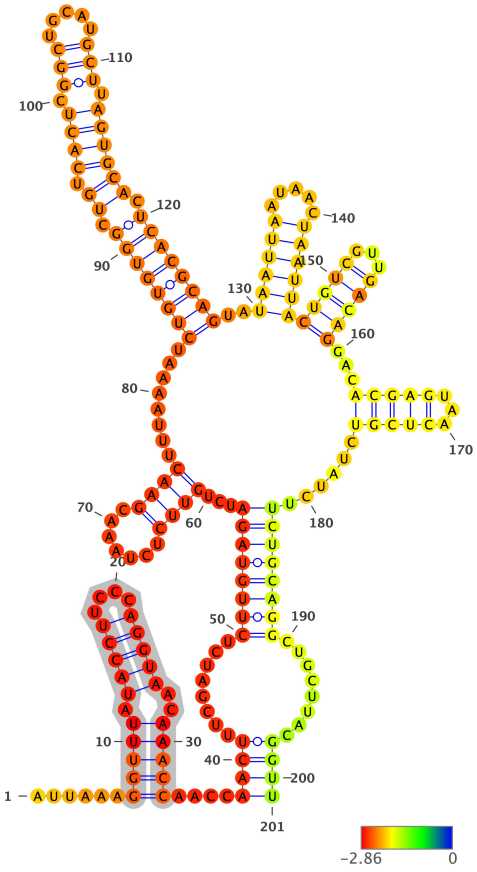
NC_045512.2 (forward strand): Structure number 1 from nt 7 to 33 (nt 7 to 33)

```
5'-GGUUUAUACCUUCCCAGGUAACAAACC-3'
5'-(((...(((((....)))))....)))-3'
Motif MFE = -7.0; z-score = -3.82; 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 1 to 201 (motif highlighted in silver):

```
5'-AUUAAAGGUUUAUACCUUCCCAGGUAACAAACCAACCAACUUUCGAUCUCUUGUAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCU
UAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUU-3
5'-......(((((.((((((....)))))).)))))....((((........(((((((((...((((.......))))).......(((((((((.((.(((((.(((.....)))
.))))))).)))))))..((((((.....))))))(((((...))))))...((((((...))))))......)))))))).......))))-3'
MFE = -51.1; z-score = -2.65; 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(+)

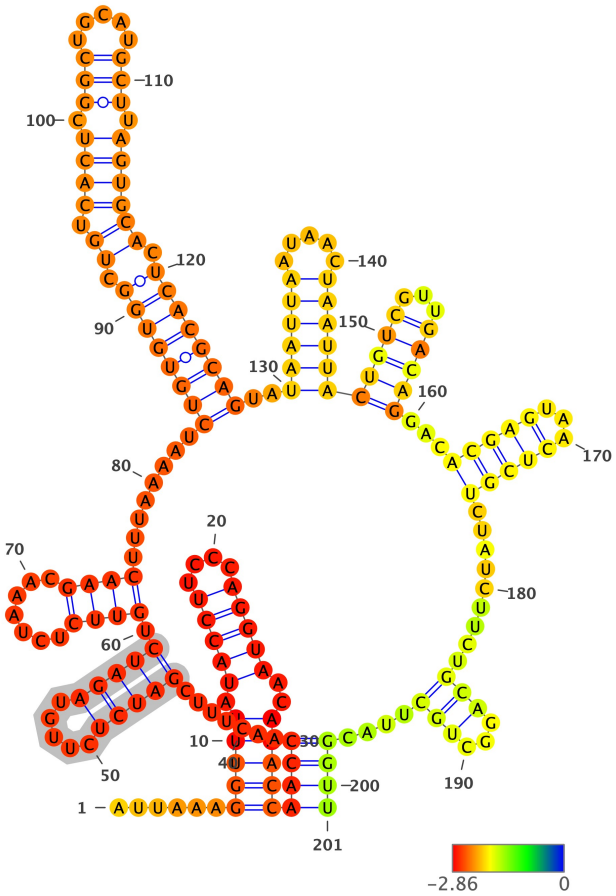
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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'-GAUCUCUUGUAGAUC-3'
5'-(((((.....)))))-3'
Motif MFE = -2.3; z-score = -2.27; 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 = -2.7; 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(+)

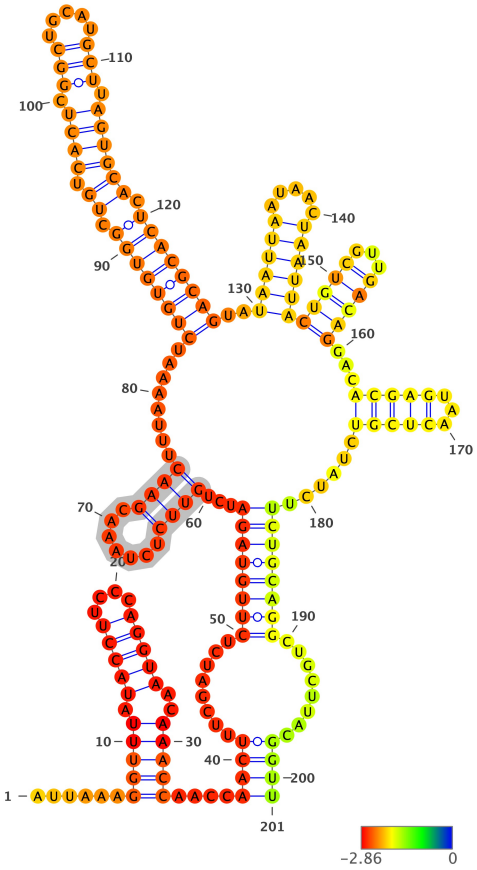
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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'-GUUCUCUAAACGAAC-3'
5'-((((.......))))-3'
Motif MFE = -0.9; z-score = -1.09; 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 = -2.88; 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(+)

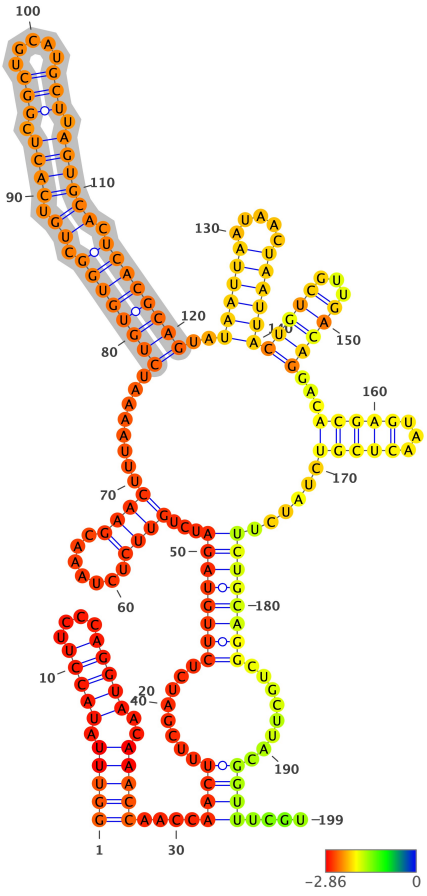
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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'-CUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAG-3'
5'-((((((((.((.((((.(((.....))).)))))).))))))))-3'
Motif MFE = -20.1; z-score = -3.47; 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 = -2.75; 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(+)

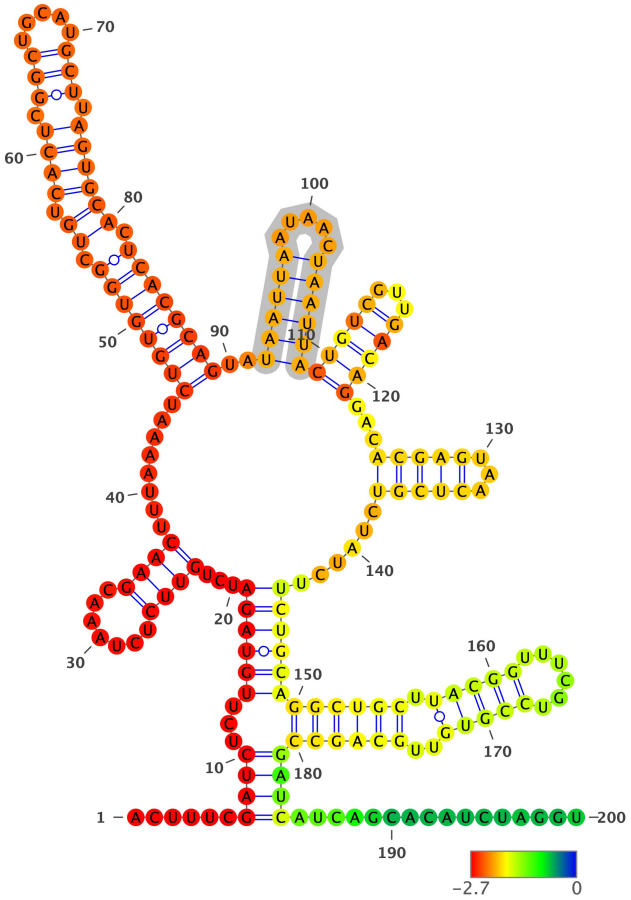
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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'-UAAUUAAUAACUAAUUA-3'
5'-((((((.....))))))-3'
Motif MFE = 0.0; z-score = 0.1; 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 = -3.94; 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(+)

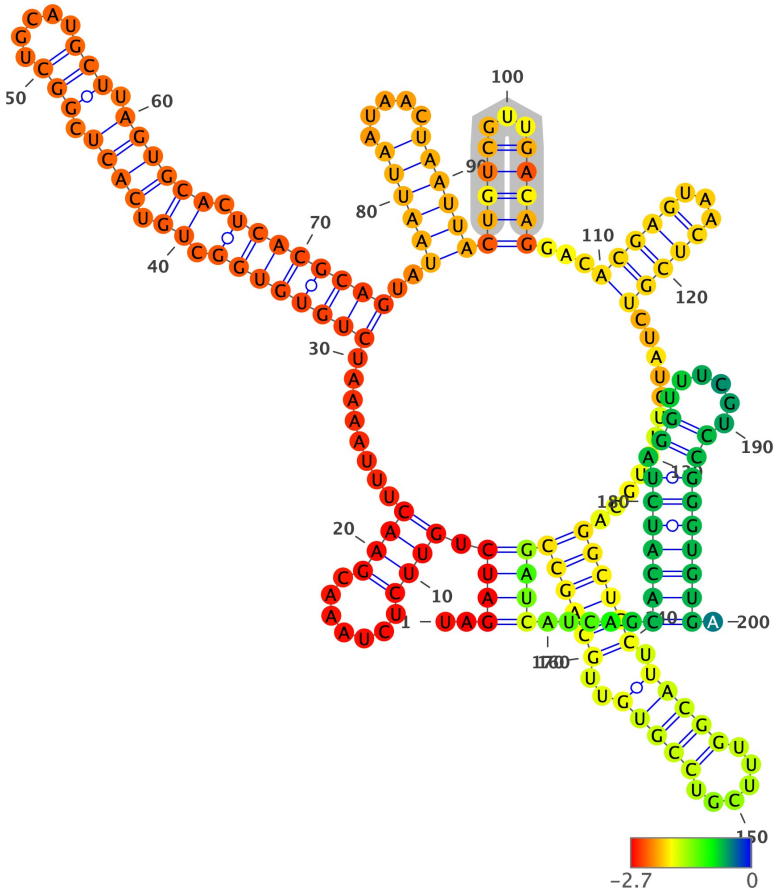
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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'-UGUCGUUGACA-3'
5'-(..(...)..)-3'
Motif MFE = -0.8; z-score = -2.72; 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 = -3.85; 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(+)

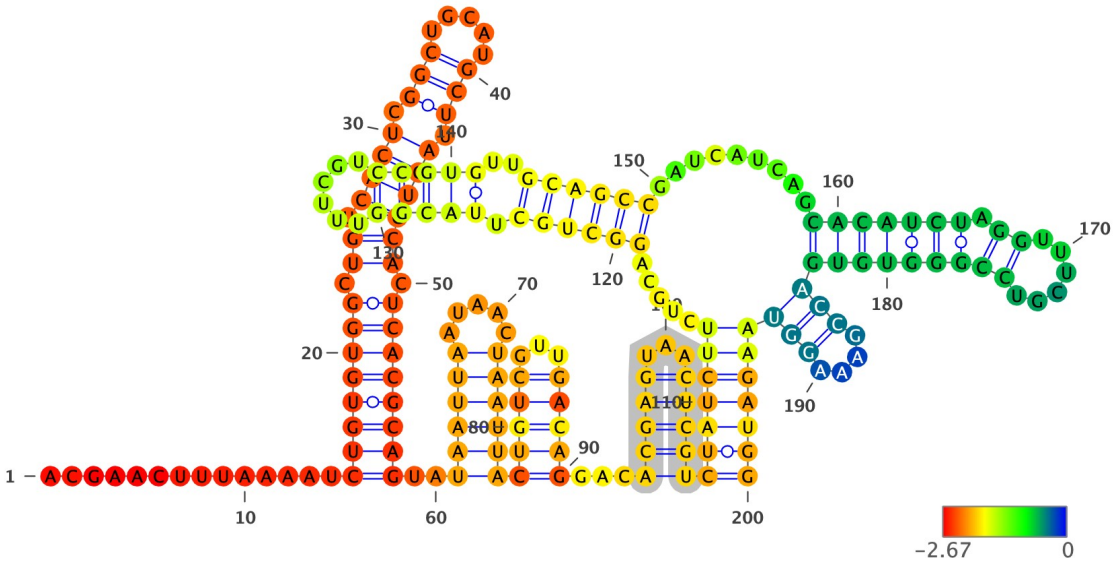
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 163 to 175 (nt 94 to 106)

```
5'-ACGAGUAACUCGU-3'
5'-(((((...)))))-3'
Motif MFE = -3.2; z-score = -5.62; 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 70 to 269 (motif highlighted in silver):

```
5'-ACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUC
UUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGG-3
5'-.............(((((((((.((.((((.(((.....))).))))))).)))))))..((((((.....))))))(((((...))))))...((((((...))))))(((((
((.....((((((.(((((.....)))))..))))))........(((((((.((.....)))))))))))(((....)))))))))-3'
MFE = -65.2; z-score = -2.54; ED = 17.02
```

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

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

3-- nt 197 to 200--gene, gene-GU280_gp01, 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 197 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

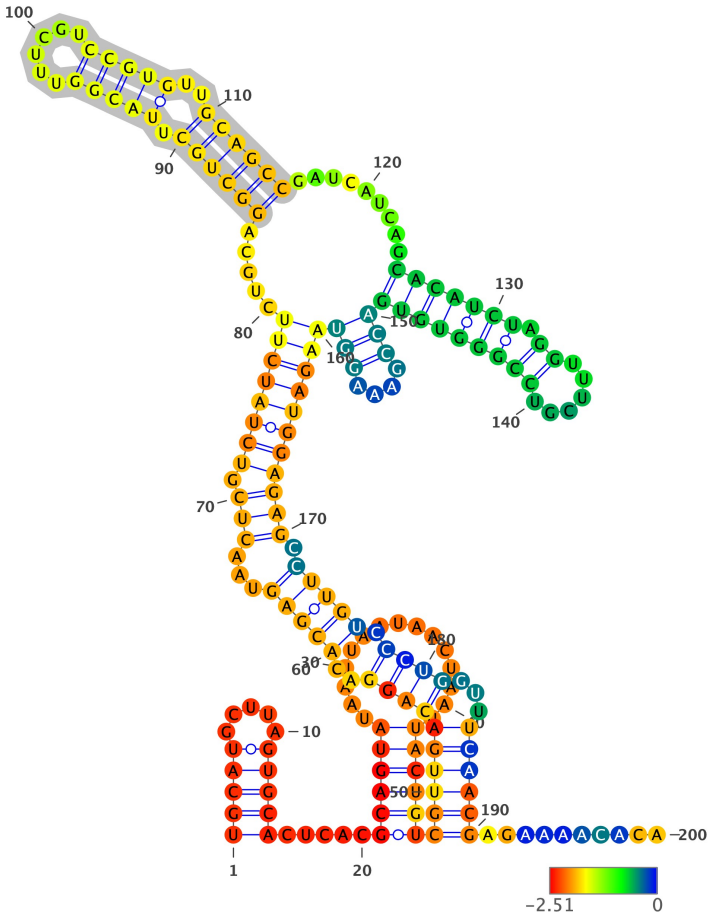
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

5-- nt 197 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'-GGCUGCUUACGGUUUCGUCCGUGUUGCAGCC-3'
5'-((((((.(((((.....)))))..)))))))-3'
Motif MFE = -17.2; z-score = -4.35; 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 = -2.62; 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(+)

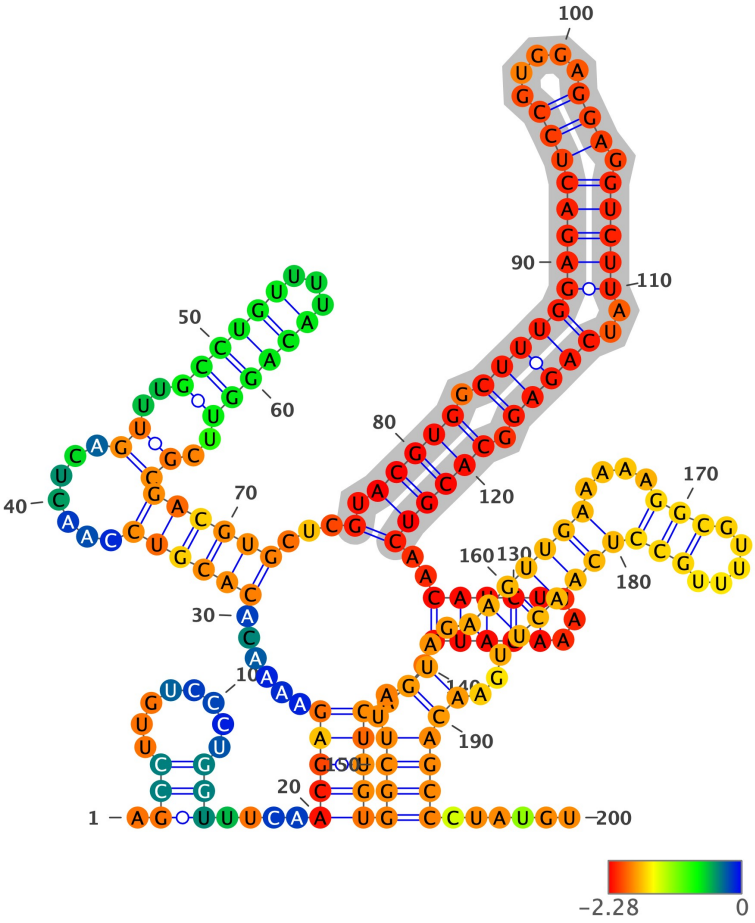
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 347 to 395 (nt 76 to 124)

```
5'-GUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUC-3'
5'-(.(((((.(((((((((((((.....))).)))))..)))))).))))))-3'
Motif MFE = -22.6; z-score = -4.27; 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 = -1.77; 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(+)

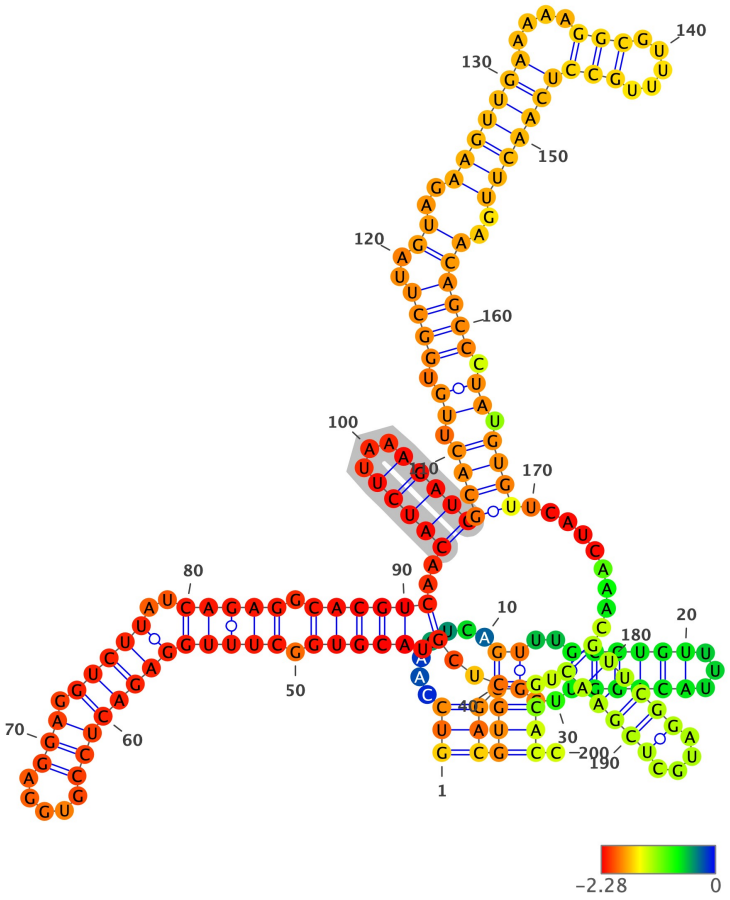
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 10 from nt 398 to 410 (nt 94 to 106)

```
5'-CAUCUUAAAGAUG-3'
5'-(((((...)))))-3'
Motif MFE = -1.8; z-score = -7.06; 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 305 to 504 (motif highlighted in silver):

```
5'-GUCCAACUCAGUUUGCCUGUUUUACAGGUUCGCGACGUGCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACU
UGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACC-3
5'-(((.......((..((((((...))))))..)))))(((((..(.(((((.((((((((((((.....))).))))))..))))))..))))))).))))))..((((((...))))))(((((.
((.(((((..((..(((((((....(((.....)))))))))))..))))))).)).)))).........((((((....)))))).)))).-3'
MFE = -66.2; z-score = -2.33; ED = 15.16
```

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(+)

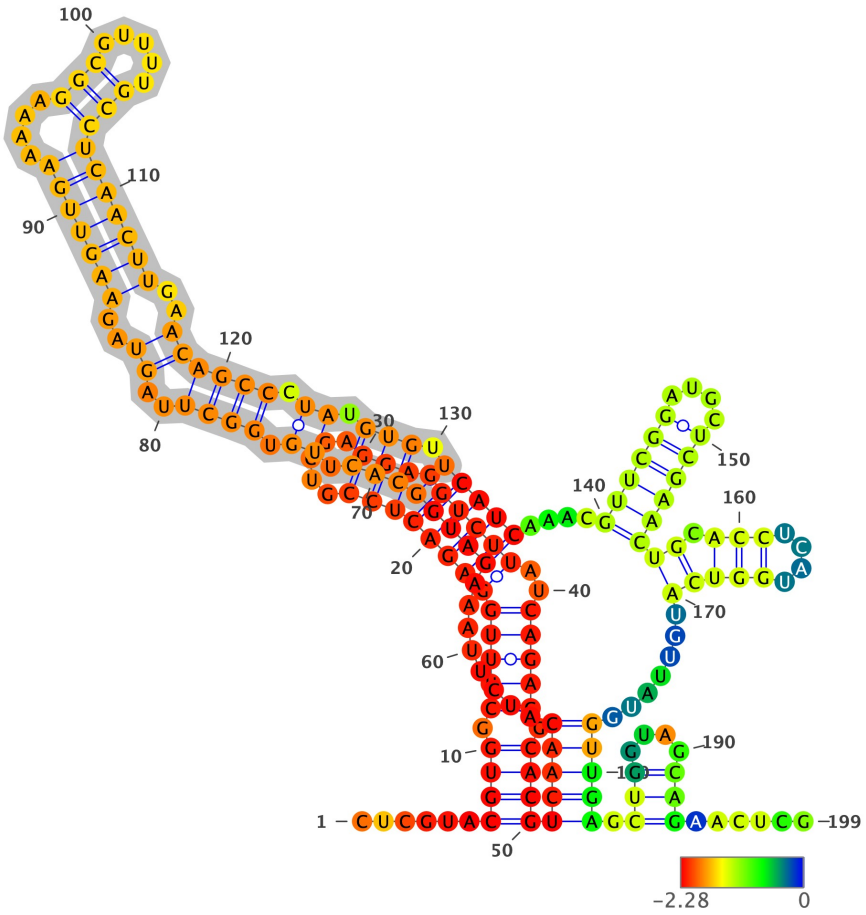
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 11 from nt 411 to 474 (nt 68 to 131)

```
5'-GCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGUU-3'
5'-((((.((.((((..((..(((((((....(((.....))))))))))..)))))).)).))).)-3'
Motif MFE = -20.9; z-score = -3.16; ED = 3.48
```



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 344 to 542 (motif highlighted in silver):

```
5'-CUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAA
CUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCG-3
5'-......((((.(((((((((((((.....))).)))))..)))))).))))(((((........((((((((.((.((((..((..(((((((....(((.....)))))))
)))..)))))).)).))).)))))....((((((....))))))((.(((....)))))).......)))))).(((....))).....-3'
MFE = -62.0; z-score = -1.73; ED = 26.51
```

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(+)

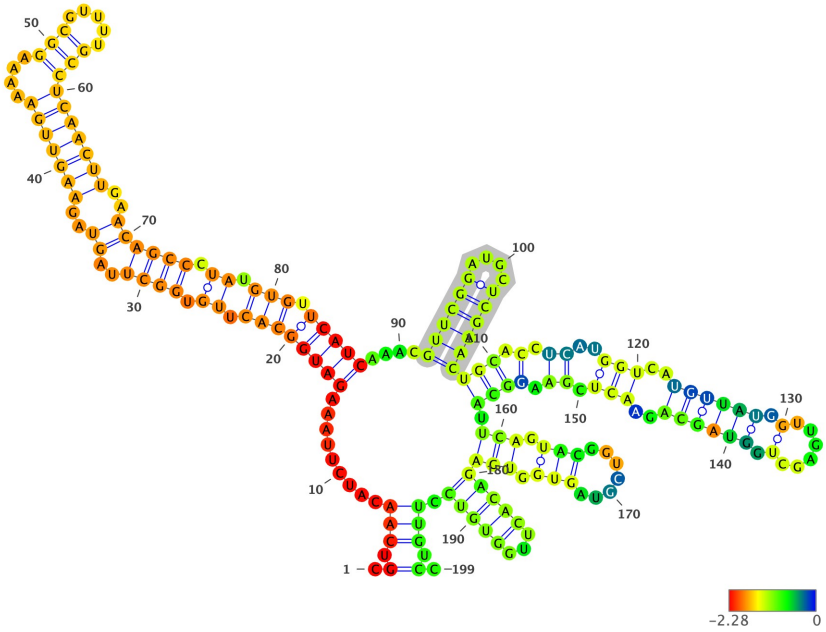
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-GUUCGGAUGCUCGAAC-3'
5'-((((((....))))))-3'
Motif MFE = -4.3; z-score = -2.57; 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 = -0.61; 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(+)

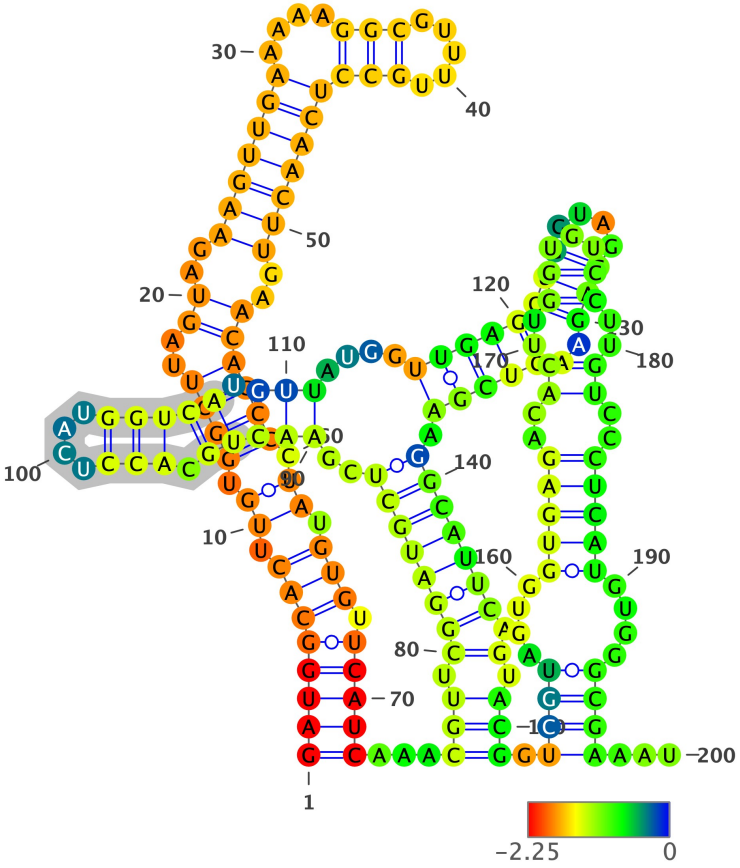
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 499 to 513 (nt 93 to 107)

```
5'-UGCACCUCAUGGUCA-3'
5'-((.(((....)))))-3'
Motif MFE = -2.2; z-score = -2.4; 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 407 to 606 (motif highlighted in silver):

```
5'-GAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUU
AUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAU-3
5'-((((((((.((.((((..((..(((((((....(((.....)))))))))..)))))).)).))).)))))...(((.((((((((..(((((.(((....)))))).)))
....((((((((....)))..)))))).))))))).).))).((((....(((((..((..((...))..))..)))))....))))...-3'
MFE = -57.6; z-score = -0.9; ED = 50.62
```

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(+)

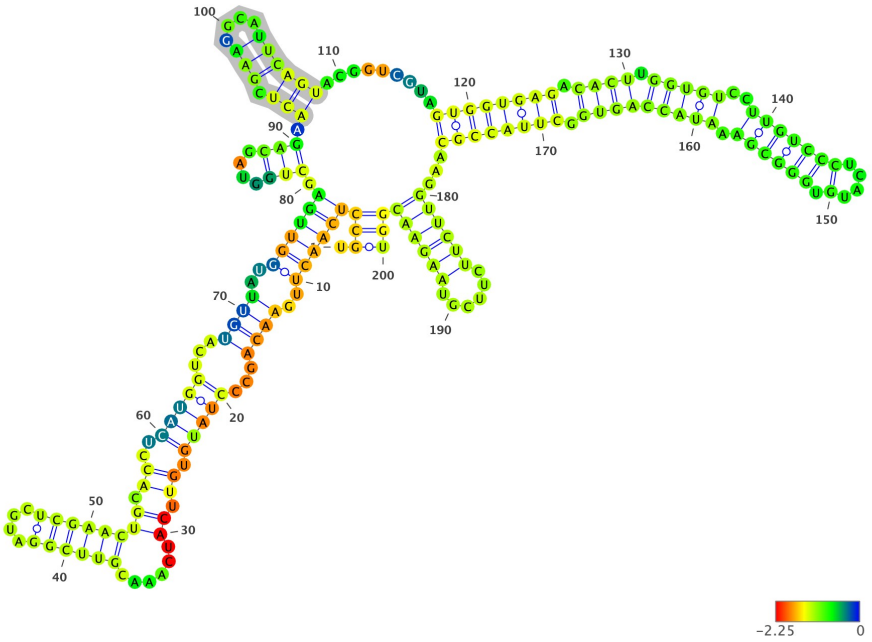
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 14 from nt 538 to 554 (nt 92 to 108)

```
5'-ACUCGAAGGCAUUCAGU-3'
5'-(((.((......)))))-3'
Motif MFE = -1.0; z-score = -0.18; 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 = -1.28; 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(+)

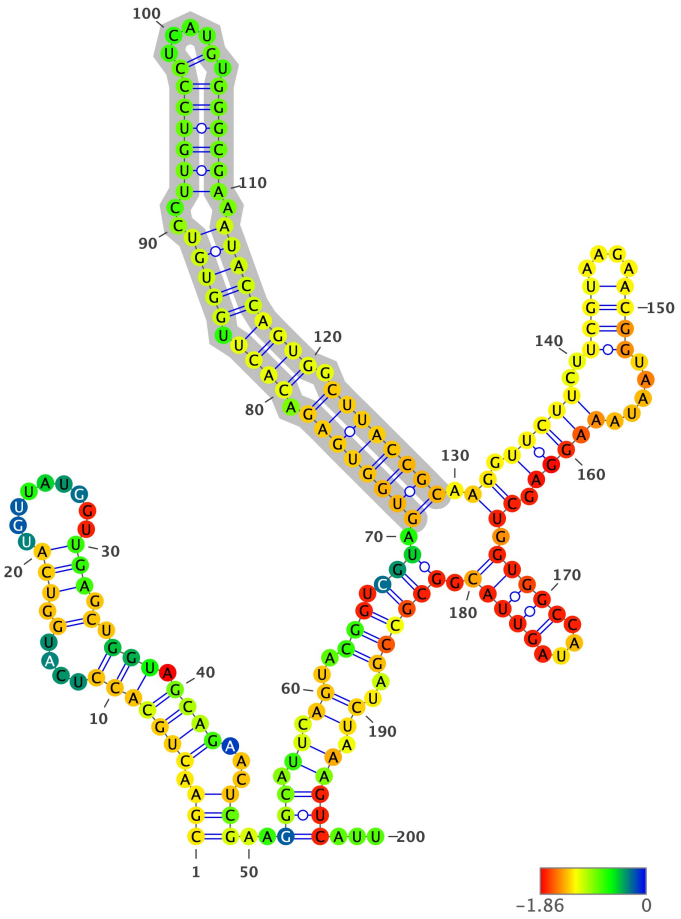
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 15 from nt 564 to 622 (nt 71 to 129)

```
5'-GUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGC-3'
5'-((((((((.((((.(((((.....................)))))))))).))))))))-3'
Motif MFE = -28.2; z-score = -3.86; 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 = -0.53; 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(+)

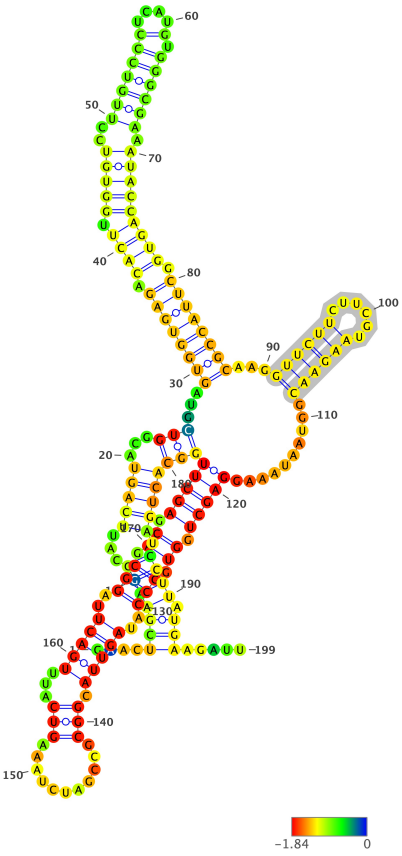
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 16 from nt 626 to 643 (nt 91 to 108)

```
5'-GUUCUUCUUCGUAAGAAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -3.27; 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 = -2.63; 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(+)

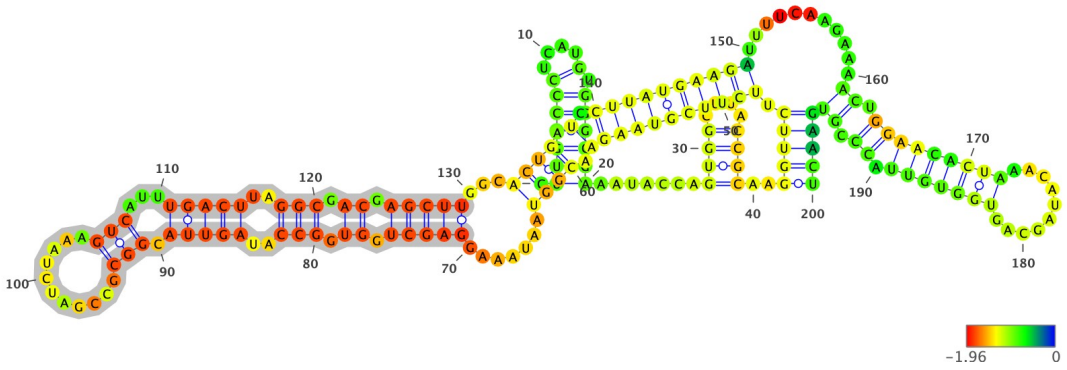
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 17 from nt 654 to 712 (nt 71 to 129)

```
5'-GAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUUAGGCGACGAGCUU-3'
5'-(((((.((.(((..(((((.(((...........)))...)))))..))).)).)))))-3'
Motif MFE = -21.7; z-score = -2.24; ED = 2.41
```



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 584 to 783 (motif highlighted in silver):

```
5'-CUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUU
GACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACU-3
5'-.(((((((....).))))))......((((....))))..(((((.(((((((((((.((((.......(((((.((.(((..(((((.(((...........)))...)
))))..))).)).)))))...)))).).))))))))))...........((.(((((((((..........)))))))).)).)))))))-3'
MFE = -56.4; z-score = -1.1; ED = 34.2
```

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(+)

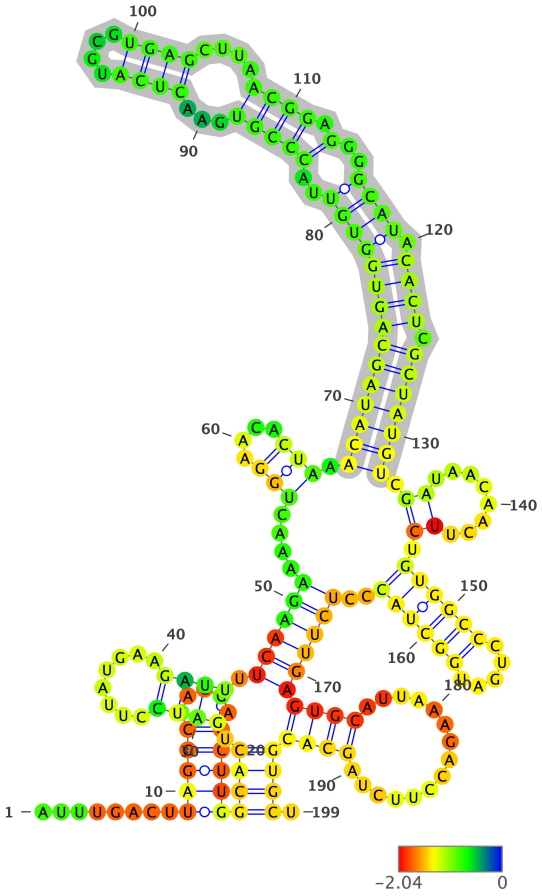
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-ACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGU-3'
5'-((((((((((.....................................))))).)))))))-3'
Motif MFE = -26.1; z-score = -2.78; 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 = -0.43; 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(+)

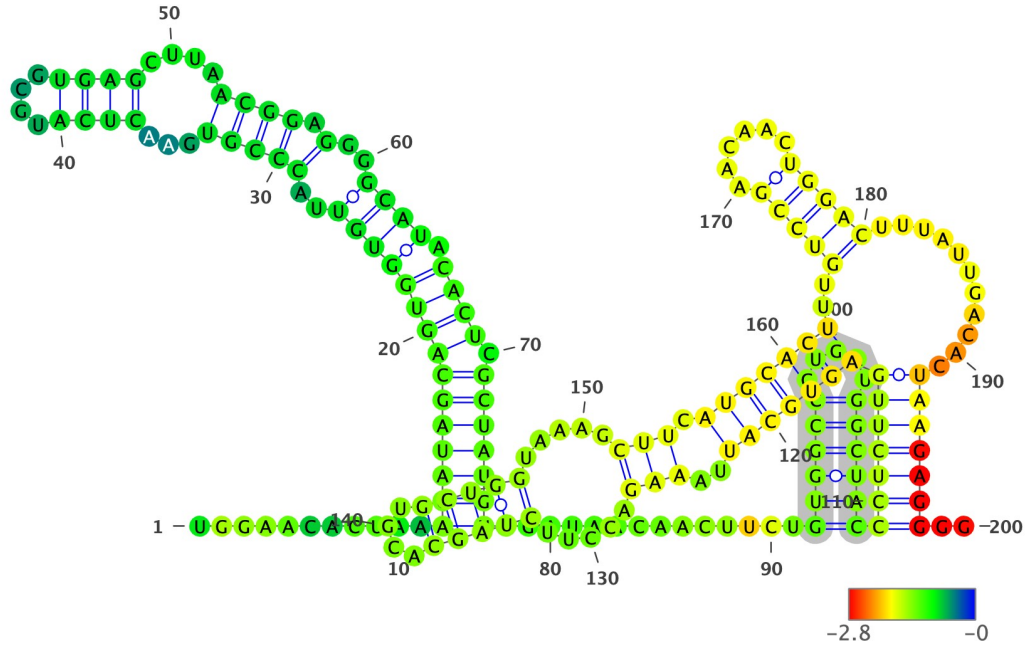
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 837 to 853 (nt 92 to 108)

```
5'-GUGGCCCUGAUGGCUAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.1; z-score = -2.82; 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 746 to 945 (motif highlighted in silver):

```
5'-UGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCU
CUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGG-3
5'-...........(((((((((((((((..((((((...((((....))))....)))))..)..))))).))))).)))))).............((((((.....))))))(((
((((((((((..(((.....(((((....)))))).....))).)))))))..(((((.....)))))).........)))))))..-3'
MFE = -63.4; z-score = -2.24; ED = 20.12
```

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(+)

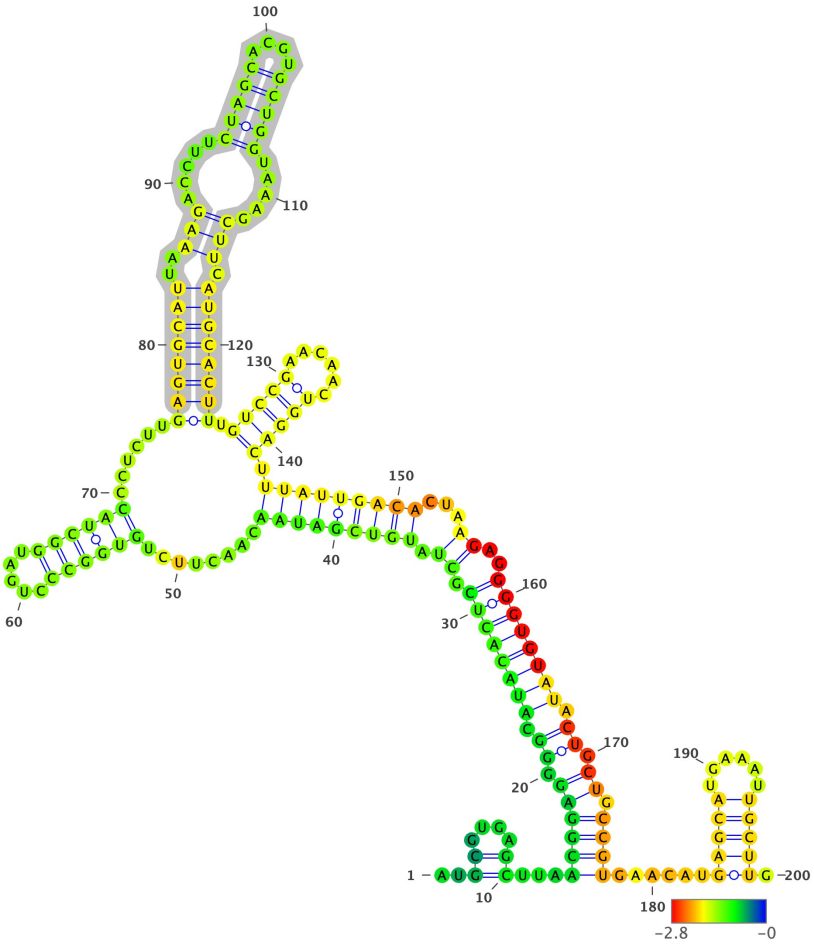
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-AGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACU-3'
5'-(((((((..(((.....(((((....)))))).....))).)))))))-3'
Motif MFE = -15.2; z-score = -3.0; 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 = -2.6; 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(+)

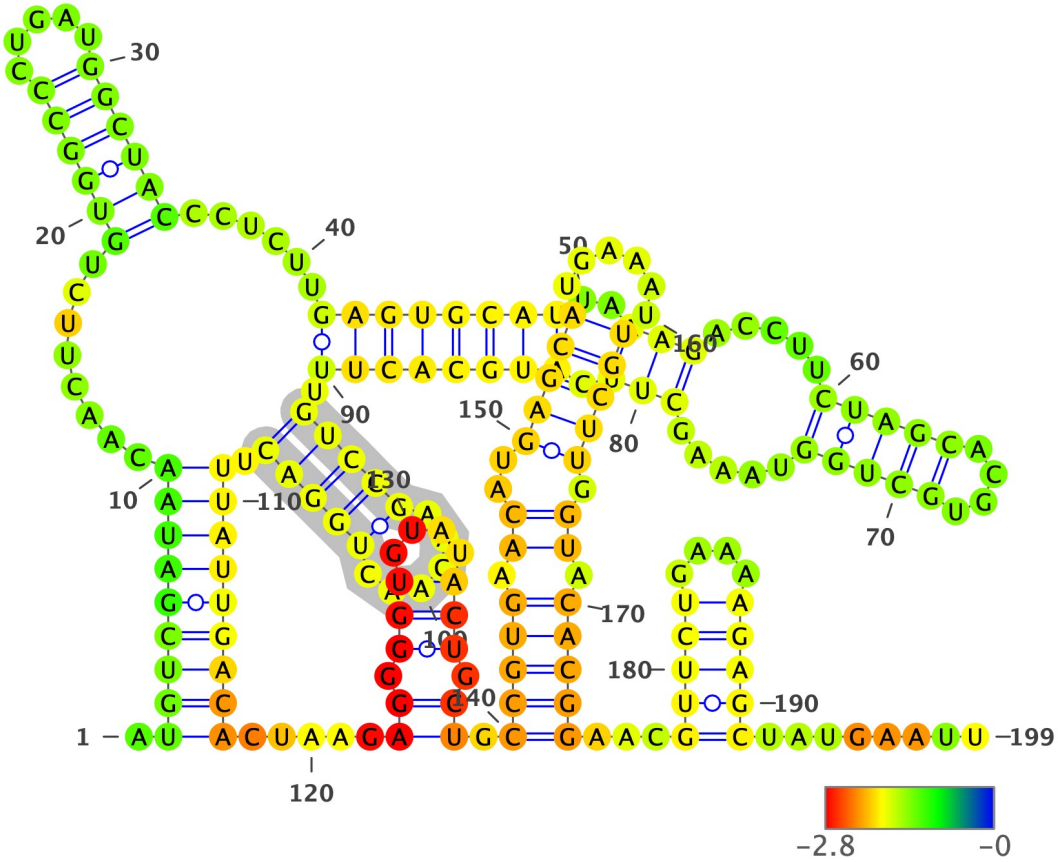
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GUCCGAACAACUGGAC-3'
5'-(((((......)))))-3'
Motif MFE = -4.4; z-score = -2.86; 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 = -2.62; 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(+)

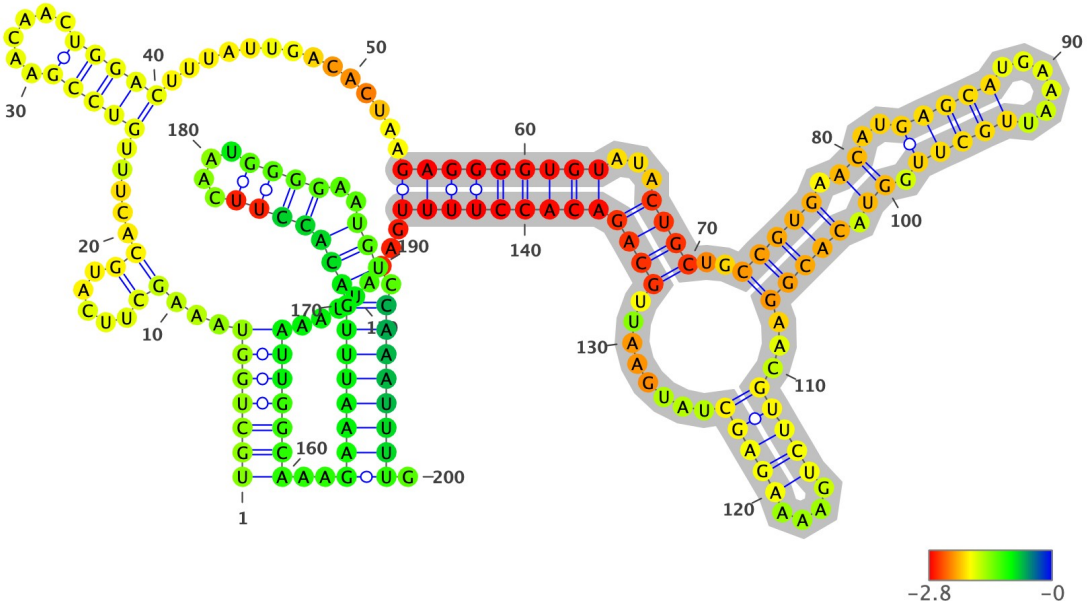
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACGUUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUU-3'
5'-(((((((((...((((..(((((.((..(((((......))))).)).)))))...(((((....)))))........)))))))))))))-3'
Motif MFE = -32.3; z-score = -3.86; 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(+)

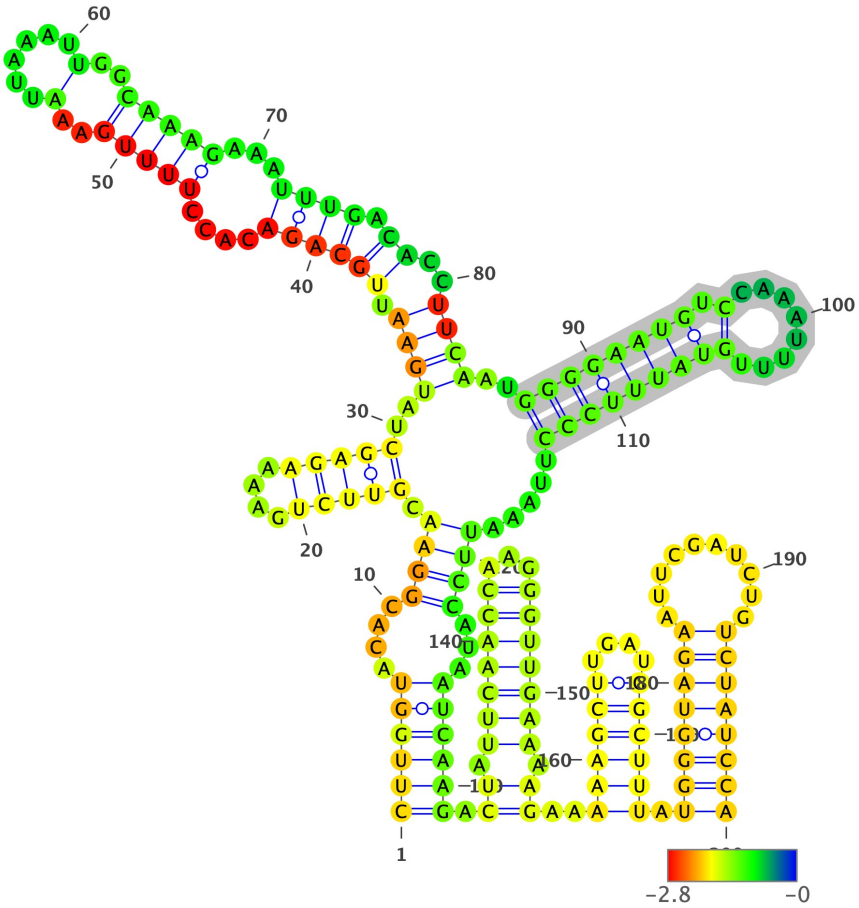
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GGGGAAUGUCCAAAUUUUGUAUUUCCC-3'
5'-((((((((.(........)))))))))-3'
Motif MFE = -6.4; z-score = -1.8; 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 = -1.84; ED = 25.17
```

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(+)

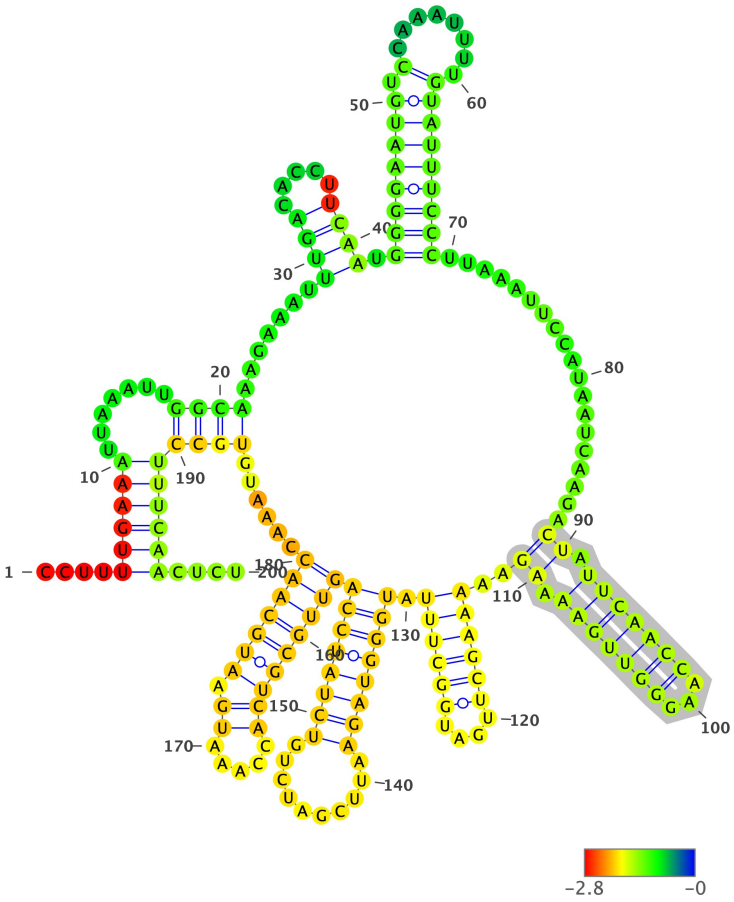
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 24 from nt 1113 to 1135 (nt 89 to 111)

```
5'-CUAUUCAACCAAGGGUUGAAAAG-3'
5'-((.(((((((...)))))))).))-3'
Motif MFE = -6.7; z-score = -4.09; ED = 1.35
```



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

Extracted structure model with flanking nucleotides 1025 to 1224 (motif highlighted in silver):

```
5'-CCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAG
AAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCU-3
5'-....((((((.......(((((.......(((((.....)))))..(((((((((.(........)))))))))..................((.(((((((...)))))))).))
..((((((....)))))).(((((((((.........)))))))))(((((((((.....)).)))))))......))))))))))....-3'
MFE = -44.8; z-score = -2.68; ED = 28.38
```

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(+)

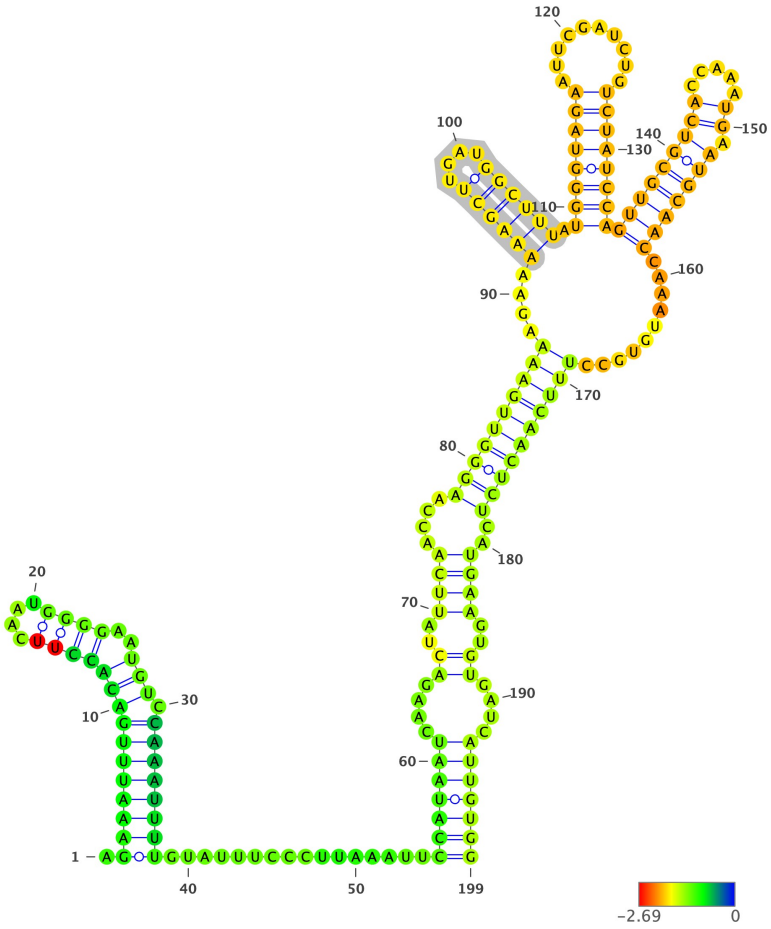
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 25 from nt 1138 to 1153 (nt 92 to 107)

```
5'-AAAGCUUGAUGGCUUU-3'
5'-((((((....))))))-3'
Motif MFE = -4.2; z-score = -5.48; 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 1047 to 1245 (motif highlighted in silver):

```
5'-AGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGGCUUUAUGG
GUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGG-3
5'-.(((((((((((((((....)))))..)))).)))))))).................(((((((....((..((((....((((((((((....((((((....)))))).(((
(((((.........)))))))))((((((((((.....)).)))))))).........))))))))))..)))))..))....)))))))-3'
MFE = -49.0; z-score = -2.16; ED = 28.22
```

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(+)

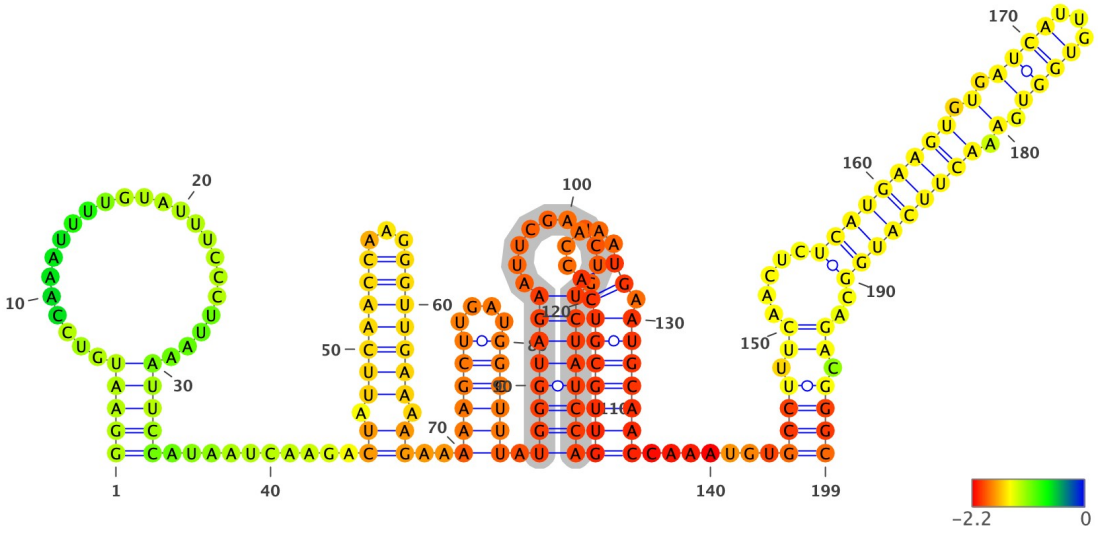
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 26 from nt 1155 to 1180 (nt 87 to 112)

```
5'-UGGGUAGAAUUCGAUCUGUCUAUCCA-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -7.4; z-score = -2.64; 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 = -1.83; 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(+)

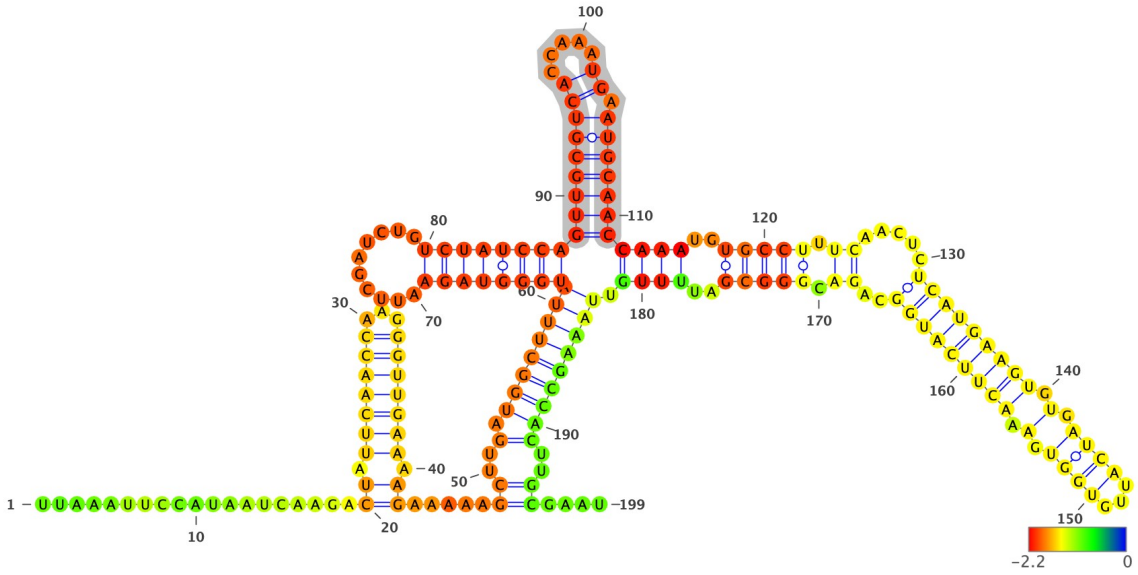
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 27 from nt 1181 to 1204 (nt 88 to 111)

```
5'-GUUGCGUCACCAAAUGAAUGCAAC-3'
5'-(((((((((.....)).)))))))-3'
Motif MFE = -6.5; z-score = -3.0; 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 = -3.34; 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(+)

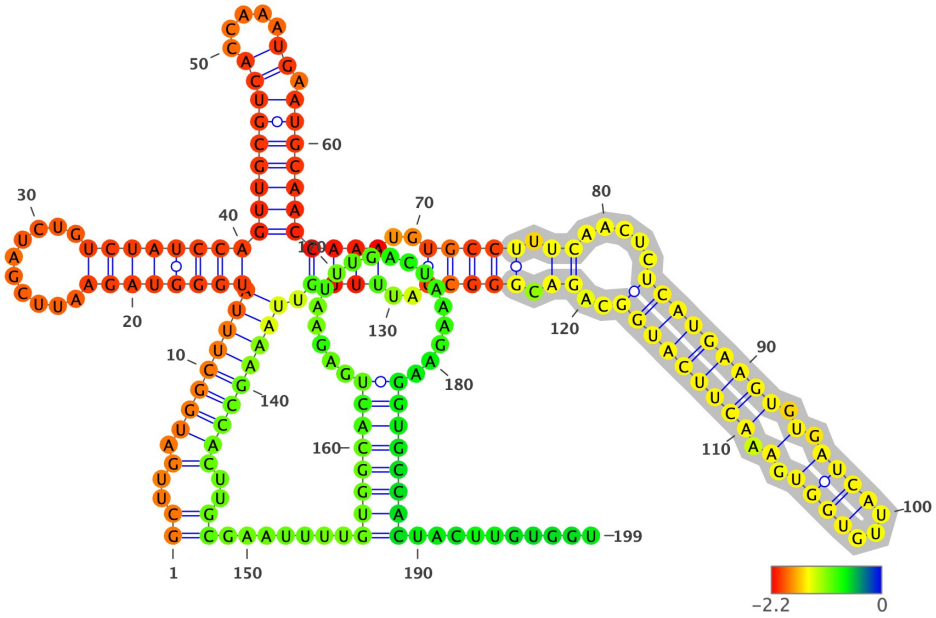
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 28 from nt 1215 to 1264 (nt 75 to 124)

```
5'-UUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACG-3'
5'-(.((.....((((((((((.(.((((...)))).).)))))))))..)).)-3'
Motif MFE = -13.6; z-score = -1.99; ED = 3.26
```



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 1141 to 1339 (motif highlighted in silver):

```
5'-GCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAAC
UUCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGU-3
5'-((..(.(((((((((((((((((.........))))))))(((((((((.....)).)))))))((((..(((((.((.....((((((((((.(.((((...)))).).))
)))))))..)).)))))..)))).))))))))))..)).......((((((((.................))))))))..........-3'
MFE = -62.3; z-score = -3.36; ED = 10.21
```

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, 266-13468(+)

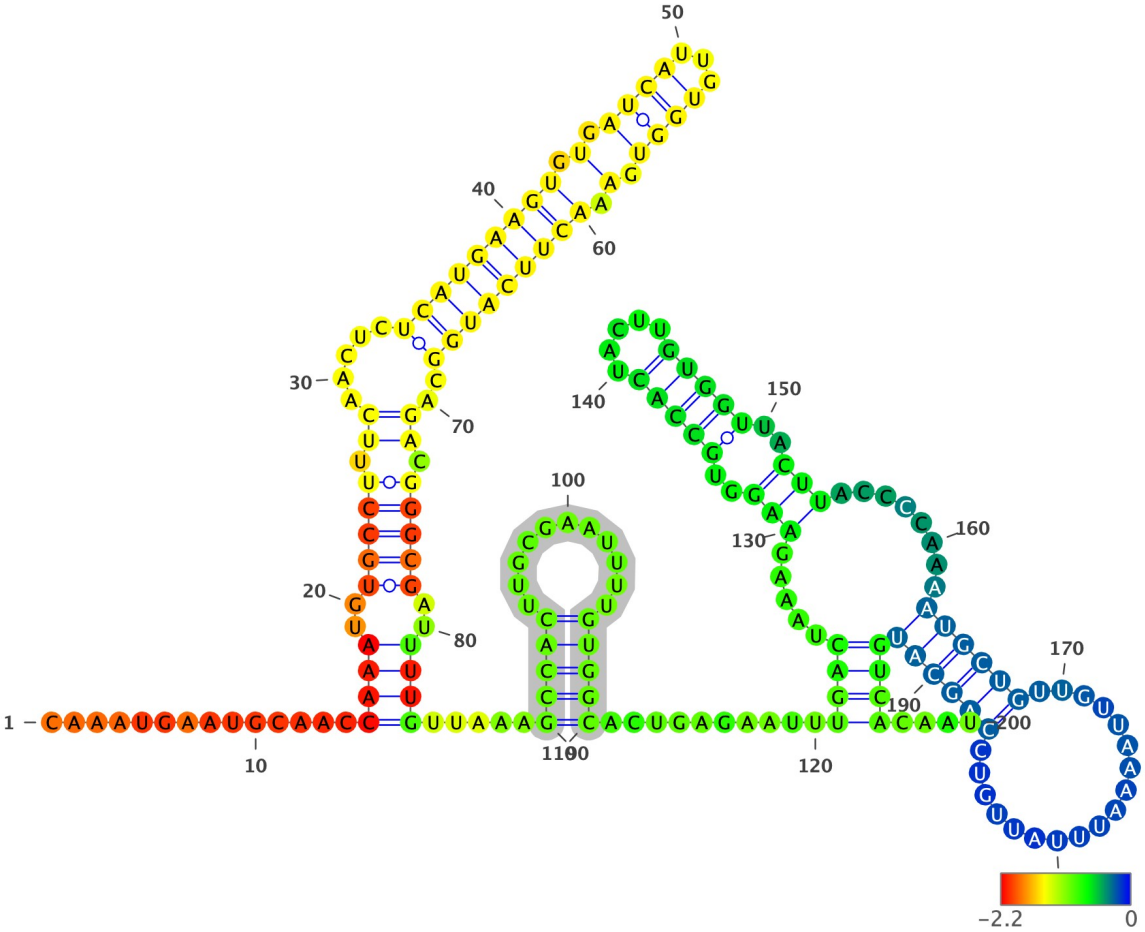
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 29 from nt 1280 to 1300 (nt 90 to 110)

```
5'-GCCACUUGCGAAUUUUGUGGC-3'
5'-(((((...........)))))-3'
Motif MFE = -6.5; z-score = -2.27; 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 = -0.71; 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(+)

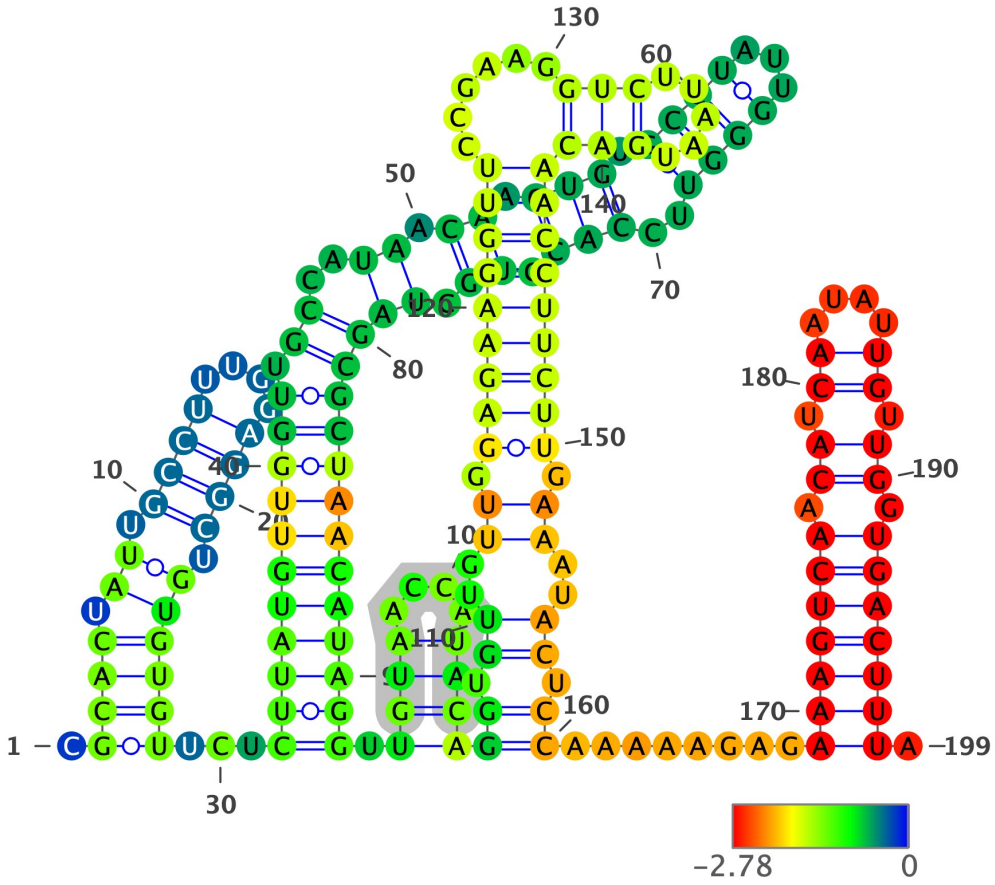
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 30 from nt 1563 to 1572 (nt 95 to 104)

```
5'-GUAACCAUAC-3'
5'-(.(....).)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 1469 to 1667 (motif highlighted in silver):

```
5'-CGCACUAUUGCCUUUGGAGGCUGUGUGUUCUCUUAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUU
GUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUA-3
5'-.((((.((.((((....)))).))))))...(((((((((((.((..((.((.(((.((((...))))..))).)).))))))))))))))).((((....))))((.((.
.((.((((((((.......(((.....)))))))))))).))..)).)).........(((((((.((.((....)).)).)))))))).-3'
MFE = -56.0; z-score = -2.29; ED = 24.02
```

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

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

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

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

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

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

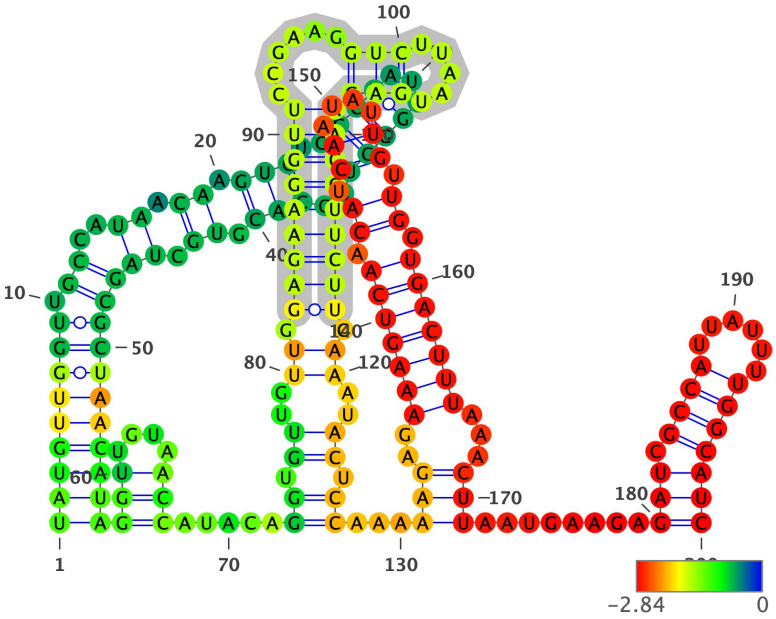
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 31 from nt 1584 to 1618 (nt 83 to 117)

```
5'-GAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUU-3'
5'-((((((((((......(((.....)))))))))))))-3'
Motif MFE = -10.8; z-score = -2.69; 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 1502 to 1701 (motif highlighted in silver):

```
5'-UAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAAC
CUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUC-3
5'-((((((((((.((..((.((.(((.((((...)))))..))).)).)))))))))))))))(((....))))).....((.((..((.((((((((((......(((.....)))))))
))))))).))..)).))...(((..(((((((.((.((....)).)).)))))))...))).........(((.((((......)))))))-3'
MFE = -51.5; z-score = -2.35; ED = 26.58
```

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(+)

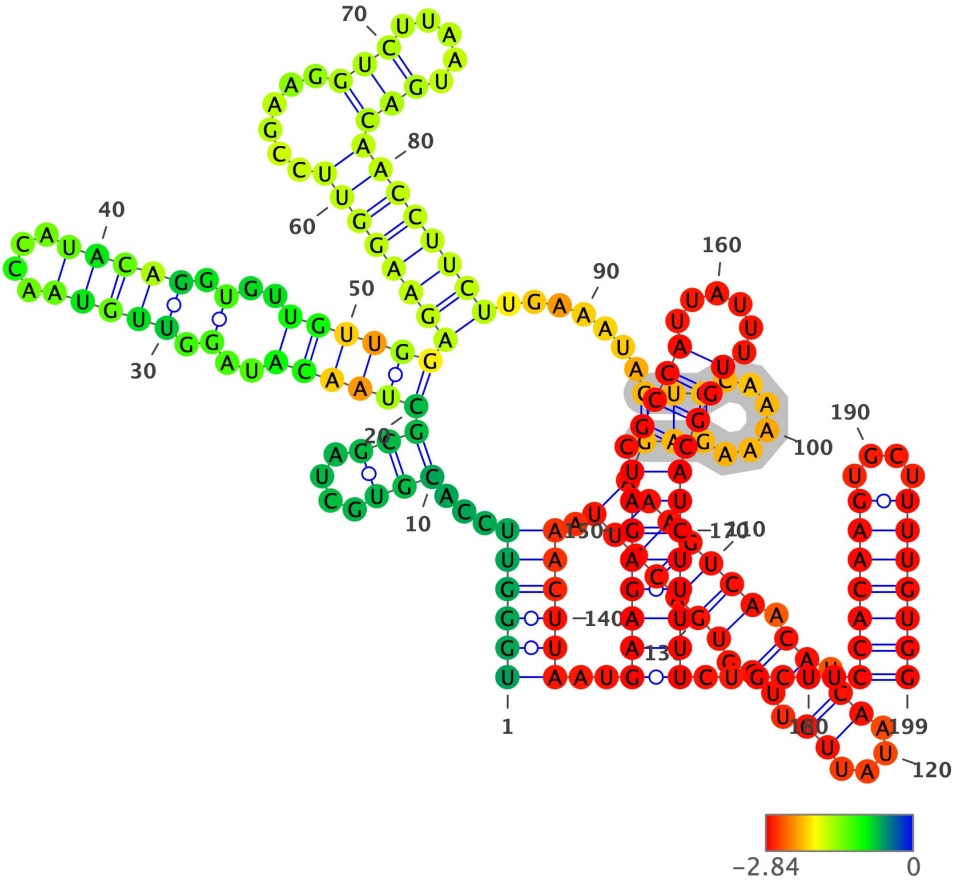
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-CUCCAAAAAGAG-3'
5'-(((.....)))-3'
Motif MFE = -0.1; z-score = -0.37; 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 = -2.51; 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(+)

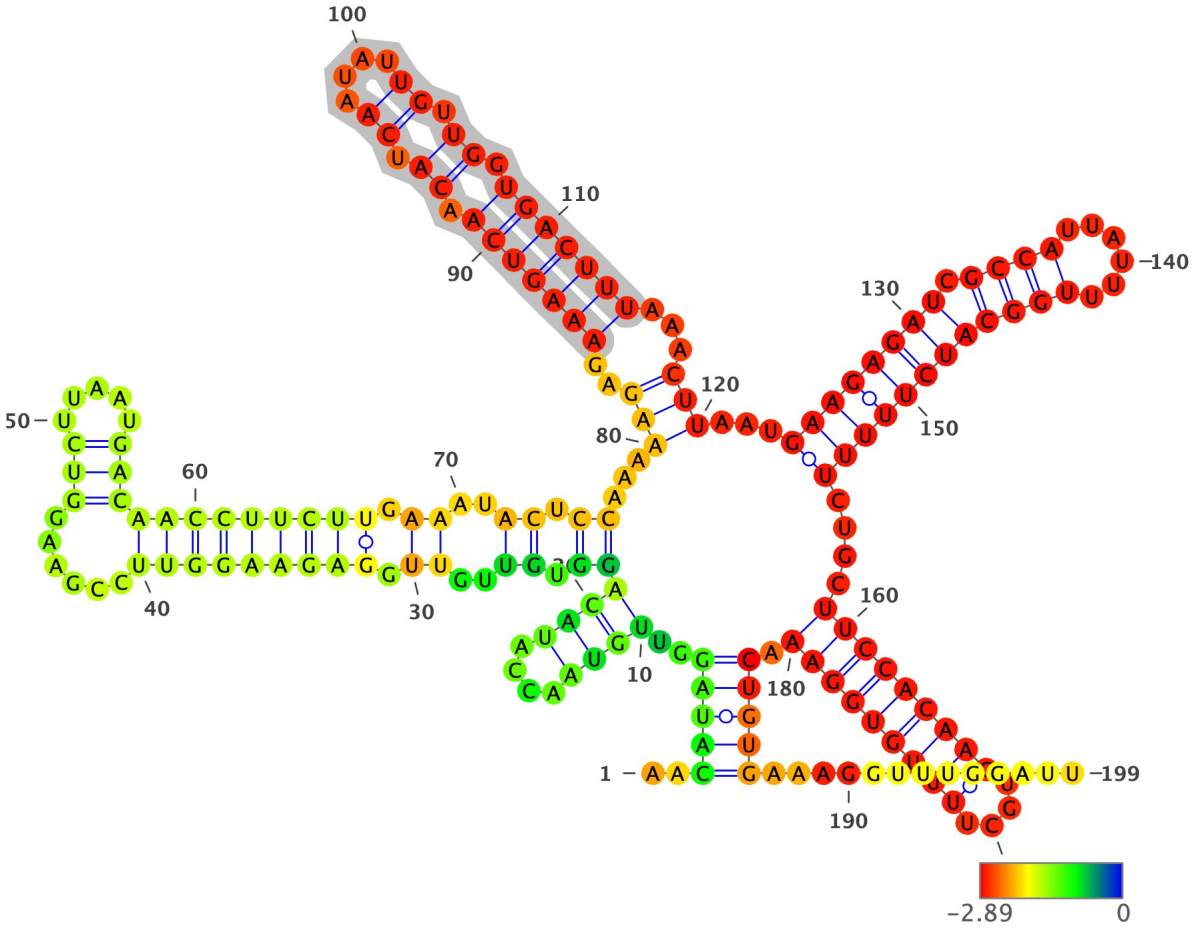
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-AAAGUCAACAUCAAUAUUGUUGGUGACUUU-3'
5'-(((((((.((.((....)).)).)))))))-3'
Motif MFE = -7.2; z-score = -3.24; 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 = -3.63; 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(+)

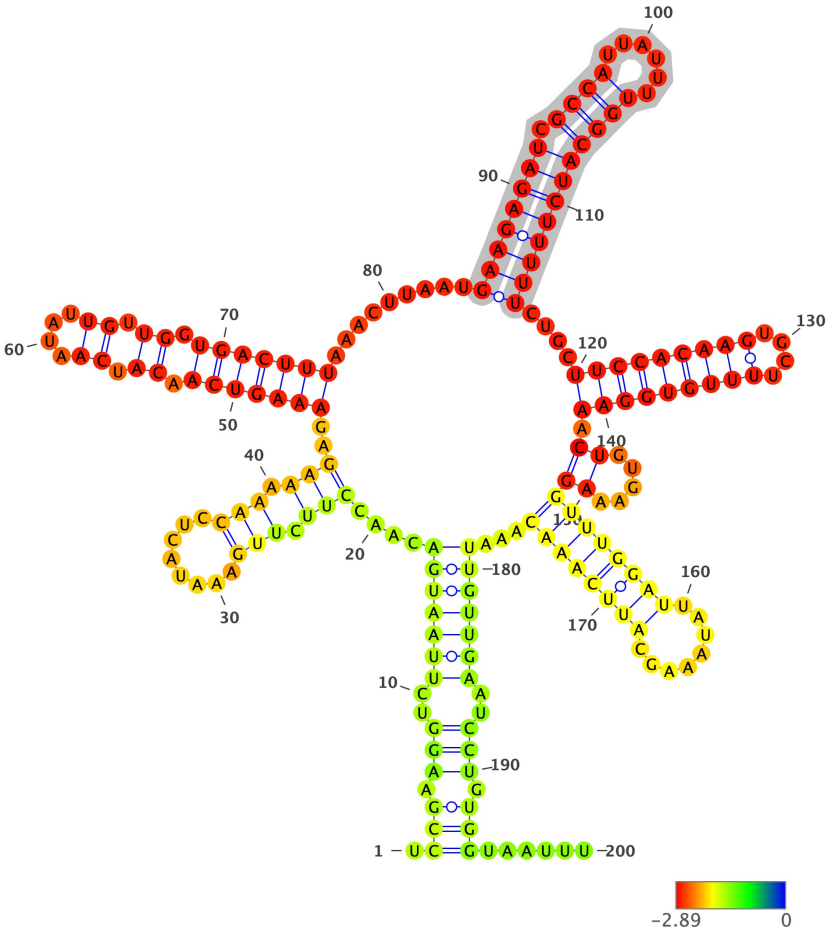
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GAAGAGAUCGCCAUUAUUUUGGCAUCUUUUU-3'
5'-((((((((.((((......)))))))))))-3'
Motif MFE = -12.1; z-score = -4.81; 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 = -2.52; 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(+)

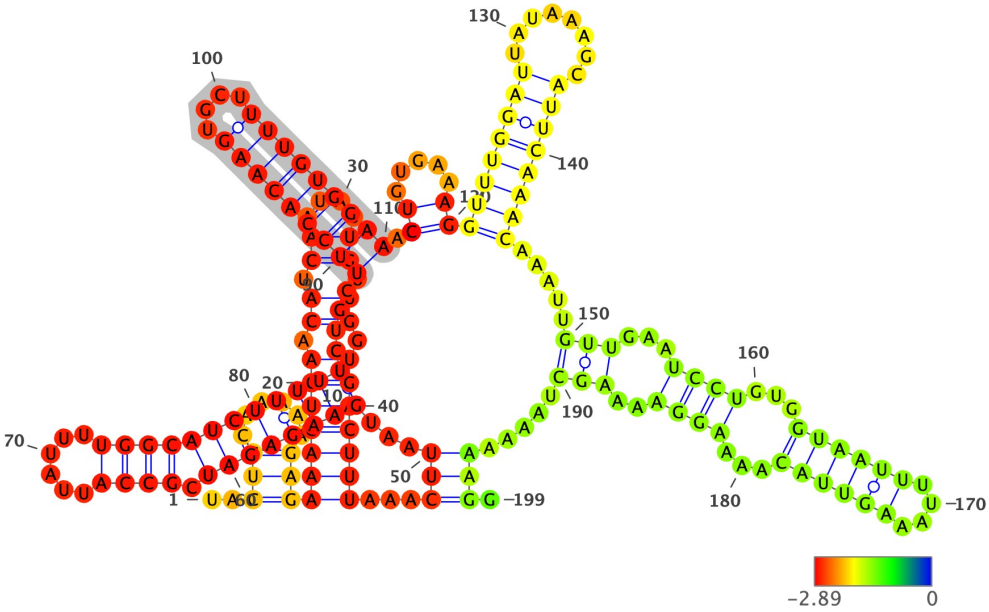
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-UUCCACAAGUGCUUUUGUGGAA-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -9.5; z-score = -5.0; 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 = -2.82; 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(+)

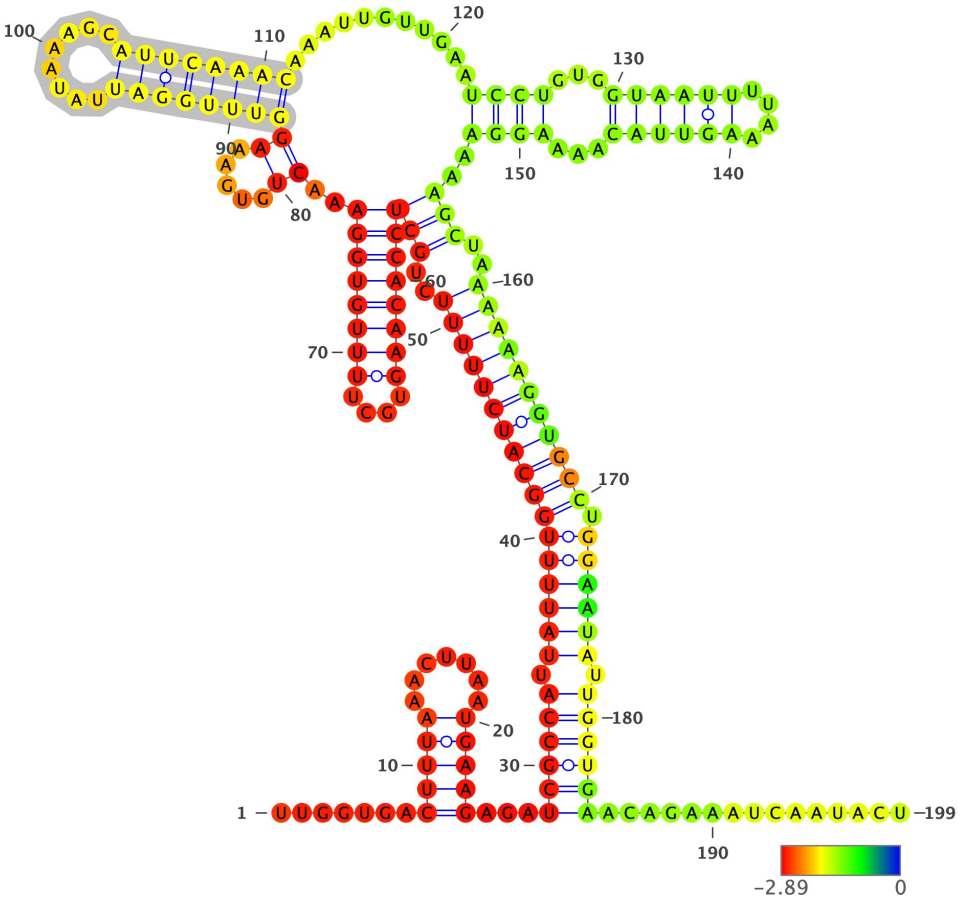
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GUUUGGAUUAUAAAGCAUUCAAAC-3'
5'-(((((((.......)))))))-3'
Motif MFE = -4.6; z-score = -2.35; ED = 0.53
```



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

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

```
5'-UUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAAC
AAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACU-3
5'-.......(((((.......)))))...((((((.(((((((((((((((..(((((((((((....)))))))))..((.....))(((((((.........)))))))).
..........((((...((((((....))))))...))))..))))..)))))))))))).)))))).)))))).............-3'
MFE = -55.0; z-score = -3.72; 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(+)

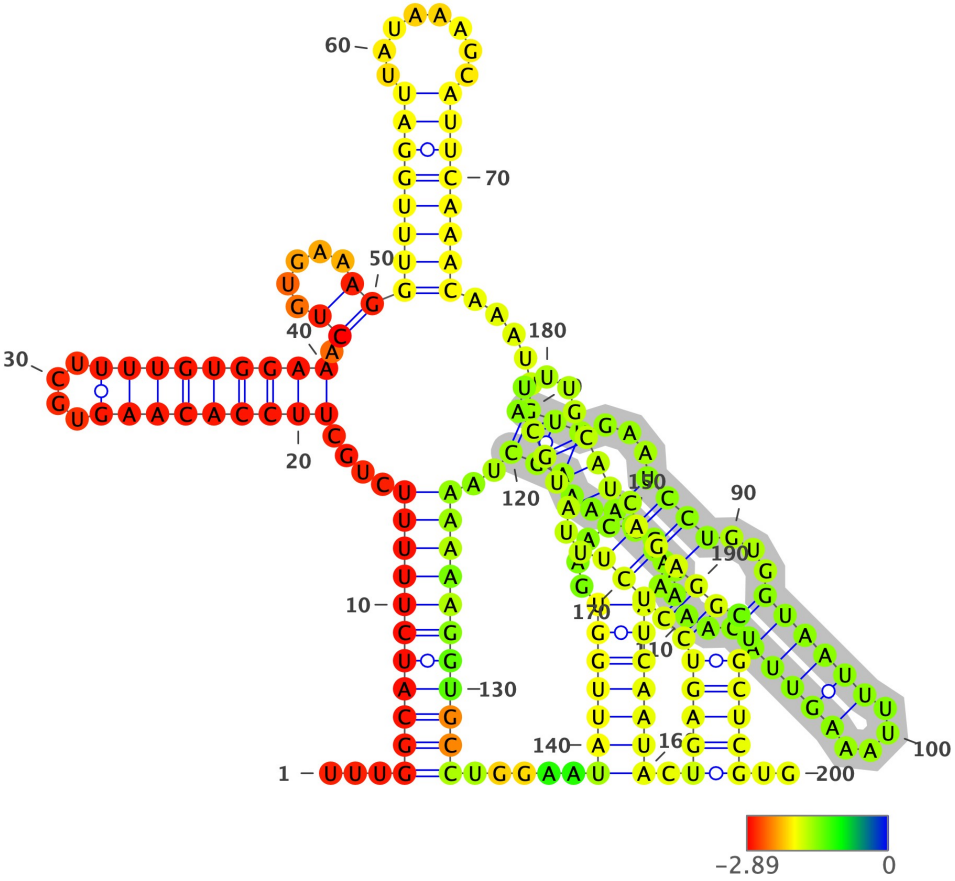
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-GUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGC-3'
5'-(((...(((((...((((((....)))))))...)))))..)))-3'
Motif MFE = -8.2; z-score = -2.69; 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 = -4.12; 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']

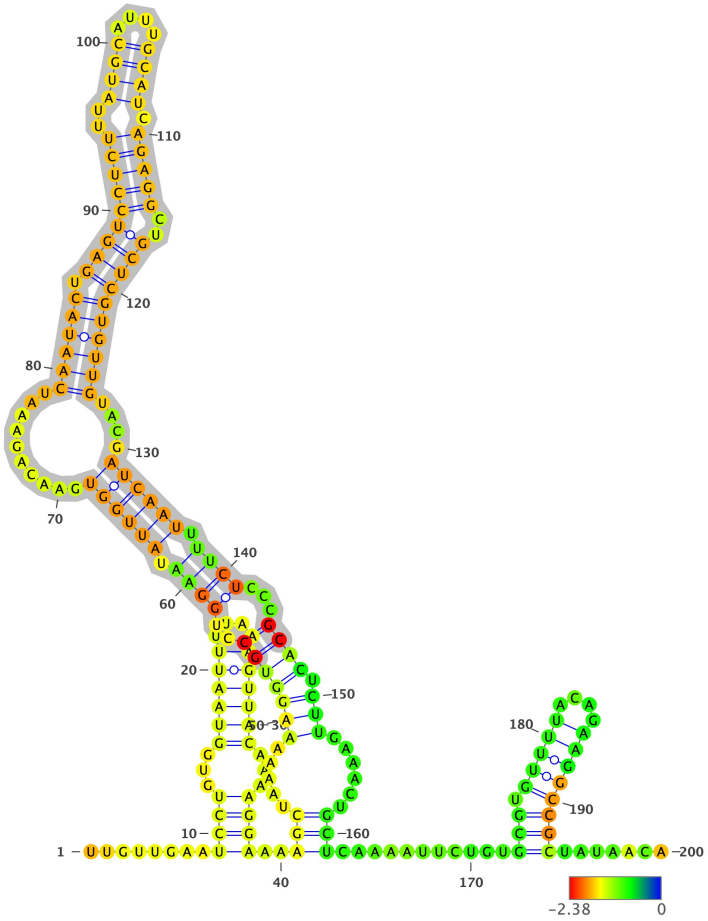
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

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'-GCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGC-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 = -2.09; ED = 23.62
```

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(+)

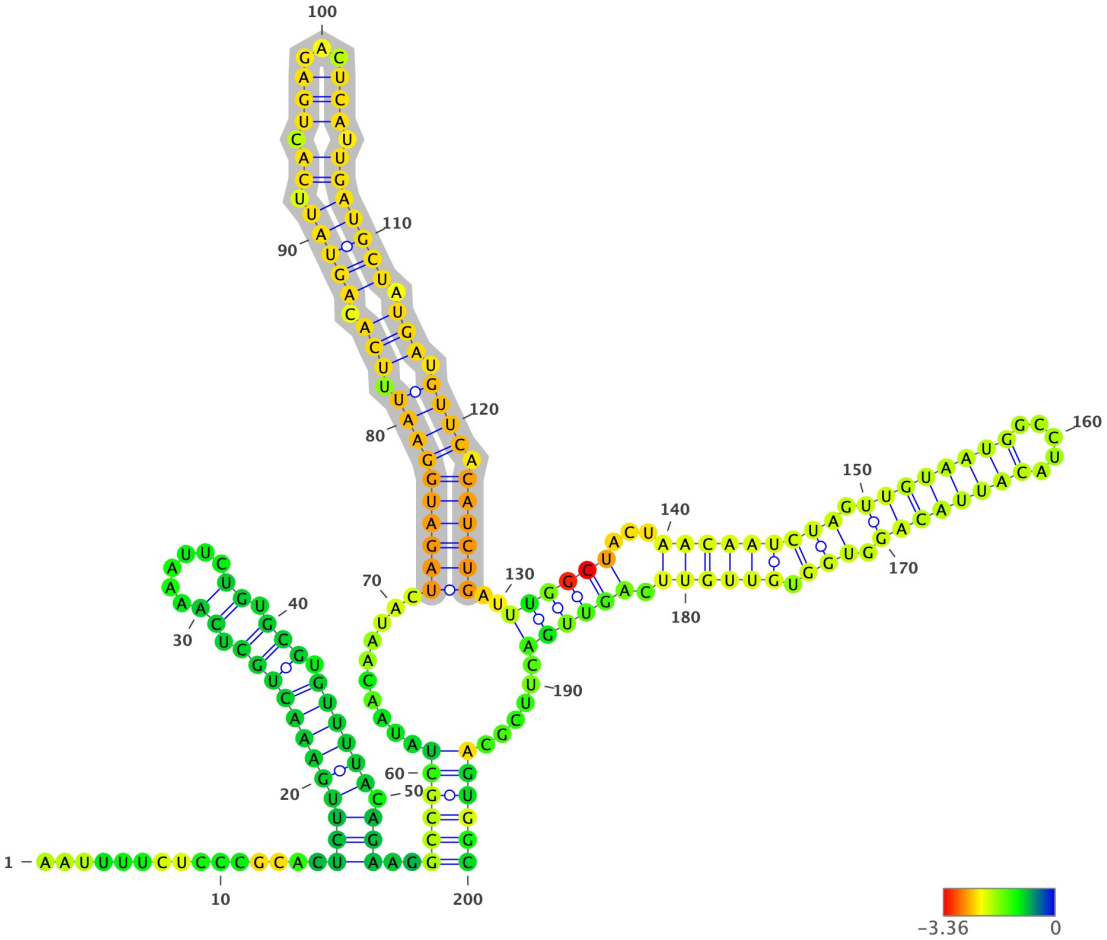
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 39 from nt 1974 to 2030 (nt 72 to 128)

```
5'-UAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUG-3'
5'-((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).))))))-3'
Motif MFE = -17.5; z-score = -3.39; 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 = -2.09; 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(+)

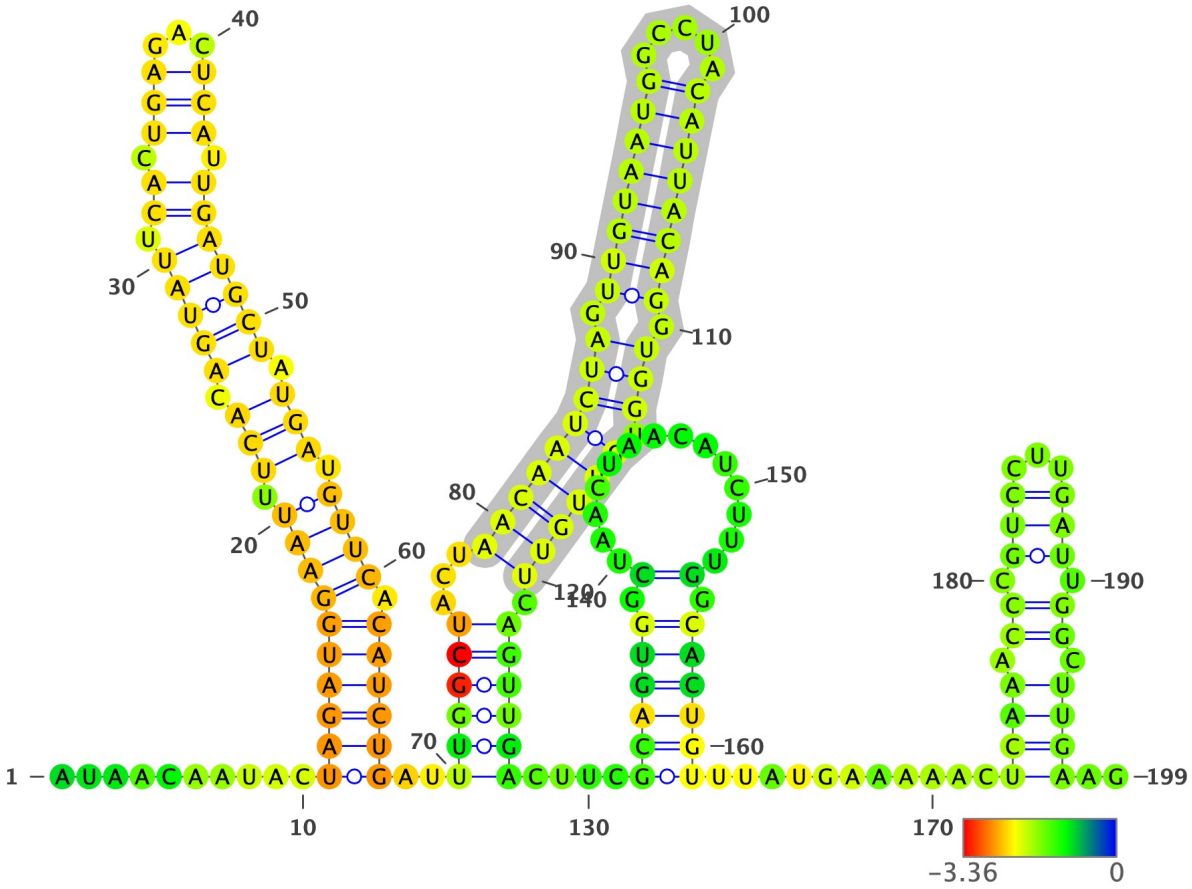
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 40 from nt 2042 to 2083 (nt 79 to 120)

```
5'-AACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUU-3'
5'-(((((((((.((((((((.....)))))))).))).))))))-3'
Motif MFE = -15.6; z-score = -3.94; 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 = -2.63; 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(+)

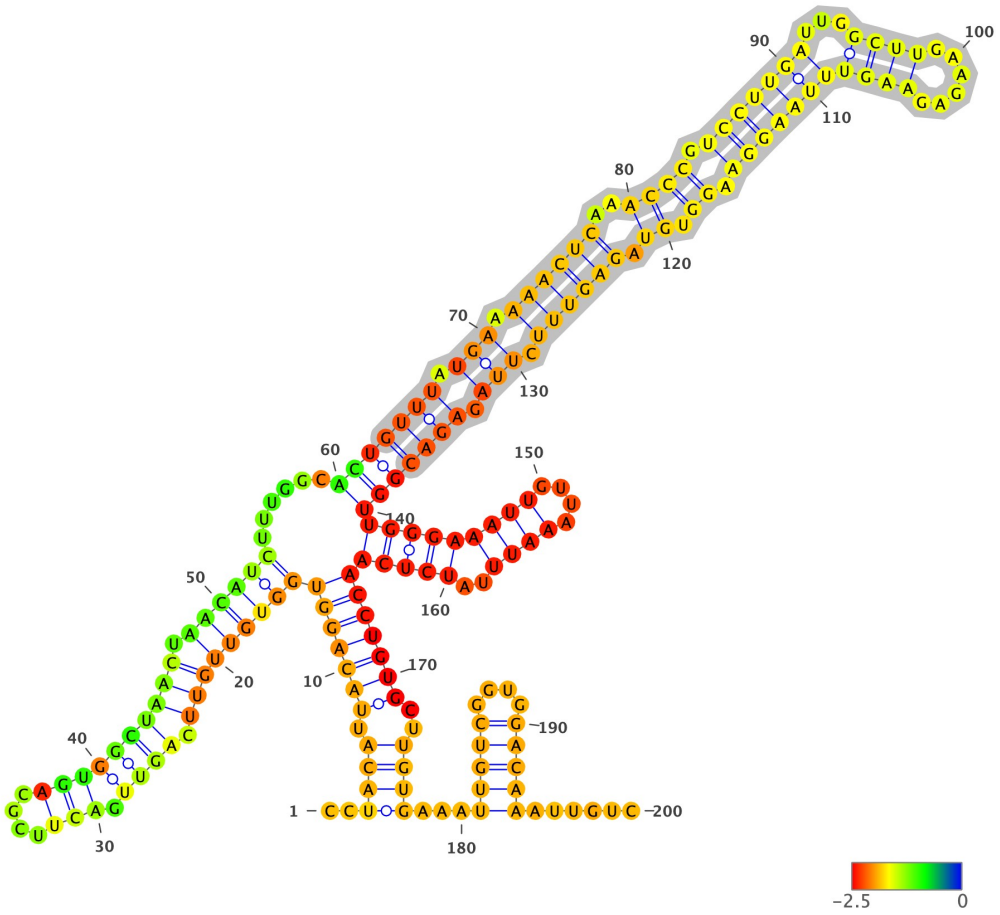
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 41 from nt 2123 to 2197 (nt 63 to 137)

```
5'-GUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGAC-3'
5'-((((..((.((((((..((((.(((((((...((((......)))))))))))).)).)).))))))).))..))))-3'
Motif MFE = -20.3; z-score = -3.65; ED = 10.26
```



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 2061 to 2260 (motif highlighted in silver):

```
5'-CCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUA
AGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUC-3
5'-..((((.((((((((((((((((.((((.(((....)))))))))).))))))......(((((((.(((.((((((..((((.(((((((...((((......)))))))
))))).)).)).)))))).))).)))))))((((((((....))))..))))))))))))..))))...(((((....)))))......-3'
MFE = -54.3; z-score = -1.75; ED = 40.72
```

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(+)

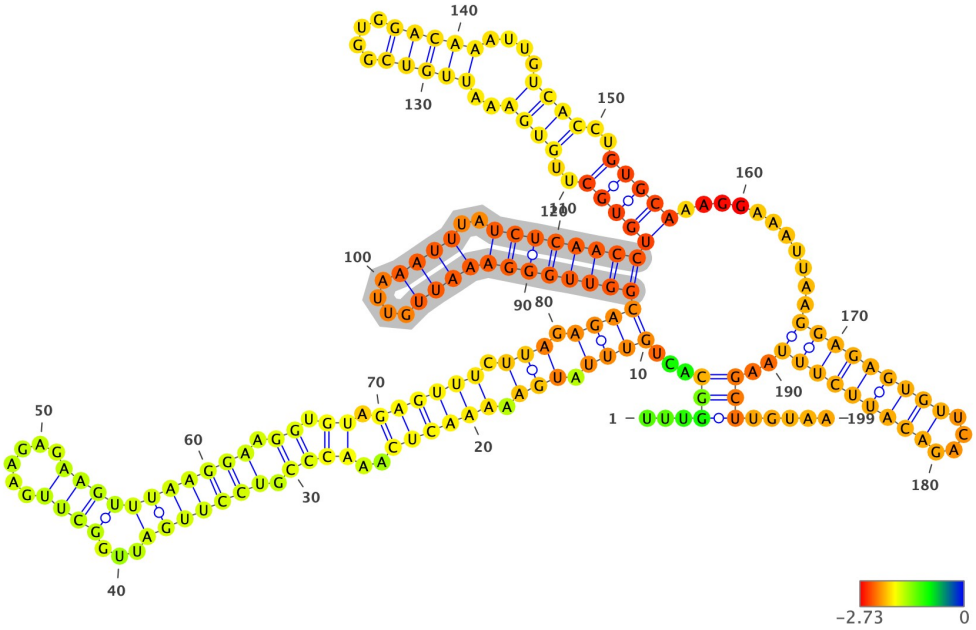
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 42 from nt 2198 to 2227 (nt 85 to 114)

```
5'-GGUUGGGAAAUUGUUAAAUUUAUCUCAACC-3'
5'-(((((((((((((....))))..))))))))-3'
Motif MFE = -9.5; z-score = -3.83; 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 = -3.45; 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(+)

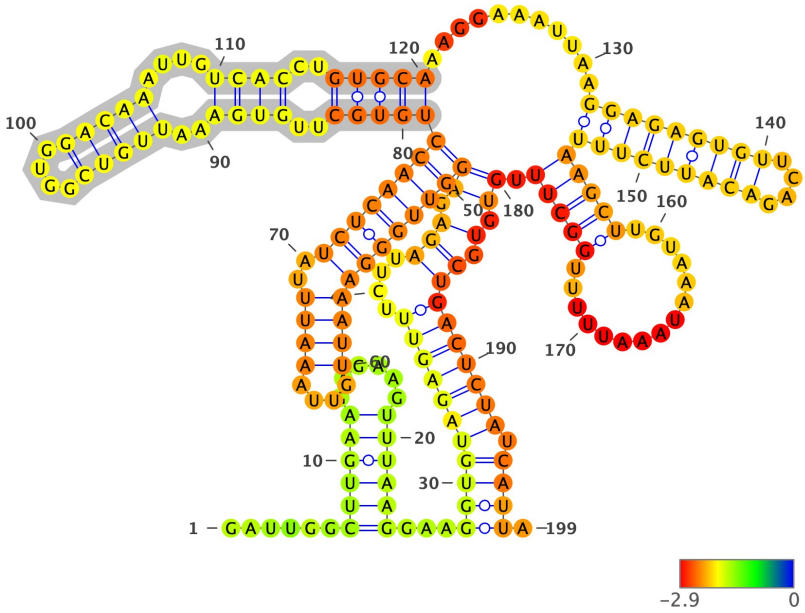
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 43 from nt 2228 to 2269 (nt 79 to 120)

```
5'-UGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCA-3'
5'-((((((..((((..(((((....)))))....))))).))))))-3'
Motif MFE = -13.1; z-score = -2.87; 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 = -1.79; 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(+)

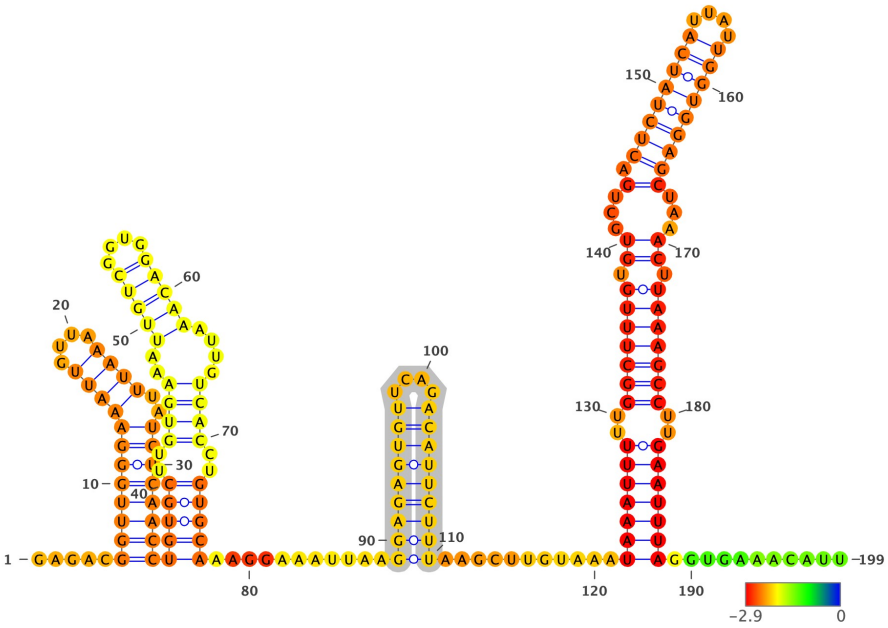
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 44 from nt 2281 to 2302 (nt 89 to 110)

```
5'-GGAGAGUGUUCAGACAUUCUUU-3'
5'-((((((((((....)))))))))-3'
Motif MFE = -6.9; z-score = -3.12; 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 = -3.97; 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(+)

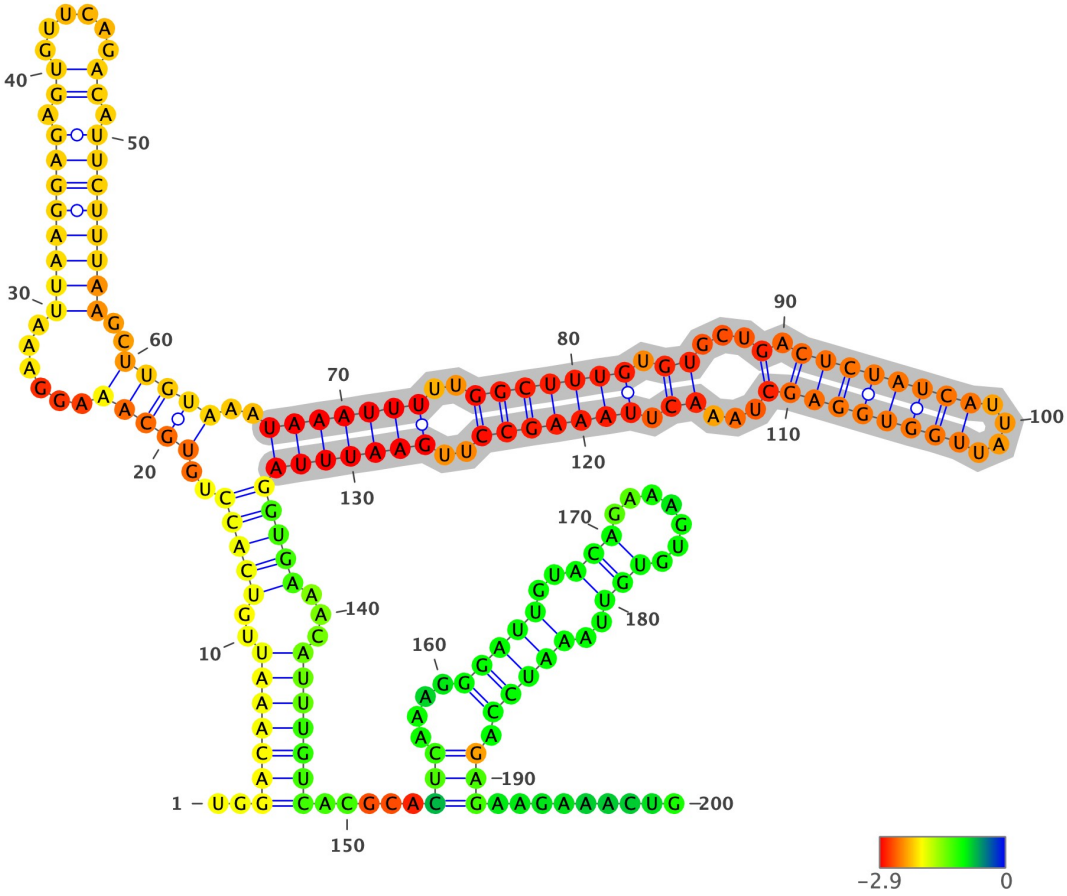
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 45 from nt 2314 to 2380 (nt 67 to 133)

```
5'-UAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUA-3'
5'-(((((((..(((((((.((...(.((((((((....)))))))))...)).)))))))..)))))))-3'
Motif MFE = -24.1; z-score = -5.12; ED = 2.11
```



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

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

```
5'-UGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGC
UAAACUUAAAGCCUUGAAUUUAGGUGAAACAUUUGUCACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUG-3
5'-..(((((((..(((((..(((((......((((((((.((......)).))))))))..)))))..(((((((..(((((((.((...(.((((((((....)))))))))
...)).)))))))..))))))))))))...)))))))).....(((....(((((..(((.......)))..)))))).)))..........-3'
MFE = -52.5; z-score = -2.81; 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(+)

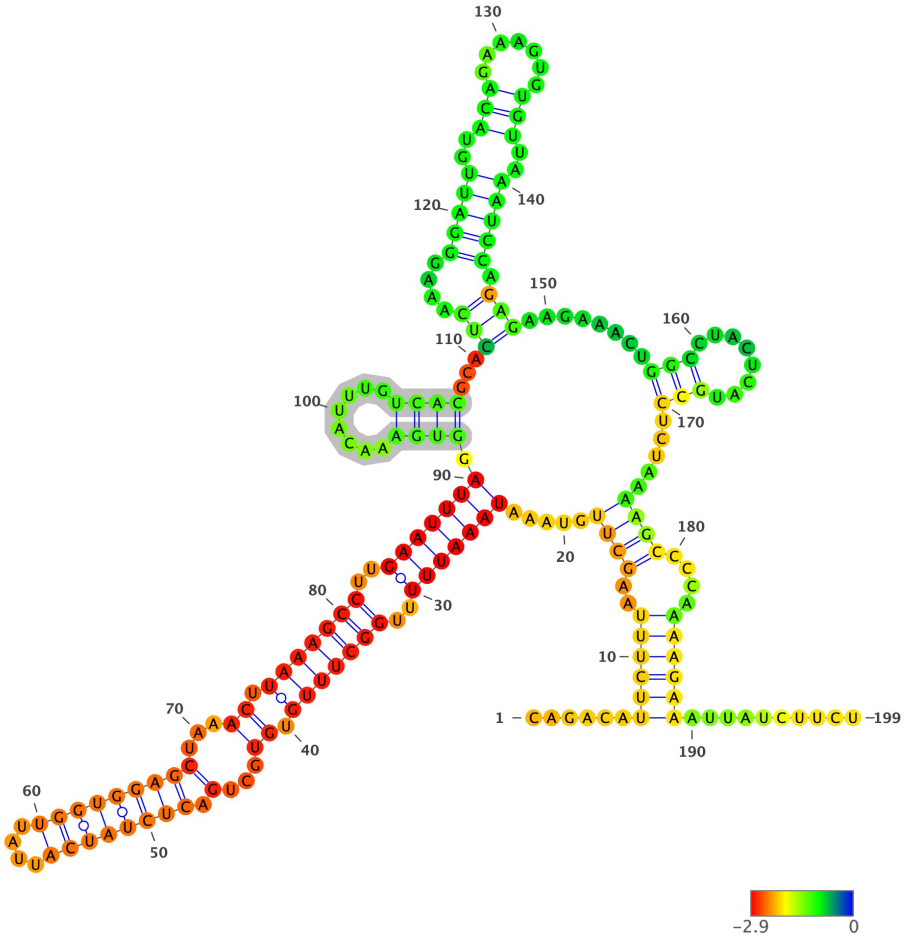
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 46 from nt 2382 to 2397 (nt 92 to 107)

```
5'-GUGAAACAUUUGUCAC-3'
5'-((((........))))-3'
Motif MFE = -1.5; z-score = -2.18; 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 = -2.17; ED = 17.47
```

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

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

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

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

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

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

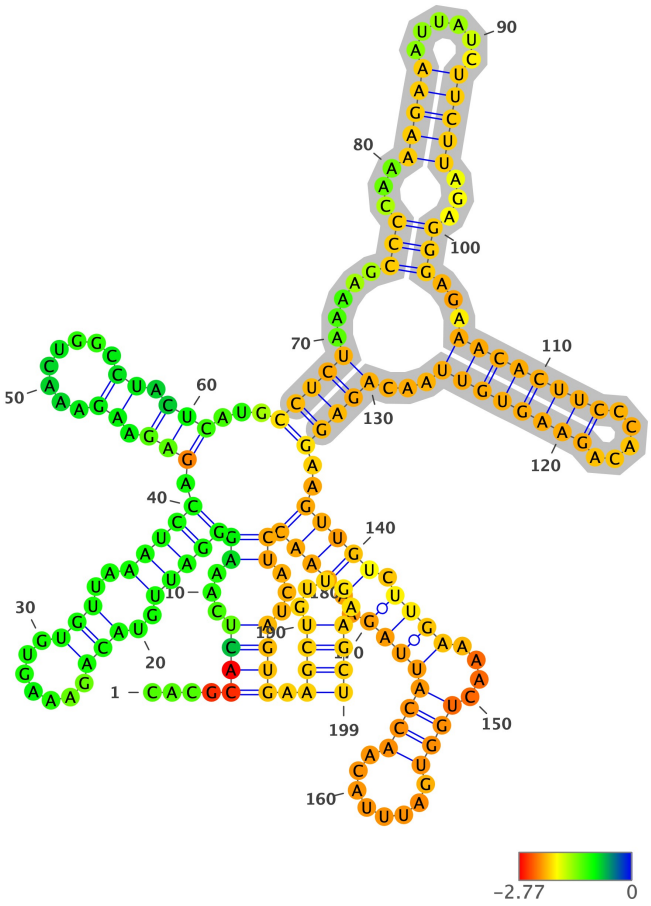
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 47 from nt 2460 to 2527 (nt 66 to 133)

```
5'-CUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAG-3'
5'-((.......(((...(((((.....)))))...)))...((((((((.....)))))))).....))-3'
Motif MFE = -15.5; z-score = -3.3; ED = 7.17
```



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 2395 to 2593 (motif highlighted in silver):

```
5'-CACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACU
UCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCU-3
5'-....((((...(((((((..(((.......)))..))))).(((.((........)).)))...(((((.....(((...(((((.....)))))...)))...((((((
((.....))))))))...)))))..(((((.((((....((((........))))))))).)))))))...)))).((((.....))))-3'
MFE = -45.3; z-score = -1.92; ED = 14.01
```

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(+)

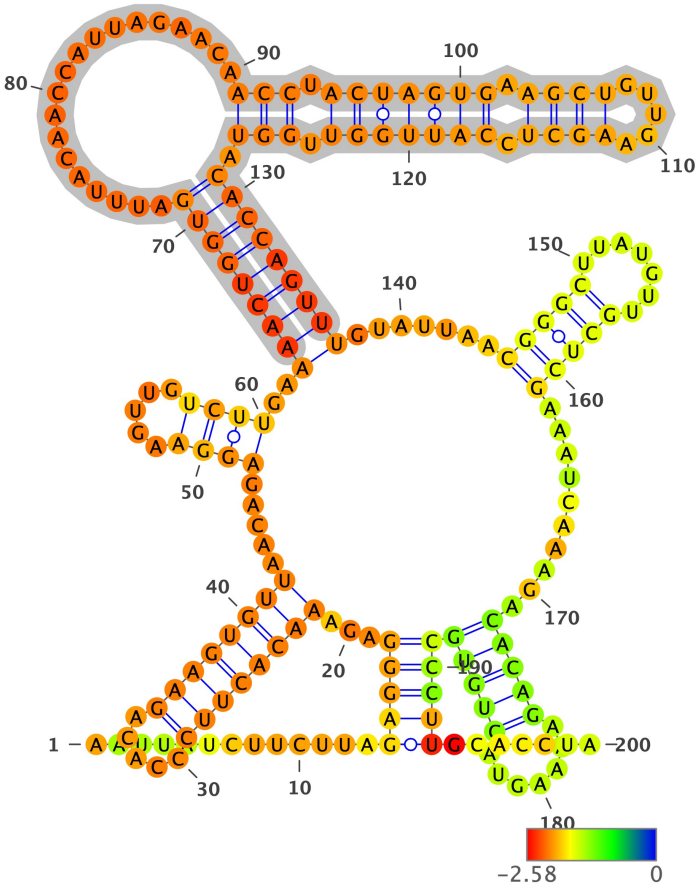
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 48 from nt 2542 to 2614 (nt 64 to 136)

```
5'-AACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUU-3'
5'-((((.......................(((.(((((((.((((.....)))).)))))))).)))).....))))-3'
Motif MFE = -23.3; z-score = -4.07; ED = 8.57
```



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 2479 to 2678 (motif highlighted in silver):

```
5'-AAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGA
AGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUA-3
5'-.............(((((...((((((((.....))))))))).....((((.....)))).((((((((((.....................(((.(((((((.((((.....
)))).)))))))).))).))))))))).......(((((.......)))))..........(((((.......))))))))))).......-3'
MFE = -53.0; z-score = -2.72; ED = 27.3
```

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

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

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

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

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

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

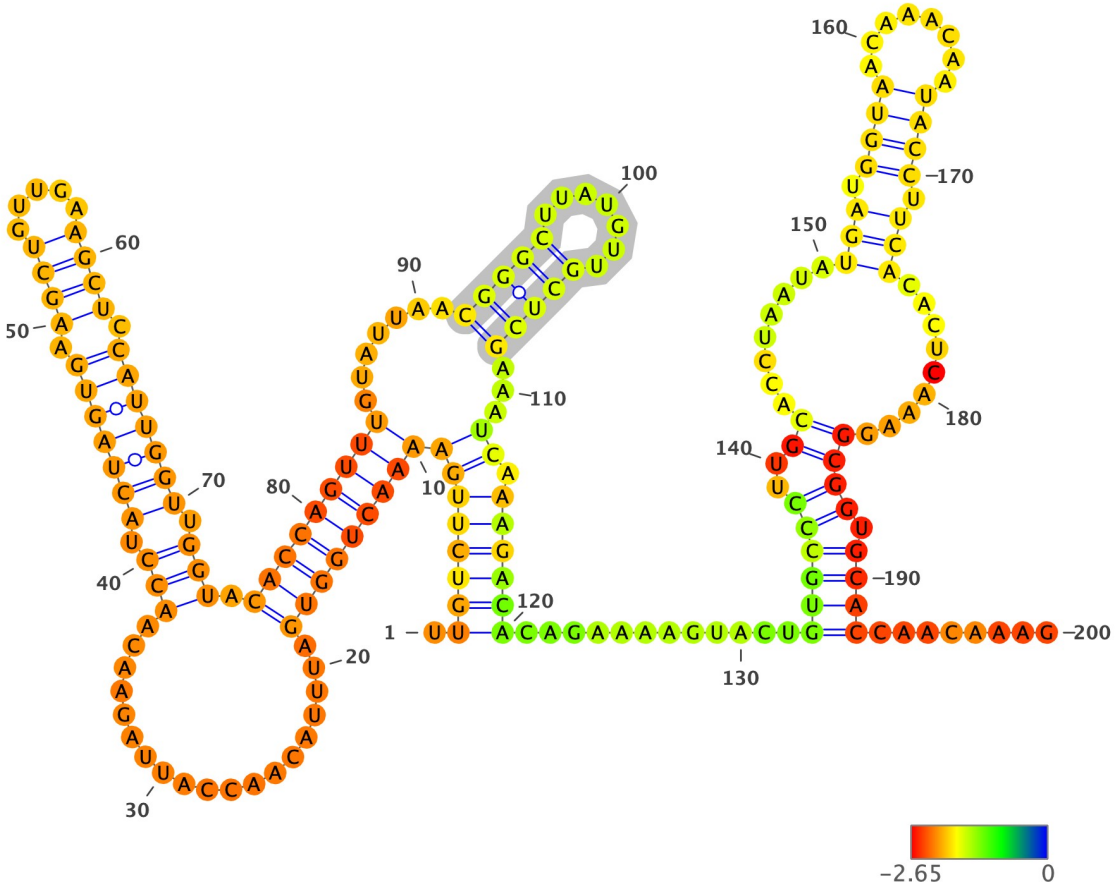
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 49 from nt 2623 to 2639 (nt 92 to 108)

```
5'-CGGGCUUAUGUUGCUCG-3'
5'-(((((.......)))))-3'
Motif MFE = -5.5; z-score = -2.26; 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 = -2.59; 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(+)

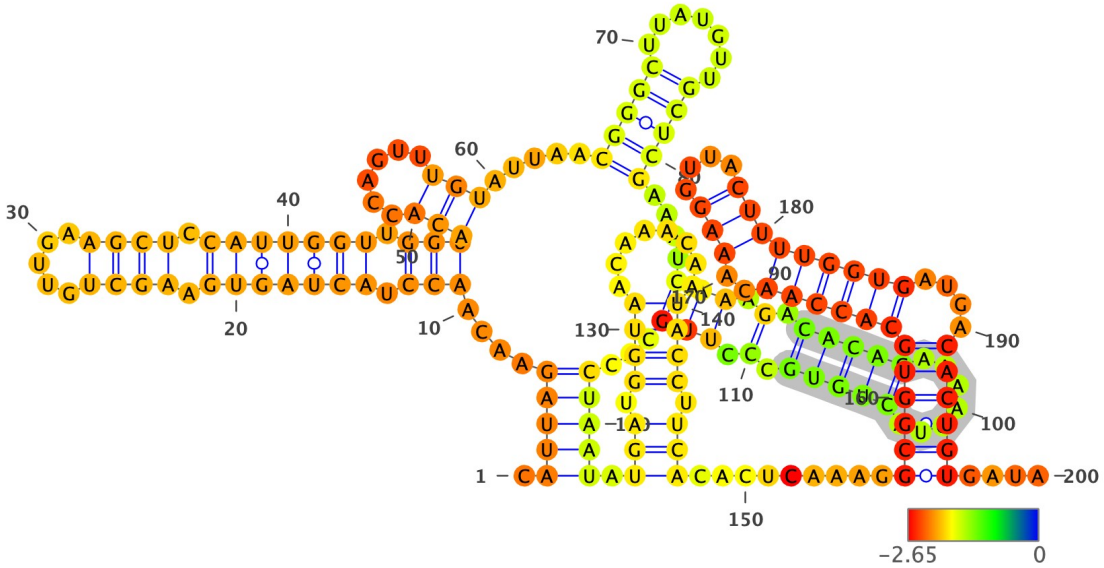
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 50 from nt 2650 to 2666 (nt 92 to 108)

```
5'-CACAGAAAAGUACUGUG-3'
5'-(((((.......)))))-3'
Motif MFE = -3.6; z-score = -4.48; 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 = -1.85; 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(+)

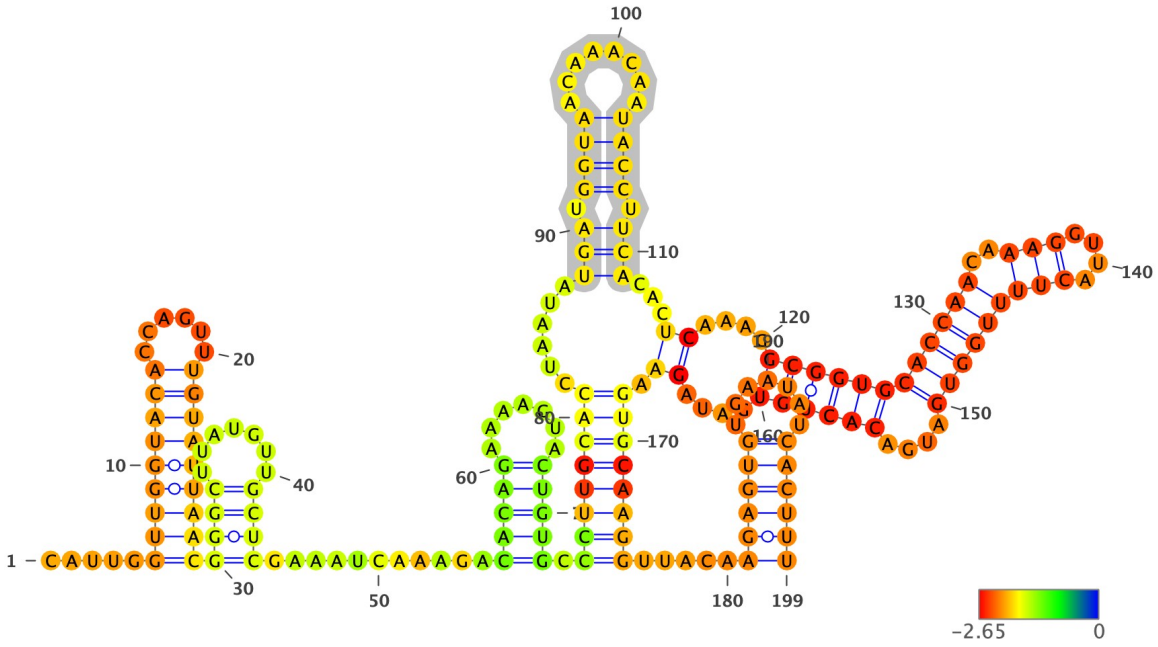
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 51 from nt 2682 to 2705 (nt 88 to 111)

```
5'-UGAUGGUAACAAACAAUACCUUCA-3'
5'-(((.((((........)))).)))-3'
Motif MFE = -4.8; z-score = -3.35; 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 = -2.36; 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(+)

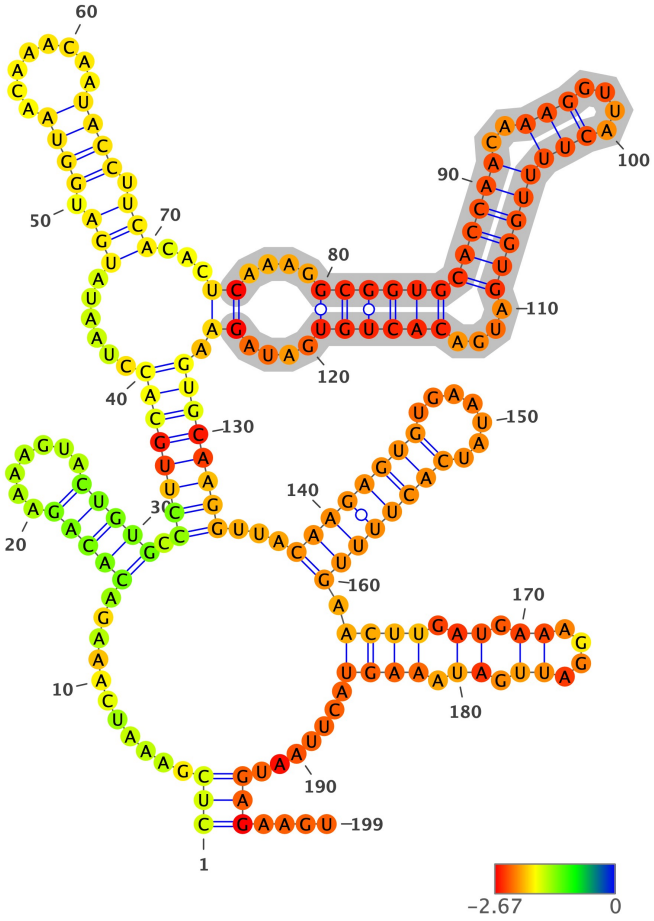
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 52 from nt 2710 to 2759 (nt 75 to 124)

```
5'-CAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAG-3'
5'-(....((((((((((((..(((....)))))))))....))))))....)-3'
Motif MFE = -13.7; z-score = -1.97; 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 = -2.31; 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(+)

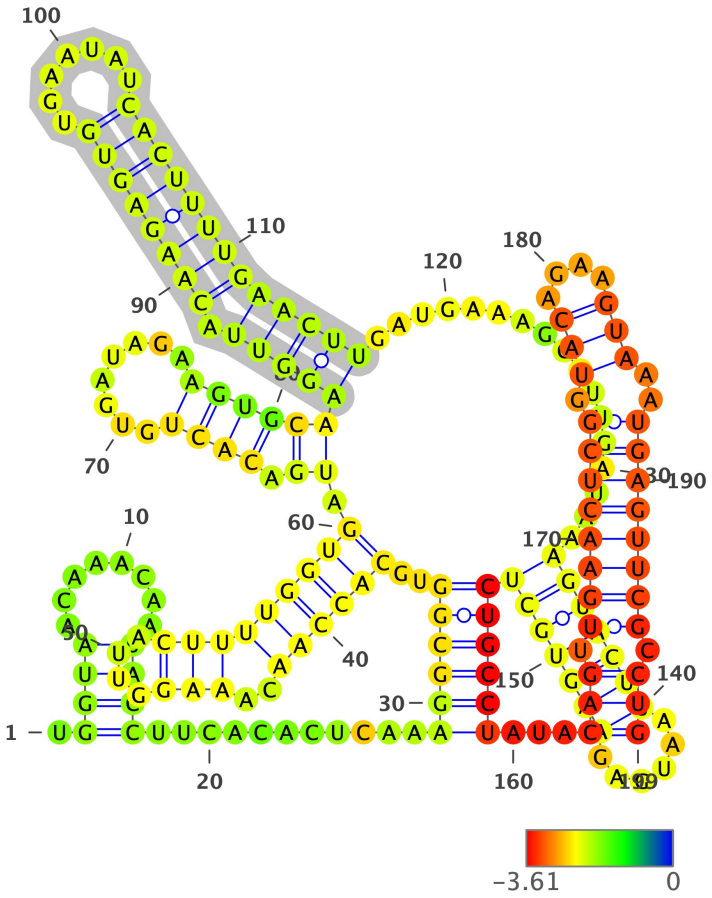
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 53 from nt 2767 to 2800 (nt 83 to 116)

```
5'-AGGUUACAAGAGUGUGAAUAUCACUUUUGAACUU-3'
5'-(((((.(((((((((.......)))))))))))))))-3'
Motif MFE = -10.9; z-score = -4.18; ED = 0.81
```



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

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

```
5'-UGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUG
AACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUG-3
5'-.((((........))))..........((((((..((((((..(((....)))))))))).((.((((........))))))((((((.(((((((((.......)))))))))
))))).................(((((((......)))))))))))...(((.(((((((((.(((....))))..)))))))))..))).)))-3'
MFE = -55.0; z-score = -3.49; 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(+)

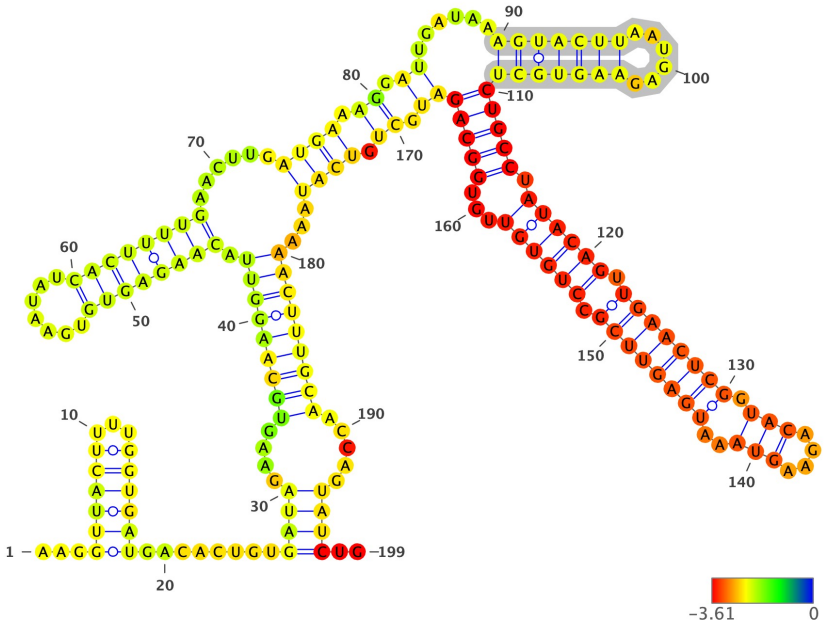
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 54 from nt 2818 to 2837 (nt 90 to 109)

```
5'-AGUACUUAAUGAGAAGUGCU-3'
5'-(((((((......)))))))-3'
Motif MFE = -5.4; z-score = -4.14; 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 = -3.37; 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(+)

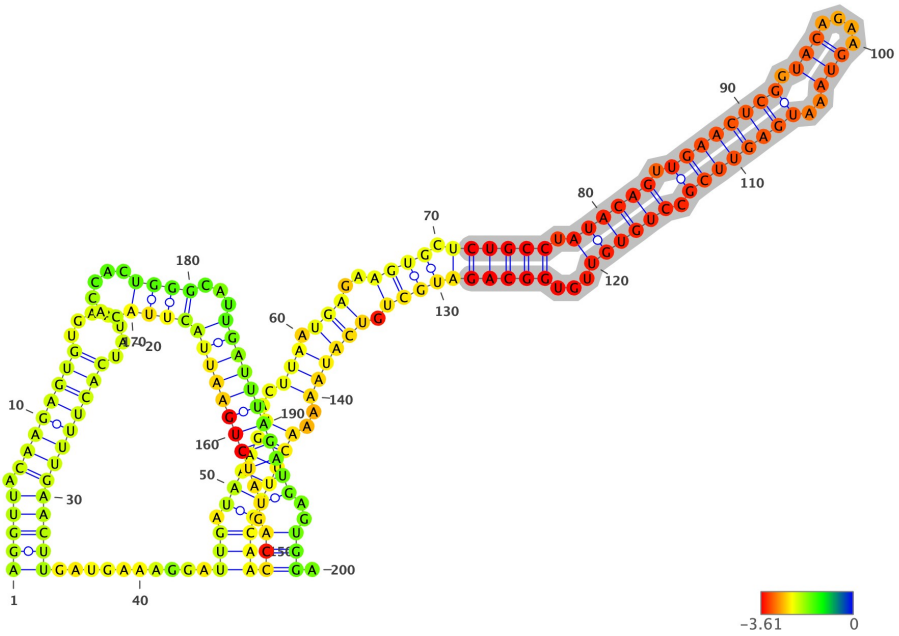
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 55 from nt 2838 to 2894 (nt 72 to 128)

```
5'-CUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAG-3'
5'-(((((.((((((.(((((((((.(((....))))..)))))))))..)))))))...))))-3'
Motif MFE = -25.1; z-score = -4.41; 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 = -3.82; 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(+)

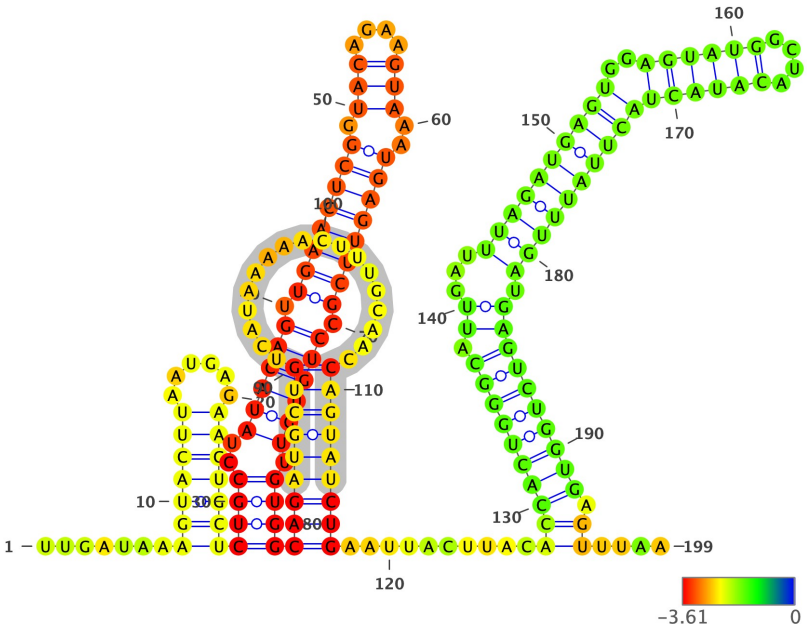
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 56 from nt 2895 to 2924 (nt 85 to 114)

```
5'-AUGCUGUCAUAAAAACUUUGCAACCAGUAU-3'
5'-(((((...................)))))-3'
Motif MFE = -2.2; z-score = -0.42; ED = 4.79
```



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

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

```
5'-UUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAG
UAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAA-3
5'-.......(((((((......)))))))((((..((((((.(((((((.(((....))))..)))))))).))))))..)))))))))(((((((.....................)))
))))))).........((((((((((.((...((((((((((..((((((....))))))))))))))))))).))))))))))..))....-3'
MFE = -60.2; z-score = -4.81; ED = 20.33
```

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

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

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

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

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', '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(+)

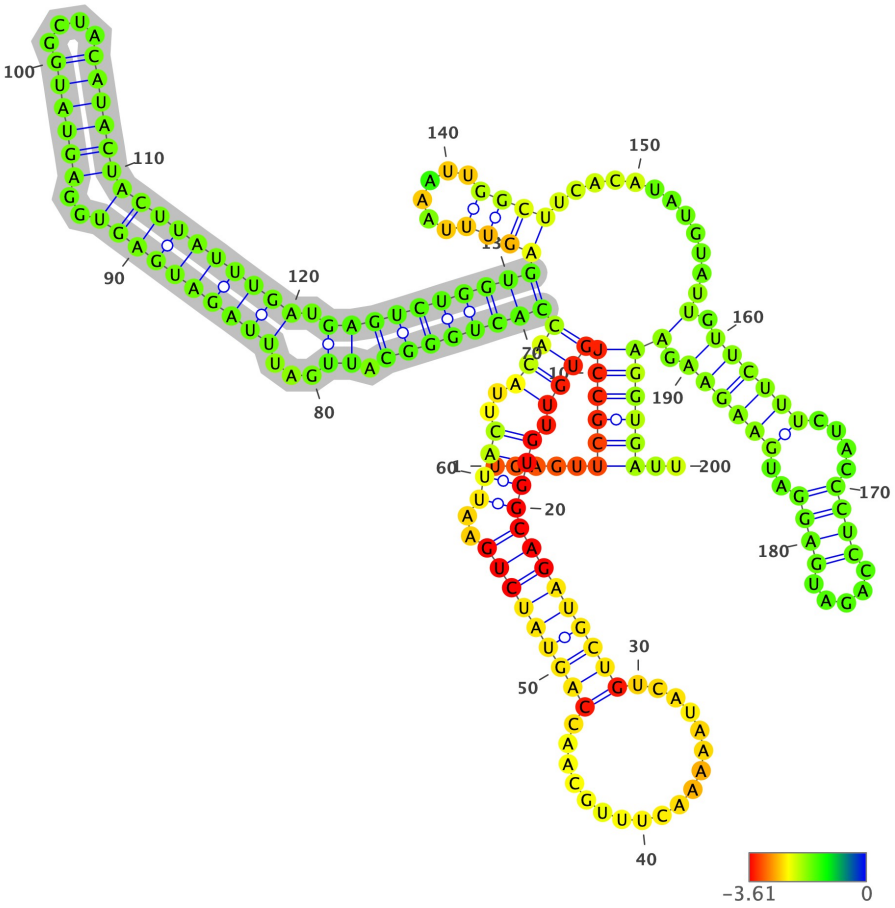
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 2940 to 3002 (nt 69 to 131)

```
5'-CACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUG-3'
5'-(((((((((.((...((((((((((..((((((....))))))))))))))))).))))))))))-3'
Motif MFE = -21.9; z-score = -3.89; ED = 5.39
```



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 2872 to 3071 (motif highlighted in silver):

```
5'-UGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUA
CUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUU-3
5'-.....((((((((((.((((((((((((((.................)))))))))..))))..))))((((((((.((...((((((((((..((((((....)))))))
))))))))).))))))))))((((......)))).............(.((((((....((((.....))))..)))))).)))))))..-3'
MFE = -54.6; z-score = -2.33; ED = 22.51
```

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

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

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

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

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

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

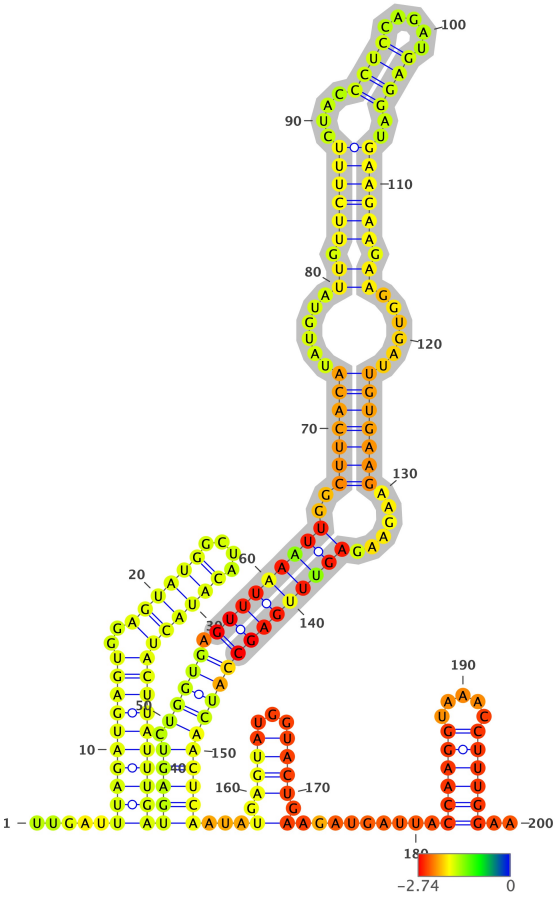
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-GUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGC-3'
5'-((((.(.((..(((((((.....((.((((((....((((.....))))..)))))))..))).....)))))))).....)).).))))-3'
Motif MFE = -23.1; z-score = -2.84; 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 = -3.73; 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(+)

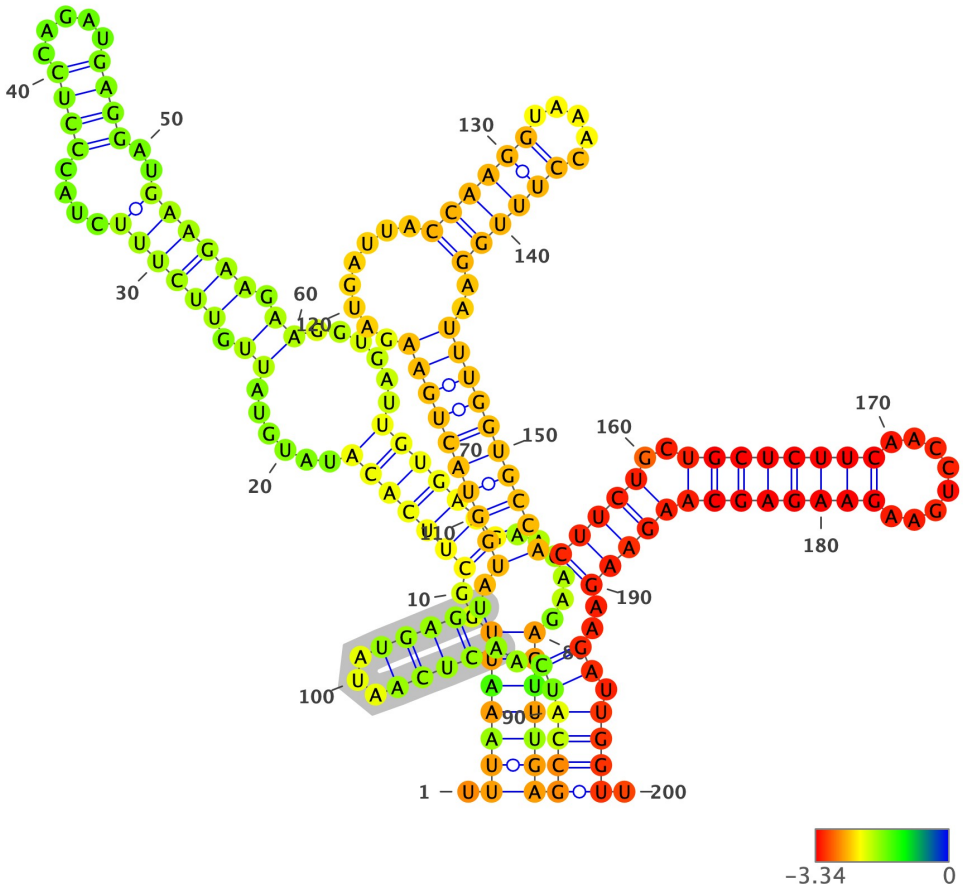
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 59 from nt 3098 to 3110 (nt 94 to 106)

```
5'-ACUCAAUAUGAGU-3'
5'-(((((...)))))-3'
Motif MFE = -2.4; z-score = -6.52; 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 = -3.7; 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(+)

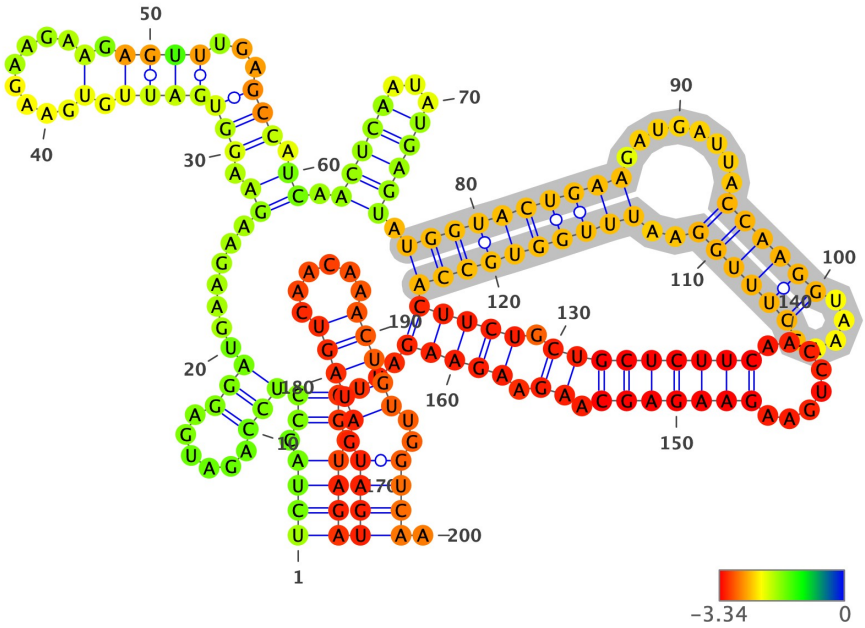
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 60 from nt 3112 to 3158 (nt 77 to 123)

```
5'-UGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCA-3'
5'-((((((((((........((((((.....))))))..))))))))))-3'
Motif MFE = -13.7; z-score = -2.96; ED = 7.14
```



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 3036 to 3235 (motif highlighted in silver):

```
5'-UCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGG
AAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAA-3
5'-((((.(((((......)))).......((.(((((((.(........).))))...))).)).(((((...))))).((((((((((........((((((.....))))))
..))))))))))(((((.((((((((((........)))))))).)).)))))...)).))))((((.(((((......)))))..)))).-3'
MFE = -51.6; z-score = -2.43; 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(+)

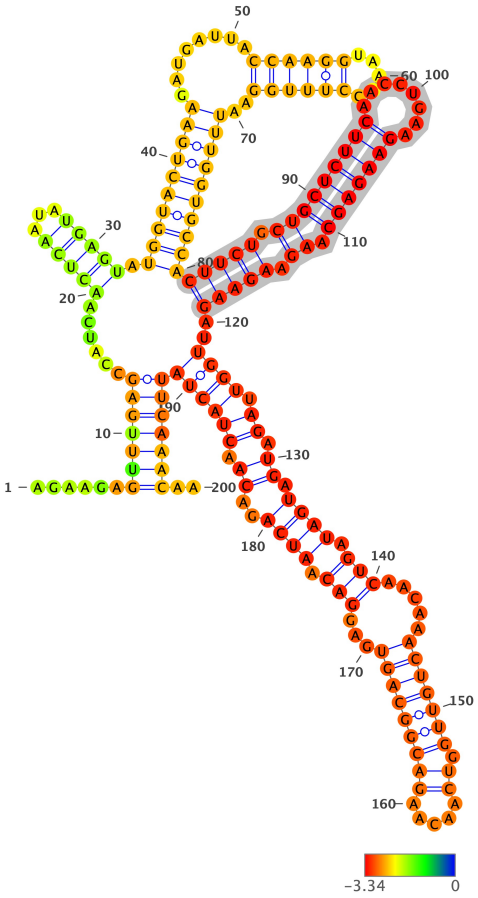
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 61 from nt 3159 to 3197 (nt 81 to 119)

```
5'-CUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAG-3'
5'-(((((.(((((((((.........)))))))).)).)))))-3'
Motif MFE = -16.2; z-score = -4.82; 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 = -5.02; 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(+)

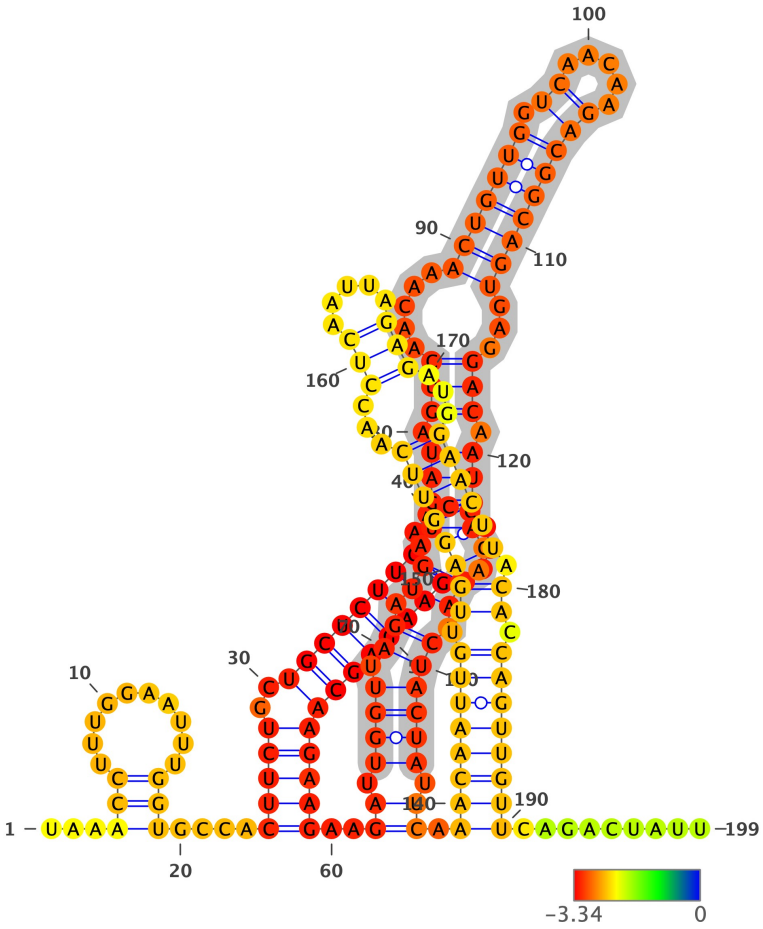
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 62 from nt 3200 to 3269 (nt 65 to 134)

```
5'-UGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUA-3'
5'-(((((.((.((.(((((.(((.....(((((((.((.....)))))))))...)))).)))))..)).)))))-3'
Motif MFE = -17.4; z-score = -2.92; ED = 6.97
```



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 3136 to 3334 (motif highlighted in silver):

```
5'-UAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAG
UGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUU-3
5'-...(((..........)))....((((((..(((((((((........)))))))))))))..((.(((((.((.((.(((((.(((.....(((((((.((.....)))))))))
)...)))).)))))..)).)))))).)).(((((((((.(((((((((...(((.....)))...)))))))).)).)))))))).........-3'
MFE = -55.7; z-score = -3.8; ED = 40.62
```

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(+)

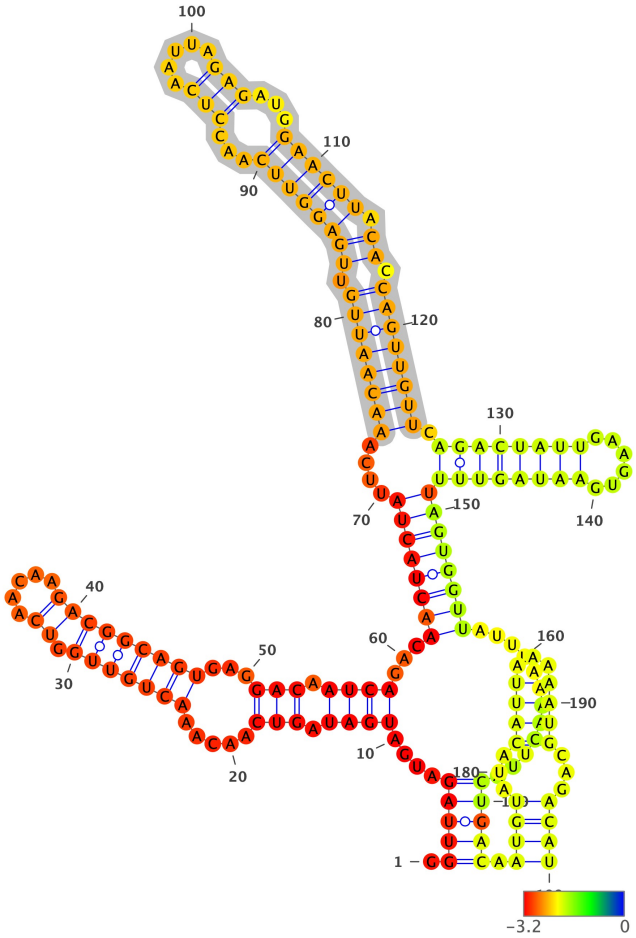
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 63 from nt 3274 to 3325 (nt 74 to 125)

```
5'-AACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUU-3'
5'-(((((((((.(((((((((...(((.....)))...))))))).)).)))))))))-3'
Motif MFE = -16.5; z-score = -4.15; 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 = -2.38; 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(+)

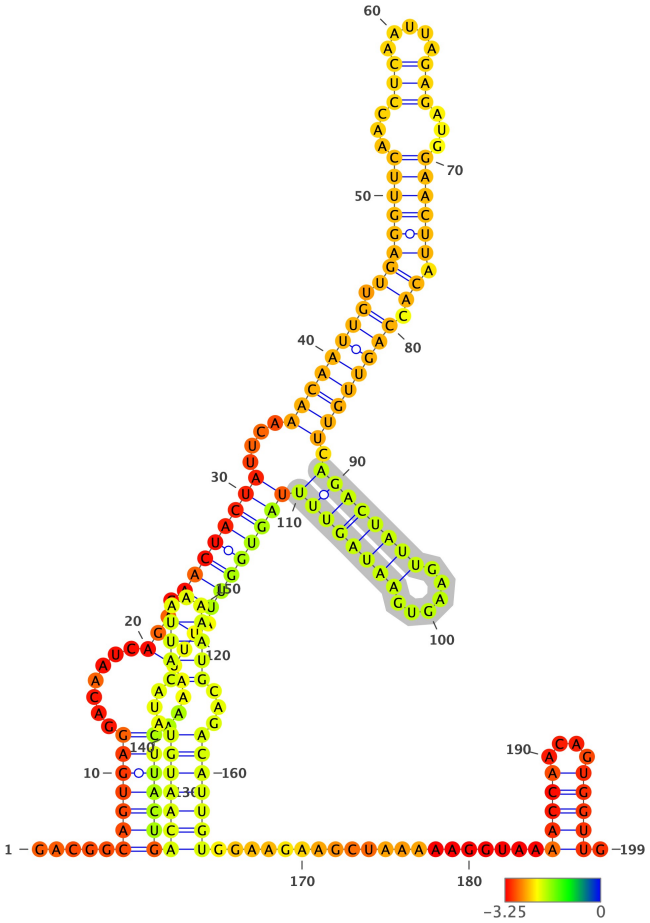
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 64 from nt 3327 to 3348 (nt 89 to 110)

```
5'-AGACUAUUGAAGUGAAUAGUUU-3'
5'-((((((((......))))))))-3'
Motif MFE = -5.2; z-score = -4.87; 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 = -3.29; 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(+)

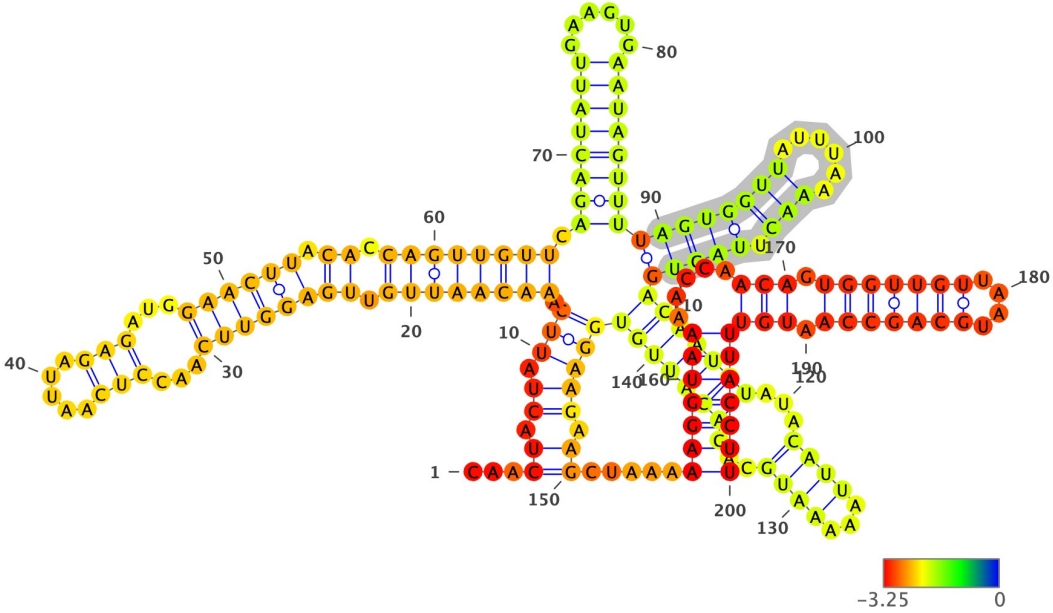
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 65 from nt 3350 to 3370 (nt 90 to 110)

```
5'-AGUGGUUAUUUAAAACUUACU-3'
5'-(((((((......))).))))-3'
Motif MFE = -1.3; z-score = -0.95; 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 = -4.81; 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(+)

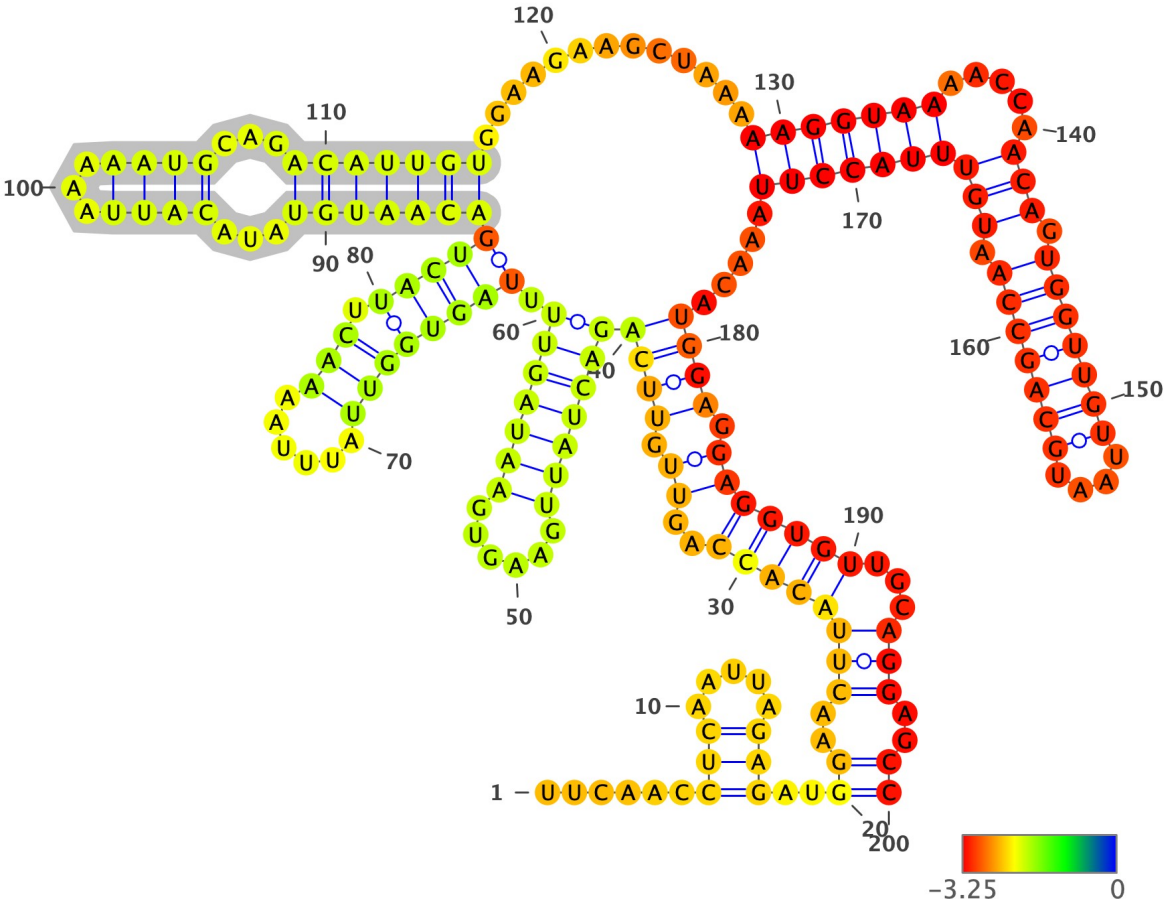
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 66 from nt 3372 to 3402 (nt 85 to 115)

```
5'-ACAAUGUAUACAUUAAAAAUGCAGACAUUGU-3'
5'-(((((((...((((...))))...)))))))-3'
Motif MFE = -6.4; z-score = -3.72; 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 = -1.91; 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(+)

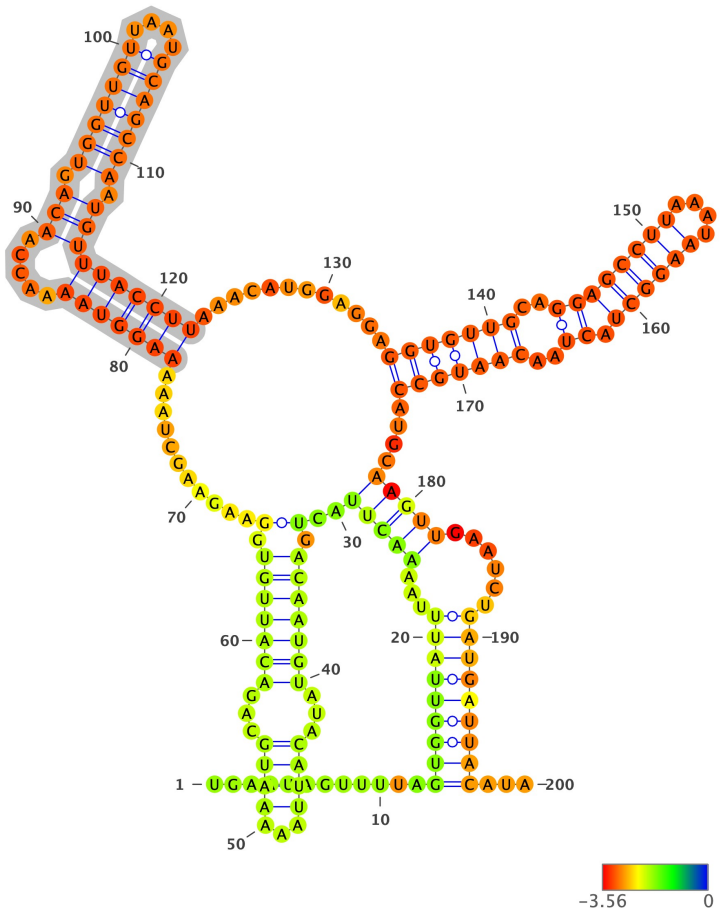
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 67 from nt 3416 to 3460 (nt 78 to 122)

```
5'-AAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUU-3'
5'-(((((((.....(((.(((((((....)))))))..)))))))))-3'
Motif MFE = -16.0; z-score = -3.78; 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 = -4.01; 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(+)

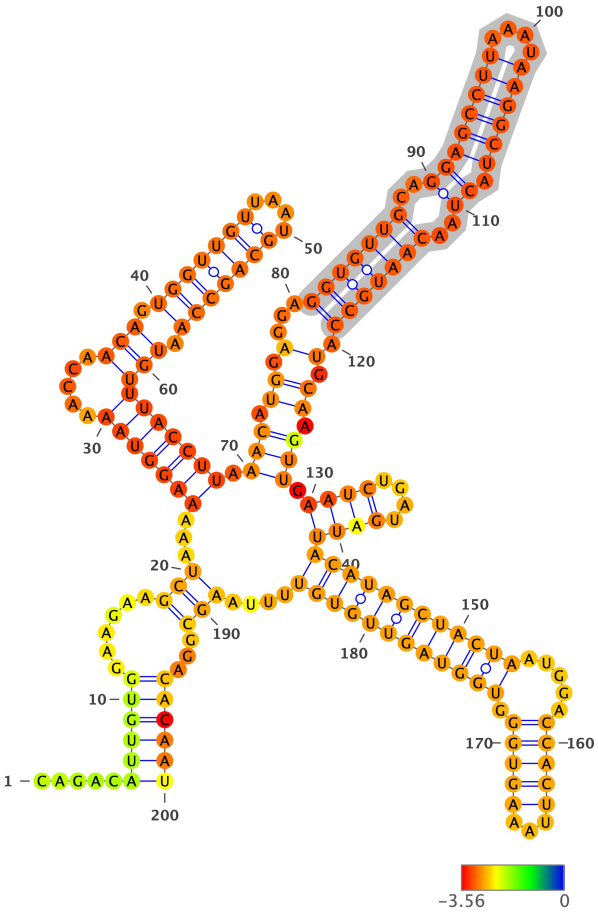
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 68 from nt 3473 to 3511 (nt 81 to 119)

```
5'-GGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCC-3'
5'-(((((((..((((((((....)))))).))..)))))))-3'
Motif MFE = -15.6; z-score = -4.0; 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 = -4.86; 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(+)

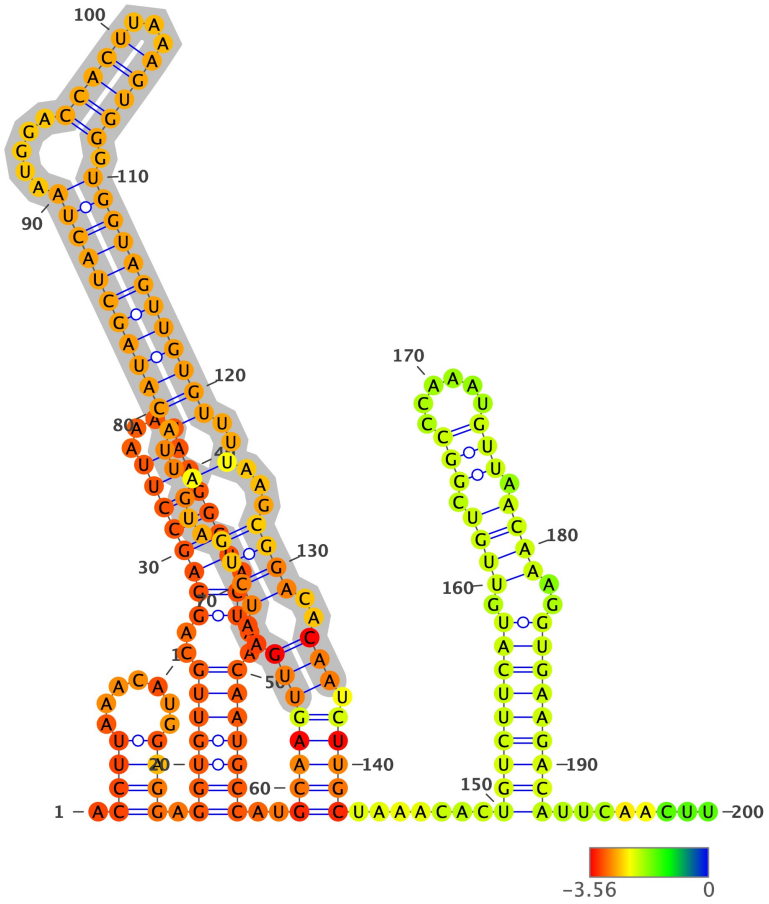
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 69 from nt 3519 to 3591 (nt 64 to 136)

```
5'-UUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAA-3'
5'-((...((........((((((((((((.....(((((...))))).))))))))))))........))...))-3'
Motif MFE = -21.9; z-score = -3.87; 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 = -5.19; ED = 11.2
```

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(+)

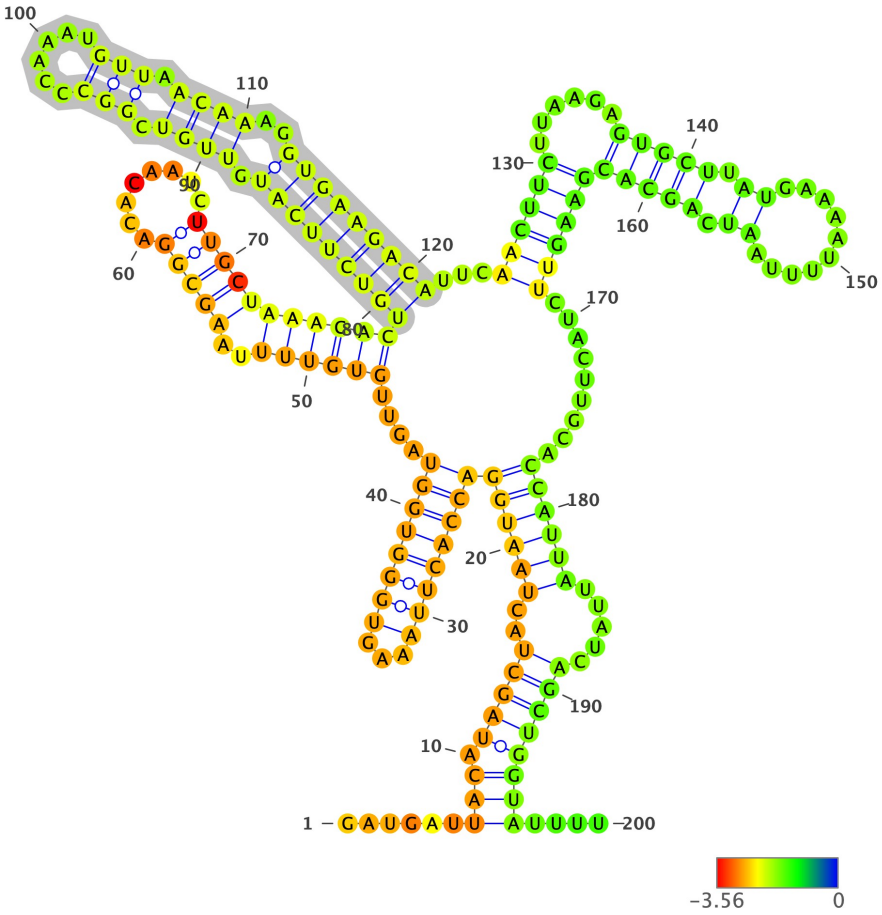
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 70 from nt 3605 to 3647 (nt 79 to 121)

```
5'-UGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACA-3'
5'-(((((((((.((((.(((......))).))))..)))))))))-3'
Motif MFE = -14.2; z-score = -3.53; 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 = -2.87; 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(+)

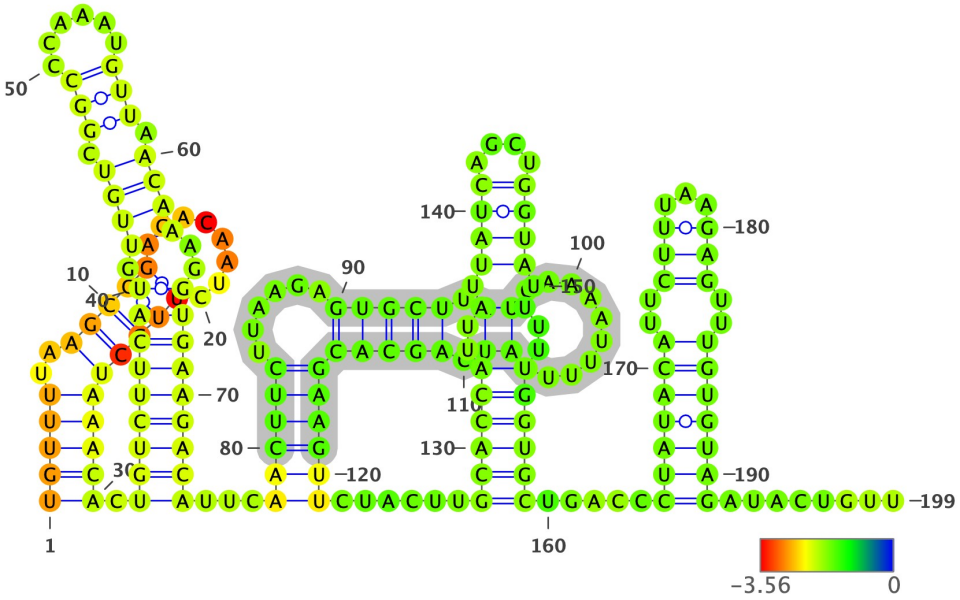
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 71 from nt 3653 to 3692 (nt 80 to 119)

```
5'-CUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAG-3'
5'-((((......(((((.((..........)).)))))))))-3'
Motif MFE = -5.4; z-score = -0.77; ED = 5.85
```



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 3574 to 3772 (motif highlighted in silver):

```
5'-UGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCA
GCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUU-3
5'-(((((..(((((........)))))))))).((((((((((.((((.(((......))).)))).))))))))))...((((((......(((((.(..........)).)
))))))))))......((((((..(.((((....)))).).))))))).....(((((((..(((...))))..)))))))........-3'
MFE = -49.4; z-score = -2.84; ED = 14.78
```

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

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

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

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

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

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

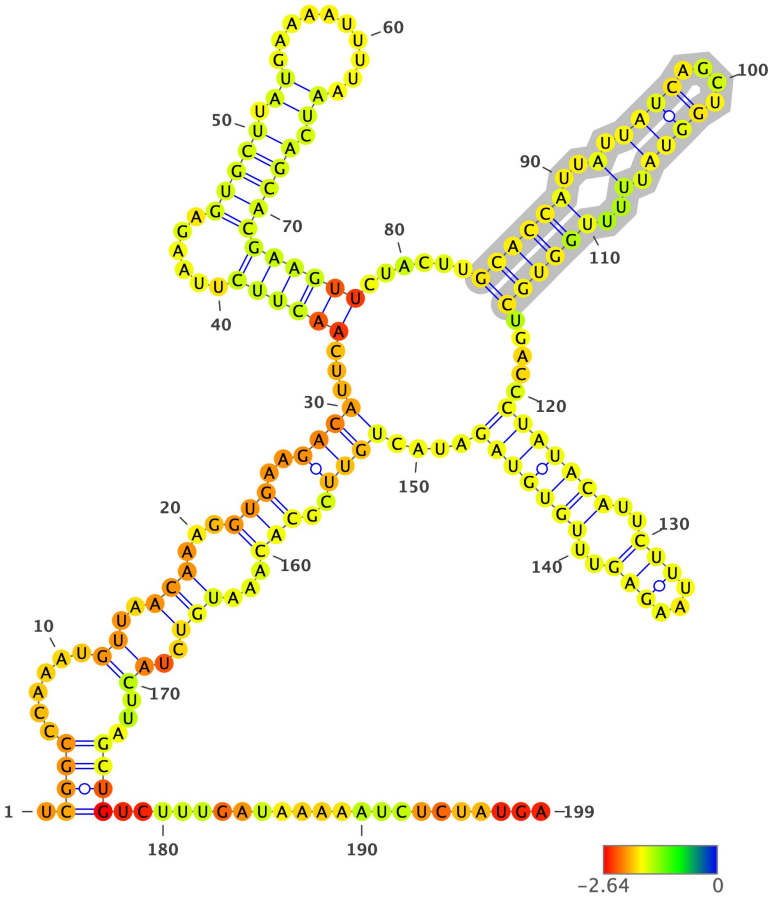
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 72 from nt 3701 to 3732 (nt 84 to 115)

```
5'-GCACCAUUAUUAUCAGCUGGUAUUUUUGGUGC-3'
5'-((.........................))-3'
Motif MFE = -11.2; z-score = -4.08; 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 = -1.11; ED = 36.28
```

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(+)

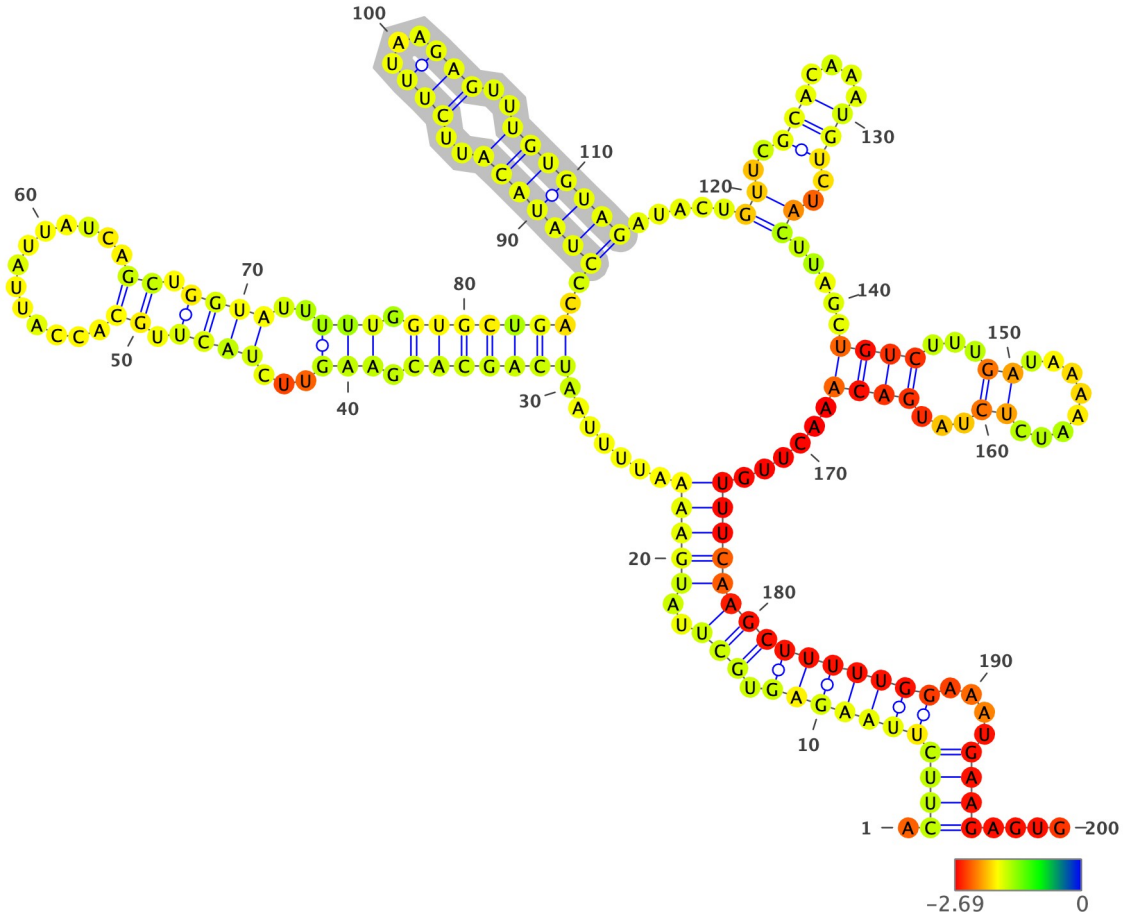
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 73 from nt 3738 to 3764 (nt 87 to 113)

```
5'-CUAUACAUUCUUUAAGAGUUUGUGUAG-3'
5'-(((((((..(((...)))..)))))))-3'
Motif MFE = -7.6; z-score = -3.4; ED = 1.45
```



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

Extracted structure model with flanking nucleotides 3652 to 3851 (motif highlighted in silver):

```
5'-ACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGU
AGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUG-3
5'-.((((((((((.(((..(((((.......(((((((.(((...((((.((............)).)))))..))))..)))))))..(((((((..(((...)))..)))))
))).....((..(((....)))..)).....((((...((........))...))))......))))))))))))....))))).....-3'
MFE = -38.6; z-score = -1.04; ED = 49.95
```

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(+)

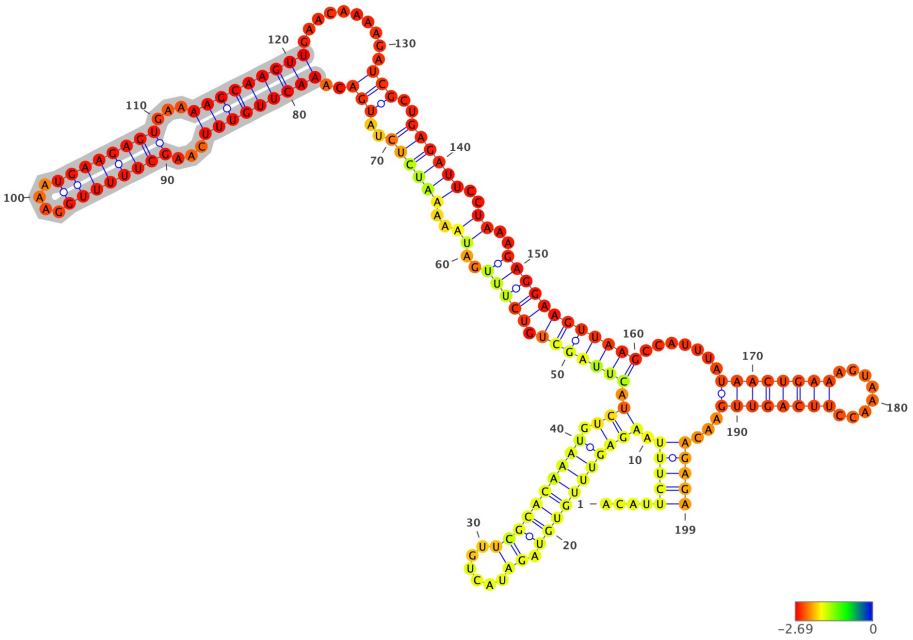
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 74 from nt 3819 to 3862 (nt 78 to 121)

```
5'-AACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUU-3'
5'-((((((((((...((((((((....))))))))...)))))))))-3'
Motif MFE = -13.1; z-score = -3.93; ED = 3.73
```



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

Extracted structure model with flanking nucleotides 3742 to 3940 (motif highlighted in silver):

```
5'-ACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGA
AAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGA-3
5'-....(((((.((((((((((((.((......)))))))))).))).(((((((.(((((..((..((((((..(((..(((((((((...((((((((....))))))))..
.)))))))))..........)))..))))))..))..))))))))))))).......((((((((........))))))))...)))))-3'
MFE = -47.3; z-score = -2.48; 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(+)

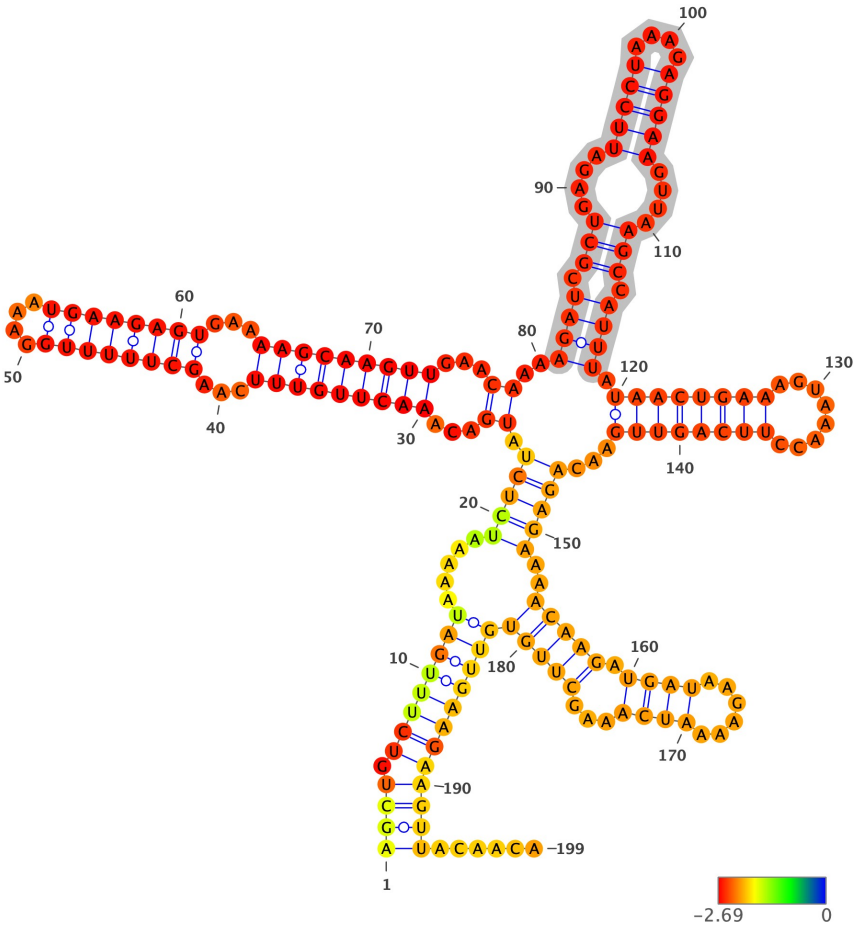
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 75 from nt 3870 to 3907 (nt 81 to 118)

```
5'-AGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUU-3'
5'-((((.(((....(((((....)))))....))).))))-3'
Motif MFE = -8.8; z-score = -2.1; 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 = -3.99; 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(+)

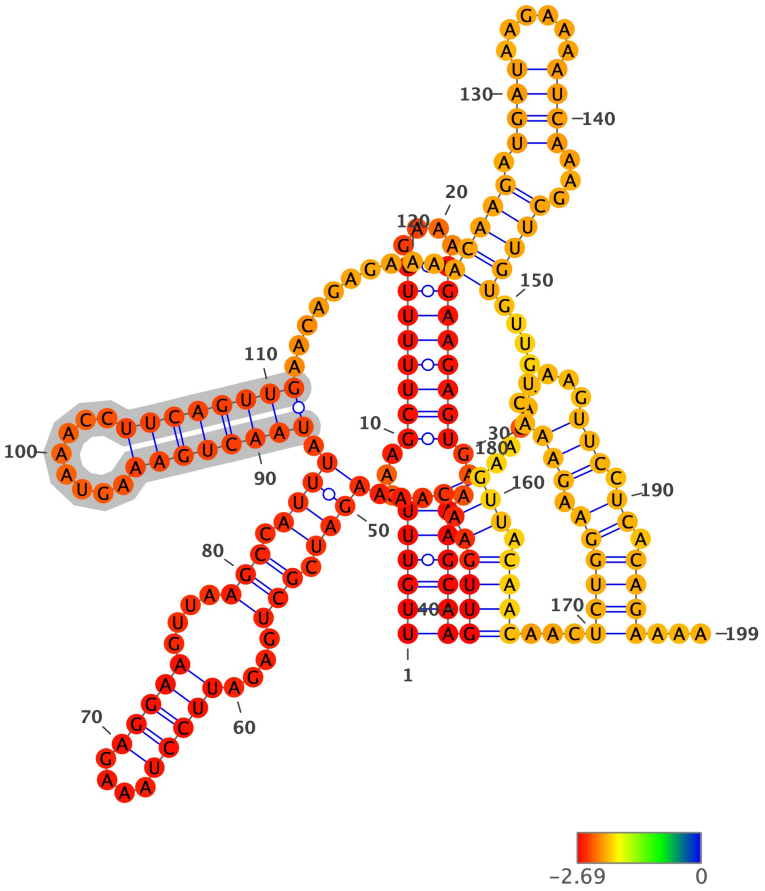
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 76 from nt 3909 to 3932 (nt 88 to 111)

```
5'-UAACUGAAAGUAAACCUUCAGUUG-3'
5'-((((((((........))))))))-3'
Motif MFE = -6.1; z-score = -3.81; 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 = -2.94; 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(+)

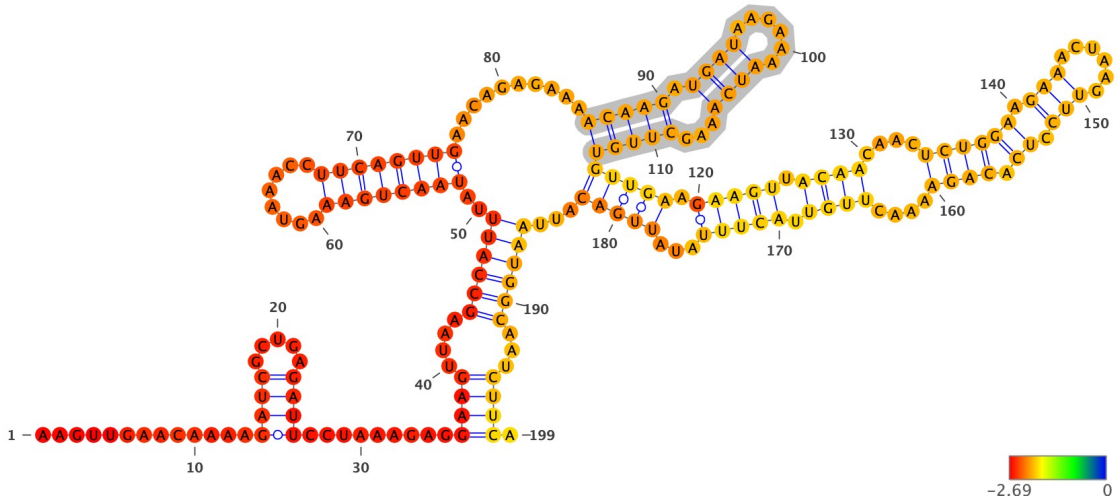
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 77 from nt 3943 to 3970 (nt 86 to 113)

```
5'-ACAAGAUGAUAAGAAAAUCAAAGCUUGU-3'
5'-(((((.((((......)))).)))))-3'
Motif MFE = -4.5; z-score = -3.53; 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 = -2.1; 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(+)

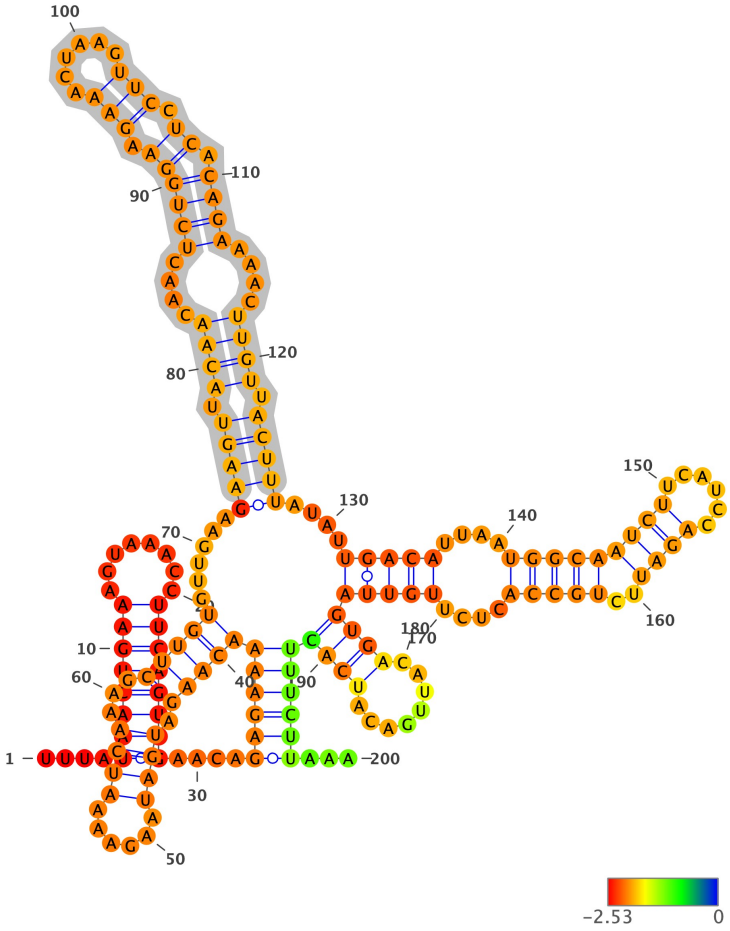
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 78 from nt 3978 to 4030 (nt 74 to 126)

```
5'-AAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUU-3'
5'-((((.((((....((((((.(((......))).)).)))).....)))).))))-3'
Motif MFE = -10.0; z-score = -2.51; 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 = -2.73; ED = 25.66
```

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(+)

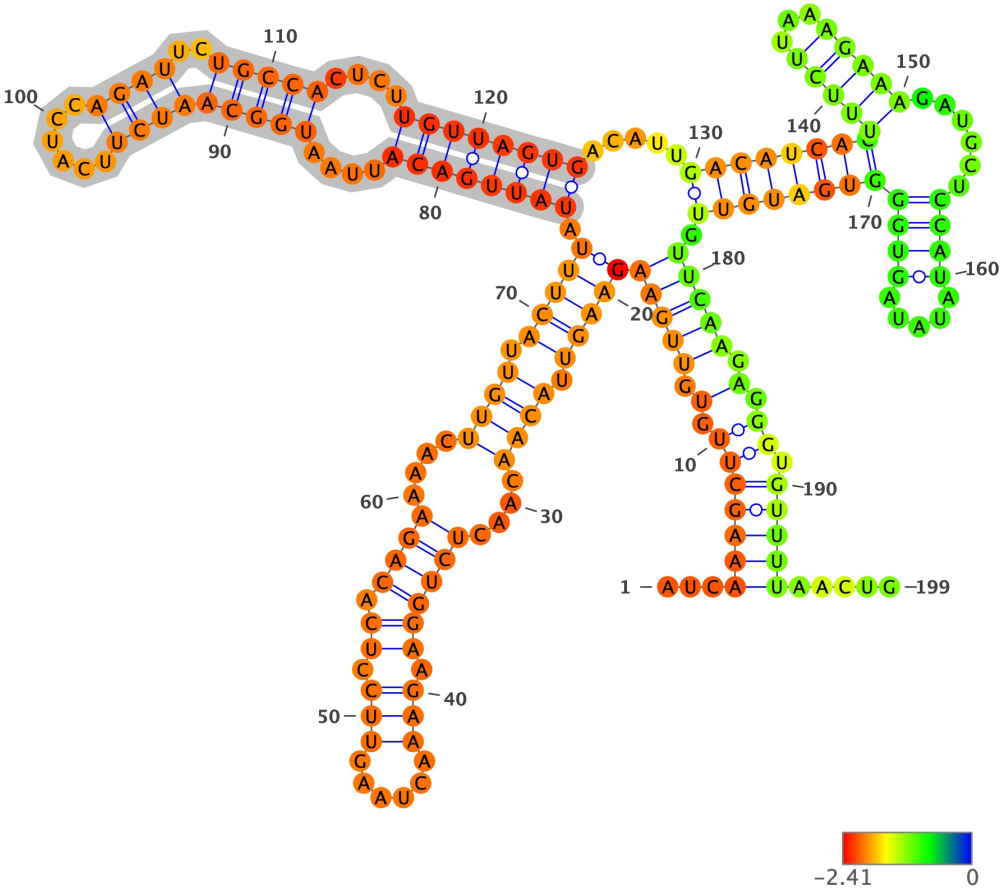
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 79 from nt 4033 to 4082 (nt 75 to 124)

```
5'-UAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUCUUGUUAGUG-3'
5'-((((((((....((((((((((......))))..)))))....))))))))-3'
Motif MFE = -13.4; z-score = -3.18; 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 = -1.61; 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(+)

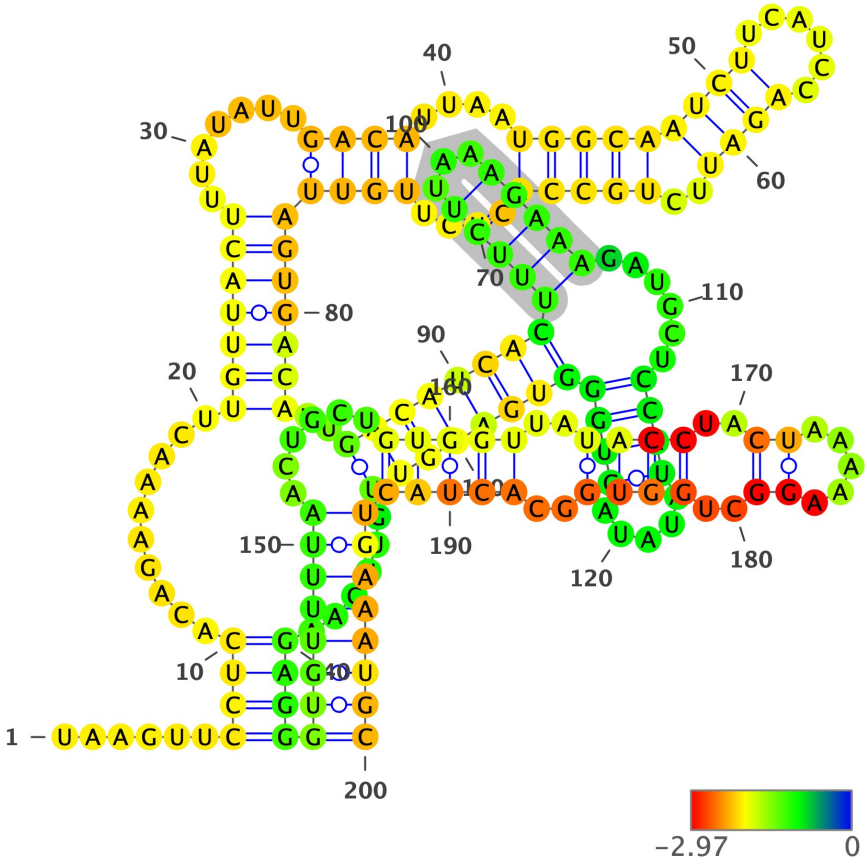
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 80 from nt 4096 to 4108 (nt 94 to 106)

```
5'-UUUCUUAAAGAAA-3'
5'-(((((...)))))-3'
Motif MFE = 0.0; z-score = 0.15; 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(+)

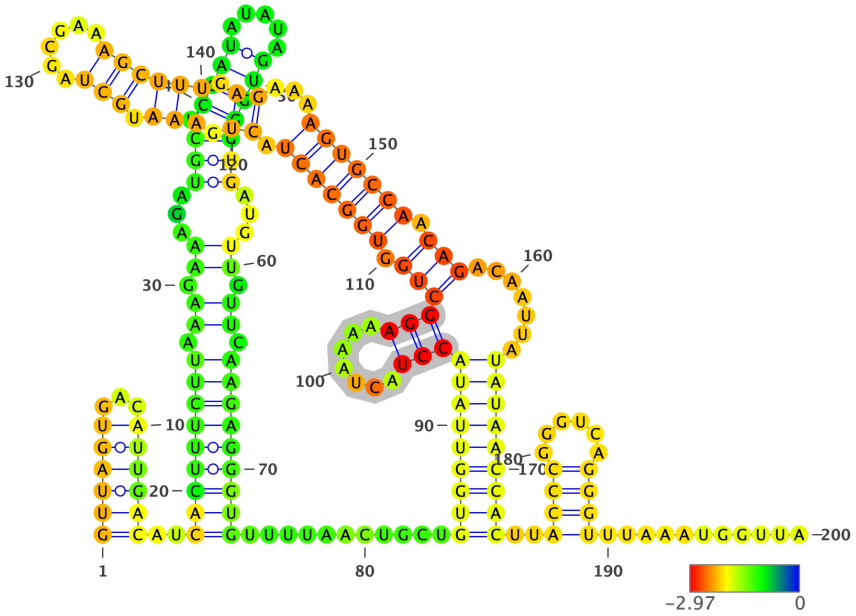
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 81 from nt 4169 to 4181 (nt 94 to 106)

```
5'-CCUACUAAAAAGG-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.24; 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 4076 to 4275 (motif highlighted in silver):

```
5'-GUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGU
GGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUA-3
5'-((((((...))))))..(((((((((.((.((...(((.((((.....)))))))...)).)).))))))))).........((((((((((((.......)))(((.(
((((((.((.(((.(((......))))))).))...)))))))).)))).......))))))))..((((......)))).........-3'
MFE = -53.0; z-score = -2.24; ED = 26.99
```

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

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

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

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

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

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

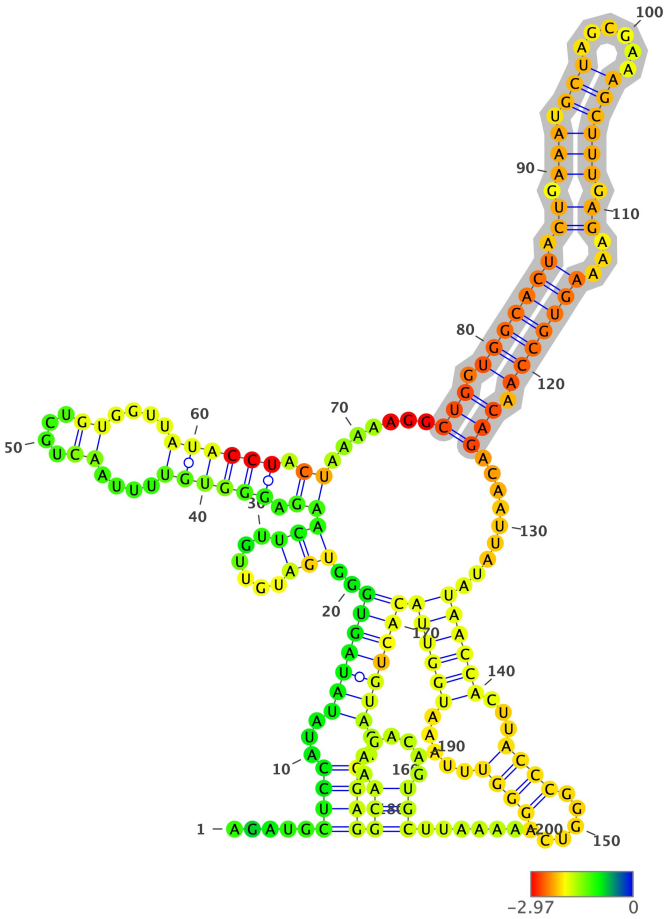
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 82 from nt 4182 to 4232 (nt 75 to 125)

```
5'-CUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAG-3'
5'-(((.(((((((.((.(((.(((......)))))).))...))))))).)))-3'
Motif MFE = -18.7; z-score = -4.23; ED = 1.63
```



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

Extracted structure model with flanking nucleotides 4108 to 4307 (motif highlighted in silver):

```
5'-AGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAG
AAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAA-3
5'-.....((((...(((((((..(((......)))((.((((((....((....))....)))))).))........(((.(((((((.((.(((.(((......)))))).))
...))))))).))).........((((((...((((......))))).....))))))))))))..))))(((.......)))......-3'
MFE = -54.2; z-score = -2.42; ED = 18.11
```

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

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

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

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

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

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

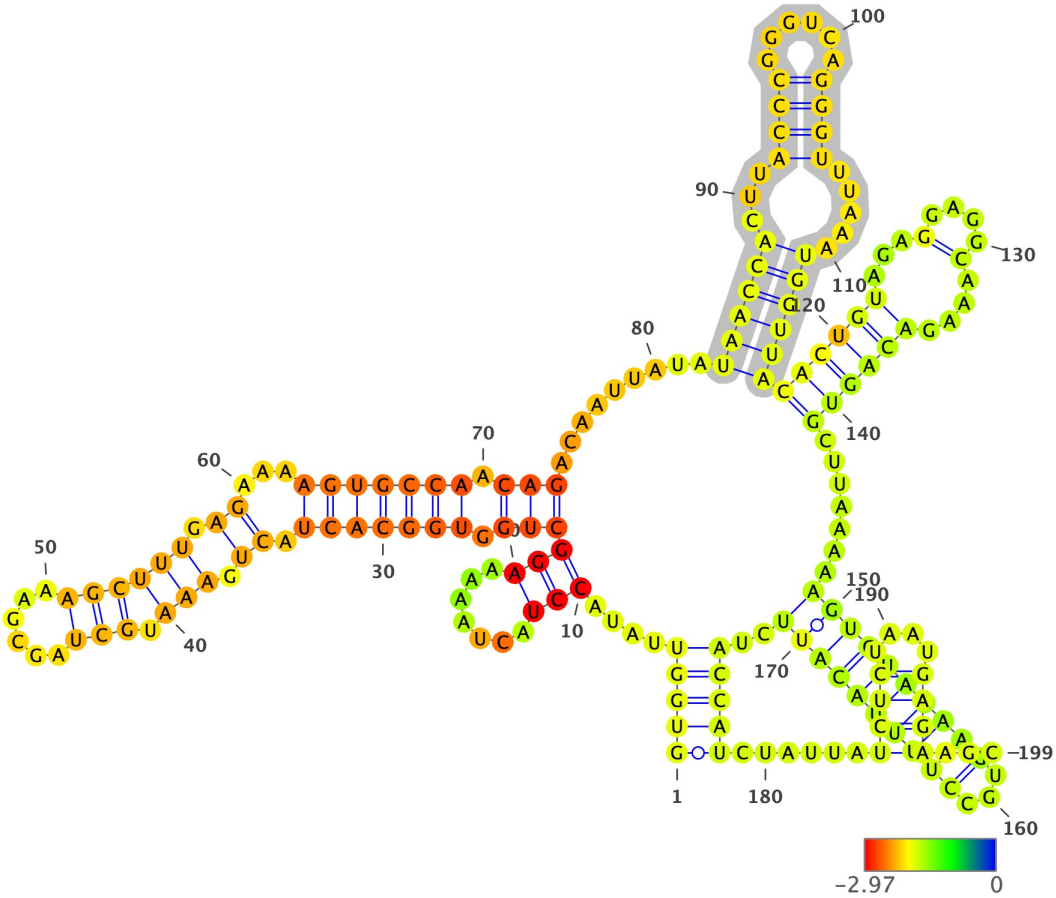
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 83 from nt 4242 to 4275 (nt 83 to 116)

```
5'-UAACCACUUACCCGGGUCAGGGUUUAAAUGGUUA-3'
5'-((((((...((((......))))).....))))))-3'
Motif MFE = -10.7; z-score = -2.53; ED = 2.31
```



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

Extracted structure model with flanking nucleotides 4160 to 4358 (motif highlighted in silver):

```
5'-GUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAU
GGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGC-3
5'-(((((....(((.......)))(((.(((((((.((.(((.(((......))))))).))...)))))))).))).........((((((...((((......))))).....)
)))))((((((...(....)....))))))).......((((((((((...)))))))))))..)))))......((((....))))...-3'
MFE = -53.7; z-score = -3.49; ED = 24.22
```

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

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

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

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

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

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

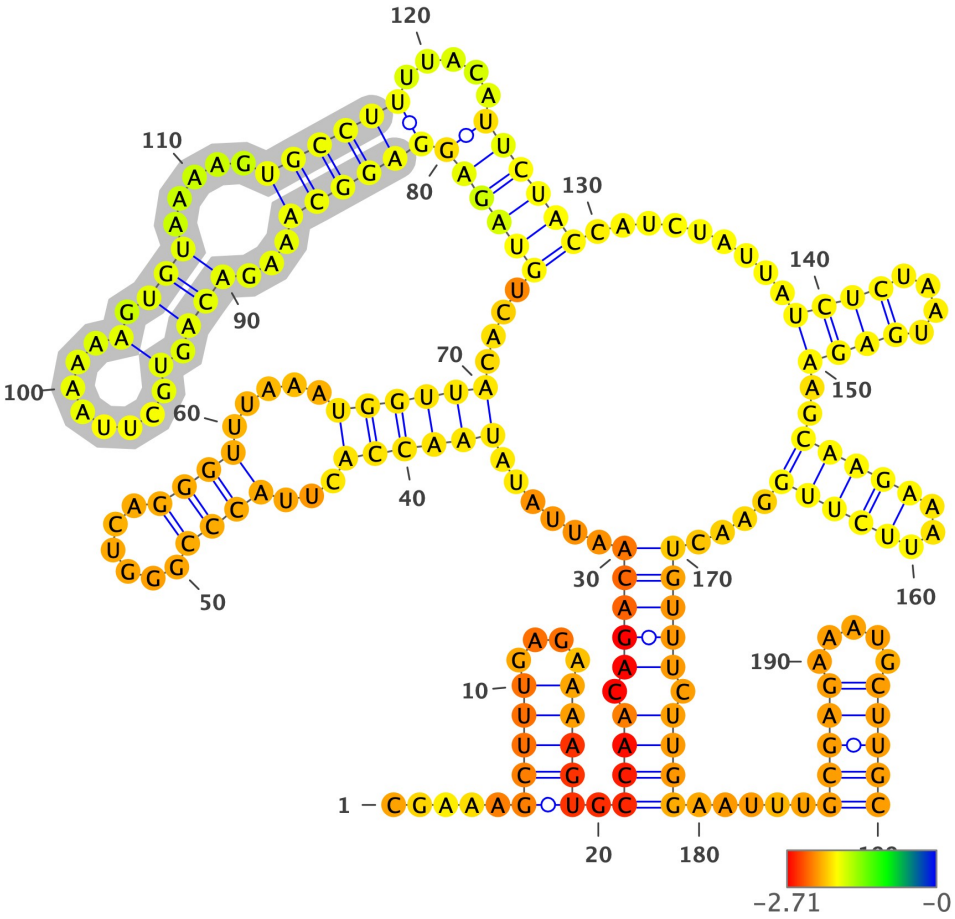
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 84 from nt 4287 to 4322 (nt 82 to 117)

```
5'-AGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCU-3'
5'-(((((...(((.(........).)))).....)))))-3'
Motif MFE = -8.1; z-score = -3.46; 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 4206 to 4404 (motif highlighted in silver):

```
5'-CGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAA
GUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGC-3
5'-.....(((((....))))).((((.(((((......((((((...((((......))))).....))))))....((((((((((((...(((.(........).)))....
.))))))).....))))))).........((((....)))).(((((...)))))....)))))).))))).....(((((.....)))))-3'
MFE = -46.0; z-score = -1.45; ED = 36.25
```

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(+)

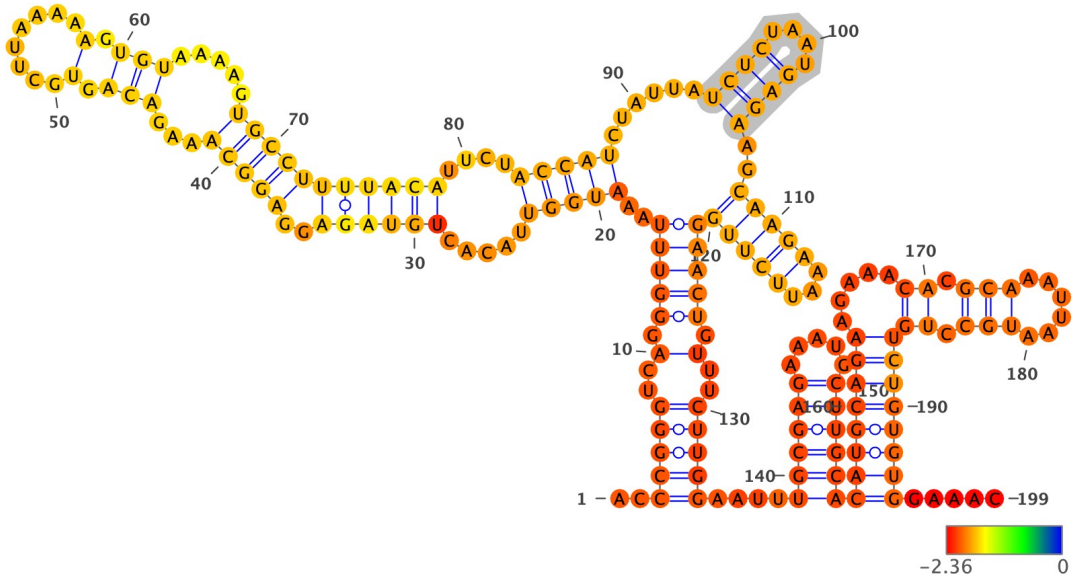
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 85 from nt 4344 to 4355 (nt 94 to 105)

```
5'-UCUCUAAUGAGA-3'
5'-((((....))))-3'
Motif MFE = -2.9; z-score = -8.1; 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 = -2.16; 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(+)

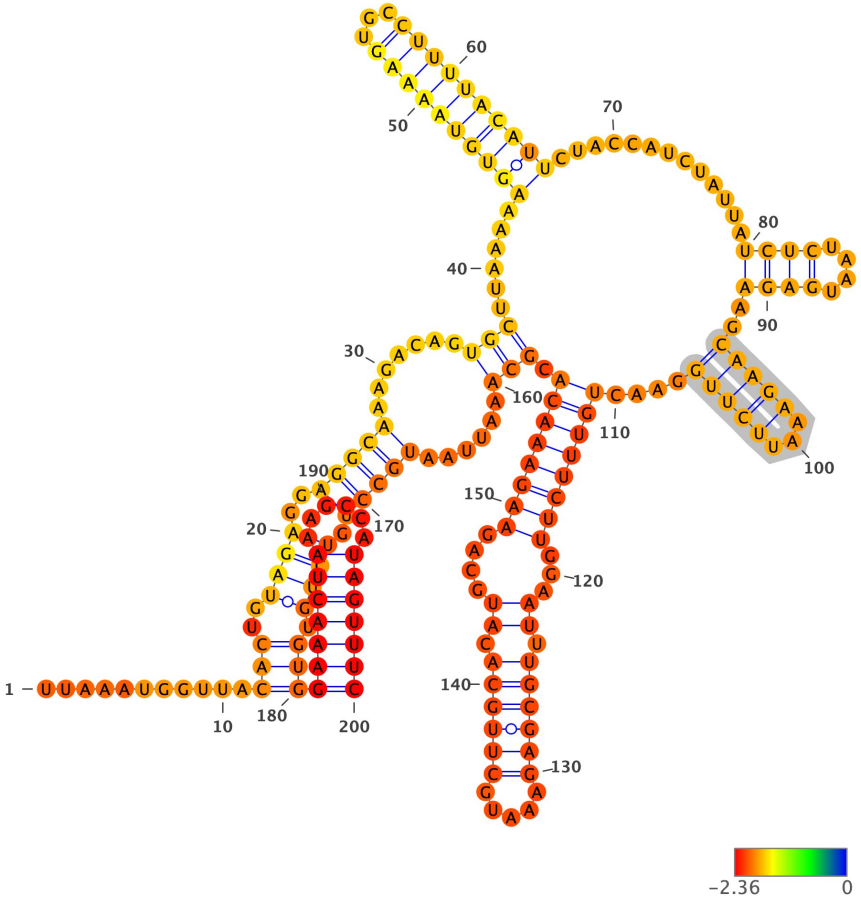
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 86 from nt 4358 to 4370 (nt 94 to 106)

```
5'-CAAGAAAUUCUUG-3'
5'-(((((...)))))-3'
Motif MFE = -1.6; z-score = -4.49; 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 = -2.52; 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(+)

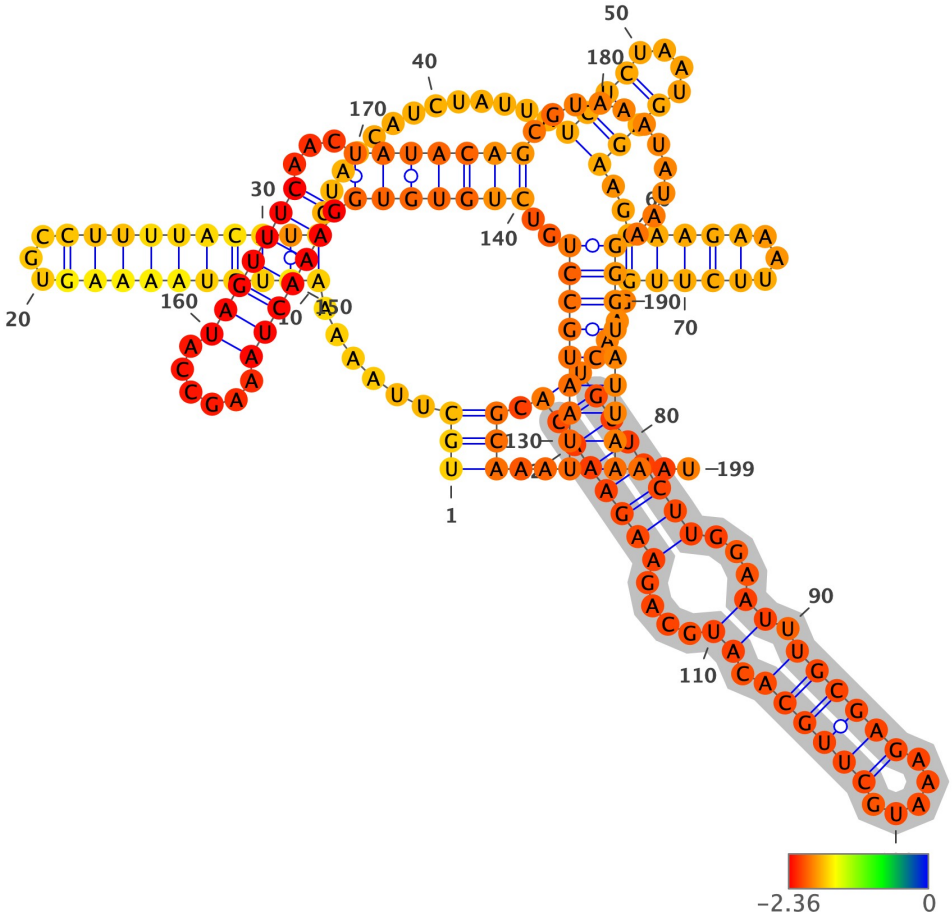
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 87 from nt 4376 to 4419 (nt 78 to 121)

```
5'-GUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAAC-3'
5'-(.....(...((.((((((.....)))))).))....).....)-3'
Motif MFE = -12.4; z-score = -2.54; 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 = -3.98; 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(+)

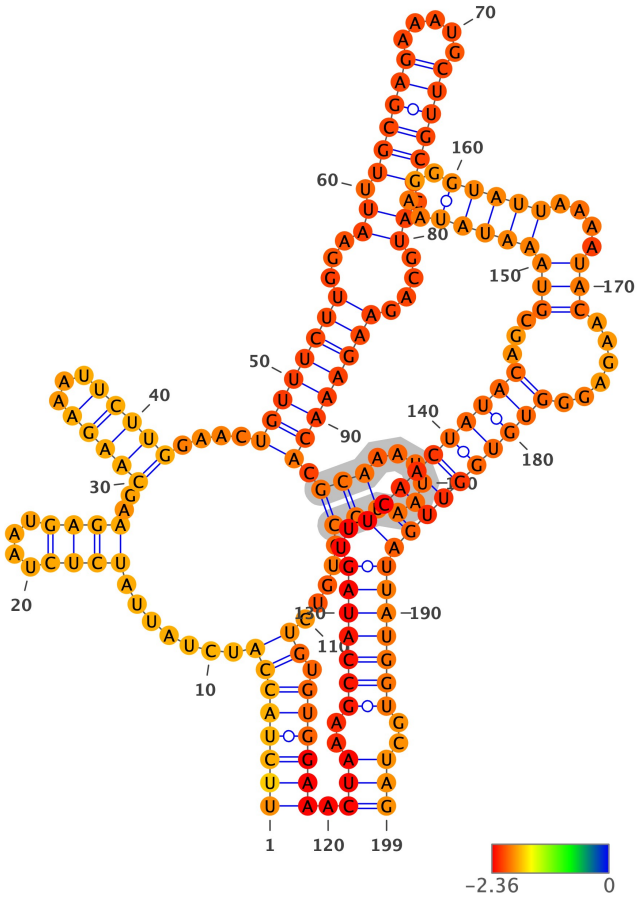
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 88 from nt 4422 to 4433 (nt 94 to 105)

```
5'-GCAAAUUAAUGC-3'
5'-(((......)))-3'
Motif MFE = -0.4; z-score = -2.15; 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 = -2.24; 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(+)

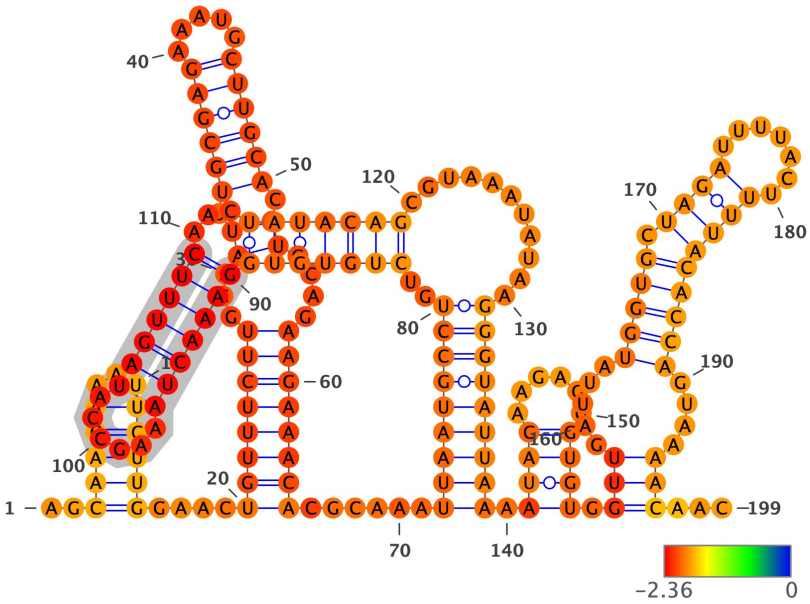
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 89 from nt 4445 to 4464 (nt 90 to 109)

```
5'-GAAACUAAAGCCAUAGUUUC-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.7; z-score = -4.21; ED = 0.29
```



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 4356 to 4554 (motif highlighted in silver):

```
5'-AGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAA
CUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAAC-3
5'-..(((((...)))))....(((((((((...((.((((((.....)))))).)).....)))))))))......(((((((((..((((((((((((((.....)))))))))))))..
.)))))))).....)))))))).((((.....)))).(((.....(((((.((((.....))))))))).....)))...-3'
MFE = -46.2; z-score = -2.14; ED = 29.11
```

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(+)

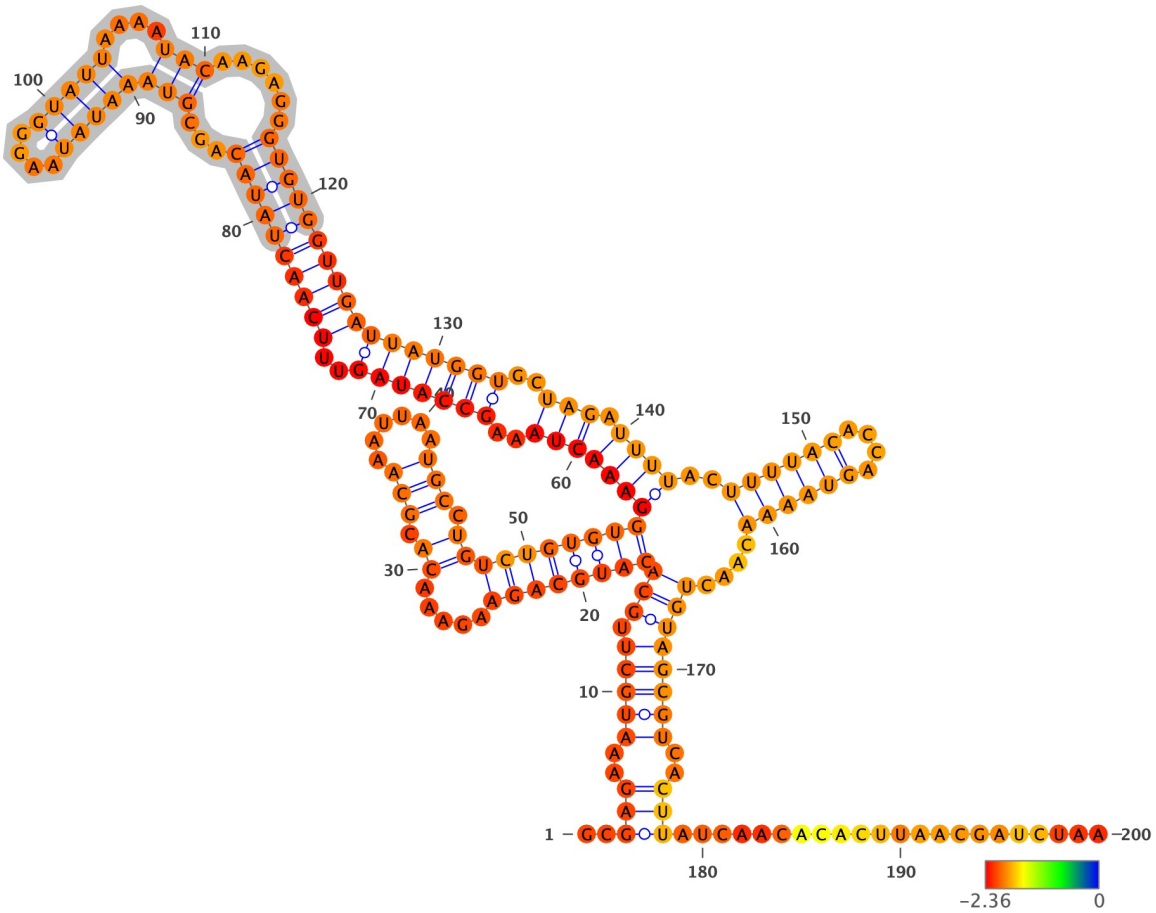
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 90 from nt 4468 to 4510 (nt 79 to 121)

```
5'-UAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUG-3'
5'-(((((...(.....................).....)))))-3'
Motif MFE = -2.2; z-score = 0.32; ED = 10.42
```



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 4390 to 4589 (motif highlighted in silver):

```
5'-GCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACA
AGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAACACACUUAACGAUCUAA-3
5'-..(((..(((((.((((((((((.....((.(((......))).)))))))))))(((((((..(((((((..((((((((((...(((((((((....)))))))))....)))).
.....)))))))))))))))))..))).)))))..((((((....))))))....))))))))..)))......................-3'
MFE = -41.4; z-score = -2.54; ED = 36.1
```

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(+)

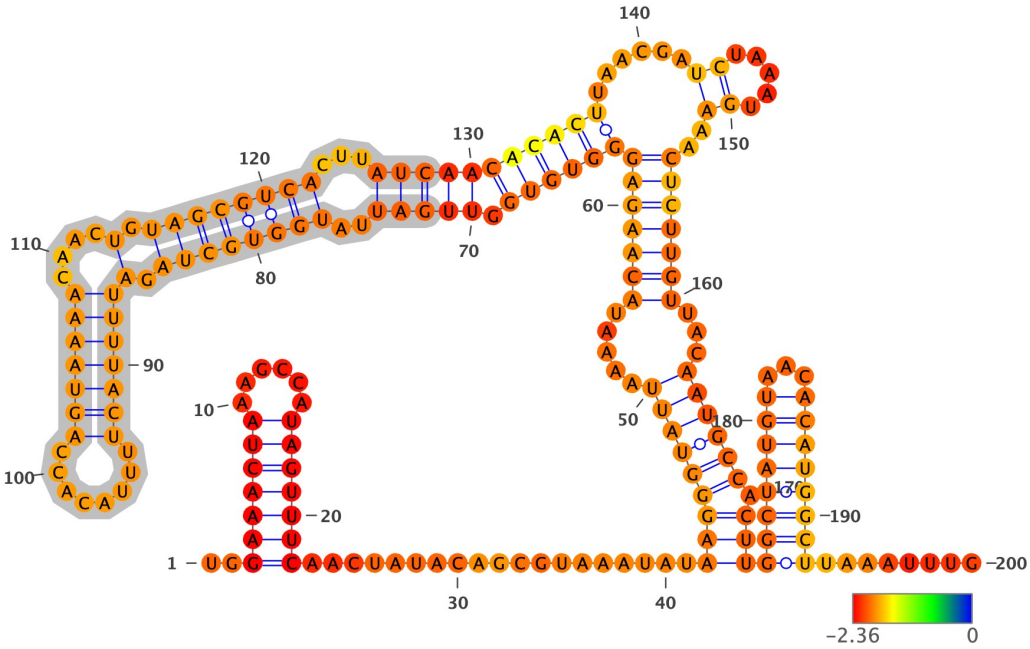
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 91 from nt 4514 to 4570 (nt 72 to 128)

```
5'-GAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUC-3'
5'-(((..(((((((((.(((((((((........)))))))....).))))))))...)))-3'
Motif MFE = -9.6; z-score = -1.11; ED = 11.22
```



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 4443 to 4642 (motif highlighted in silver):

```
5'-UGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAA
CUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUG-3
5'-..(((((((......)))))))...................(((((((((.....(((((((((((((.(((((..(((((((((.(((((((((........)))))))...
.).))))))))...)))))))))))).....((.....))..)))))))...)))))).)))((((((((...))))))))........-3'
MFE = -49.0; z-score = -3.66; ED = 21.96
```

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(+)

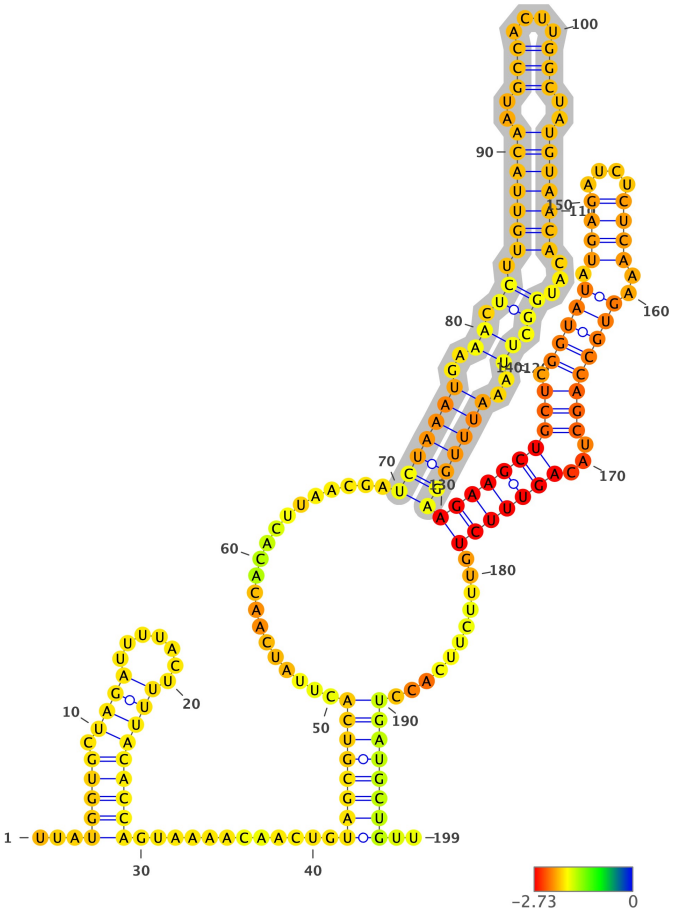
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 92 from nt 4585 to 4644 (nt 70 to 129)

```
5'-UCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUGGA-3'
5'-((.......((.((.(((((((..(((....)))).))))))))...)).)).......))-3'
Motif MFE = -15.3; z-score = -3.12; ED = 5.54
```



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 4516 to 4714 (motif highlighted in silver):

```
5'-UUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAAC
ACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUU-3
5'-...(((((.((((.......)))))))))...........(((((((.....................(((((((..((.((.(((((((..(((....))))..)))))))
)...)).))..)))))))((((((((((.(((((.((((....)))))..)))))))))...)))))))...........)))))))..-3'
MFE = -48.7; z-score = -3.19; ED = 13.84
```

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(+)

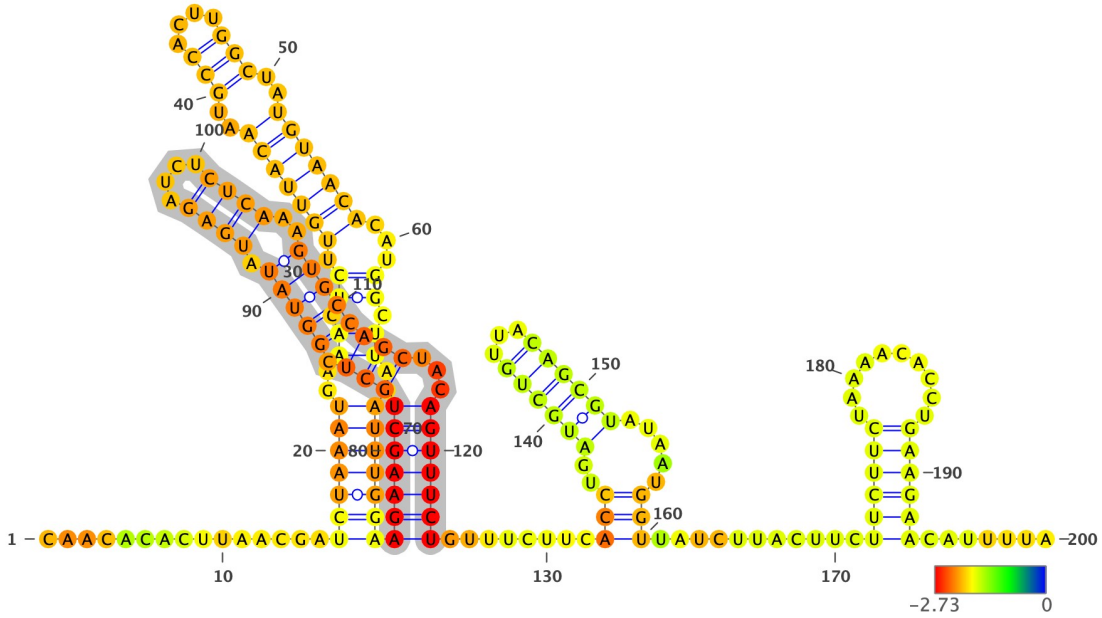
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 93 from nt 4645 to 4693 (nt 76 to 124)

```
5'-AGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCU-3'
5'-((((((((((.(((((.((((....))))..))))))))...)))))))-3'
Motif MFE = -17.2; z-score = -3.37; 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 = -2.31; 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(+)

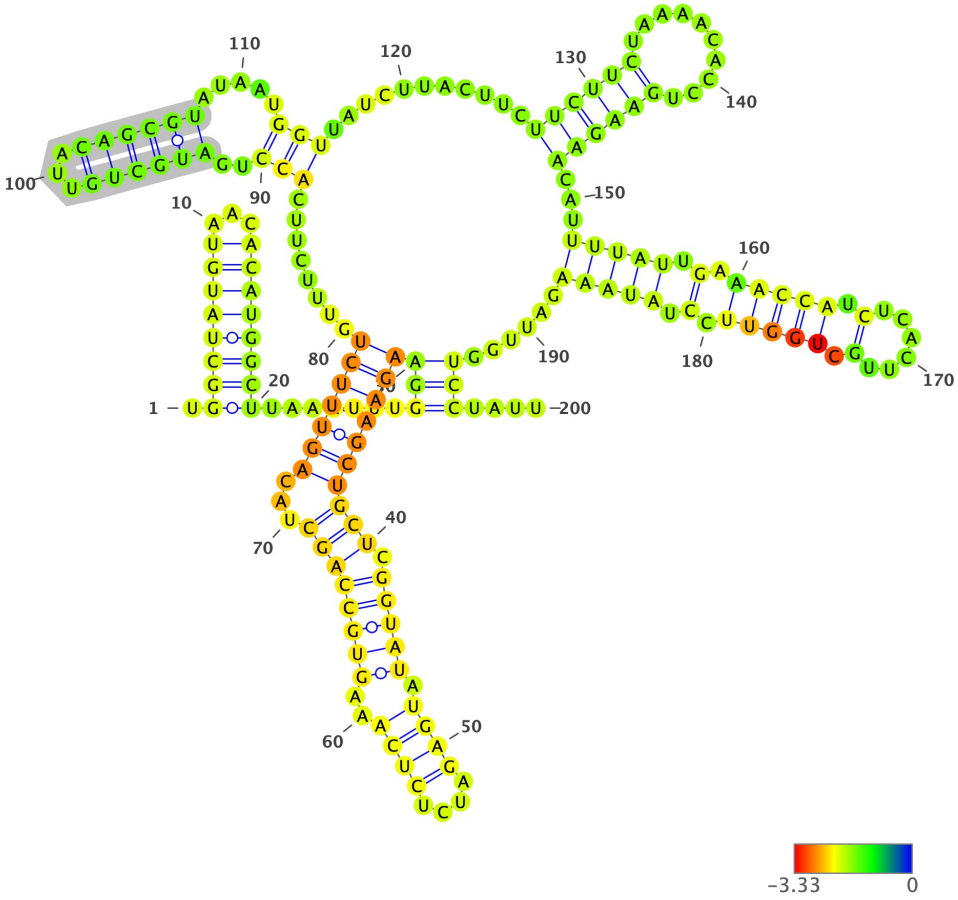
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 94 from nt 4707 to 4721 (nt 93 to 107)

```
5'-AUGCUGUUACAGCGU-3'
5'-((((((...))))))-3'
Motif MFE = -3.0; z-score = -2.36; 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 = -1.87; 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(+)

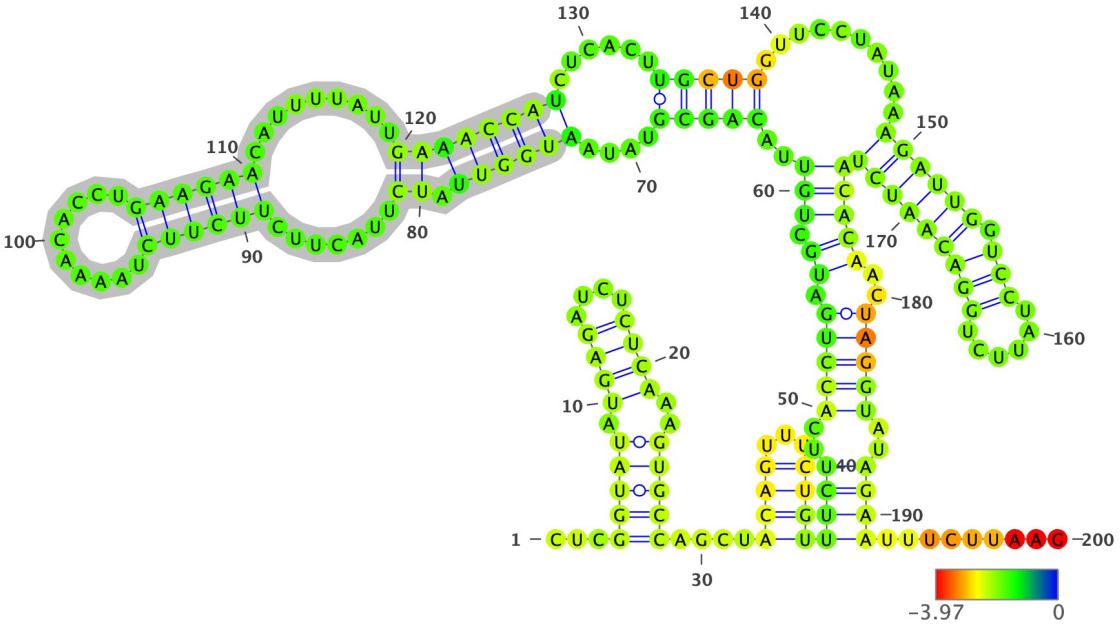
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 95 from nt 4726 to 4778 (nt 74 to 126)

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

```
5'-CUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAAC
AUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAG-3
5'-...(((((.((((....))))..)))))....((((...))))((((..(((((.((.(((..(((((....((((((.((.......((((((..........)))))).
........))))))))......)))))..........((((((.(((......)))))))))))))))..)))))..))))..........-3'
MFE = -41.5; z-score = -1.97; 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(+)

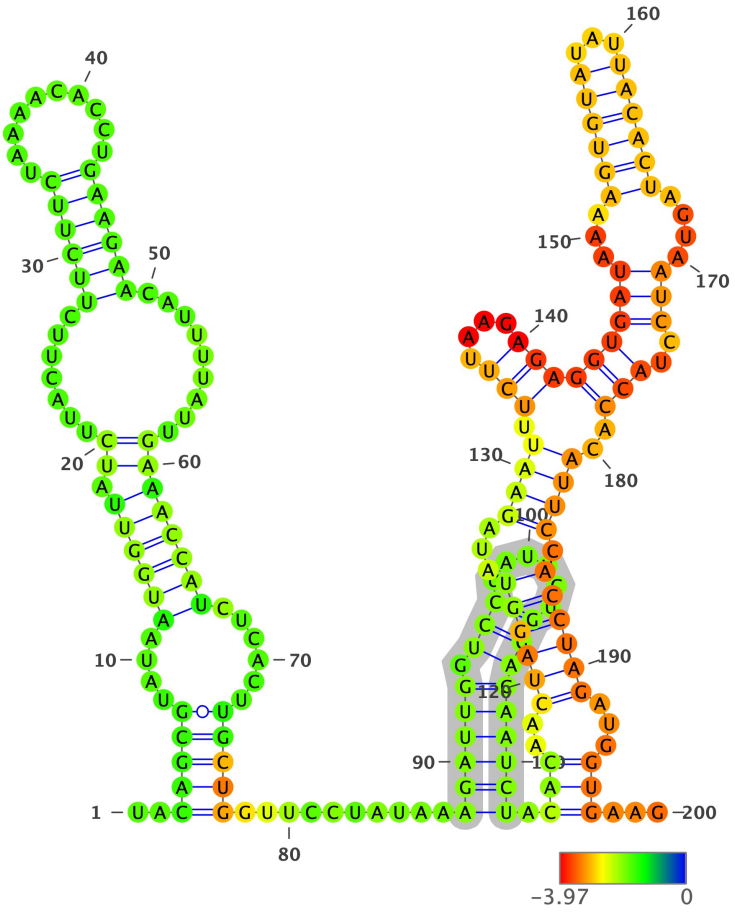
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 96 from nt 4801 to 4825 (nt 88 to 112)

```
5'-AGAUUGGUCCUAUUCUGGACAAUCU-3'
5'-((((((.(((......)))))))))-3'
Motif MFE = -8.9; z-score = -3.77; 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 = -2.07; 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(+)

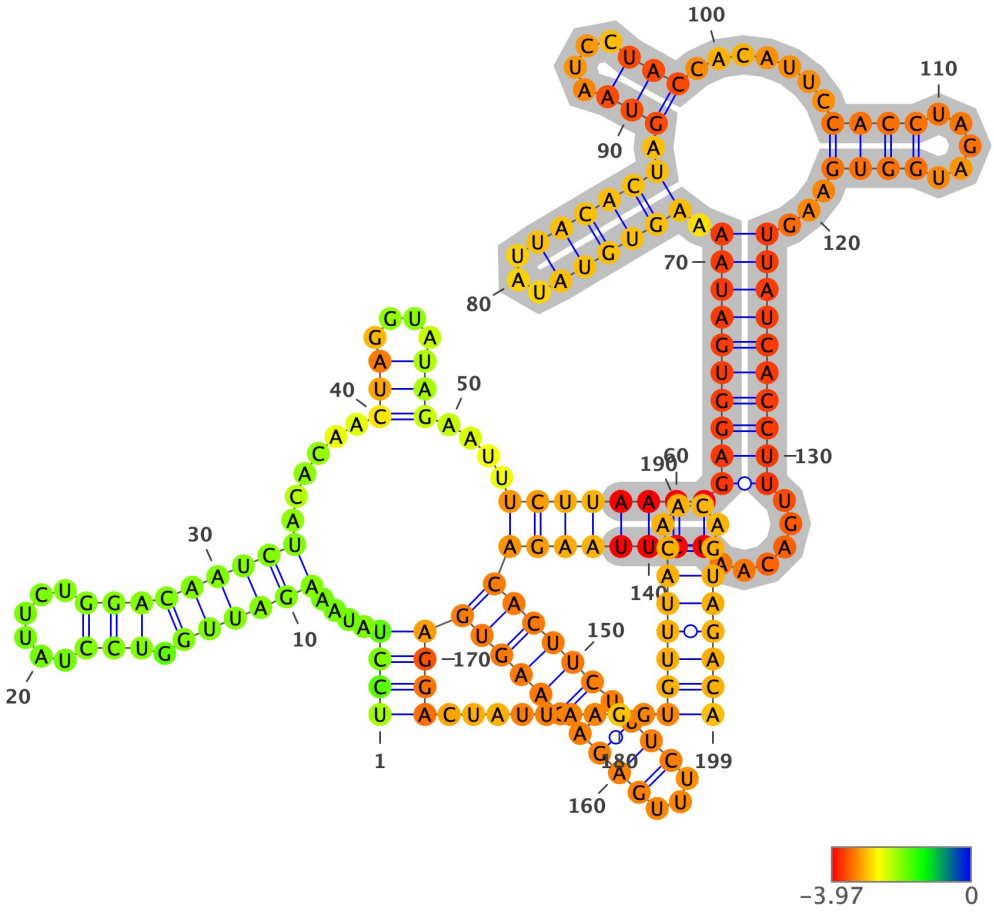
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 97 from nt 4850 to 4933 (nt 58 to 141)

```
5'-AAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUU-3'
5'-(((((((((((((((.((((((...)))))).(((....)))).......((((.....))))...)))))))))).....))))-3'
Motif MFE = -22.0; z-score = -4.17; ED = 8.98
```



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 4793 to 4991 (motif highlighted in silver):

```
5'-UCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUA
GAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACA-3
5'-((((....((((((.(((......)))))))))......(((....)))....((((((((((((((((((.((((((...)))))).(((....)))).......((((..
...))))...)))))))))).....))))))))((((((((((...)))))))))))))).........(((((((....)))))))-3'
MFE = -58.3; z-score = -5.04; ED = 18.03
```

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

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

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

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

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

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

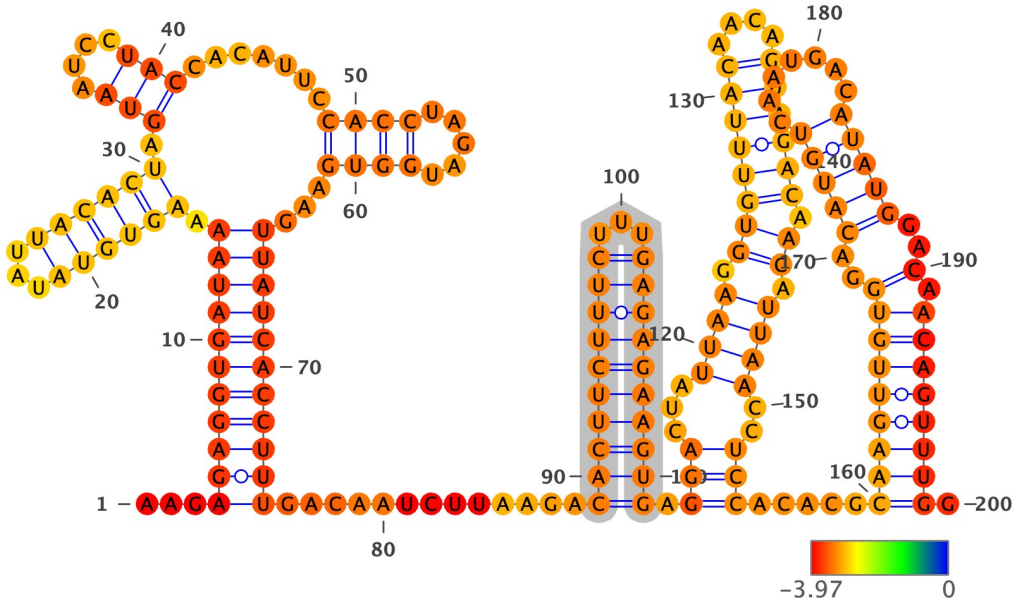
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 98 from nt 4938 to 4960 (nt 89 to 111)

```
5'-CACUUCUUUCUUUGAGAGAAGUG-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -10.7; z-score = -4.15; ED = 0.18
```



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

Extracted structure model with flanking nucleotides 4850 to 5049 (motif highlighted in silver):

```
5'-AAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUG
AGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGG-3
5'-...((((((((((.((((((...)))))).(((....))).......((((.....))))...))))))))))..............((((((((((...))))))))))
.(((...((((.(((((((((....)))))))).)).))))..))).....(((((((((..(((((.......)))))..).)))))))).-3'
MFE = -52.1; z-score = -2.99; ED = 36.8
```

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

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

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

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

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

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

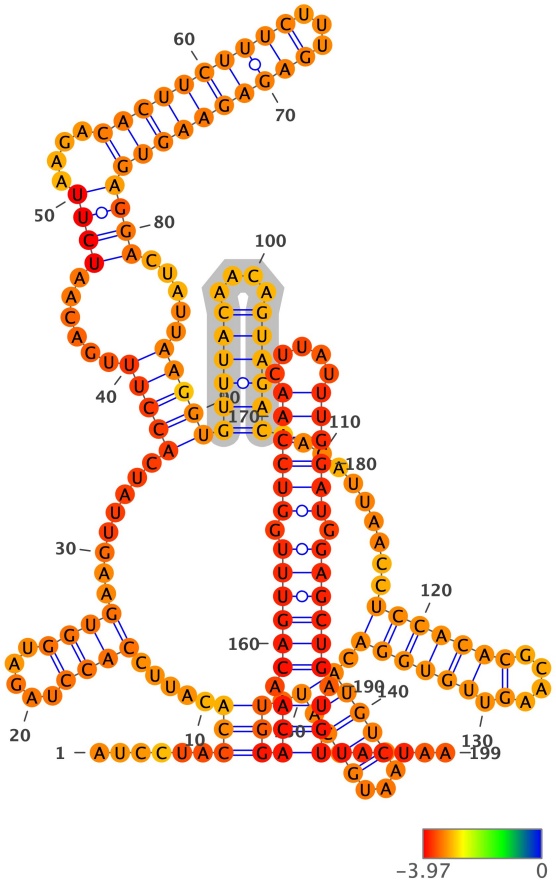
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 99 from nt 4975 to 4990 (nt 92 to 107)

```
5'-GUUUACAACAGUAGAC-3'
5'-((((((....))))))-3'
Motif MFE = -3.5; z-score = -3.82; 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 = -3.52; 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(+)

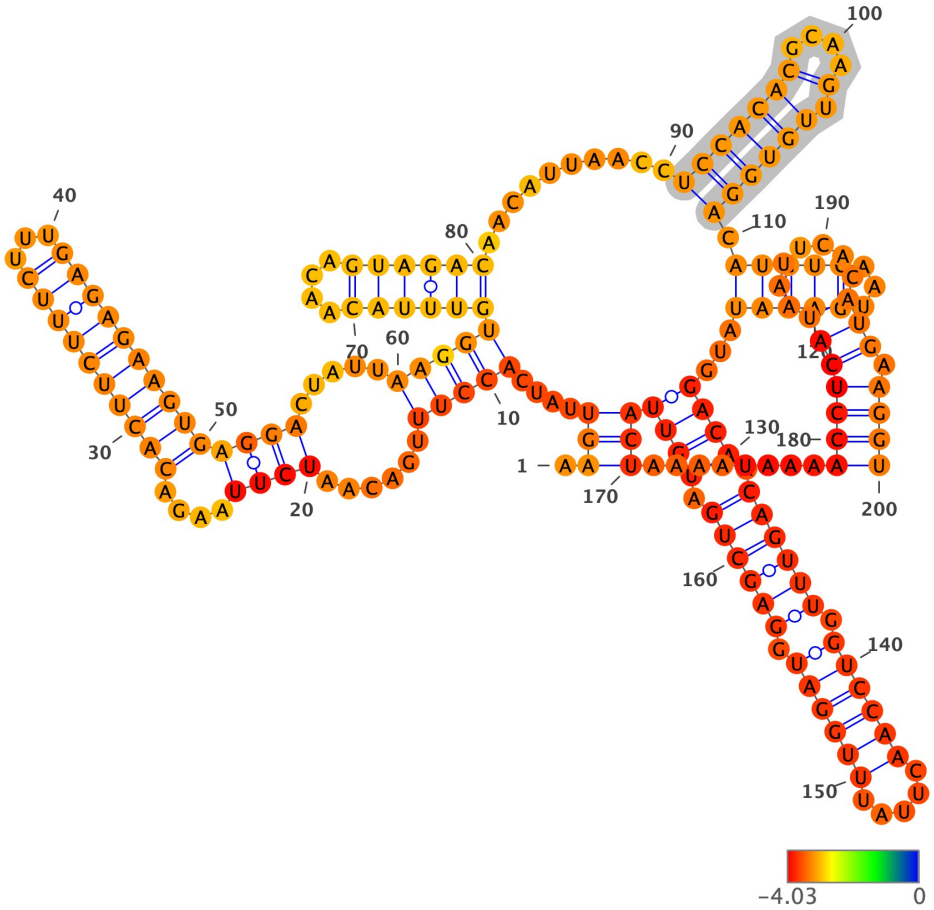
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 100 from nt 5001 to 5019 (nt 91 to 109)

```
5'-UCCACACGCAAGUUGUGGA-3'
5'-(((((((....).))))))-3'
Motif MFE = -6.7; z-score = -3.39; ED = 1.66
```



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

Extracted structure model with flanking nucleotides 4911 to 5110 (motif highlighted in silver):

```
5'-AAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACA
UGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGU-3
5'-.(((....(((((......((((....((((((((((...)))))))))))))))).....)))))((((((....))))))..........(((((((....).)))))).(
((((...)))))...((((.((((((.((((((.....)))))).)))))).)))))))........(((((((.......))).))))-3'
MFE = -54.9; z-score = -4.07; 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(+)

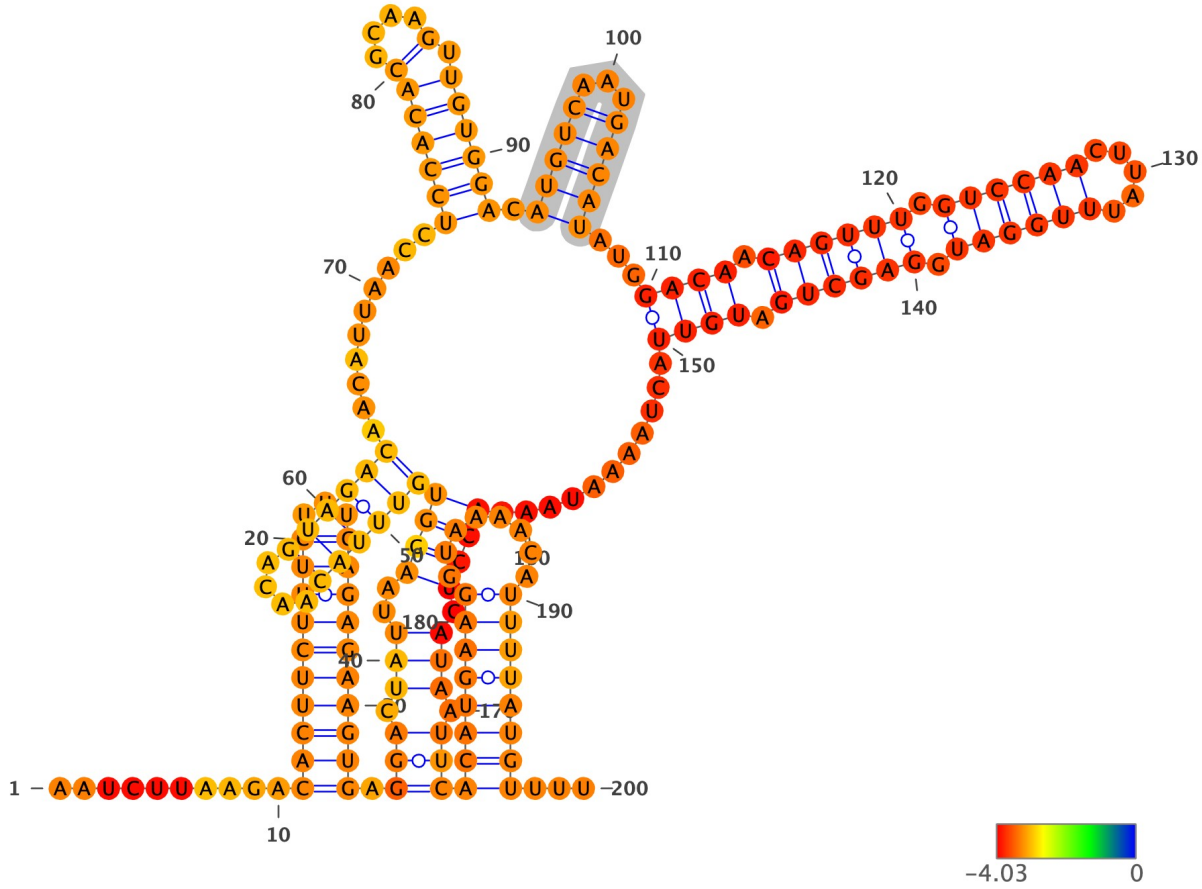
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 101 from nt 5021 to 5033 (nt 94 to 106)

```
5'-AUGUCAAUGACAU-3'
5'-(((((...)))))-3'
Motif MFE = -1.9; z-score = -7.34; 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 = -4.06; 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(+)

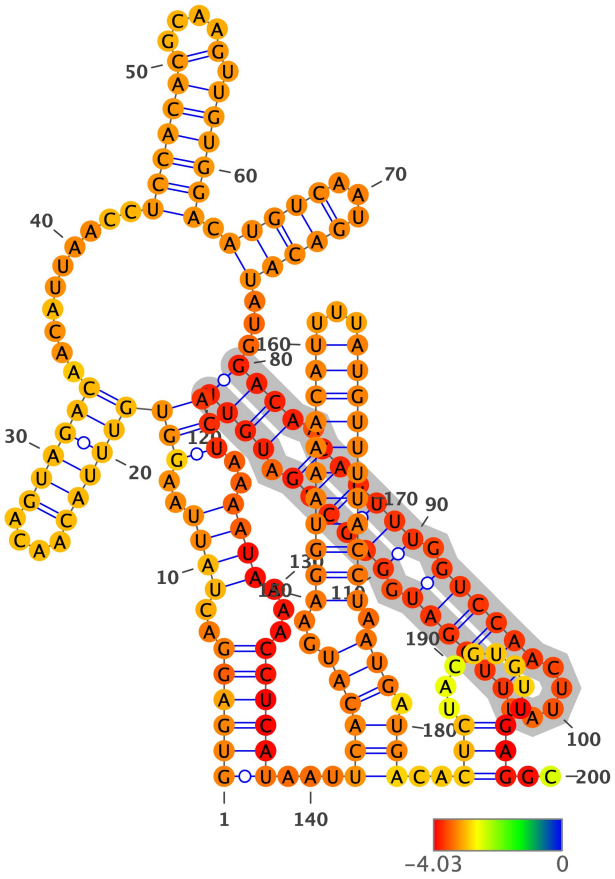
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 102 from nt 5037 to 5077 (nt 80 to 120)

```
5'-GACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUU-3'
5'-((((.((((((.((((((.....)))))).)))))).))))-3'
Motif MFE = -17.8; z-score = -4.45; 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 = -4.41; 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(+)

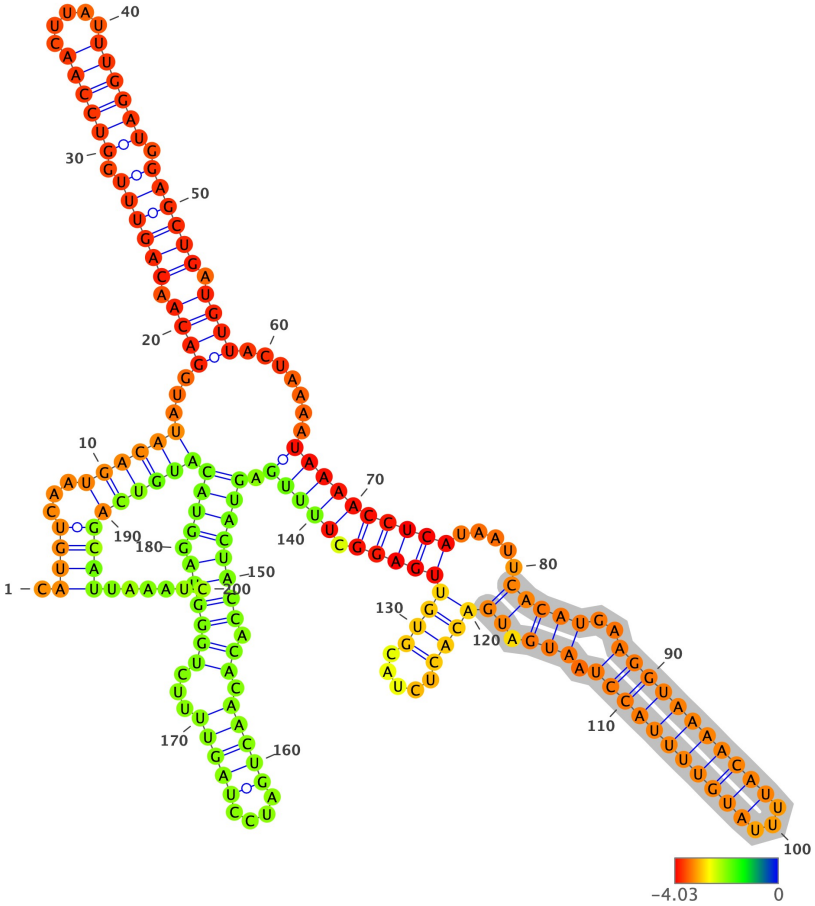
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 103 from nt 5100 to 5138 (nt 81 to 119)

```
5'-CACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUG-3'
5'-(((((..(((((((((((...)))))))))))).))).))-3'
Motif MFE = -12.8; z-score = -4.92; ED = 3.26
```



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 5020 to 5219 (motif highlighted in silver):

```
5'-CAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACC
UAAUGAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUC-3
5'-.((((...((((((...((((.((((((.((((((.....)))))).)))))).))))).......((((((((((.....(((((..((((((((((((...)))))))))))
).))).))((((.....)))))))))).))))).((((((((.((.(((((....)))))...)))))).))))))))))))))).....-3'
MFE = -57.9; z-score = -4.48; ED = 15.18
```

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(+)

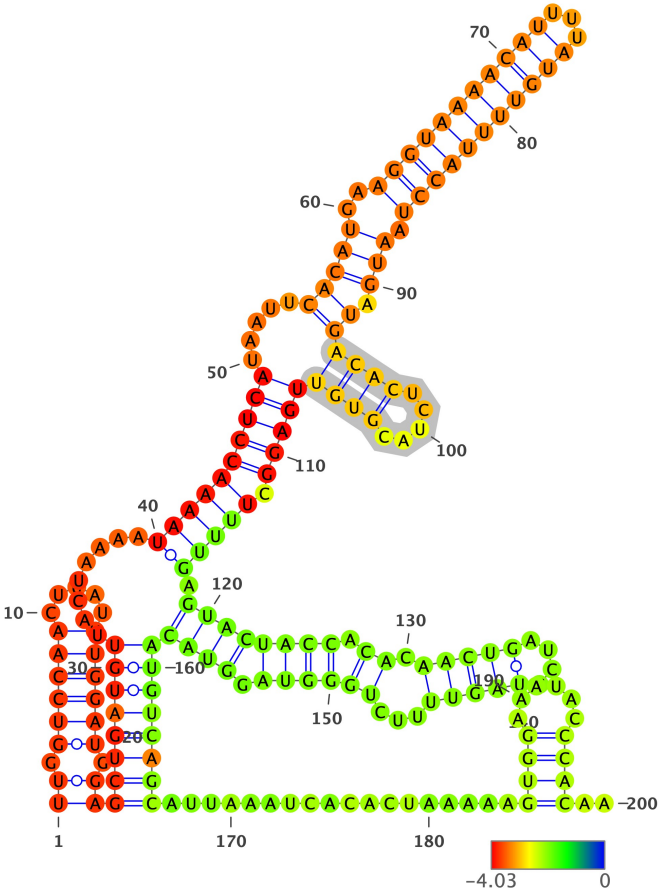
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 104 from nt 5139 to 5151 (nt 94 to 106)

```
5'-ACACUCUACGUGU-3'
5'-((((.....))))-3'
Motif MFE = -1.7; z-score = -4.45; 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 5046 to 5245 (motif highlighted in silver):

```
5'-UUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGG
CUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAA-3
5'-((.((((((.....)))))).))((((((((.........((((((((((.....(((((..((((((((((((...)))))))))))).))).))((((.....)))))))))
.))))).((((((((.((.(((((....)))))...)))))).))))))))))))).................((((......))))..-3'
MFE = -52.5; z-score = -3.65; ED = 20.73
```

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

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

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

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

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

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

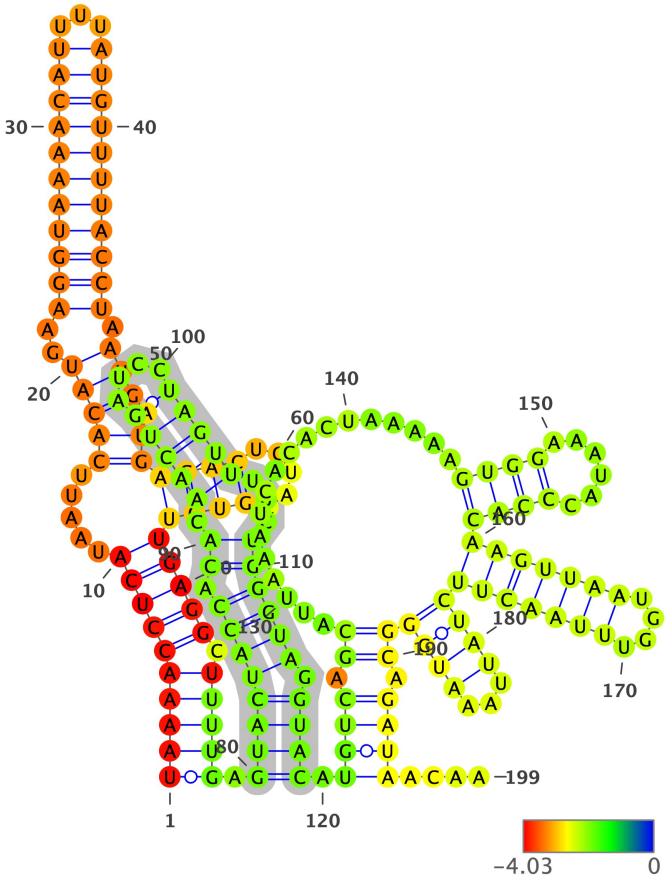
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 105 from nt 5164 to 5203 (nt 80 to 119)

```
5'-GUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUAC-3'
5'-((((((((.((.(((((....)))))...)))))).))))-3'
Motif MFE = -9.8; z-score = -2.14; ED = 4.77
```



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

Extracted structure model with flanking nucleotides 5085 to 5283 (motif highlighted in silver):

```
5'-UAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGG
GUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAA-3
5'-(((((((((((.....(((((..((((((((((((...)))))))))))).))).))((((.....))))))))).))))).((((((((.((.(((((....)))))...)))
))).)))).((((.((.....................((((......))))((((((((....)))))))((((...)))))).))))....-3'
MFE = -45.7; z-score = -3.16; 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(+)

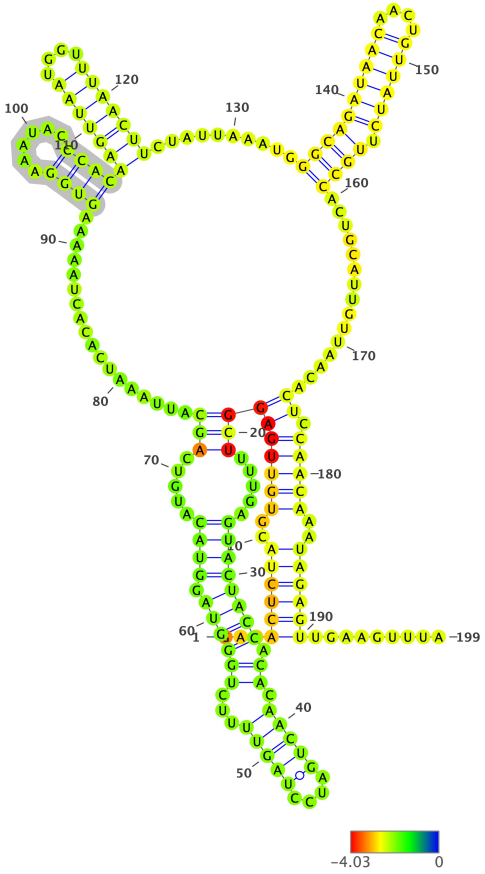
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 5230 to 5243 (nt 93 to 106)

```
5'-GUGGAAAUACCCAC-3'
5'-((((.....))))-3'
Motif MFE = -3.7; z-score = -6.26; 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 5138 to 5336 (motif highlighted in silver):

```
5'-GACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGUU
AAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUA-3
5'-...((((((..((((((((((.....((((((((.((.(((((....)))))...)))))))..))))).....)))..................((((......))))))(((((
((....)))))))..........((((((((((....))))))).))))..............)).))))))..))))))..........-3'
MFE = -48.0; z-score = -3.19; ED = 27.73
```

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(+)

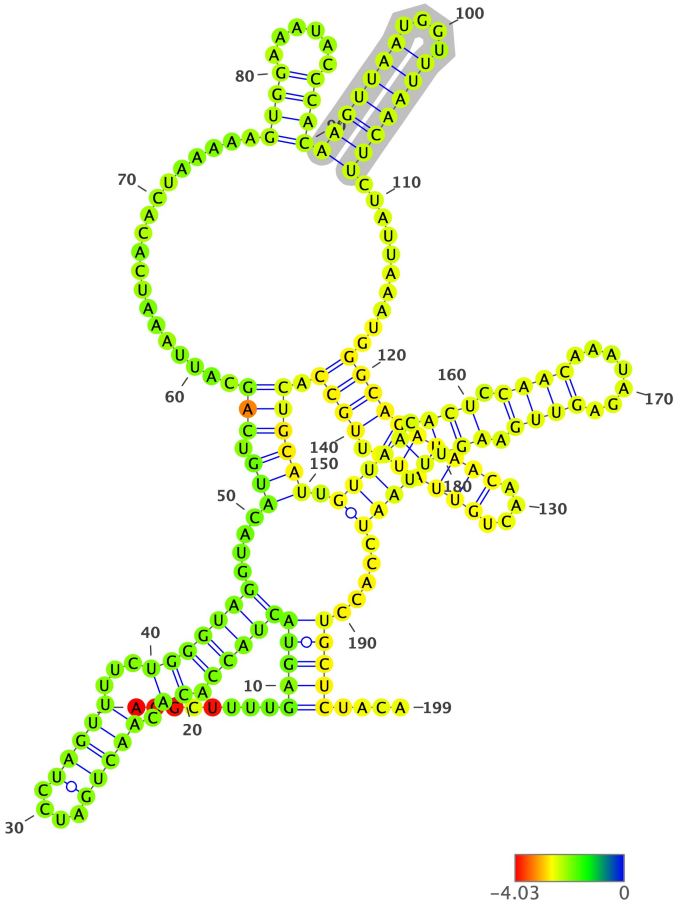
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 107 from nt 5244 to 5261 (nt 91 to 108)

```
5'-AAGUUAAUGGUUUAACUU-3'
5'-(((((((....)))))))-3'
Motif MFE = -3.4; z-score = -3.69; 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 5154 to 5352 (motif highlighted in silver):

```
5'-AGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUA
UUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACA-3
5'-........((((((((((.((.(((((....)))))...)))))))....(((.(((.....................((((......))))(((((((....)))))))...
.......((((((((((....))))))).)))).)))))).(((((.(((.((((.......)))).)))))))).....)))))....-3'
MFE = -42.6; z-score = -2.19; ED = 33.14
```

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(+)

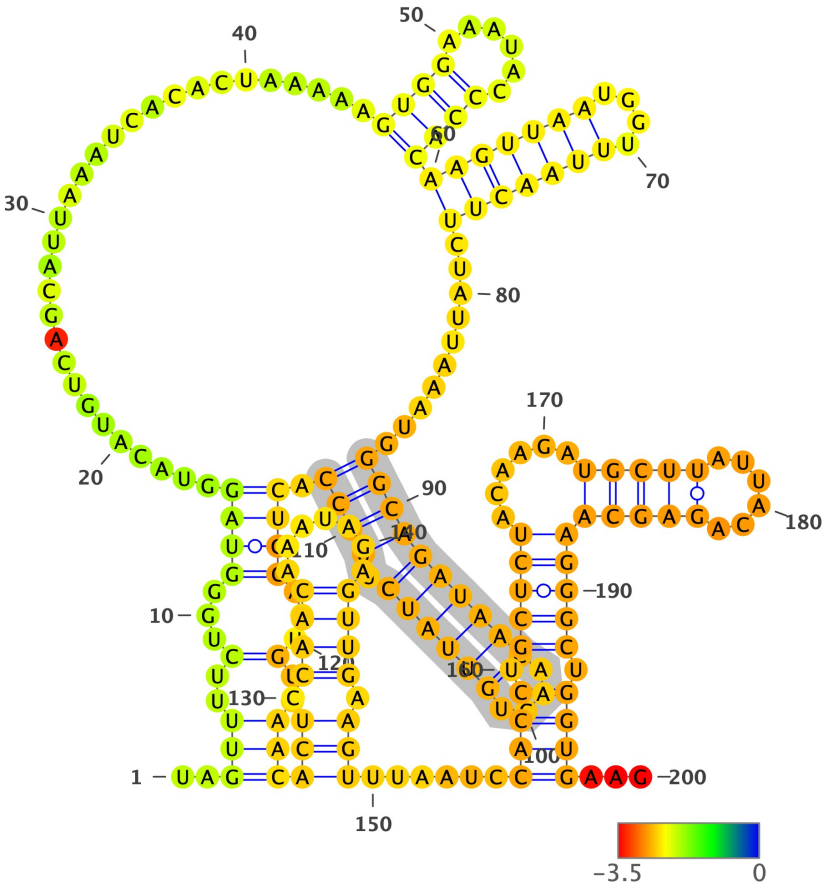
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 108 from nt 5272 to 5296 (nt 88 to 112)

```
5'-GGCAGAUAACAACUGUUAUCUUGCC-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -10.9; z-score = -4.75; 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 = -2.32; 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(+)

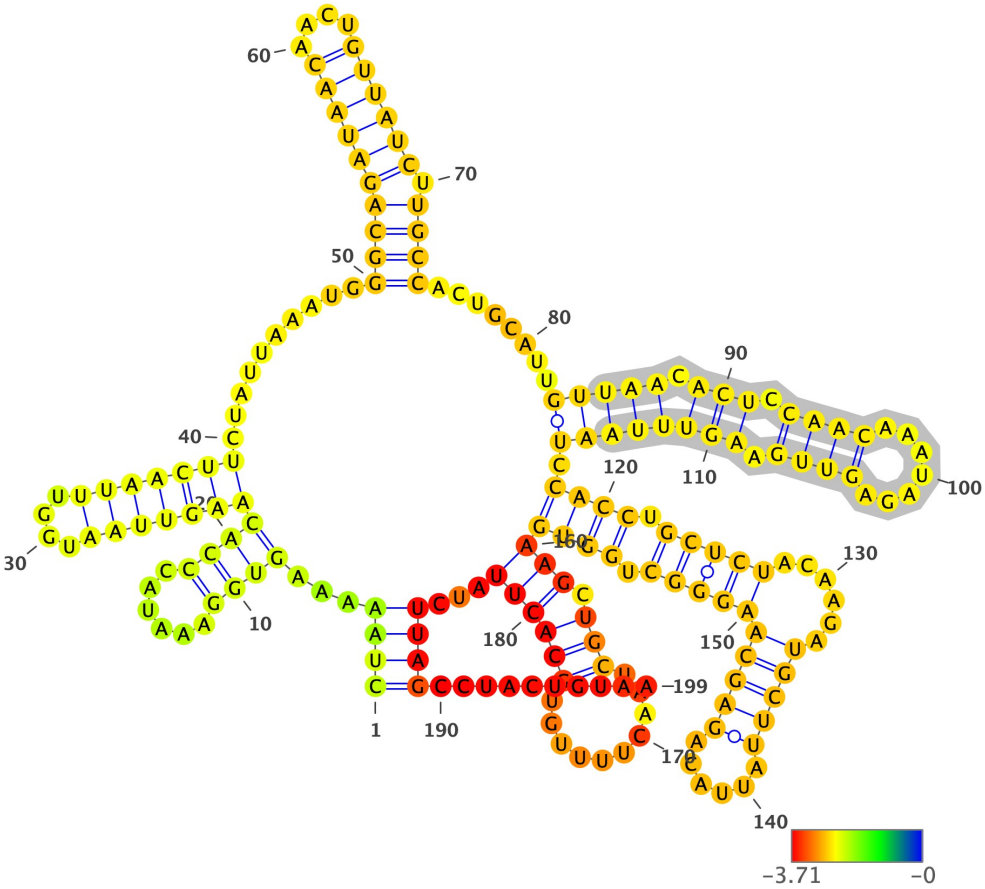
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 109 from nt 5307 to 5336 (nt 85 to 114)

```
5'-UAACACUCCAACAAAUAGAGUUGAAGUUUA-3'
5'-(((.(((.((((.......)))).))))))-3'
Motif MFE = -3.9; z-score = -1.94; 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 5223 to 5421 (motif highlighted in silver):

```
5'-CUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGU
UUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAA-3
5'-((((...((((......))))(((((((....)))))))..........((((((((((....))))))).))))........(((((.(((.((((.......)))).)))
))))).((((.(((((......(((((......)))))))))).))))(((.(((..........))))))...))))..........-3'
MFE = -48.6; z-score = -2.72; ED = 37.31
```

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(+)

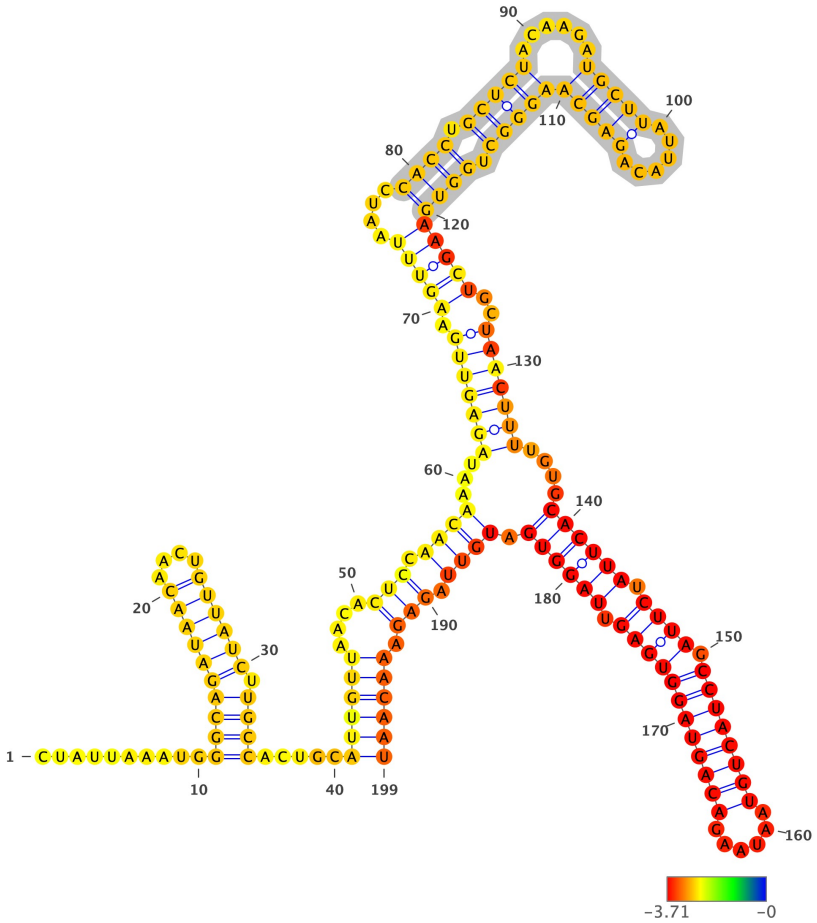
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 110 from nt 5340 to 5381 (nt 79 to 120)

```
5'-CACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUG-3'
5'-((((.(((((......(((((......)))))))))).))))-3'
Motif MFE = -14.9; z-score = -3.02; 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 = -4.75; 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(+)

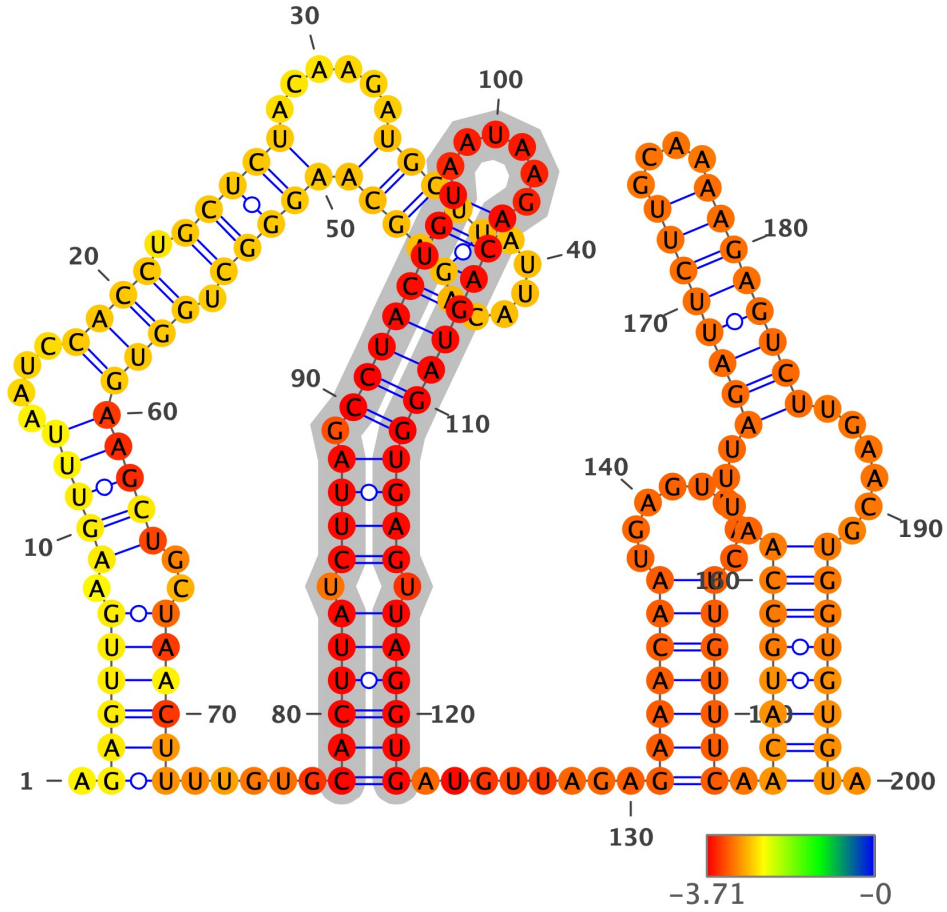
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 111 from nt 5400 to 5444 (nt 78 to 122)

```
5'-CACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUG-3'
5'-((((((.((((.((((((((.....))))))))))))).))))))-3'
Motif MFE = -20.7; z-score = -5.34; 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 = -4.85; 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(+)

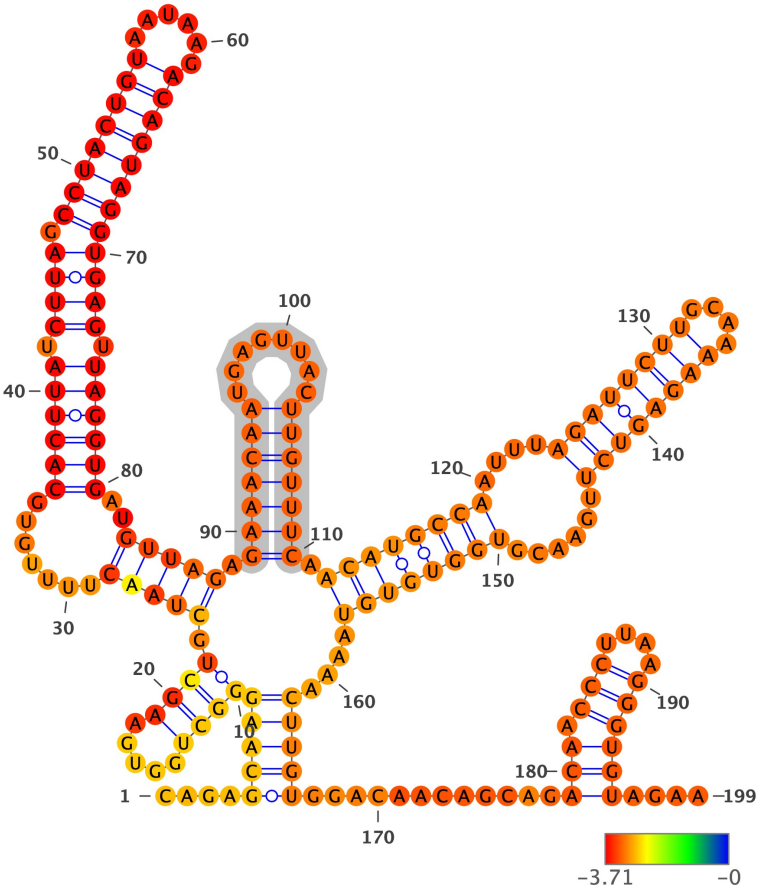
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 112 from nt 5453 to 5474 (nt 89 to 110)

```
5'-GAAACAAUGAGUUACUUGUUUC-3'
5'-(((((((........)))))))-3'
Motif MFE = -4.2; z-score = -2.36; 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 = -3.84; 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(+)

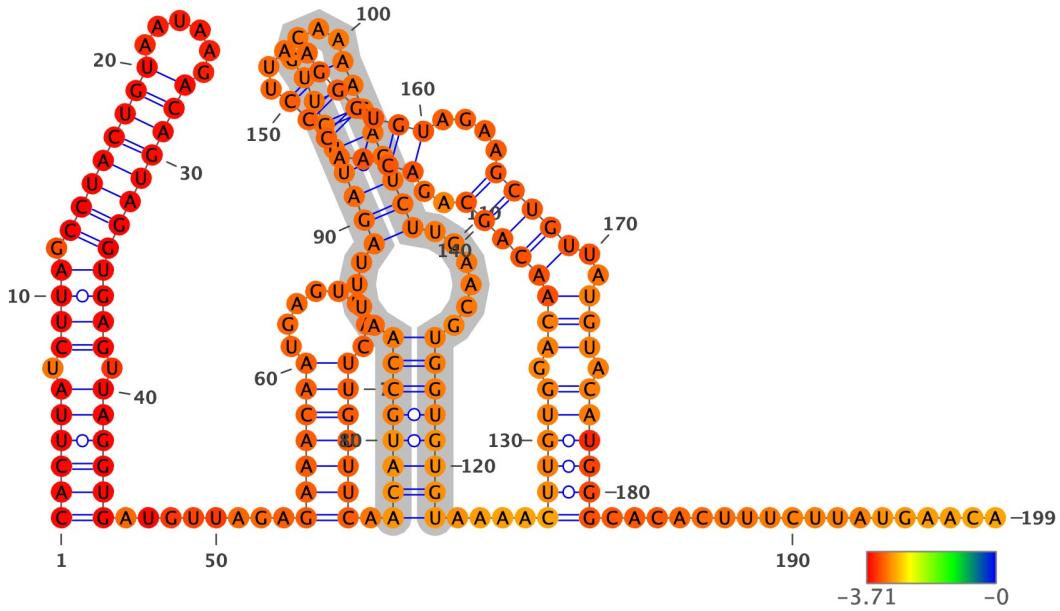
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 113 from nt 5476 to 5521 (nt 77 to 122)

```
5'-ACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGU-3'
5'-(((((((((....(((((((((....)))))))))......)))))))))-3'
Motif MFE = -16.9; z-score = -3.52; 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 = -4.67; 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(+)

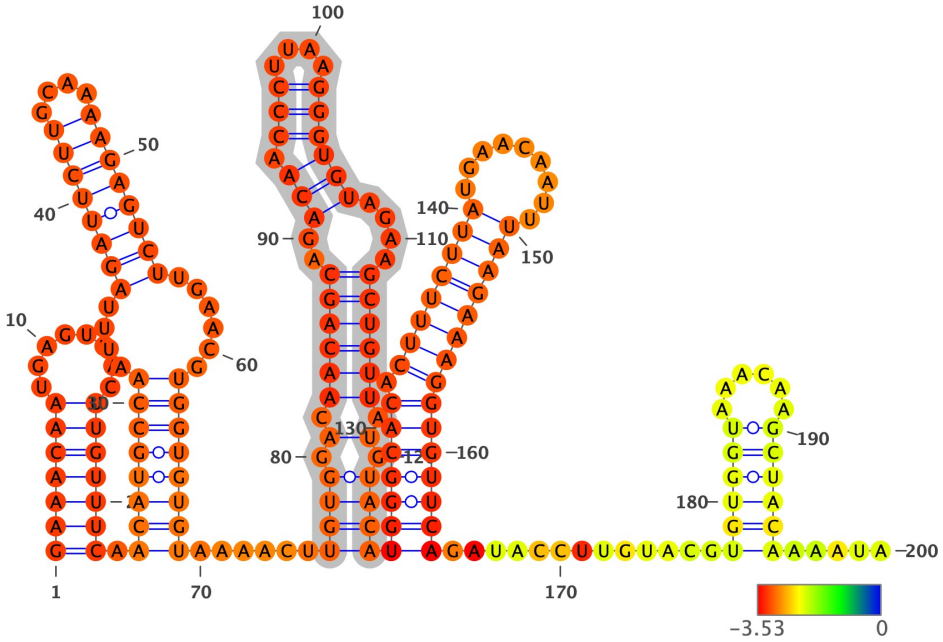
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 114 from nt 5528 to 5576 (nt 76 to 124)

```
5'-UGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACA-3'
5'-((((.(.(((((((..(((.(((....)))))))....)))))))).).))))-3'
Motif MFE = -15.9; z-score = -3.42; 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 5453 to 5652 (motif highlighted in silver):

```
5'-GAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAA
GCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUA-3
5'-(((((((........)))))))..(((((((((....(((((((((....)))))))))......)))))))).....((((.(.((((((..(((.(((....)))))))....
))))))).).))))(((((((.(((((((((.........)))))))))))))))).............((((((......))))))......-3'
MFE = -61.9; z-score = -5.36; ED = 15.42
```

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(+)

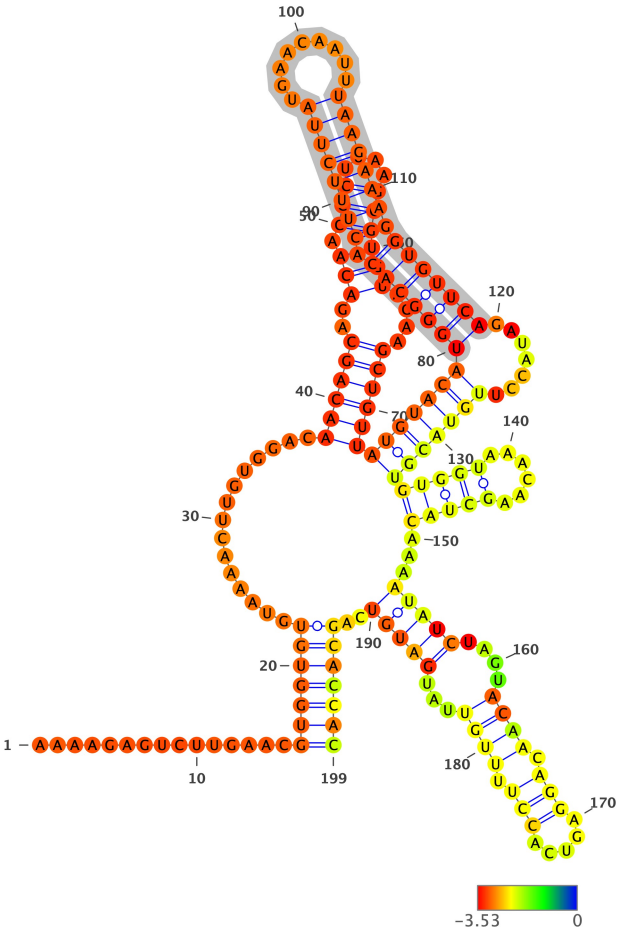
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 115 from nt 5577 to 5616 (nt 80 to 119)

```
5'-UGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCA-3'
5'-(((((((.((((((((.........)))))))))))))))-3'
Motif MFE = -15.3; z-score = -4.15; ED = 1.09
```



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

Extracted structure model with flanking nucleotides 5498 to 5696 (motif highlighted in silver):

```
5'-AAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAA
GGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCAC-3
5'-...............(((((((...............((((((..(((.(((....))))))....))))))((((((((((((((.((((((((.........)))))))
))))))))).......)))))))(((((......)))))...(((((....((((.(((.....))).))))...)))))..)))))))-3'
MFE = -56.0; z-score = -3.64; ED = 33.57
```

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

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

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

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

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

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

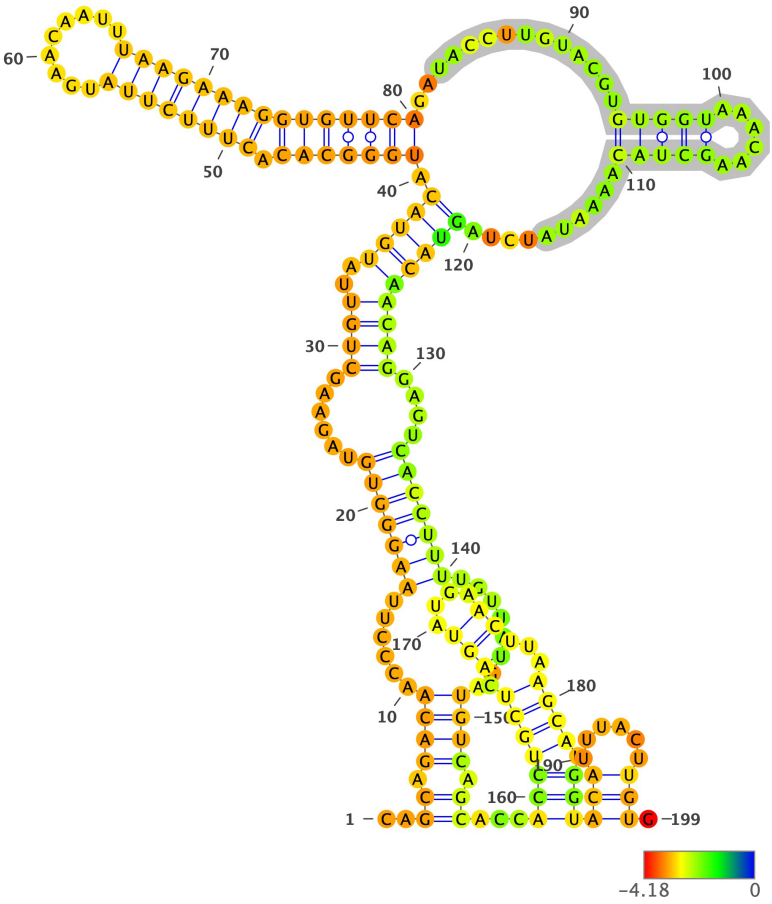
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 116 from nt 5619 to 5652 (nt 83 to 116)

```
5'-UACCUUGUACGUGUGGUAAACAAGCUACAAAAUA-3'
5'-((...(.......((..........)).)...))-3'
Motif MFE = -5.3; z-score = -1.61; ED = 8.69
```



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 5537 to 5735 (motif highlighted in silver):

```
5'-CAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACA
AAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUG-3
5'-..((.((((......(((((((......((((..(((((.(((((((.((((((((.........))))))))))))))).............(((((......))))).
.........))))))))....)))))))........)))).))...(((((((.(((....)))..)))).)))(((......))).-3'
MFE = -48.3; z-score = -2.58; ED = 22.37
```

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(+)

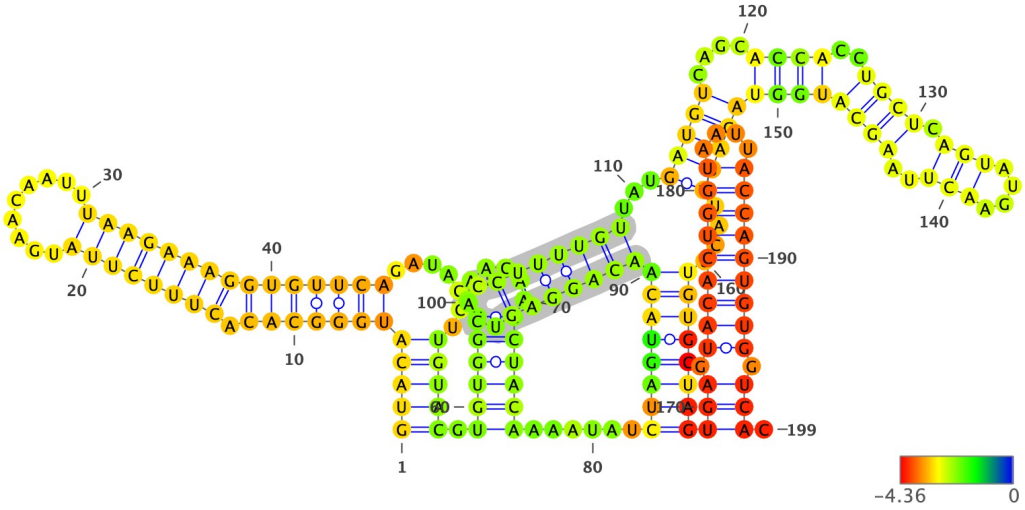
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 117 from nt 5662 to 5679 (nt 91 to 108)

```
5'-ACAGGAGUCACCUUUUGU-3'
5'-(((((((....)))))))-3'
Motif MFE = -3.7; z-score = -2.4; 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 5572 to 5770 (motif highlighted in silver):

```
5'-GUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAU
GAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCAC-3
5'-(((((((((((.((((((((.........)))))))))))))).......))))).((((((......))))))......((((((((((((((....)))))))...
(((((....((((..((((.(((....)))..)))))))))))))....))))))))(((.(((((((((....)))))))))).))).-3'
MFE = -63.5; z-score = -4.56; ED = 30.96
```

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

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

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

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

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

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

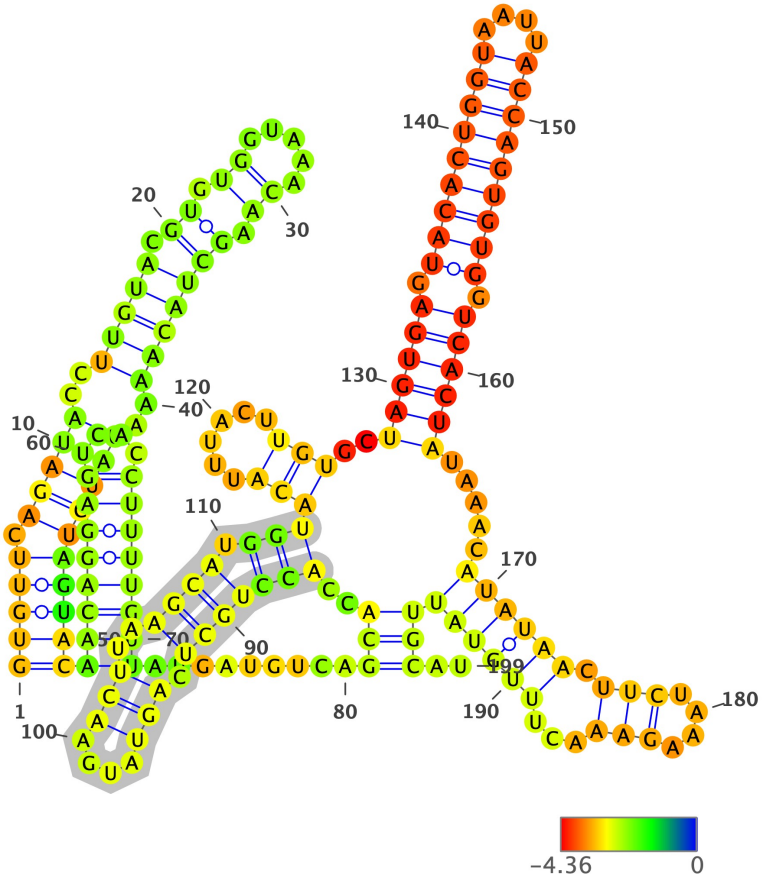
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 118 from nt 5695 to 5722 (nt 86 to 113)

```
5'-ACCUGCUCAGUAUGAACUUAAGCAUGGU-3'
5'-(..((((.(((....)))..))))...)-3'
Motif MFE = -6.4; z-score = -1.67; ED = 1.61
```



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

Extracted structure model with flanking nucleotides 5610 to 5808 (motif highlighted in silver):

```
5'-GUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUG
GUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAU-3
5'-(((((.(((((..(((((.((.((.....)).)))))))..))))))))))((((((((....))))))))).........(((..(((((((.(((....)))..)))).)
))(((......)))..((((((.((((((((((....)))))))))).))))))).....((((((.(((....)))...))))))))..-3'
MFE = -49.7; z-score = -3.22; ED = 48.21
```

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, 266-13468(+)

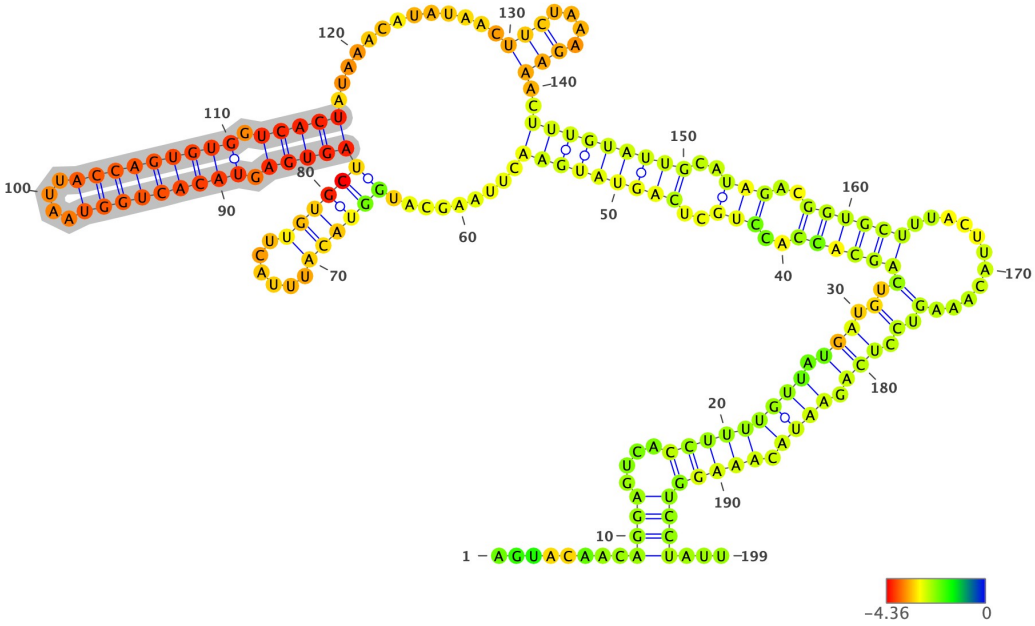
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 119 from nt 5738 to 5771 (nt 83 to 116)

```
5'-AGUGAGUACACUGGUAAUUACCAGUGUGGUCACU-3'
5'-(((((.((((((((((....)))))))))).)))))-3'
Motif MFE = -20.9; z-score = -5.78; 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 5656 to 5854 (motif highlighted in silver):

```
5'-AGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGG
UCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUU-3
5'-........((((....((((((((((.(((.(.(((((((..(((..((((((((((.........((((((......))))))(((((.((((((((((....))))))))).
)))))).............(((....)))..))))))))))..)))..))))))...........).).))).)))).))))))))))...-3'
MFE = -51.7; z-score = -3.09; ED = 63.27
```

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, 266-13468(+)

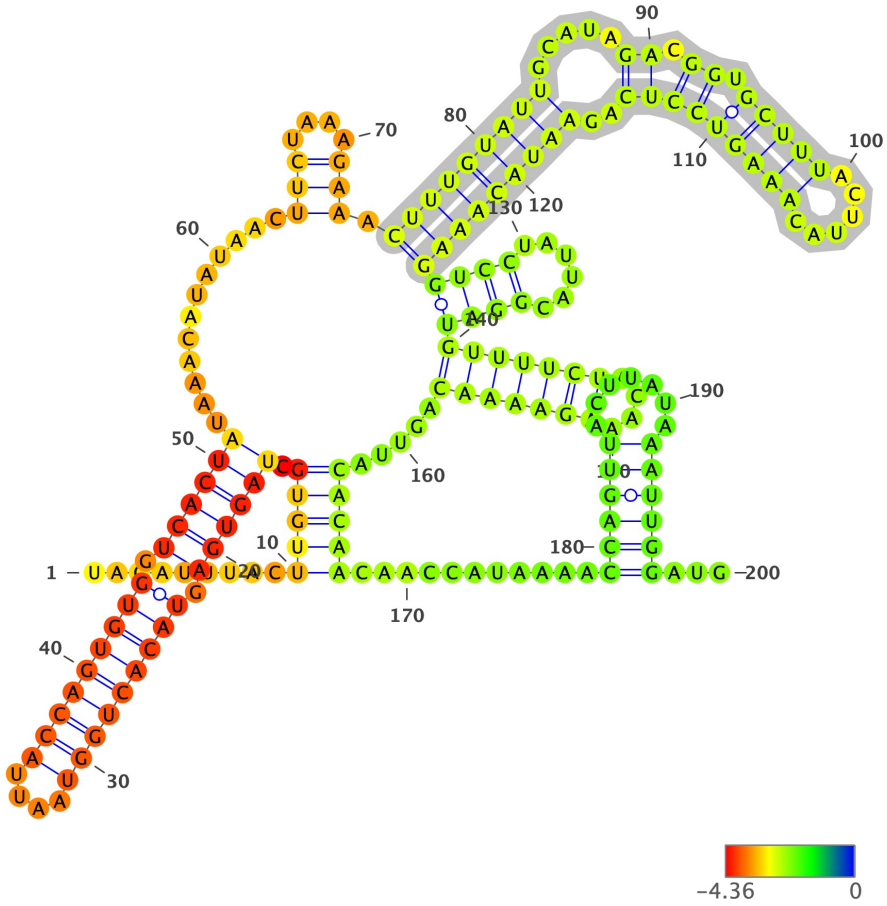
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 120 from nt 5796 to 5846 (nt 75 to 125)

```
5'-CUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAG-3'
5'-(((((((((.....((.((.(((((.....)))))))))..)))))))))-3'
Motif MFE = -10.9; z-score = -2.13; 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 = -4.62; 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(+)

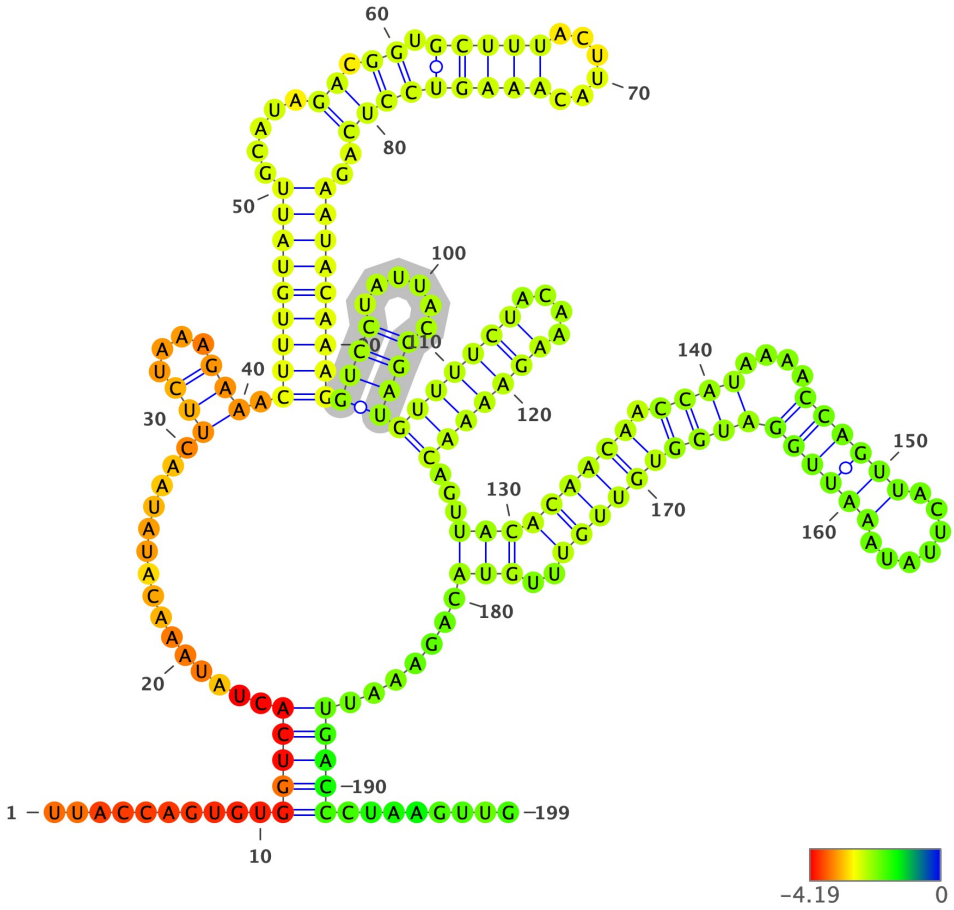
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 121 from nt 5847 to 5860 (nt 93 to 106)

```
5'-GUCCUAUUACGGAU-3'
5'-((((......))))-3'
Motif MFE = -2.6; z-score = -3.63; 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 = -2.52; 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(+)

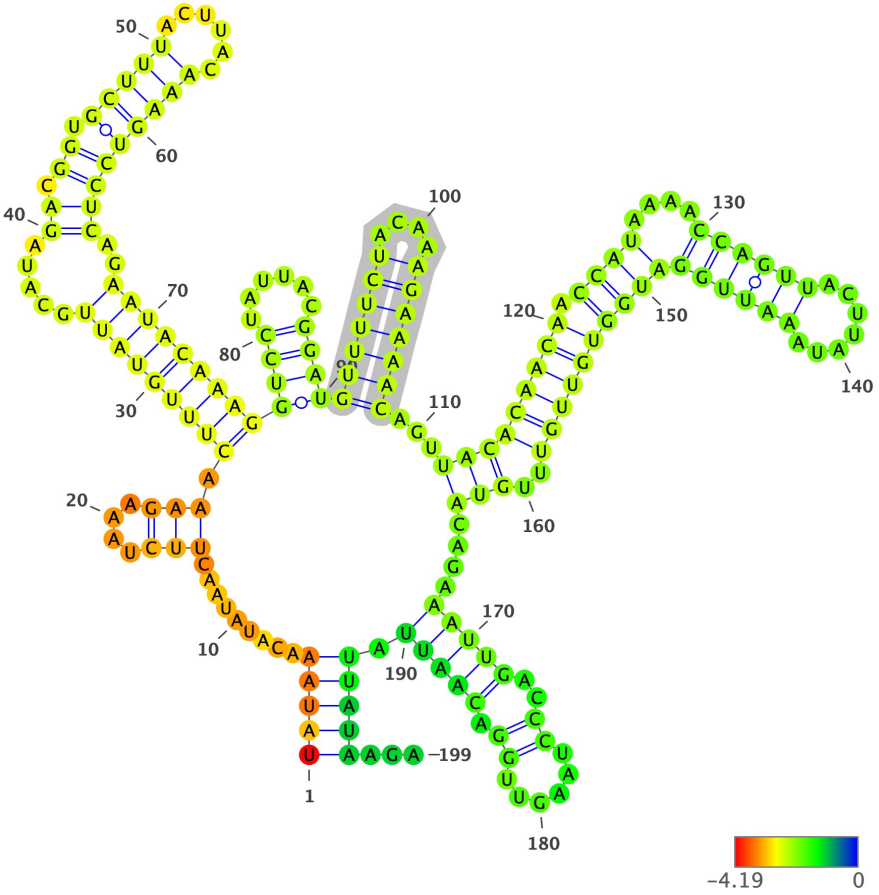
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 122 from nt 5861 to 5878 (nt 91 to 108)

```
5'-GUUUUCUACAAAGAAAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -5.51; ED = 0.35
```



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

Extracted structure model with flanking nucleotides 5771 to 5969 (motif highlighted in silver):

```
5'-UAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGU
UACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGA-3
5'-(((((.........(((....))).((((((((((.....((.((.(((((.....)))))))))..)))))))))(((.....)))))(((((((....)))))))...
(((((((((.((((....((((((.......))))))))))))))))))..)))....((((((..((.....)).)))))).))))))...-3'
MFE = -39.8; z-score = -2.37; 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(+)

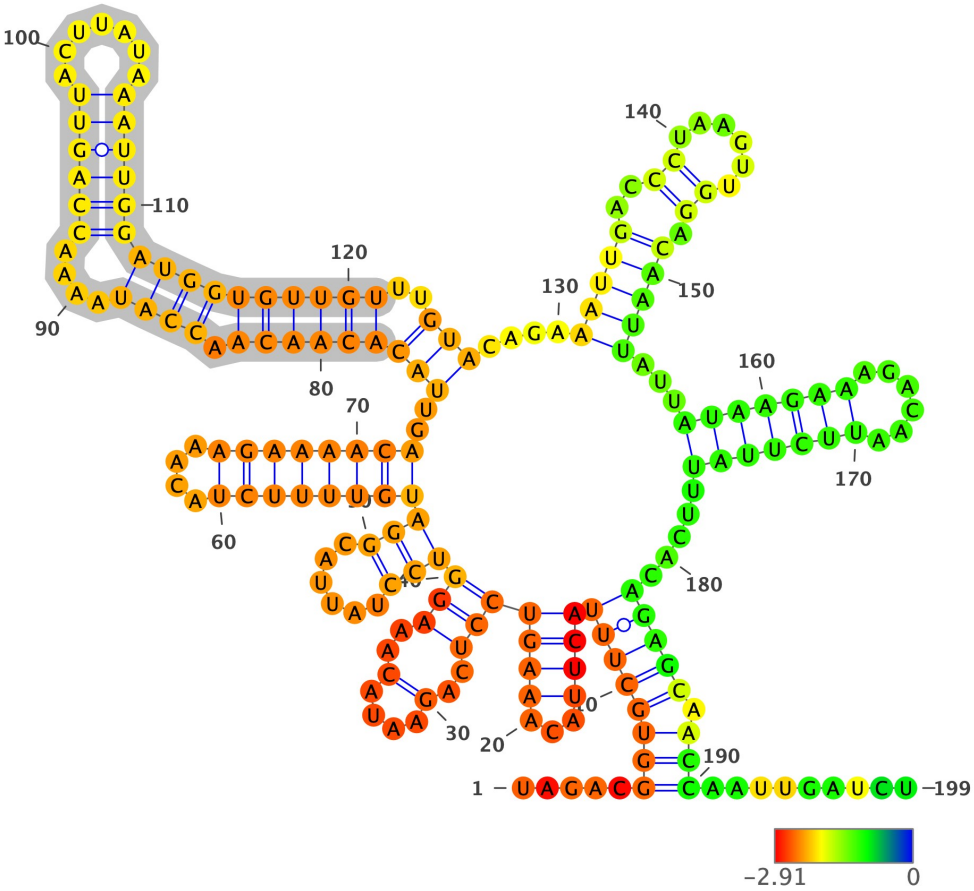
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 123 from nt 5885 to 5928 (nt 78 to 121)

```
5'-ACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGU-3'
5'-((((((.((((....((((((.......))))))))))))))))-3'
Motif MFE = -12.6; z-score = -4.34; 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'-UAGACGGUGCUUUACUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGG
AUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCU-3
5'-.....((((((((((((...))))))((..(....)..))))((......)))(((((((((....)))))))))..((((((((((.((((....((((((.......))))))
))))))))))..))).....((((((..((.......)).))))))...(((((((.....)))))))).....))))).)))..........-3'
MFE = -39.1; z-score = -2.21; 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(+)

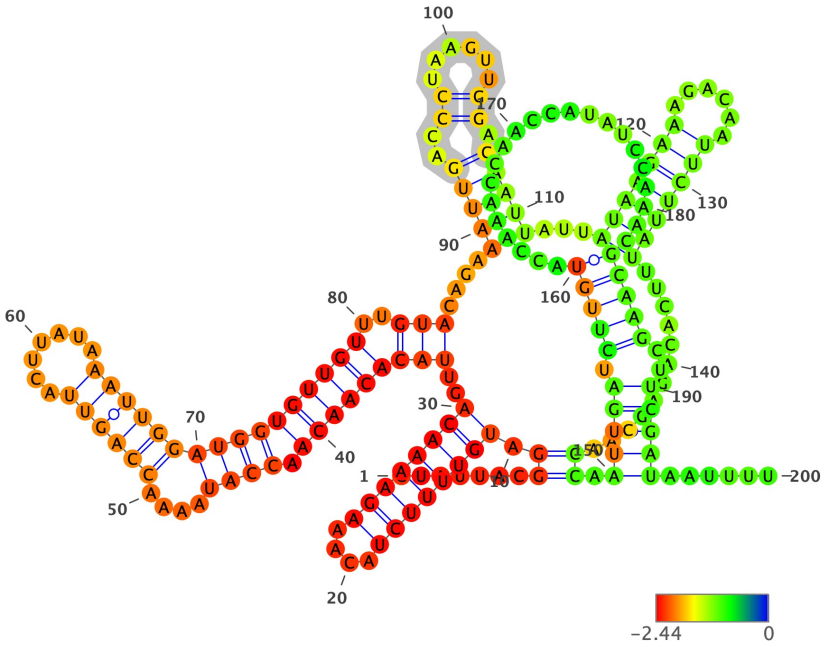
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 124 from nt 5942 to 5956 (nt 93 to 107)

```
5'-GACCCUAAGUUGGAC-3'
5'-(..((......)).)-3'
Motif MFE = -1.5; z-score = -0.97; 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 = -1.49; ED = 34.74
```

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(+)

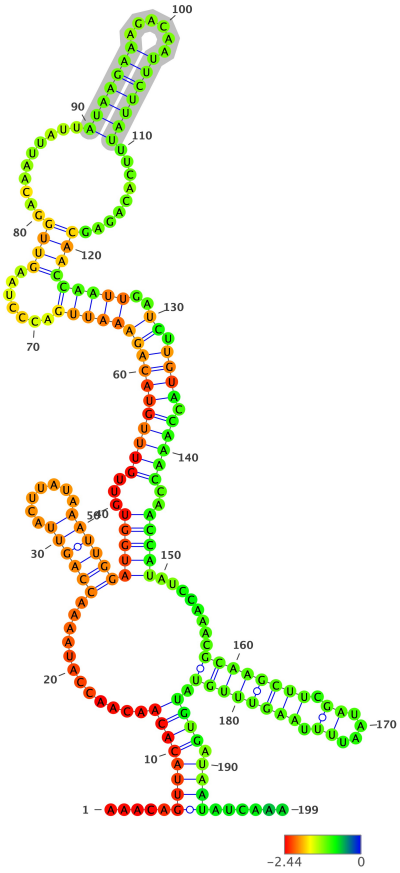
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 125 from nt 5964 to 5983 (nt 90 to 109)

```
5'-AUAAGAAAGACAAUUCUUAU-3'
5'-(((((((......)))))))-3'
Motif MFE = -3.1; z-score = -4.66; 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 = -2.2; 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(+)

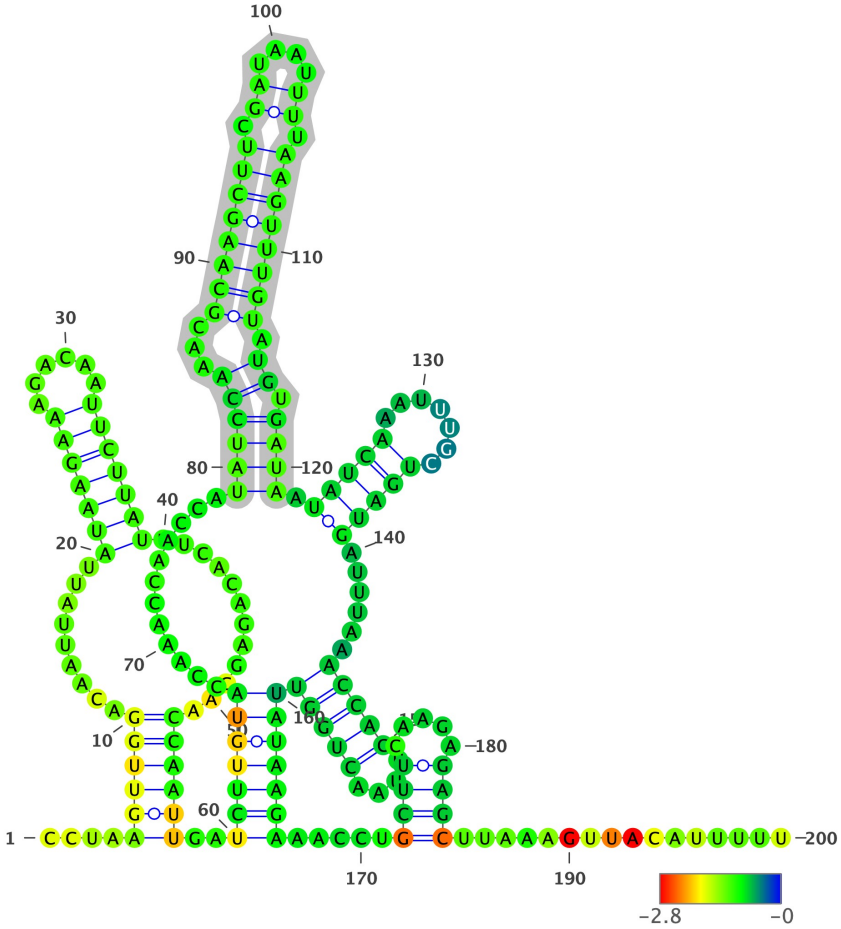
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 126 from nt 6023 to 6065 (nt 79 to 121)

```
5'-UAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUGUAUGUGAUA-3'
5'-(((......((((((((.((....)).))))))))).....)))-3'
Motif MFE = -8.8; z-score = -2.06; 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 = -0.47; ED = 41.45
```

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(+)

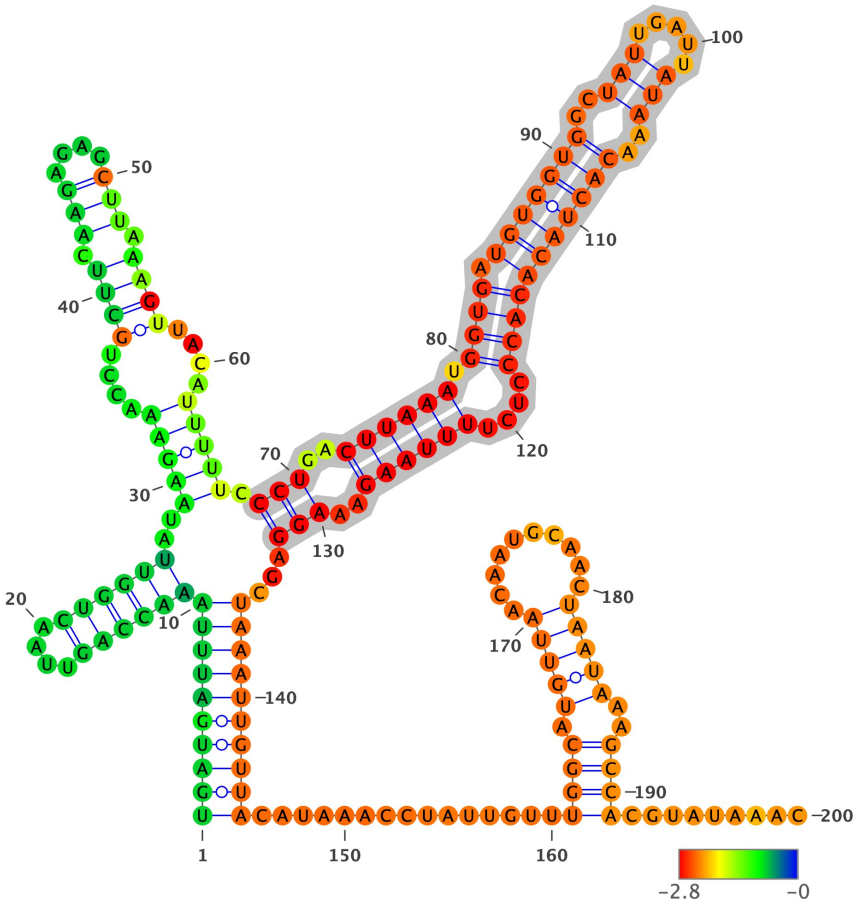
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 127 from nt 6146 to 6210 (nt 68 to 132)

```
5'-CCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGG-3'
5'-(((..(((((((.(((((.(((((((..(((.....)))..)))))))))))).....)))))))..)))-3'
Motif MFE = -21.2; z-score = -4.1; ED = 1.74
```



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

Extracted structure model with flanking nucleotides 6079 to 6278 (motif highlighted in silver):

```
5'-UGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUA
CACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAAC-3
5'-((((((((((((((((....))))))..((((((....((((.((((....)))).))))....))))))..(((..((((((.((((.(((((((..(((.....)))..)))))
))))))....))))))..)))...))))))))))..............((((.(((((..........))))))..))))........-3'
MFE = -40.5; z-score = -1.85; 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(+)

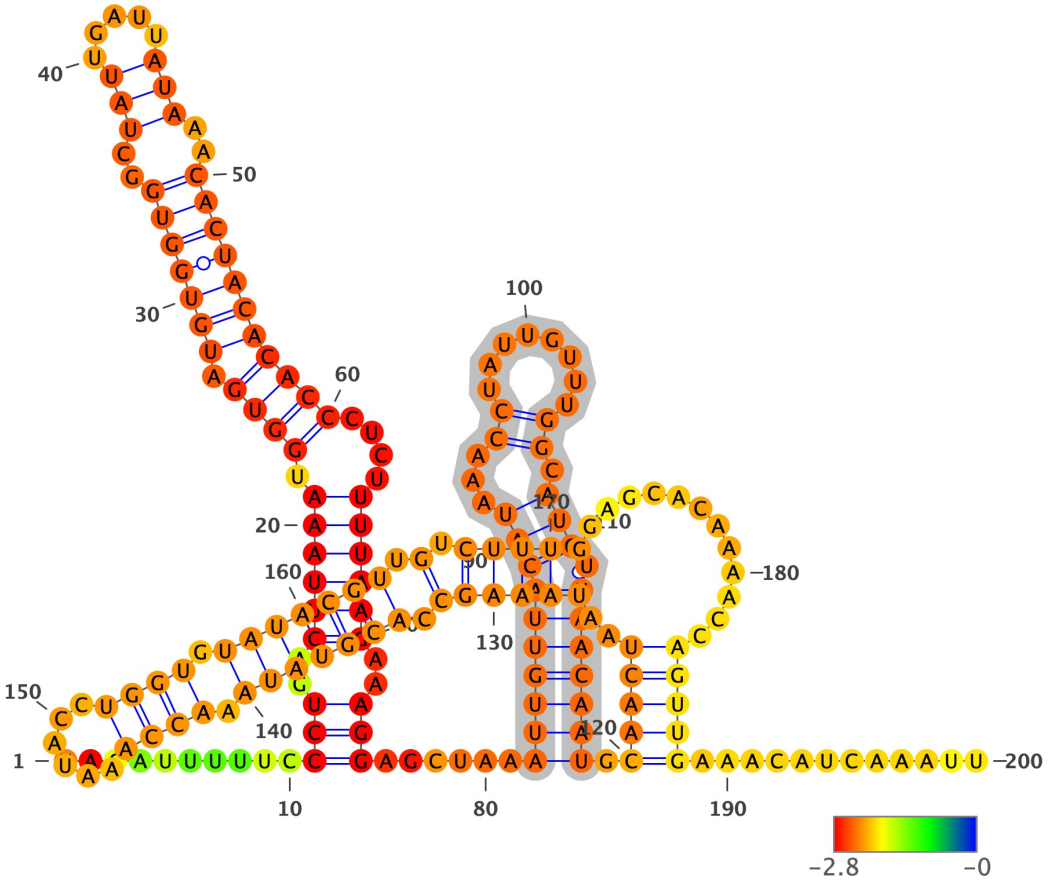
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 128 from nt 6217 to 6253 (nt 82 to 118)

```
5'-AUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAU-3'
5'-(((((((((((...((........)).))).)))))))-3'
Motif MFE = -6.5; z-score = -2.06; 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 6136 to 6335 (motif highlighted in silver):

```
5'-UACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGU
UAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUU-3
5'-..........(((..((((((.((((.(((((((..(((.....)))..))))))))))).....))))))..)))......((((((((((...((........)).))).
)))))))).(((((..((((((.(((((((.((((.....)))).)))))))).).)))))............)))))............-3'
MFE = -47.2; z-score = -3.27; ED = 23.78
```

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

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

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

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

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

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

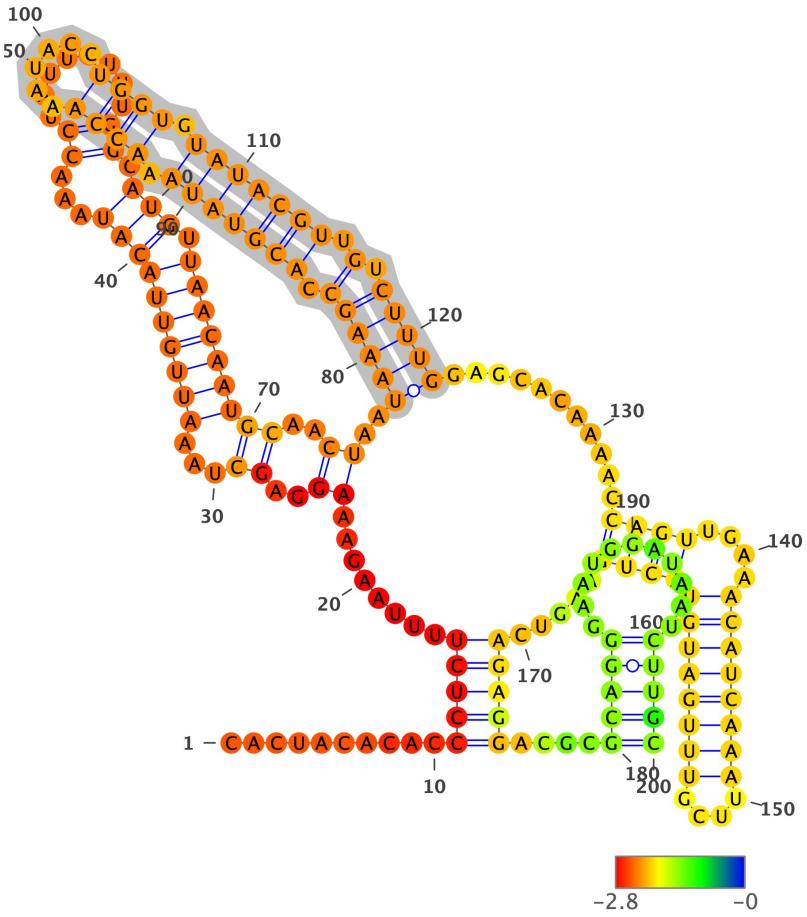
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 129 from nt 6262 to 6306 (nt 78 to 122)

```
5'-UAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUG-3'
5'-((((((.(((((((.((((......)))).)))))))).).)))))-3'
Motif MFE = -14.1; z-score = -3.92; 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 = -1.51; 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(+)

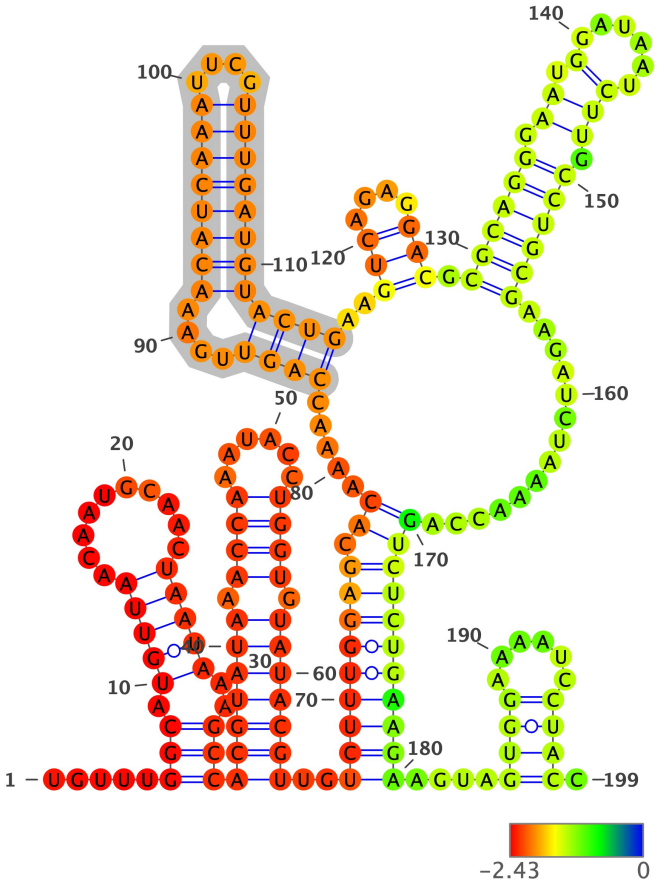
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 130 from nt 6318 to 6349 (nt 84 to 115)

```
5'-CAGUUGAAACAUCAAAUUCGUUUGAUGUACUG-3'
5'-((((....((((((((....))))))))))))-3'
Motif MFE = -8.0; z-score = -2.75; ED = 1.64
```



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

Extracted structure model with flanking nucleotides 6235 to 6433 (motif highlighted in silver):

```
5'-UGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGU
ACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACC-3
5'-.....(((.(((((.........)))))..)))(((((((.((((......)))).)))))))..(((((((((.((.....((((....((((((((....))))))))
))))..(((....))).((((((.((.(......))).))))))..............)))))))))))....((((......)))).-3'
MFE = -50.1; z-score = -2.43; ED = 27.41
```

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(+)

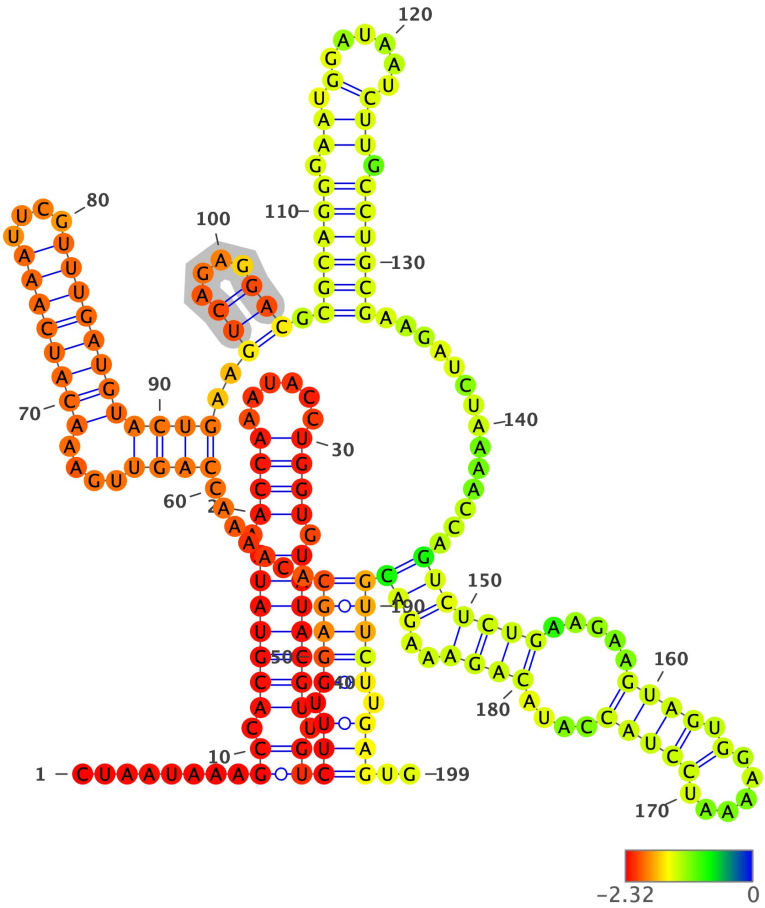
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 131 from nt 6353 to 6360 (nt 96 to 103)

```
5'-UCAGAGGA-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.13
```



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

Extracted structure model with flanking nucleotides 6258 to 6456 (motif highlighted in silver):

```
5'-CUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGG
GAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUG-3
5'-........((.(((((((.((((......)))).)))))))).))(((.(((((.......((((....((((((((....)))))))))))))..(((....))).((((((
.((.(......))).))))))..............(((((((.....((((.(......)))))....))))..)))))))).)))..-3'
MFE = -49.4; z-score = -2.53; ED = 28.46
```

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

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

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

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

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

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

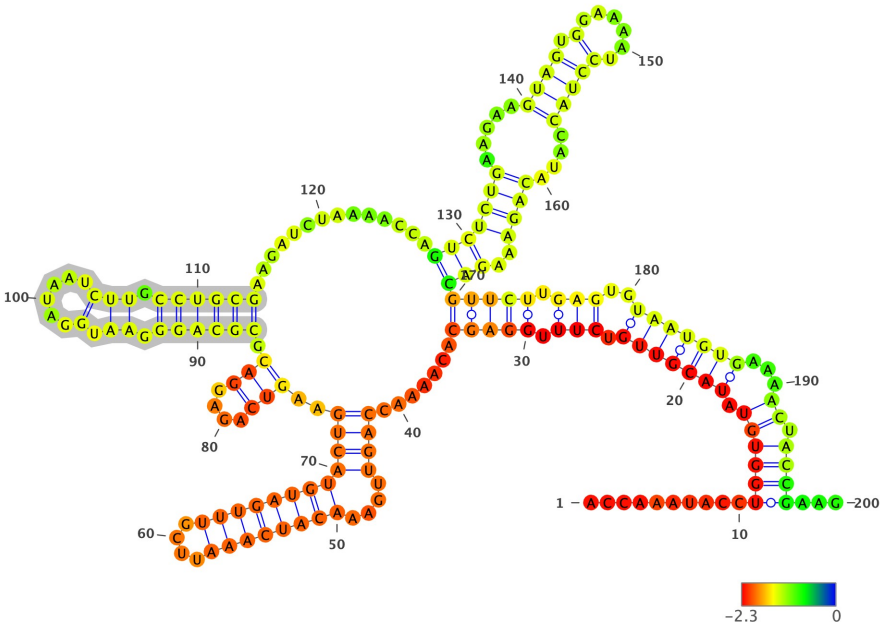
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 132 from nt 6363 to 6389 (nt 87 to 113)

```
5'-CGCAGGGAAUGGAUAAUCUUGCCUGCG-3'
5'-((((((.((.(.....))).)))))))-3'
Motif MFE = -10.0; z-score = -2.51; ED = 3.35
```



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

Extracted structure model with flanking nucleotides 6277 to 6476 (motif highlighted in silver):

```
5'-ACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUG
CGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAG-3
5'-..........((((((.(((((((.(((.(((((.......(((((....(((((((((....)))))))))))))..(((....))).((((((.((.(......))).))))
)).............(((((((.....((((.(......))))))....))))..)))))))).))))..)))))))...)).))))...-3'
MFE = -45.8; z-score = -0.99; ED = 32.23
```

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

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

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

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

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

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

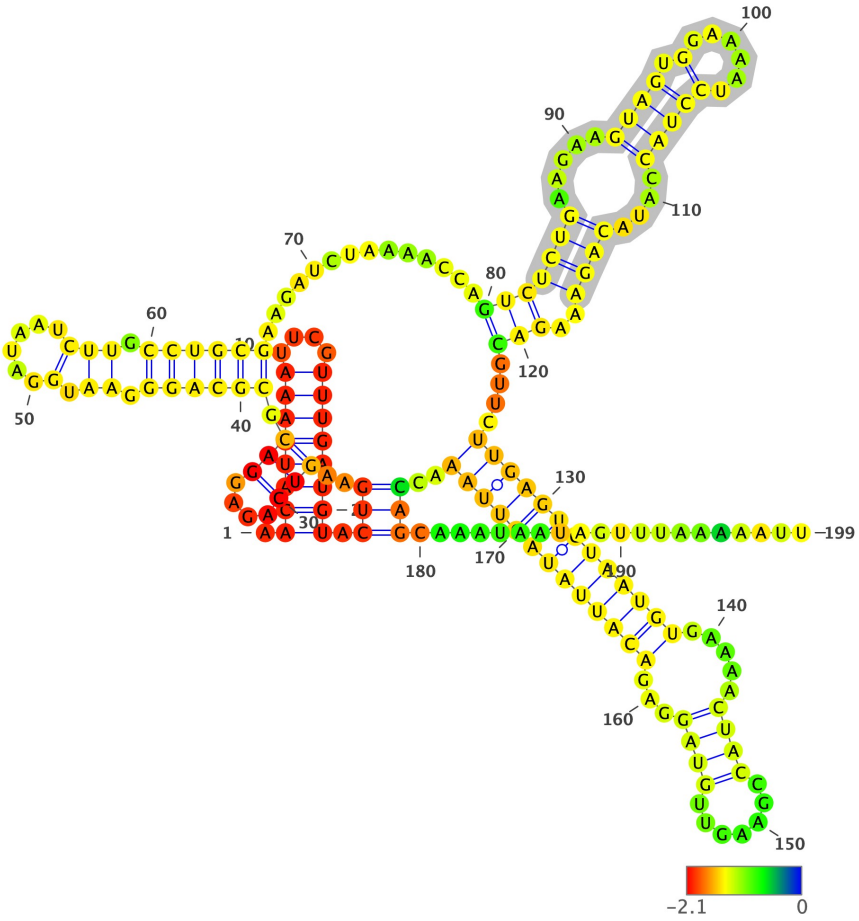
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 133 from nt 6407 to 6440 (nt 83 to 116)

```
5'-UCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGA-3'
5'-((((.....((((.(......)))))....))))-3'
Motif MFE = -4.3; z-score = -0.94; ED = 5.84
```



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 6325 to 6523 (motif highlighted in silver):

```
5'-AACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAU
ACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUU-3
5'-.((((((((....)))))))).(((..(((....))).((((((.((.(......))).))))))..............(((((((.....((((.(......)))))...
.))))..)))....((((((((((((.....((((.......))))...)))))))))))))..)))....................-3'
MFE = -45.5; z-score = -2.33; ED = 22.44
```

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

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

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

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

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

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

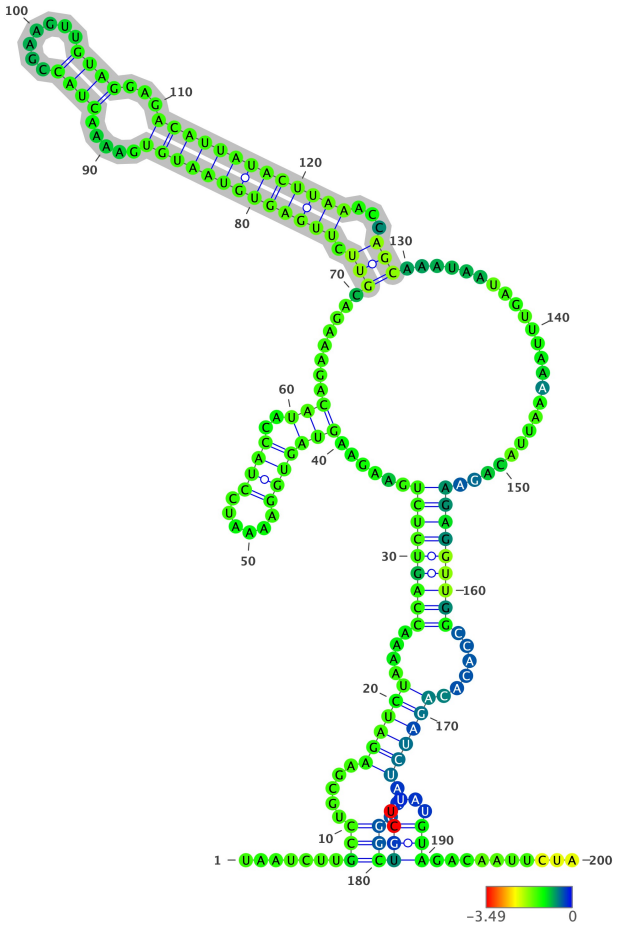
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 134 from nt 6446 to 6504 (nt 71 to 129)

```
5'-GUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUACUUAAACCAGC-3'
5'-(((.(((((((((((((.....((((.......))))...)))))))))))))...)))-3'
Motif MFE = -16.2; z-score = -3.04; 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 = -0.66; 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(+)

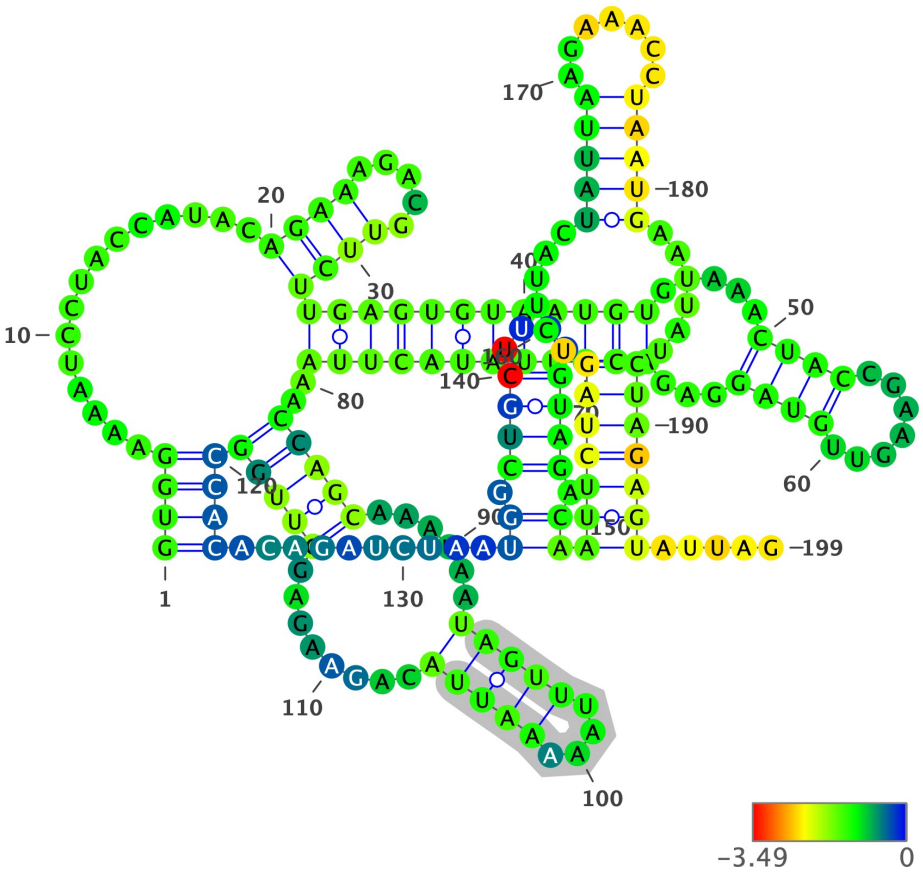
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 135 from nt 6512 to 6523 (nt 94 to 105)

```
5'-AGUUUAAAAAUU-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 = -0.68; 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(+)

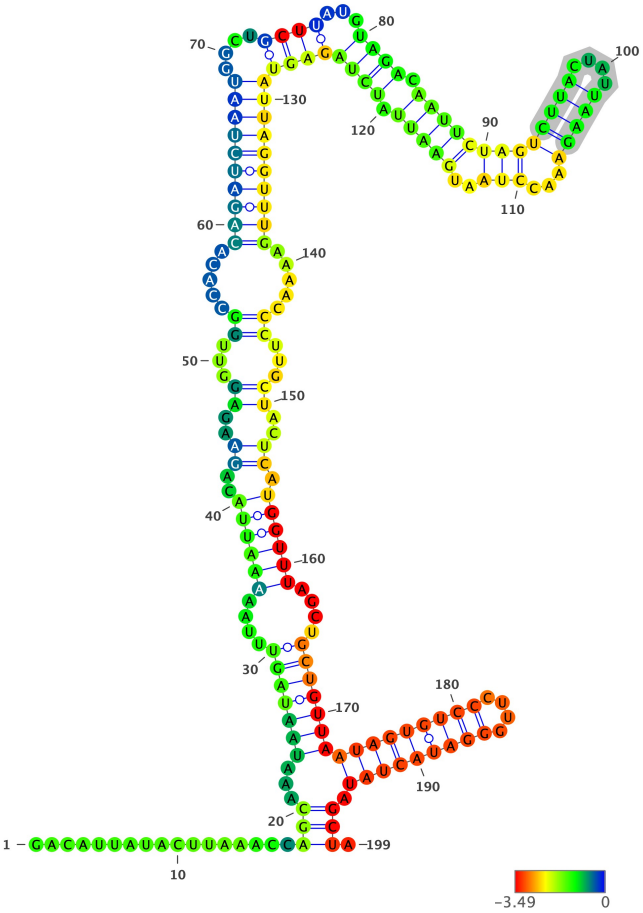
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 136 from nt 6578 to 6589 (nt 94 to 105)

```
5'-CUUACUAUUAAG-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = 0.1; 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 6485 to 6683 (motif highlighted in silver):

```
5'-GACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUAGUCUUACUAUUAAGAAACCU
AAUGAAUUAUCUAGAGUAUUAGGUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUA-3
5'-.................(((...(((((((....((((((..((..((...((.....((((((((((....((((...((((.((((((((((((....)))))...))
)..)))))).))))))))))))))))).....))...))..)).))))))....)))))))((((((((....)))))))))).))).-3'
MFE = -39.0; z-score = -0.82; ED = 53.41
```

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(+)

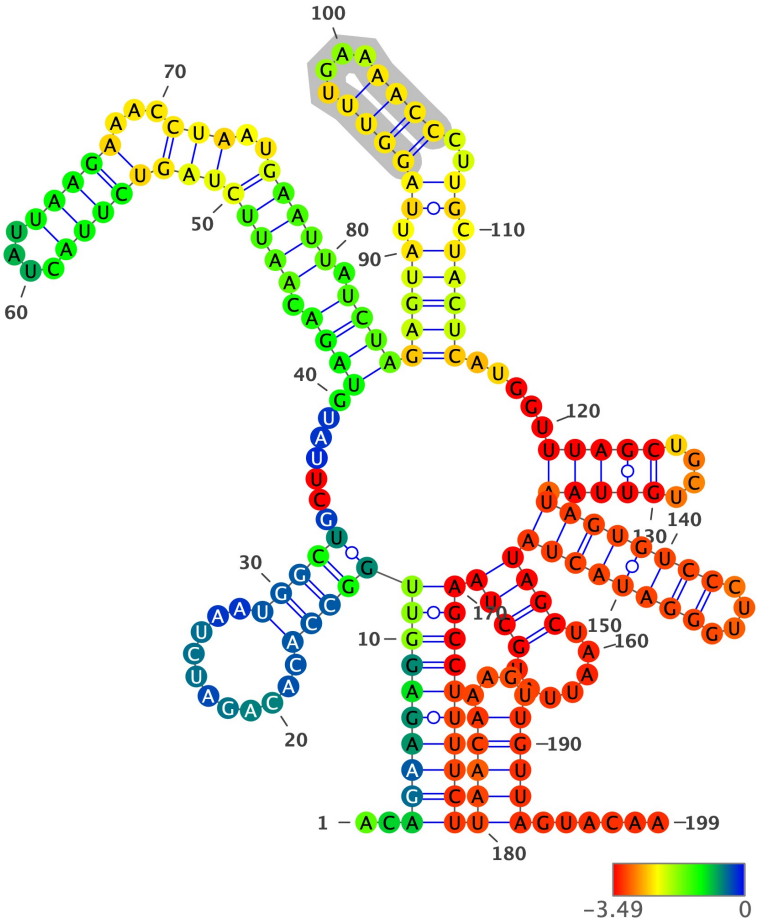
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 137 from nt 6617 to 6628 (nt 94 to 105)

```
5'-GGUUUGAAAACC-3'
5'-((((....))))-3'
Motif MFE = -1.0; z-score = -3.27; 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 6524 to 6722 (motif highlighted in silver):

```
5'-ACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAGGUUUGAAAACCCUUGCU
ACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAA-3
5'-..((((((((((((((.....))))).......((((.((((((((((((....)))))...)))..)))))).))))(((((.((((((....))))..)).)
)))).....(((((....)))))((((((((....))))))))((((.......)))))))))))))((((....)))))......-3'
MFE = -48.1; z-score = -2.44; ED = 40.34
```

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(+)

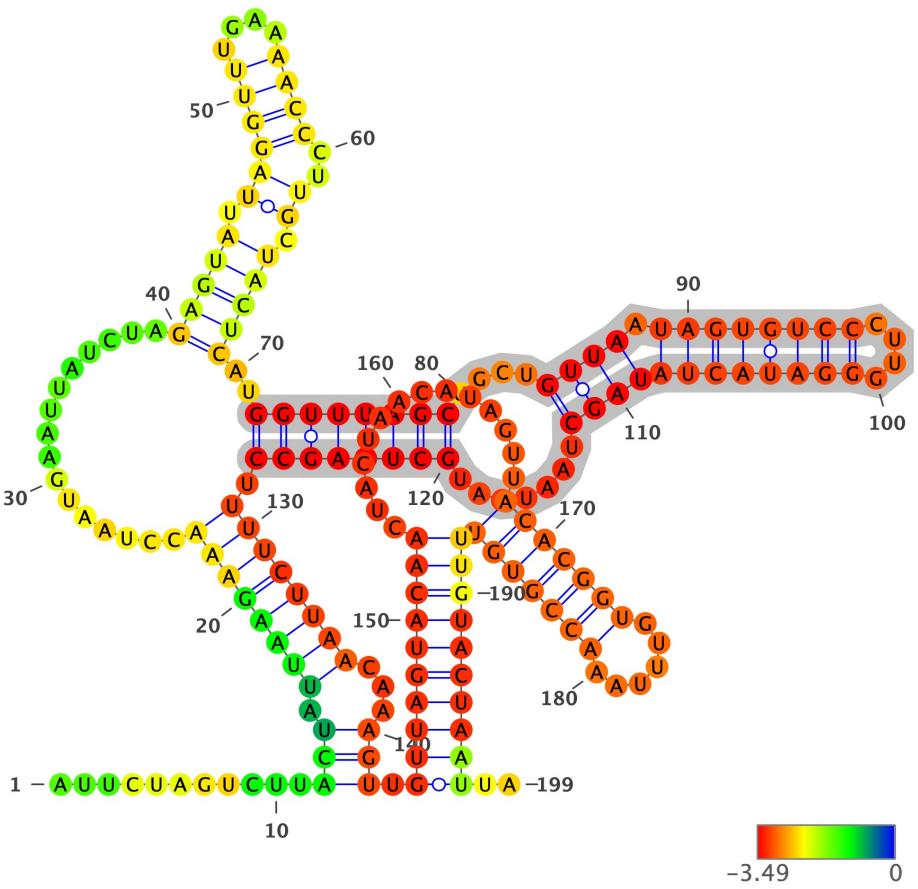
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 138 from nt 6641 to 6696 (nt 72 to 127)

```
5'-GGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCC-3'
5'-((((((((....((((.((((((((....))))))))))))).......))))))))-3'
Motif MFE = -21.7; z-score = -4.34; 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 = -3.97; 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(+)

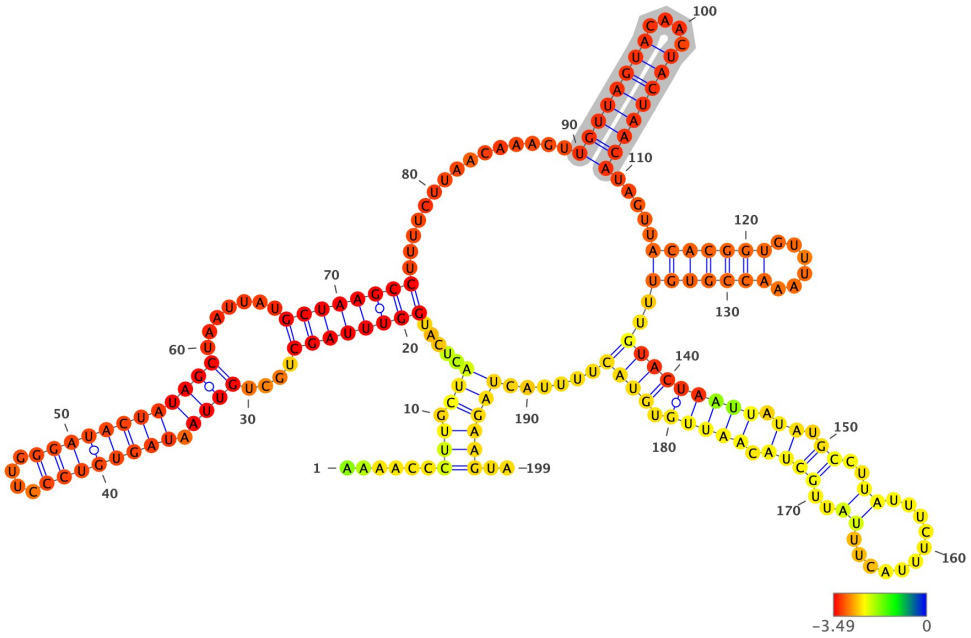
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 139 from nt 6712 to 6731 (nt 90 to 109)

```
5'-UGUUAGUACAACUACUAACA-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -6.2; z-score = -6.97; 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 6623 to 6821 (motif highlighted in silver):

```
5'-AAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUA
GUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUA-3
5'-......(((.(((.....(((((((((....(((((.(((((((((....)))))))))))).....)))))))).............(((((((....)))))))))..
...(((((((......))))))).(((((((((.((.((..((..........)).))))).)))))).)))).....))))))..-3'
MFE = -46.9; z-score = -4.19; ED = 26.1
```

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

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

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

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

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

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

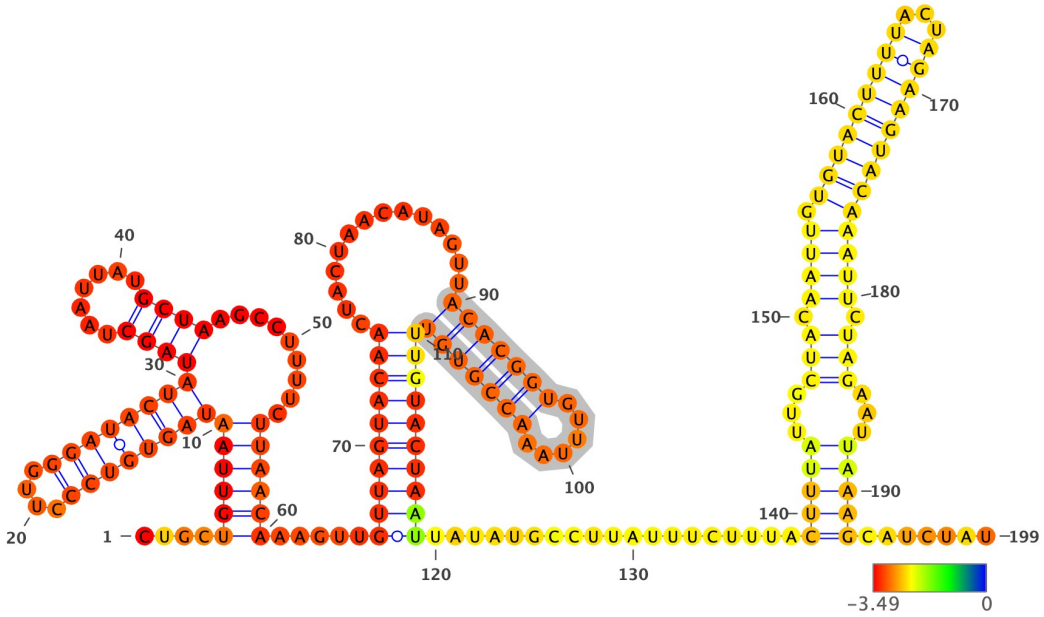
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 140 from nt 6737 to 6756 (nt 90 to 109)

```
5'-ACACGGUGUUUAAACCGUGU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -10.0; z-score = -5.63; 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 = -4.16; 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(+)

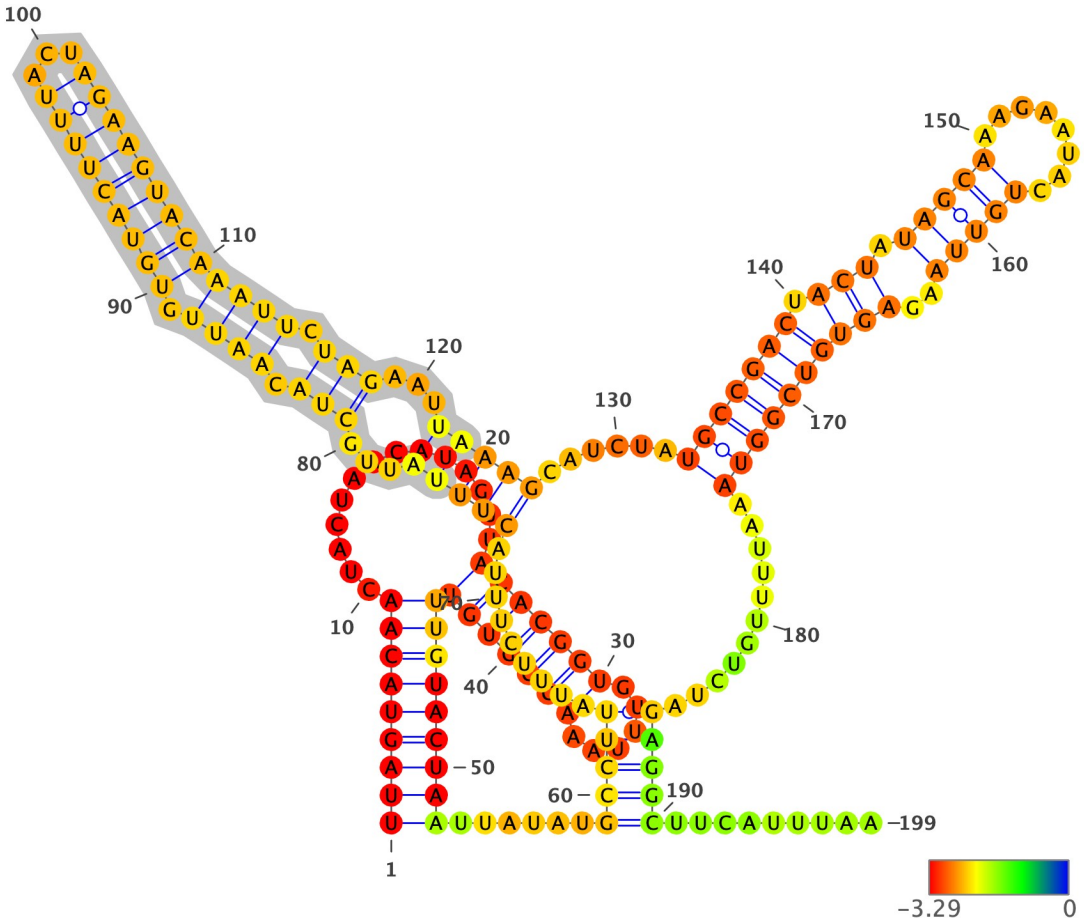
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 141 from nt 6789 to 6836 (nt 76 to 123)

```
5'-UAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUA-3'
5'-((...(((.(((((.((((((((((...)))))))))))))).)))...))-3'
Motif MFE = -9.6; z-score = -2.81; 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 6714 to 6912 (motif highlighted in silver):

```
5'-UUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAA
AUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAA-3
5'-((((((((((.............(((((((......)))))))))))))))).....((((.........(((((...(((.((((.((((((((((...))))))))))
)))).)))...)))))).....(((((((.(((.(((((........)))))..))))))))).........)))))........-3'
MFE = -51.4; z-score = -4.47; 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(+)

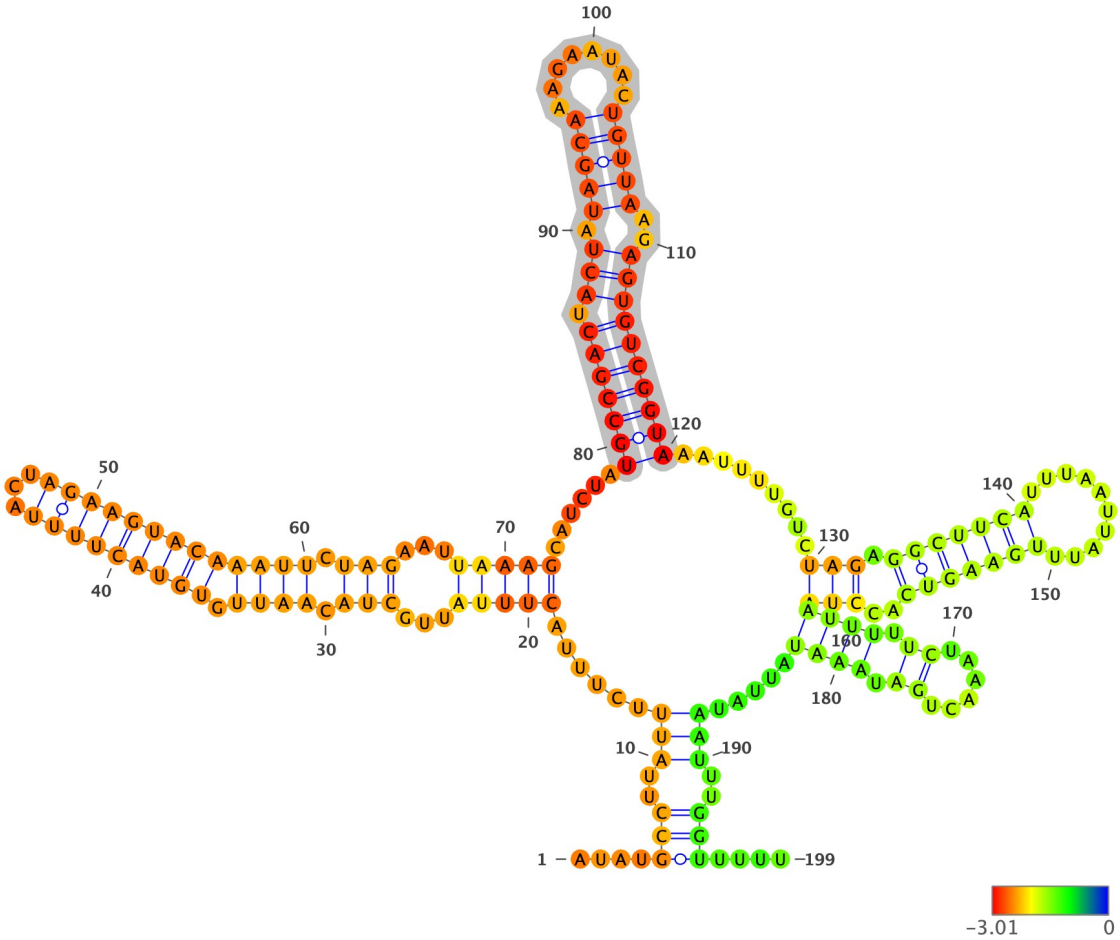
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 142 from nt 6846 to 6887 (nt 79 to 120)

```
5'-UGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUA-3'
5'-(((((((.(((.(((((........)))))..)))))))))-3'
Motif MFE = -14.8; z-score = -4.1; 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 = -2.85; ED = 21.67
```

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(+)

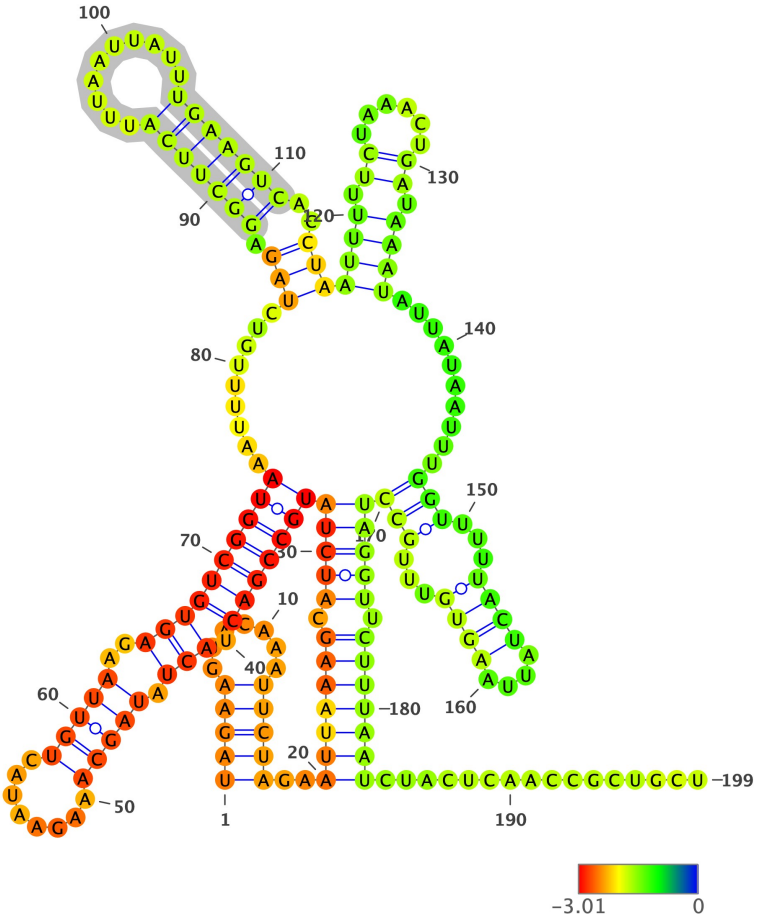
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 143 from nt 6901 to 6924 (nt 88 to 111)

```
5'-GGCUUCAUUUAAUUAUUUGAAGUC-3'
5'-(((((((..........)))))))-3'
Motif MFE = -6.2; z-score = -3.9; ED = 0.75
```



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

Extracted structure model with flanking nucleotides 6814 to 7012 (motif highlighted in silver):

```
5'-UAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUC
ACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCU-3
5'-(((((.......)))))..(((((((.(((((((((((((.(((.(((((.........)))))..))))))))))).........(((.(((((((..........)))))))
..)))((((.((......)).)))).........(((...((((....))))...)))))))).)))))))................-3'
MFE = -39.6; z-score = -1.83; ED = 45.45
```

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

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

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

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

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

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

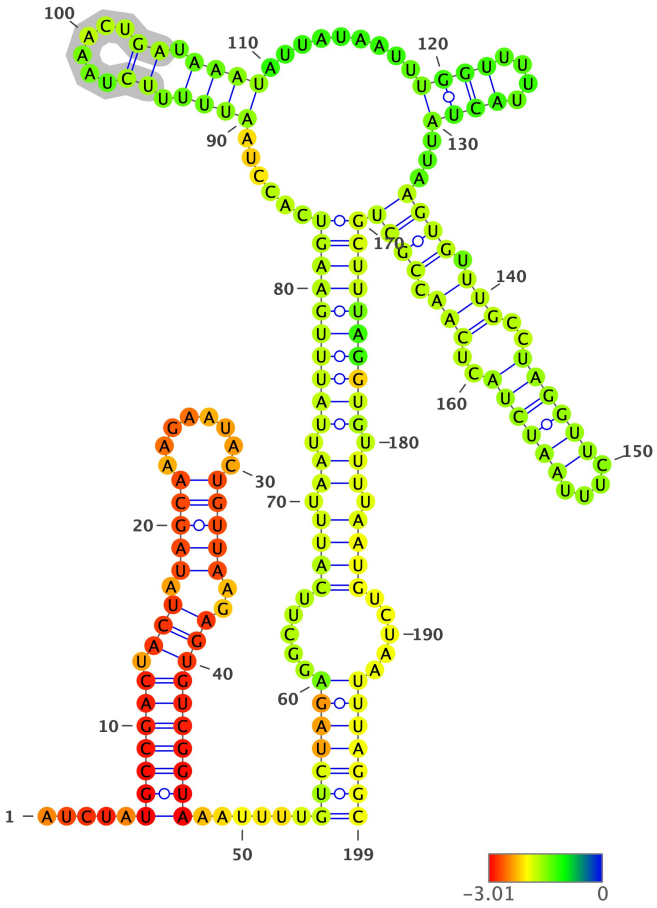
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 144 from nt 6935 to 6944 (nt 95 to 104)

```
5'-UCUAAACUGA-3'
5'-((......))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.4
```



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 6841 to 7039 (motif highlighted in silver):

```
5'-AUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAU
UAUAAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGC-3
5'-.....(((((((.(((.(((((........)))))..)))))))))).....(((((((.....((((.((.((((((((((.....((((.((.....)).)))))..
.......((((....)))).)...((((.(((..(((((((....)))))))..))).)))))))))))))).)).))))).....)))))))-3'
MFE = -41.2; z-score = -2.01; ED = 30.88
```

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(+)

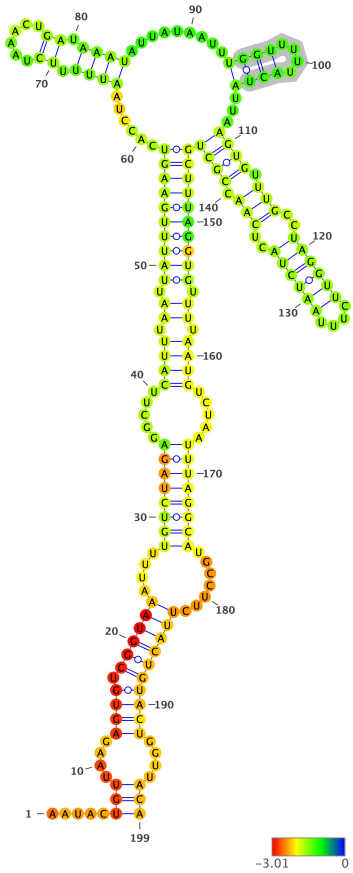
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 145 from nt 6960 to 6969 (nt 95 to 104)

```
5'-GGUUUUUACU-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 6866 to 7064 (motif highlighted in silver):

```
5'-AAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGU
GUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACA-3
5'-.....(((....((((.((((((....((((((((.....((((.((.((((((((((.....((((.((......)).))))..........((((....))))...(((
(.(((..((((((....))))))..))).))))))))))))))).)).))))).....))))))))).......))))))))))....)))-3'
MFE = -36.2; z-score = -1.2; ED = 46.79
```

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 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', '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(+)

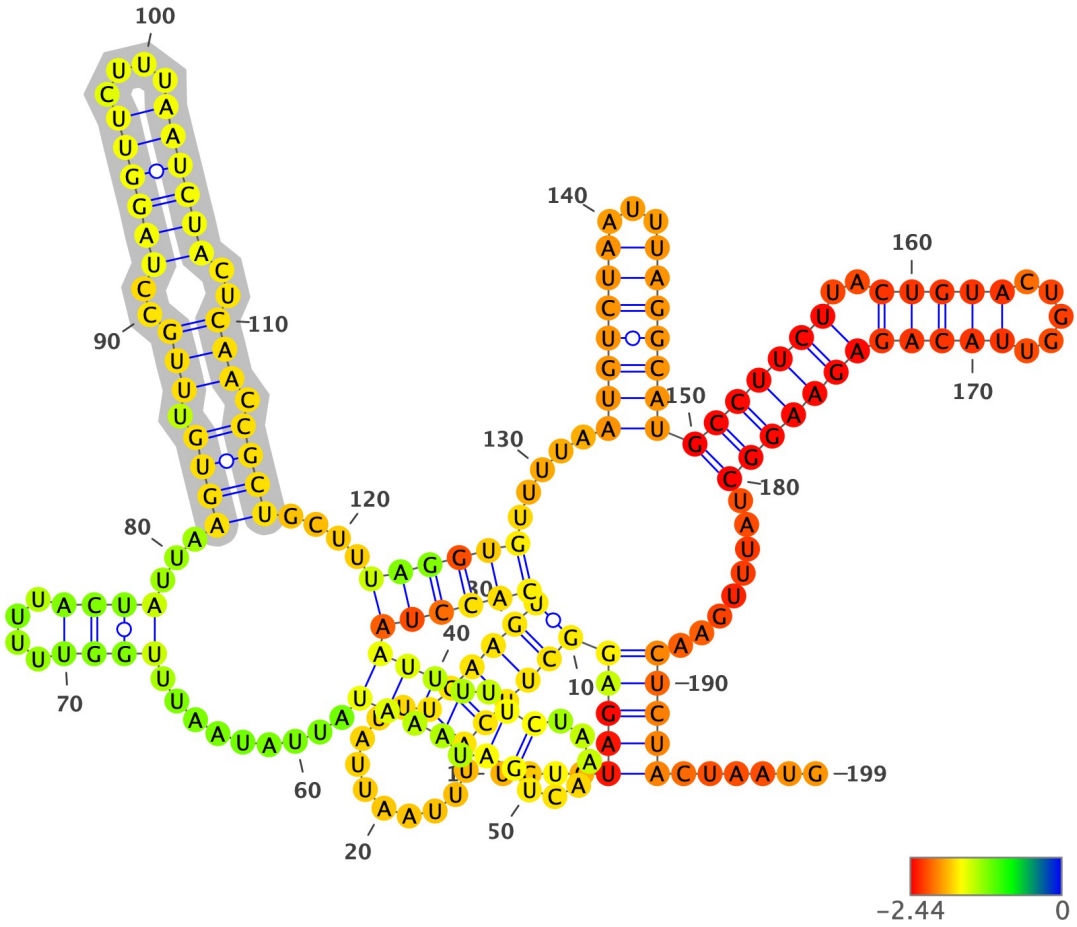
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 146 from nt 6974 to 7009 (nt 82 to 117)

```
5'-AGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCU-3'
5'-((((.(((..(((((((....)))))))..))).))))-3'
Motif MFE = -7.2; z-score = -2.16; 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 = -3.12; 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(+)

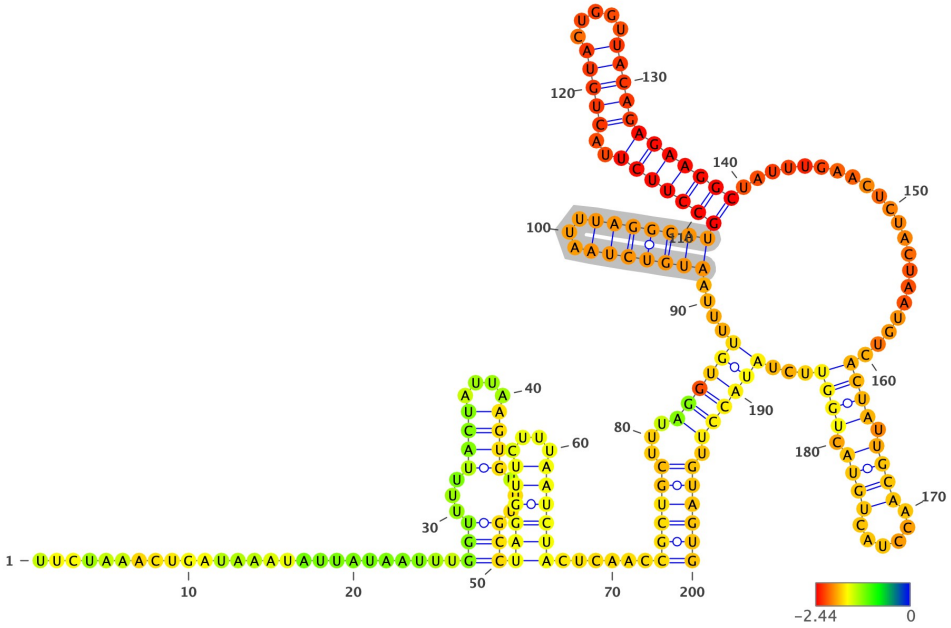
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 147 from nt 7025 to 7041 (nt 92 to 108)

```
5'-AUGUCUAAUUUAGGCAU-3'
5'-(((((((...)))))))-3'
Motif MFE = -4.2; z-score = -4.57; 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 = -2.2; 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(+)

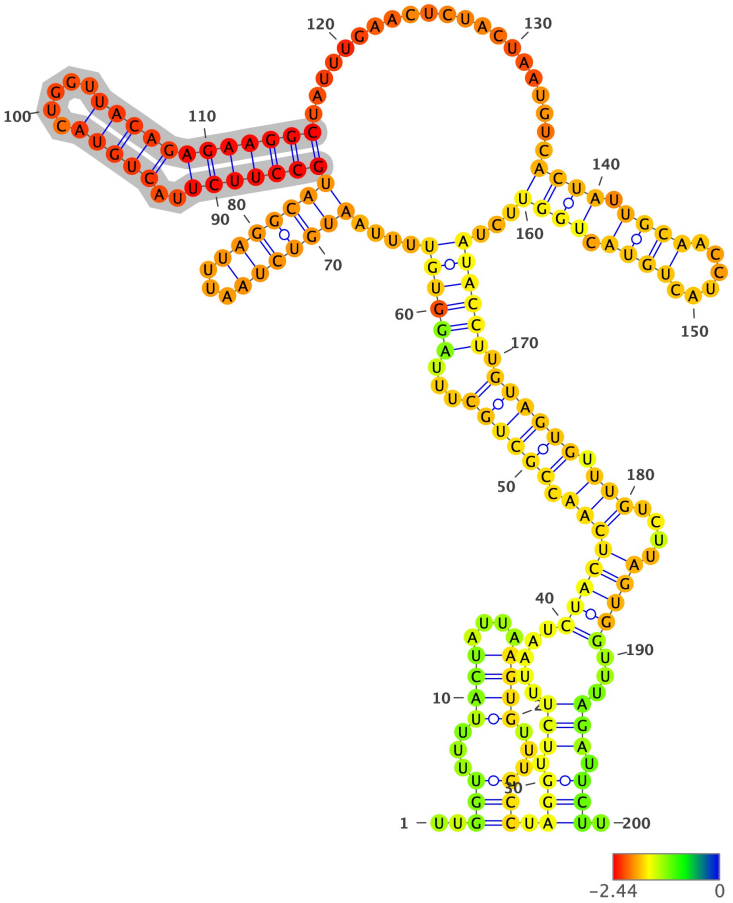
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 148 from nt 7042 to 7072 (nt 85 to 115)

```
5'-GCCUUCUUACUGUACUGGUUACAGAGAAGGC-3'
5'-(((((((..(((((.....)))))))))))-3'
Motif MFE = -13.1; z-score = -3.31; ED = 1.16
```



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

Extracted structure model with flanking nucleotides 6958 to 7157 (motif highlighted in silver):

```
5'-UUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGA
AGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUU-3
5'-..(((...((((....))))...))).(((.(((.....((((((((.((((((...((((((....(((((((...)))))))(((((((..(((((.....))))))))
))))....................((((.((((......)))).))))...)))))).)))))).)))....)))))...))).))).-3'
MFE = -48.6; z-score = -2.92; 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(+)

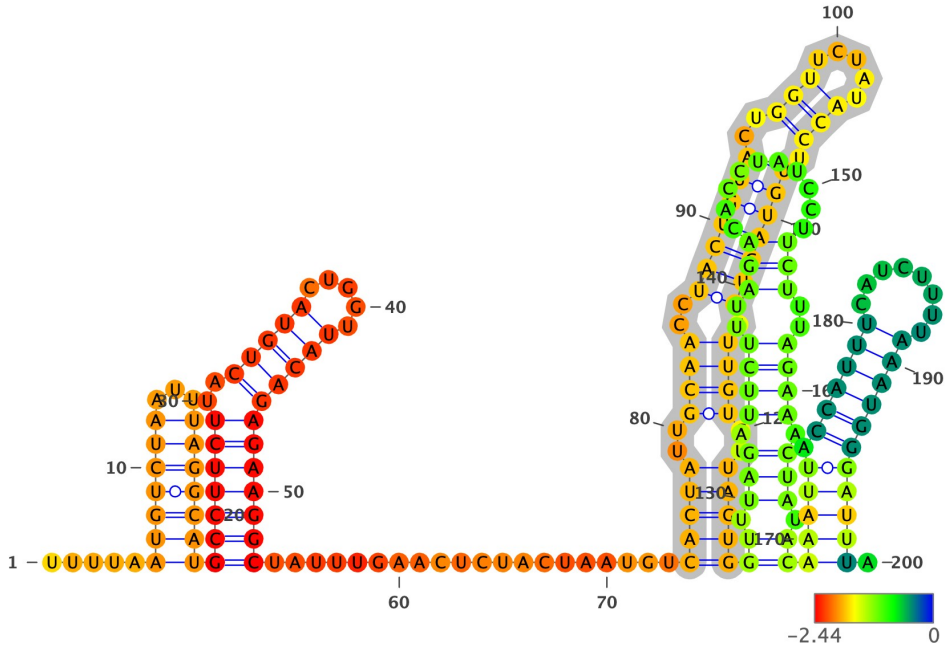
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 149 from nt 7093 to 7145 (nt 74 to 126)

```
5'-CACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUG-3'
5'-((((((..((((..(((((((..(((.....))).)))))))).)))))..))))))-3'
Motif MFE = -12.3; z-score = -2.49; 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 = -3.6; 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(+)

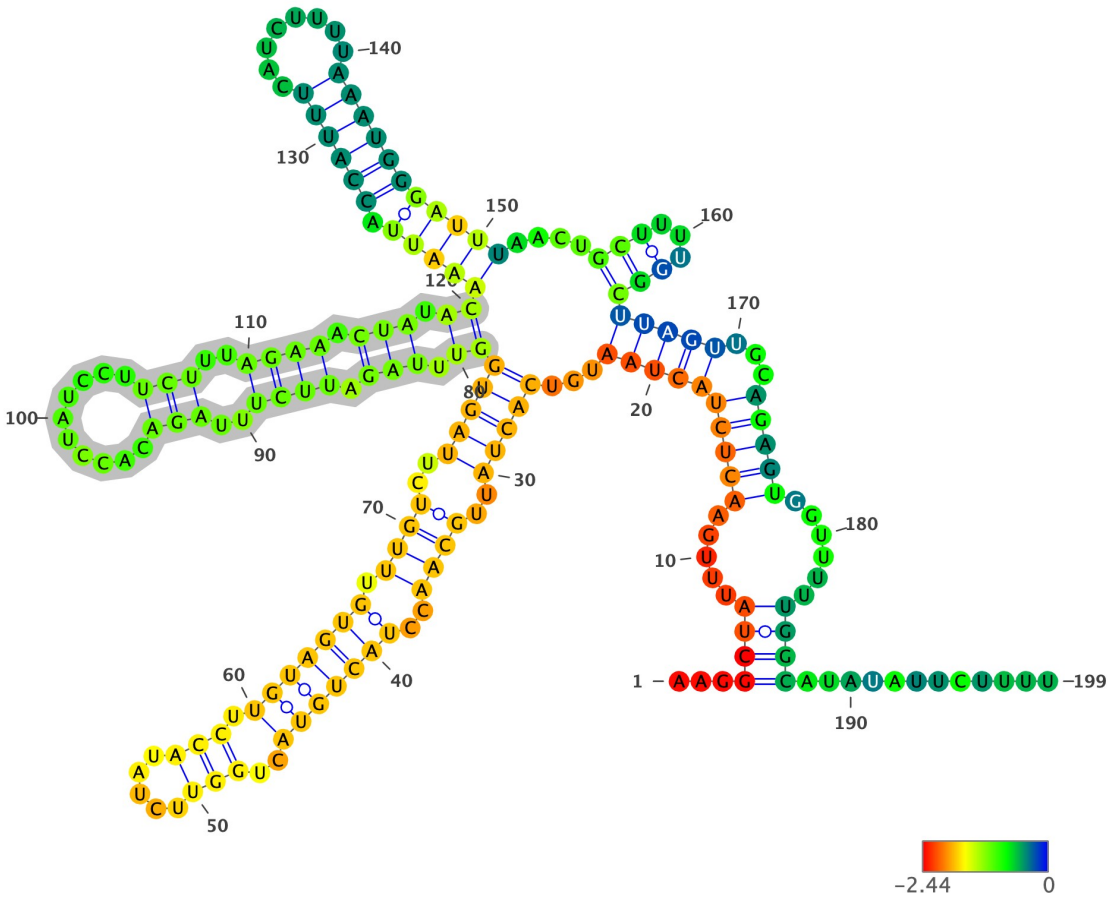
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 150 from nt 7146 to 7187 (nt 79 to 120)

```
5'-GUUUAGAUUCUUUAGACACCUAUCCUUCUUUAGAAACUAUAC-3'
5'-((.(((.((((..(((..........)))..)))).))).))-3'
Motif MFE = -5.4; z-score = -1.95; 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 = -1.4; 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(+)

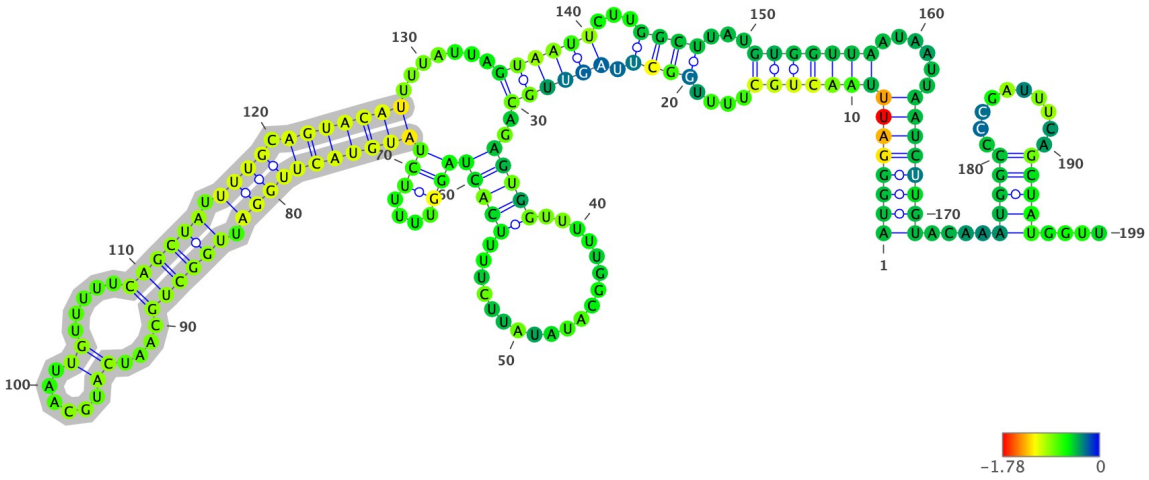
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 151 from nt 7281 to 7336 (nt 72 to 127)

```
5'-AUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAGCUAUUUUGCAGUACAU-3'
5'-(((((((((((.................................)))).)))))))-3'
Motif MFE = -14.5; z-score = -2.44; 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 = 0.21; 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(+)

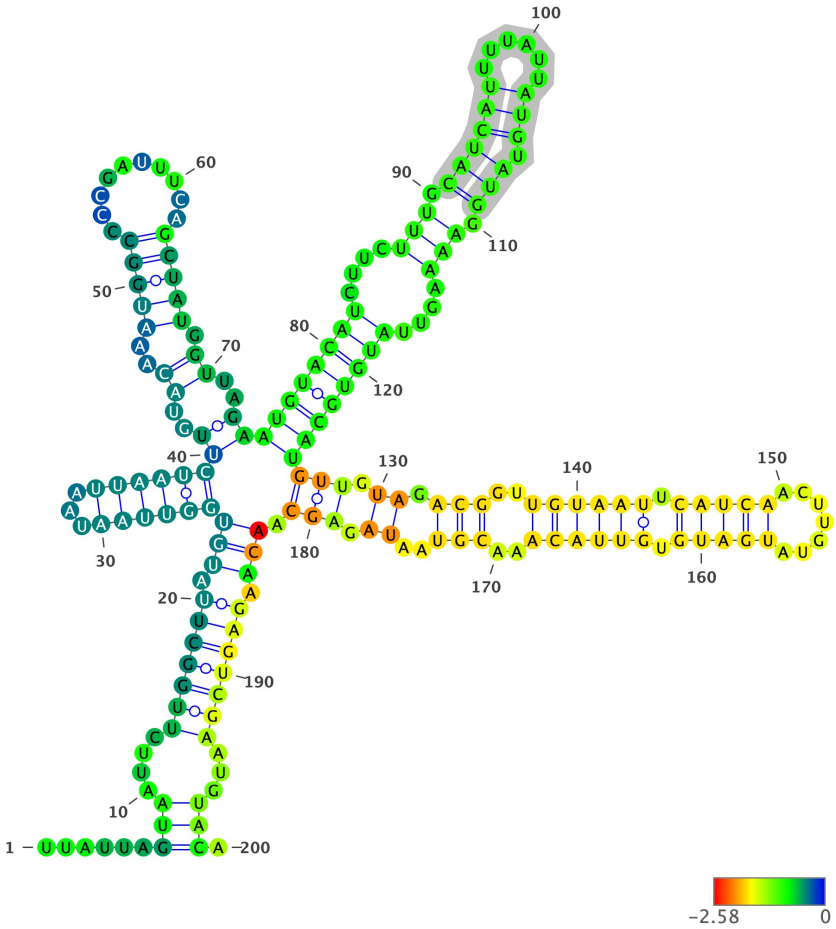
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 152 from nt 7428 to 7446 (nt 91 to 109)

```
5'-CAUCAUUUUAUUAUGUAUG-3'
5'-((((((......))).)))-3'
Motif MFE = -0.5; z-score = -0.4; 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 = -1.85; 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(+)

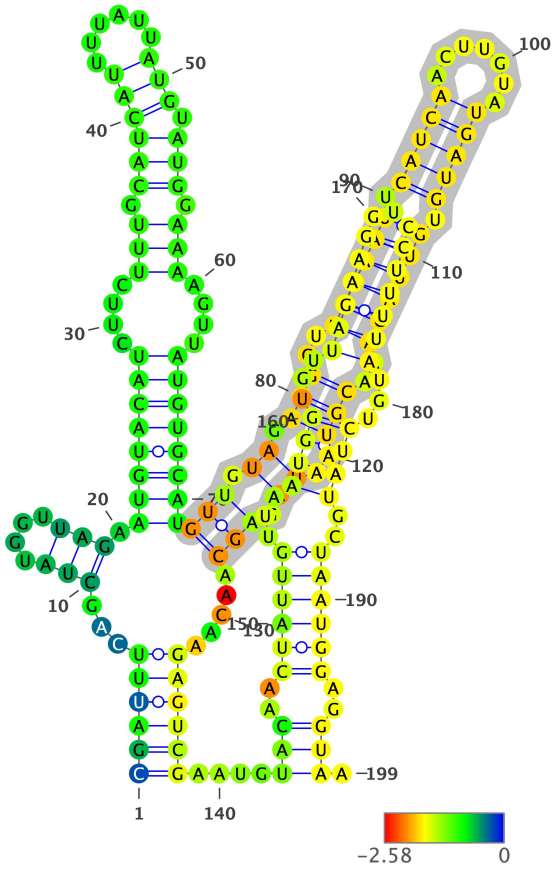
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 153 from nt 7463 to 7518 (nt 72 to 127)

```
5'-GUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGC-3'
5'-((..((.((((..((((((.(((((.......))))).))))))..))))..))..))-3'
Motif MFE = -16.3; z-score = -3.12; 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 7392 to 7590 (motif highlighted in silver):

```
5'-CGAUUUCAGCUAUGGUUAGAAUGUACAUCUUCUUUGCAUCAUUUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUU
ACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAA-3
5'-((((((...(((....))).(((((((((....(((.((((((......))).))))..))).))).....))))))))).((.(((..((((((.(((((.......))))))..))).
)))..)))..)).)))).....))))))....(((..((((((...((((...(((((((...)))))))...))))..))))))..))).-3'
MFE = -45.0; z-score = -1.48; ED = 52.78
```

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

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

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

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

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

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

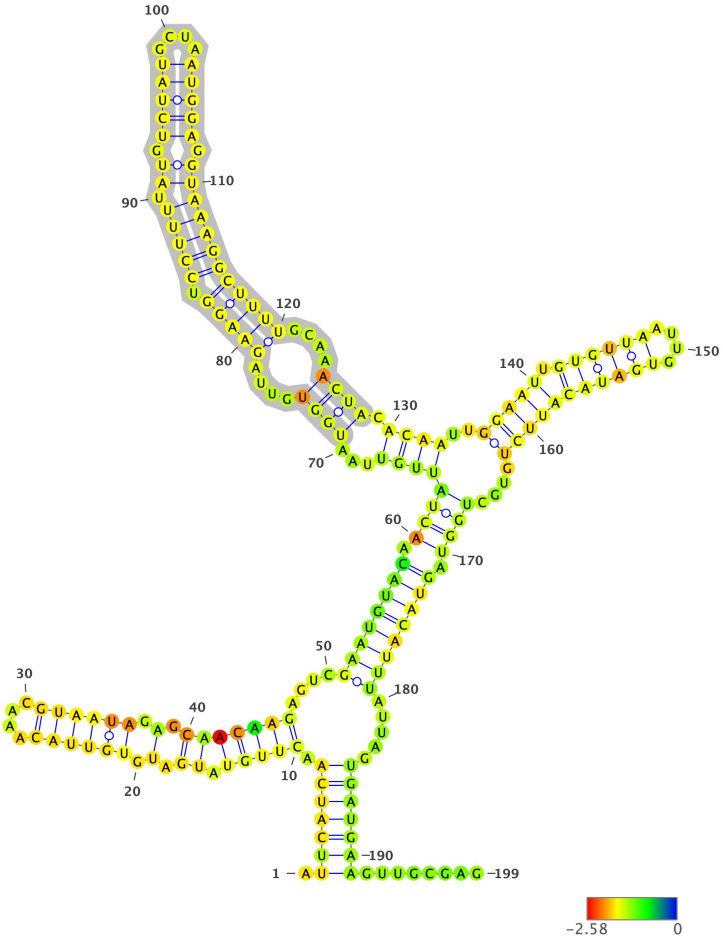
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 154 from nt 7549 to 7606 (nt 71 to 128)

```
5'-UGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUA-3'
5'-(((.....(((((.(((((.((.(((((....))))).))))))))))).....)))-3'
Motif MFE = -16.9; z-score = -3.15; 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 7479 to 7677 (motif highlighted in silver):

```
5'-AUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUA
AAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAG-3
5'-.(((((((.(((((.((.(.((((((....)))))).).)))))))....((((((((.((((((((...((((....(((((.(((((.((.(((((....))))).)))
))))))))).....)))).)))).(((((.((((((....))))))))))).....)))).)))))))).....)))))))........-3'
MFE = -49.7; z-score = -2.52; 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(+)

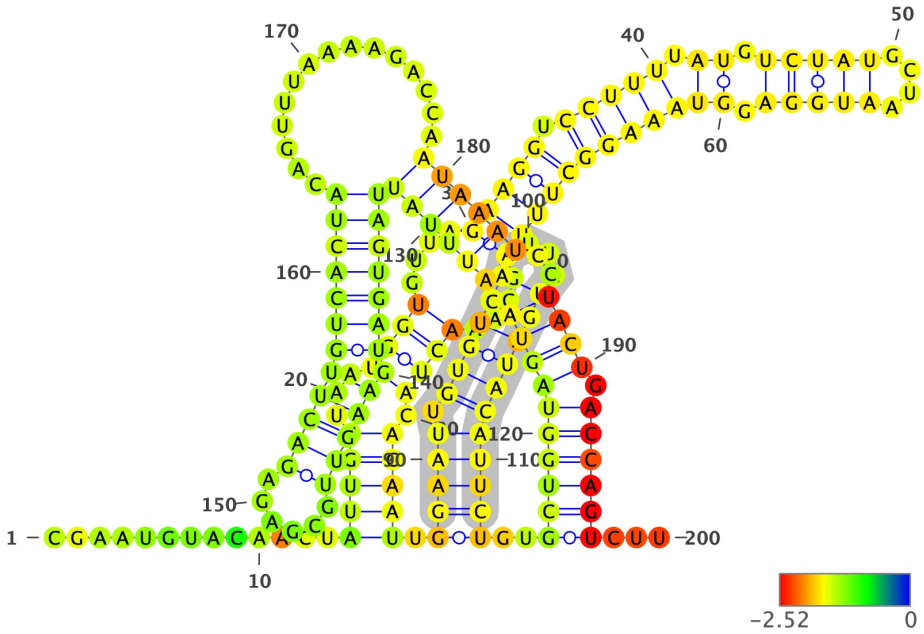
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 155 from nt 7615 to 7639 (nt 88 to 112)

```
5'-GAAUUGUGUUAAUUGUGAUACAUUC-3'
5'-(.(..(((.((....)).))).).)-3'
Motif MFE = -4.3; z-score = -2.05; ED = 2.65
```



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 7528 to 7727 (motif highlighted in silver):

```
5'-CGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUU
CUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUU-3
5'-.............(((((...((((....(((((.(((((.((.(((((....))))).))))))))))))....)))).))))).(((((.((((((....)))))))))
))..((((((((((.((((((((((((.(((((......)))))))))))).................))))))..)))).))))))...-3'
MFE = -47.9; z-score = -2.68; ED = 36.4
```

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

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

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

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

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

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

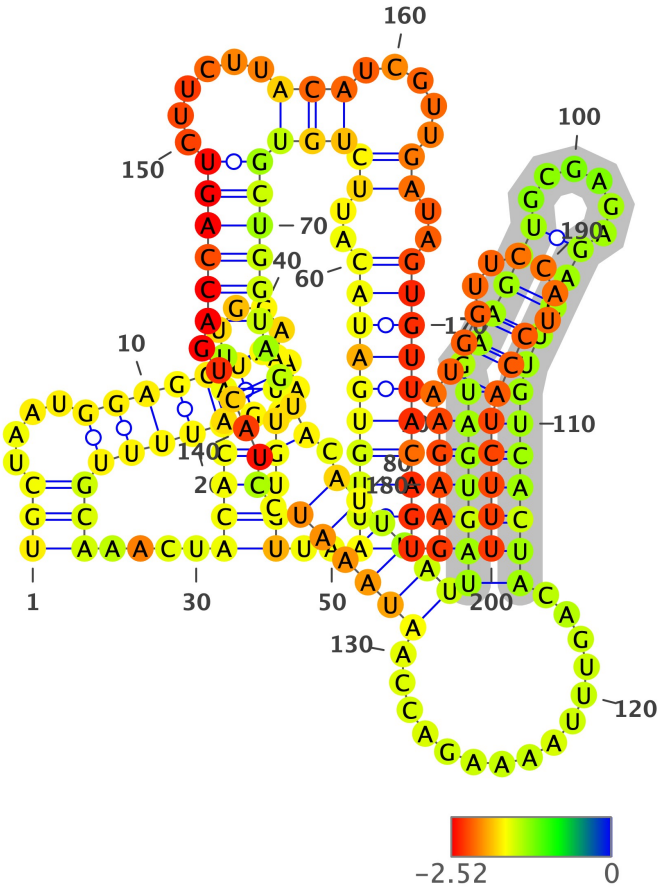
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 156 from nt 7660 to 7690 (nt 85 to 115)

```
5'-UAGUGAUGAAGUUGCGAGAGACUUGUCACUA-3'
5'-((.((((.(((((.....)))))))))).))-3'
Motif MFE = -10.2; z-score = -3.38; ED = 2.13
```



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

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

```
5'-UGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUC
ACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUU-3
5'-(((....((((((....))))))))).....(((((((....))))))).((((((((((..((((((((((((((.((((((((((((.(((((.....)))))))))))))))))))))))))))))
))))).............))))))..)))).))))))......)))).....))..))))))))))(((((.(((.....)))))))))-3'
MFE = -44.5; z-score = -1.66; ED = 55.73
```

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

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

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

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

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

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

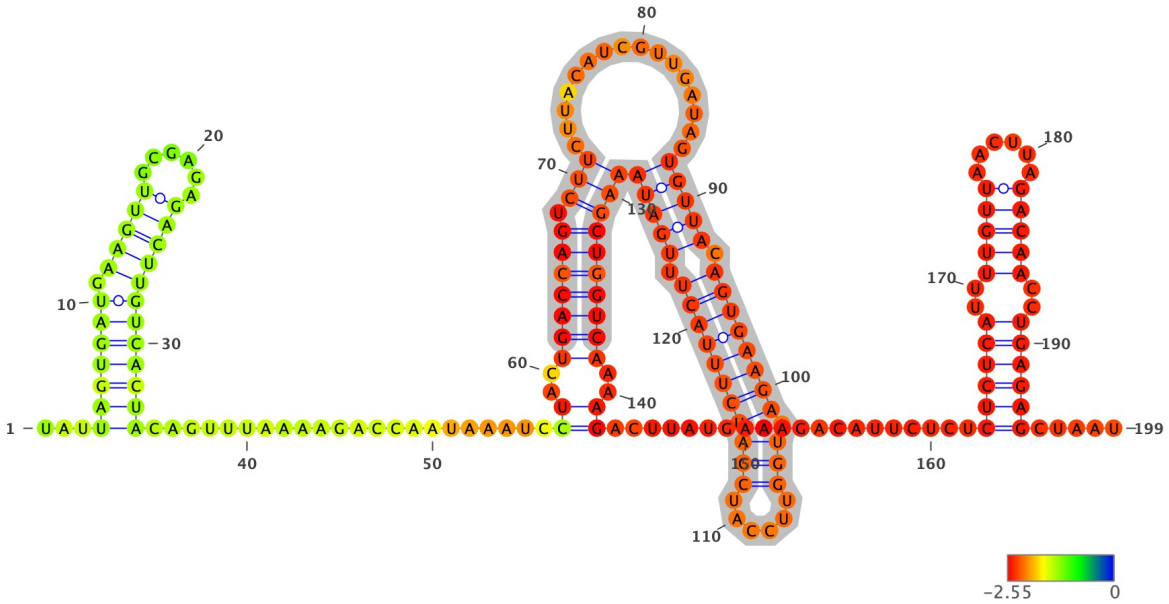
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 157 from nt 7718 to 7793 (nt 62 to 137)

```
5'-GACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUC-3'
5'-(((.((....................(((((.(((((((((.(((......))))))))))).)))))...)).)))-3'
Motif MFE = -22.0; z-score = -3.41; 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 = -2.64; ED = 25.16
```

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(+)

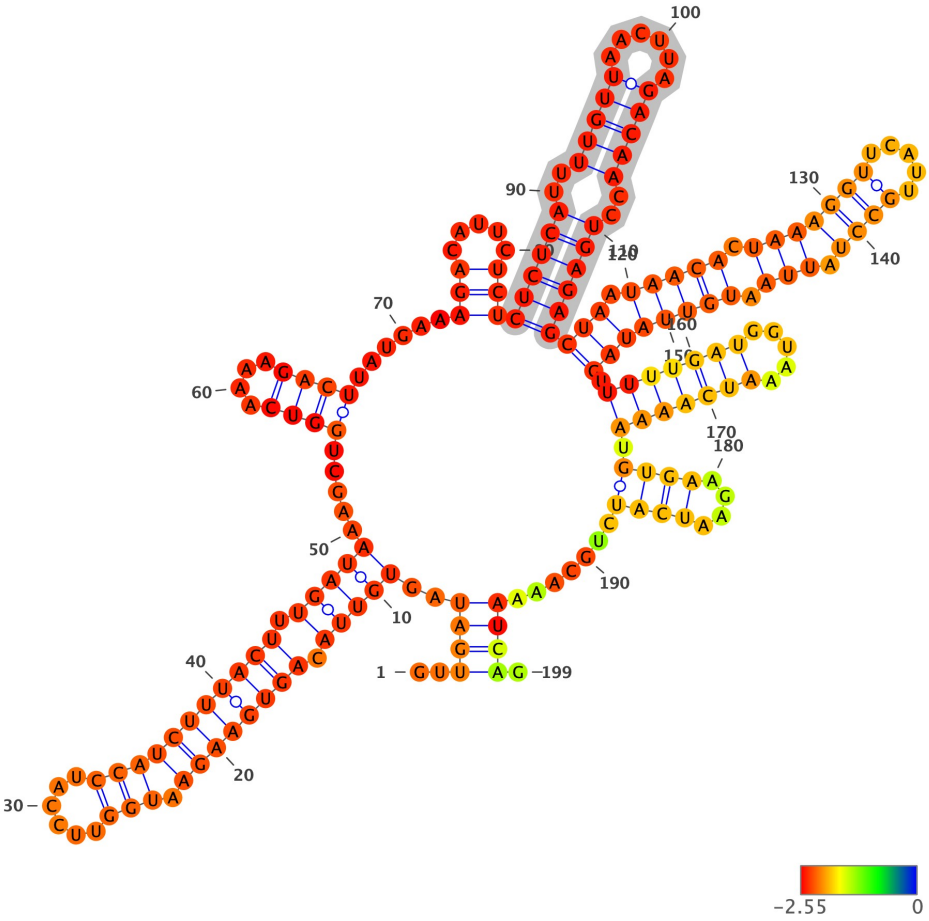
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 158 from nt 7819 to 7850 (nt 84 to 115)

```
5'-CUCUCAUUUUGUUAACUUAGACAACCUGAGAG-3'
5'-((((((..(((((......)))))..))))))-3'
Motif MFE = -10.3; z-score = -4.33; 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 = -2.37; 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(+)

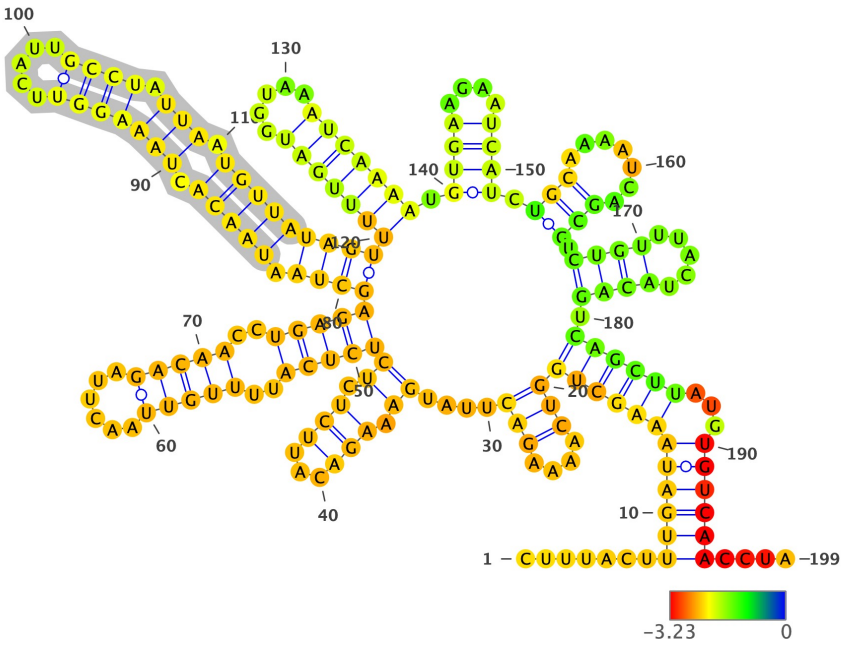
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 159 from nt 7855 to 7886 (nt 84 to 115)

```
5'-UAACACUAAAGGUUCAUUGCCUAUUAAUGUUA-3'
5'-(((((.(((((((.....)))).))).)))))-3'
Motif MFE = -6.5; z-score = -2.34; ED = 1.37
```



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

Extracted structure model with flanking nucleotides 7772 to 7970 (motif highlighted in silver):

```
5'-CUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAU
GUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUA-3
5'-.......(((((((((((((((....)))....((.(((...))).))(((((..(((((......)))))..)))))((((.(((((.(((((((.....)))).))).)
))))))))(((((((.....)))))))).((((....)))).(((.......))).((((.....)))).))))))...))))))....-3'
MFE = -43.5; z-score = -2.63; ED = 28.74
```

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

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

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

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

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

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

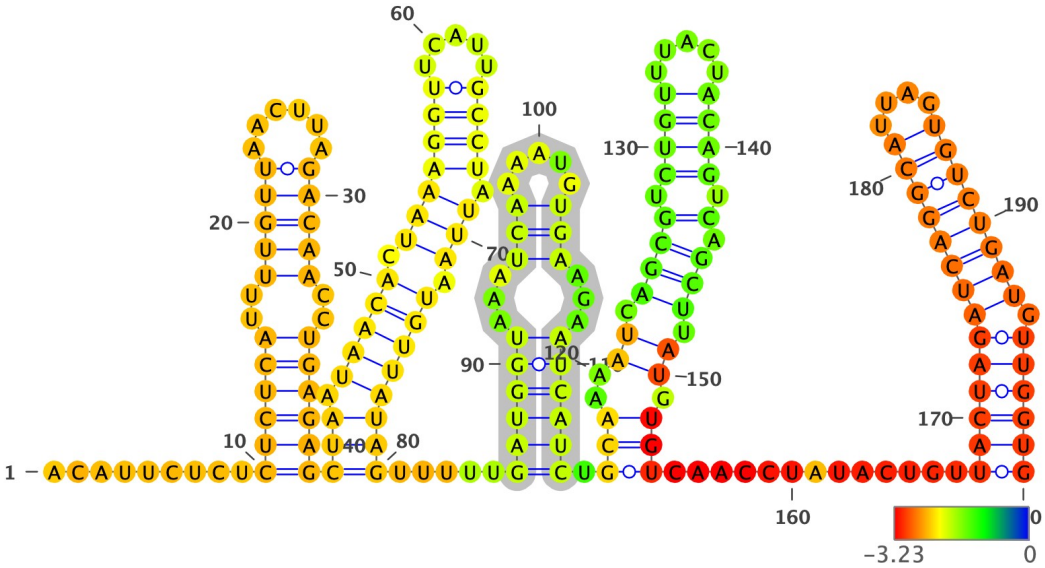
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 160 from nt 7895 to 7923 (nt 86 to 114)

```
5'-GAUGGUAAAUCAAAAUGUGAAGAAUCAUC-3'
5'-((((((...(((.....)))...)))))))-3'
Motif MFE = -4.2; z-score = -1.84; ED = 1.56
```



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

Extracted structure model with flanking nucleotides 7810 to 8009 (motif highlighted in silver):

```
5'-ACAUUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUC
AUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUG-3
5'-.........((((((..(((((......)))))..)))))))(((.((((((.(((((((.....)))))).))).)))))))).....((((((...(((.....)))...)))
))).(((..((.((((.((((.....)))).).))).)).))).............((((((((((((((....))))))))).)))))-3'
MFE = -44.9; z-score = -1.97; ED = 19.3
```

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

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

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

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

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

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

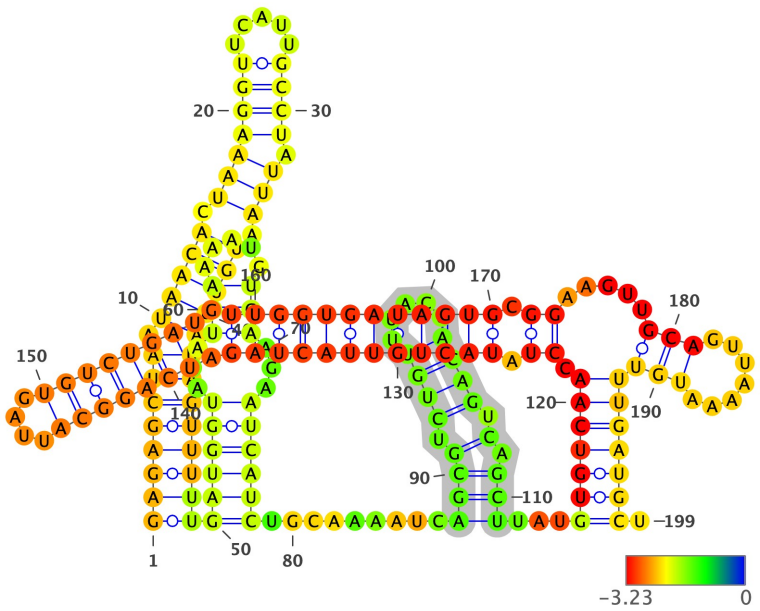
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-AGCGUCUGUUUACUACAGUCAGCU-3'
5'-((((.((((.....)))))).).)))-3'
Motif MFE = -5.8; z-score = -2.24; 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 = -3.31; 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(+)

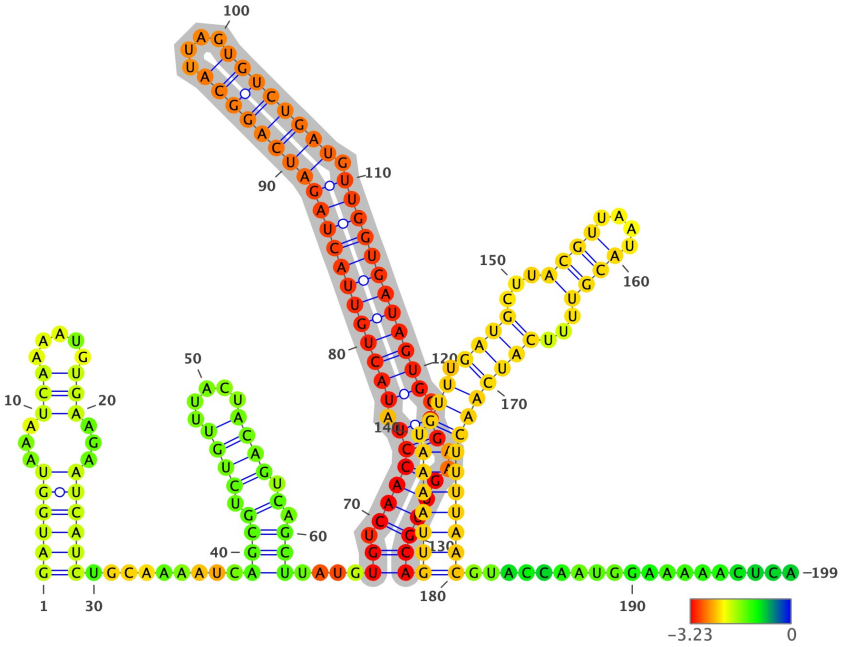
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 162 from nt 7961 to 8026 (nt 67 to 132)

```
5'-UGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCA-3'
5'-((.((((((.(((((((((((((((((((((....))))))))).))))))))))))).)).)))))))-3'
Motif MFE = -25.5; z-score = -4.16; ED = 3.41
```



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 7895 to 8093 (motif highlighted in silver):

```
5'-GAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUU
GGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCA-3
5'-((((((...(((.....)))...))))))..........((((.((((.....)))).).)))....((.((((((.(((((((((((((((((((....))))))))).))
))))))))))).))..))))))(((((((.(((.((((...((((....))))...))))))))))))))).....................-3'
MFE = -51.9; z-score = -3.4; ED = 18.49
```

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(+)

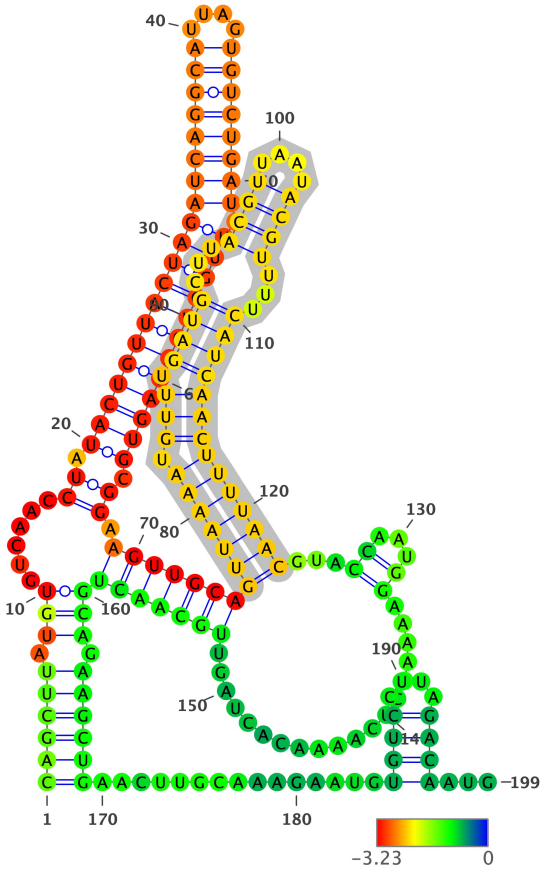
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 163 from nt 8027 to 8074 (nt 76 to 123)

```
5'-GUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAAC-3'
5'-(((((((.(((.((((...((((....))))...)))))))))))))-3'
Motif MFE = -12.4; z-score = -3.5; ED = 2.68
```



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

Extracted structure model with flanking nucleotides 7952 to 8150 (motif highlighted in silver):

```
5'-CAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCA
UCAACUUUUAACGUACCAAUGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUG-3
5'-((((((.(((......((.((((((((((((((((((((....))))))))).))))))))))))).)).((((((((((((((.(((.((((...((((....))))...))
))))))))))))...((...))...................))))))))))).))))))...............((((....))))...-3'
MFE = -54.0; z-score = -3.09; 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, 266-13468(+)

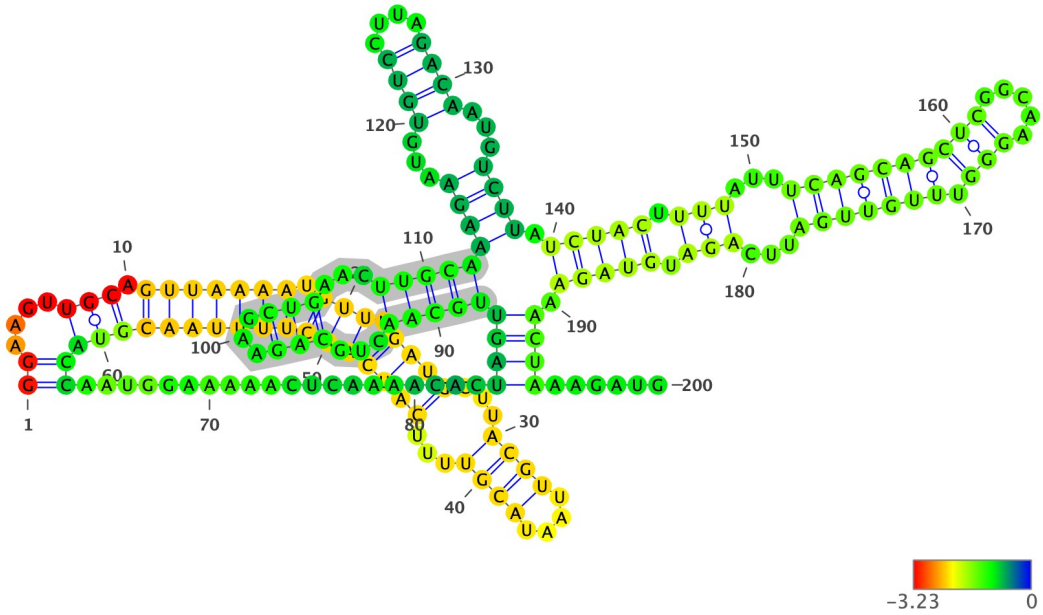
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 8104 to 8128 (nt 88 to 112)

```
5'-UGCAACUGCAGAAGCUGAACUUGCA-3'
5'-(((((...(((...)))...)))))-3'
Motif MFE = -4.9; z-score = -1.21; ED = 2.59
```



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 8017 to 8216 (motif highlighted in silver):

```
5'-GGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGC
AAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAUUCAGAUGUAGAAACUAAAGAUG-3
5'-((....(((.(((((((.(((.((((...((((....))))...))))))))))))))))))).....................((((((((...(((...)))...))))
)((((...((((....))))...)))).(((((.(((...((((((((((.....))).)))))))...))).))))).))))......-3'
MFE = -43.9; z-score = -1.47; ED = 25.68
```

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(+)

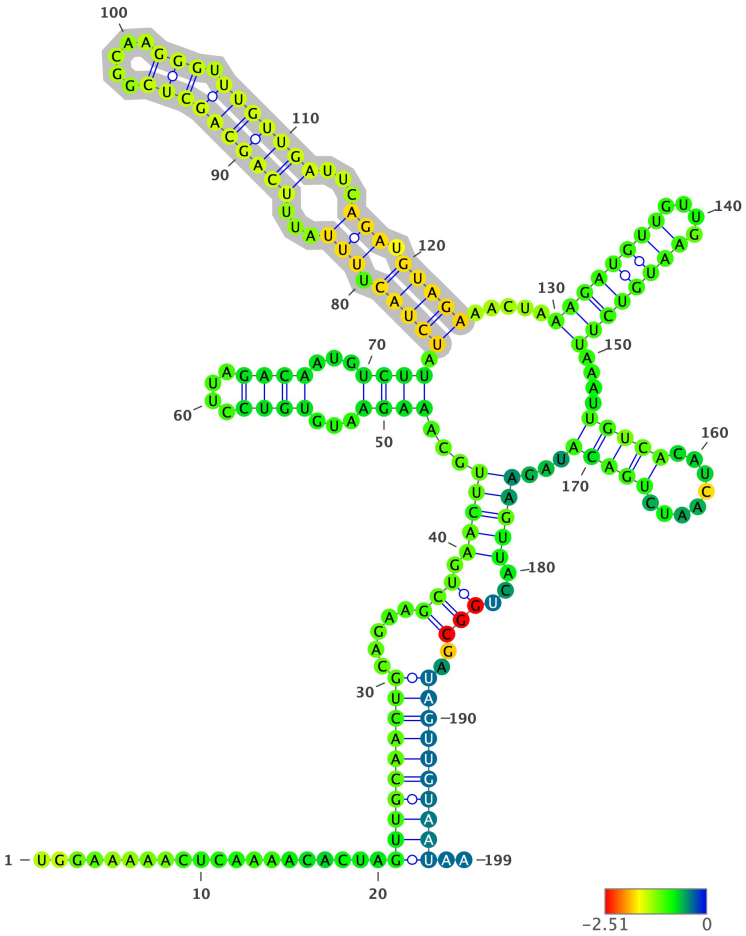
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 165 from nt 8156 to 8205 (nt 75 to 124)

```
5'-UCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAUUCAGAUGUAGA-3'
5'-(((((.(((...((((((((((.....))).)))))))...))).)))))-3'
Motif MFE = -15.0; z-score = -2.78; 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 = -1.98; 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(+)

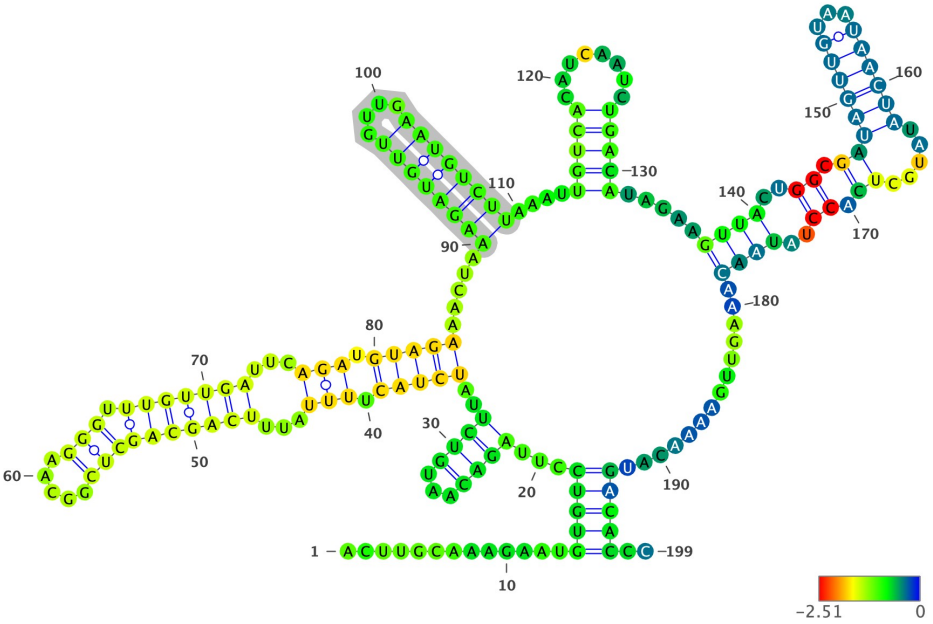
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 166 from nt 8211 to 8230 (nt 90 to 109)

```
5'-AAGAUGUUGUUGAAUGUCUU-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -4.2; z-score = -4.51; 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 = -1.41; 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, 266-13468(+)

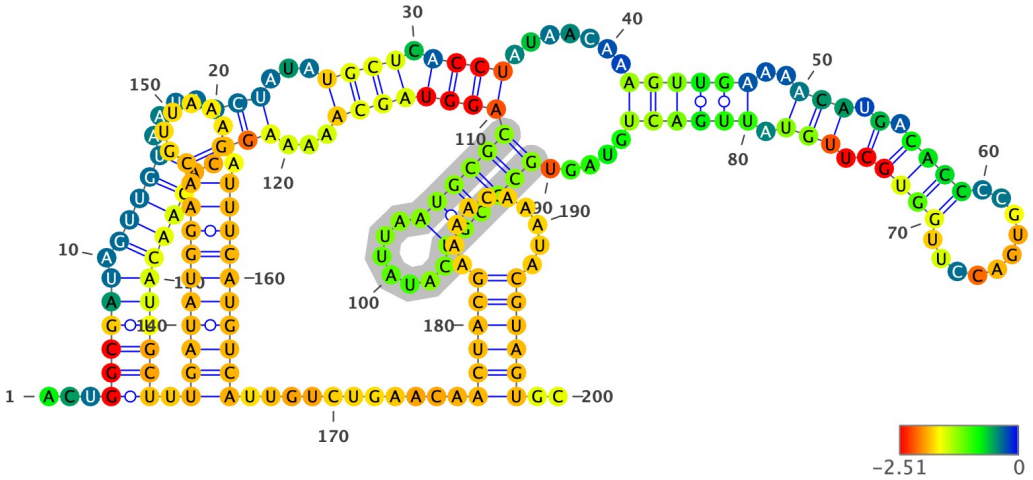
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 8351 to 8369 (nt 91 to 109)

```
5'-GCGCGUCAUAUUAAUGCGC-3'
5'-((((((.......))))))-3'
Motif MFE = -6.2; z-score = -3.1; 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 8261 to 8460 (motif highlighted in silver):

```
5'-ACUGGCGAUAGUUGUAAUAACUAUAUGCUCACCUAUAACAAAGUUGAAAACAUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAG
GUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGC-3
5'-...((((((.(((((....(((...((((.((((.......((((((..(((.(.((((..........)))))).))).))))))).....((((((.......))))))))
))))))...))).)))))))))).((((((((((.....).)))))))))..........((((((..........))))))..-3'
MFE = -48.1; z-score = -2.08; ED = 11.9
```

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

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

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

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

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

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

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

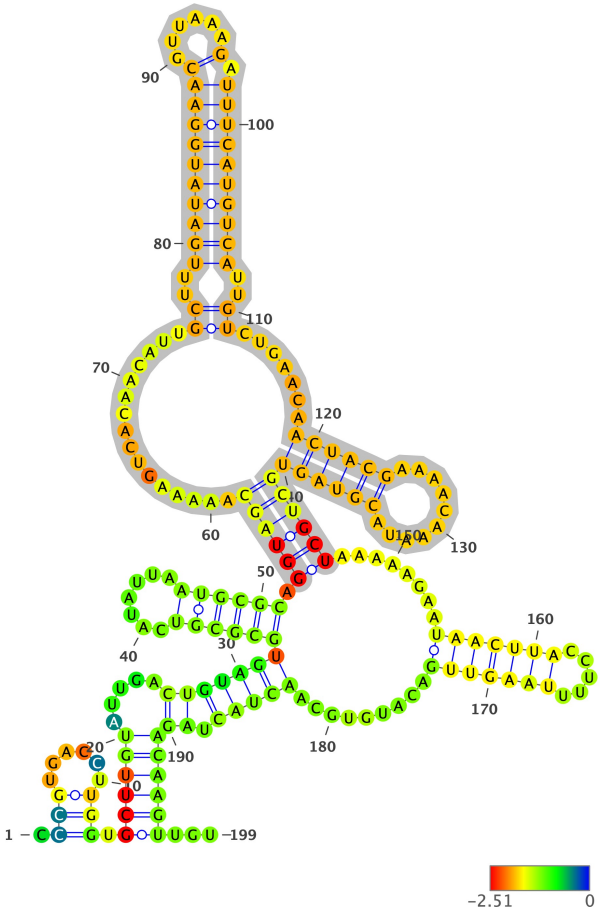
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

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

NC_045512.2 (forward strand): Structure number 168 from nt 8371 to 8464 (nt 53 to 146)

```
5'-GGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCU-3'

5'-(((...................((..(((((((((((......).))))))))))..)).......((((((..........))))))...)))-3'
Motif MFE = -22.4; z-score = -2.76; ED = 9.66
```



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 8319 to 8517 (motif highlighted in silver):

```
5'-CCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGU
CUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGU-3
5'-.(((......))).((((((.....(((((((((((((.......))))))).((((((.................((..(((((((((((......).))))))))))..))
.......((((((..........))))))))))))).........(((((((.....)))))))..........))))).))))))))...-3'
MFE = -43.5; z-score = -0.93; ED = 30.37
```

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(+)

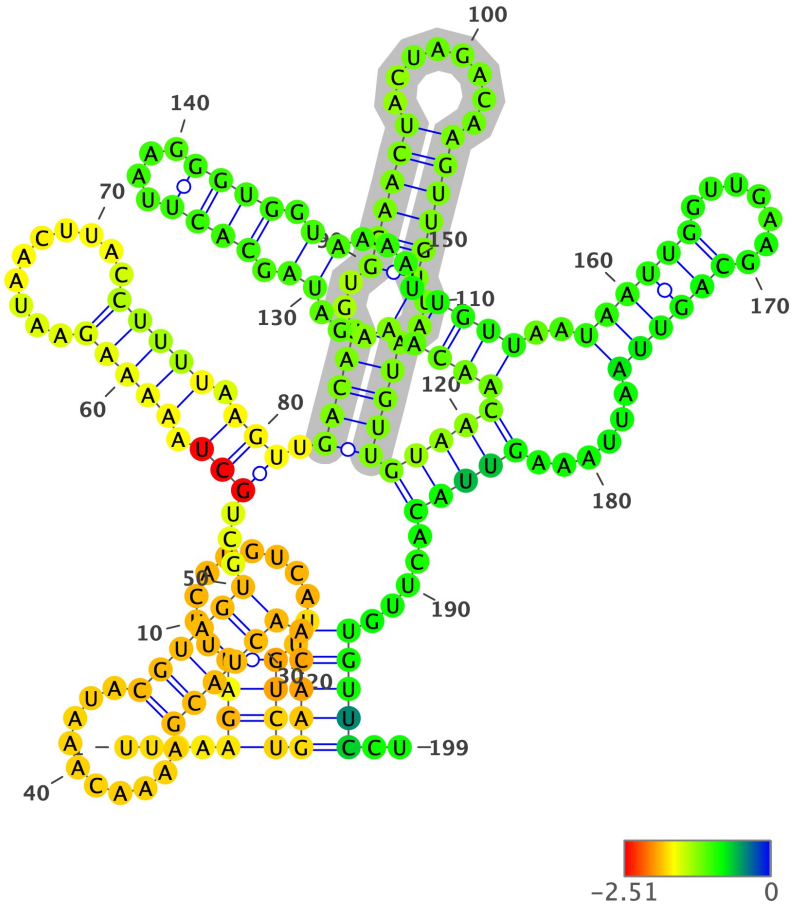
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 169 from nt 8491 to 8524 (nt 83 to 116)

```
5'-GACAUGUGCAACUACUAGACAAGUUGUUAAUGUU-3'
5'-((((((..((((((........)))))))..))))))-3'
Motif MFE = -9.3; z-score = -3.33; 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 = -0.63; 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(+)

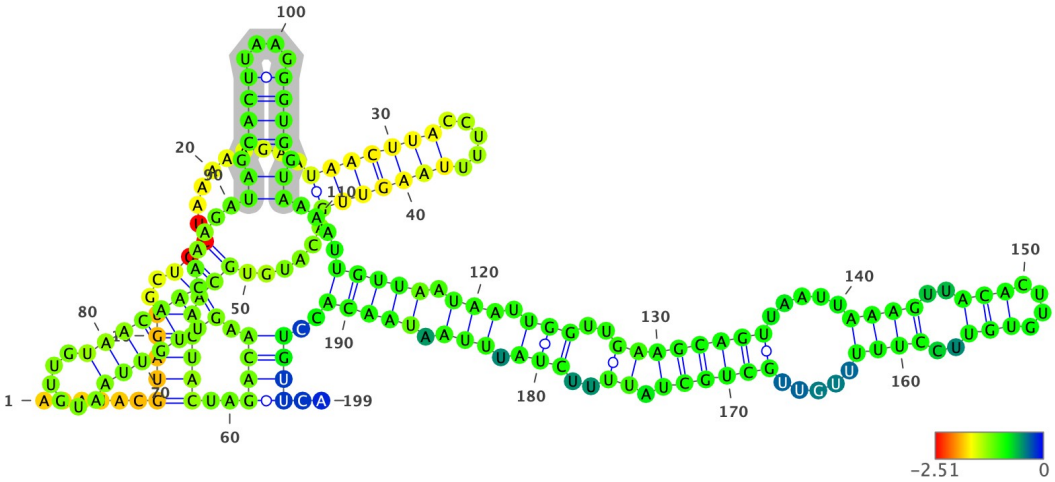
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 170 from nt 8538 to 8555 (nt 91 to 108)

```
5'-UAGCACUUAAGGGUGGUA-3'
5'-((.((((....)))).))-3'
Motif MFE = -3.2; z-score = -2.69; 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 = -1.01; 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(+)

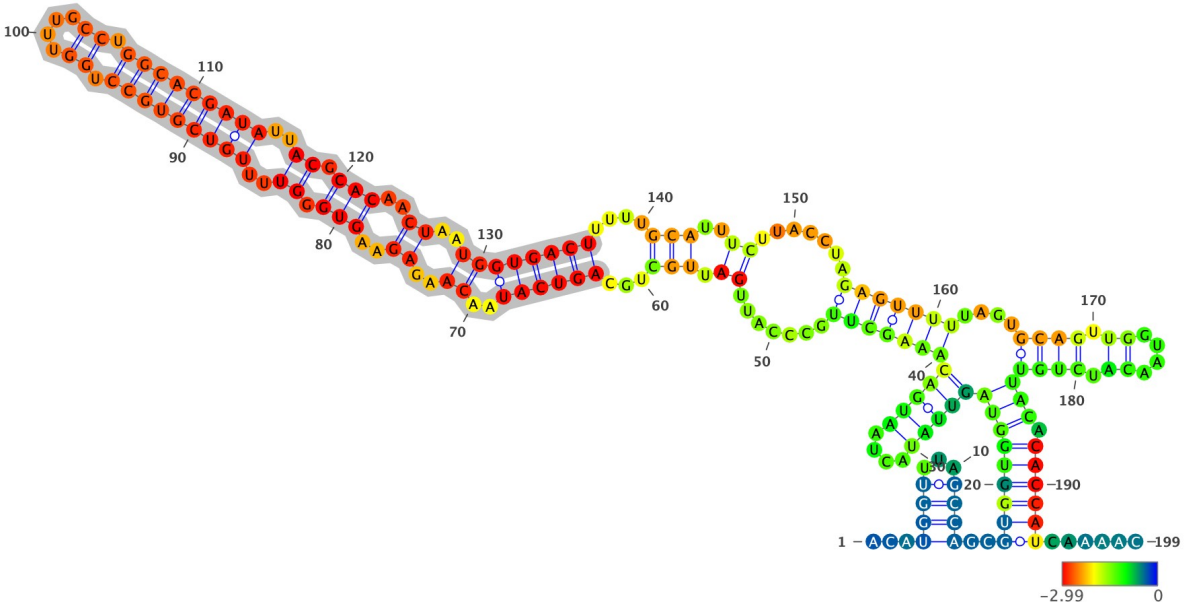
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 171 from nt 8833 to 8906 (nt 63 to 136)

```
5'-AGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACU-3'
5'-((((((..((..((..(((.((..((((((((((.((....)).)))))))))..)).))))..))..))))))))-3'
Motif MFE = -32.0; z-score = -4.92; 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 = -2.79; 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(+)

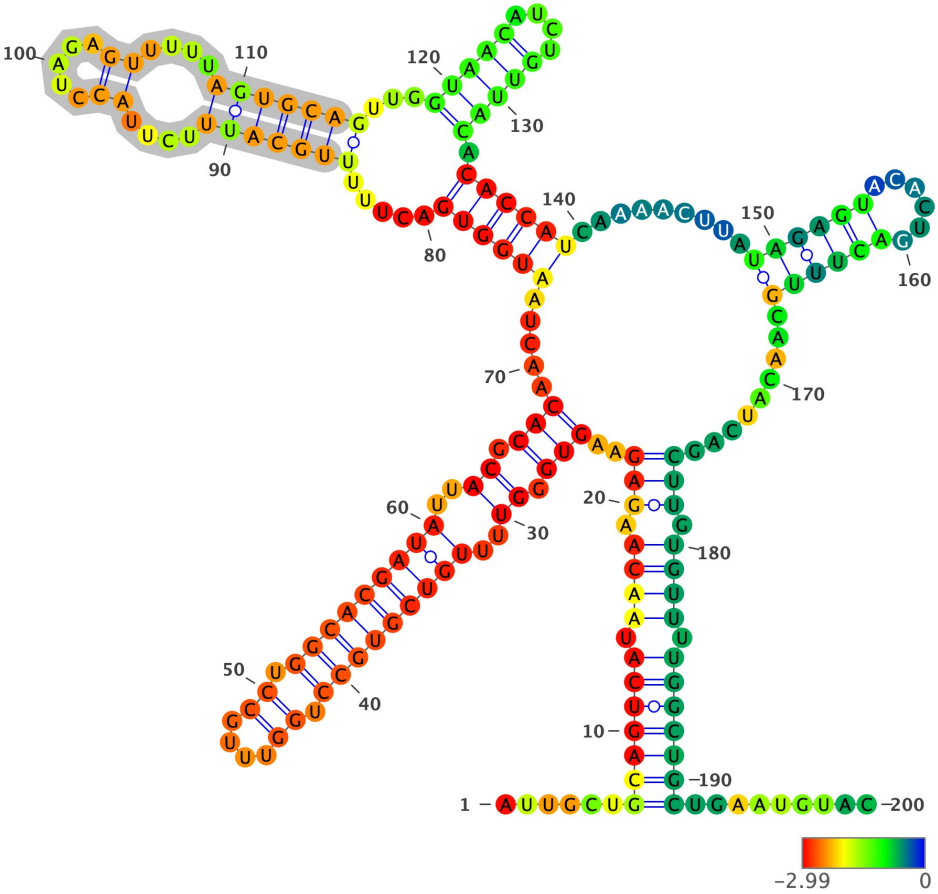
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 172 from nt 8910 to 8938 (nt 86 to 114)

```
5'-UGCAUUUCUUACCUAGAGUUUUUAGUGCA-3'
5'-((((.(....((.....)).....).))))-3'
Motif MFE = -4.1; z-score = -1.33; 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 = -58.8; z-score = -3.62; ED = 20.44
```

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(+)

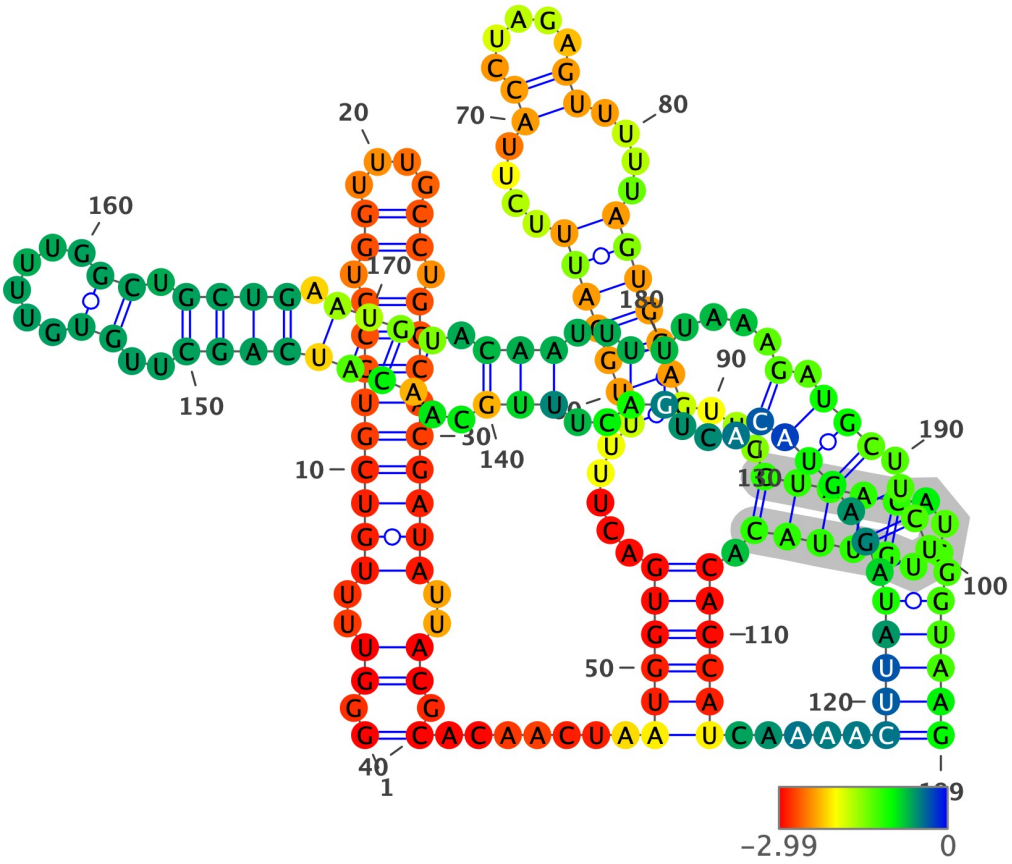
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 173 from nt 8943 to 8956 (nt 93 to 106)

```
5'-GUAACAUCUGUUAC-3'
5'-(((((....)))))-3'
Motif MFE = -2.5; z-score = -5.35; ED = 0.27
```



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 8851 to 9049 (motif highlighted in silver):

```
5'-GGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGUGCAGUUGGUAACAUCUGUUACACACC
AUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAG-3
5'-(.((..((((((((((.((....)).)))))))))..)).).......((((((.....(((((((....((.....)).....)))))))...(((((....))))).))))
)).....((((((((((((...((..(((..((((((((..((......)).)))).)))).)))..)).....).))).))).)))))-3'
MFE = -50.0; z-score = -1.69; ED = 45.39
```

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']

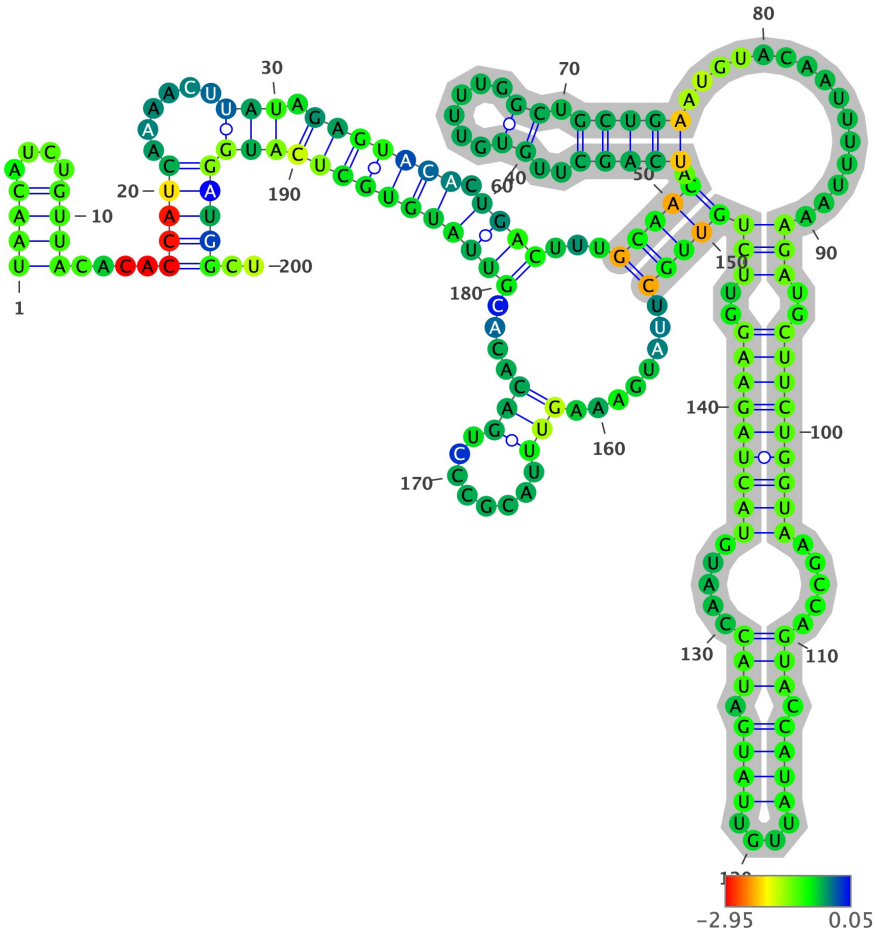
4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

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 174 from nt 8990 to 9096 (nt 47 to 153)

```
5'-GCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCAAUGUACUAGAAGGUUCUGUUGC-3'

5'-(..(..(.....................).................(((..((((((((((.....(((.((((....)))).)))).....)))))))))..))).)..)-3'
Motif MFE = -29.0; z-score = -2.37; ED = 9.52
```



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 8944 to 9143 (motif highlighted in silver):

```
5'-UAACAUCUGUUACACACCAUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGU
ACCAUAUUGUUAUGAUACCAAUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGCCCUGACACACGUUAUGUGCUCAUGGAUGGCU-3
5'-((((....))))....(((((......(((.(((((((.((((...(((((.(((((..((......)).)))))...............(((..((((((((.....((
(.((((....)))).)))).....))))))))))..))))))))).........(((........)))....))))))))))))))))))))..-3'
MFE = -45.3; z-score = -1.55; ED = 23.48
```

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

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

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

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

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

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

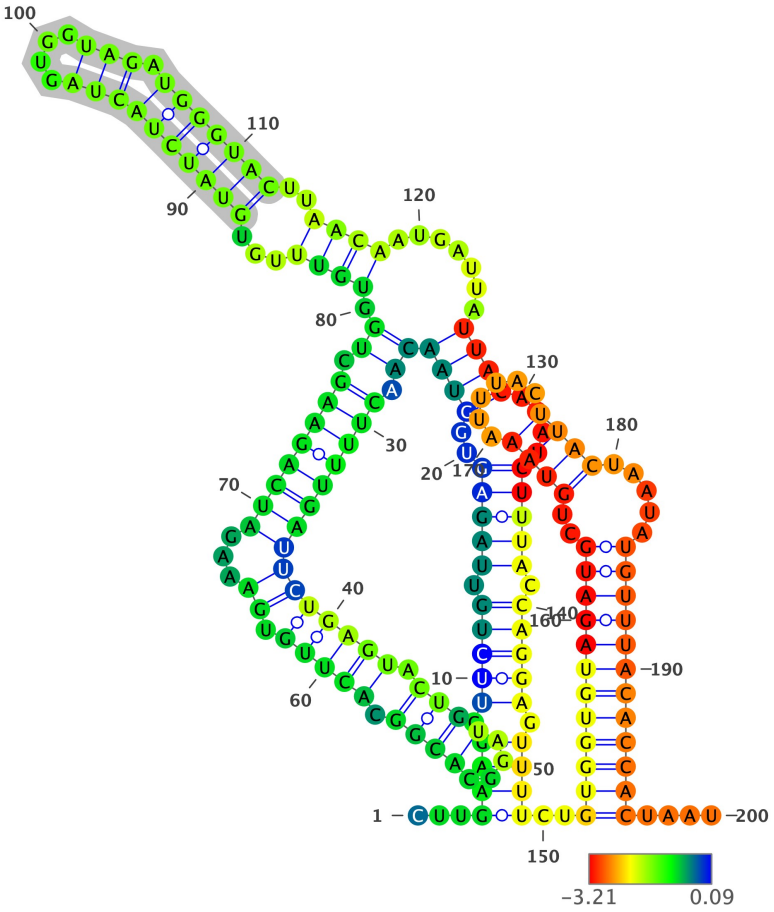
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 175 from nt 9257 to 9281 (nt 88 to 112)

```
5'-GUAUCUACUAGUGGUAGAUGGGUAC-3'
5'-((((((((((....))).)))))))-3'
Motif MFE = -6.8; z-score = -2.98; 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 = -2.0; 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(+)

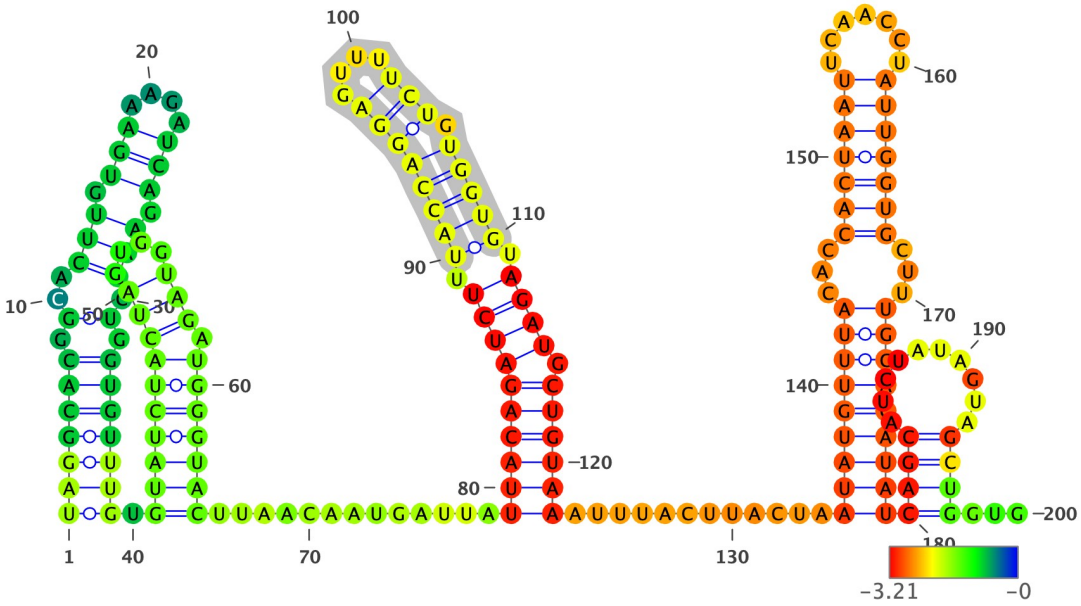
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 176 from nt 9306 to 9326 (nt 90 to 110)

```
5'-UACCAGGAGUUUUCUGUGGUG-3'
5'-((((((((....))).)))))-3'
Motif MFE = -4.3; z-score = -1.9; ED = 3.62
```



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 9217 to 9416 (motif highlighted in silver):

```
5'-UAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGU
AGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG-3
5'-(((((((.(..(((.(((....))).))).).)))))))).((((((((((....))).)))))))..............((((((((((.((((((((....))).)))))).
)))).))))))............((((((((...(((((((.......)))))))...)))))))))((((..........))))...-3'
MFE = -51.1; z-score = -2.45; ED = 51.42
```

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(+)

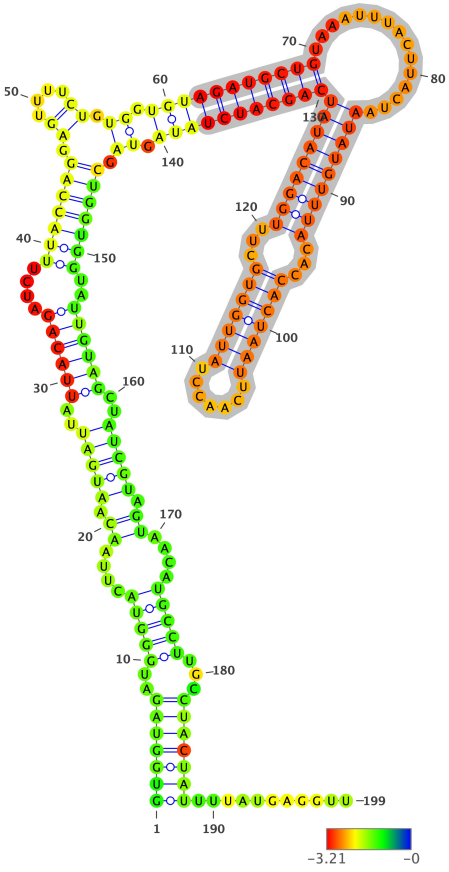
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 177 from nt 9328 to 9403 (nt 62 to 137)

```
5'-AGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCU-3'
5'-((((((((...............(((((((((...(((((((.......)))))))...)))))))))))))))))-3'
Motif MFE = -21.1; z-score = -4.6; ED = 5.1
```



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 9267 to 9465 (motif highlighted in silver):

```
5'-GUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUA
UUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUU-3
5'-(((((((..(((((....((.(((((..((((((....(((((((.((....)).((.(((((((((((.................(((((((((...(((((((.......)
))))))...))))))))))))))))))).)).)))))))..))))))..))))).))....)))))...)))))))...........-3'
MFE = -51.9; z-score = -2.82; ED = 19.49
```

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(+)

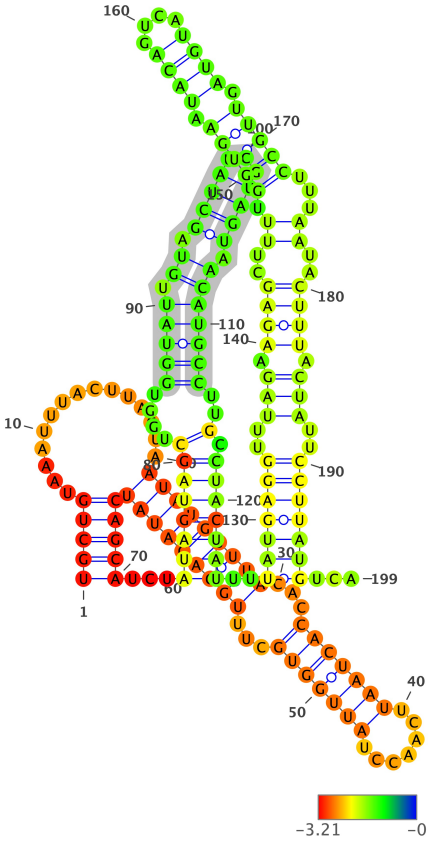
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 178 from nt 9416 to 9443 (nt 86 to 113)

```
5'-GGUAUUGUAGCUAUCGUAGUAACAUGCC-3'
5'-((((((.((.((((...)))).)))))))-3'
Motif MFE = -6.5; z-score = -1.53; 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 = -3.03; 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(+)

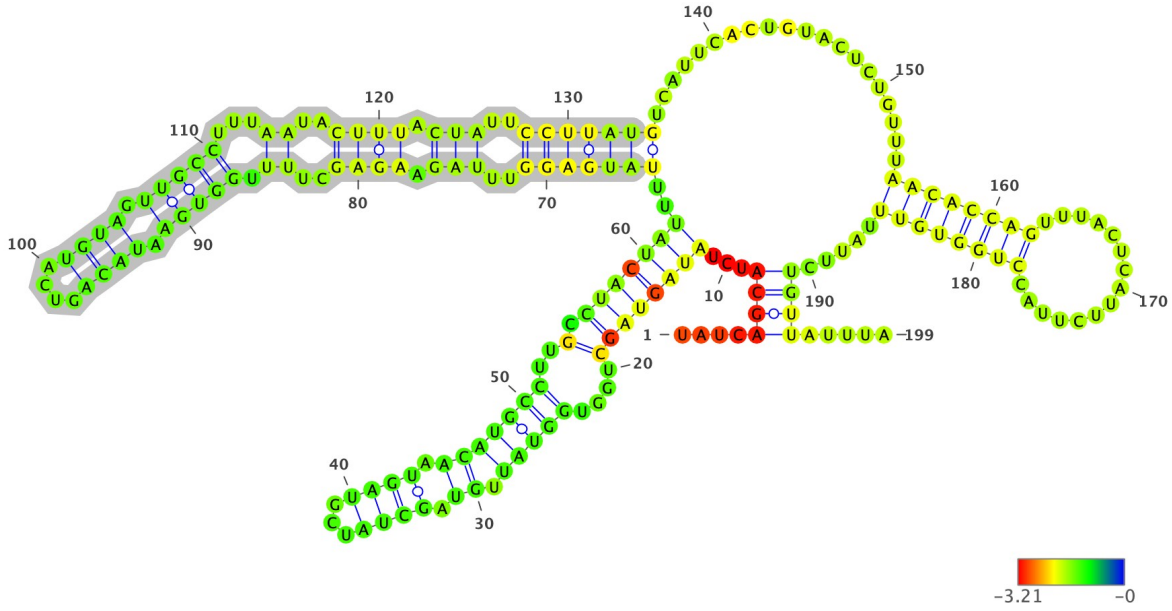
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 179 from nt 9458 to 9525 (nt 66 to 133)

```
5'-AUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAU-3'
5'-((......(((.......((.(((((.((((....)))).)))))...)).......)))......))-3'
Motif MFE = -17.7; z-score = -3.11; 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 = -1.88; ED = 22.82
```

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(+)

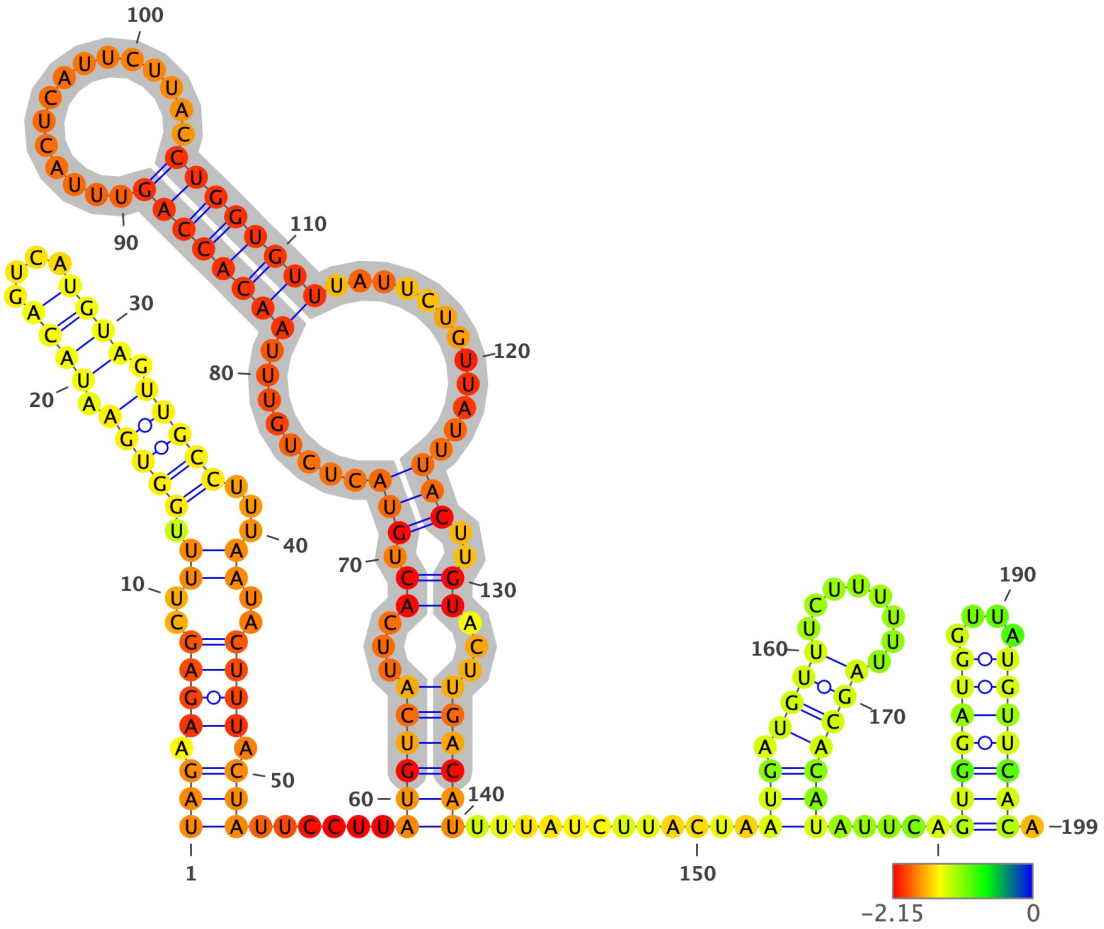
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 180 from nt 9526 to 9603 (nt 61 to 138)

```
5'-GUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGAC-3'
5'-(......((.(..........(((((((.............)))))))).............)..)).....)-3'
Motif MFE = -11.3; z-score = -2.11; 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 = -1.25; ED = 36.43
```

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(+)

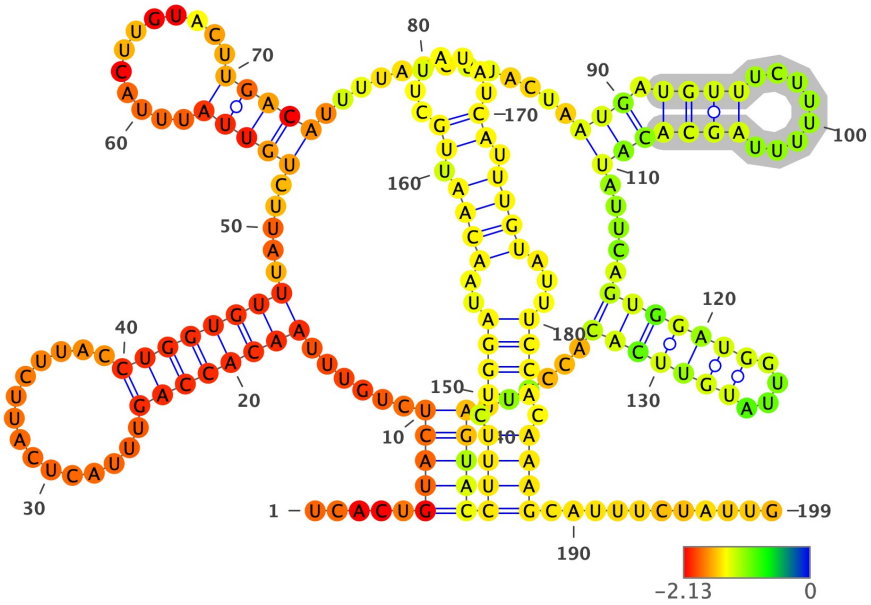
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 181 from nt 9622 to 9637 (nt 92 to 107)

```
5'-UGUUUCUUUUUUAGCA-3'
5'-((((........))))-3'
Motif MFE = -0.1; z-score = -0.88; ED = 1.83
```



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

Extracted structure model with flanking nucleotides 9531 to 9729 (motif highlighted in silver):

```
5'-UCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUA
UUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUG-3
5'-.....(((((......(((((((.............)))))))).....(((((...........)))))).............(((.((((........)))))))).
....(((((((....))))))).....)))))(((((.(((((..(((((.((.......)).)))))...))))).)))).....-3'
MFE = -29.4; z-score = -1.43; ED = 39.81
```

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

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

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

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

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

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

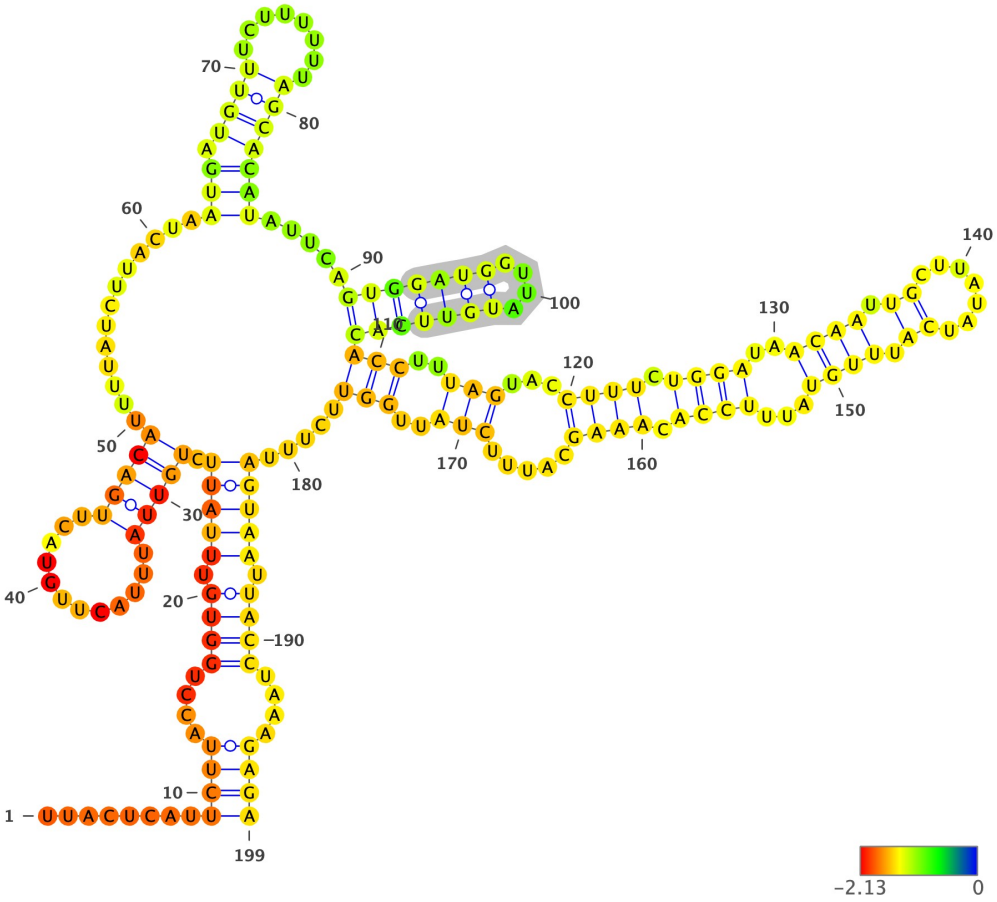
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 182 from nt 9649 to 9660 (nt 94 to 105)

```
5'-GAUGGUUAUGUU-3'
5'-(.((....)).)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.22
```



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

Extracted structure model with flanking nucleotides 9556 to 9754 (motif highlighted in silver):

```
5'-UUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACC
UUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGA-3
5'-........((((....((((.(((((.(((((............)))))).............(((.((((........)))))))).....(((((((....)))))))))(((
..(((...((((.((((..((((.((.......)).)))))...)))))..))))).....)))..)))).....))))).))))....))))-3'
MFE = -29.7; z-score = -0.96; ED = 29.42
```

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, 266-13468(+)

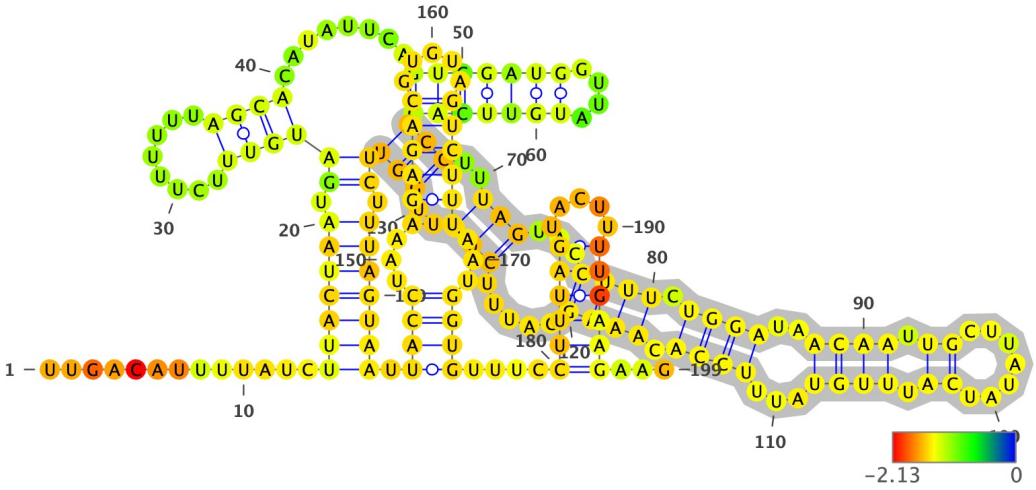
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 183 from nt 9664 to 9731 (nt 66 to 133)

```
5'-ACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGU-3'
5'-(((...((...((((.((((..((((.((.......)).))))...)))).)))).....))...)))-3'
Motif MFE = -12.1; z-score = -2.66; ED = 2.89
```



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

Extracted structure model with flanking nucleotides 9599 to 9797 (motif highlighted in silver):

```
5'-UUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUU
UCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAG-3
5'-.............(((((((.((((((........))))........(((((((....)))))))(((..(((...((((.((((..((((.((.......)).))))...
)))).)))).....)))..))))).))))))).((((...((((((.....))))))...)))).....((((((.....))))))...-3'
MFE = -36.1; z-score = -1.1; ED = 51.94
```

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

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

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

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

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

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

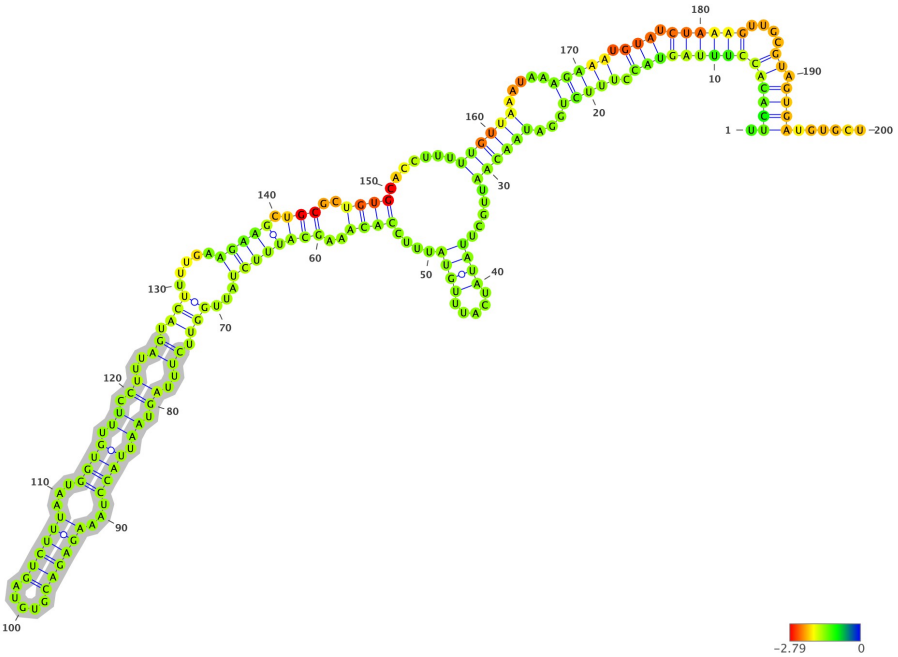
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 184 from nt 9733 to 9783 (nt 75 to 125)

```
5'-CUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAG-3'
5'-((..(.....((((...((((((.....))))))...))))).....)..))-3'
Motif MFE = -11.2; z-score = -2.4; ED = 3.51
```



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

Extracted structure model with flanking nucleotides 9659 to 9858 (motif highlighted in silver):

```
5'-UUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAU
GGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCU-3
5'-.(((((((((((((((.(((((...((((((.....((((.....))))....((((..((((((((...(((.((..((.((.((((...((((((.....))))))...
)))).)).))..)).))).....))))).)))..))))).......))))))).....))))).))).))))))....)).))))......-3'
MFE = -40.2; z-score = -1.15; ED = 43.54
```

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(+)

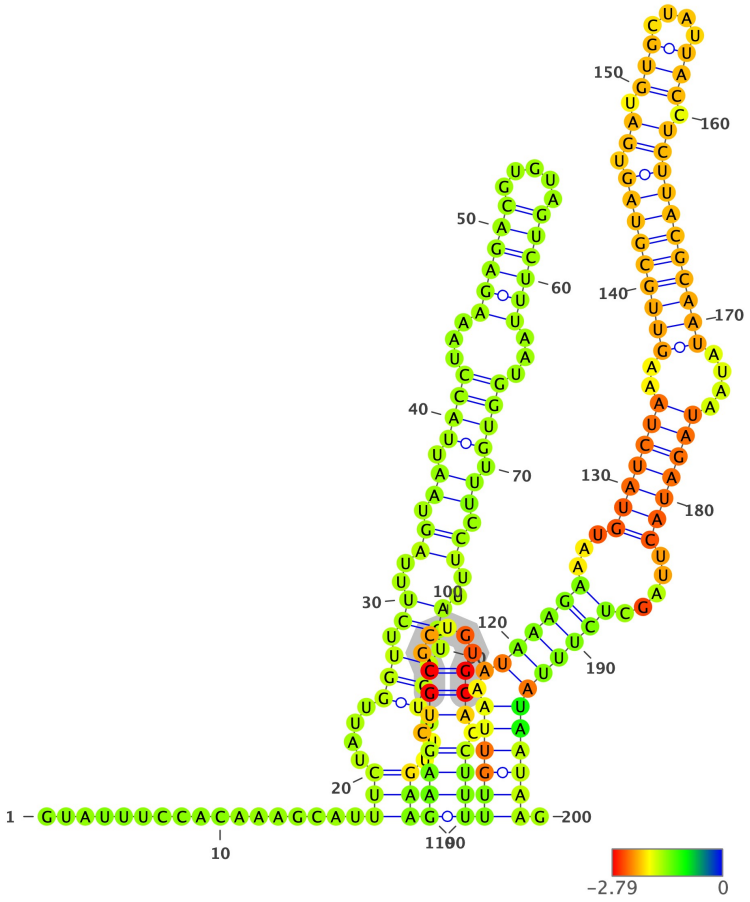
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 185 from nt 9800 to 9808 (nt 96 to 104)

```
5'-GCGCUGUGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.23; 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 9705 to 9904 (motif highlighted in silver):

```
5'-GUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUU
UGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAG-3
5'-.................(((....(((.(((..(((.(((.((((...((((((.....))))))...)))))..)).)).)).)))...)))(((((.(((.....))).)))))(
((((((..(((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....))))))))))).-3'
MFE = -44.1; z-score = -3.15; ED = 32.31
```

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(+)

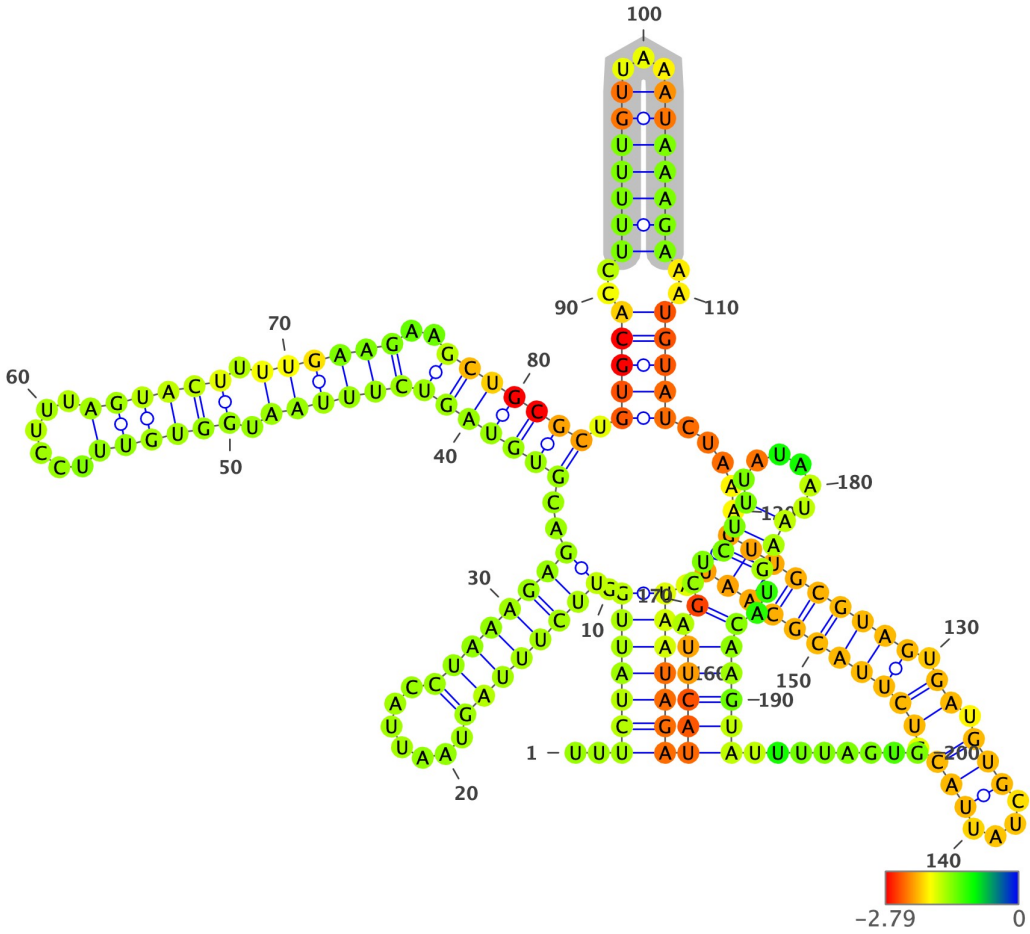
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 186 from nt 9812 to 9828 (nt 92 to 108)

```
5'-UUUUUGUUAAAUAAAGA-3'
5'-(((((.......)))))-3'
Motif MFE = 0.0; z-score = 0.17; ED = 4.13
```



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 9721 to 9920 (motif highlighted in silver):

```
5'-UUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAU
GUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAGUG-3
5'-..(((((((.((((((((.......))))))))..(((((((((((((.((((((.....)))))).))))))..))))))).(((((..(((((((...)))))))..)
))))).....((((((((.((.(((....))).))))))))))).)))))))(((((.(..(((......)))..))))))........-3'
MFE = -44.9; z-score = -2.86; ED = 22.96
```

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

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

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

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

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', '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(+)

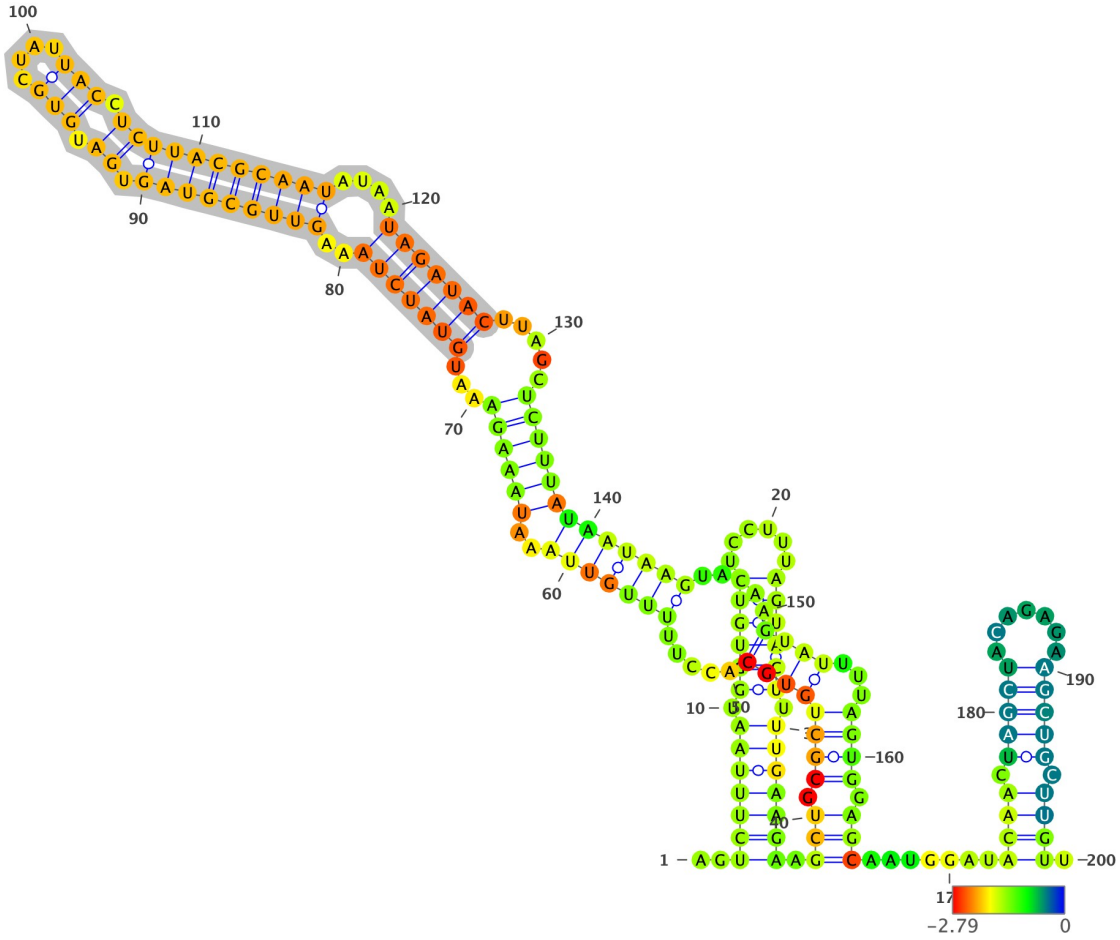
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 9832 to 9886 (nt 73 to 127)

```
5'-GUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUAC-3'
5'-(((((((..((((((((((.((.(((....))).))))))))))....)))))))-3'
Motif MFE = -17.4; z-score = -4.02; ED = 3.76
```



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

Extracted structure model with flanking nucleotides 9760 to 9959 (motif highlighted in silver):

```
5'-AGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUAC
GCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAGUGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUU-3
5'-..(((((((.((((((......))))))).)))))))).(((.(((((((((.....(((((((..((((((...(((((((..((((((((((.((.(((....))).))))))
))))).....)))))))).....))))))))))))).....))))...)))).))).......((((.(((((.......))))).)))).-3'
MFE = -50.0; z-score = -2.69; ED = 14.76
```

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(+)

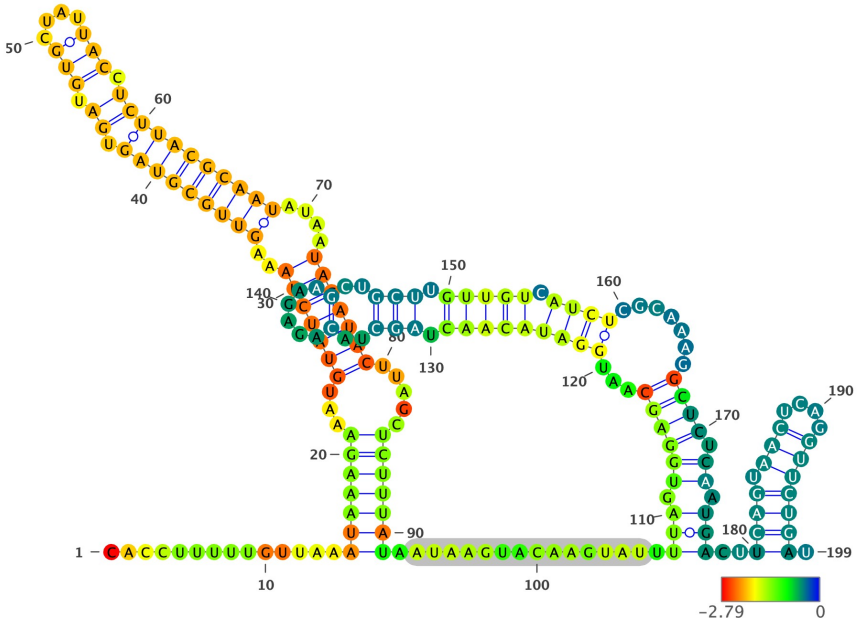
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 188 from nt 9900 to 9913 (nt 93 to 106)

```
5'-AUAAGUACAAGUAU-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.16; 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'-CACCUUUUUGUUAAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAG
UGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUUGUCAUCUCGCAAAGGCUCUCAAUGACUUCAGUAACUCAGGUUCUGAU-3
5'-..............(((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....)))))).............(((.
((((((...((((((((((.(((..(......)..))).)))))).))))).......)))))).))..))))..((((.(((....)))))))).-3'
MFE = -43.8; z-score = -1.84; 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(+)

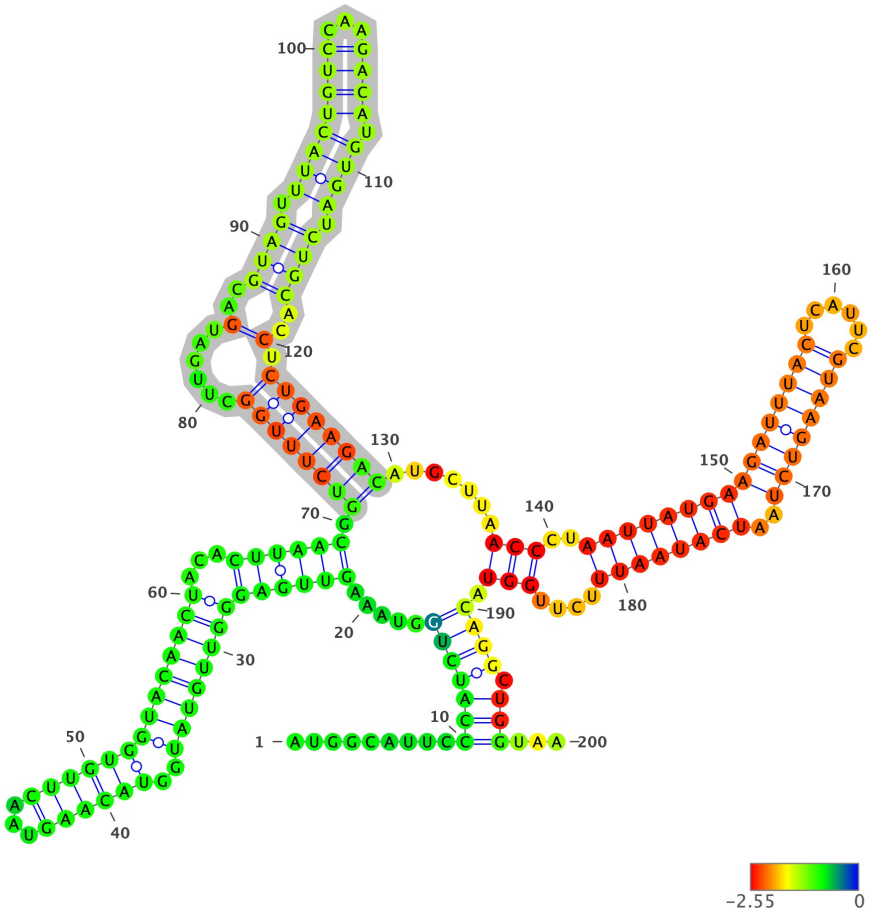
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 189 from nt 10140 to 10198 (nt 71 to 129)

```
5'-GUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGAC-3'
5'-((...............((((.((((((((...)))).)))).)))).........))-3'
Motif MFE = -14.0; z-score = -0.77; ED = 9.97
```



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 10070 to 10269 (motif highlighted in silver):

```
5'-AUGGCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUG
AUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAA-3
5'-.........(((((((.....(((((((((((((..((((((...)))))))))))))...)))))).((((((((......(..((((.((((((((...)))).)))
).))))..).))))))))).......(((..((((((((((((((((.....))))))))..))))))))....))).)))).)))...-3'
MFE = -53.1; z-score = -2.2; ED = 17.67
```

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(+)

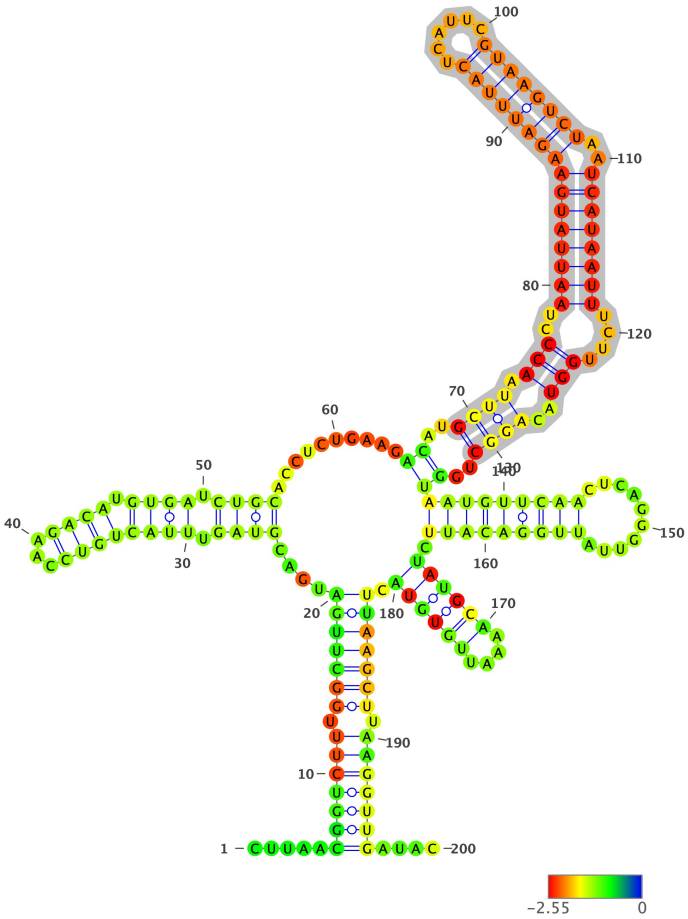
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 190 from nt 10201 to 10263 (nt 69 to 131)

```
5'-GCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGC-3'
5'-(....(((..(((((((((((((((((.....))))))))..))))))))....)))).....)-3'
Motif MFE = -17.5; z-score = -3.64; ED = 2.15
```



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 10133 to 10332 (motif highlighted in silver):

```
5'-CUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAU
CAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUAC-3
5'-.....(((((((.(((((((....((((.((((((((...)))).)))).))))..........((..((((.(((..(((((((((((((((.....))))))))..)
)))))))....)))..))))..))((((((((.........))))))))).((((((....)))))).))))))).))))))....-3'
MFE = -49.6; z-score = -3.09; 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(+)

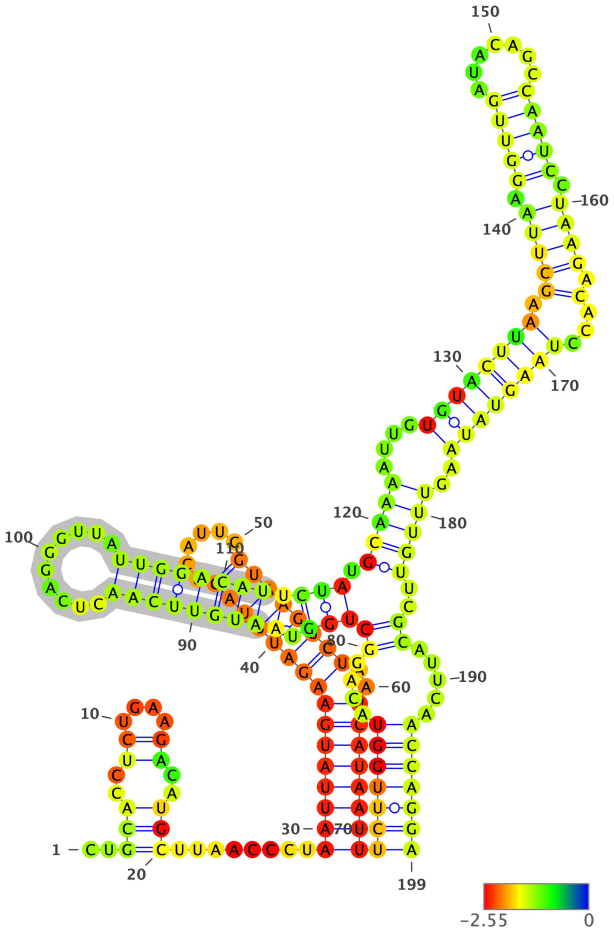
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 191 from nt 10269 to 10294 (nt 87 to 112)

```
5'-AUGUUCAACUCAGGGUUAUUGGACAU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -4.3; z-score = -1.05; 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 10183 to 10381 (motif highlighted in silver):

```
5'-CUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACA
UUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGA-3
5'-..(((..((....))..))).........(((((((((((((((.....))))))))..))))))))(((((((....(((((.((((((((.........)))))))
))))).(((((....((((((((.(((((.(((((.......))))).)))).)...)))))))))..)))))..))).....)))))))-3'
MFE = -45.2; z-score = -1.91; ED = 39.47
```

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(+)

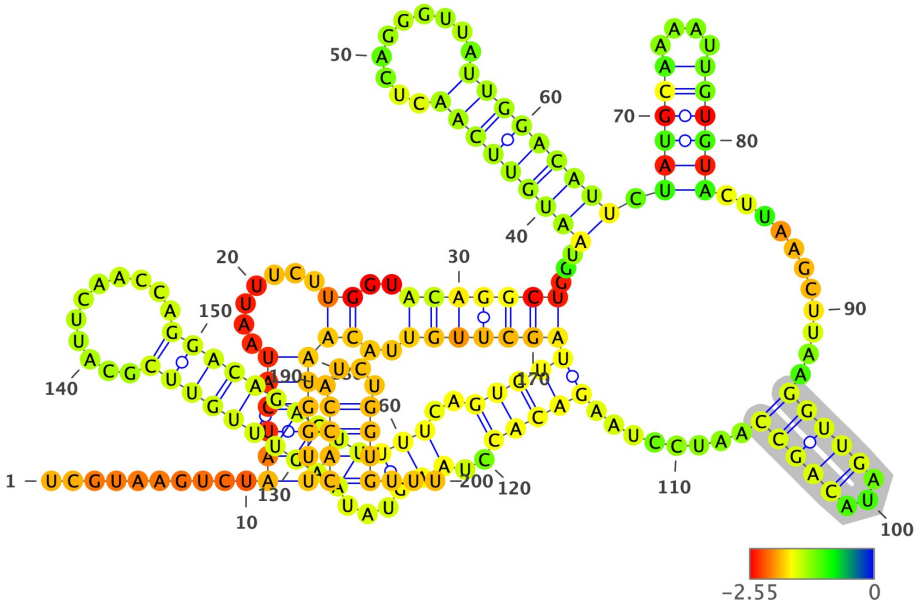
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 192 from nt 10324 to 10336 (nt 94 to 106)

```
5'-GGUUGAUACAGCC-3'
5'-(((((...)))))-3'
Motif MFE = -3.1; z-score = -2.74; ED = 0.22
```



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

Extracted structure model with flanking nucleotides 10231 to 10430 (motif highlighted in silver):

```
5'-UCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCC
UAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUU-3
5'-..........((((((.......((..(((((((...((((((((((..........))))))))).((((((....)))))).........(((((...)))))).....
...(((((..(((...((((((((((.........))))))))))))..))))))))))))..))))))))((((....))))...-3'
MFE = -42.7; z-score = -0.82; ED = 30.48
```

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

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

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

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

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

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

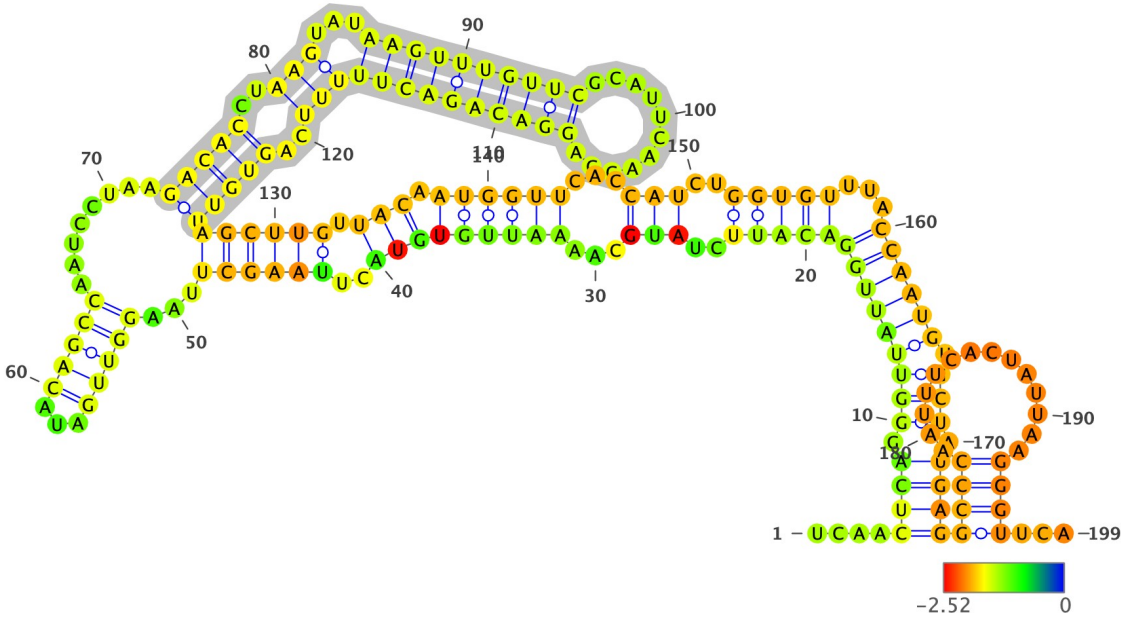
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 193 from nt 10345 to 10398 (nt 73 to 126)

```
5'-GACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUU-3'
5'-(((((..(((...(((((((((((.........))))))))))))..)))))-3'
Motif MFE = -12.9; z-score = -1.98; ED = 3.56
```



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 10273 to 10471 (motif highlighted in silver):

```
5'-UCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACA
GACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCA-3
5'-....((((.(((((((((((((..(((...(((((((((..((((((...(((((...)))))........(((((..(((...(((((((((((.........))))))
))))))))..))))))))))).))).))))))...)))..)))))...))))))).))).))))((((..............))))...-3'
MFE = -44.5; z-score = -1.46; ED = 45.15
```

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(+)

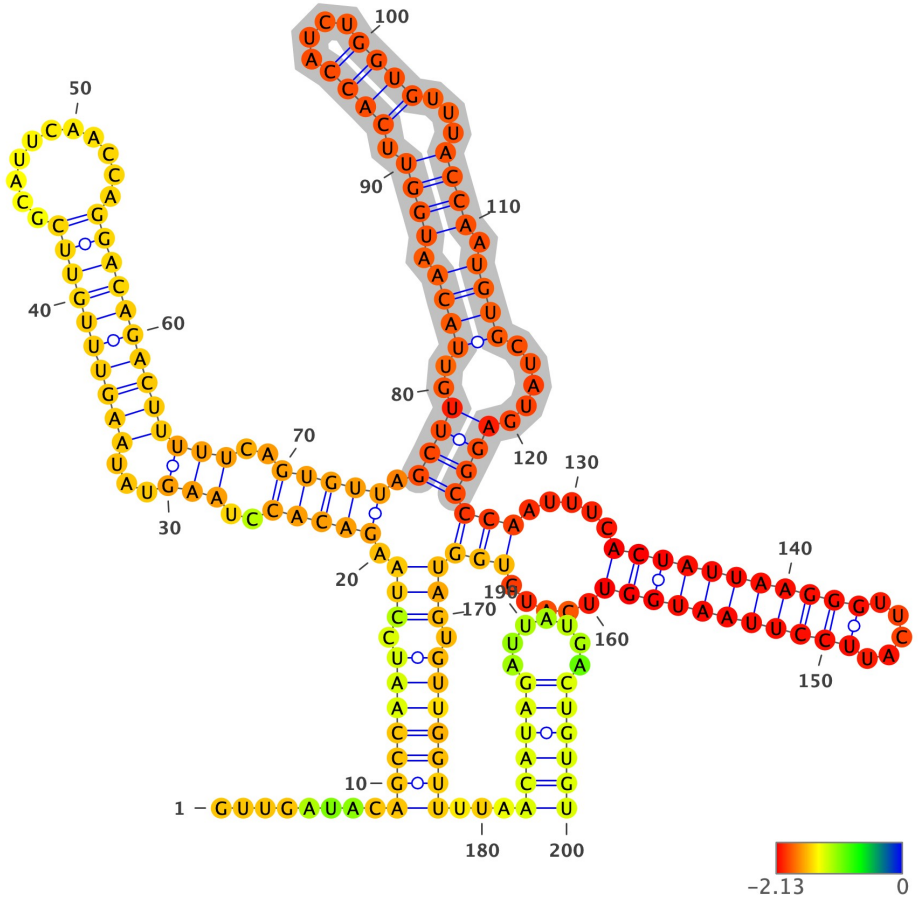
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 194 from nt 10400 to 10448 (nt 76 to 124)

```
5'-GCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGC-3'
5'-(((...((((.((((.((((....))))...)))).))))......)))-3'
Motif MFE = -13.6; z-score = -2.02; ED = 5.82
```



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 10325 to 10524 (motif highlighted in silver):

```
5'-GUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAA
UGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGU-3
5'-........(((((((.(((.(((((..(((...((((((((((.....)))))))))))))..))))).((((..((((.((((.((((....))))...)))).
)))).....))))(((.....((((((((((.....)))))))))).....)))))).)))))))...((((((.......))))))-3'
MFE = -54.6; z-score = -2.95; ED = 12.84
```

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

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

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

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

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

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

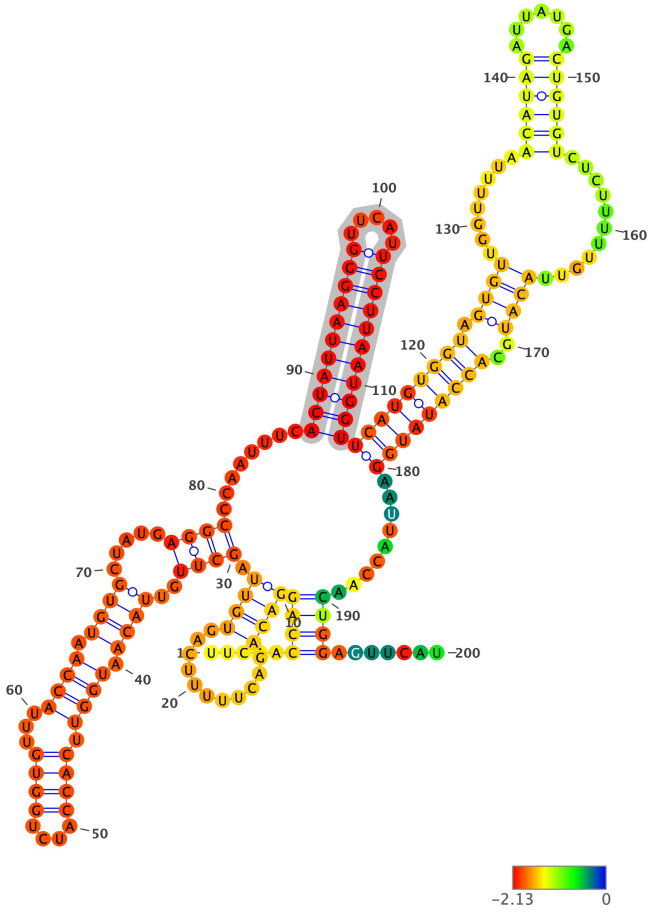
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-ACUAUUAAGGGUUCAUUCCUUAAUGGU-3'
5'-(((((((((((.....)))))))))))-3'
Motif MFE = -11.2; z-score = -5.5; 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 = -1.65; 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(+)

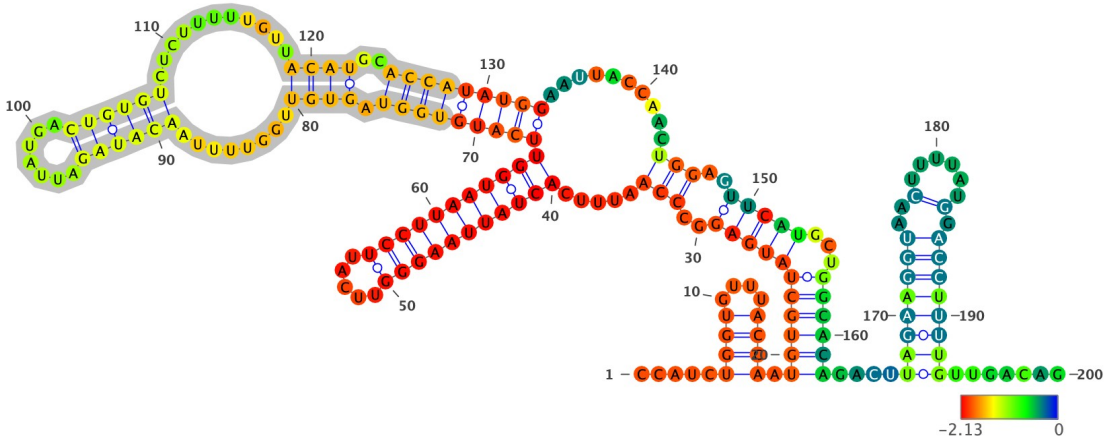
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 196 from nt 10489 to 10545 (nt 72 to 128)

```
5'-UGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCA-3'
5'-((((.((((........((((((.......))))))...........))))..))))-3'
Motif MFE = -8.3; z-score = -0.18; ED = 14.92
```



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 10418 to 10617 (motif highlighted in silver):

```
5'-CCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCU
UUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAG-3
5'-.....((((....)))).(((((((((((..(((.....((((((((((((.....)))))))))))((((((((((.((((........((((((.......))))))....
.......))))..))))))))))..........)))..)))))...))))))....((((((((..(......).))))))))).......-3'
MFE = -50.0; z-score = -1.45; ED = 19.76
```

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

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

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

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

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

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

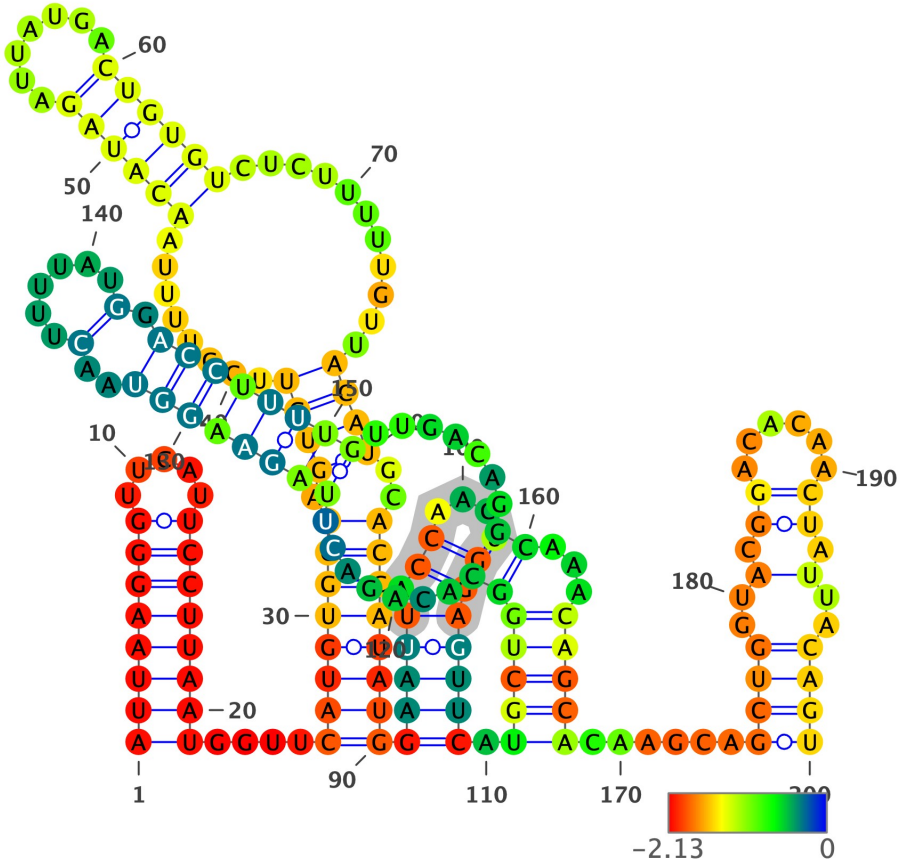
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 197 from nt 10554 to 10564 (nt 95 to 105)

```
5'-UACCAACUGGA-3'
5'-(.((....)))-3'
Motif MFE = -0.3; z-score = -3.06; ED = 0.97
```



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 10460 to 10659 (motif highlighted in silver):

```
5'-AUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAU
GCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGU-3
5'-(((((((((.....)))))))))....(((((((((.((((........((((((........))))))..........))))..)))))))))((((((.((....)))))))).(
((((((.......((((((((..(......).))))))))).......))...)))))......(((((..(.((......)).)..))))-3'
MFE = -44.1; z-score = -0.68; ED = 63.23
```

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(+)

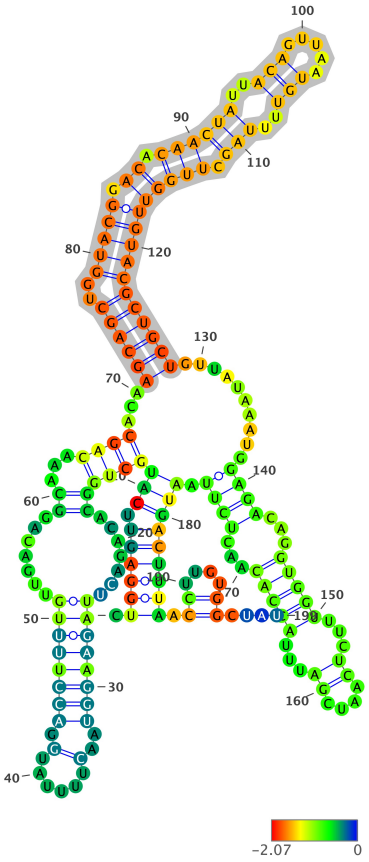
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 198 from nt 10630 to 10687 (nt 71 to 128)

```
5'-AGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCU-3'
5'-((((((..(((((.((.((((((..(((.....)))..))).)))))))))))))))-3'
Motif MFE = -19.9; z-score = -2.72; 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 = -1.09; 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(+)

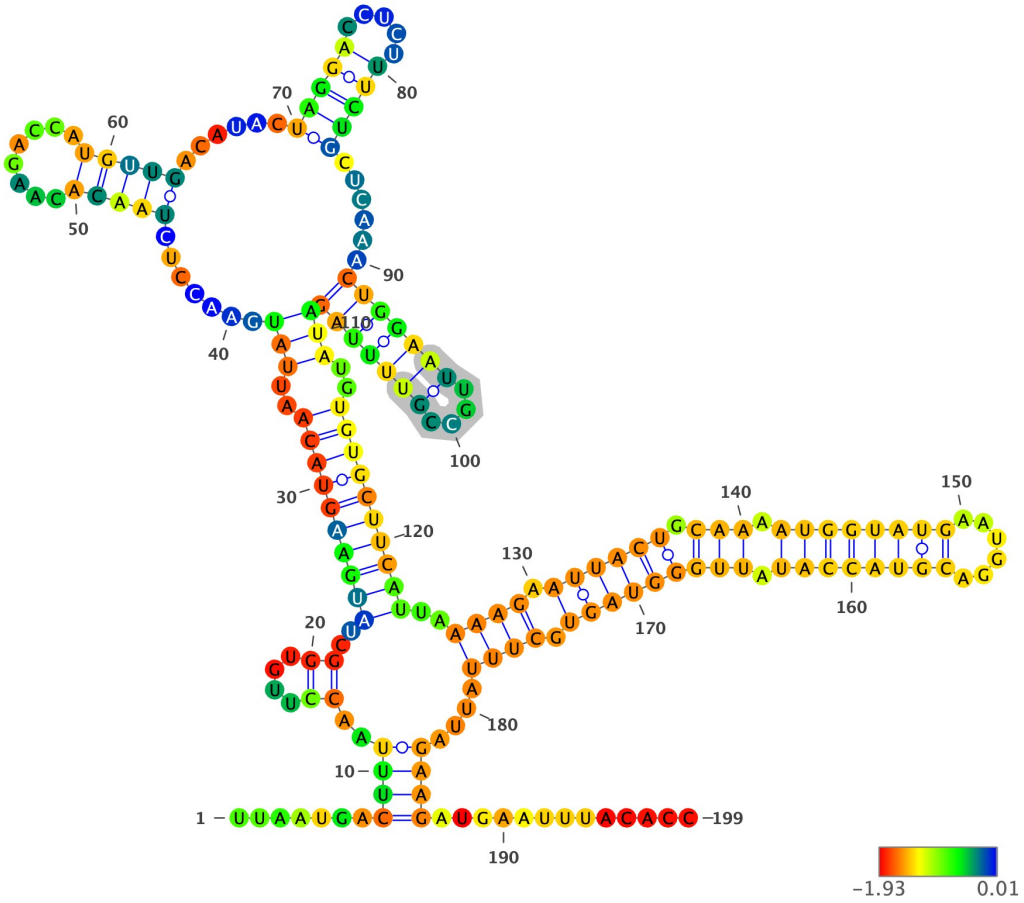
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 199 from nt 10829 to 10836 (nt 96 to 103)

```
5'-AUUGCCGU-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 10734 to 10932 (motif highlighted in silver):

```
5'-UUAAUGACUUUAACCUUGUGGCUAUGAAGUACAAUUAUGAACCUCUAACACAAGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUA
UGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACC-3
5'-.......((((..((....))..((((((((((..(((.......(((((........)))))......(((((.....)))))......(((((((....)))))))))
..)))))))))..((((.((((((.(((.((((((((.....))))))))).))))))))).))))....))))............-3'
MFE = -36.6; z-score = -0.76; ED = 47.2
```

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(+)

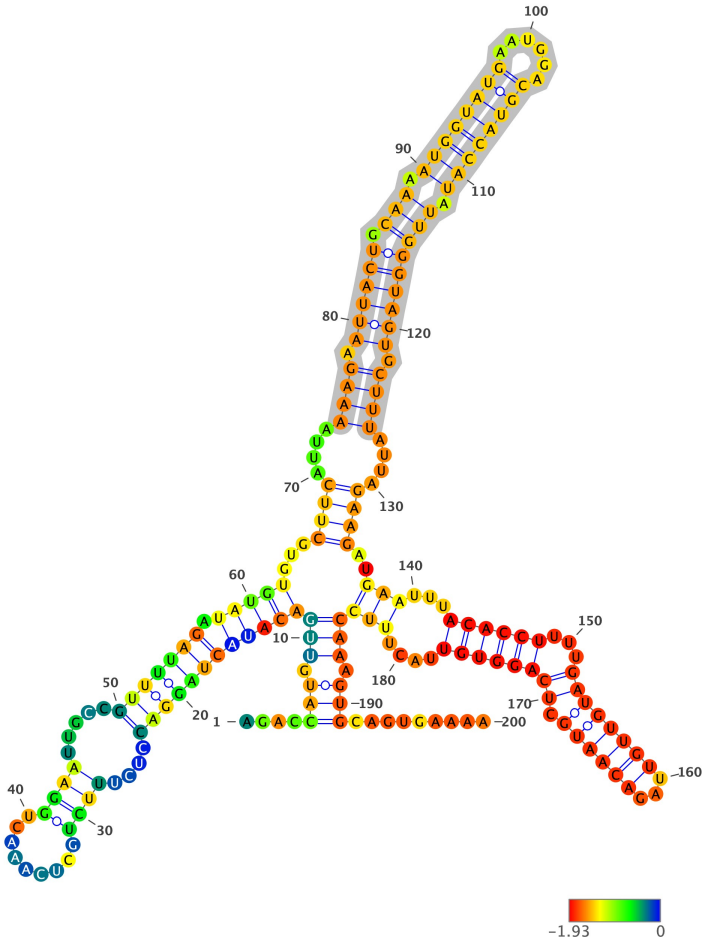
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 200 from nt 10859 to 10911 (nt 74 to 126)

```
5'-AAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUU-3'
5'-((((.(((((((.(((.(((((((((.....)))))))))..)))))))))..))))-3'
Motif MFE = -17.1; z-score = -3.47; ED = 2.91
```



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

Extracted structure model with flanking nucleotides 10786 to 10985 (motif highlighted in silver):

```
5'-AGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUAUGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAU
AUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAA-3
5'-....(((.(((((((((((((((....((((.........)))).....)))))))..)))))...((((....((((.((((((.(((.(((((((((.....)))))))))
.))))))))).))))....))))..(((...(((((((...(((((((((...)))))))..)))))))))....)))))).)))........-3'
MFE = -42.2; z-score = -0.21; ED = 30.47
```

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

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

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

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

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

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

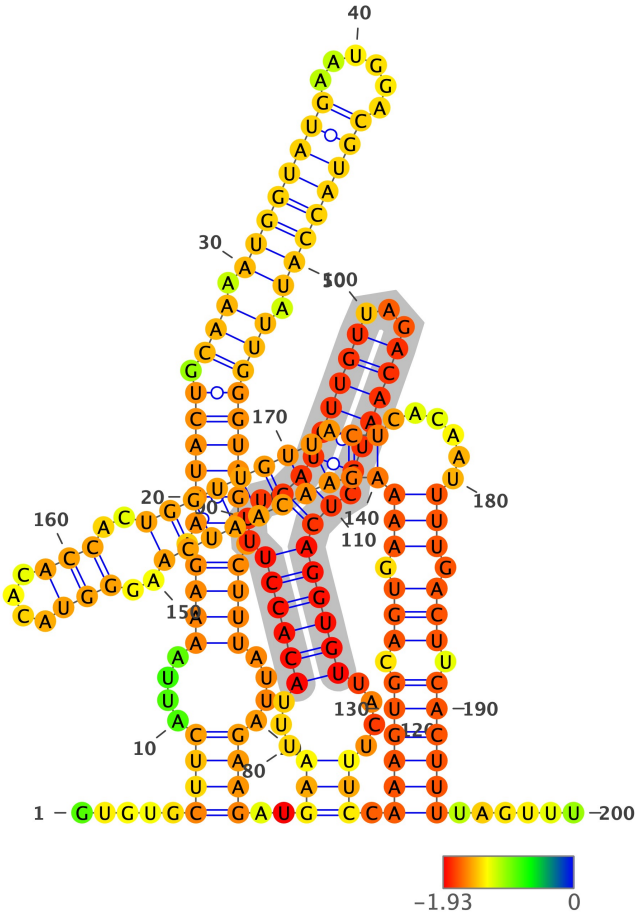
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 201 from nt 10928 to 10962 (nt 83 to 117)

```
5'-ACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGU-3'
5'-((((((...((((((((...)))))).))))))))-3'
Motif MFE = -8.1; z-score = -1.92; ED = 6.74
```



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

Extracted structure model with flanking nucleotides 10846 to 11045 (motif highlighted in silver):

```
5'-GUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUC
AGGUGUUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUU-3
5'-.....((((....((((.((((((.(((.((((((((......)))))))).))))))))).))))....))))..(((...((((((...((((((((...)))))).))
))))))....))).((((((.(((.(((((((((((((..(((....)))..)))))))).))......))).))).))))))......-3'
MFE = -50.7; z-score = -2.48; ED = 26.54
```

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(+)

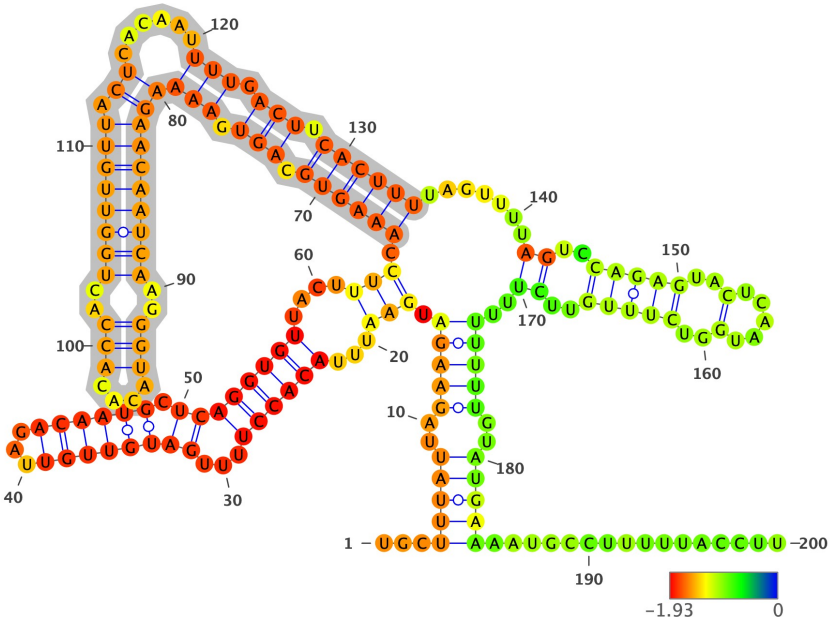
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 202 from nt 10971 to 11039 (nt 66 to 134)

```
5'-AAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUUACUCACAAUUUUGACUUCACUUU-3'
5'-((((((.(((.((((((((((((((..(((....))))..))))))))).))......))).))).))))))-3'
Motif MFE = -19.0; z-score = -3.93; 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 = -38.2; z-score = -1.07; ED = 36.6
```

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(+)

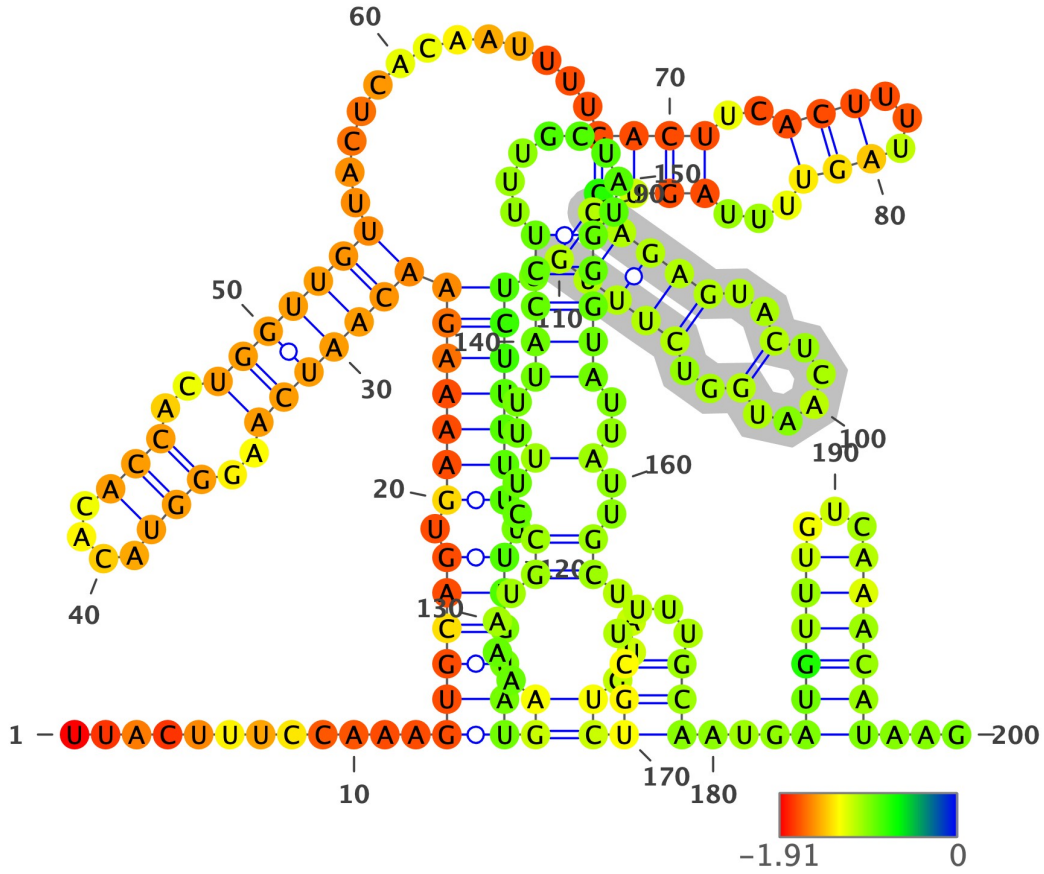
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 203 from nt 11051 to 11071 (nt 90 to 110)

```
5'-CAGAGUACUCAAUGGUCUUUG-3'
5'-((((((..(.....)..))))))-3'
Motif MFE = -4.0; z-score = -1.86; 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 10962 to 11161 (motif highlighted in silver):

```
5'-UUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGU
UCUUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAG-3
5'-...........((((((.(((((((((((((((..(((....)))..)))))))).............((((..(((...))))...))))((((((..(.....)..)))))).
)))))))).)))))))((....((..(..(((((........))))))..)..))....))(((....))))...((((((...))))))...-3'
MFE = -38.5; z-score = -0.68; ED = 53.31
```

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(+)

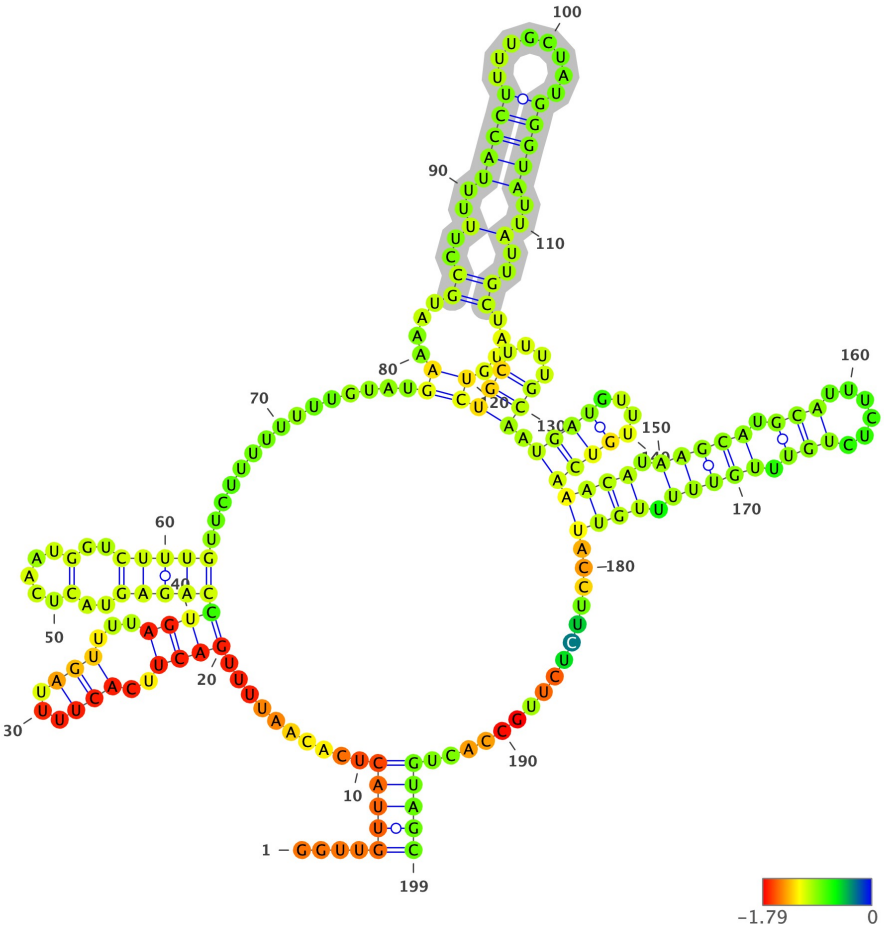
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 204 from nt 11093 to 11124 (nt 84 to 115)

```
5'-GCCUUUUUACCUUUUGCUAUGGGUAUUAUUGC-3'
5'-((..(.....................)..))-3'
Motif MFE = -5.9; z-score = -2.49; 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 11010 to 11208 (motif highlighted in silver):

```
5'-GGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUA
UUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGC-3
5'-....(((((..........((((..(((...)))...))))(((((..(.....)..)))))...............((....((..(..(((((........)))))..)
..))....))(((....))).((((....))))((((.(((((.(((......))).)))))).))))................)))))-3'
MFE = -31.5; z-score = -0.59; ED = 39.66
```

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(+)

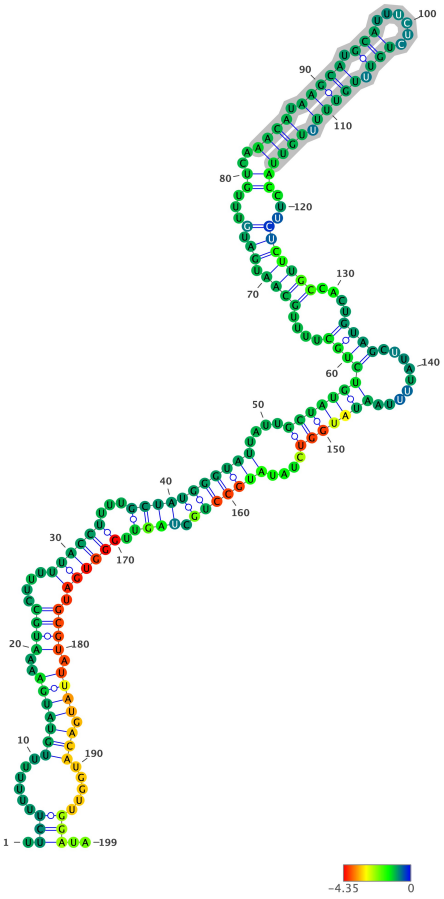
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 205 from nt 11154 to 11187 (nt 83 to 116)

```
5'-AACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUU-3'
5'-((((.........................))))-3'
Motif MFE = -7.2; z-score = -2.97; 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 11072 to 11270 (motif highlighted in silver):

```
5'-UUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUU
UUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUA-3
5'-.(((......(((((((..((((....((((((...((((((((((((....((((((((((((....((((.((.(...((..((((.(((((.(((......))).)))))
.))))))...)))))))....))))).........)))))))....)))))))).)))).)))))).)))).)))).)))).....)))..-3'
MFE = -38.7; z-score = -1.47; ED = 28.04
```

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

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

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

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

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

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

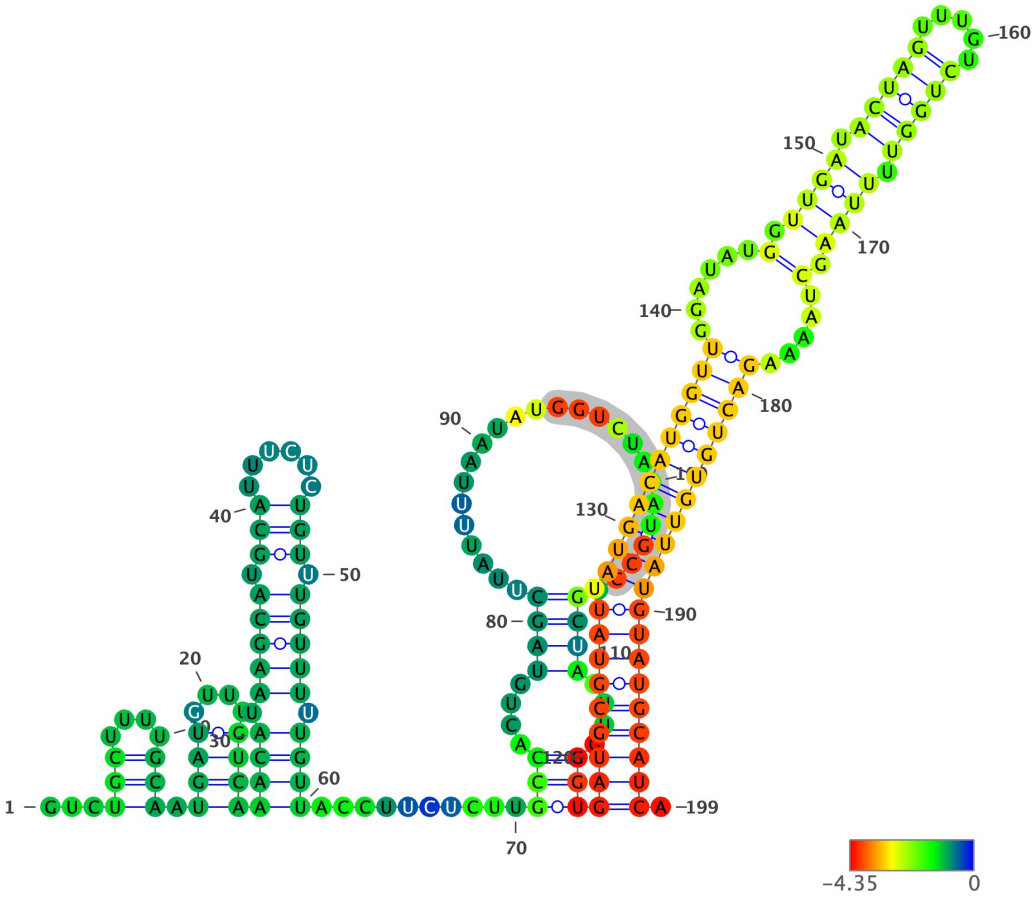
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 206 from nt 11221 to 11232 (nt 94 to 105)

```
5'-GGUCUAUAUGCC-3'
5'-(((......)))-3'
Motif MFE = -0.4; z-score = -1.01; 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 = -2.88; 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(+)

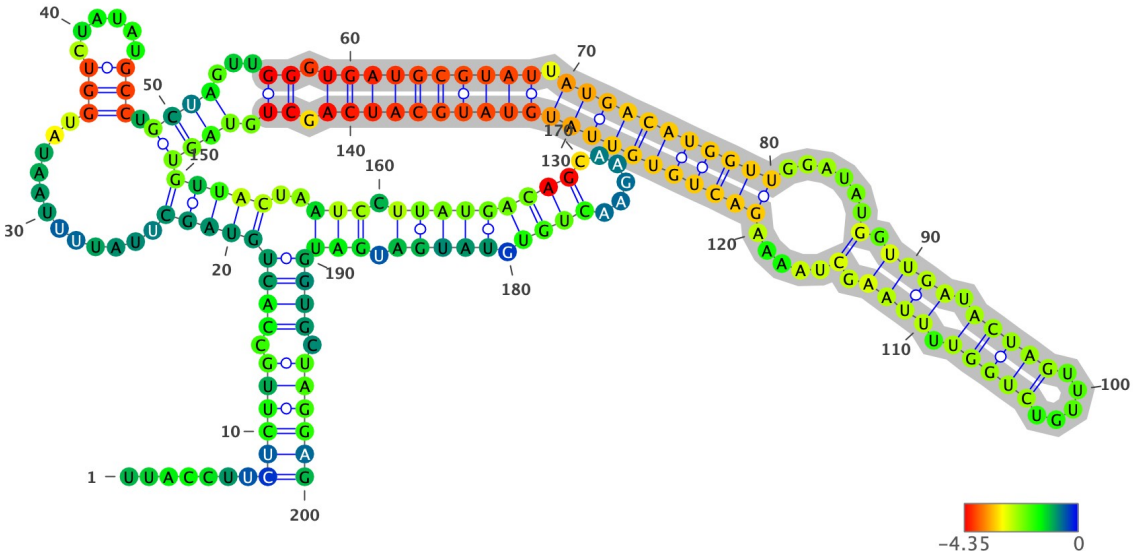
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 207 from nt 11241 to 11329 (nt 56 to 144)

```
5'-GGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCU-3'
5'-((.((((((((((.((((((((((.......(.((((.(((((.....))))).)))).).....)))))))))))))))))))).))-3'
Motif MFE = -35.3; z-score = -5.6; 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 = -2.61; 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(+)

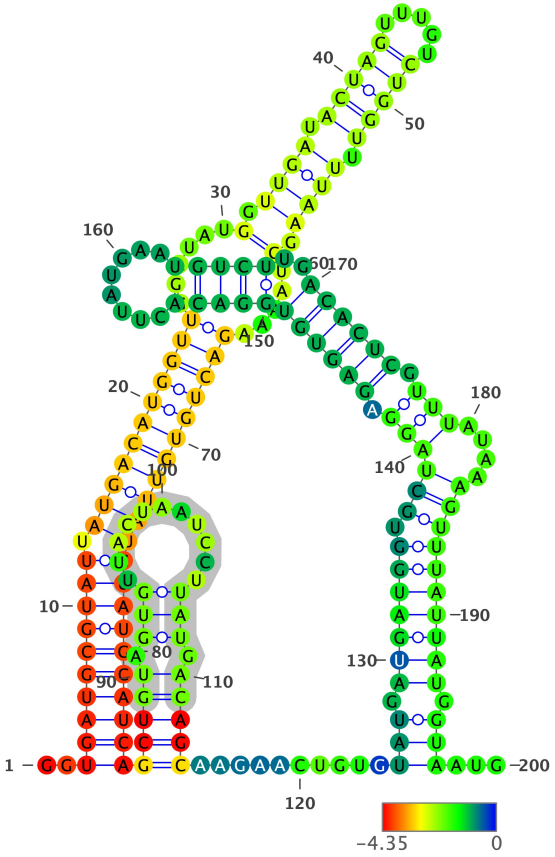
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 208 from nt 11330 to 11352 (nt 89 to 111)

```
5'-GUAGUGUUACUAAUCCUUAUGAC-3'
5'-((.(((...........))).))-3'
Motif MFE = 0.0; z-score = 0.76; ED = 4.0
```



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 11242 to 11441 (motif highlighted in silver):

```
5'-GGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGAC
AGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAGAGUGUGGACACUUAUGAAUGUCUUGACACUCGUUUAUAAAGUUUAUUAUGGUAAUG-3
5'-..(((((((((((.(((((((((((......(.((((.(((((.....))))).))))).).....))))))))))))))))))))))(((((.(((...........))).))
)))..........(((.(((((((.((((((.((((((((((.........))))).)))))).))).....)))))))))).)))...-3'
MFE = -57.1; z-score = -3.7; ED = 23.87
```

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

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

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

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

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', '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(+)

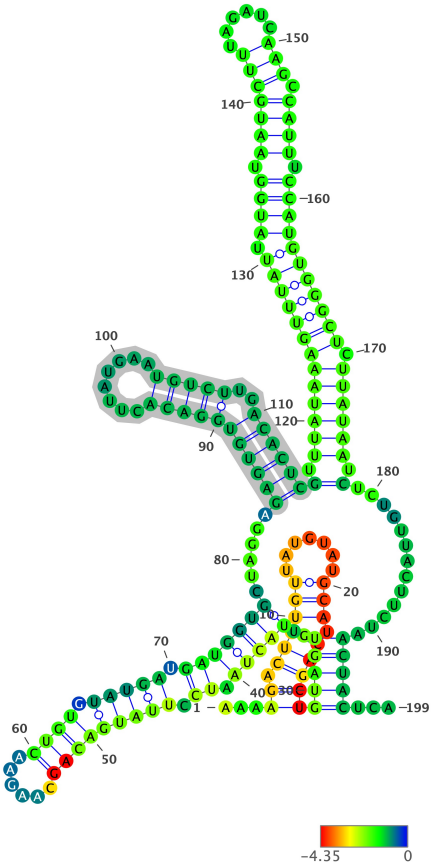
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 209 from nt 11385 to 11416 (nt 84 to 115)

```
5'-GAGUGUGGACACUUAUGAAUGUCUUGACACUC-3'
5'-((....(((((........)))))......))-3'
Motif MFE = -10.6; z-score = -2.89; 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 = -0.67; ED = 20.35
```

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, 266-13468(+)

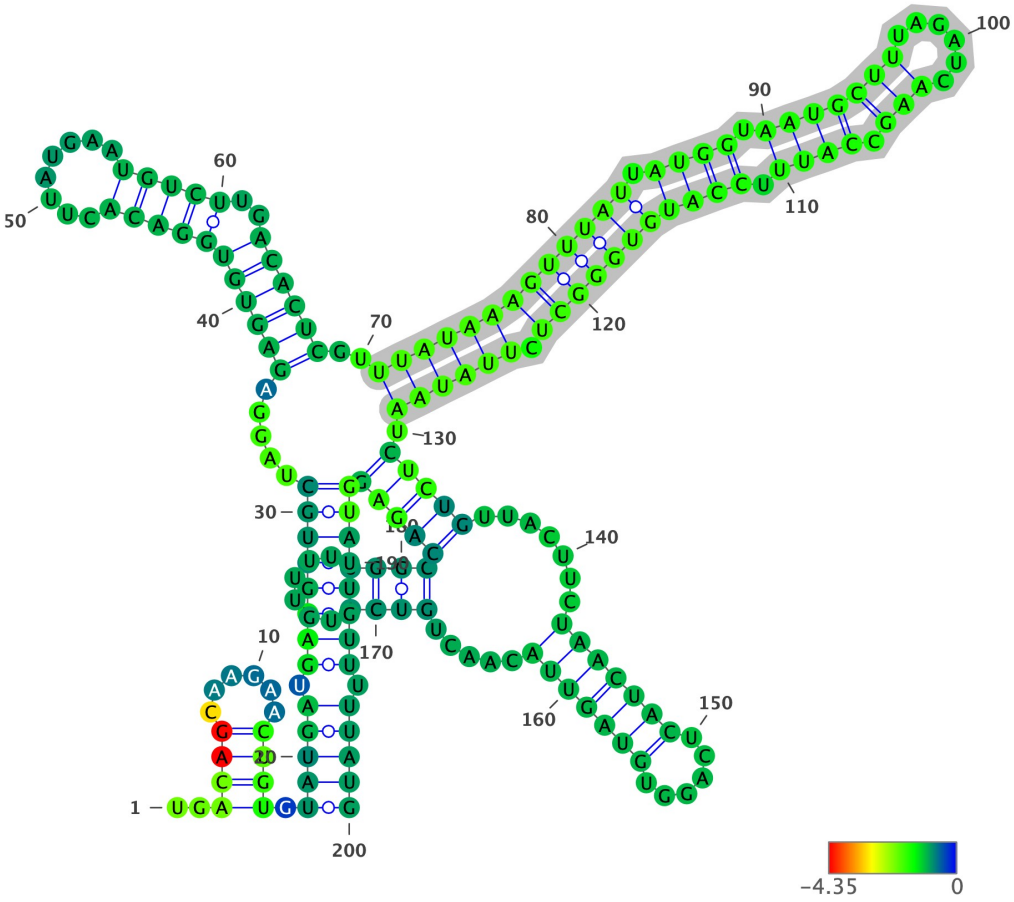
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-UUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUUCCAUGUGGGCUCUUAUAA-3'
5'-(((((((((((((.((((.(((((((.....))).)))).)))))))))))).)))))-3'
Motif MFE = -14.1; z-score = -2.69; 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 = -1.45; 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(+)

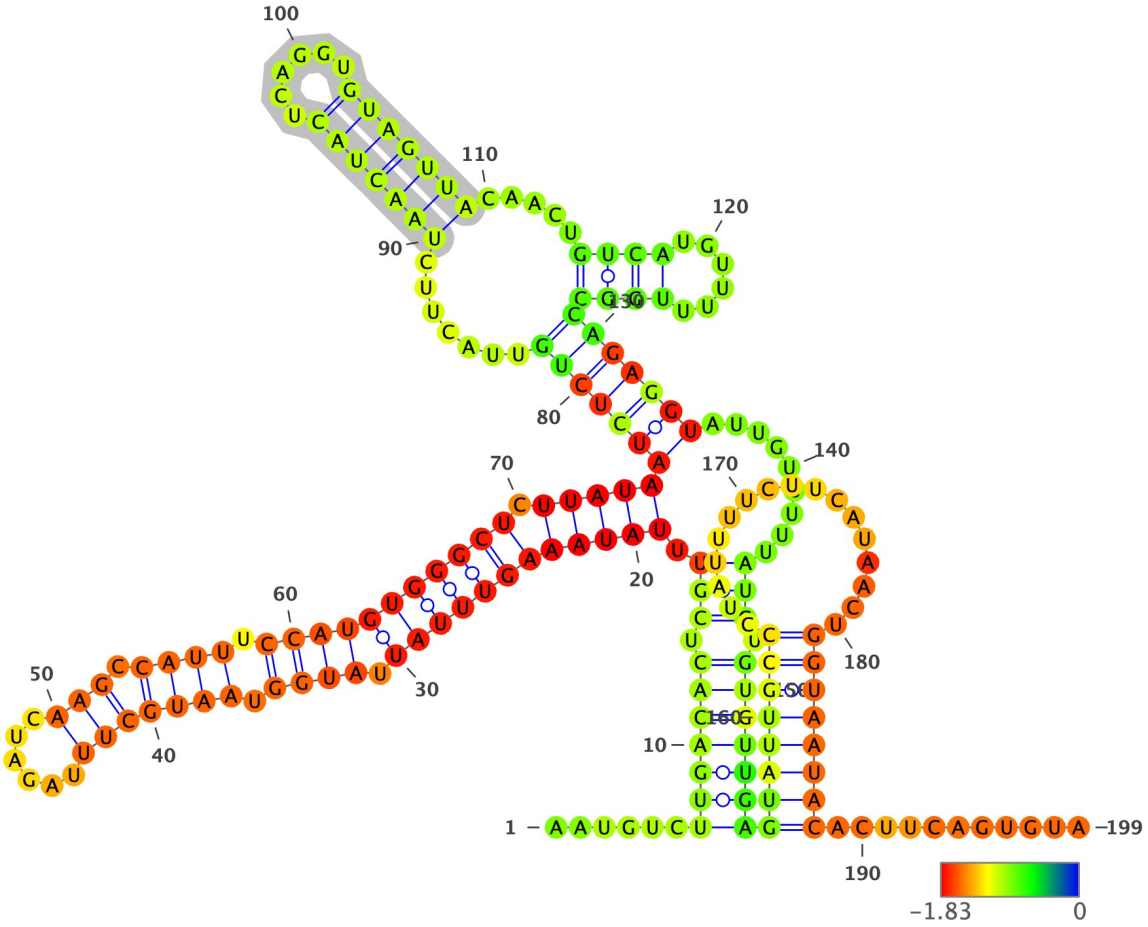
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 211 from nt 11491 to 11510 (nt 90 to 109)

```
5'-UAACUACUCAGGUGUAGUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.2; z-score = -4.7; 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 = -1.83; 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(+)

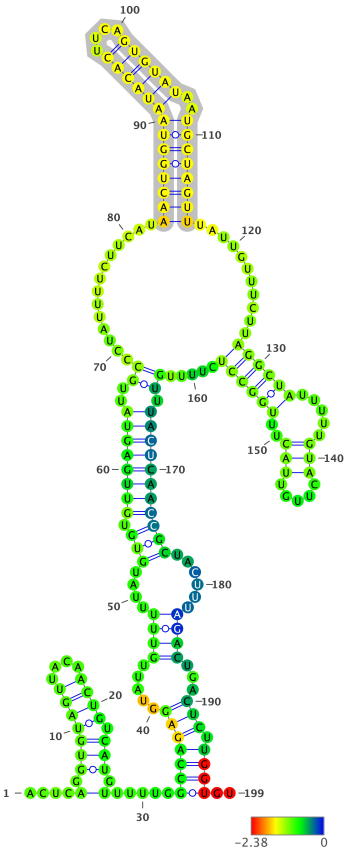
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 212 from nt 11578 to 11611 (nt 83 to 116)

```
5'-AACUGGUAAUACACUUCAGUGUAUAAUGCUAGUU-3'
5'-(((((((((((((((....))))))..))))))))-3'
Motif MFE = -11.8; z-score = -4.84; ED = 1.22
```



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

Extracted structure model with flanking nucleotides 11496 to 11694 (motif highlighted in silver):

```
5'-ACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGC
UAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGU-3
5'-....(.(((((((....)))).))).).....(((((((.....((((....(((.((((((((..((..............((((((((((((((....))))))..)))
)))))..........((((((.....(((.....)))..))))))).....)).)))))))))))).....))))...))).)))).-3'
MFE = -42.0; z-score = -1.59; ED = 31.11
```

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

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

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

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

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

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

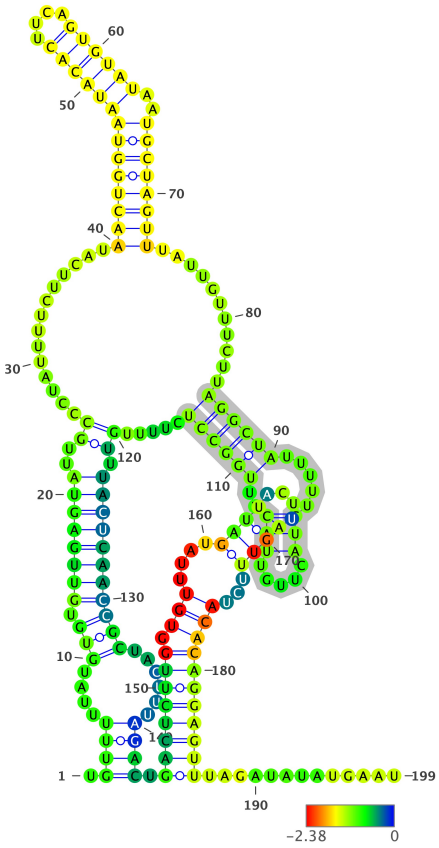
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 213 from nt 11623 to 11652 (nt 85 to 114)

```
5'-AGGCUAUUUUUGUACUUGUUACUUUGGCCU-3'
5'-((((((.....(((.....)))..))))))-3'
Motif MFE = -6.0; z-score = -2.15; 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 = -2.21; 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(+)

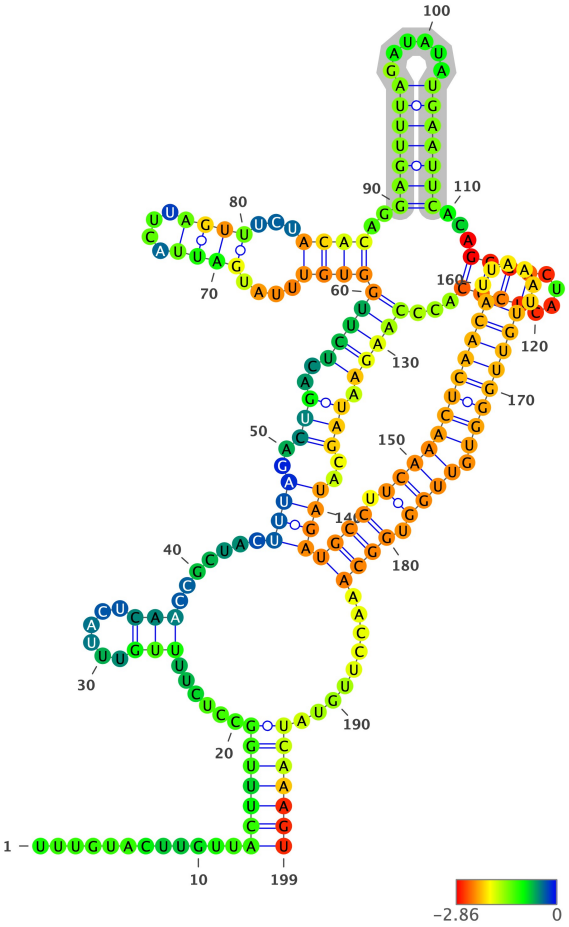
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 214 from nt 11720 to 11739 (nt 90 to 109)

```
5'-GAGUUUAGAUAUAUGAAUUC-3'
5'-(((((((......)))))))-3'
Motif MFE = -3.4; z-score = -3.69; 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 = -0.62; 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']

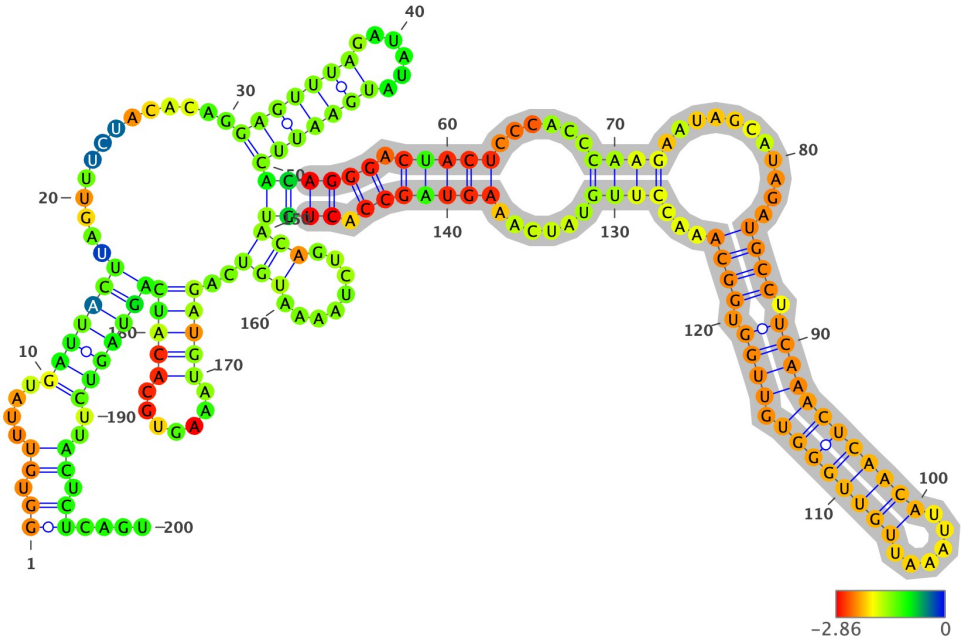
4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

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 215 from nt 11742 to 11836 (nt 53 to 147)

```
5'-AGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACU-3'

5'-((((.(.(((.....................((((.(((((((((((.....))))))))).)))).))))..............))).))).))-3'
Motif MFE = -25.3; z-score = -2.94; ED = 21.73
```



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 11690 to 11889 (motif highlighted in silver):

```
5'-GGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUG
GGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGU-3
5'-((.((....(((((((.............(((((((......)))))))((((((.(((((......((((...........((((.(((((((((((.....)))))
))).)))).))))...))))......))))))).))))(((........)))..(((((.......)))))))))))))..)).)).....-3'
MFE = -45.1; z-score = -1.48; ED = 22.17
```

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(+)

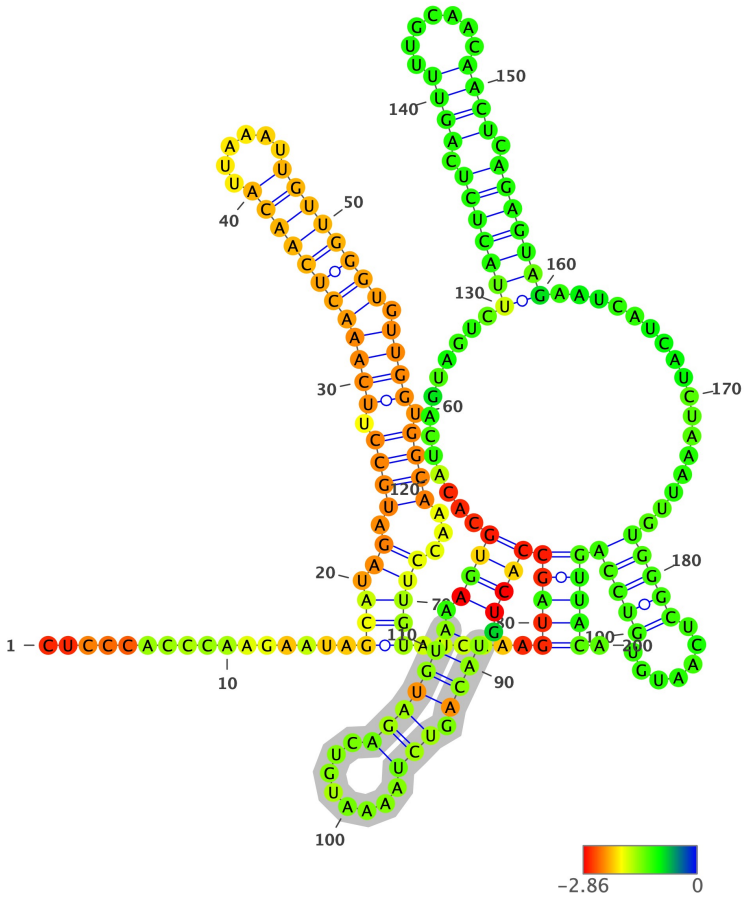
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 216 from nt 11838 to 11860 (nt 89 to 111)

```
5'-UACAGUCUAAAAUGUCAGAUGUA-3'
5'-(((..((..........)).)))-3'
Motif MFE = -1.7; z-score = -0.9; 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 11750 to 11949 (motif highlighted in silver):

```
5'-CUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUA
AAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACA-3
5'-................(((.((.((((.((((((((((((.....))))))))).)))).))))...)))))......(((((((((.((((.(((........)))))))
.))))............(((((((.((((.......)))).)))))))................(((((.......)))))))))).-3'
MFE = -44.7; z-score = -1.27; ED = 31.22
```

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

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

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

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

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

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

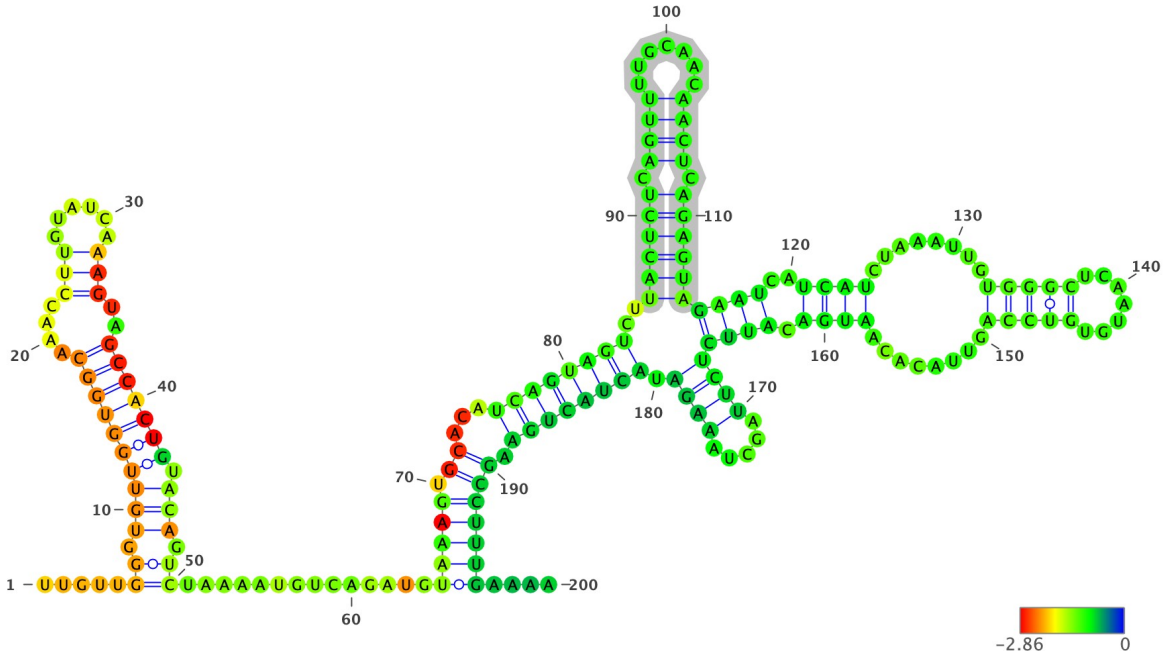
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 217 from nt 11880 to 11908 (nt 86 to 114)

```
5'-UACUCUCAGUUUUGCAACAACUCAGAGUA-3'
5'-((((((.((((.......)))).))))))-3'
Motif MFE = -7.0; z-score = -3.19; ED = 1.35
```



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

Extracted structure model with flanking nucleotides 11795 to 11994 (motif highlighted in silver):

```
5'-UUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGA
GUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAA-3
5'-.....((.(((((((((((....(((.....)))..)))))))).))).))..............(((((.((...((((((((..((((((.((((.......)))).)))
)))((((..((((........(((((.......)))))........)))).))))((((.....)))).))))))))).)))))))....-3'
MFE = -45.6; z-score = -1.35; ED = 32.99
```

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

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

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

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

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

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

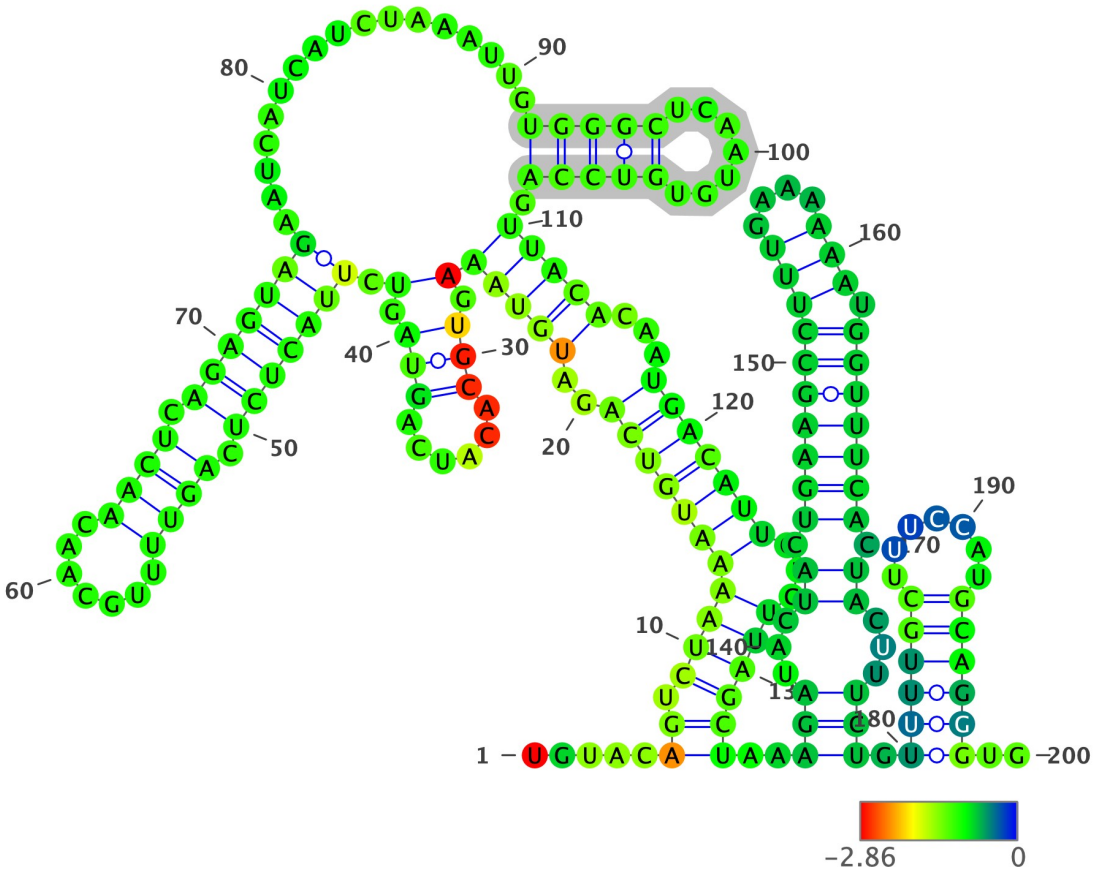
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 218 from nt 11927 to 11943 (nt 92 to 108)

```
5'-UGGGCUCAAUGUGUCCA-3'
5'-(.(((.......))).)-3'
Motif MFE = -5.0; z-score = -2.07; 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 = -0.71; 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']

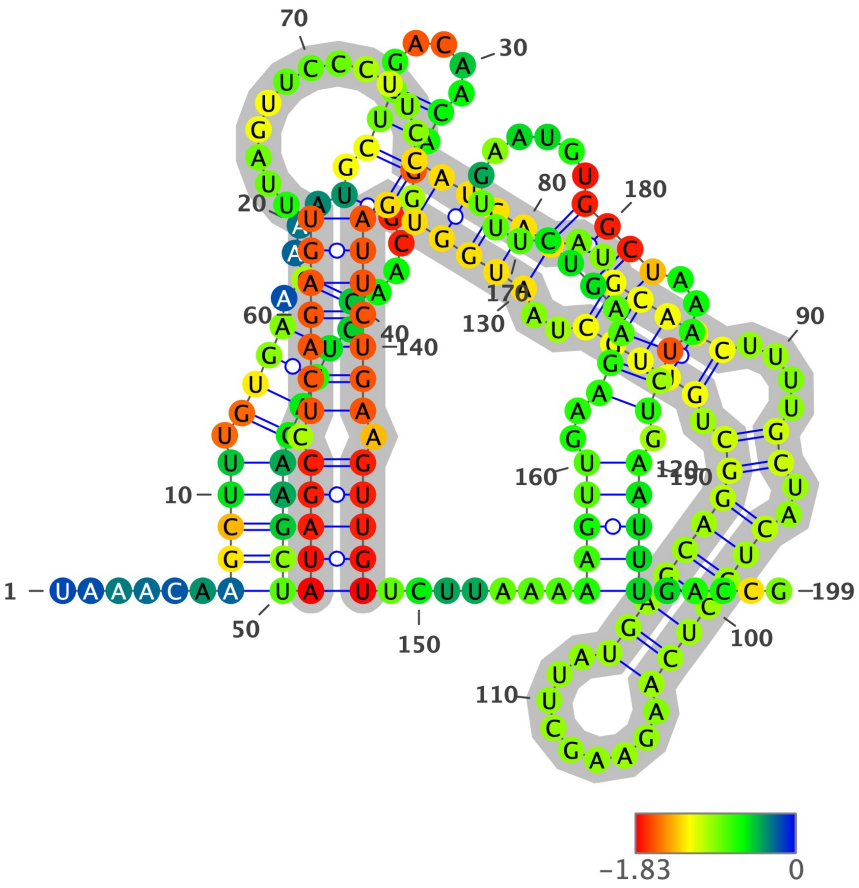
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

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 219 from nt 12095 to 12192 (nt 51 to 148)

```
5'-AUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUUAUGAGCAGGCUGUUGCUAAUGGUGAUUCUGAAGUUGU-3'

5'-(((((.(((((((.............((((((..(((((....((..(.....................))).)))))..)))))))))))))).)))))-3'
Motif MFE = -29.1; z-score = -2.55; ED = 8.22
```



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 12045 to 12243 (motif highlighted in silver):

```
5'-UAAACAAGCUUUGUGAAGAAAUGCUGGACAACAGGGCAACCUUACAAGCUAUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUU
AUGAGCAGGCUGUUGCUAAUGGUGAUUCUGAAGUUGUUCUUAAAAAGUUGAAGAAGUCUUUGAAUGUGGCUAAAUCUGAAUUUGACCG-3
5'-......(((((.((((.(...(.(((.....))).)...).))))))))))(((((.(((((((.............((((((..(((((....((..(((((((.........
.)))))))))).)))))..)))))))))))))).)))))).......(((((..(((((((.........))))...))).)))))).....-3'
MFE = -43.8; z-score = -0.11; ED = 27.71
```

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

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

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

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

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

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

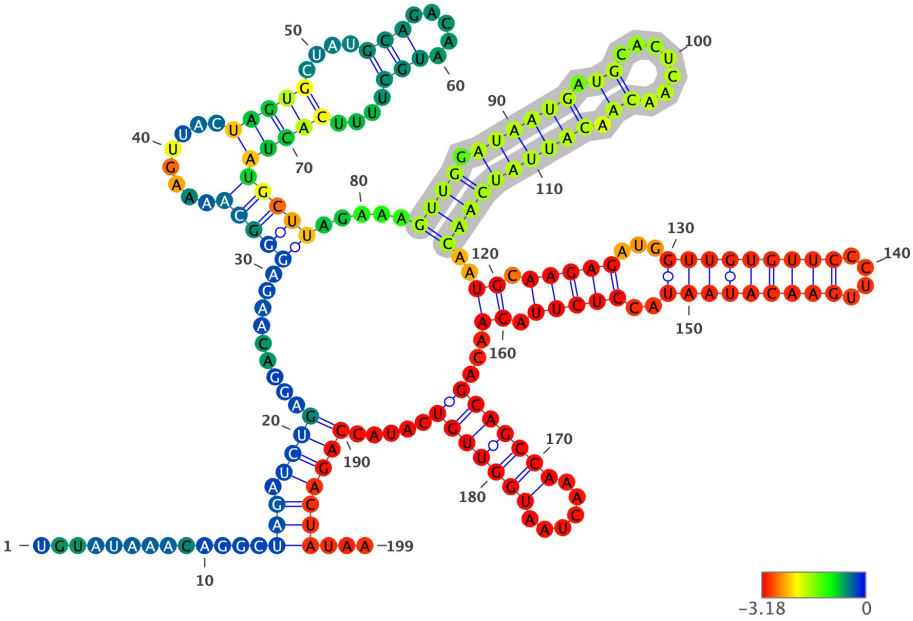
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 220 from nt 12382 to 12415 (nt 83 to 116)

```
5'-GUUGGAUAAUGAUGCACUCAACAACAUUAUCAAC-3'
5'-((((.((((((.((.......)).))))))))))-3'
Motif MFE = -6.3; z-score = -2.35; 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 = -2.16; 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(+)

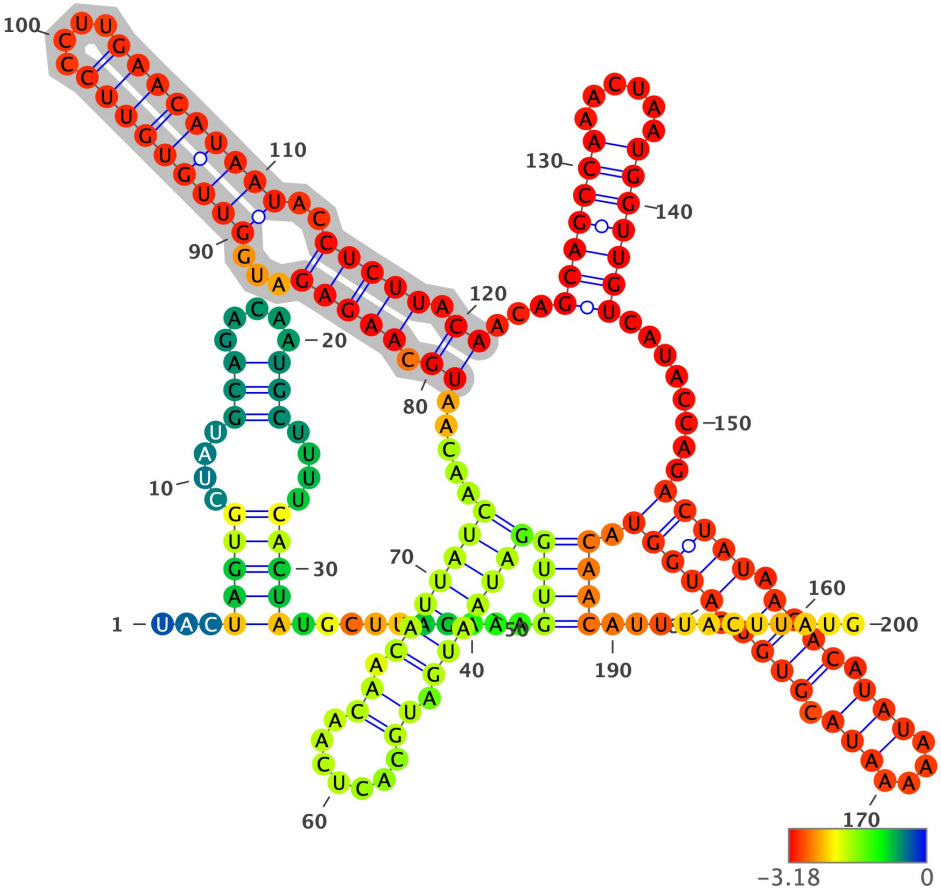
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 221 from nt 12418 to 12460 (nt 79 to 121)

```
5'-UGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACA-3'
5'-((.((((((...((((((((((....))))))))))..))))))..))-3'
Motif MFE = -12.6; z-score = -2.93; 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 = -3.6; 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(+)

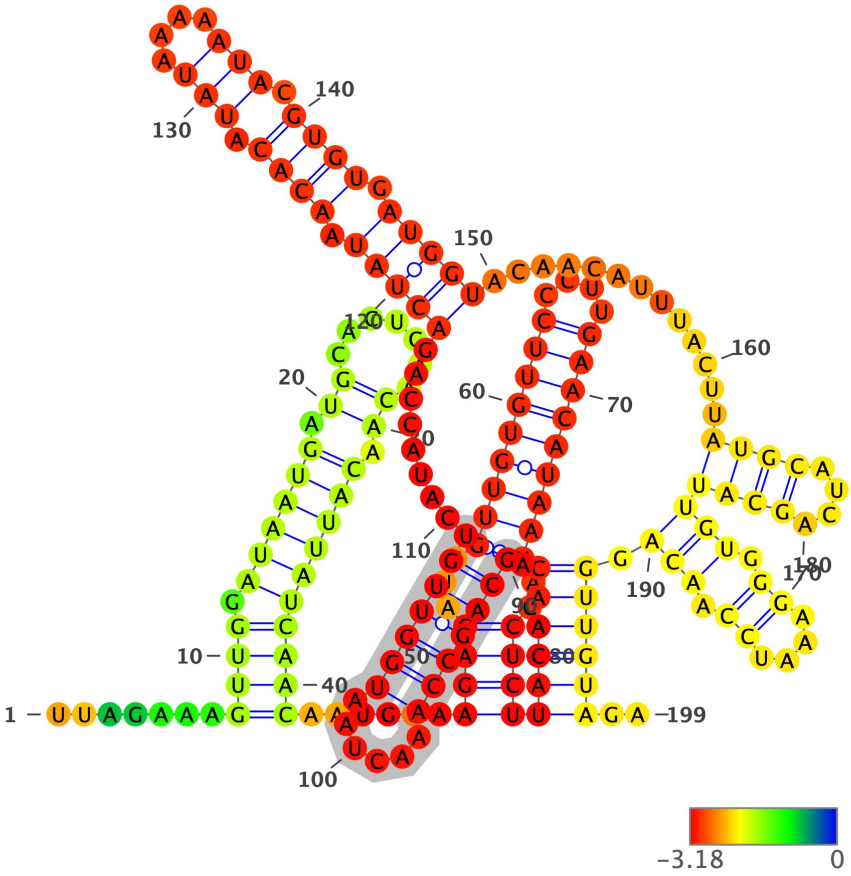
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 222 from nt 12464 to 12483 (nt 90 to 109)

```
5'-GCAGCCAAACUAAUGGUUGU-3'
5'-(((((((......)))))))-3'
Motif MFE = -7.5; z-score = -3.62; ED = 0.6
```



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

Extracted structure model with flanking nucleotides 12375 to 12573 (motif highlighted in silver):

```
5'-UUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCA
UACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGA-3
5'-.......((((.((((((.((.......)).))))))))))......((((...((((((((((....)))))))))..))))((((((.(((((((......)))))))..
......(((((.((((.(((....))).)))).)))))..............((((....))))(((.((....)).))).))))))..-3'
MFE = -46.3; z-score = -3.42; 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(+)

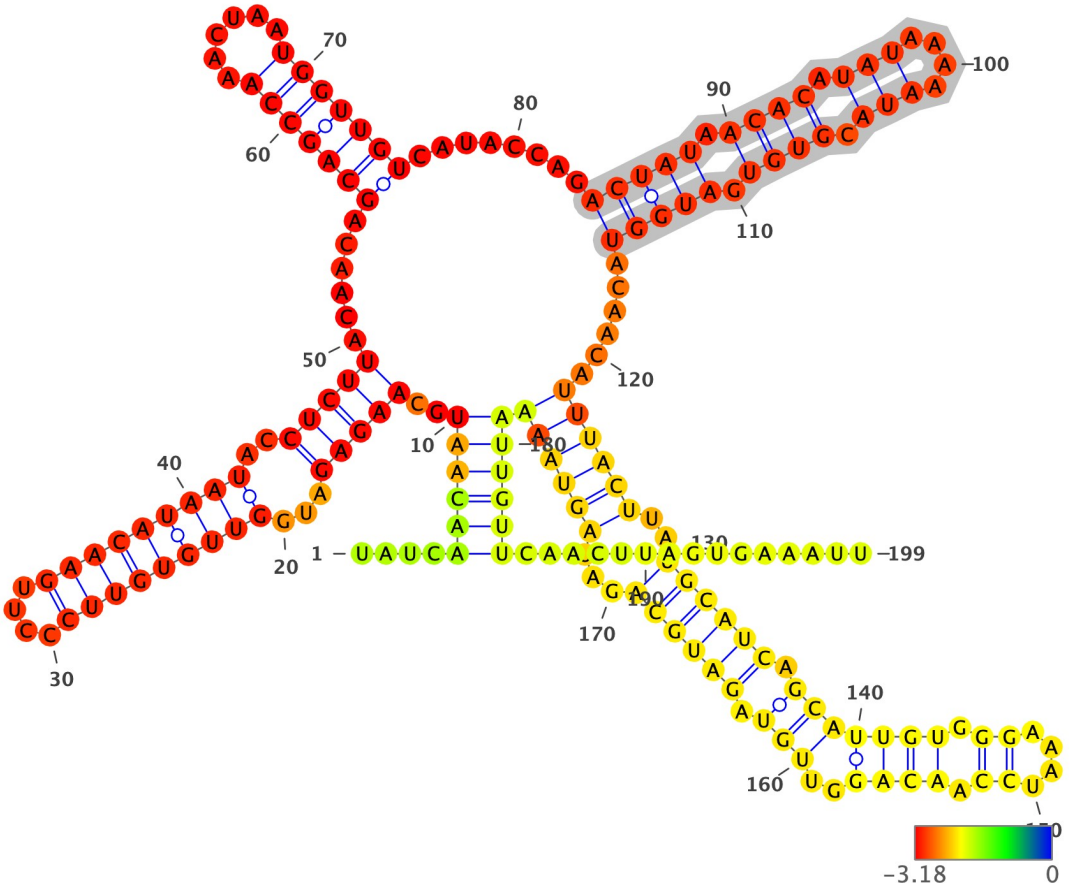
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 223 from nt 12492 to 12523 (nt 84 to 115)

```
5'-ACUAUAACACAUAUAAAAAUACGUGUGAUGGU-3'
5'-(((((.(((((.(((....))).))))).))))))-3'
Motif MFE = -6.6; z-score = -2.72; 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 12409 to 12607 (motif highlighted in silver):

```
5'-UAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGA
UGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUU-3
5'-....((((((..((((((...((((((((((....))))))))))..))))))......(((((((......)))))))).......((((.((((.((((....)))).)))))))))
))))......((((((..((((((.(((((((.((....)).)))))..))))..))))))...)))))))))))))).............-3'
MFE = -49.2; z-score = -3.64; ED = 23.37
```

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

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

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

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

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

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

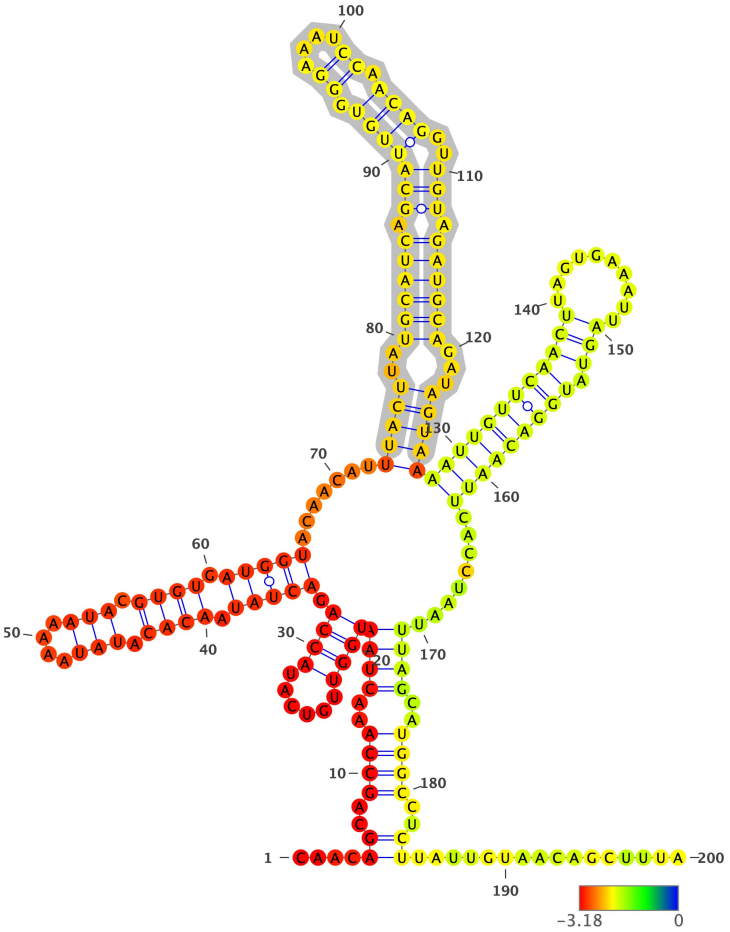
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-UACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUA-3'
5'-((((..((((((.(((((((.((....)).))))..))).))))))...))))-3'
Motif MFE = -15.1; z-score = -3.13; 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 = -2.71; 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(+)

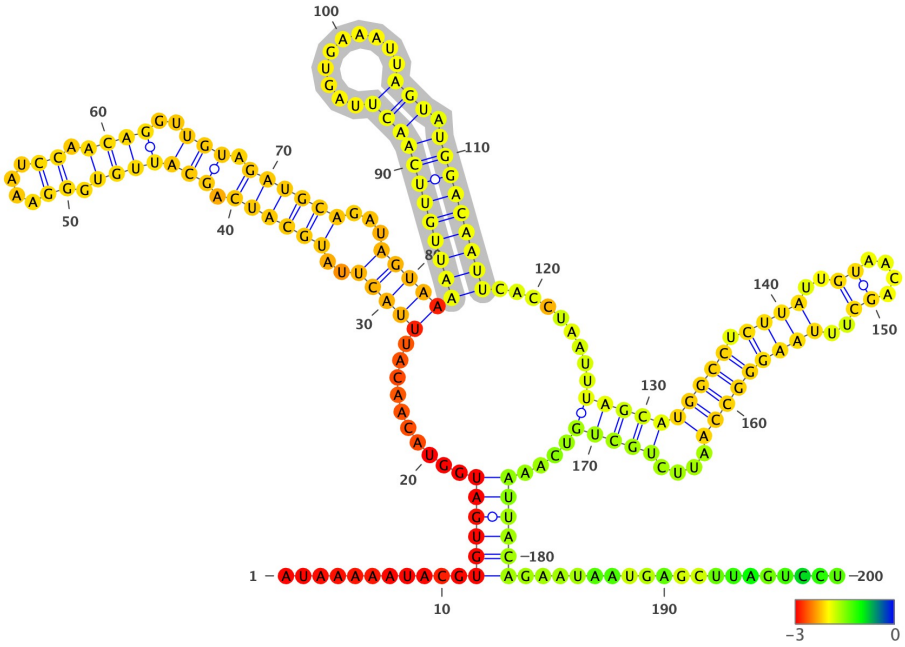
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 225 from nt 12586 to 12620 (nt 83 to 117)

```
5'-AAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUU-3'
5'-((((((((((((.........))).))))))))))-3'
Motif MFE = -7.4; z-score = -2.79; 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 = -1.78; 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(+)

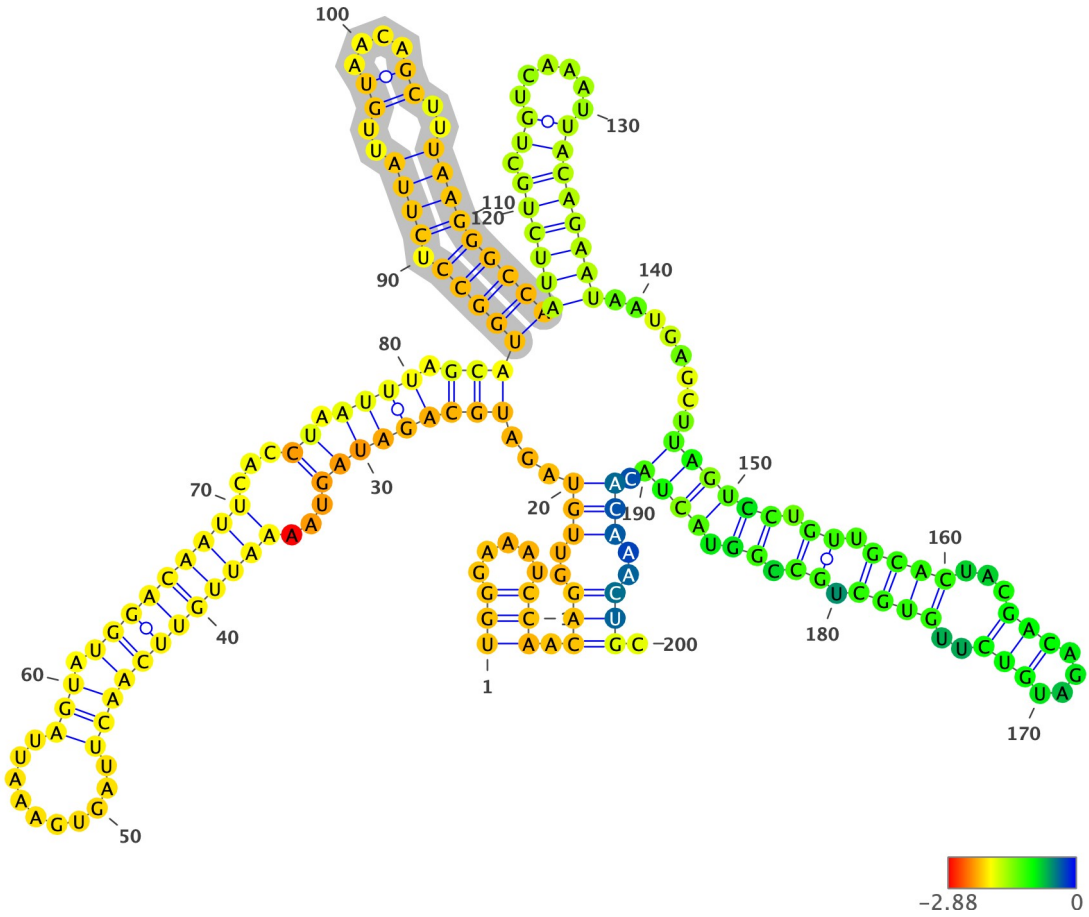
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 226 from nt 12635 to 12665 (nt 85 to 115)

```
5'-UGGCCUCUUAUUGUAACAGCUUUAAGGGCCA-3'
5'-(((((.((((..((....))..)))))))))-3'
Motif MFE = -12.7; z-score = -4.88; 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 = -2.1; 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(+)

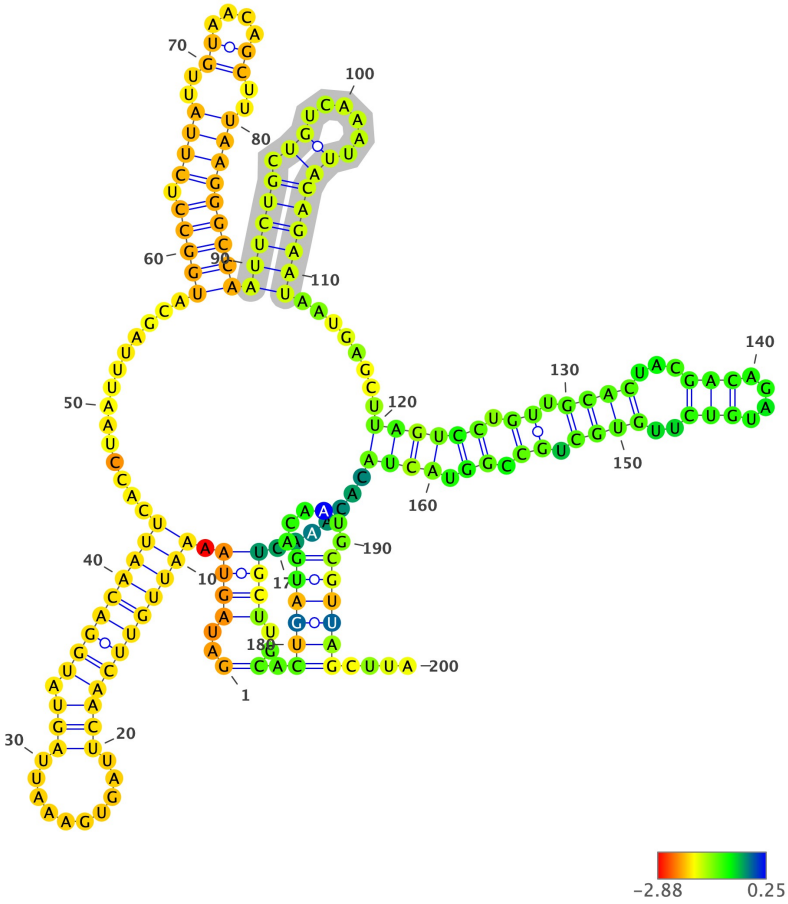
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 227 from nt 12666 to 12688 (nt 89 to 111)

```
5'-AUUCUGCUGUCAAAUUACAGAAU-3'
5'-((((((.((......))))))))-3'
Motif MFE = -3.1; z-score = -1.72; 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 = -2.11; 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(+)

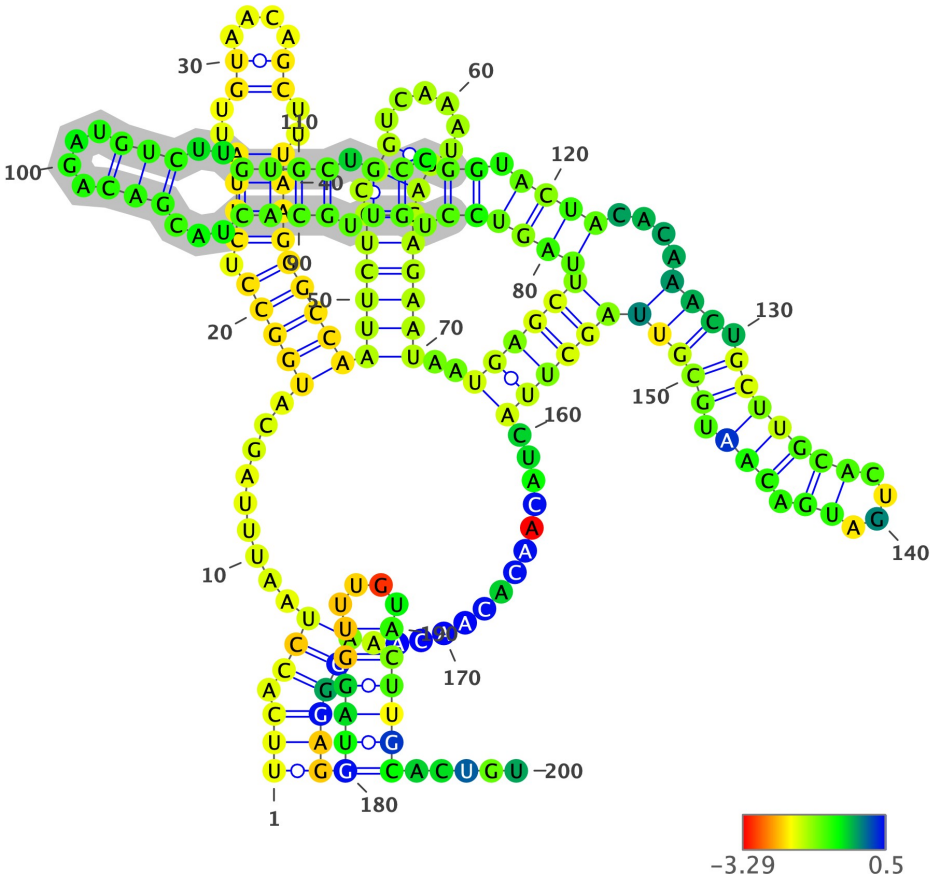
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 228 from nt 12702 to 12734 (nt 84 to 116)

```
5'-CUGUUGCACUACGACAGAUGUCUUGUGCUGCCG-3'
5'-(.((.((((...............)))).)).)-3'
Motif MFE = -8.1; z-score = -1.2; 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 12619 to 12818 (motif highlighted in silver):

```
5'-UUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGCCAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCUGUUGCACUACGACAGAUGUCUUGUGC
UGCCGGUACUACACAAACUGCUUGCACUGAUGACAAUGCGUUAGCUUACUACAACACAACAAAGGGAGGUAGGUUUGUACUUGCACUGU-3
5'-(((.(((.........(((((.((((..((....))..)))))))))((((((.((......))))))))..((((((((((((.((.((((...(((....)))..))))
.)).)).)))).....(((.(((((((....)).))).))))))))))).............))))))((((((....))))))).....-3'
MFE = -46.7; z-score = -0.75; ED = 38.12
```

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(+)

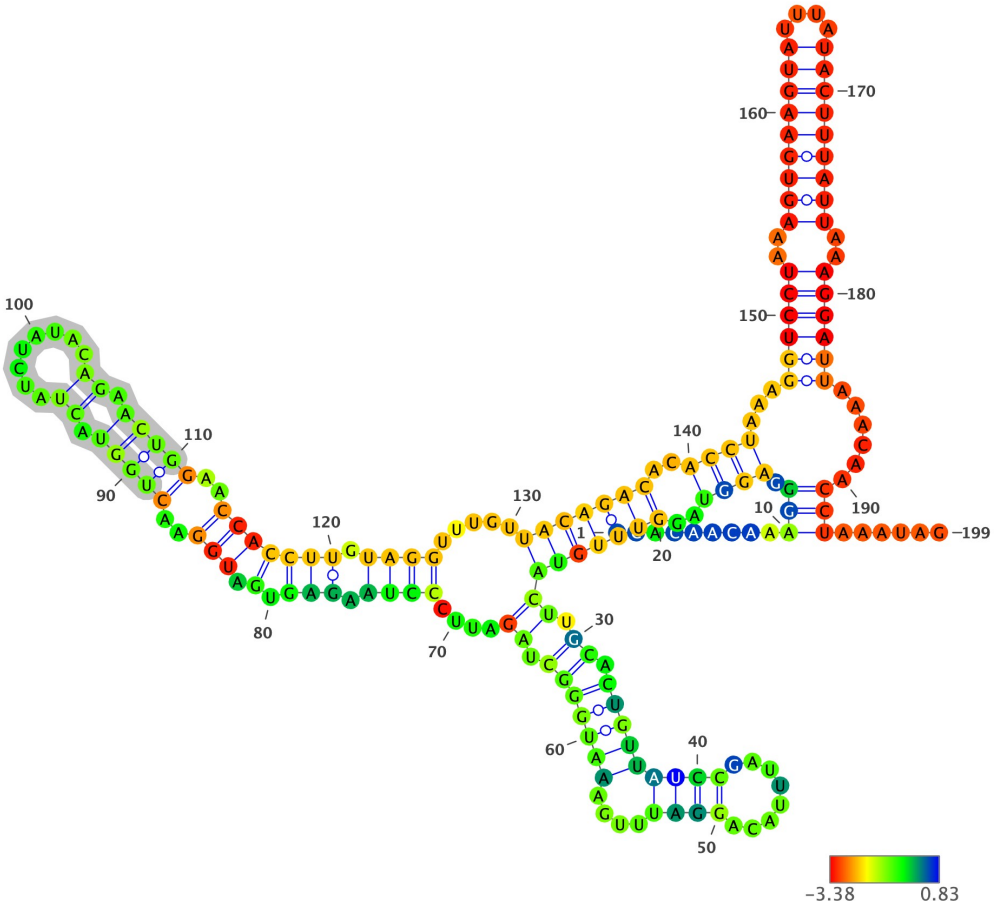
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 229 from nt 12871 to 12892 (nt 89 to 110)

```
5'-UGGUACUAUCUAUACAGAACUG-3'
5'-((..................))-3'
Motif MFE = -0.3; z-score = 0.53; 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 12783 to 12981 (motif highlighted in silver):

```
5'-ACACAACAAAGGGAGGUAGGUUUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGG
AACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAG-3
5'-.........(((.(((((..((((((((((.((.((((((((((........)))).....)))))))).)).....((((.(((.(.(((..((((((.((........)).)))))
..)))))))).))))).....)))))))..)))))...((((((..((((((((((....))))))))))..))))))......)))......-3'
MFE = -44.9; z-score = -1.67; ED = 45.24
```

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(+)

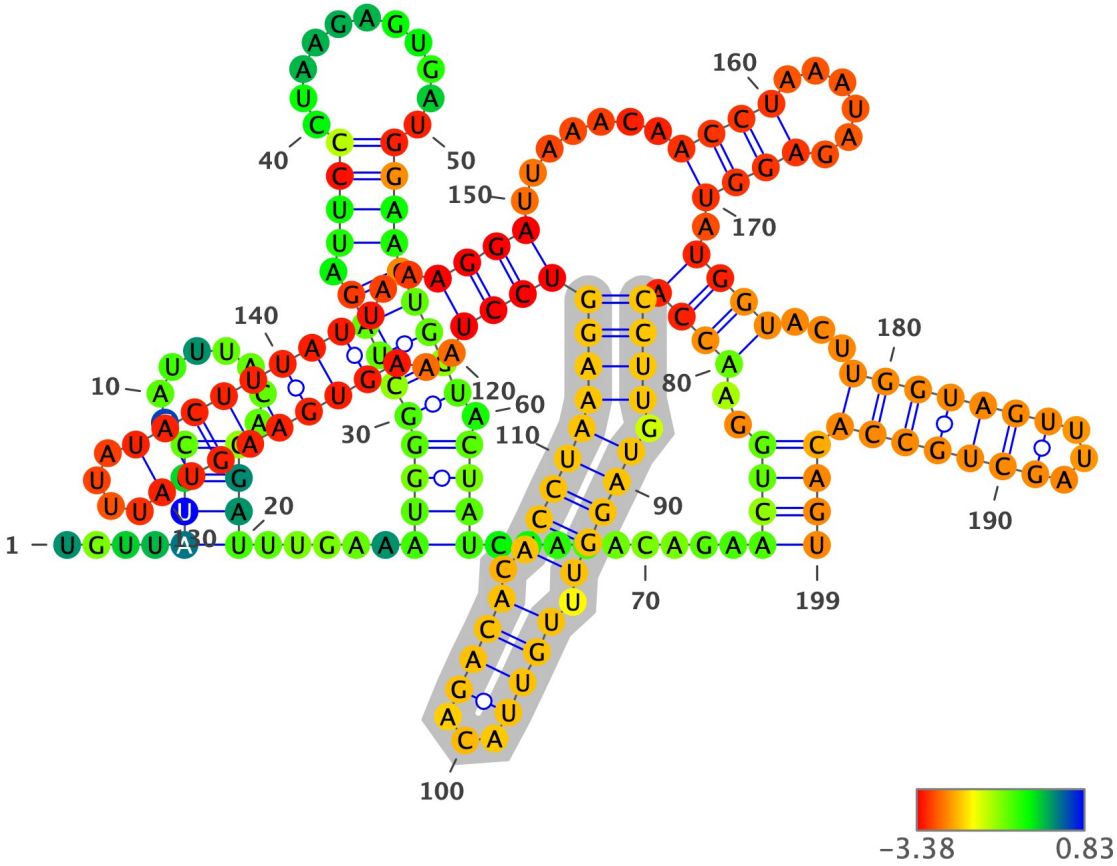
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 230 from nt 12899 to 12930 (nt 84 to 115)

```
5'-CCUUGUAGGUUUGUUACAGACACACCUAAAGG-3'
5'-((((.(((((.((((...)))).)))))))))-3'
Motif MFE = -10.1; z-score = -3.4; 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 = -2.21; 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(+)

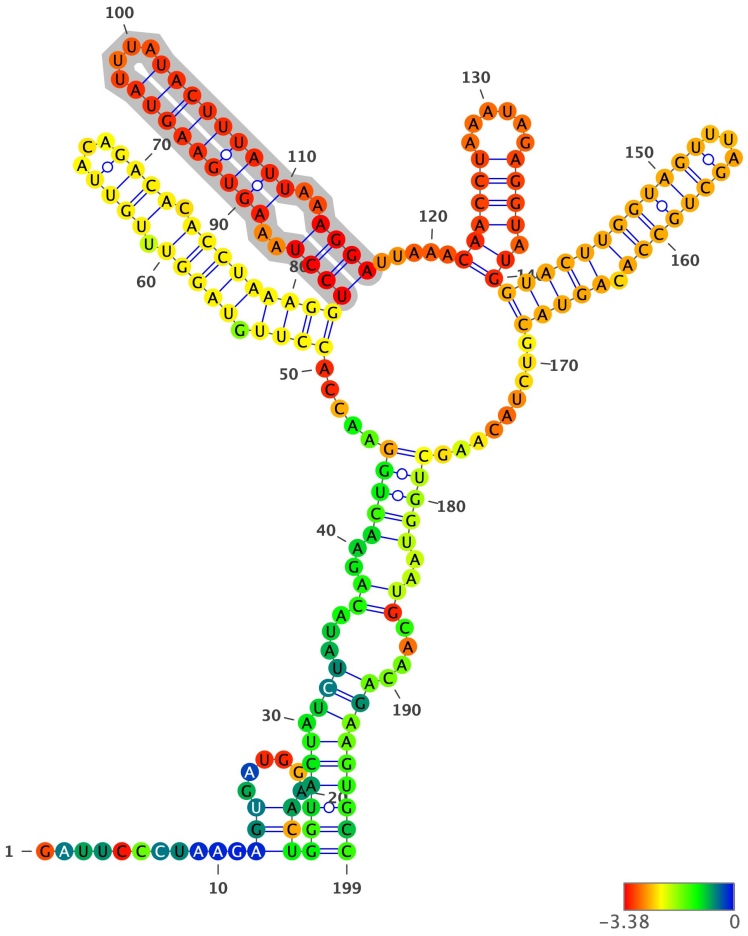
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 231 from nt 12931 to 12964 (nt 83 to 116)

```
5'-UCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGA-3'
5'-((((..((((((((((....)))))))))..))))-3'
Motif MFE = -9.8; z-score = -4.24; ED = 1.18
```



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

Extracted structure model with flanking nucleotides 12849 to 13047 (motif highlighted in silver):

```
5'-GAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUA
AAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCC-3
5'-...........(((......)))((((((.(((...((..(((((.....((((.(((((.((((...)))).)))))))))((((..(((((((((....)))))))))).
.))))).....((((((......)))).))((((((((((((...)))))))).)))))..........)))))..))....)))))))))-3'
MFE = -52.8; z-score = -3.31; ED = 29.81
```

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

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

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

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

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

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

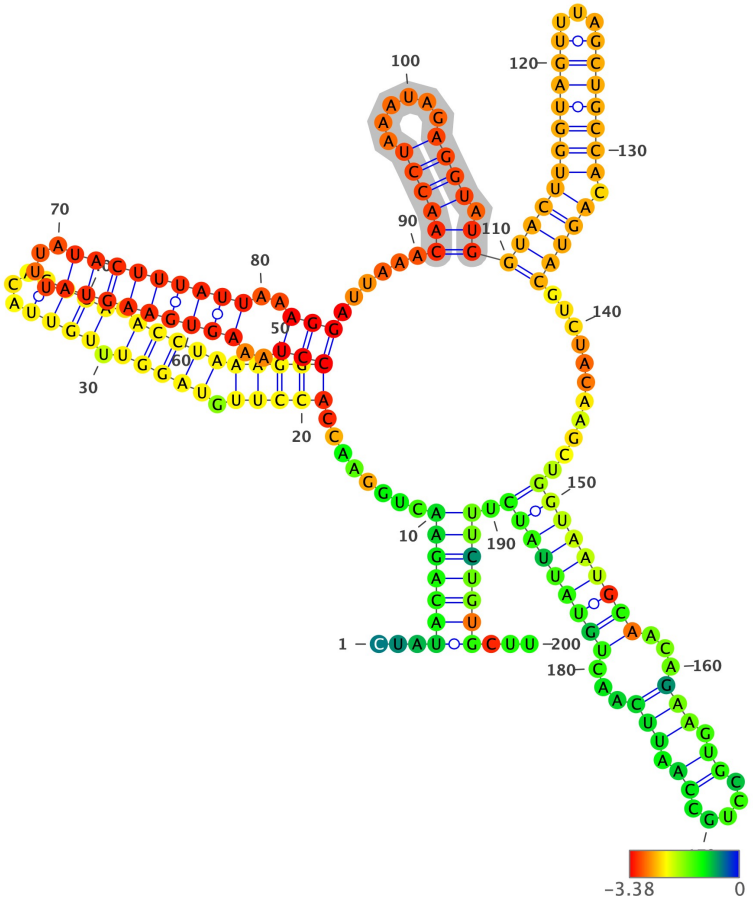
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 232 from nt 12970 to 12988 (nt 91 to 109)

```
5'-CAACCUAAAUAGAGGUAUG-3'
5'-((((((......)))).))-3'
Motif MFE = -3.2; z-score = -2.46; 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 12880 to 13079 (motif highlighted in silver):

```
5'-CUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGU
ACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCUU-3
5'-...(((((((.........(((((.(((((.((((...)))).)))))))))))(((..((((((((((....)))))))))..)))......((((((......)))).))((
((((((((((...)))))))).)))))...........(((((((((...(((.((.....)).)))...)))))))))).)))))))...-3'
MFE = -55.3; z-score = -3.61; ED = 29.11
```

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

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

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

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

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

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

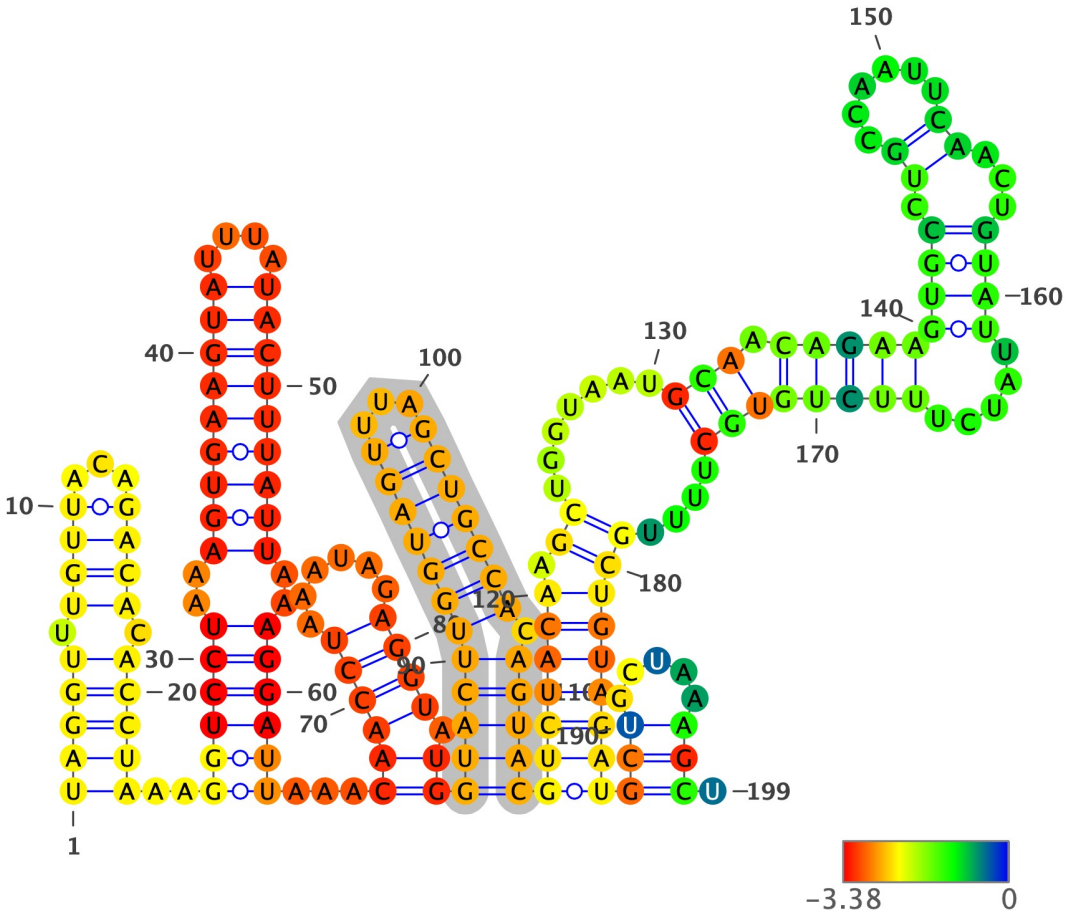
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 233 from nt 12989 to 13016 (nt 86 to 113)

```
5'-GUACUUGGUAGUUUAGCUGCCACAGUAC-3'
5'-(((((((((((...)))))))).)))))-3'
Motif MFE = -12.5; z-score = -3.98; 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 = -3.15; 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(+)

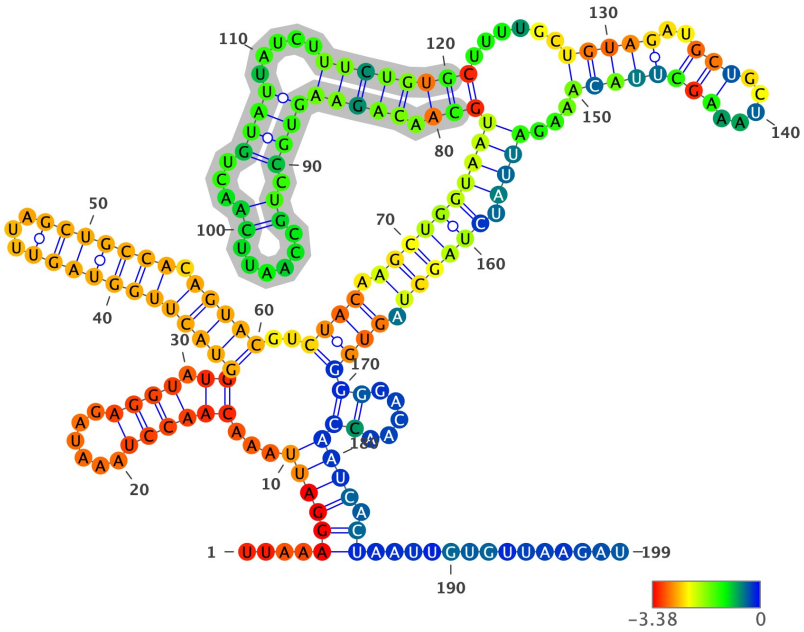
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 234 from nt 13035 to 13076 (nt 79 to 120)

```
5'-CAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUG-3'
5'-(........((................)).............)-3'
Motif MFE = -4.4; z-score = 0.16; ED = 7.45
```



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

Extracted structure model with flanking nucleotides 12957 to 13155 (motif highlighted in silver):

```
5'-UUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAU
CUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAU-3
5'-....((((((...((((((......)))).))((((((((((((...)))))))).)))))..((((.(((((((((((((.(((((((((.((......))...))))...
..))))))))......(((((..(((.....))))))))...)))).)))))).))))((.....)))))).))...............-3'
MFE = -44.6; z-score = -1.17; ED = 43.46
```

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(+)

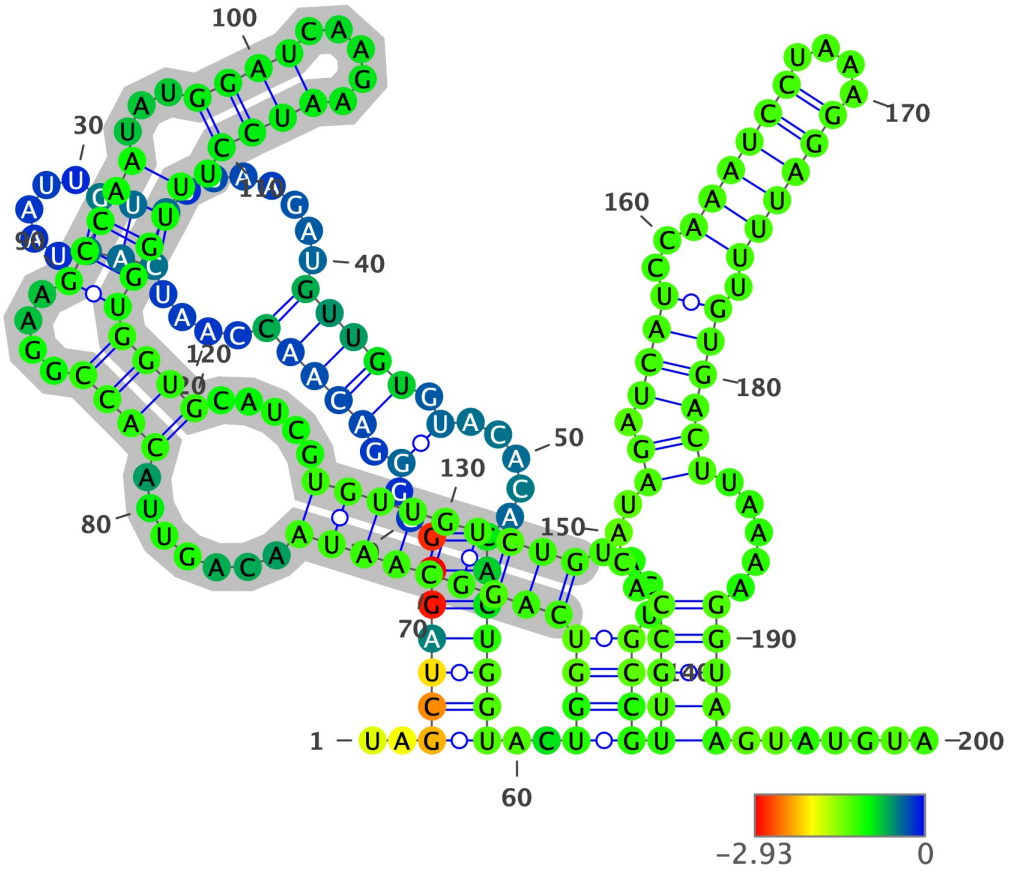
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 235 from nt 13181 to 13249 (nt 66 to 134)

```
5'-CAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUG-3'
5'-((.((((((.......((((....(((((.................)))))))))).....)))))).))-3'
Motif MFE = -20.4; z-score = -2.27; ED = 9.06
```



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 13116 to 13315 (motif highlighted in silver):

```
5'-UAGCUAGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAUGUUGUGUACACACACUGGUACUGGUCAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCU
UUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUA-3
5'-..(((((((..(.(((((....(((.....))).......))))).).....)))))))..((((((((((((.......((((....(((((...((((.....)))).
))))))))).....))))))))).....))))(((((....((.((((..((((((....)))))).)))))).....)))))).......-3'
MFE = -50.1; z-score = -1.02; ED = 31.37
```

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

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

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

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

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

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

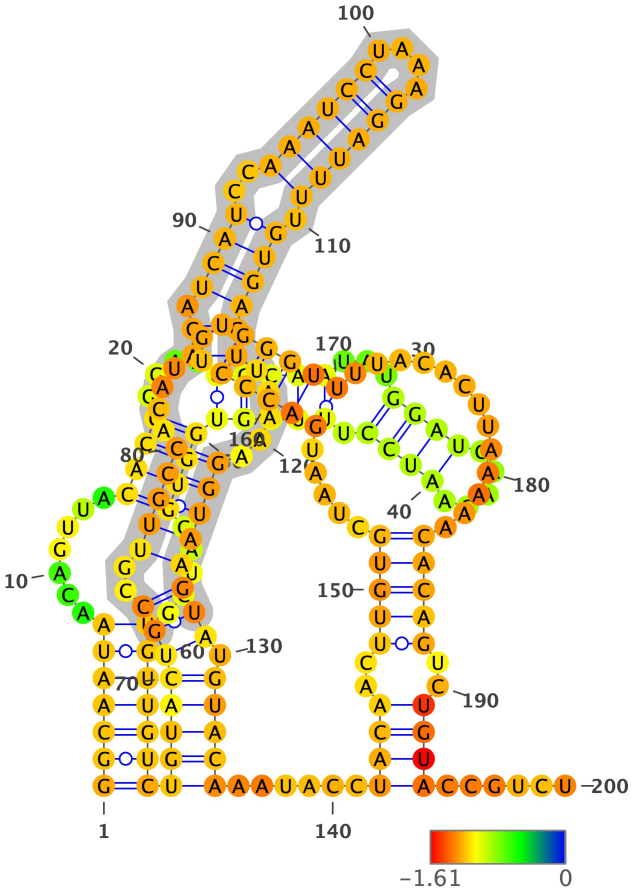
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 236 from nt 13254 to 13310 (nt 72 to 128)

```
5'-GCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGU-3'
5'-((...((((....((.((((..((((((....)))))).))))))).....)))).))-3'
Motif MFE = -11.6; z-score = -1.55; ED = 5.19
```



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 13183 to 13382 (motif highlighted in silver):

```
5'-GGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUG
UGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCU-3
5'-(((((((.......((((....(((((...((((.....)))).))))))))).....)))))))((((((((..(((((....((.((((..((((((....)))))).)
))))).....)))))))).)))))......((((..(((((.....(((((...)))))..............)))))..))))......-3'
MFE = -43.9; z-score = -0.8; ED = 42.3
```

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

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

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

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

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

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

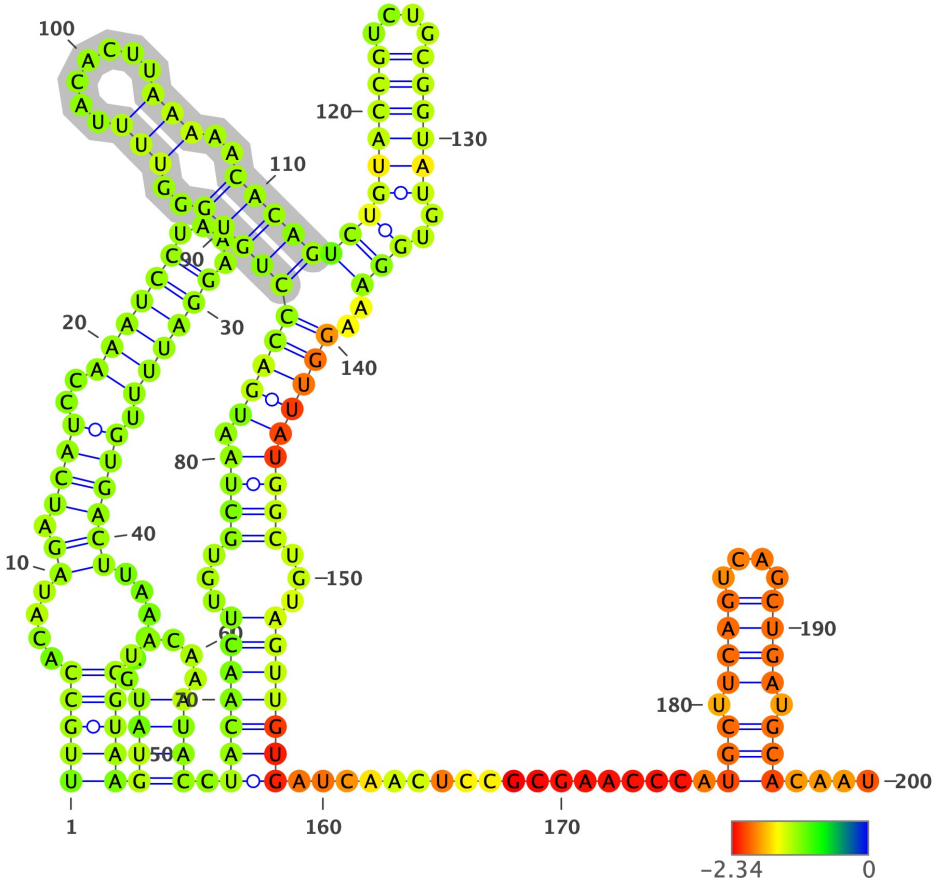
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 237 from nt 13344 to 13370 (nt 87 to 113)

```
5'-CUGUGGGUUUUACACUUAAAAACACAG-3'
5'-(.(((.................))).)-3'
Motif MFE = -5.6; z-score = -2.49; ED = 4.21
```



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 13258 to 13457 (motif highlighted in silver):

```
5'-UUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACAC
AGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAU-3
5'-(((((....((.((((..((((((....)))))).))))))....)))))(((.....)))).(((((((...((((.((((((((((..(((.......)))..)))
))(((((((((....))))))..))))..))))))))...)))))))..................(((.((((....)))).))).....-3'
MFE = -49.4; z-score = -1.8; ED = 56.32
```

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(+)

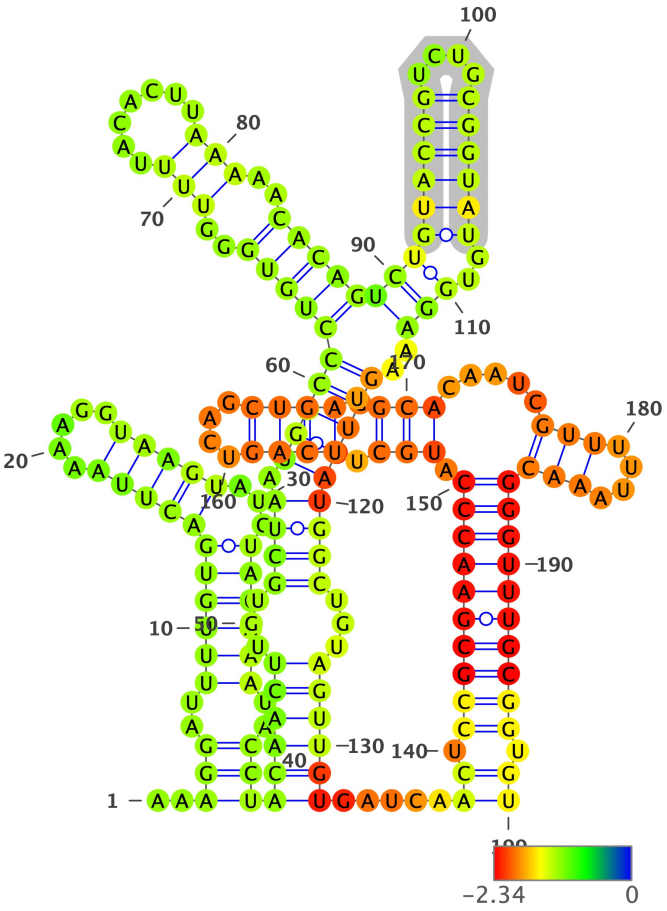
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 238 from nt 13374 to 13389 (nt 92 to 107)

```
5'-GUACCGUCUGCGGUAU-3'
5'-(.((((....)))).)-3'
Motif MFE = -5.6; z-score = -2.84; 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 13283 to 13481 (motif highlighted in silver):

```
5'-AAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGG
AAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGU-3
5'-..(((..((((((((((((.....)))))...))))))..)))((((((...((((.((((((((((..(((.......)))..)))))((((((((....))))))..))
)..))))))))...))))))).....((.((((((((((.(((.((((....)))).)))).....(((....)))))))))))))).))-3'
MFE = -60.9; z-score = -3.04; 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 186--CDS, cds-YP_009724389.1, 266-13468(+)

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

4-- nt 186 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

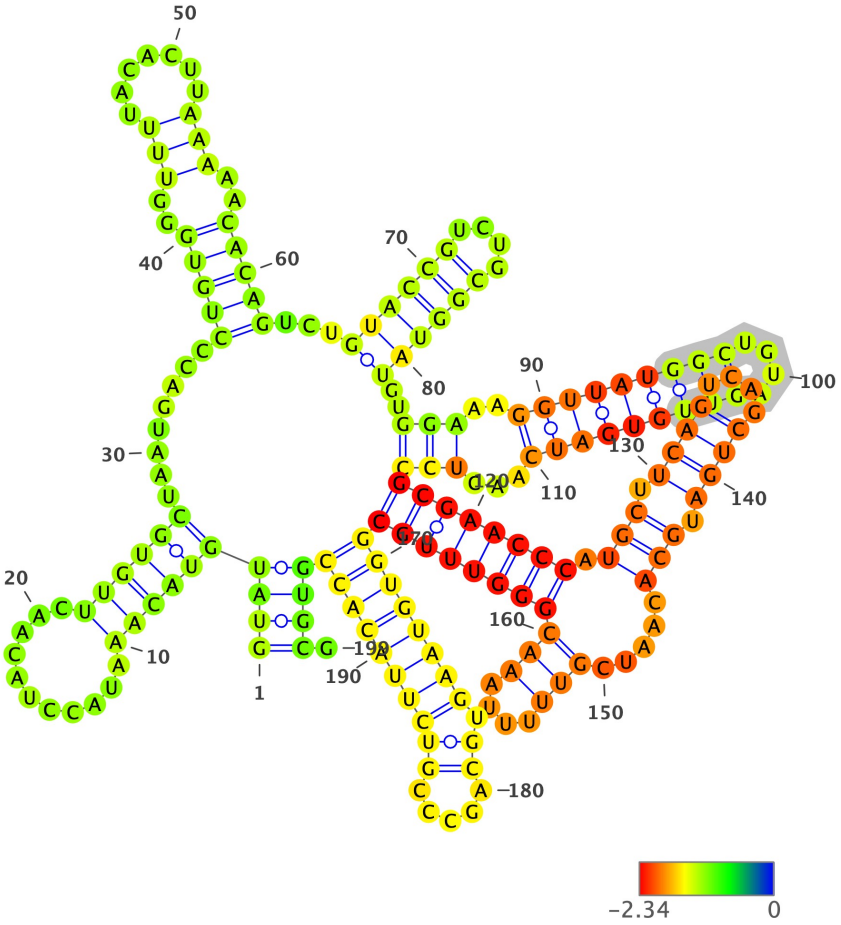
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

5-- nt 1 to 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 239 from nt 13403 to 13412 (nt 95 to 104)

```
5'-GGCUGUAGUU-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 13309 to 13507 (motif highlighted in silver):

```
5'-GUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCA
ACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCG-3
5'-((((((((((...........))))))).......((((..(((.......))))..))))))...((((((....))))))..(((..(((((((((....)))))))))).
..)))(((((((((.(((.((((....)))).))).....(((....)))))))))))(((((((((.((.....))))))))))))).-3'
MFE = -59.2; z-score = -2.34; ED = 37.69
```

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

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

4-- nt 160 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

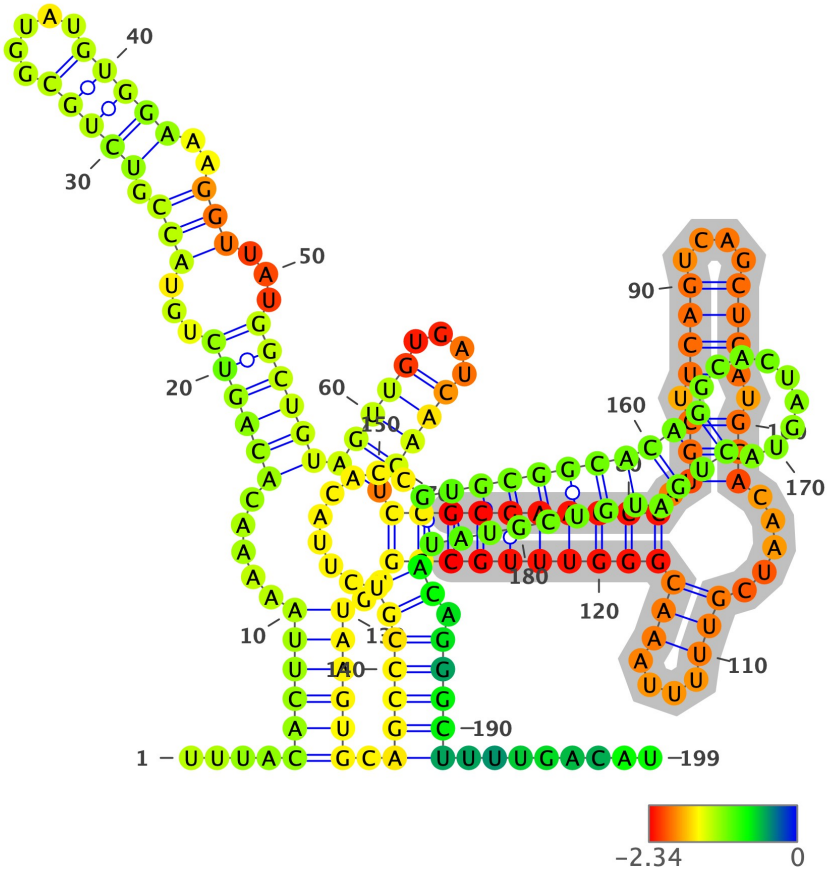
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

5-- nt 1 to 175--CDS, cds-YP_009725295.1, 266-13483(+)

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

NC_045512.2 (forward strand): Structure number 240 from nt 13425 to 13476 (nt 74 to 125)

```
5'-GCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGC-3'
5'-(((((((((.(((.((((....)))))..))).....(((....)))))))))))-3'
Motif MFE = -16.8; z-score = -3.19; ED = 2.45
```



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

Extracted structure model with flanking nucleotides 13352 to 13550 (motif highlighted in silver):

```
5'-UUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUU
UUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAU-3
5'-....((((((.....((((((...(((.(((((.....)))))..)))...)))))))((((....))))))(((((((((.(((.((((....)))).))).....(((.
...)))))))))))))..)))))).(((((((.......((((((((((.........))).)))))))))..)))))........-3'
MFE = -65.5; z-score = -2.4; ED = 19.9
```

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 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(+)

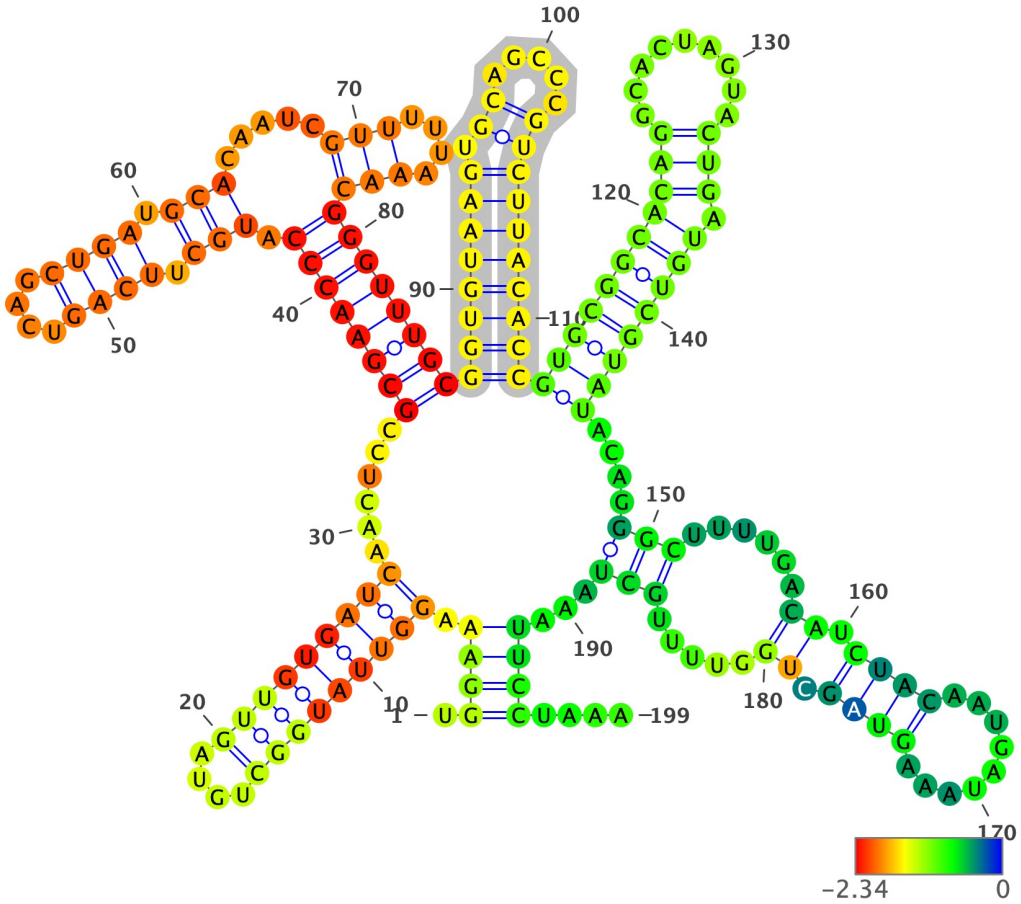
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 241 from nt 13477 to 13502 (nt 87 to 112)

```
5'-GGUGUAAGUGCAGCCCGUCUUACACC-3'
5'-(((((((((.((.....)))))))))))-3'
Motif MFE = -10.1; z-score = -3.15; ED = 1.5
```



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

Extracted structure model with flanking nucleotides 13391 to 13589 (motif highlighted in silver):

```
5'-UGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACAC
CGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAA-3
5'-.((((.((((((((((....))))))))).....(((((((.(((.((((....)))).))).....(((....)))))))))))(((((((.((.....)))))))))
)((((((((((.........))).)))))))....(((......((.((((.........)))).))).....)))...))))....-3'
MFE = -58.8; z-score = -1.59; ED = 38.45
```

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

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

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

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

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

3-- nt 1 to 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(+)

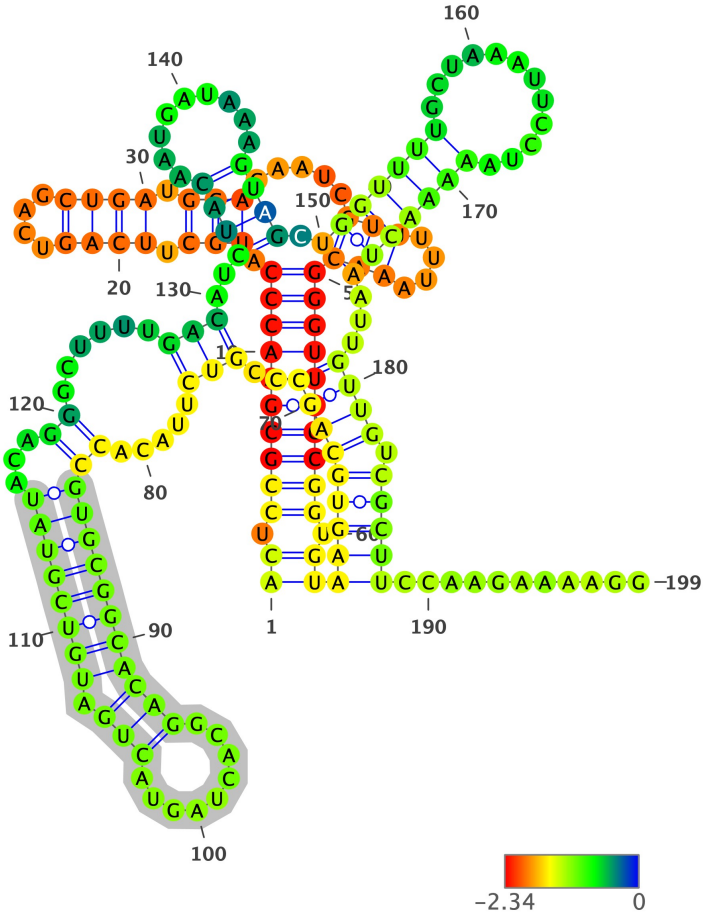
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 242 from nt 13503 to 13534 (nt 84 to 115)

```
5'-GUGCGGCACAGGCACUAGUACUGAUGUCGUAU-3'
5'-(((((((((((.........))).))))))))-3'
Motif MFE = -11.6; z-score = -2.08; 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 = -1.18; 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(+)

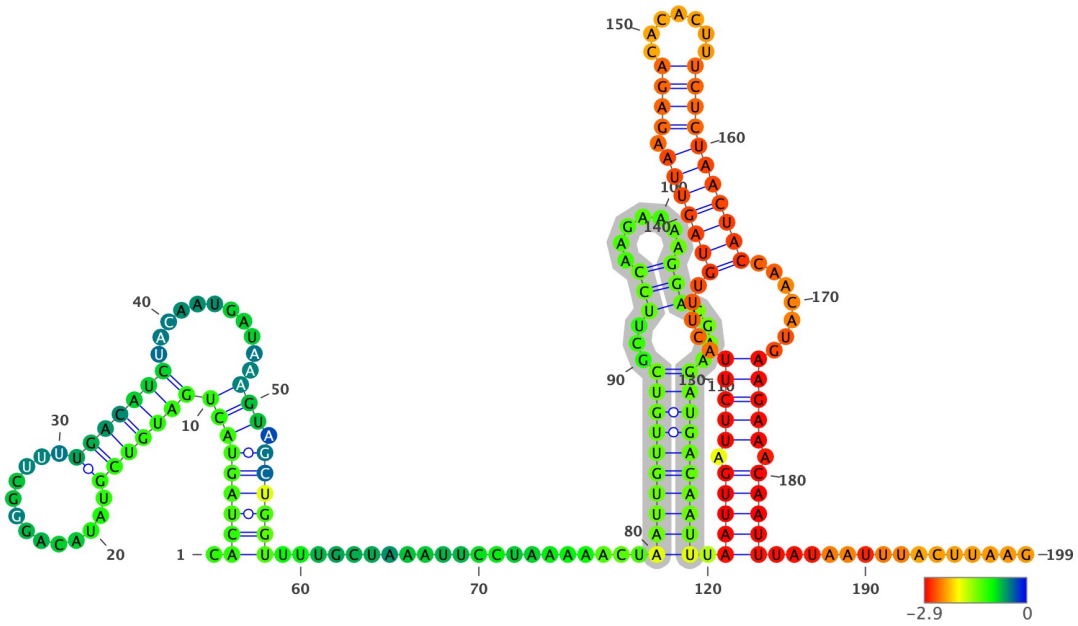
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 243 from nt 13594 to 13633 (nt 80 to 119)

```
5'-AAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAUGACAAUU-3'
5'-((((((((((...(((.......)))....)))))))))-3'
Motif MFE = -10.3; z-score = -2.41; 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'-CACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGA
UGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAG-3
5'-.((((((((((((((((.............))))))).............))).)))))).....................((((((((((...(((.......))).....))
))))))))).(((((.(((((.....(((((((.((((.......))))))))))).......)))))).)))))..............-3'
MFE = -38.3; z-score = -2.07; 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(+)

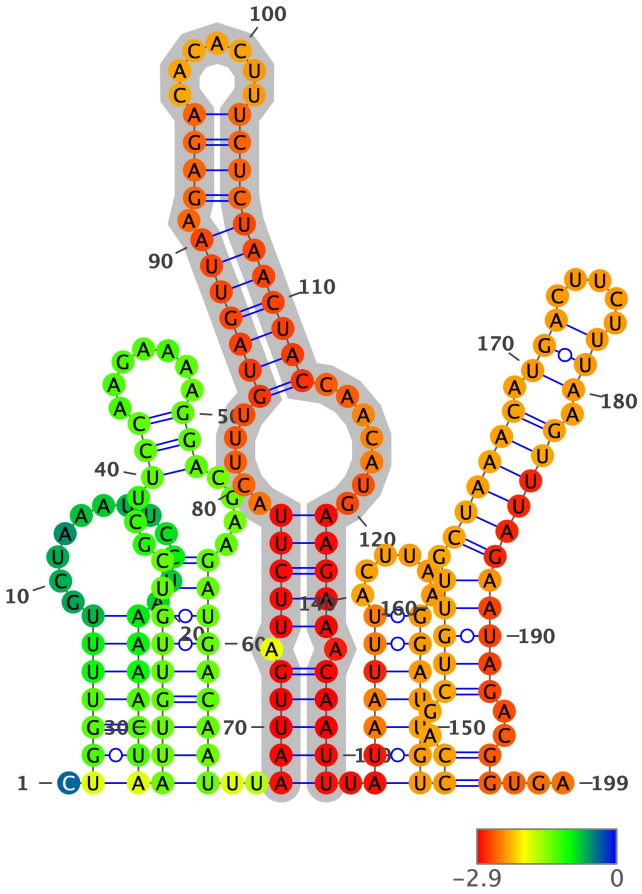
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-AAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUU-3'
5'-(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))-3'
Motif MFE = -15.2; z-score = -4.11; 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 = -1.84; 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(+)

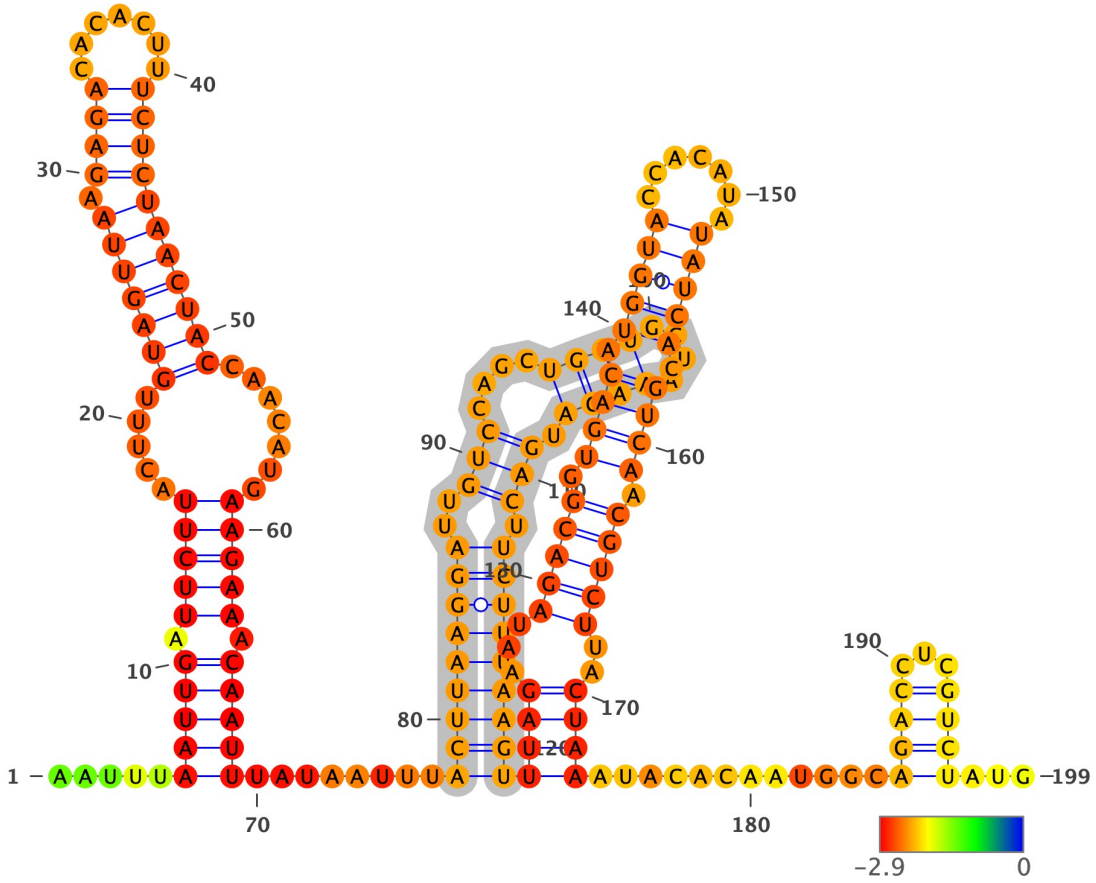
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-ACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGU-3'
5'-(((((((((..(((....((((....)))).))).)))))))))-3'
Motif MFE = -11.0; z-score = -2.88; 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 = -3.95; 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(+)

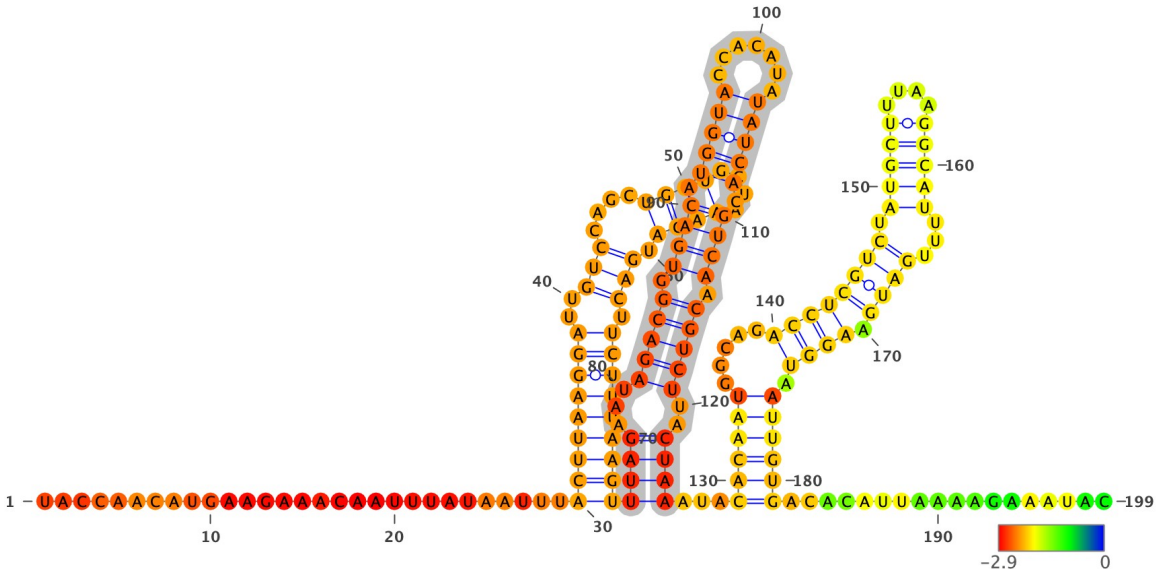
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAA-3'
5'-((((...(((((.((((.(((((.......))))).)))).)))))..))))-3'
Motif MFE = -14.7; z-score = -2.99; 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 = -2.31; 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(+)

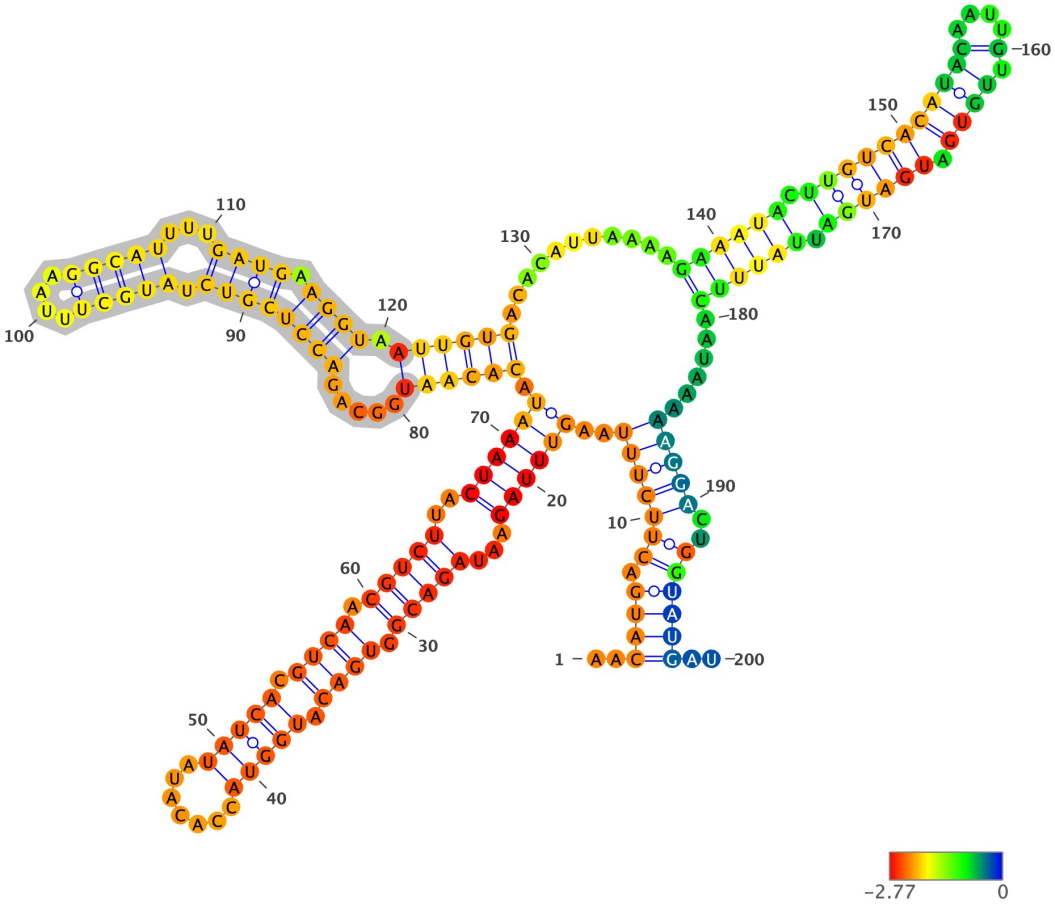
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUGAAGGUAA-3'
5'-(.....((((((((.(((((....)))))...)))).)))).)-3'
Motif MFE = -12.3; z-score = -2.33; 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 = -2.86; 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(+)

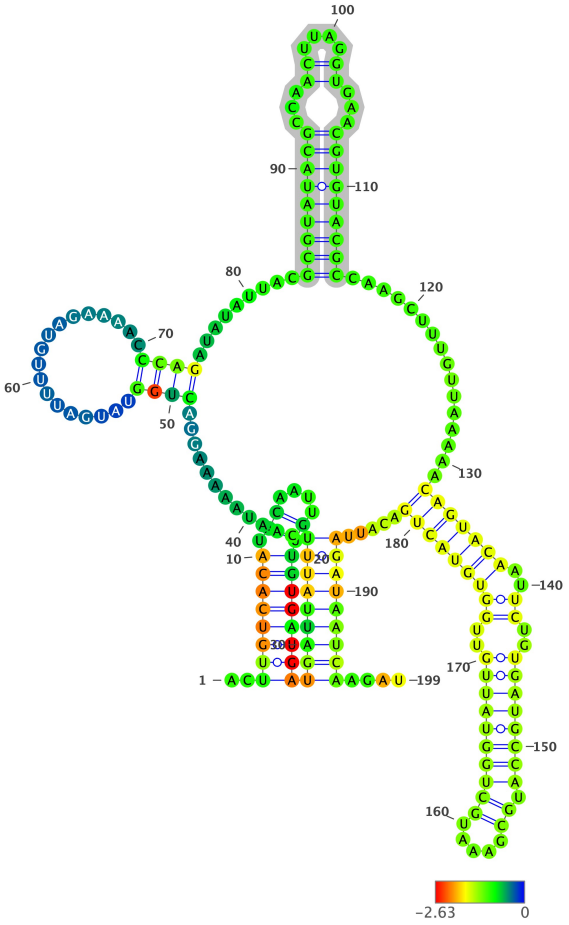
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 248 from nt 13958 to 13989 (nt 84 to 115)

```
5'-GCGUAUACGCCAACUUAGGUGAACGUGUACGC-3'
5'-((((((((((...((....))...)))))))))-3'
Motif MFE = -13.3; z-score = -3.28; 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 = -1.49; 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(+)

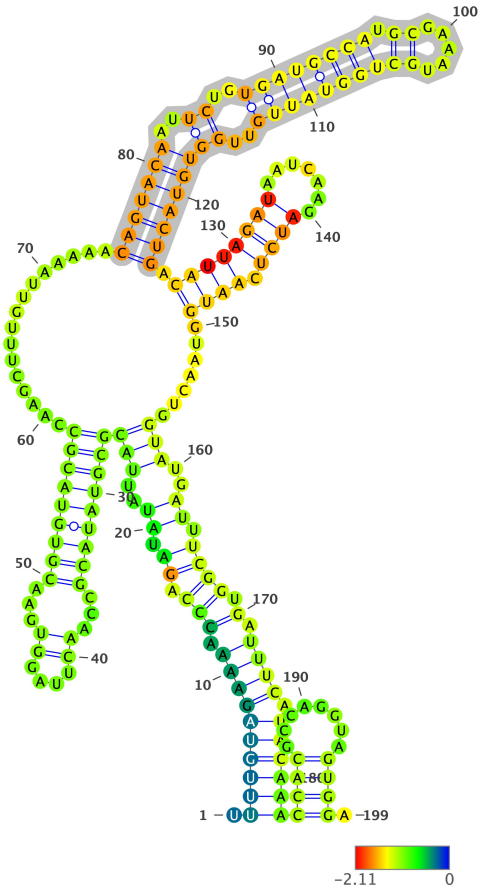
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-CAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUG-3'
5'-(((((((..((..((((((((.((.....))))))))))..)))))))))-3'
Motif MFE = -16.7; z-score = -3.05; ED = 3.57
```



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

Extracted structure model with flanking nucleotides 13932 to 14130 (motif highlighted in silver):

```
5'-UUUUGUAGAAAACCCAGAUAUAUUACGCGUAUACGCCAACUUAGGUGAACGUGUACGCCAAGCUUUGUUAAAAACAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAU
UGUUGGUGUACUGACAUUAGAUAAUCAAGAUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCCAGGUAGUGGA-3
5'-.(((((((((((.(((.((.((..(((((((((((((...((....))...)))))))))).................(((((((..((..((((((((.((.....))))))))
))..))))))))).((((((((.......)))).))))).......)))..)).)))).).)))).))))))((((........)))).-3'
MFE = -52.0; z-score = -2.52; ED = 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(+)

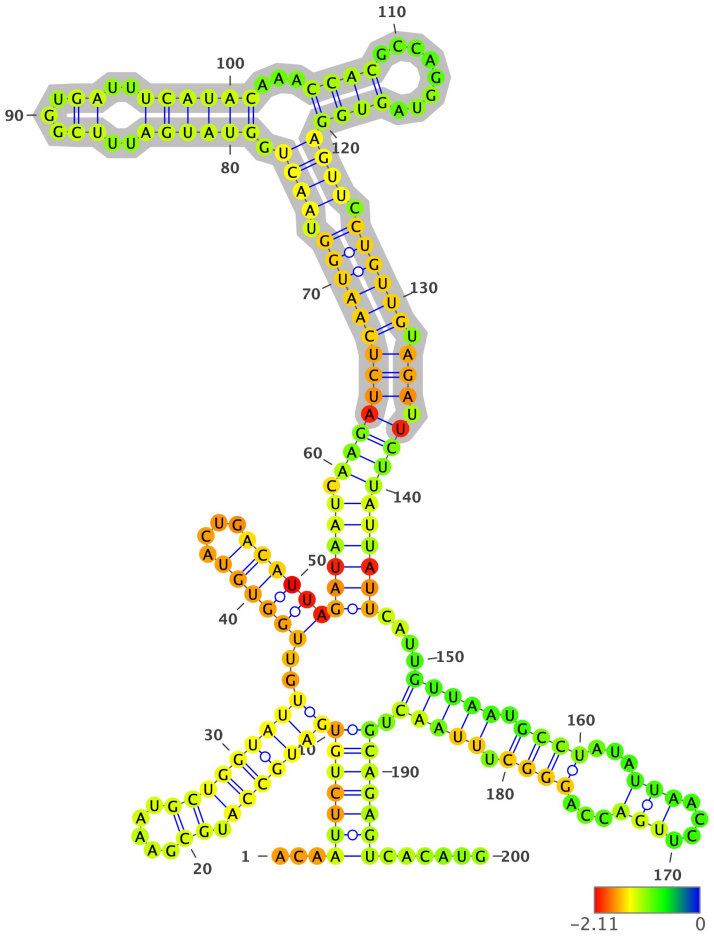
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 250 from nt 14072 to 14146 (nt 63 to 137)

```
5'-AUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUU-3'
5'-((((((((((.((((.((((((..((...))..))))))...((((........))))))))).)))))).))).)-3'
Motif MFE = -20.5; z-score = -2.07; 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 = -1.97; ED = 36.75
```

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

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

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

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

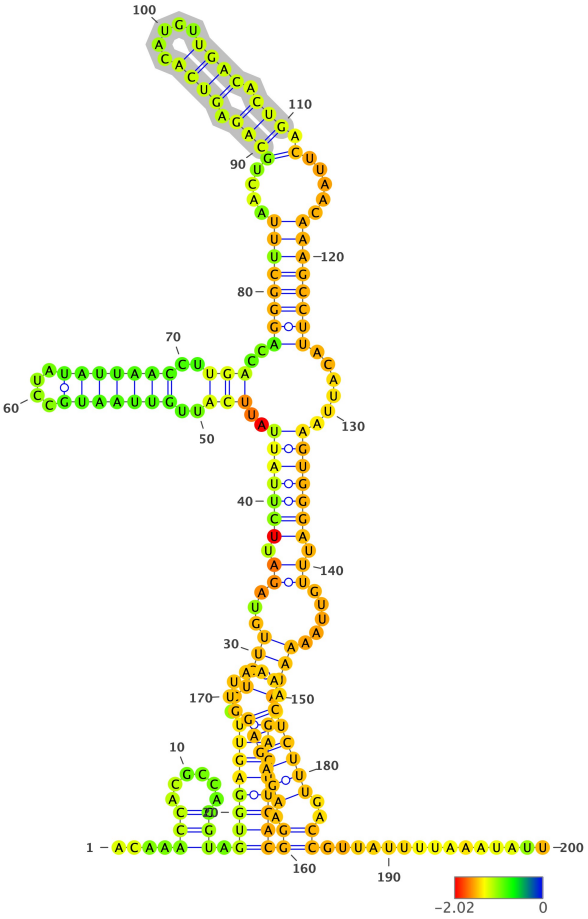
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 251 from nt 14198 to 14218 (nt 90 to 110)

```
5'-CAGAGUCACAUGUUGACACUG-3'
5'-(((.((((.....)))).)))-3'
Motif MFE = -4.5; z-score = -1.66; 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 = -0.97; 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(+)

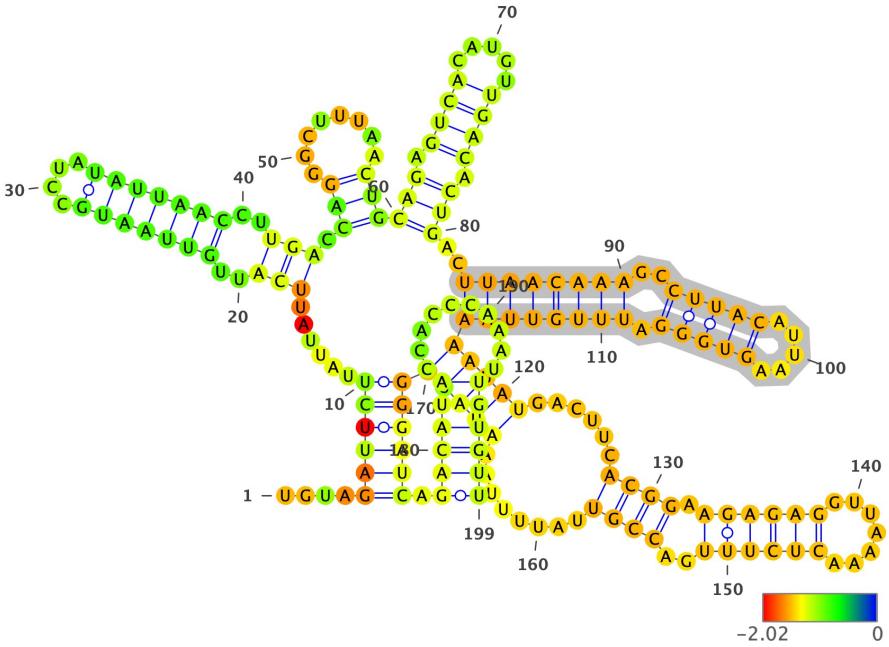
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAA-3'
5'-((((((((..(((((.....))))).))))))))-3'
Motif MFE = -8.5; z-score = -3.09; 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 = -1.2; 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(+)

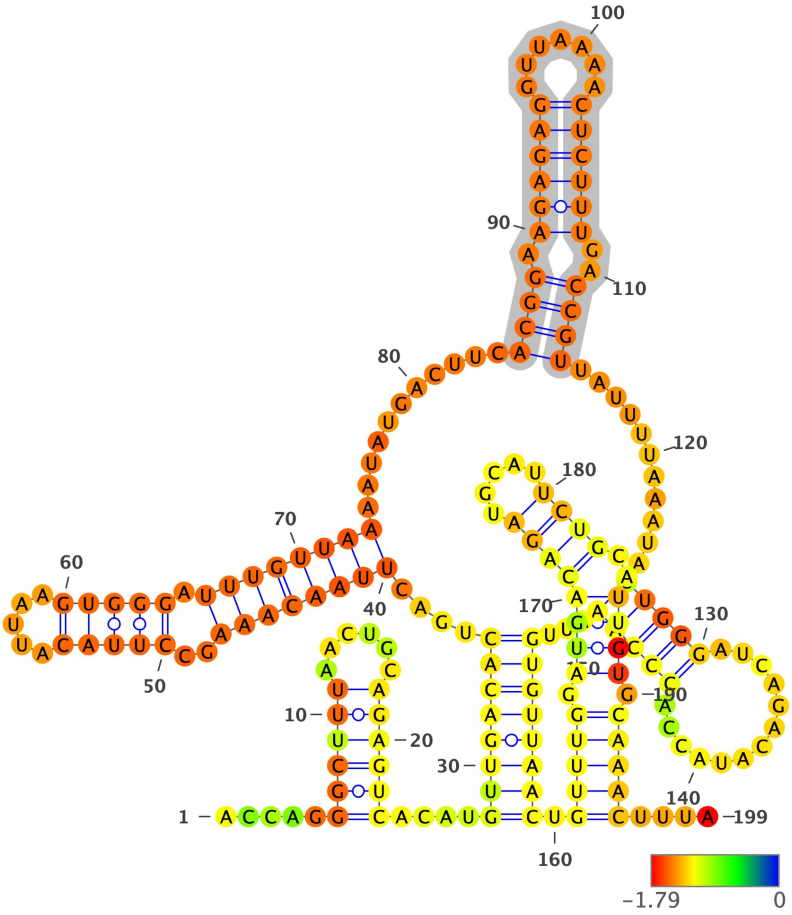
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-ACGGAAGAGAGGUUAAAACUCUUUGACCGU-3'
5'-((((.((((((.......))))))..))))-3'
Motif MFE = -10.5; z-score = -3.78; ED = 0.72
```



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

Extracted structure model with flanking nucleotides 14182 to 14380 (motif highlighted in silver):

```
5'-ACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGAC
CGUUAUUUUAAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUA-3
5'-.....((((((......))))))....(((((((((....(((((((((..(((((.....)))))).)))))))))..........((((.((((((.......))))))..)
)))).........((((((.............))))))...)))))))).((((((.(((((((((.....)))))..)))).)))))).....-3'
MFE = -47.5; z-score = -2.05; 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(+)

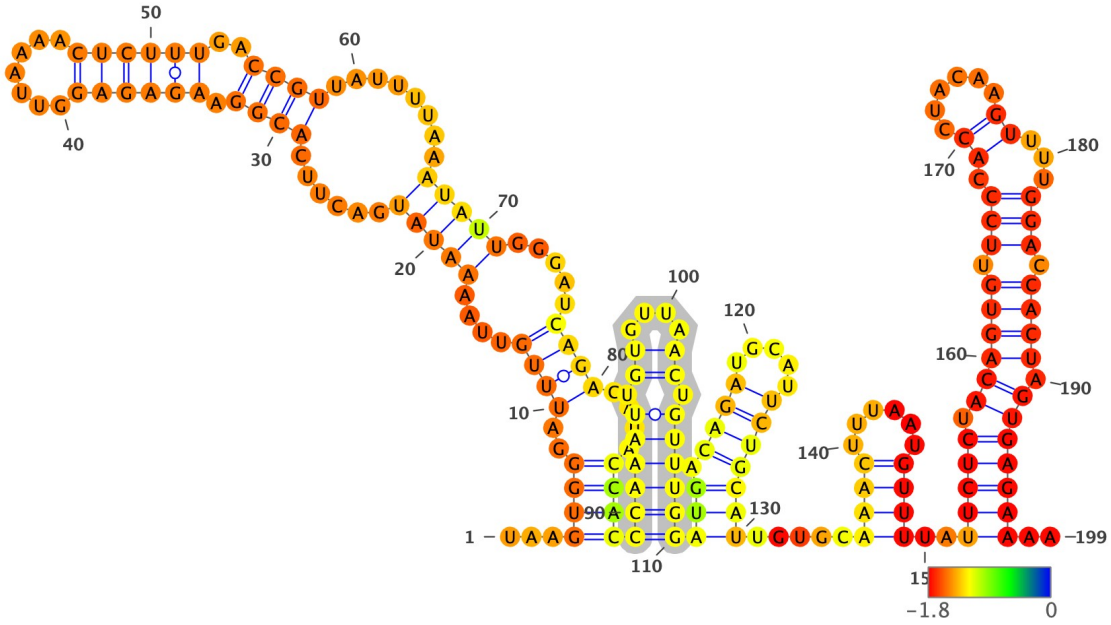
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-CCAAAUUGUGUUAACUGUUUGG-3'
5'-((((((.((....)).))))))-3'
Motif MFE = -5.6; z-score = -2.94; 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 = -1.34; 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(+)

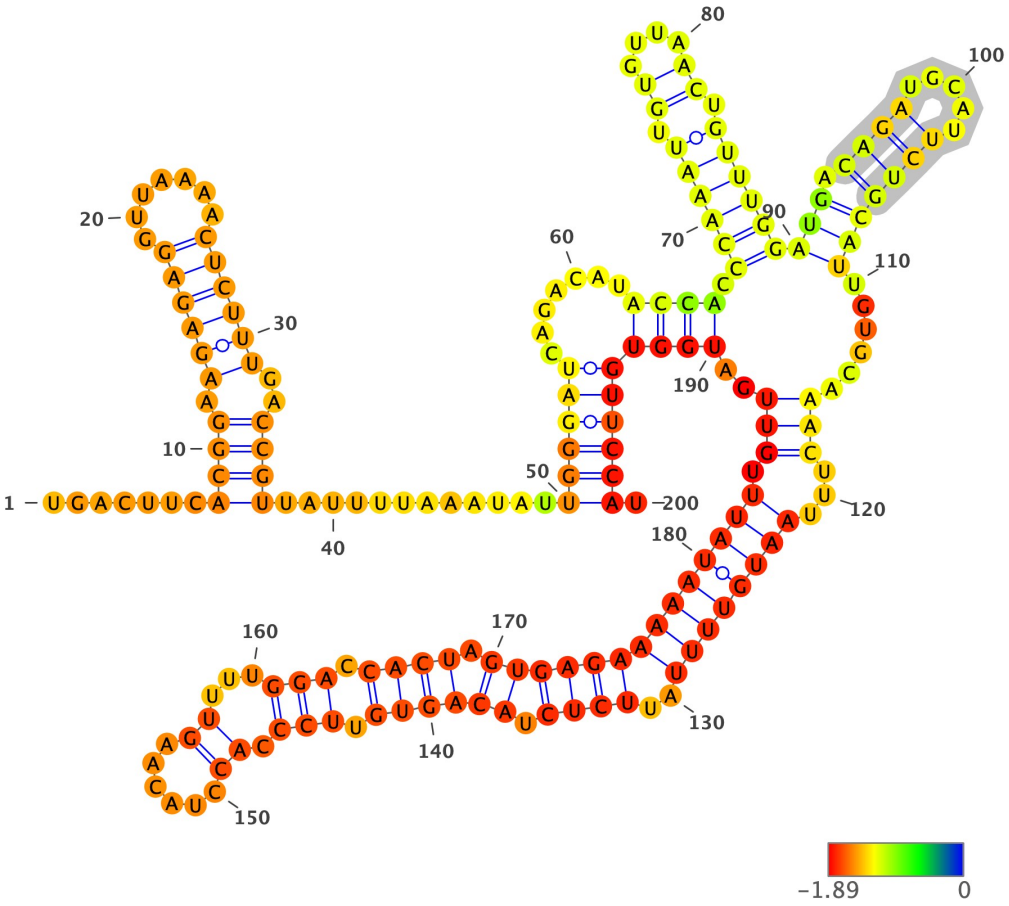
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 255 from nt 14352 to 14364 (nt 94 to 106)

```
5'-CAGAUGCAUUCUG-3'
5'-((.........))-3'
Motif MFE = -2.1; z-score = -4.53; 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 = -1.79; 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(+)

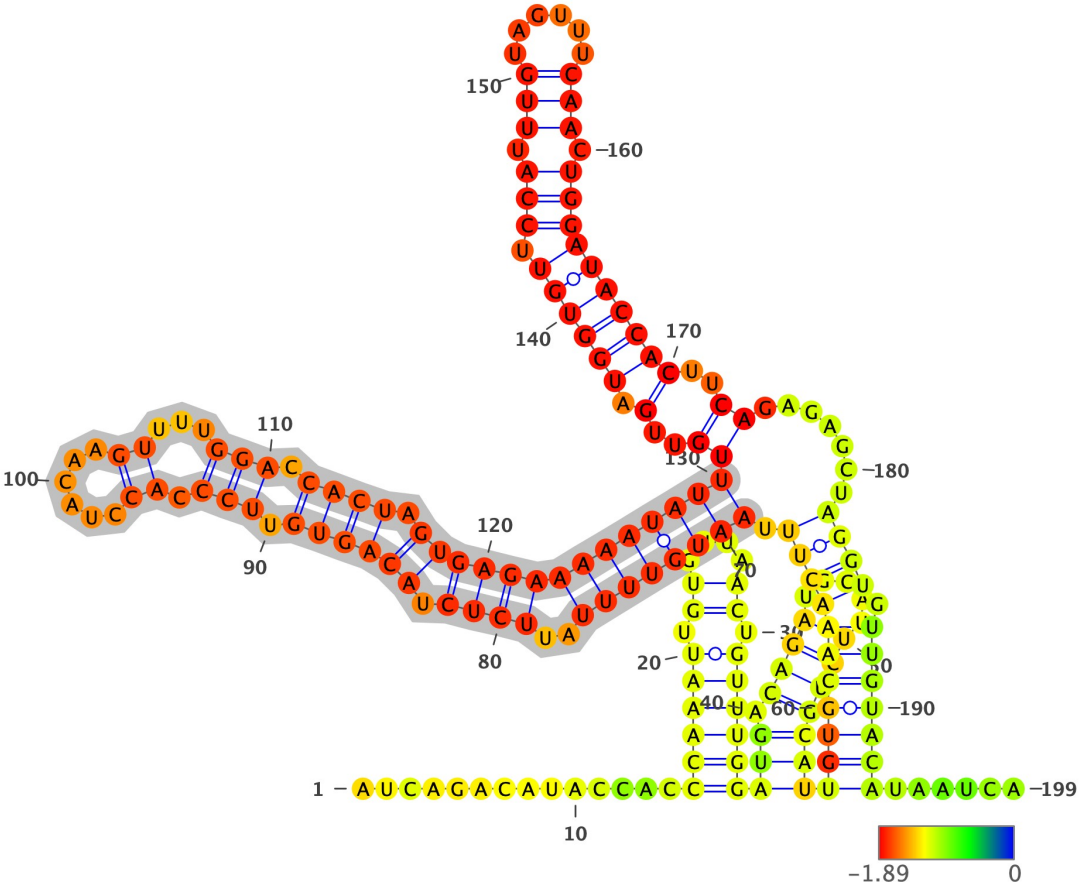
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-AAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUU-3'
5'-((((((((..((((.((((((.(((.((......))...))).)))).)))))))))))))-3'
Motif MFE = -14.2; z-score = -2.86; 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 = -1.85; ED = 29.95
```

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(+)

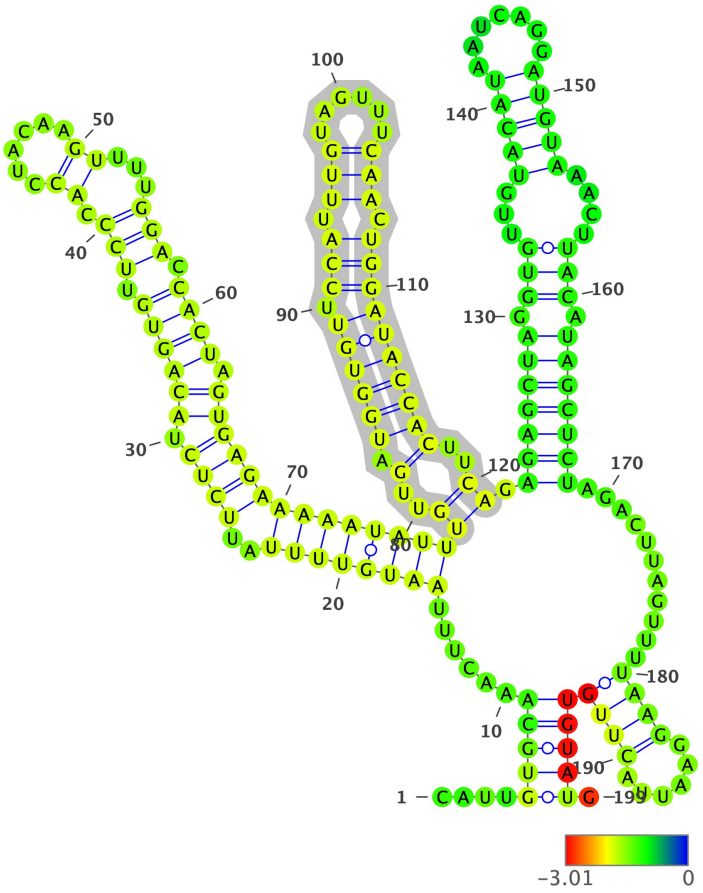
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCA-3'
5'-((..(.(((((((.(((.(((......))).))))))))))..))-3'
Motif MFE = -11.9; z-score = -2.88; 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 = -1.57; 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(+)

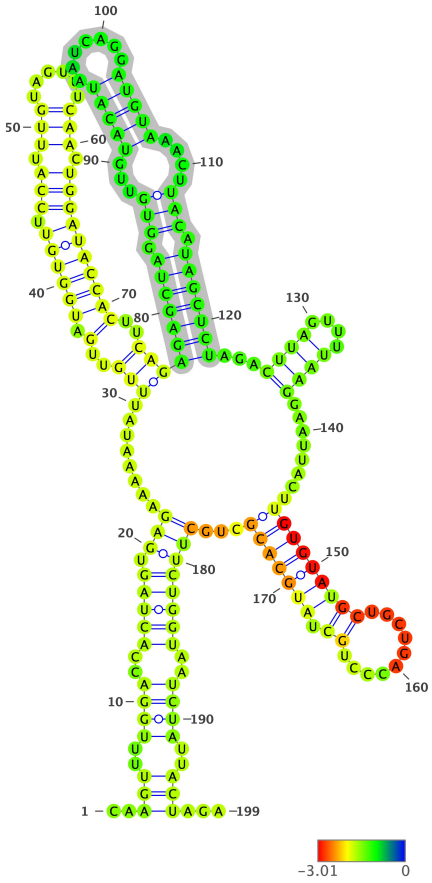
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 258 from nt 14487 to 14532 (nt 77 to 122)

```
5'-AGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCU-3'
5'-(((((((.(((...(((((.......)))))....))).)))))))-3'
Motif MFE = -13.4; z-score = -3.17; 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 = -1.58; ED = 45.93
```

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(+)

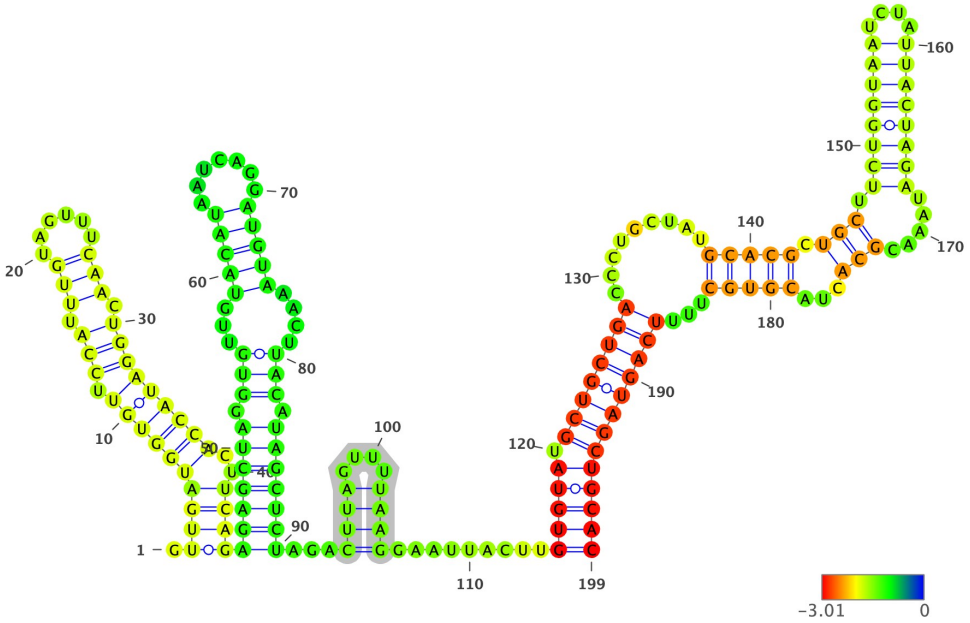
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 14536 to 14547 (nt 94 to 105)

```
5'-CUUAGUUUUAAG-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = 0.11; 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 14443 to 14641 (motif highlighted in silver):

```
5'-GUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUA
CUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAUAAACGCACUACGUGCUUUUCAGUAGCUGCAC-3
5'-.((((((((((.(((.(((......))).)))))))))..))))(((((((.(((...(((((.......)))))....))).)))))))...((((....)))).....
...(((((.(((((((((.........(((((.(((.(((((((((....)))))))))).....)))...))))))...)))))))))))))-3'
MFE = -58.1; z-score = -3.19; ED = 13.97
```

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(+)

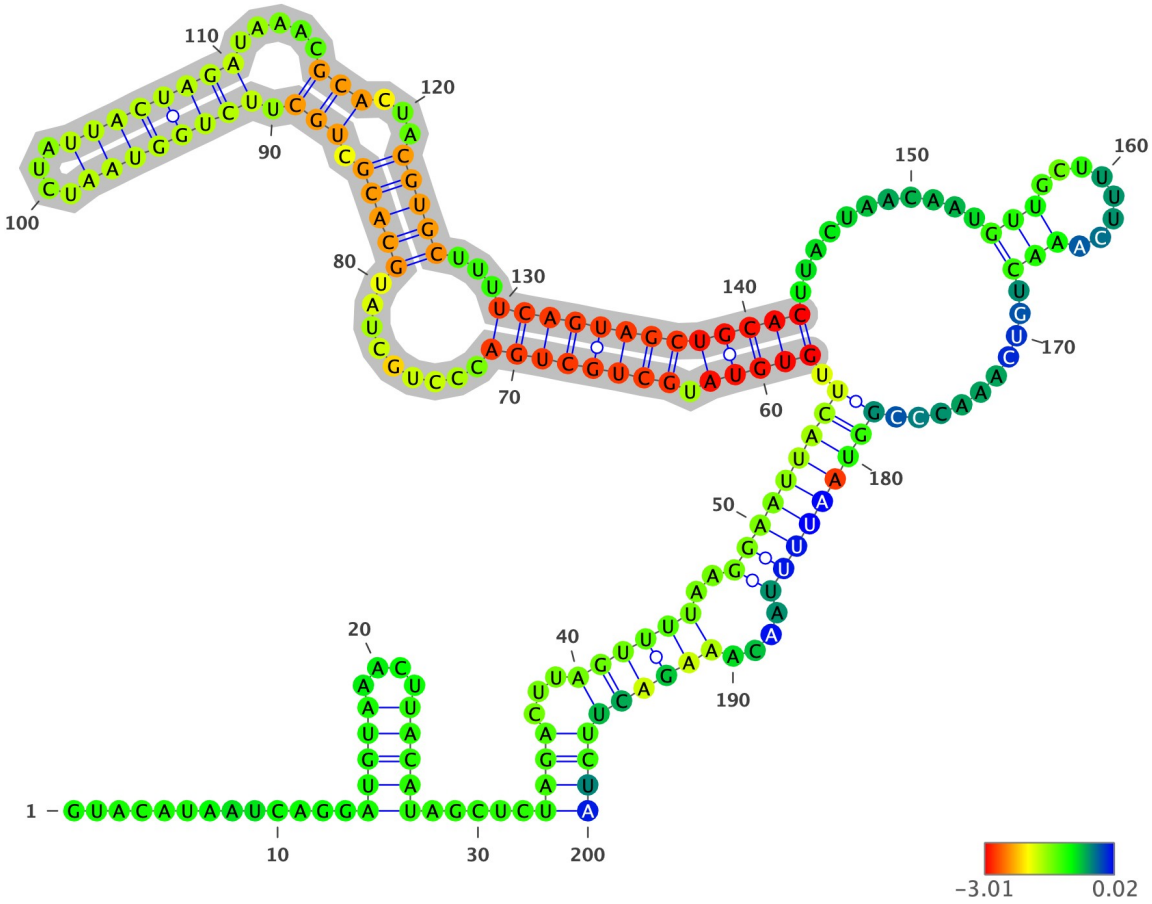
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 260 from nt 14557 to 14641 (nt 58 to 142)

```
5'-GUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAUAAACGCACUACGUGCUUUUCAGUAGCUGCAC-3'
5'-(((((.(((((((((.........(((((.(((.(((((((((....)))))))))).....)))...))))))...)))))))))))))-3'
Motif MFE = -29.9; z-score = -4.25; 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 = -1.74; 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(+)

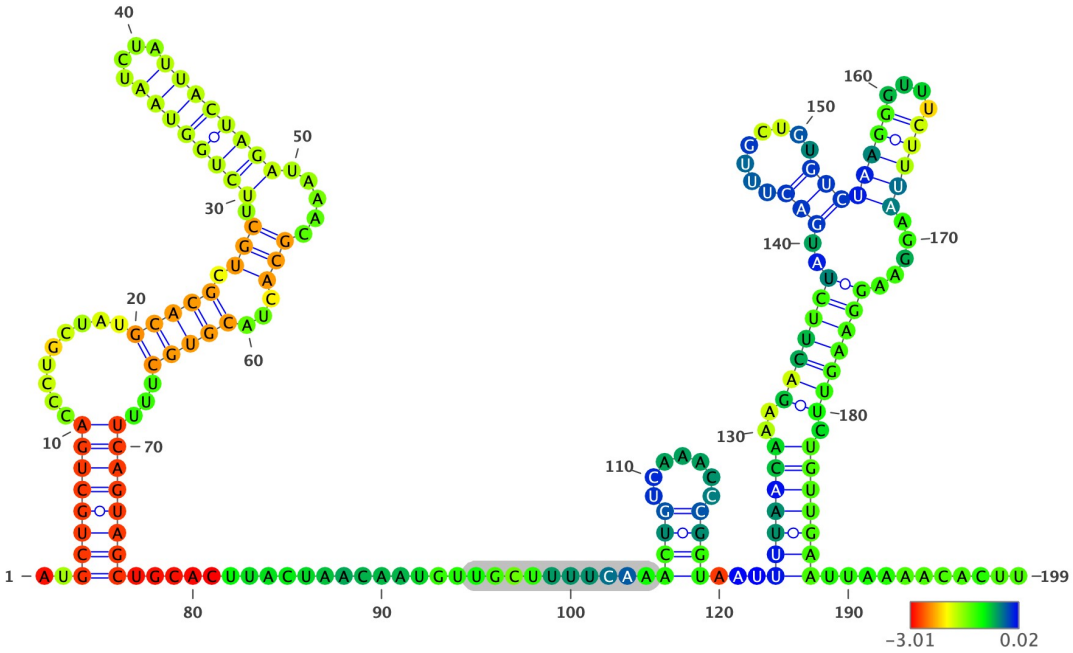
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UGCUUUUCAA-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 = -0.41; 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(+)

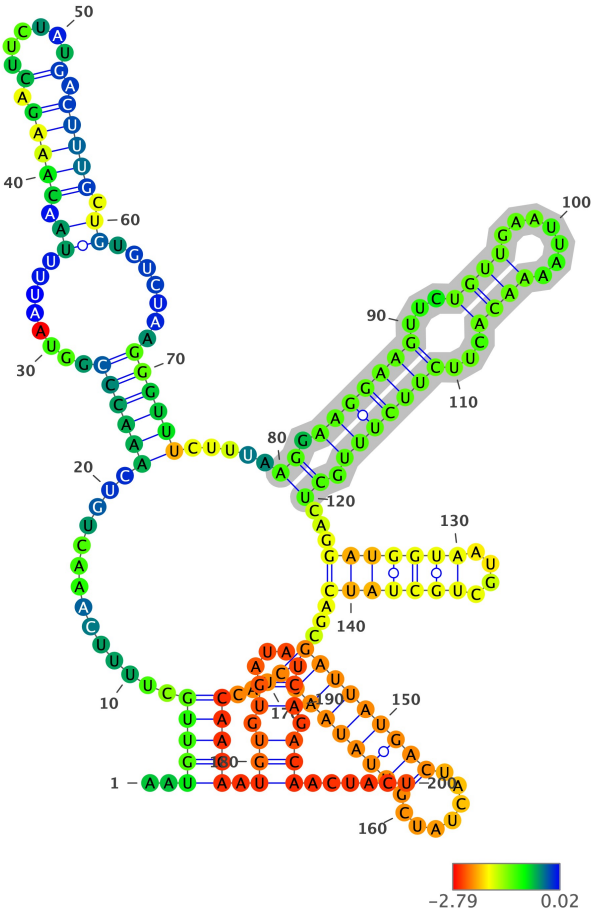
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 262 from nt 14729 to 14769 (nt 80 to 120)

```
5'-AGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCU-3'
5'-((.(((((((...((((.......)))))...)))))))).))-3'
Motif MFE = -10.6; z-score = -2.05; ED = 1.6
```



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

Extracted structure model with flanking nucleotides 14650 to 14849 (motif highlighted in silver):

```
5'-AAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUC
UUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACU-3
5'-..(((((.............((((((........((.(((((.(......).)))))).)).......))))))).....((.(((((((...((((.......)))))...)
))))))).))...(((((((....)))))))...(((((((((.......)))))))))...)))))).(((.((....)).))).......-3'
MFE = -42.4; z-score = -1.29; ED = 33.66
```

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(+)

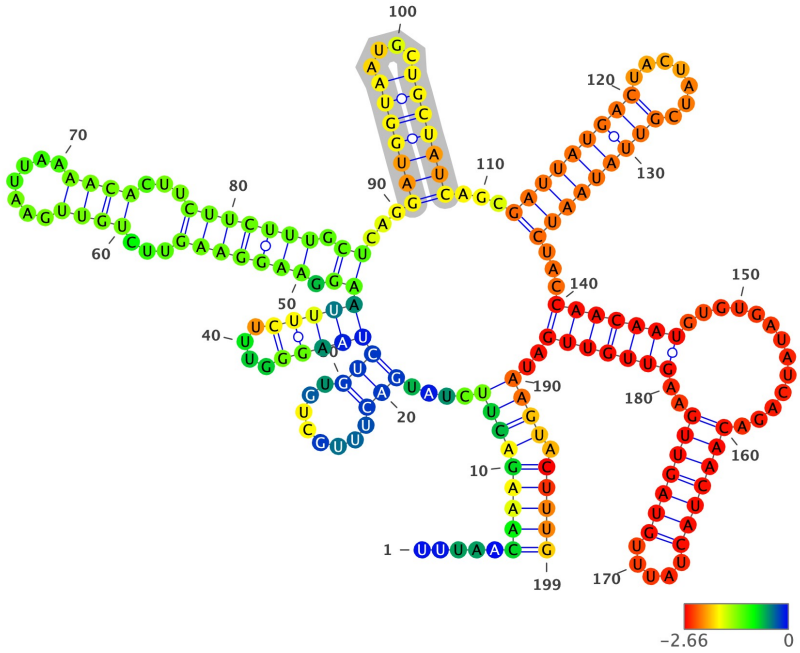
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 14773 to 14790 (nt 91 to 108)

```
5'-GAUGGUAAUGCUGCUAUC-3'
5'-(..((((....)))))..)-3'
Motif MFE = -5.0; z-score = -3.1; ED = 0.39
```



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 14683 to 14881 (motif highlighted in silver):

```
5'-UUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGC
GAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUG-3
5'-.....((((((((((....(((........)))((((....))))))).(((((((...((((........))))...)))))))).))...(((((((....)))))))...
(((((((((.......)))))))))...(((((((.............(((((((.....)))))))..)))))))..)))).)))))-3'
MFE = -49.5; z-score = -2.54; ED = 40.81
```

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

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

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

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

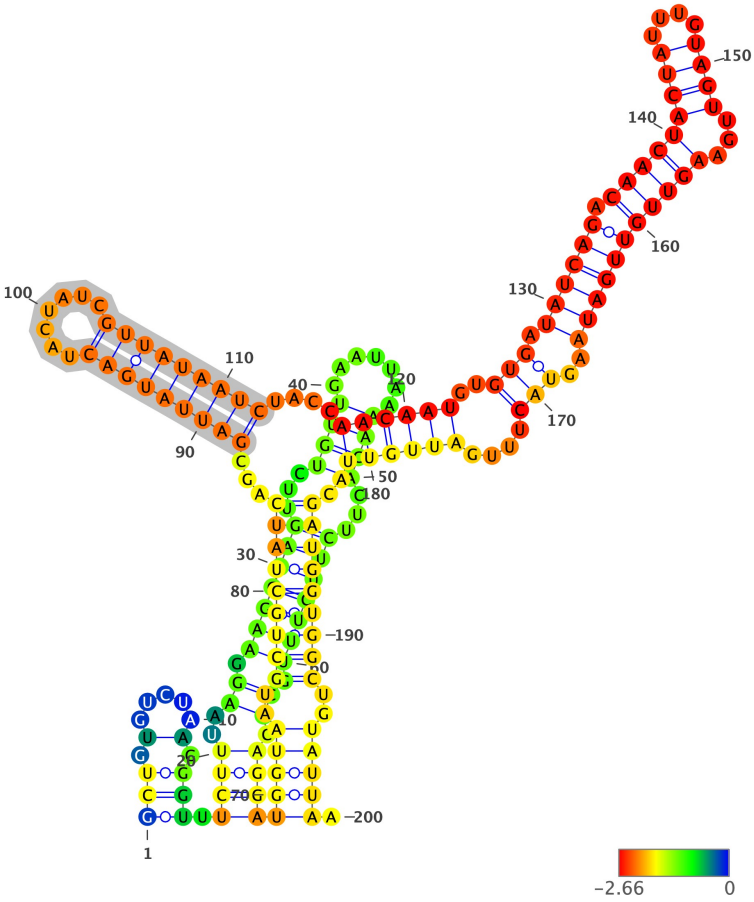
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 264 from nt 14794 to 14818 (nt 88 to 112)

```
5'-GAUUAUGACUACUAUCGUUAUAAUC-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.7; z-score = -4.47; 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 = -2.53; 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(+)

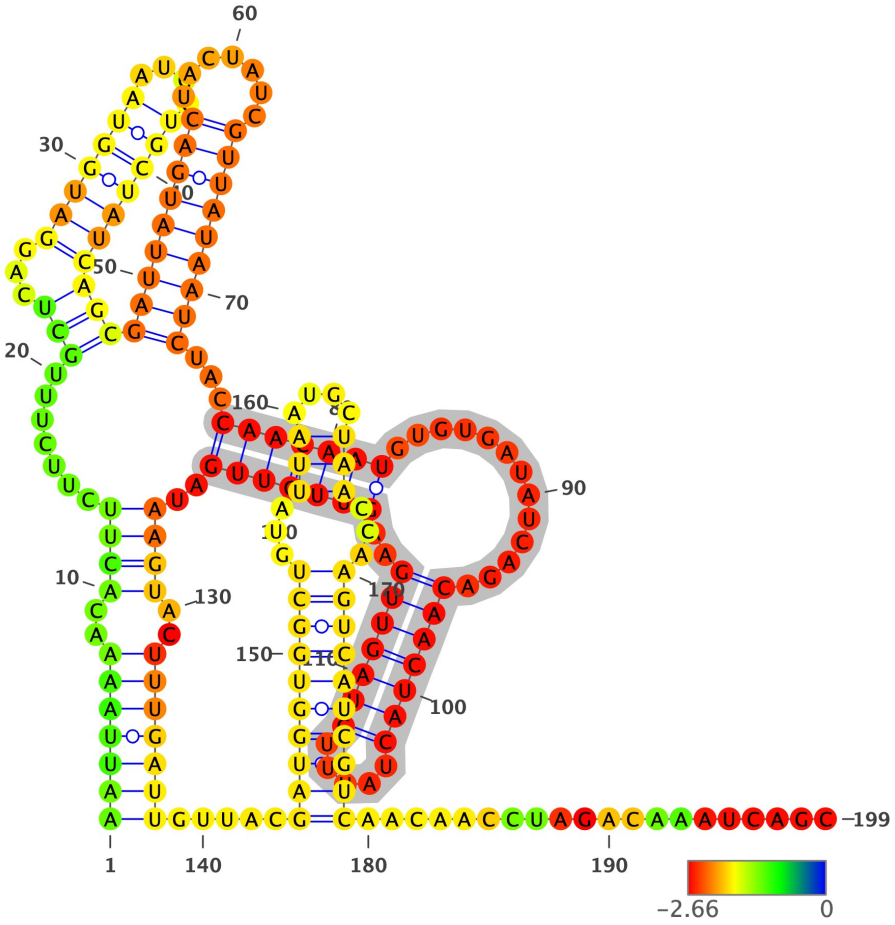
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-CAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUG-3'
5'-(((((((.............(((((((.....)))))))..)))))))-3'
Motif MFE = -11.2; z-score = -2.26; 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 = -2.72; 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(+)

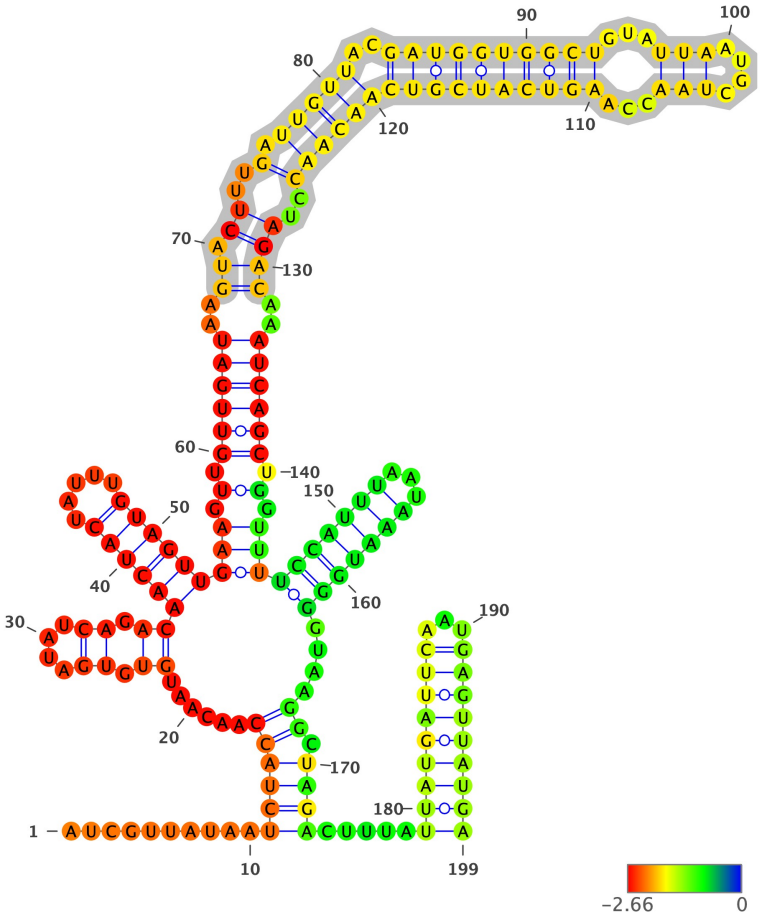
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 266 from nt 14874 to 14937 (nt 68 to 131)

```
5'-GUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGAC-3'
5'-((.....(.((((((..((((((((((...(((....)))...))))))))))))))))....))-3'
Motif MFE = -14.2; z-score = -1.47; 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 = -1.91; ED = 35.5
```

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

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

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

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

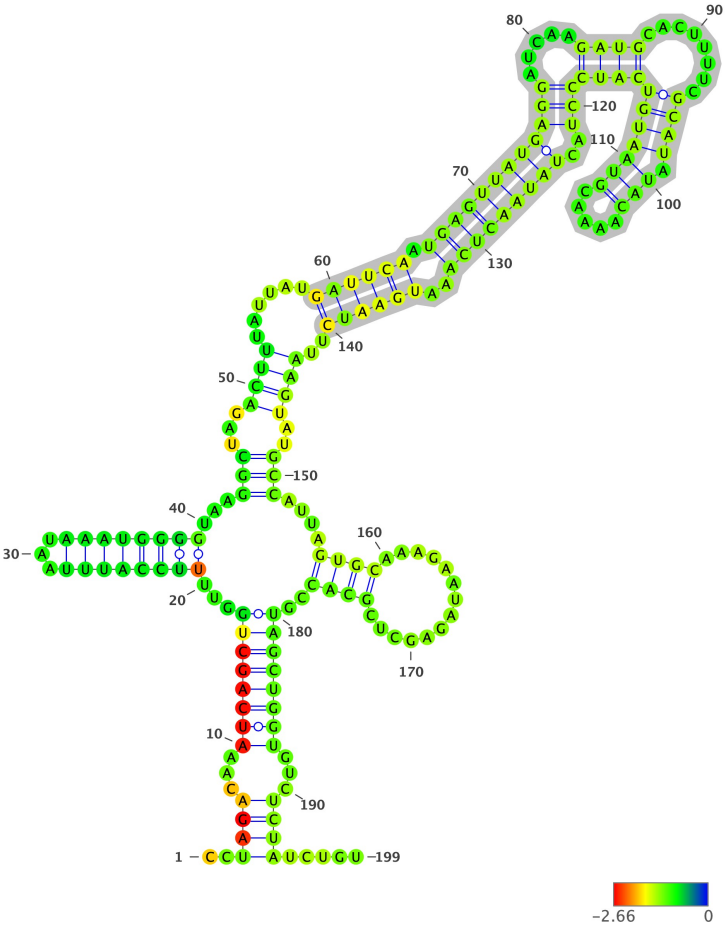
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 267 from nt 14989 to 15070 (nt 59 to 140)

```
5'-GAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUCAAAUGAAUC-3'
5'-(.((((.....(((((((((.....((((........((((.(((.....)))))))))))))))..)))))).....)))).)-3'
Motif MFE = -18.4; z-score = -2.84; 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 = -44.8; z-score = -1.5; ED = 35.55
```

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(+)

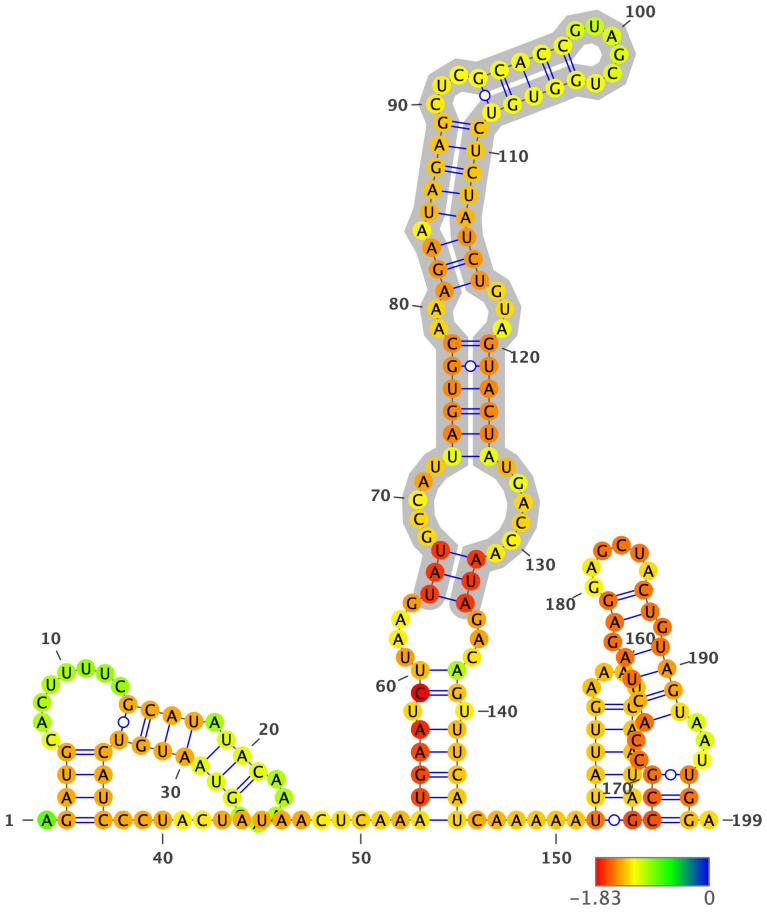
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 268 from nt 15076 to 15145 (nt 65 to 134)

```
5'-UAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUA-3'
5'-(((......(((((..(((.(((((...(((((......))))))))))))...)))))).......)))-3'
Motif MFE = -20.0; z-score = -2.08; 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 = -0.62; ED = 34.9
```

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(+)

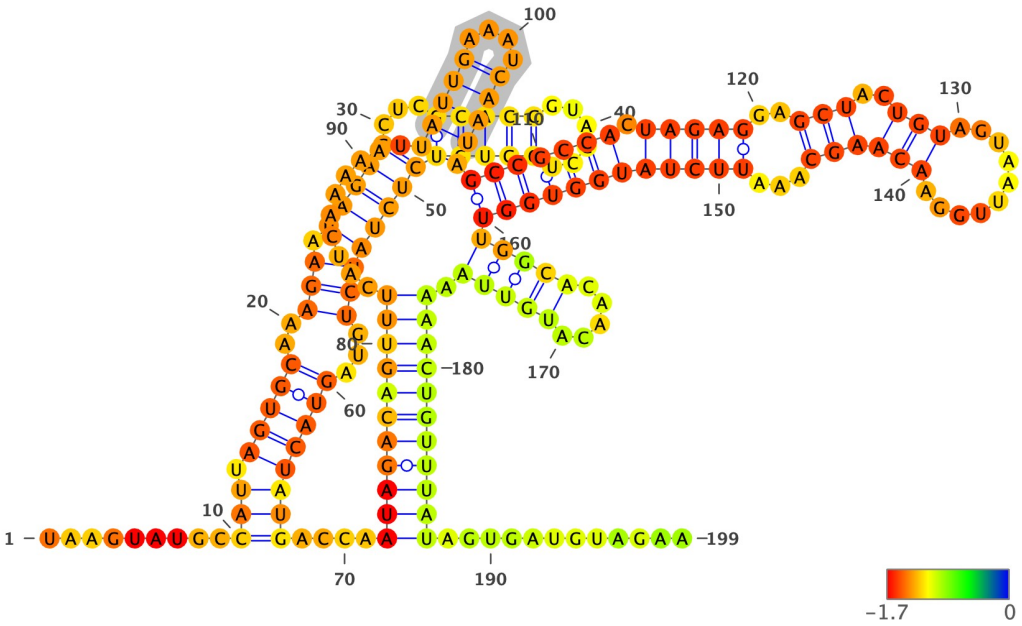
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 269 from nt 15165 to 15176 (nt 94 to 105)

```
5'-AUUGAAAUCAAU-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.83
```



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

Extracted structure model with flanking nucleotides 15072 to 15270 (motif highlighted in silver):

```
5'-UAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGC
CACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAA-3
5'-.........(((.(((((..(((.(((((...(((((......)))))))))))))...))))))))....((((((((((.........(((((....)))))(((((
((.(((((..(((..(((.........))))))...))))))))))))(((((.....))))).))))))))))).............-3'
MFE = -49.3; z-score = -2.8; ED = 31.08
```

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

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

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

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

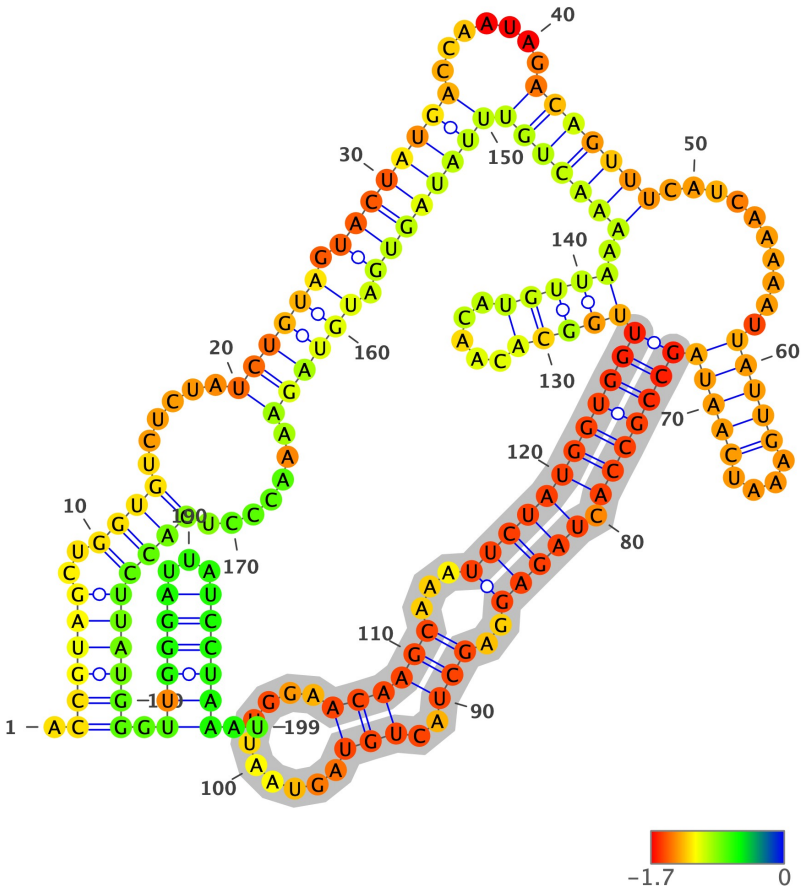
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 270 from nt 15178 to 15231 (nt 73 to 126)

```
5'-GCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGU-3'
5'-(((((((.(((((..(((..(((..........))))))...)))))))))))))-3'
Motif MFE = -16.1; z-score = -2.45; 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 = -2.26; ED = 18.98
```

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(+)

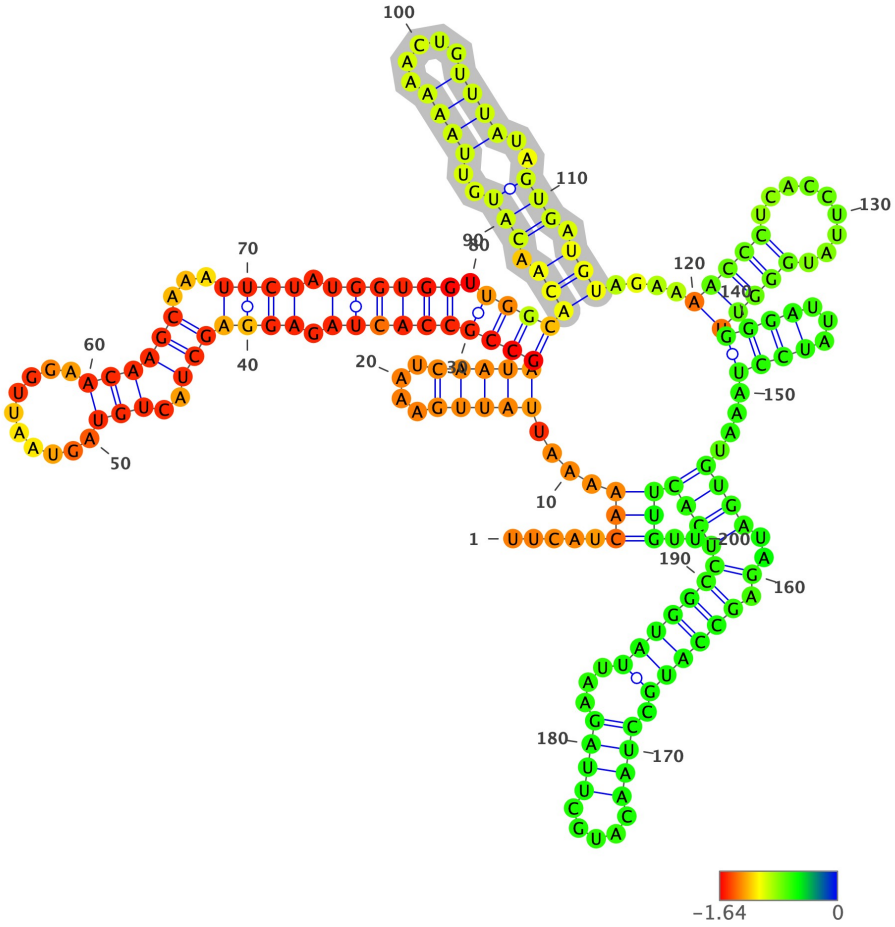
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 271 from nt 15236 to 15266 (nt 85 to 115)

```
5'-ACAACAUGUUAAAAACUGUUUAUAGUGAUGU-3'
5'-(((.........................)))-3'
Motif MFE = -3.5; z-score = -1.13; 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 = -1.28; 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(+)

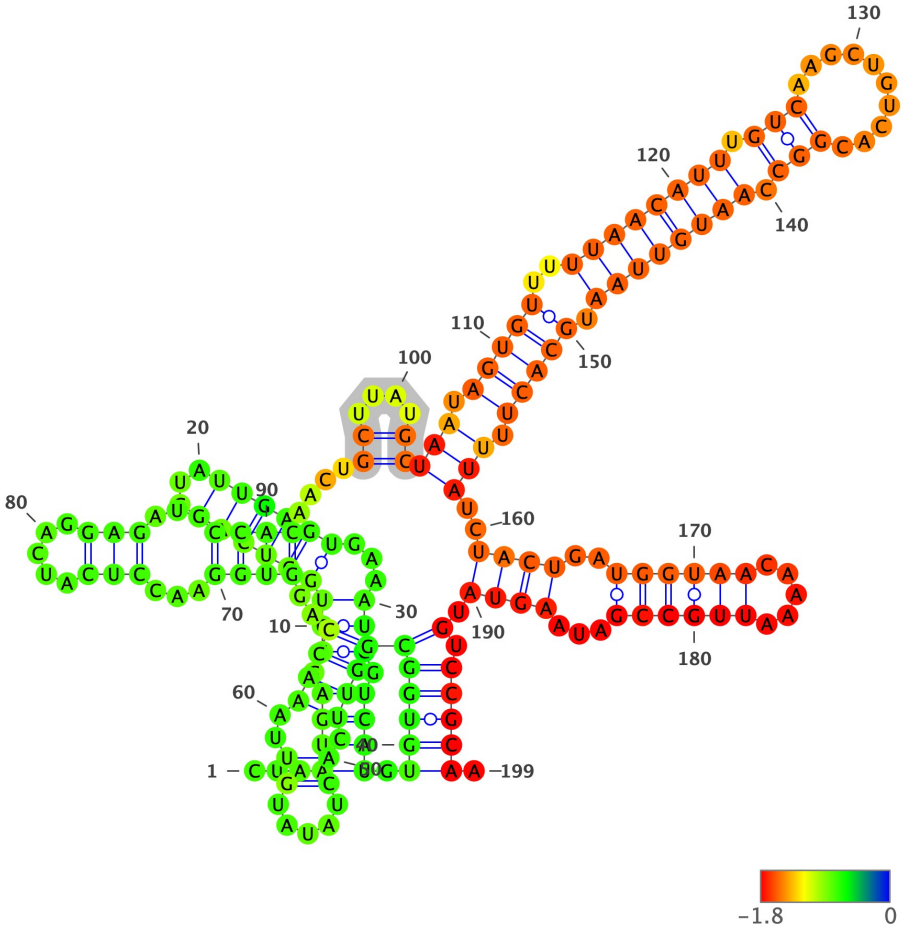
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 272 from nt 15502 to 15509 (nt 96 to 103)

```
5'-GCUUAUGC-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 = -0.74; 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(+)

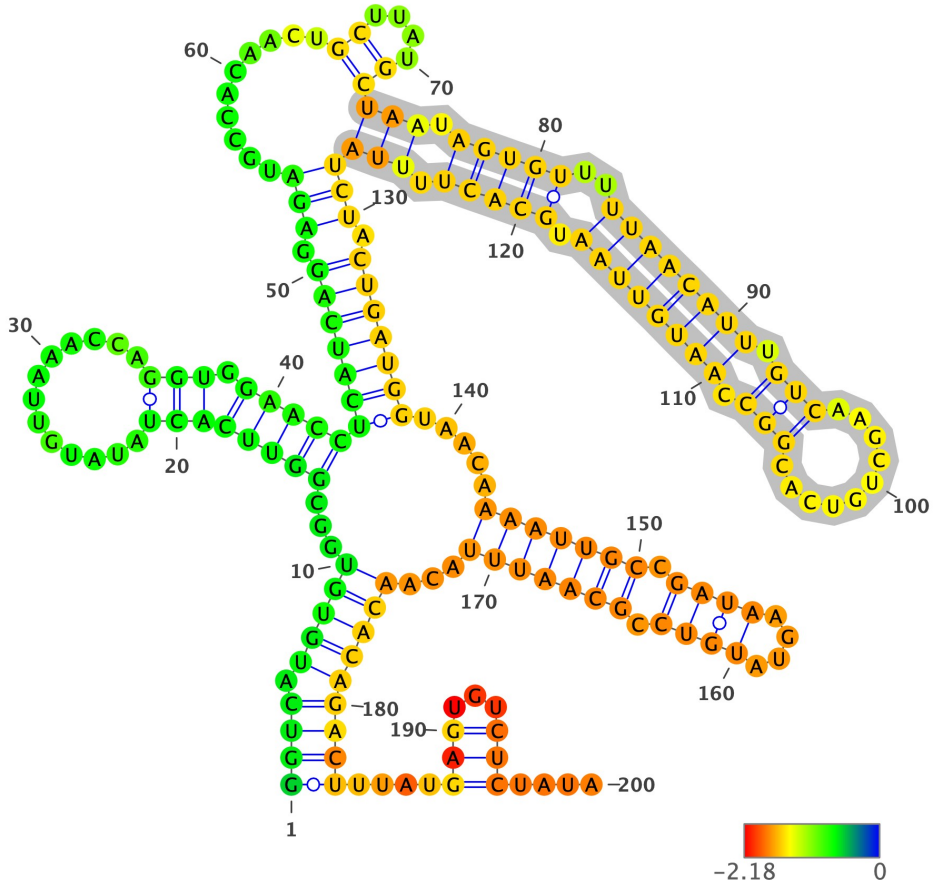
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUA-3'
5'-((..(((((..(((((((((.(((..........))).)))))))).)))))..))-3'
Motif MFE = -13.3; z-score = -3.05; 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 = -1.62; 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(+)

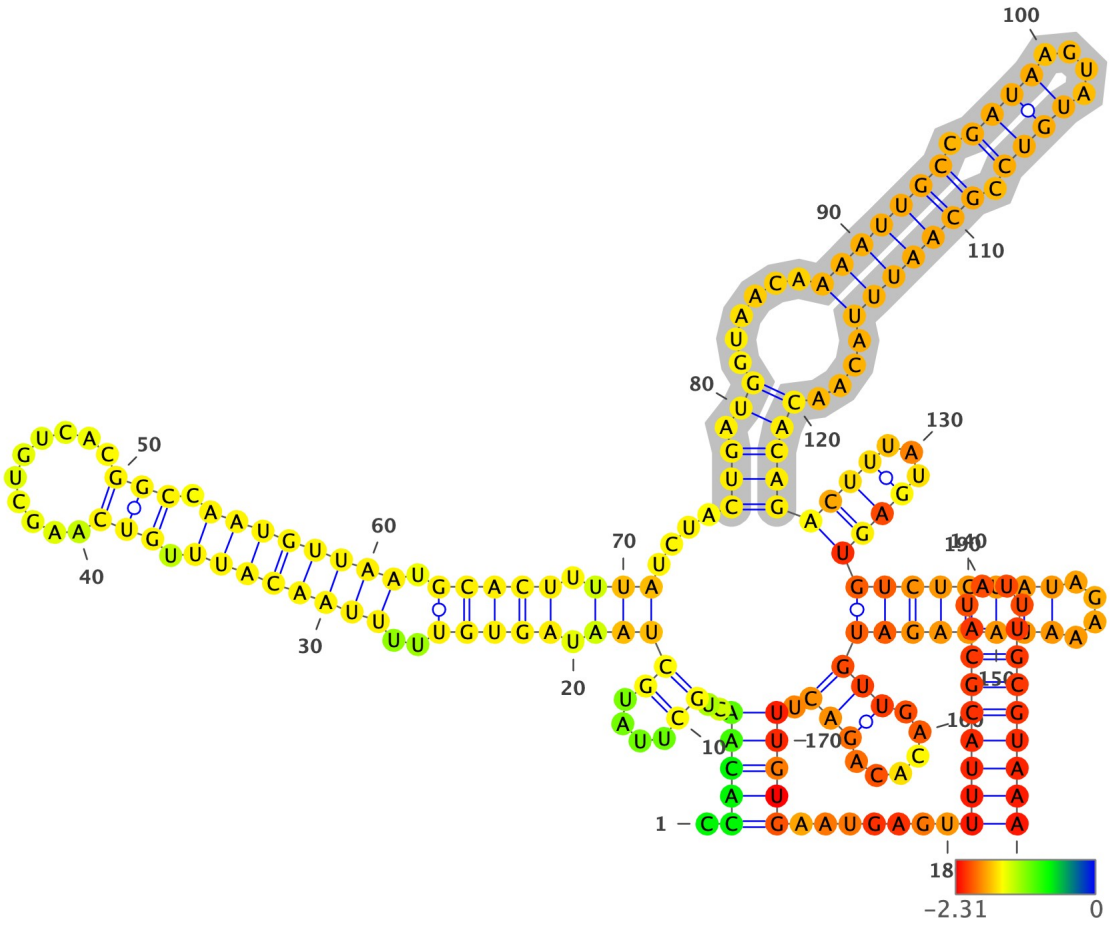
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 274 from nt 15569 to 15617 (nt 76 to 124)

```
5'-CUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAG-3'
5'-(((.((......(((((((.((((....)))).)))))))....)))))-3'
Motif MFE = -9.6; z-score = -1.77; ED = 6.02
```



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

Extracted structure model with flanking nucleotides 15494 to 15693 (motif highlighted in silver):

```
5'-CCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCA
AUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAA-3
5'-.(((((..((....))(((.(((((..((((((((.(((..........))).)))))))).))))).)))....(((.((......(((((((.((((....)))).)))
)))).....)))))((((...))))((((((((....))))))))(((......))).)))))........((((((((....))))))))-3'
MFE = -49.0; z-score = -3.26; ED = 24.75
```

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

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

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

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

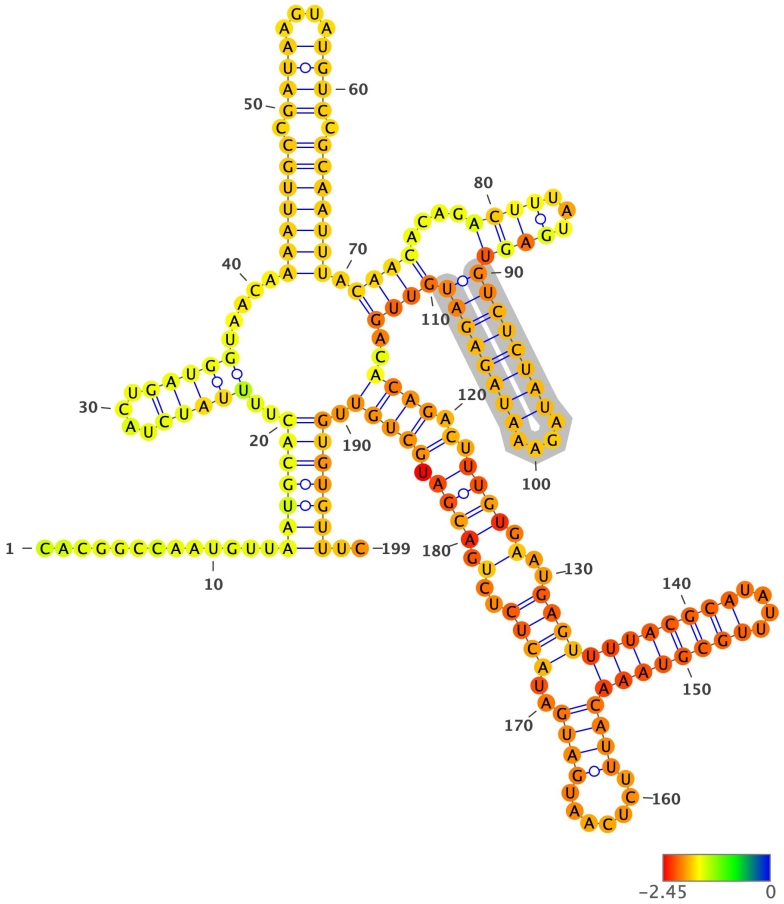
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 275 from nt 15629 to 15648 (nt 90 to 109)

```
5'-GUCUCUAUAGAAAUAGAGAU-3'
5'-((((((((....))))))))-3'
Motif MFE = -7.2; z-score = -5.28; ED = 0.7
```



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

Extracted structure model with flanking nucleotides 15540 to 15738 (motif highlighted in silver):

```
5'-CACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGU
UGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUC-3
5'-.............(((((((..(((((....))))).....(((((((.((((....)))).)))))))).((((....((((...))))((((((((....))))))))))
))..((((.(.((((.(..((((((((((((....))))))))((((.......))))..))))..).)))).))))).)))))))..-3'
MFE = -44.7; z-score = -1.3; ED = 54.61
```

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(+)

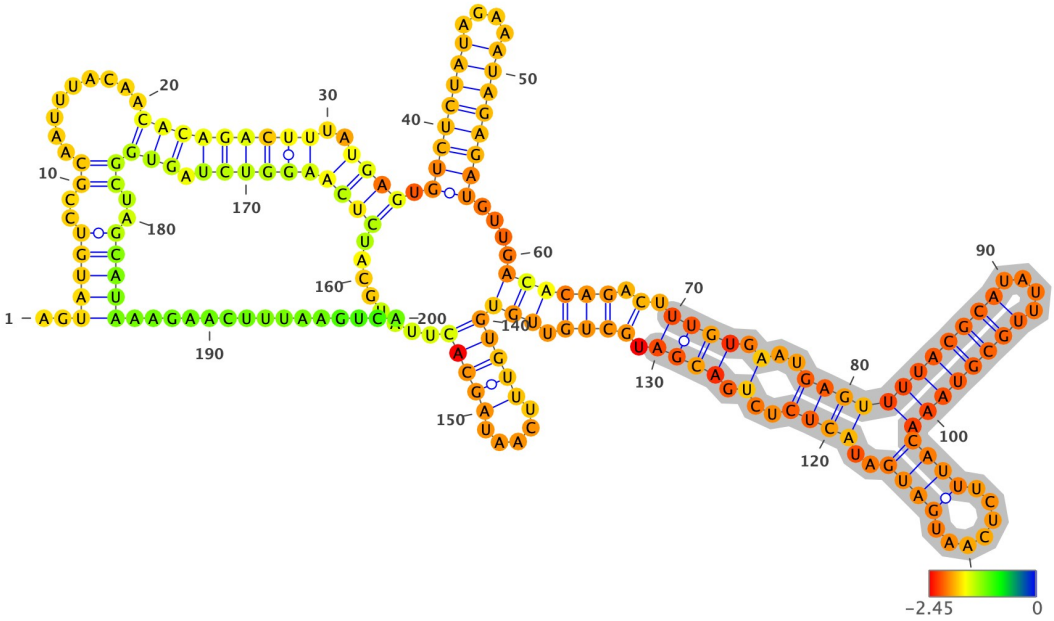
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 15662 to 15722 (nt 70 to 130)

```
5'-UUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGA-3'
5'-((......((..((((((((....))))))))...................))......))-3'
Motif MFE = -13.7; z-score = -2.36; ED = 8.57
```



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 15593 to 15792 (motif highlighted in silver):

```
5'-AGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAA
UGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCA-3
5'-..(((((..((.........(((((((((..((((.((((((((....))))))))....((((((.(.((((.(..((((((((((((....))))))))((((......
.))))..))))..).)))).)))).)))(((((.....)))))........))))))))))).)))))..)))))................-3'
MFE = -46.0; z-score = -2.69; ED = 45.56
```

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

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

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

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

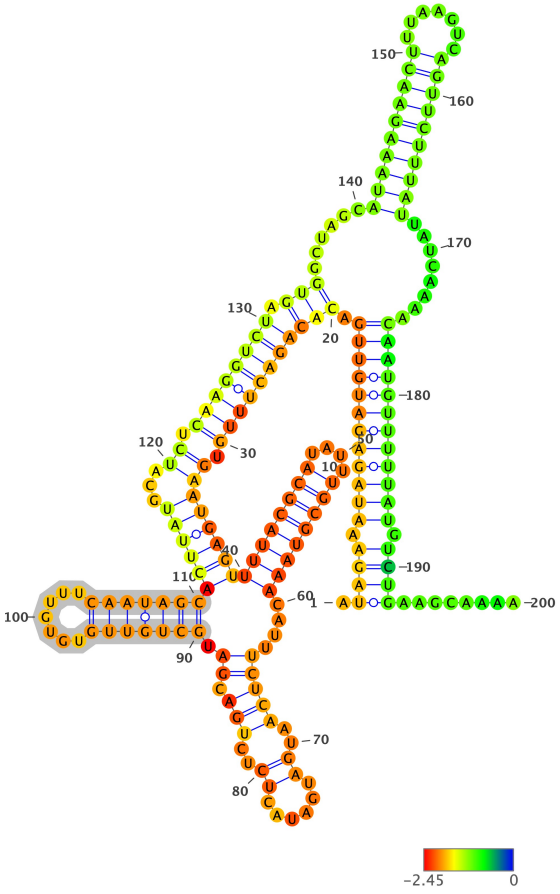
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 277 from nt 15724 to 15744 (nt 90 to 110)

```
5'-GCUGUUGUGUGUUUCAAUAGC-3'
5'-(((((((.......)))))))-3'
Motif MFE = -6.5; z-score = -2.96; ED = 0.17
```



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 15635 to 15834 (motif highlighted in silver):

```
5'-AUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCA
CUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAA-3
5'-.((((.(((((((((((((.((((((((((((.(((((((((((((((((....))))))))....(((((..((......))..))).)).(((((((.......))))))))
)))))...)).)))))))).)))......((((((((((.......))))))))))........))))))))))))).))))........-3'
MFE = -53.5; z-score = -3.45; ED = 15.0
```

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(+)

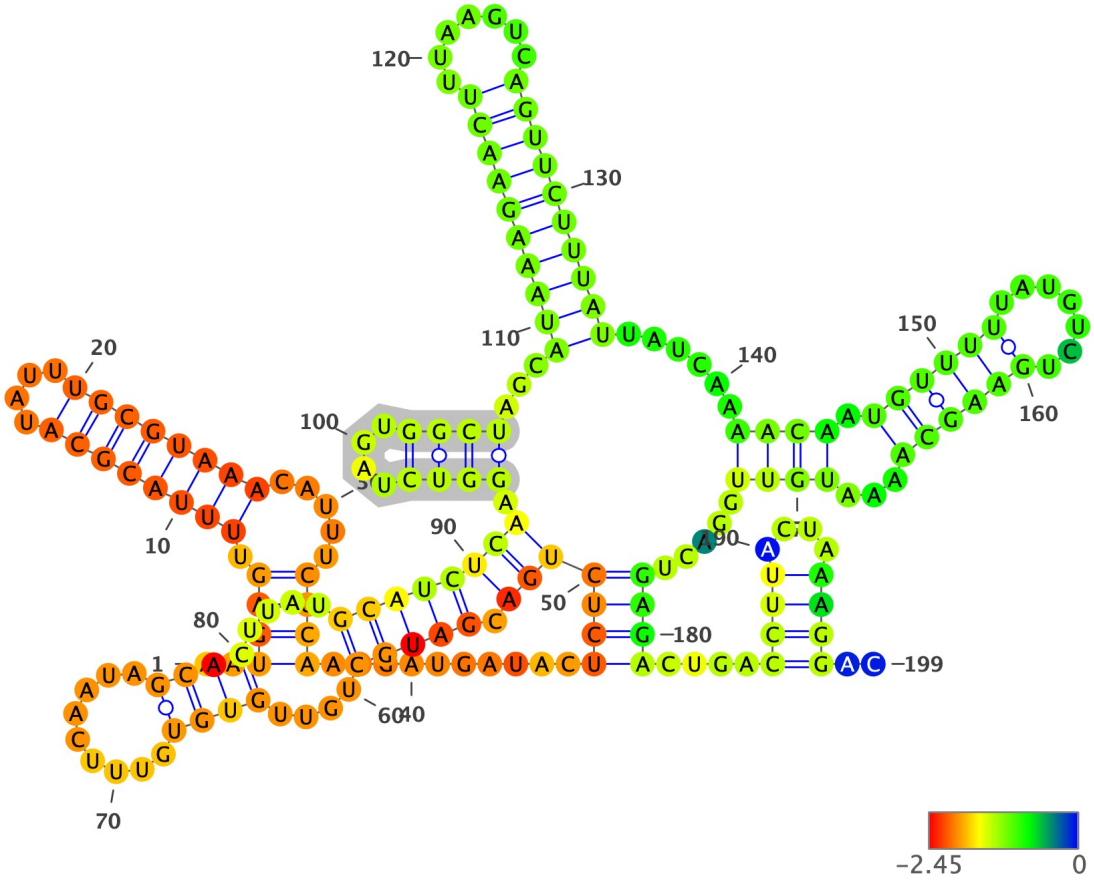
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 15760 to 15771 (nt 94 to 105)

```
5'-GGUCUAGUGGCU-3'
5'-((((....))))-3'
Motif MFE = -2.1; z-score = -4.08; 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 = -1.83; 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(+)

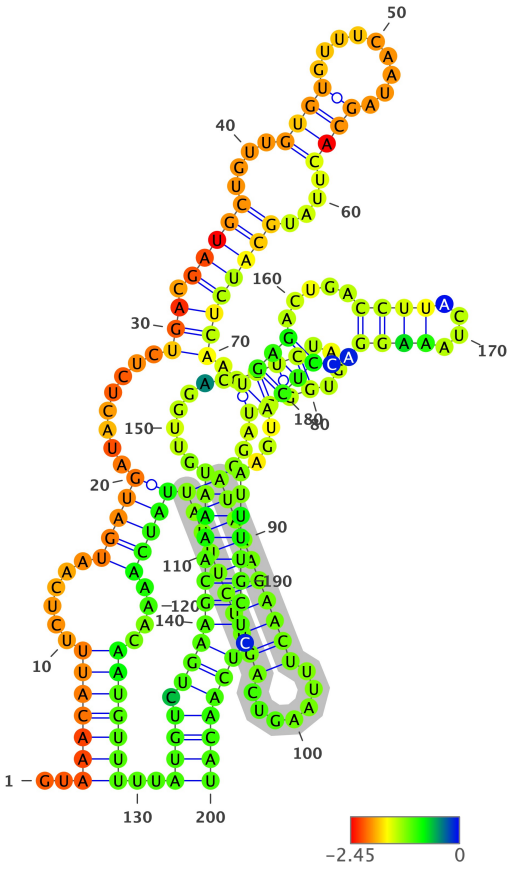
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-AUAAAGAACUUUAAGUCAGUUCUUUAU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -7.5; z-score = -4.23; 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 = -1.55; 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(+)

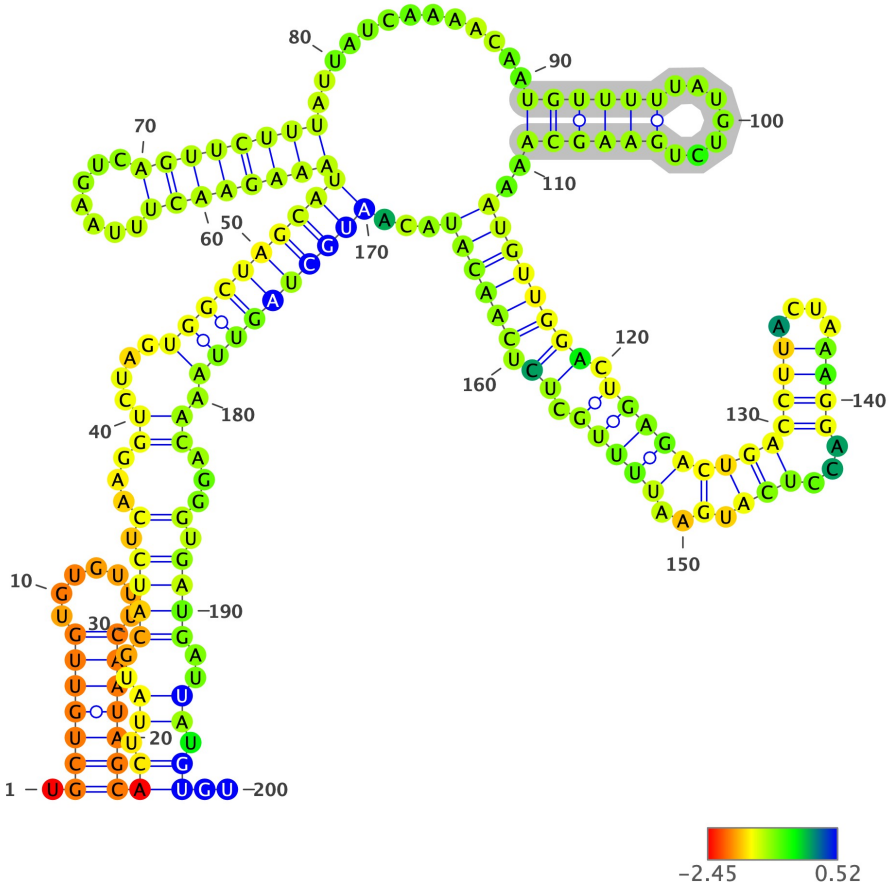
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UGUUUUUAUGUCUGAAGCA-3'
5'-((((((.......))))))-3'
Motif MFE = -1.8; z-score = -1.91; 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 = -1.36; 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(+)

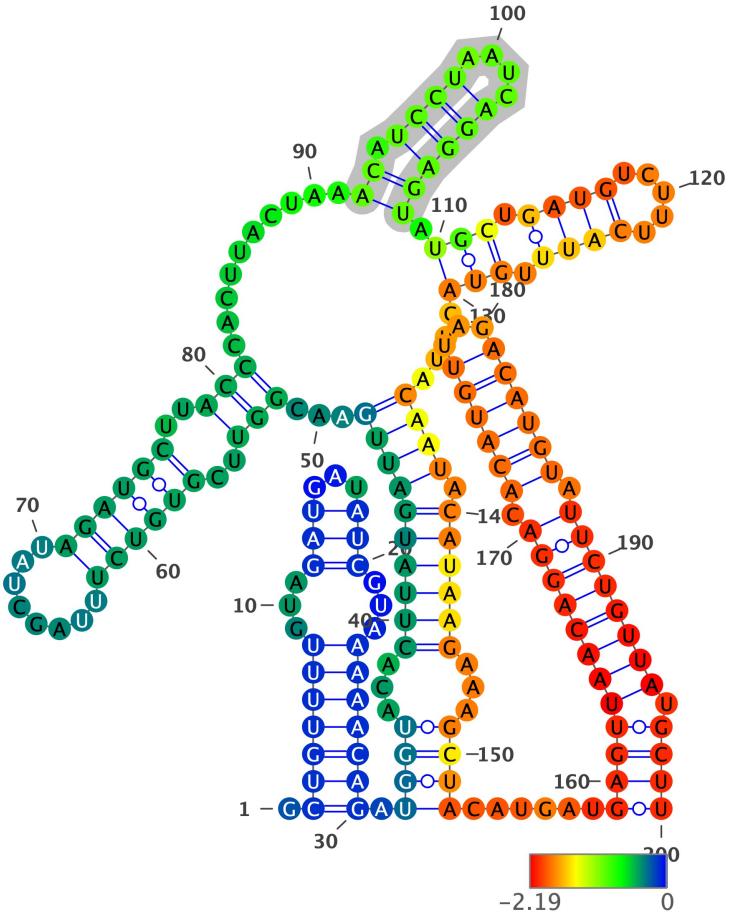
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 281 from nt 16053 to 16069 (nt 92 to 108)

```
5'-ACAUCCUAAUCAGGAGU-3'
5'-((.............))-3'
Motif MFE = -2.8; z-score = -2.48; 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 15962 to 16161 (motif highlighted in silver):

```
5'-GCUGUUUUGUAGAUGAUAUCGUAAAAACAGAUGGUACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUG
CUGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUU-3
5'-.(((((((...(((...)))...))))))).((((...((((((((((...(((..((((((.........))))))..)))..........((.((((....)))))).((
(.((((.....)))).)))....)))).))))))...))))......((((((((((((.((((((...)))))).)))))))).))))-3'
MFE = -46.9; z-score = -1.94; ED = 13.1
```

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 282 from nt 16074 to 16118 (nt 78 to 122)

```
5'-UGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGA-3'
5'-(.(((((((((...((((.......))))...)))))..)))).)-3'
Motif MFE = -6.7; z-score = -1.42; 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 = -1.74; 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(+)

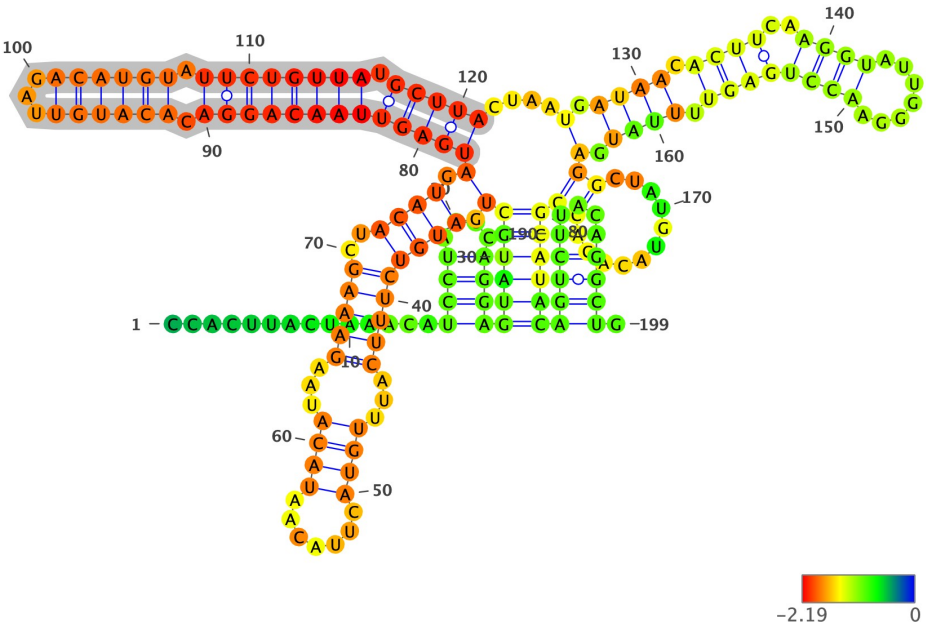
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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

```
5'-UGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUA-3'
5'-(((((((((((((.((((((...)))))).)))))))).)))))-3'
Motif MFE = -16.5; z-score = -4.75; 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 = -1.58; 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(+)

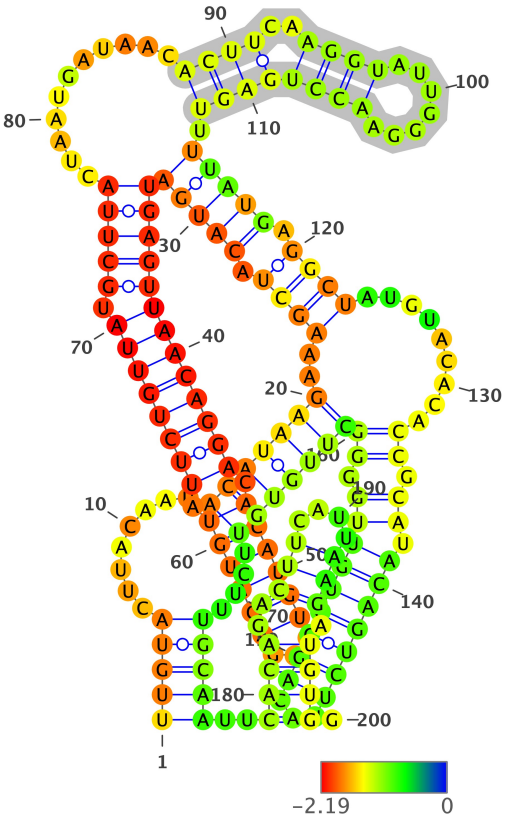
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 284 from nt 16174 to 16198 (nt 88 to 112)

```
5'-ACUUCAAGGUAUUGGGAACCUGAGU-3'
5'-((((..((((.......))))))))-3'
Motif MFE = -3.7; z-score = -0.8; 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 = -1.33; 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(+)

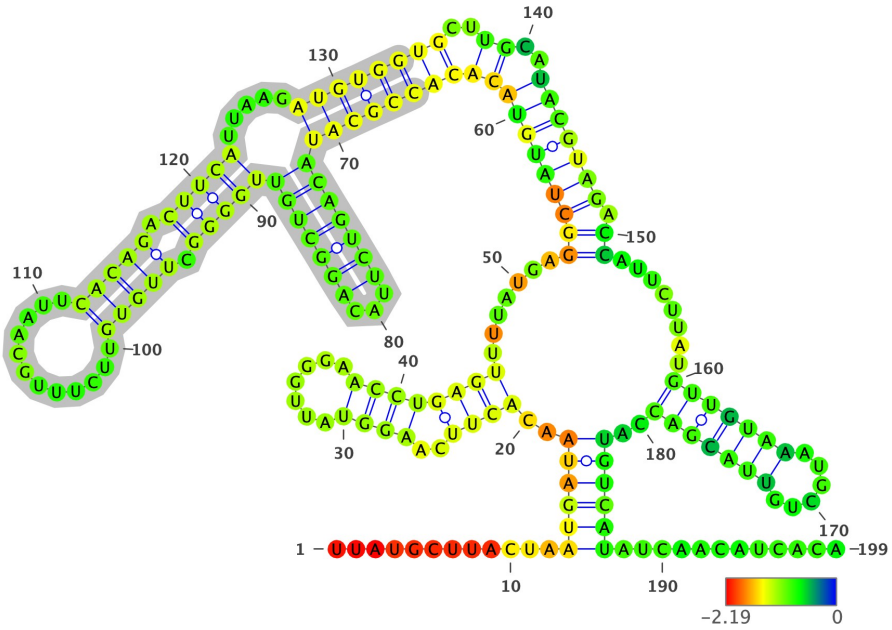
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 285 from nt 16219 to 16286 (nt 66 to 133)

```
5'-CCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUUCACAGACUUCAUUAAGAUGUGG-3'
5'-((((((.................(((((.(((((............)))))).)))))).....))))))-3'
Motif MFE = -18.2; z-score = -1.47; ED = 8.91
```



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 16154 to 16352 (motif highlighted in silver):

```
5'-UUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUU
CACAGACUUCAUUAAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACA-3
5'-............((((((..((((..((((.......))))))))).......(((((((((((((((((((((((...)))))))))))))))))))))))))))(((((.(((((.....
)))))).)))))).....)))))))))..))..)))))))..)).......(((((((.....)))))))..))))))............-3'
MFE = -44.2; z-score = -0.54; ED = 34.39
```

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(+)

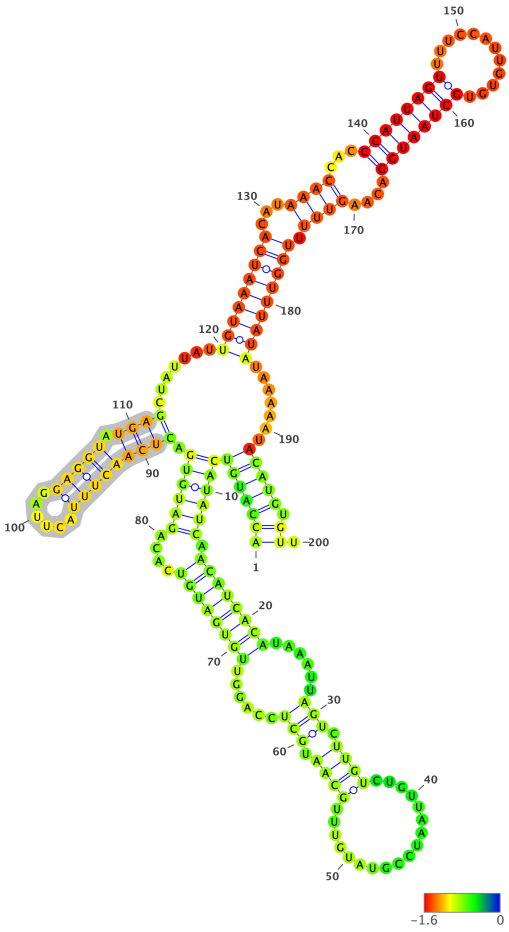
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 16419 to 16441 (nt 89 to 111)

```
5'-UCAACUUUACUUAGGAGGUAUGA-3'
5'-(((((((.....))))))).)))-3'
Motif MFE = -2.5; z-score = -0.72; 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 = -1.38; ED = 16.26
```

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

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

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

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

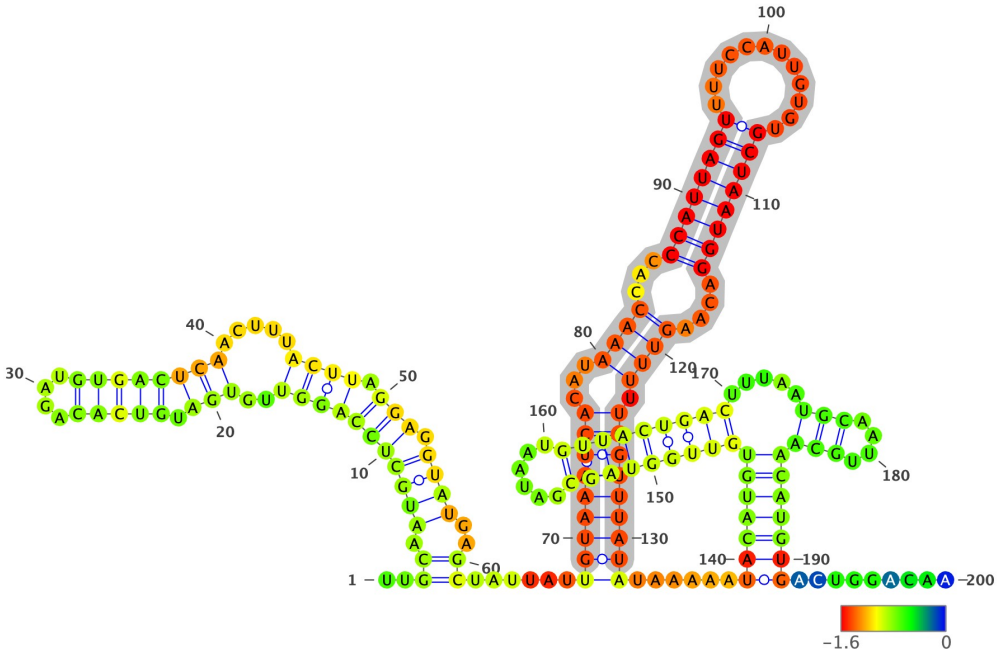
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 287 from nt 16451 to 16513 (nt 69 to 131)

```
5'-GUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAU-3'
5'-((((((((...((((...((((((((.............))))))))....)))).))))))))-3'
Motif MFE = -14.1; z-score = -2.55; 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 = -2.55; 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(+)

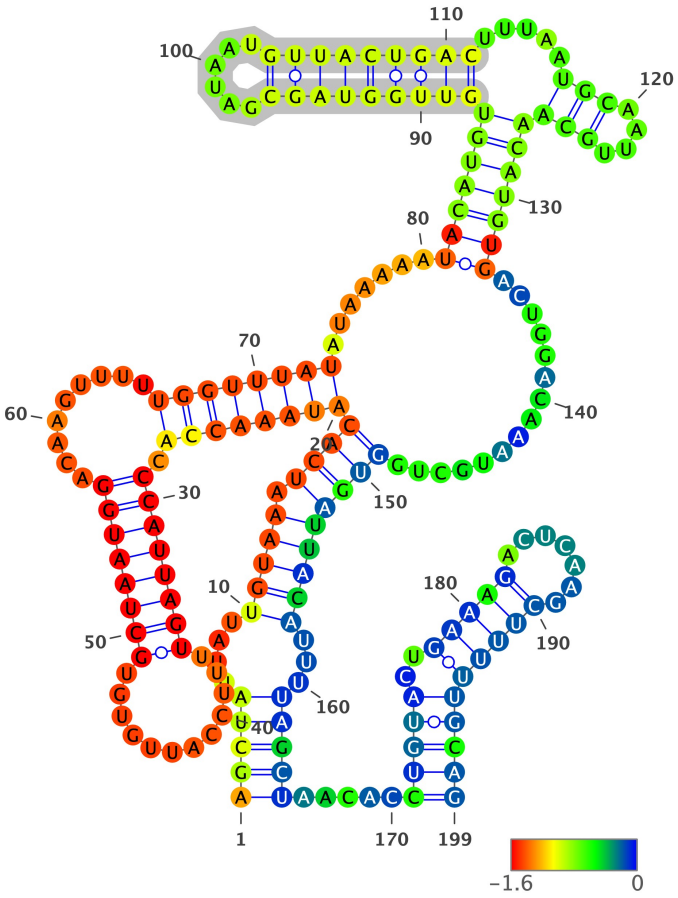
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 288 from nt 16528 to 16551 (nt 88 to 111)

```
5'-GUUGGUAGCGAUAAUGUUACUGAC-3'
5'-(......................)-3'
Motif MFE = -8.0; z-score = -3.9; 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 = -2.11; 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(+)

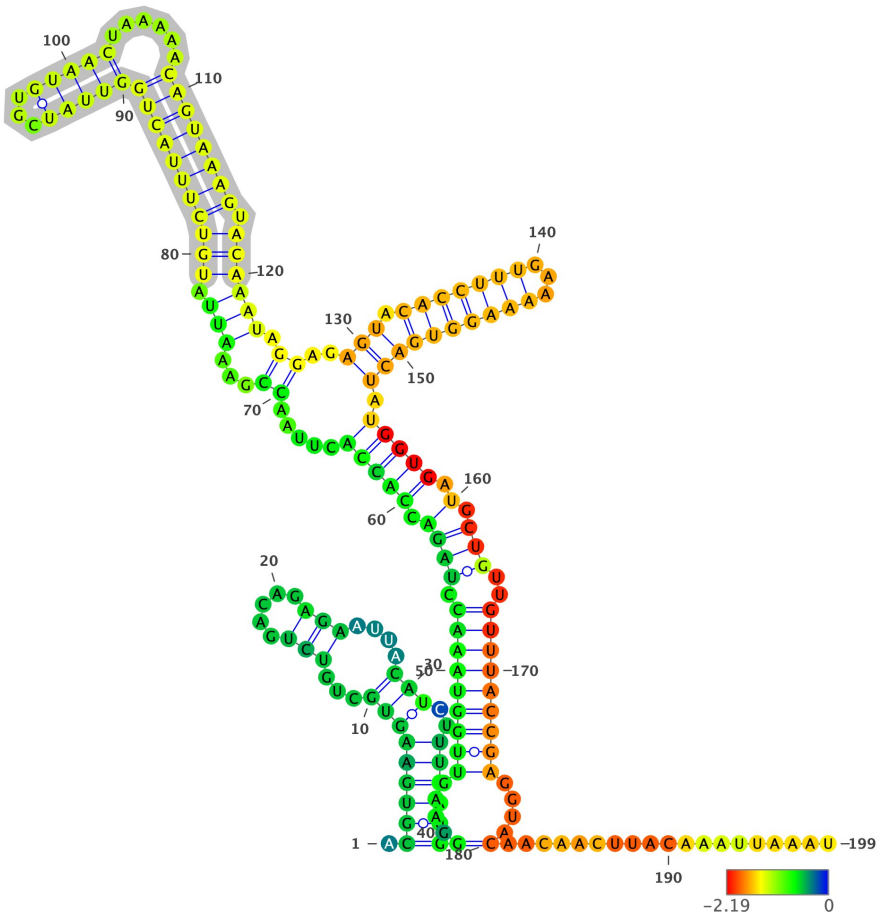
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 289 from nt 16776 to 16817 (nt 79 to 120)

```
5'-UGUCUUUACUGGUUAUCGUGUAACUAAAAACAGUAAAGUACA-3'
5'-(((((((((((((((...)))))......)))))))).)))-3'
Motif MFE = -9.5; z-score = -2.04; 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 = -1.15; 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(+)

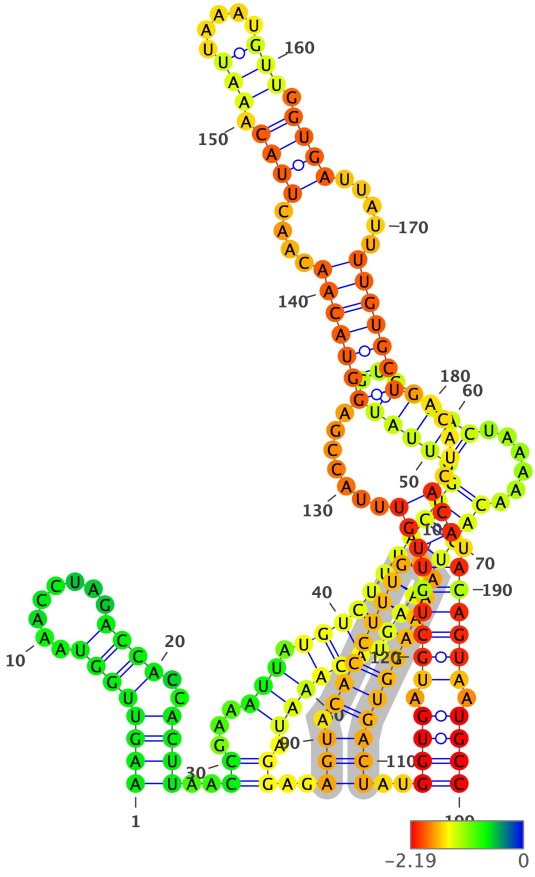
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 290 from nt 16826 to 16849 (nt 88 to 111)

```
5'-AGUACACCUUUGAAAAAGGUGACU-3'
5'-(((.(((((((...))))))))))-3'
Motif MFE = -8.0; z-score = -4.65; 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 = -1.41; 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(+)

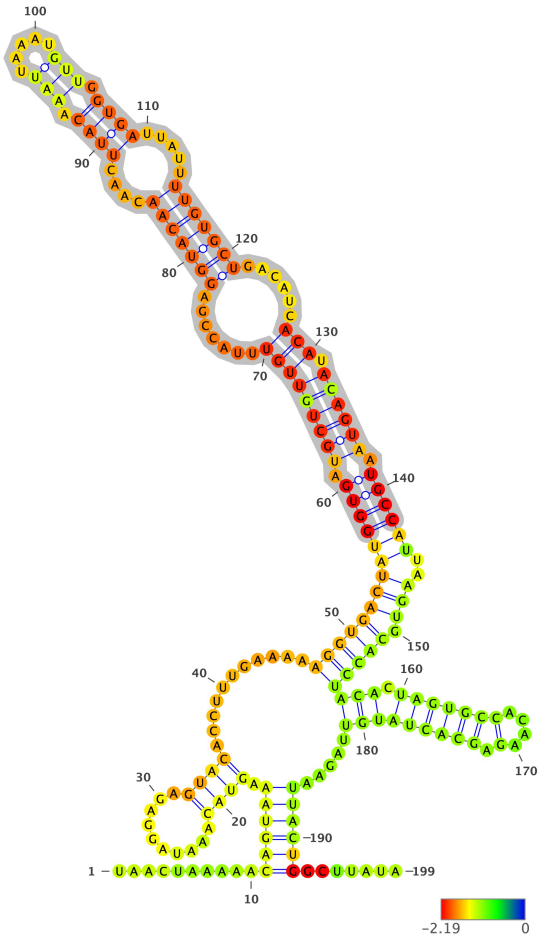
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 291 from nt 16852 to 16937 (nt 57 to 142)

```
5'-GGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCC-3'
5'-((((..(((.((((.......(((((((....((((.............))))).....)))))))......))).).)))..))))-3'
Motif MFE = -18.3; z-score = -1.12; 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 = -2.4; 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(+)

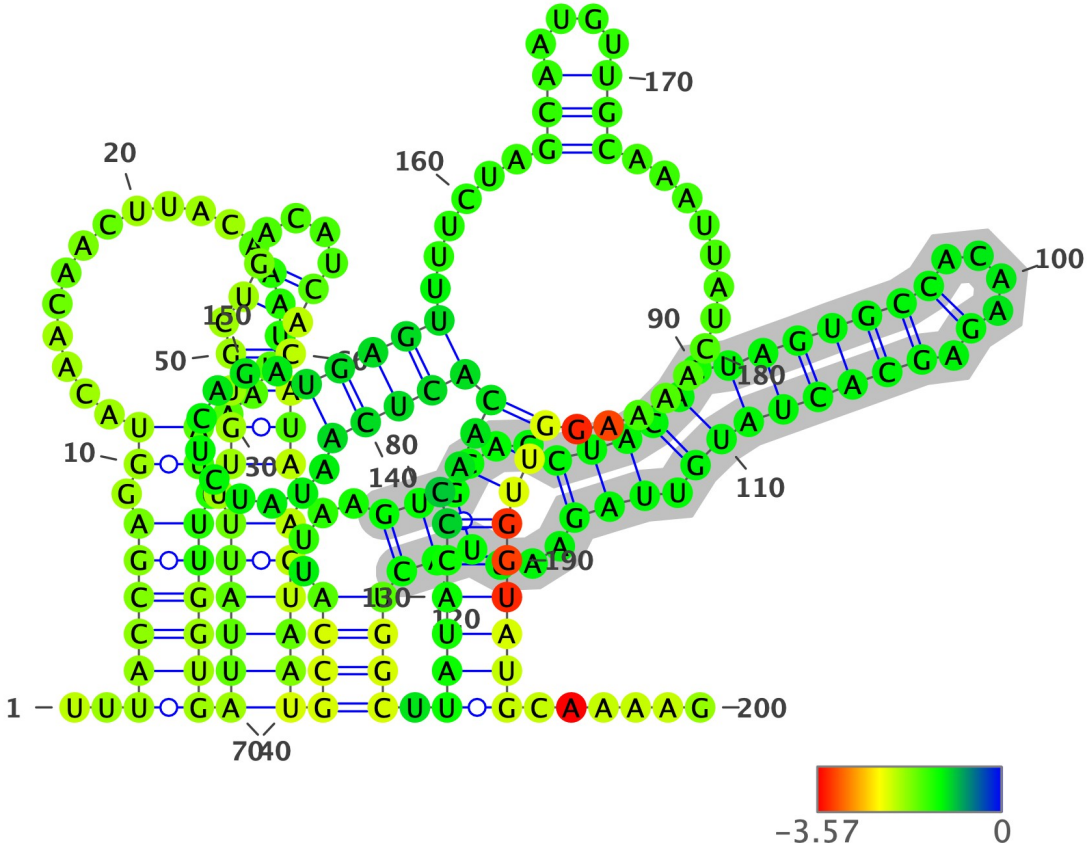
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 292 from nt 16943 to 16985 (nt 79 to 121)

```
5'-GUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUAC-3'
5'-(((...(((((.(((((((....).))))))))).)))...)))-3'
Motif MFE = -9.2; z-score = -2.14; 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 = -0.12; 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(+)

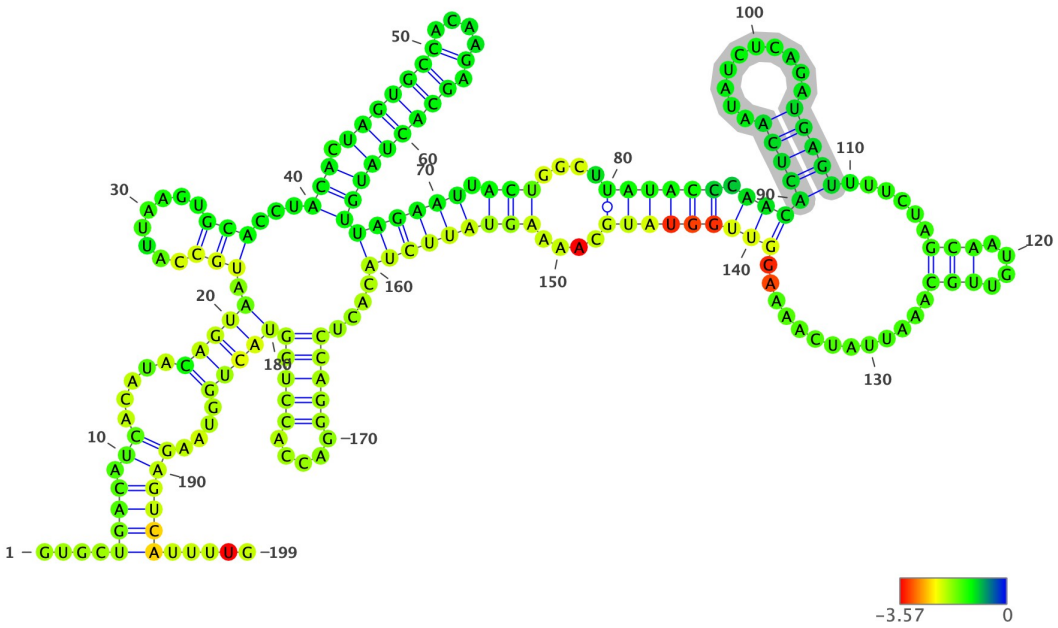
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 293 from nt 17001 to 17020 (nt 90 to 109)

```
5'-ACUCAAUAUCUCAGAUGAGU-3'
5'-(((((..........)))))-3'
Motif MFE = -2.1; z-score = -2.27; ED = 2.73
```



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

Extracted structure model with flanking nucleotides 16912 to 17110 (motif highlighted in silver):

```
5'-GUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUU
UCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUG-3
5'-....((((.((.....(((((.(((........)))...(((.(((((((....).)))))))))((((((.(((....((((((.((((((((..........)))))..
....(((....)))............)))))))))....)))))))))....(((((.....))))))))))....))))))).....-3'
MFE = -43.0; z-score = -1.06; ED = 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(+)

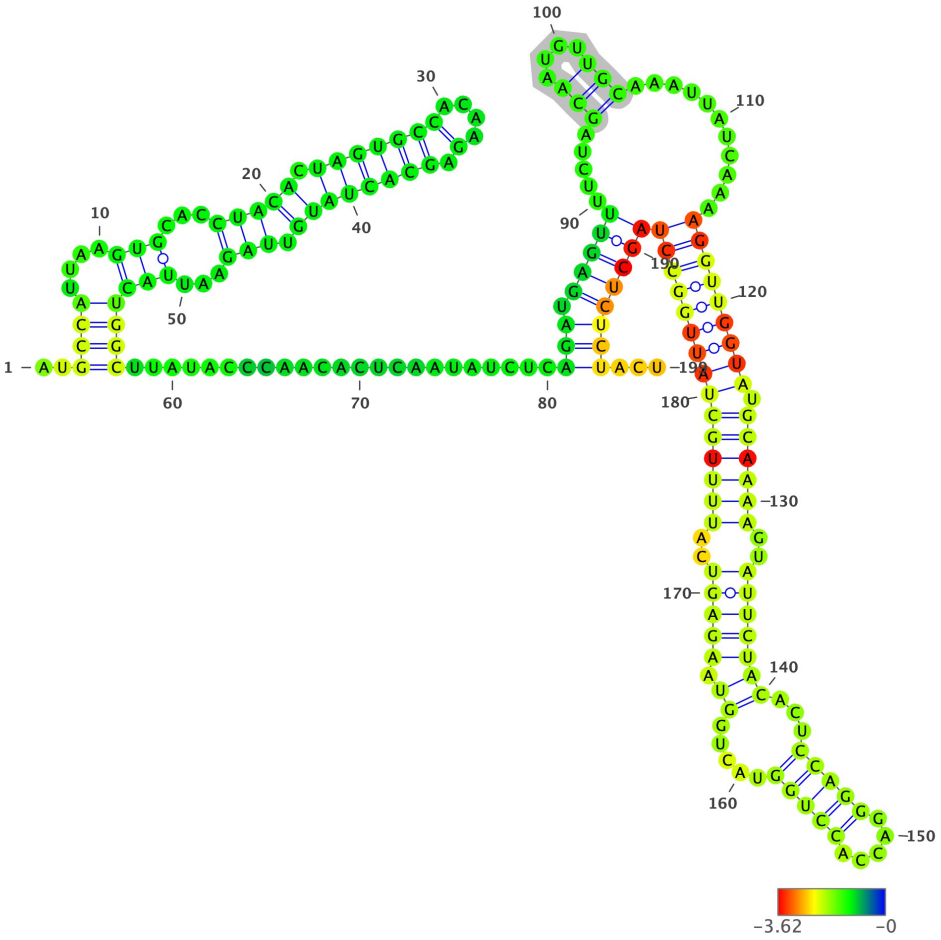
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 294 from nt 17027 to 17036 (nt 95 to 104)

```
5'-GCAAUGUUGC-3'
5'-(((....)))-3'
Motif MFE = -0.4; z-score = -2.76; 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 = -2.53; 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(+)

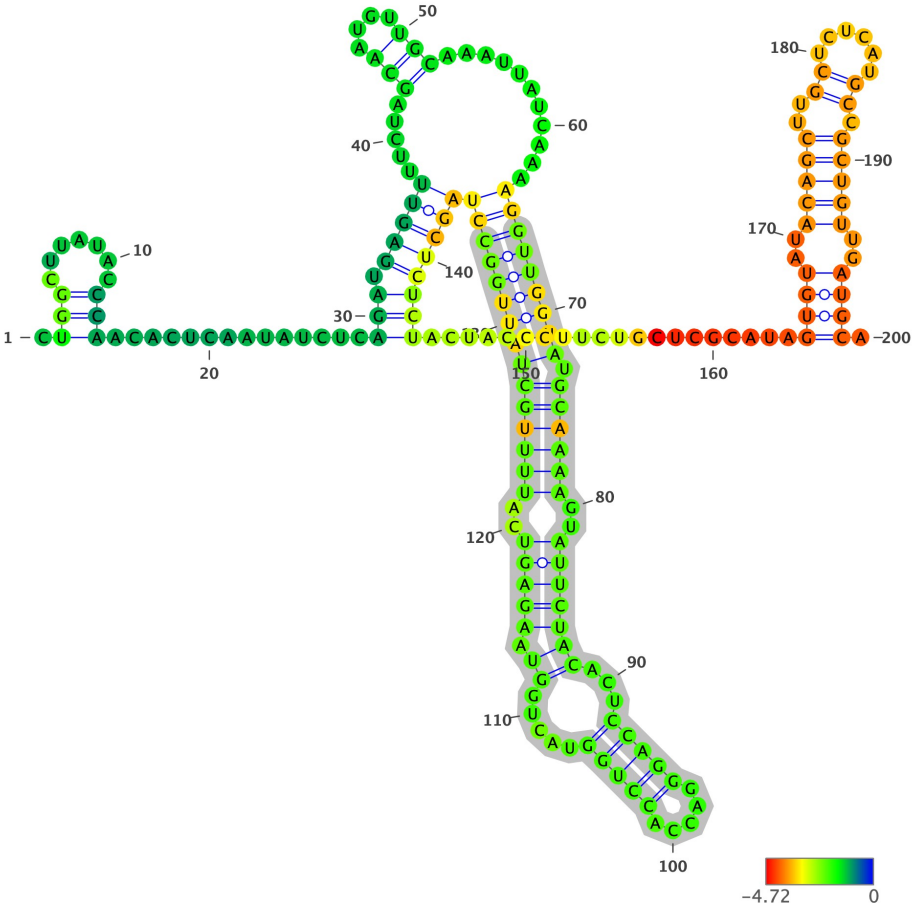
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 295 from nt 17050 to 17118 (nt 66 to 134)

```
5'-GUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUGCUAUUGGC-3'
5'-(((...(.((.(((..(((((((...(((((.....)))))).....)).)))))..))).)))...)))-3'
Motif MFE = -22.3; z-score = -2.85; 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 = -1.1; 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(+)

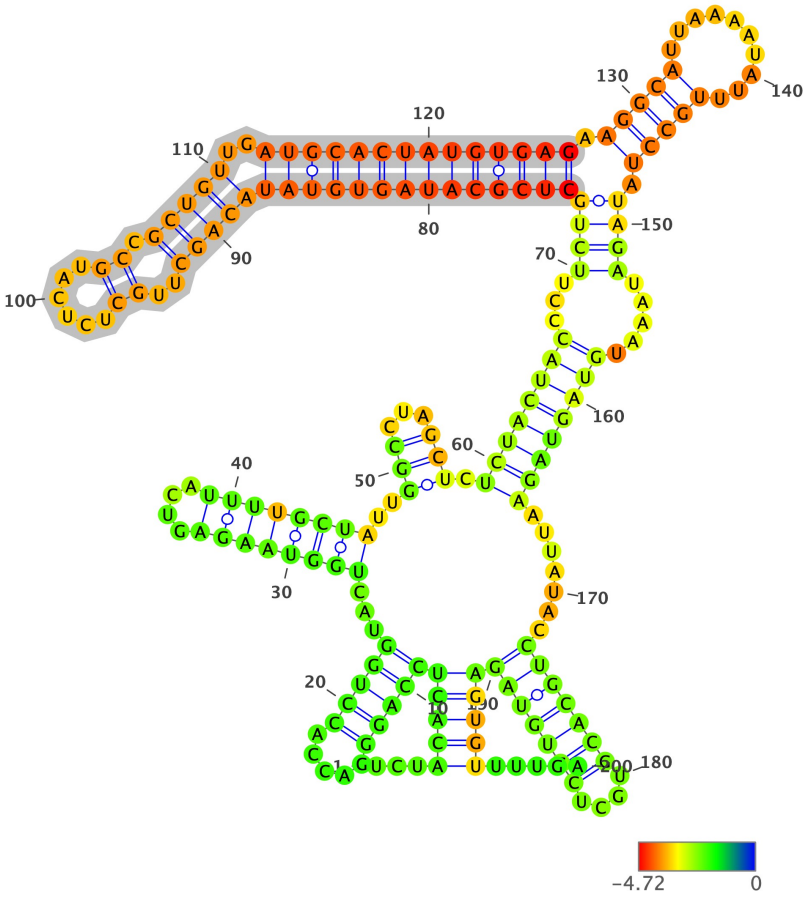
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 296 from nt 17141 to 17193 (nt 74 to 126)

```
5'-CUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAG-3'
5'-(((((((((((((((((((..((......)).)))))..))))))))))))))-3'
Motif MFE = -27.7; z-score = -5.42; 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(+)

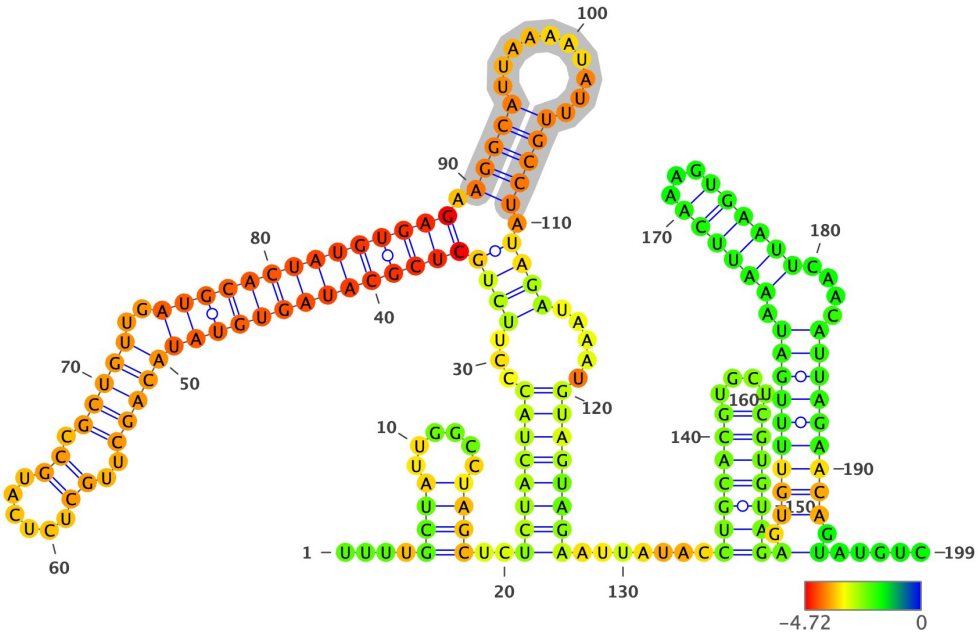
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 297 from nt 17195 to 17214 (nt 90 to 109)

```
5'-AGGCAUUAAAAUAUUUGCCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.1; z-score = -4.45; 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 = -5.39; 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(+)

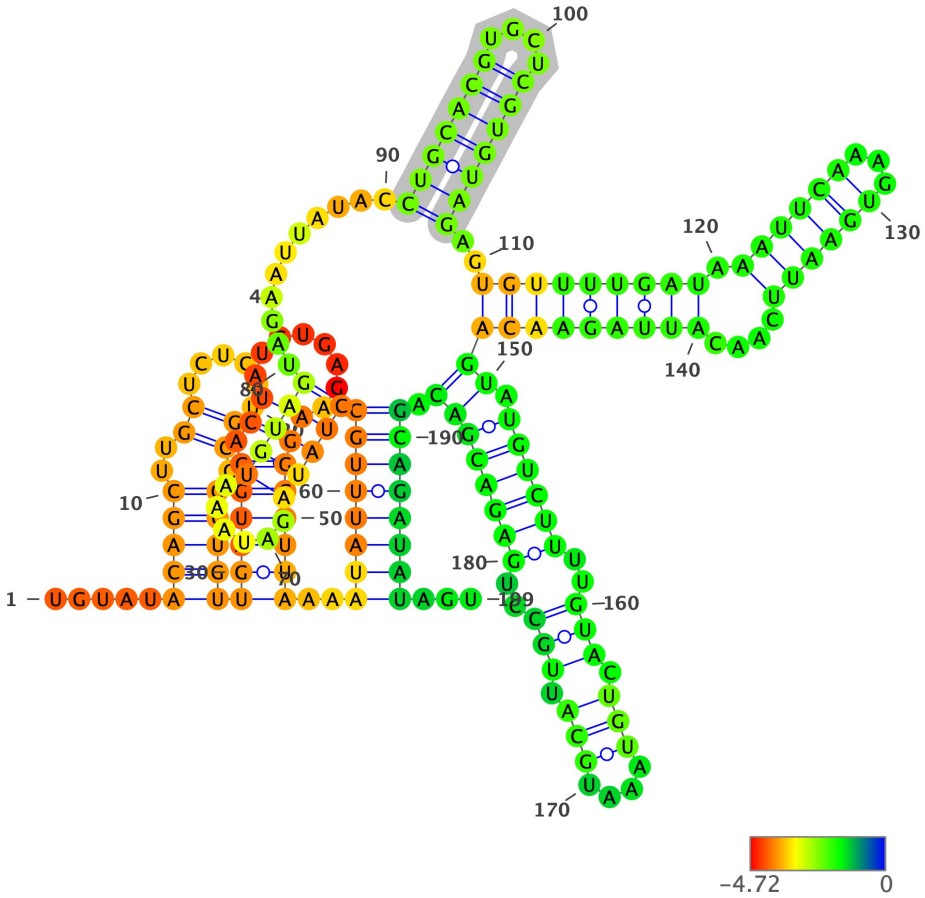
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 298 from nt 17240 to 17257 (nt 91 to 108)

```
5'-CUGCACGUGCUCGUGUAG-3'
5'-(((((((....)))))))-3'
Motif MFE = -8.3; z-score = -3.36; ED = 0.22
```



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

Extracted structure model with flanking nucleotides 17150 to 17348 (motif highlighted in silver):

```
5'-UGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGU
GUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGU-3
5'-.....(((((..((......)).)))))((((((.((........))))))))..((((((((((((((......)))))...........(((((((....)))))))..(
((((((((.((((((...))))))....)))))))))((.((((((..(((.(((....))).))).)))))))).))))))))...-3'
MFE = -50.1; z-score = -1.91; ED = 56.56
```

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(+)

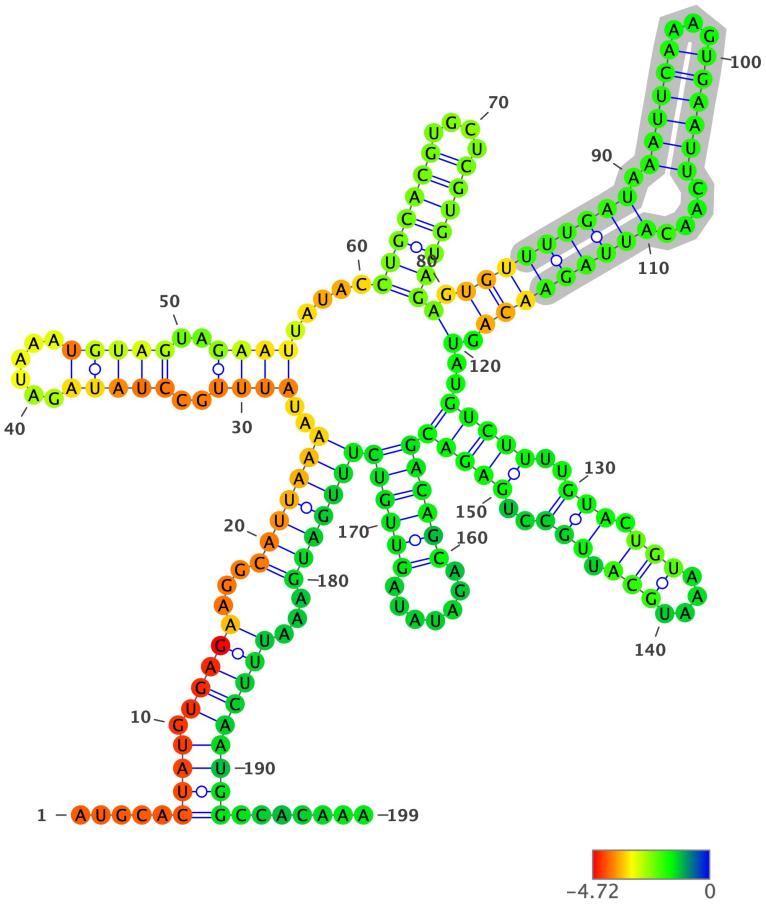
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 299 from nt 17263 to 17294 (nt 84 to 115)

```
5'-UUUGAUAAAUUCAAAGUGAAUUCAACAUUAGA-3'
5'-(((((..((((((...))))))).....)))))-3'
Motif MFE = -2.1; z-score = -0.5; ED = 8.72
```



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 17180 to 17378 (motif highlighted in silver):

```
5'-AUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAU
UAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAA-3
5'-.....((((.(((((...(((((((..((((..(((((......)))))..))))).....(((((((....)))))))(.(((((((((.((((((...))))))....))
))))))).)..(((((..(((.(((....))).)))..)))))((((((.......)))))))))))))...))))))))).......-3'
MFE = -47.5; z-score = -2.27; ED = 28.24
```

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(+)

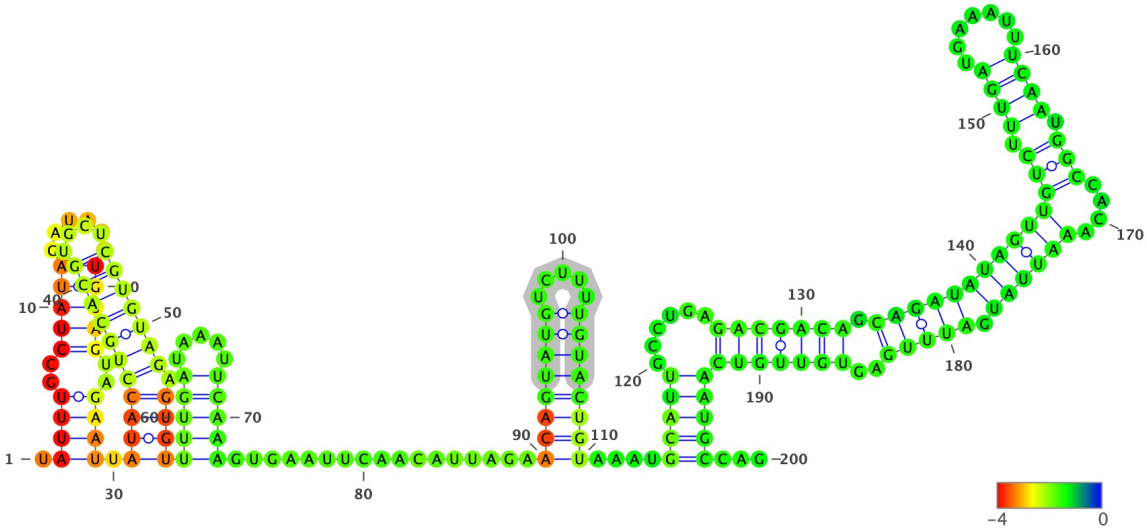
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 300 from nt 17299 to 17311 (nt 94 to 106)

```
5'-UAUGUCUUUUGUA-3'
5'-((((.....))))-3'
Motif MFE = 0.0; z-score = 0.13; 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 17206 to 17405 (motif highlighted in silver):

```
5'-UAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUA
AAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAG-3
5'-.((((..(((((......)))))..)))).(((((((((((....)))))))).))))(((((.....)))))..................((((((((.....)))))))).
...(((((......(((((((.((((((((((((((.((((.......)))).)))....)))))).)))))..))))))))))))...-3'
MFE = -46.0; z-score = -1.47; ED = 31.62
```

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

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

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

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

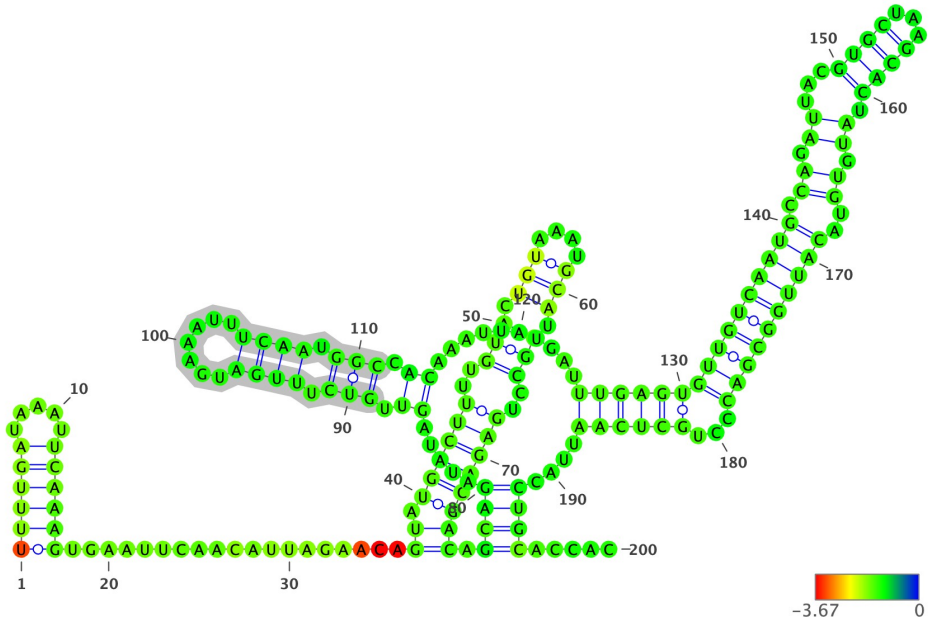
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 301 from nt 17350 to 17372 (nt 89 to 111)

```
5'-GUCUUUGAUGAAAUUUCAAUGGC-3'
5'-(((.((((.......)))))..)))-3'
Motif MFE = -3.8; z-score = -1.6; 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 = -1.34; 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(+)

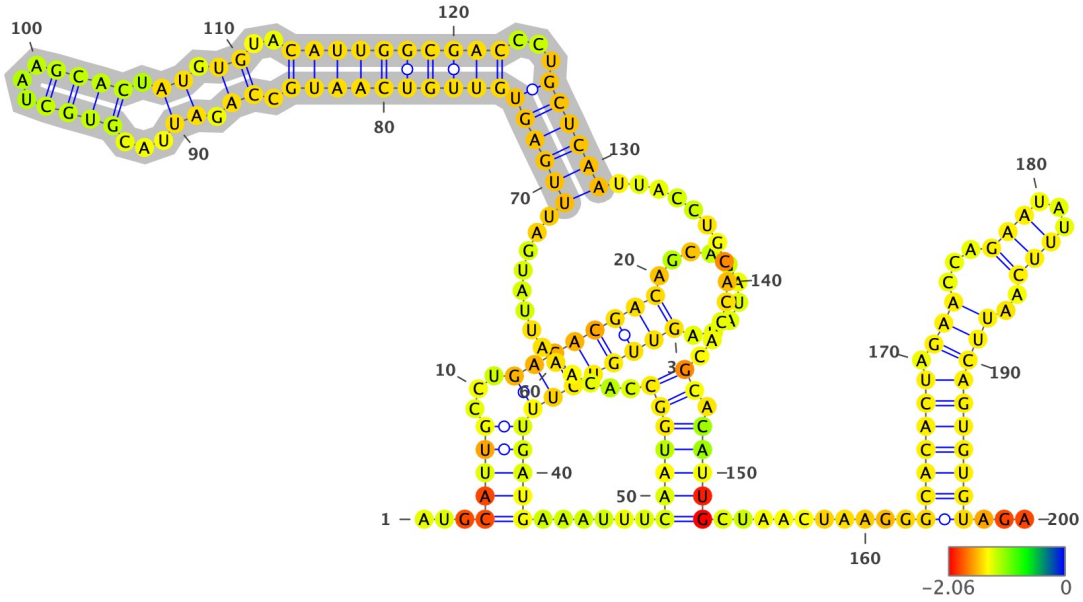
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 302 from nt 17386 to 17448 (nt 69 to 131)

```
5'-UUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAA-3'
5'-(((((((((((((((.((.((...((((...)))).)).)).)).)))))))))))...)))))))-3'
Motif MFE = -21.9; z-score = -3.08; ED = 3.43
```



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

Extracted structure model with flanking nucleotides 17318 to 17517 (motif highlighted in silver):

```
5'-AUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGU
ACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGA-3
5'-...((((((...(((((((((.........)))))))))))))).....(((((((.............((((((((((((((((.((.((...((((...)))).)).)).
.))))))))))...))))))).............)).)))))).........(((((((.(((...(((...))).))..)))))))))...-3'
MFE = -47.0; z-score = -1.17; 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(+)

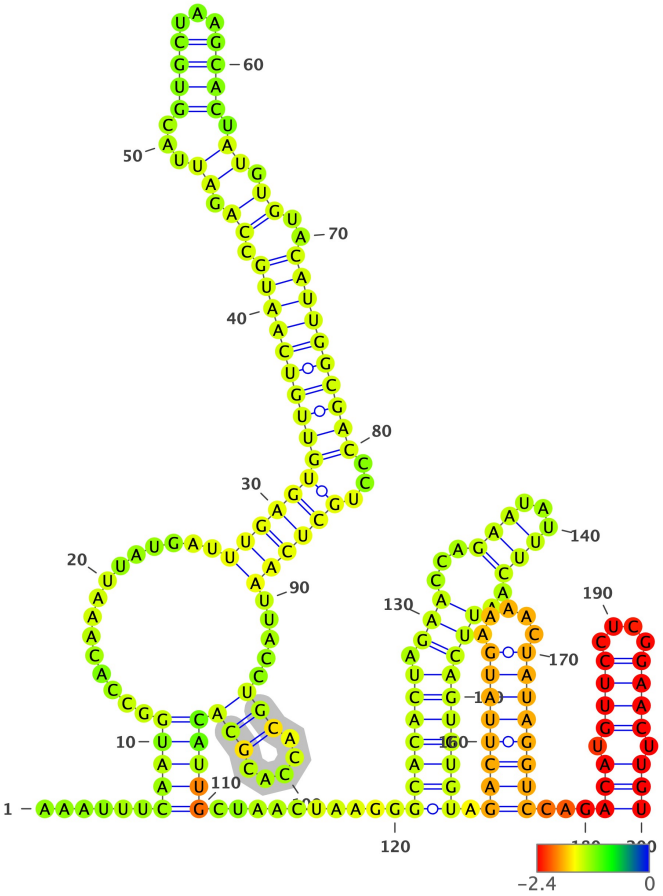
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 303 from nt 17455 to 17463 (nt 96 to 104)

```
5'-GCACCACGC-3'
5'-(.......)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 17360 to 17559 (motif highlighted in silver):

```
5'-AAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGC
UAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGU-3
5'-......(((((...............(((((((((((((((.((.((...((((...)))).)).))..))))))))))...))))))).....(((.....)))))))).
.........(((((((.(((...(((...)))..))))))))))).((((((((.....))))))))...(((.((((....)))).)))-3'
MFE = -48.2; z-score = -2.38; ED = 18.12
```

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

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

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

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

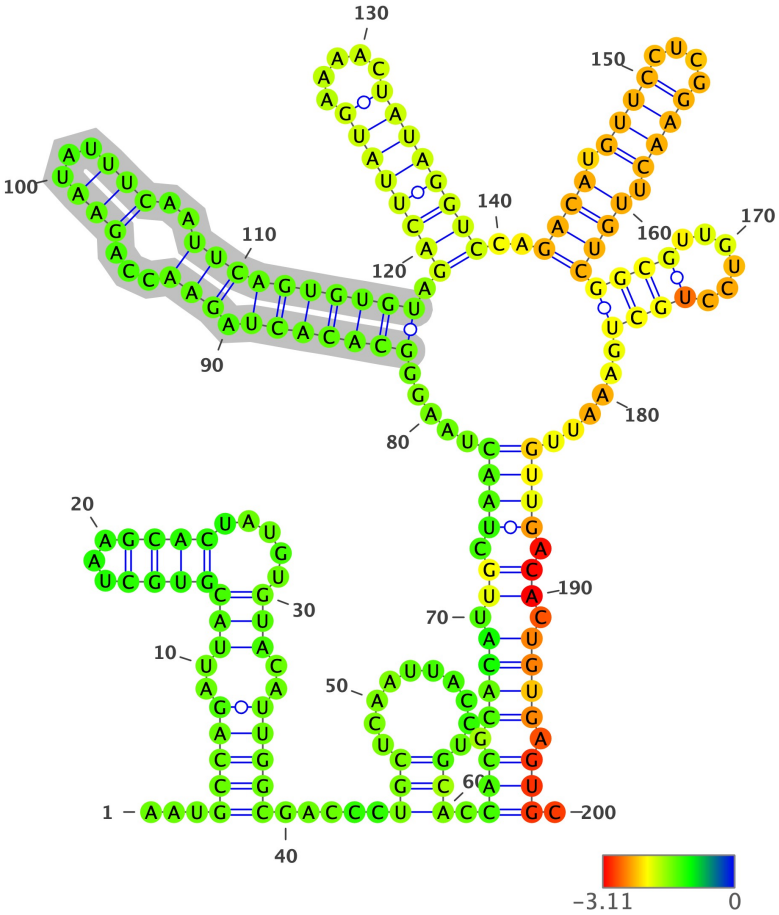
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17480 to 17514 (nt 83 to 117)

```
5'-GCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGU-3'
5'-(((((((.(((...(((...)))..))))))))))-3'
Motif MFE = -8.4; z-score = -3.02; 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 = -0.94; 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(+)

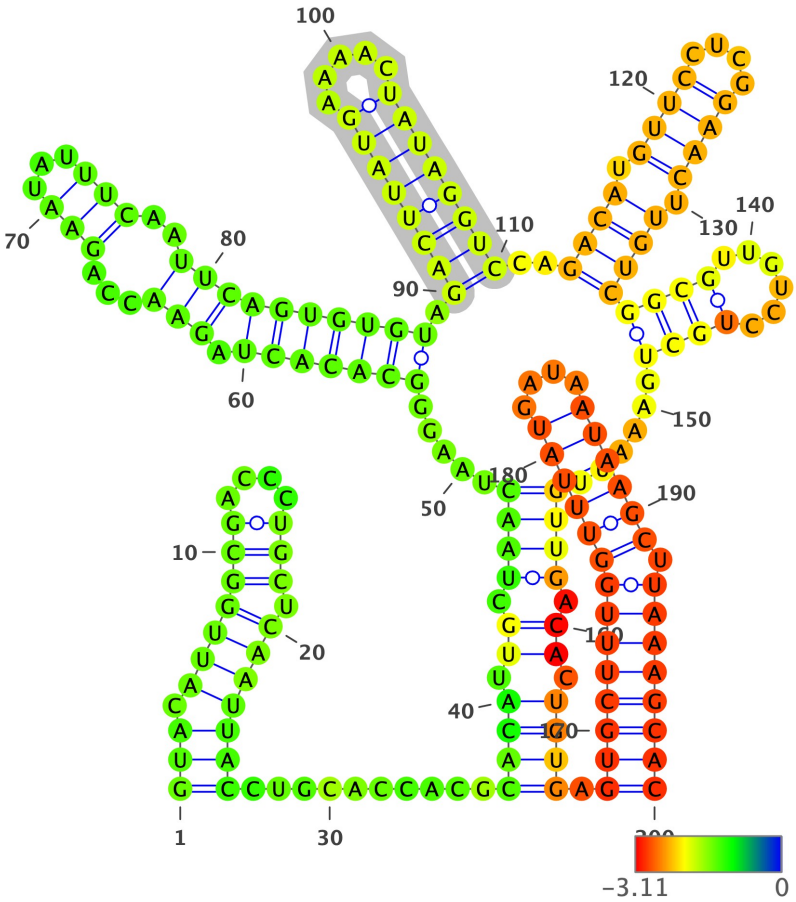
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 305 from nt 17516 to 17536 (nt 90 to 110)

```
5'-GACUUAUGAAAACUAUAGGUC-3'
5'-(((((((.....)))))))-3'
Motif MFE = -5.5; z-score = -3.18; ED = 0.4
```



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 17427 to 17626 (motif highlighted in silver):

```
5'-GUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCC
AGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCAC-3
5'-(((.(((((((....))).)))))))..........((((.((.((((.....(((((((.(((...(((...)))..))..)))))))))).(((((((.....)))))))).
.((((.((((....)))).))))(((((.....)))).....)))).)).)))).((((((((((((((....))))))).))))))-3'
MFE = -53.7; z-score = -2.18; ED = 34.29
```

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

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

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

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

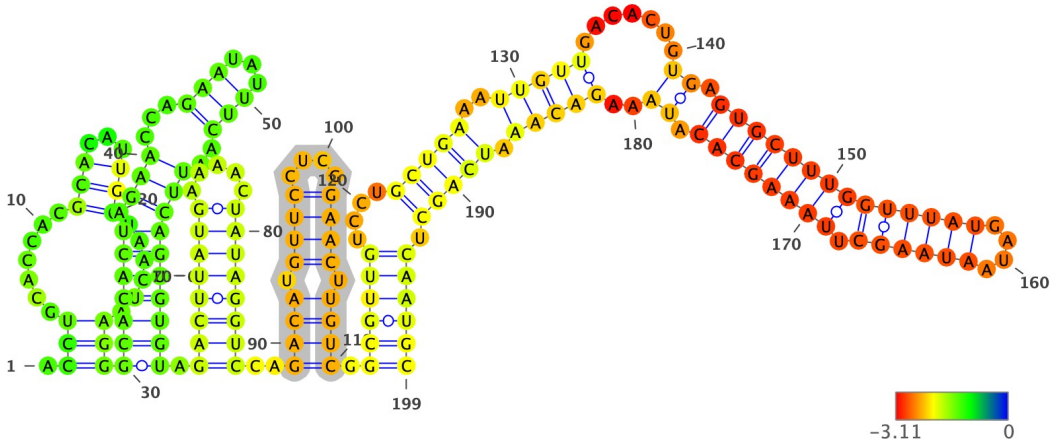
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 306 from nt 17539 to 17560 (nt 89 to 110)

```
5'-GACAUGUUCCUCGGAACUUGUC-3'
5'-((((.((((....)))).))))-3'
Motif MFE = -8.9; z-score = -3.1; 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 = -3.15; 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(+)

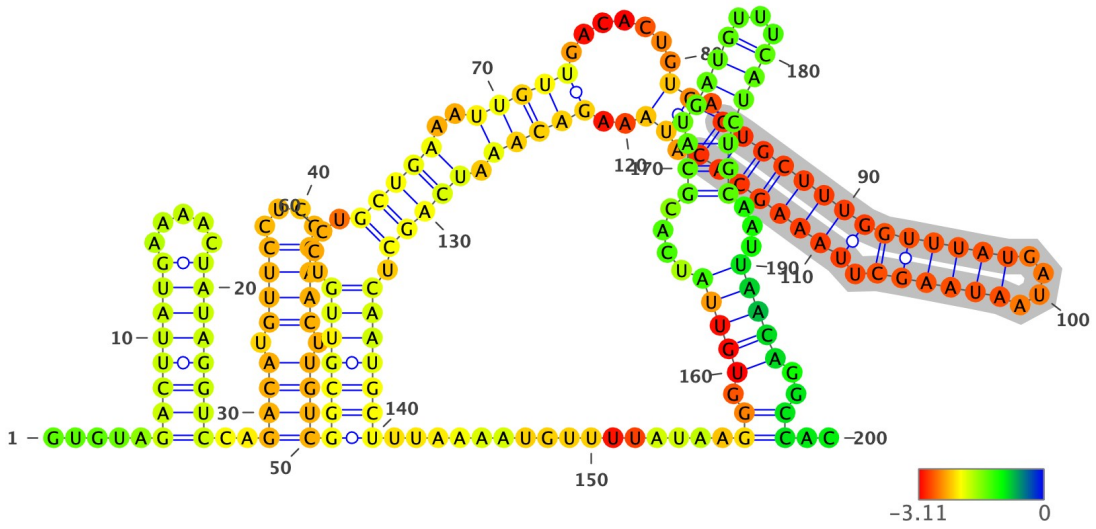
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 307 from nt 17594 to 17626 (nt 84 to 116)

```
5'-GUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCAC-3'
5'-((((((((((((((....)))))))).))))))))-3'
Motif MFE = -13.2; z-score = -5.07; 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 = -3.0; 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(+)

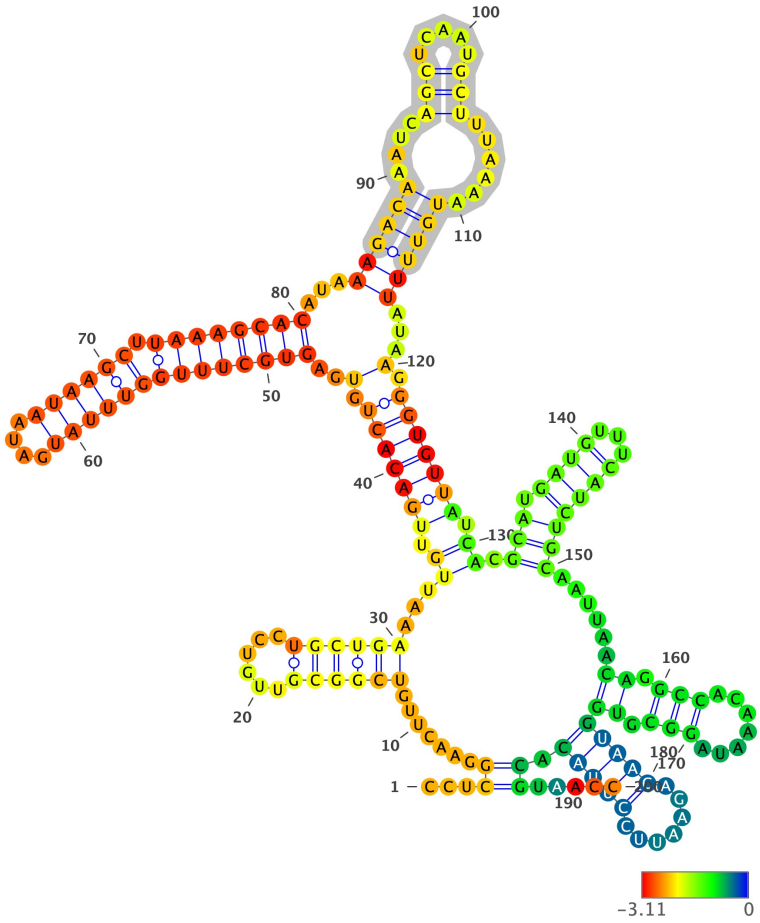
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 308 from nt 17632 to 17660 (nt 86 to 114)

```
5'-GACAAAUCAGCUCAAUGCUUUAAAAUGUU-3'
5'-((((....(((.....)))......))))-3'
Motif MFE = -2.0; z-score = -0.17; 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 17547 to 17746 (motif highlighted in silver):

```
5'-CCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAU
GUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACC-3
5'-...((.......((((((.....))))))...((.(((((((.(..(((((((((((((((....)))))))).)))))))))...((((((....(((.....)))).....)
))))))...).)))))))..)).(((.((((...)))))))......((.(((.......))).))(((((.......))))))..))......-3'
MFE = -49.1; z-score = -1.92; ED = 34.63
```

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

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

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

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

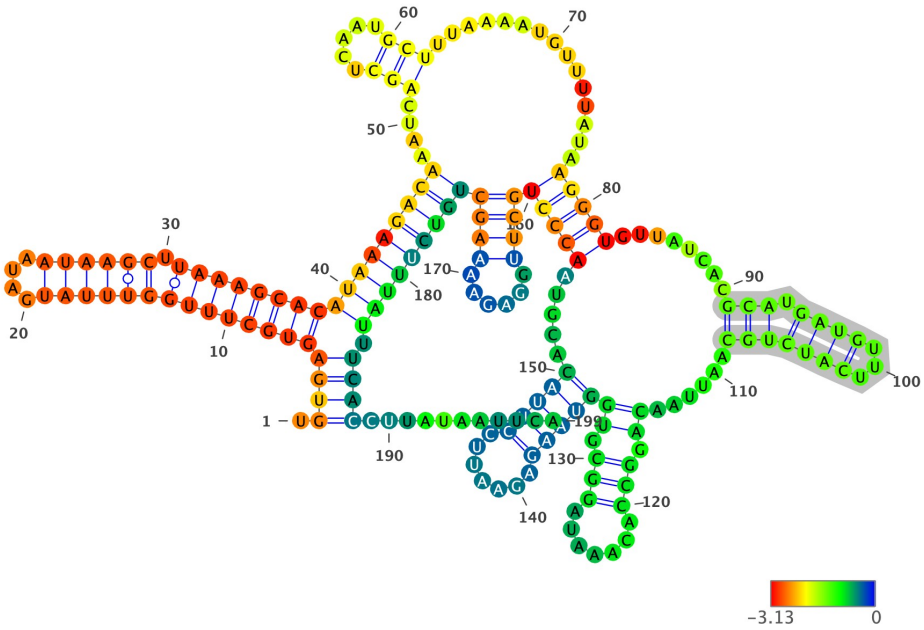
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 17679 to 17696 (nt 91 to 108)

```
5'-GCAUGAUGUUUCAUCUGC-3'
5'-(((.((((...)))))))-3'
Motif MFE = -4.0; z-score = -2.65; 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 = -3.19; 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(+)

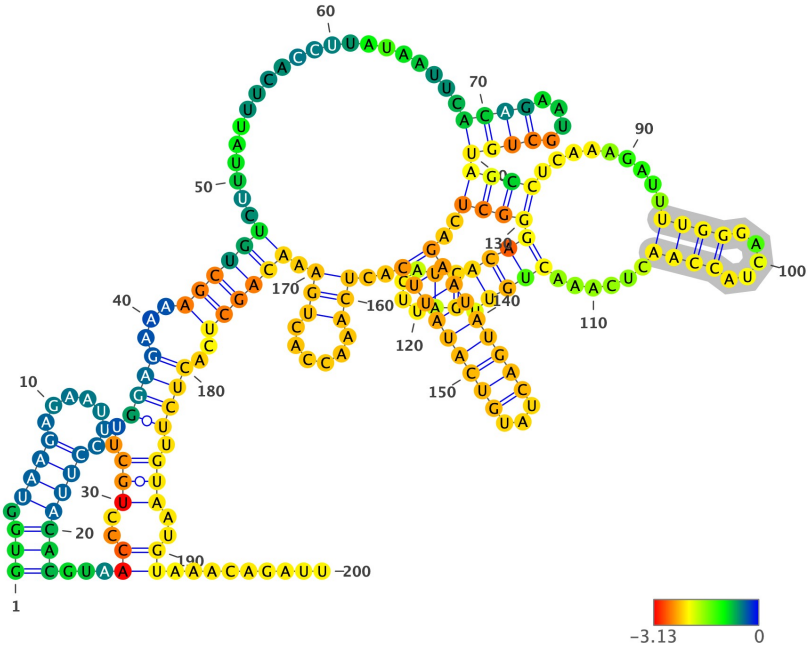
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 310 from nt 17812 to 17824 (nt 94 to 106)

```
5'-UUGGGACUACCAA-3'
5'-((((.....))))-3'
Motif MFE = -2.7; z-score = -3.78; 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 17719 to 17918 (motif highlighted in silver):

```
5'-GUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAA
ACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUU-3
5'-(((.((((.......)))))))...((..((((..((((...((((((.....................((((....))))))(((((.........((((.....)))))).....
.((((.((....))))))))))..(((((((((...)))))))))..(((......))).)))))).))..))..........-3'
MFE = -38.7; z-score = -2.0; ED = 24.48
```

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

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

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

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

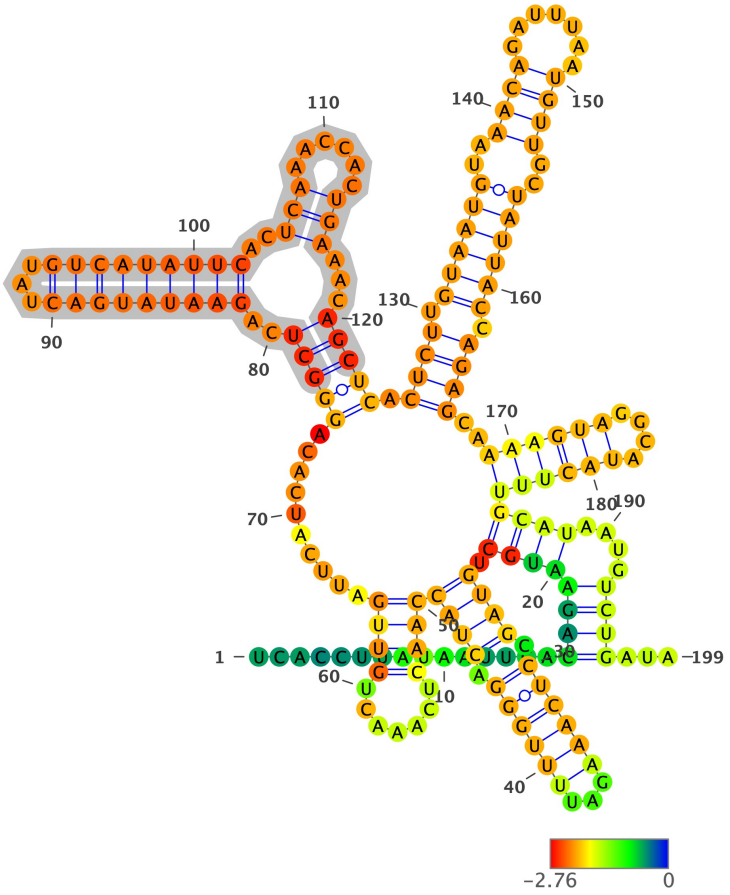
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 311 from nt 17849 to 17894 (nt 77 to 122)

```
5'-GCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGC-3'
5'-(((..((((((((((...)))))))))..(((......)))...)))-3'
Motif MFE = -9.7; z-score = -3.21; ED = 3.31
```



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 17773 to 17971 (motif highlighted in silver):

```
5'-UCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACC
ACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUA-3
5'-...............((((((((.((((.((((((...)))))).))))((((.......))))..........(((((..((((((((((...)))))))))..(((....
..)))...))))).((((.((((((..((((.......))))..)))))).))))..((((((....))))))))))....))))...-3'
MFE = -45.5; z-score = -3.04; ED = 18.14
```

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(+)

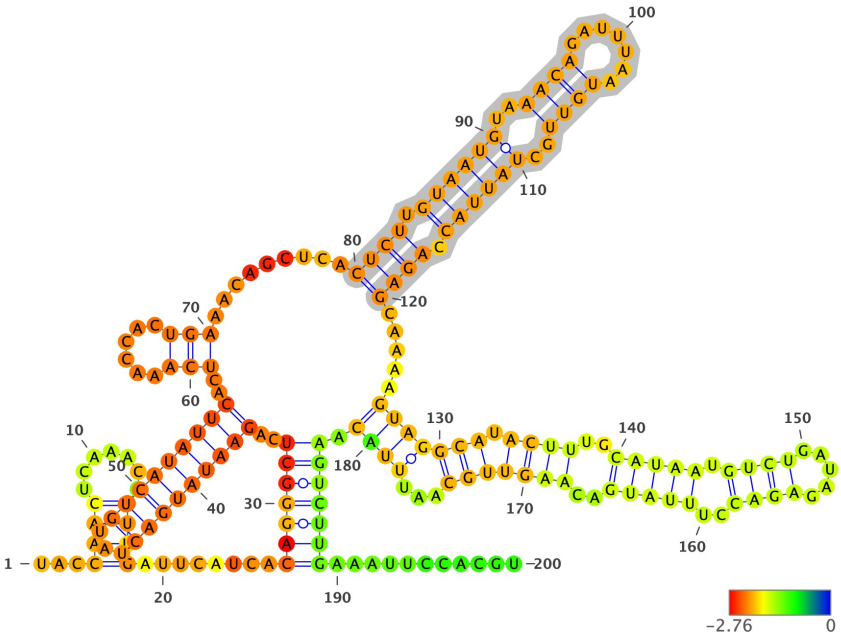
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 312 from nt 17898 to 17938 (nt 80 to 120)

```
5'-CUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAG-3'
5'-((((.((((((..((((.......))))..)))))).))))-3'
Motif MFE = -9.7; z-score = -2.52; 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 = -2.74; 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(+)

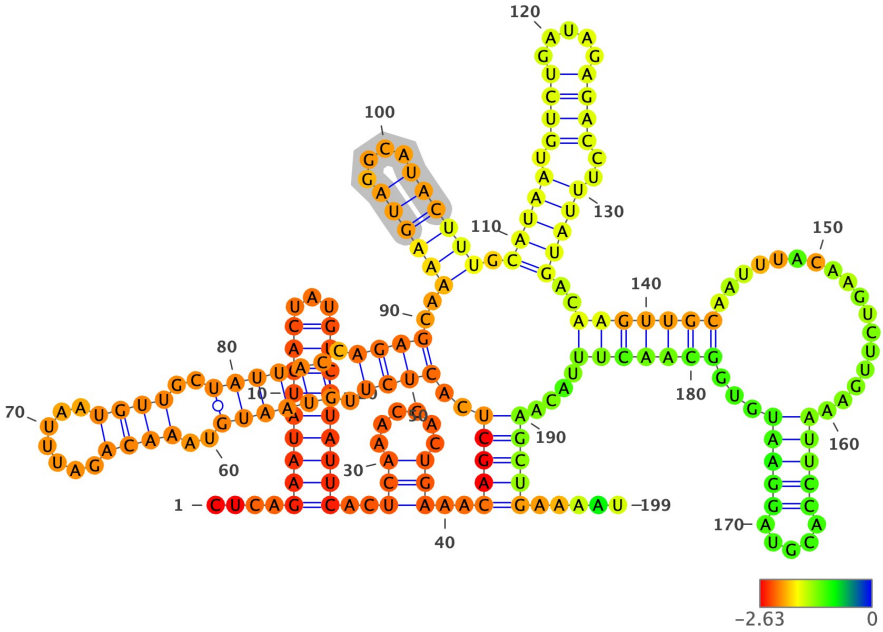
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 313 from nt 17944 to 17953 (nt 95 to 104)

```
5'-GUAGGCAUAC-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = 0.17; ED = 0.97
```



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 17850 to 18048 (motif highlighted in silver):

```
5'-CUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAU
AAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGCUGAAAAU-3
5'-....((((((((((...))))))))))..(((......)))..((((((..((((.((((((..((((.......))))..))))))).))))).((((((....))))))).(((
((.((((.....))))..))))))..(((((((.................(((((.....)))))...)))))))....))))).....-3'
MFE = -47.3; z-score = -2.97; ED = 23.69
```

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

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

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

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

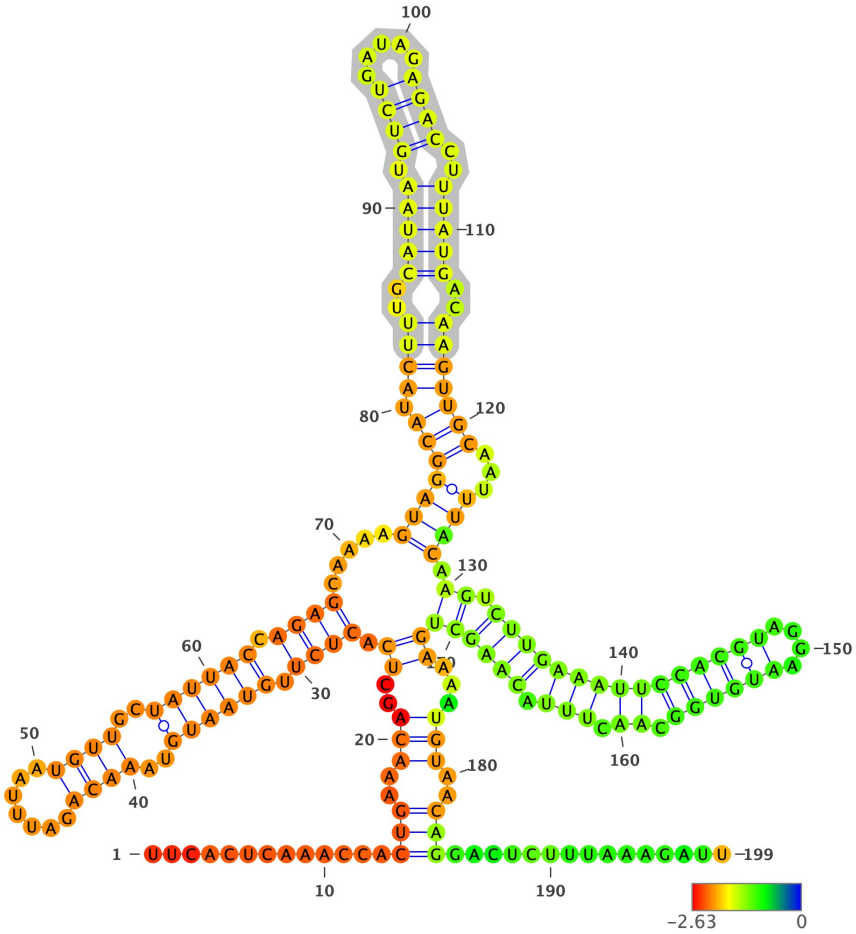
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 314 from nt 17954 to 17987 (nt 83 to 116)

```
5'-UUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAA-3'
5'-((..(((((.((((.....)))).)))))..))-3'
Motif MFE = -8.0; z-score = -2.83; 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 17872 to 18070 (motif highlighted in silver):

```
5'-UUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAU
GACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUU-3
5'-.............(((..(((..((.((((.((((((..((((.......)))).)))))).))))).....(((((((.((((..(((((.((((.....)))).)))))
)..)))))))...)))).((.((((((((((((((....)))))).)).))).))))))))...)))..))).................-3'
MFE = -38.1; z-score = -1.44; ED = 41.04
```

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

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

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

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

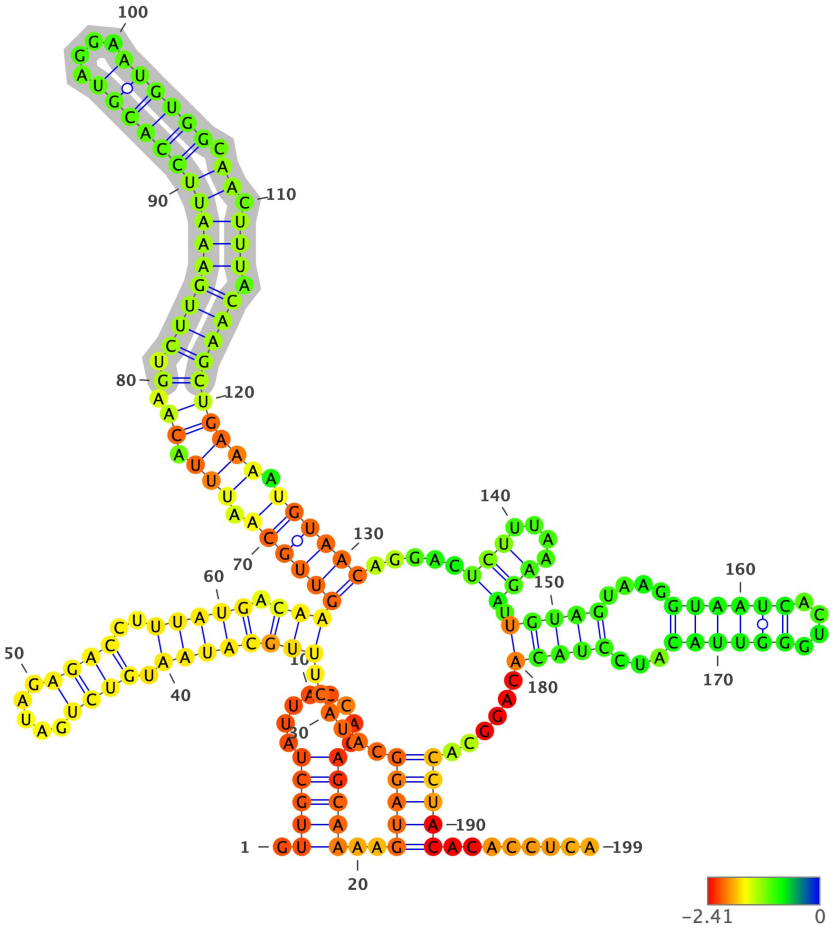
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 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 18002 to 18041 (nt 80 to 119)

```
5'-GUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGC-3'
5'-(.(((((((((((((((....)))))).)).))).)))))-3'
Motif MFE = -8.1; z-score = -1.3; ED = 5.05
```



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

Extracted structure model with flanking nucleotides 17923 to 18121 (motif highlighted in silver):

```
5'-GUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACU
UUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCA-3
5'-.(((((........)))))..(((((......((((((((.((((.....)))).)))))).)))((((((.(((.((.(.(((((((((((((((....)))))).)).)
)).))))))))))).))))))).....(((....))).(((((....((((((....))))))...)))))......)))))........-3'
MFE = -44.1; z-score = -1.65; ED = 41.21
```

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(+)

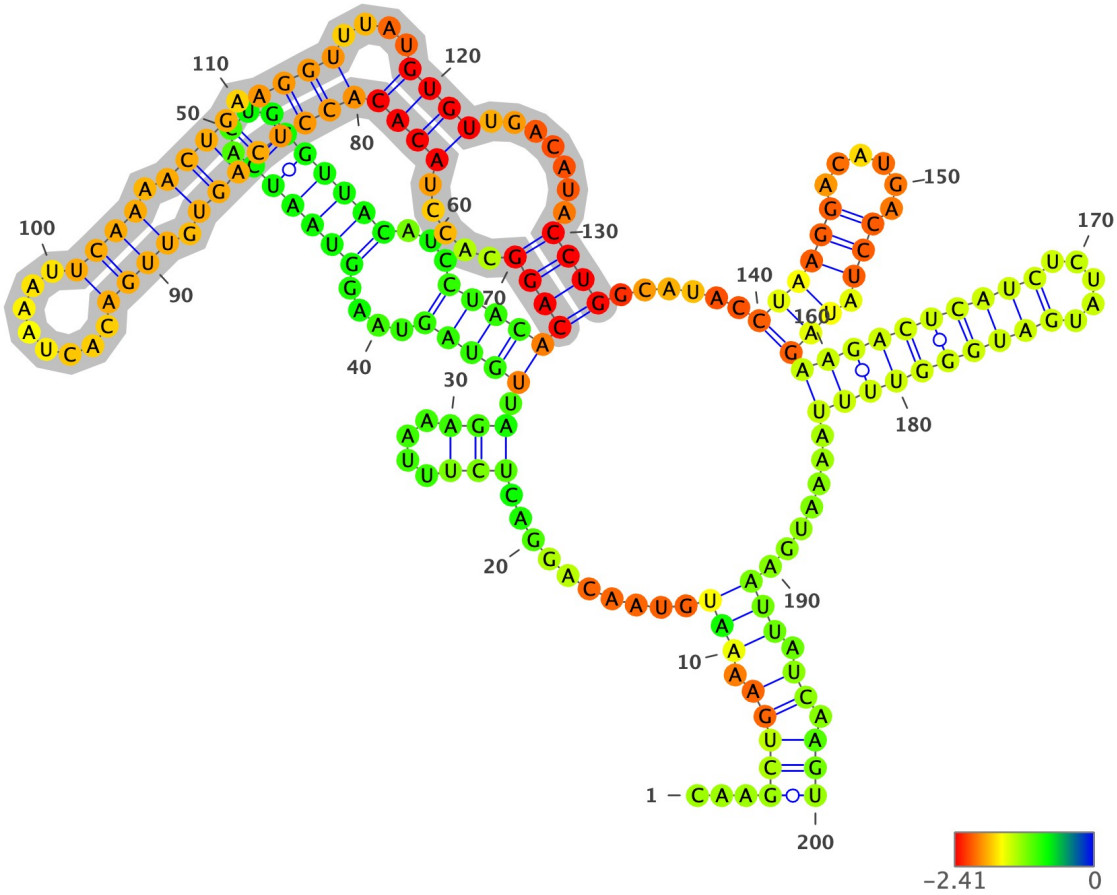
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 316 from nt 18103 to 18169 (nt 67 to 133)

```
5'-CAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUG-3'
5'-((((.....(((((((((((.((((........)))).)))).)))).....)))).......))))-3'
Motif MFE = -16.7; z-score = -2.66; 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 18037 to 18236 (motif highlighted in silver):

```
5'-CAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAA
GGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGU-3
5'-...(((((.(((..........(((....))).(((((....((((((....))))))...)))))((((.....(((((((((((.((((........)))).)))).)
)))....)))).......)))).....((((((......))).)))((((((((((.....)))))))))).......))).)).)))-3'
MFE = -43.0; z-score = -1.66; ED = 26.77
```

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

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

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

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

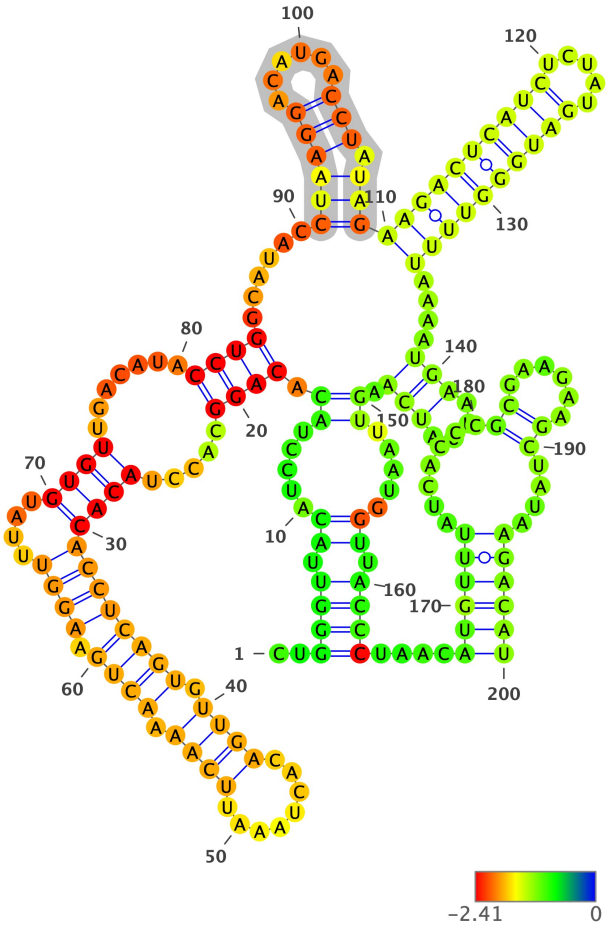
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 18176 to 18194 (nt 91 to 109)

```
5'-CUAAGGACAUGACCUAUAG-3'
5'-(..(((......)))...)-3'
Motif MFE = -1.6; z-score = -0.88; ED = 1.93
```



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 18086 to 18285 (motif highlighted in silver):

```
5'-CUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAA
GACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAU-3
5'-..((((.((.....((.((((.....(((((((((((.((((.........)))).)))).))))....))))........))))......((((((......))).)))((
((((((((.....))))))))))....(((....))).)).....)).))))....((((((.......((......))....))))))-3'
MFE = -42.0; z-score = -2.13; ED = 29.78
```

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

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

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

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

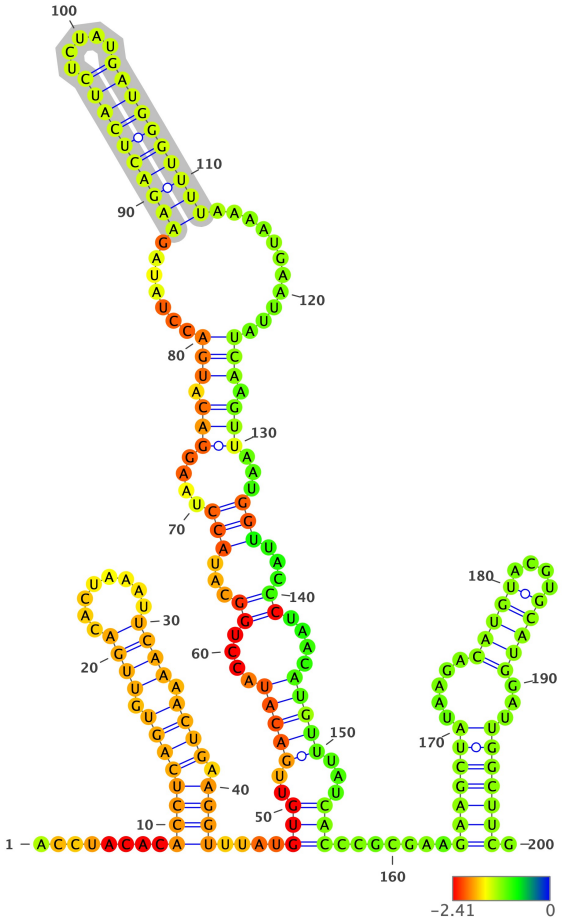
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 18195 to 18219 (nt 88 to 112)

```
5'-AAGACUCAUCUCUAUGAUGGGUUUU-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -10.1; z-score = -4.22; 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 = -2.01; 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(+)

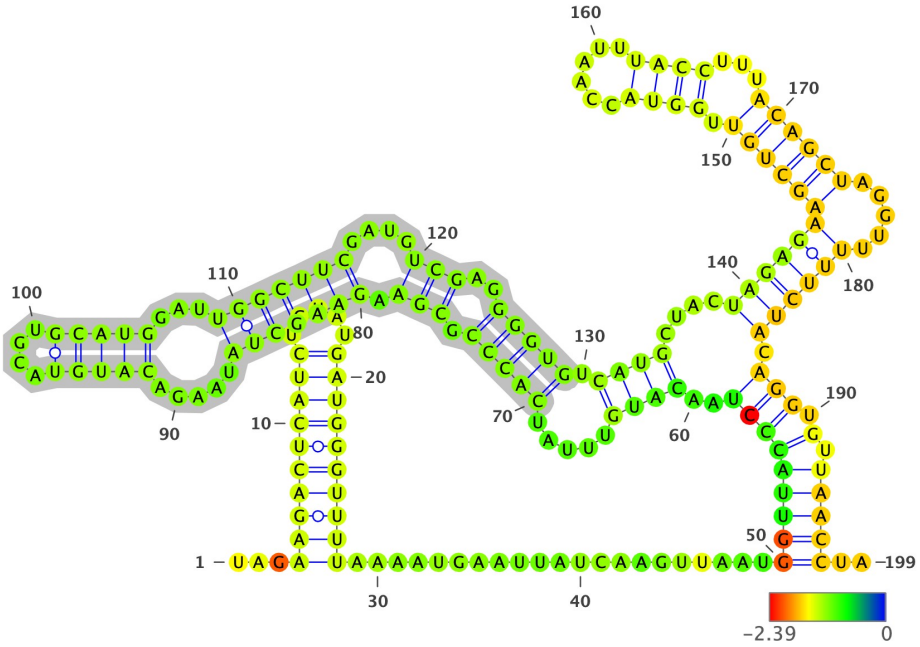
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 319 from nt 18261 to 18320 (nt 70 to 129)

```
5'-CACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUG-3'
5'-(((((.(((.(((((((.....(((((....)))))...)))))))....)))..)))))-3'
Motif MFE = -22.2; z-score = -2.43; ED = 4.38
```



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

Extracted structure model with flanking nucleotides 18192 to 18390 (motif highlighted in silver):

```
5'-UAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGG
CUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUA-3
5'-...((((((((((.....))))))))))....................(((((((((..((((.....(((((.(((.(((((((.....(((((....)))))...)))
))))....)))..)))))).))))....((((((((((((.((((......))))...))))))).....)))))).))).).)))))..-3'
MFE = -54.7; z-score = -2.47; 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 199--gene, gene-GU280_gp01, 266-21555(+)

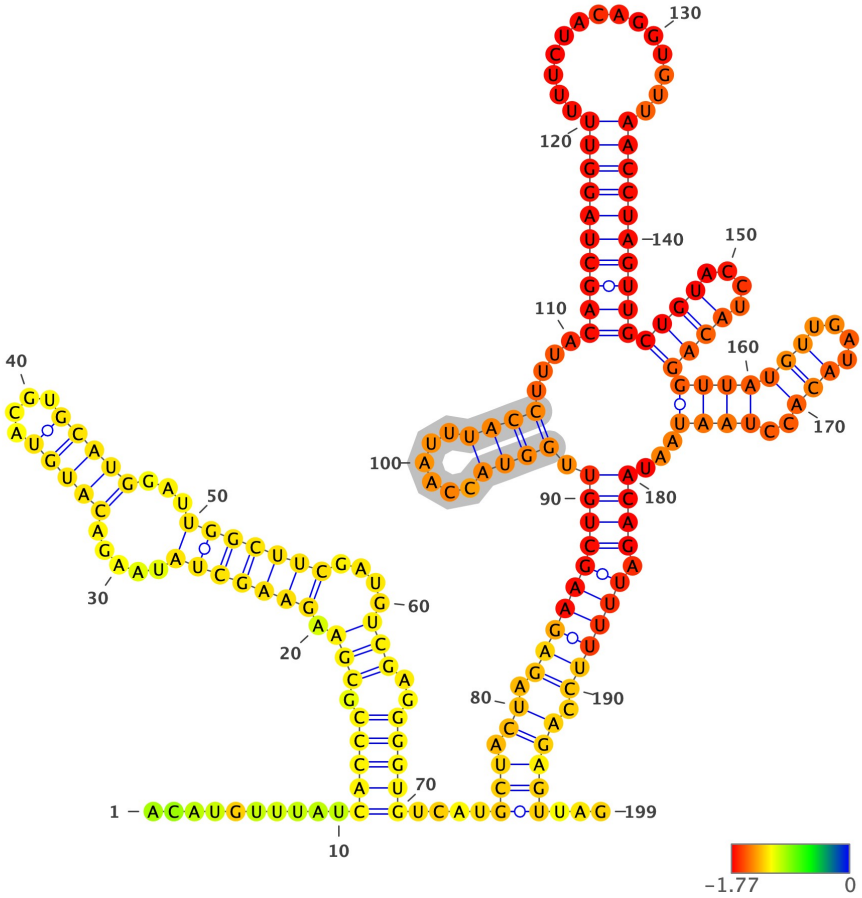
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 320 from nt 18343 to 18356 (nt 93 to 106)

```
5'-GGUACCAAUUUACC-3'
5'-((((......))))-3'
Motif MFE = -1.6; z-score = -3.56; 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 = -1.02; 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(+)

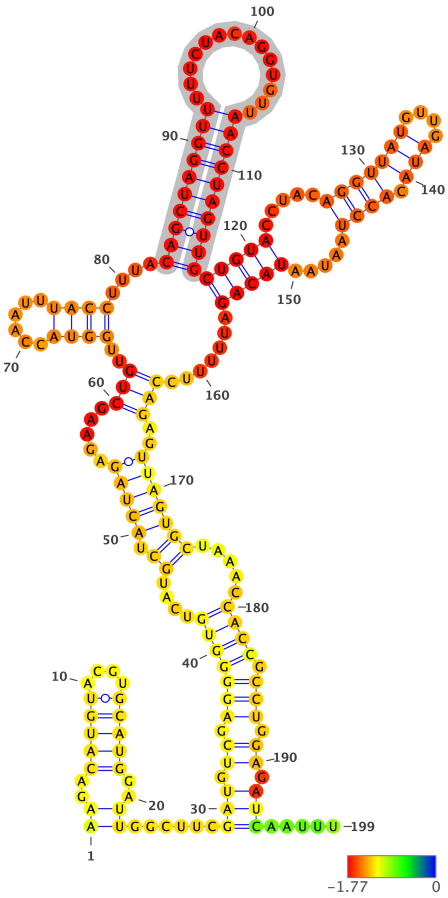
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 321 from nt 18361 to 18394 (nt 83 to 116)

```
5'-CAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUG-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -11.1; z-score = -3.02; 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 = -1.42; 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(+)

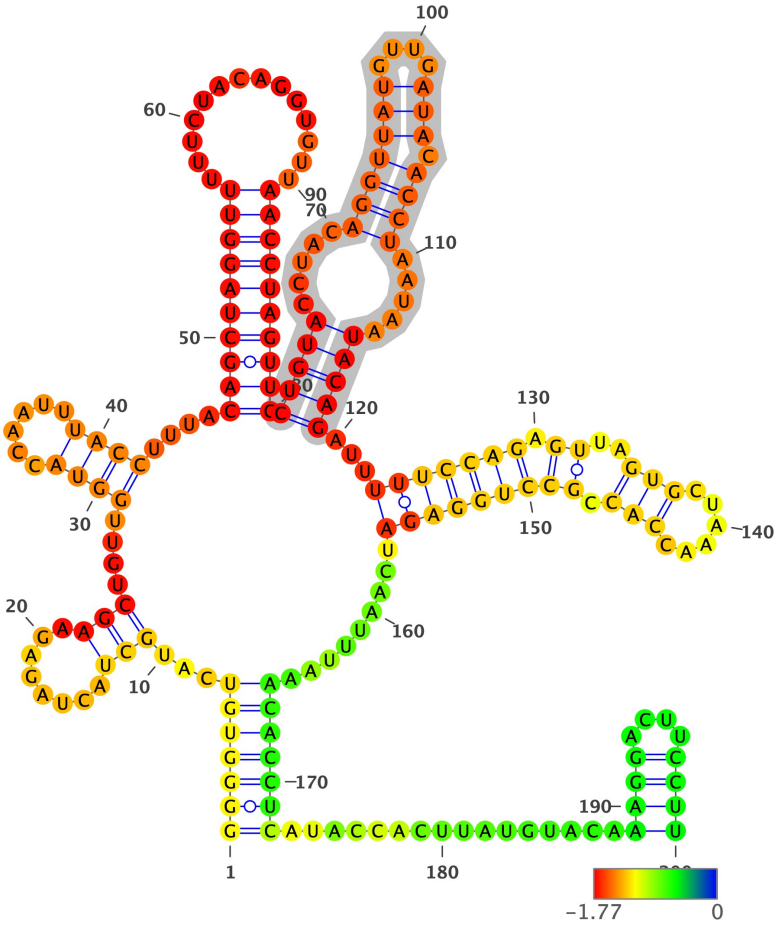
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 322 from nt 18395 to 18433 (nt 81 to 119)

```
5'-CUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAG-3'
5'-(((((.....(((((((....))).))))).....)))))-3'
Motif MFE = -6.8; z-score = -1.73; 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 18315 to 18514 (motif highlighted in silver):

```
5'-GGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAA
UAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUU-3
5'-(((((((...(((.........)))....((((......))))....((((((((((.............))))))))))(((((.....(((((((....))).))))..
...)))))...(((((((.((..(((......))).)))))))))).........)))))))................((((....))))-3'
MFE = -48.9; z-score = -2.4; ED = 18.95
```

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(+)

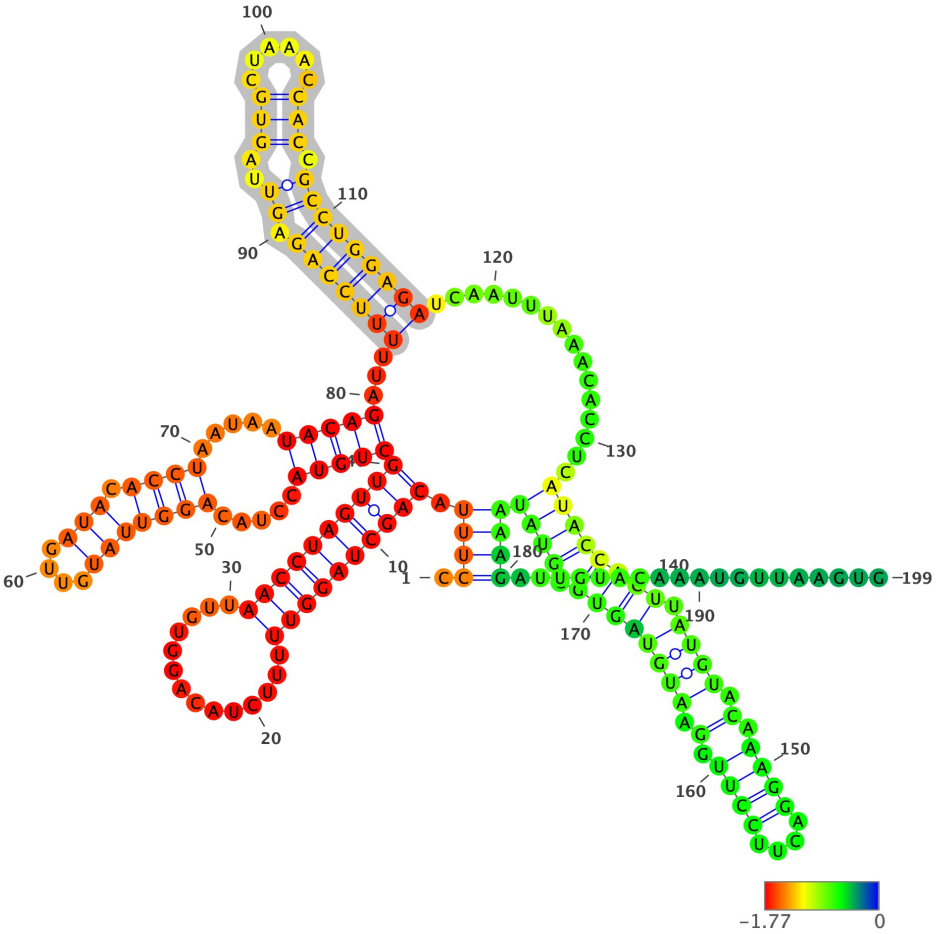
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 323 from nt 18437 to 18470 (nt 83 to 116)

```
5'-UUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGA-3'
5'-(((((((.((..(((......))).)))))))))-3'
Motif MFE = -9.9; z-score = -2.45; 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 18355 to 18553 (motif highlighted in silver):

```
5'-CCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCU
GGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUUGGAAUGUAGUGCGUAUAAAGAUUGUACAAAUGUUAAGUG-3
5'-.((((.(((((((((((.............))))))))))(((((.....(((((((....))).))))).....)))))...(((((((.((..(((......))).))))
)))))................(((((((.((((.(.((((....)))).).))))))))).))))))))...................-3'
MFE = -42.5; z-score = -1.22; ED = 26.79
```

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 199--gene, gene-GU280_gp01, 266-21555(+)

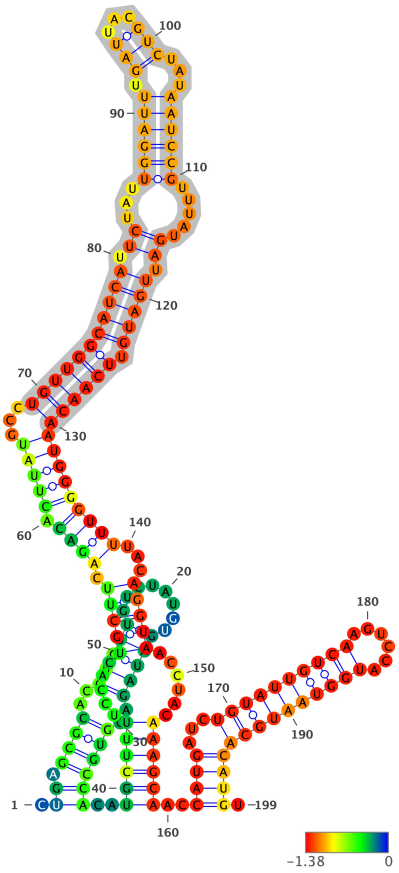
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 18715 to 18776 (nt 69 to 130)

```
5'-UGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACA-3'
5'-((((((((((.((...((((((.(((...))).)))))).....)).)))))).))))))-3'
Motif MFE = -16.9; z-score = -3.2; 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 = -0.96; 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(+)

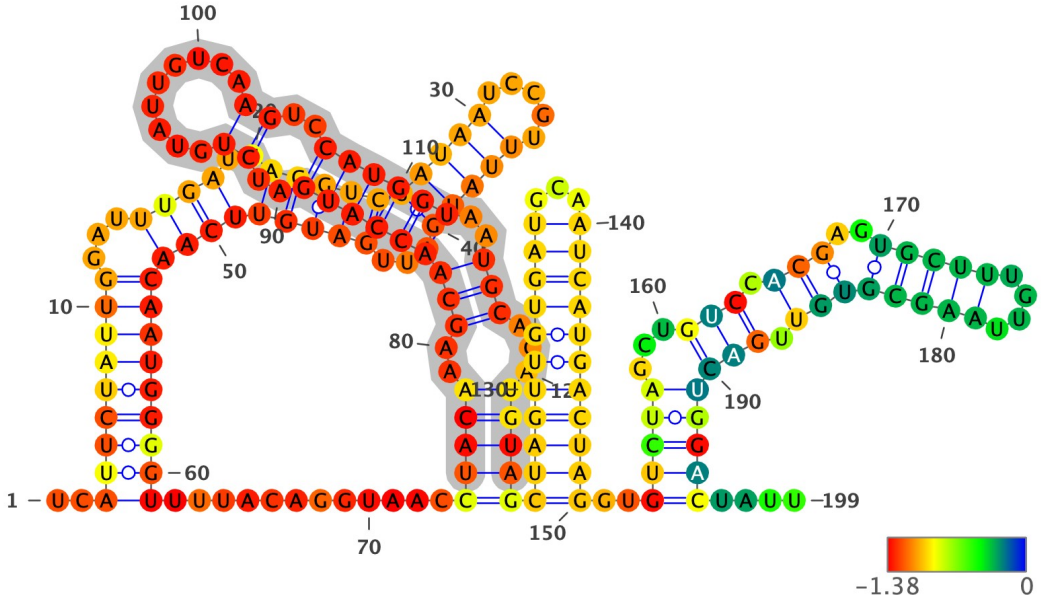
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 325 from nt 18797 to 18846 (nt 75 to 124)

```
5'-UACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUA-3'
5'-(.....((((((((((..((.........))..))))))..)))......)-3'
Motif MFE = -11.3; z-score = -2.09; 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 18723 to 18921 (motif highlighted in silver):

```
5'-UCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGG
UAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUU-3
5'-..((((((((((...((((..((((((((((.....)))))...))))))))))))))))))).............(((((..((((((((((..((.........))..)))))
)..)))...)))))((((((((((...)))))))))))..(((((...(((.(((..(((((....)))))))).))))))))....-3'
MFE = -49.4; z-score = -1.24; ED = 33.69
```

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

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

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

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

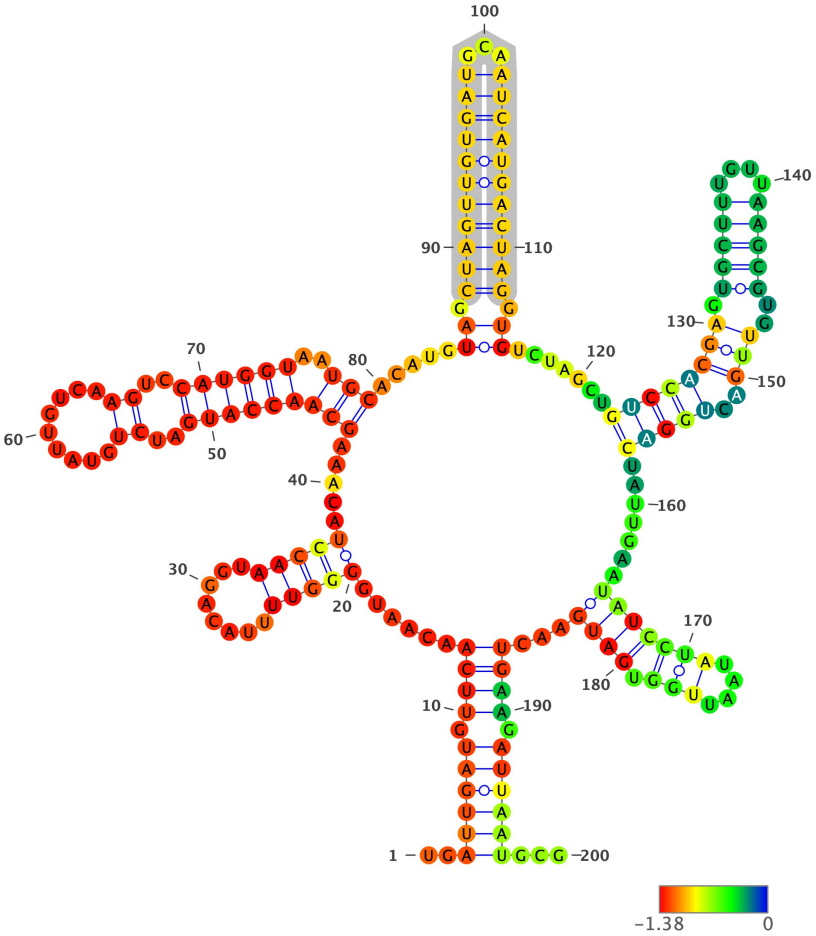
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 326 from nt 18848 to 18872 (nt 88 to 112)

```
5'-CUAGUUGUGAUGCAAUCAUGACUAG-3'
5'-(((...................)))-3'
Motif MFE = -9.8; z-score = -4.91; 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 18761 to 18960 (motif highlighted in silver):

```
5'-UGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUA
GGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGAACUGAAGAUUAAUGCG-3
5'-..((((((.((((......(((((........)))))).....(((((((((..((.........))..))))))..)))).....((.(((((((((((...)))))))))))
).)).......((((((((.(((((....)))))..)))..)))))).......(((((((....))).))))...)))).))))))...-3'
MFE = -50.2; z-score = -0.87; ED = 45.14
```

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

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

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

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

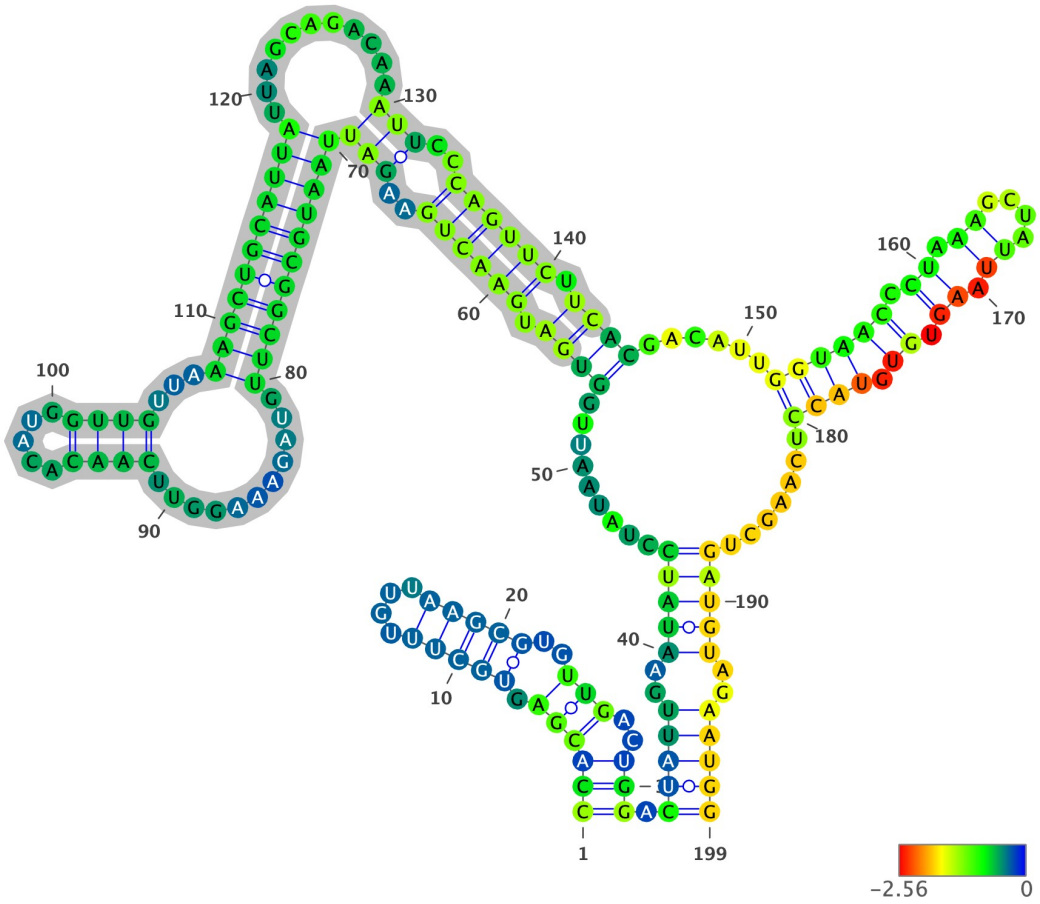
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 18940 to 19027 (nt 56 to 143)

```
5'-GAUGAACUGAAGAUUAAUGCGGCUUGUAGAAAGGUUCAACACAUGGUUGUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUC-3'
5'-((.((((((...((.....................................................))...)))))).))-3'
Motif MFE = -20.5; z-score = -1.75; 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 = 0.75; ED = 34.26
```

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(+)

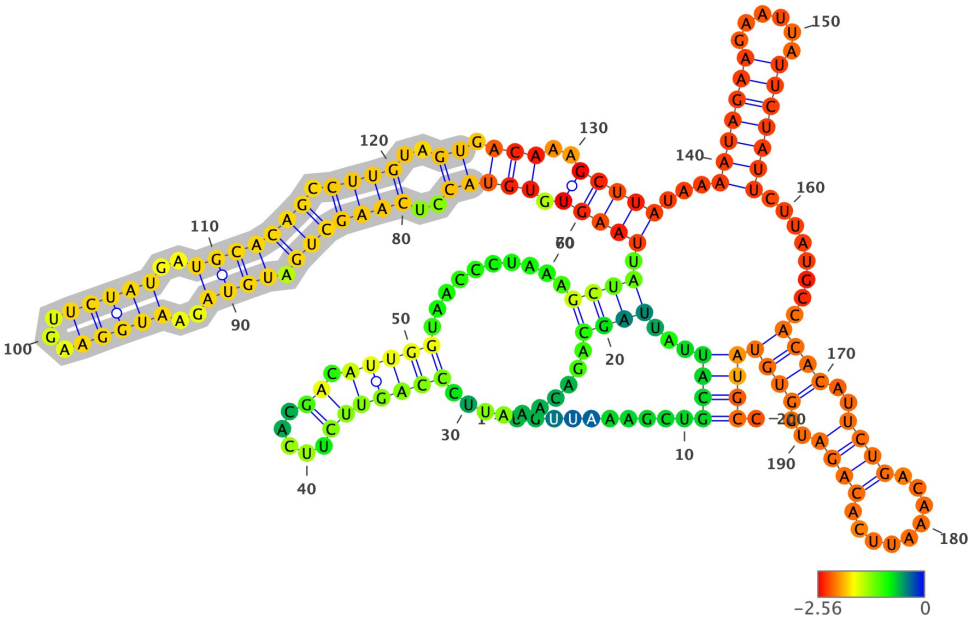
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 328 from nt 19062 to 19110 (nt 76 to 124)

```
5'-ACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGU-3'
5'-((..(((((((.(((((..((((((...))))))..))))))).))))..))-3'
Motif MFE = -15.0; z-score = -3.14; 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 18987 to 19186 (motif highlighted in silver):

```
5'-UGUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGC
ACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCC-3
5'-..........((((...((((..........(((((((.....)).)))))..........)))).(((((.(((((..(((((((.((((..(((((...)))))).))))
)))).)))))..)).)))..))))))...(((((((.....)))))))........((((..((((.........))))).))))))))).-3'
MFE = -43.6; z-score = -1.55; ED = 31.93
```

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(+)

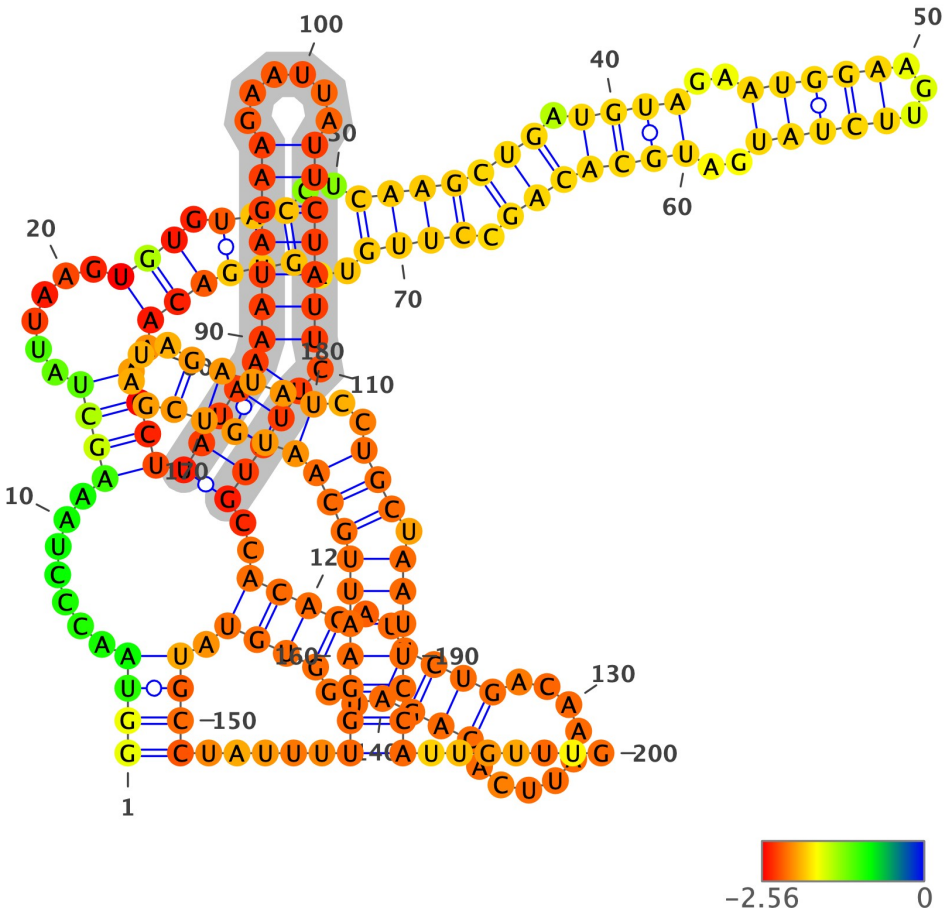
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 329 from nt 19120 to 19150 (nt 85 to 115)

```
5'-UAUAAAAUAGAAGAAUUAUUCUAUUCUUAUG-3'
5'-(((((((((((.....)))))))).)))))-3'
Motif MFE = -5.4; z-score = -3.22; 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 19036 to 19235 (motif highlighted in silver):

```
5'-GGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCU
UAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUG-3
5'-((((.......((((......(((.(((..(((((((.((((..(((((...)))))..)))))))).))))..)))))).))))((((((((((((.....)))))))).)
))))..((((..((((.........))))..)))).))))).....((((((((((((((....)))))..))).)))))))).......-3'
MFE = -50.0; z-score = -3.11; 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(+)

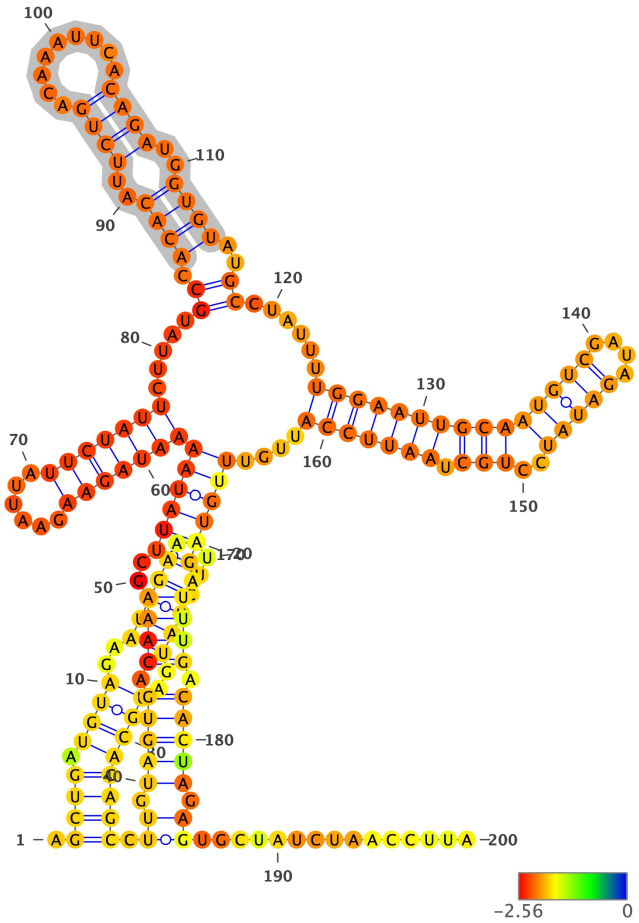
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 19153 to 19181 (nt 86 to 114)

```
5'-ACACAUUCUGACAAAUUCACAGAUGGUGU-3'
5'-((((..((((.........))))..))))-3'
Motif MFE = -7.3; z-score = -3.39; ED = 0.64
```



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

Extracted structure model with flanking nucleotides 19068 to 19267 (motif highlighted in silver):

```
5'-AGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGG
UGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUA-3
5'-.((((.((((..(((((...)))))..)))))))).((.(((((.((((..(((((((((((((.....)))))))).....((.((((..((((.........))))..)
)))..))......((((((((((((((....)))))..))).))))))).....))))))).)))).)))))).)).................-3'
MFE = -49.9; z-score = -2.81; ED = 25.47
```

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

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

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

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

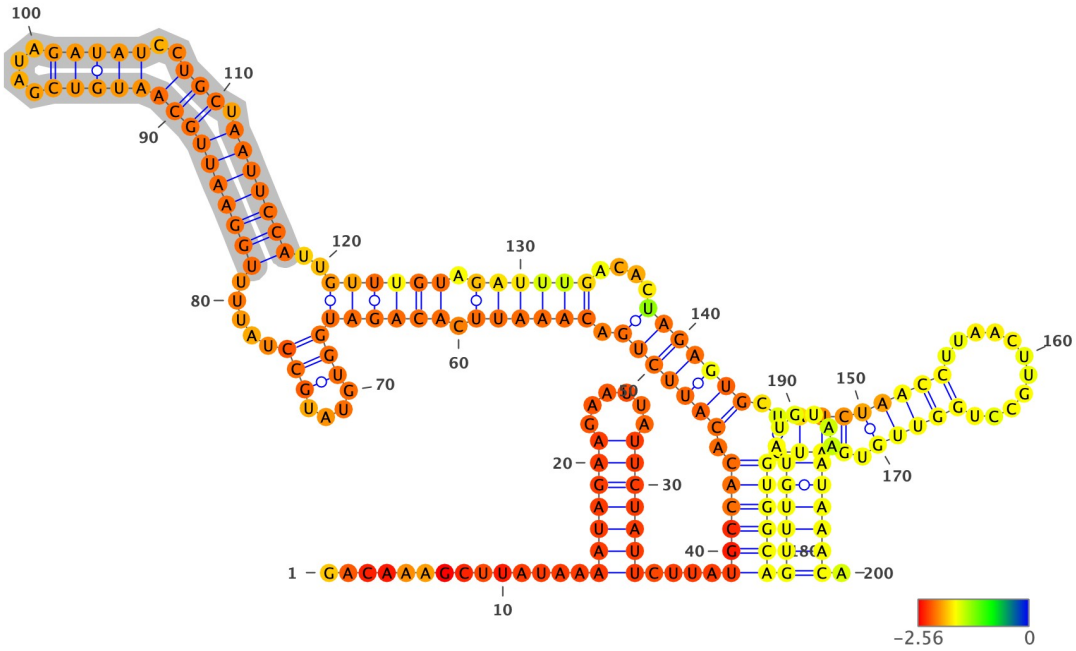
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 19192 to 19228 (nt 82 to 118)

```
5'-UGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCA-3'
5'-(((((((((((((((....)))))..))).)))))))-3'
Motif MFE = -12.8; z-score = -4.23; 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 19111 to 19310 (motif highlighted in silver):

```
5'-GACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCU
AAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACA-3
5'-..............(((((((......)))))))....((((((.(((((((.((((((.((((((((((....)))).....((((((((((((((....)))))..))).
)))))))..)))))).)))))).....))))))).((((((((((...........)))))).))))))))))((((((......)))))).-3'
MFE = -49.3; z-score = -2.43; ED = 27.45
```

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(+)

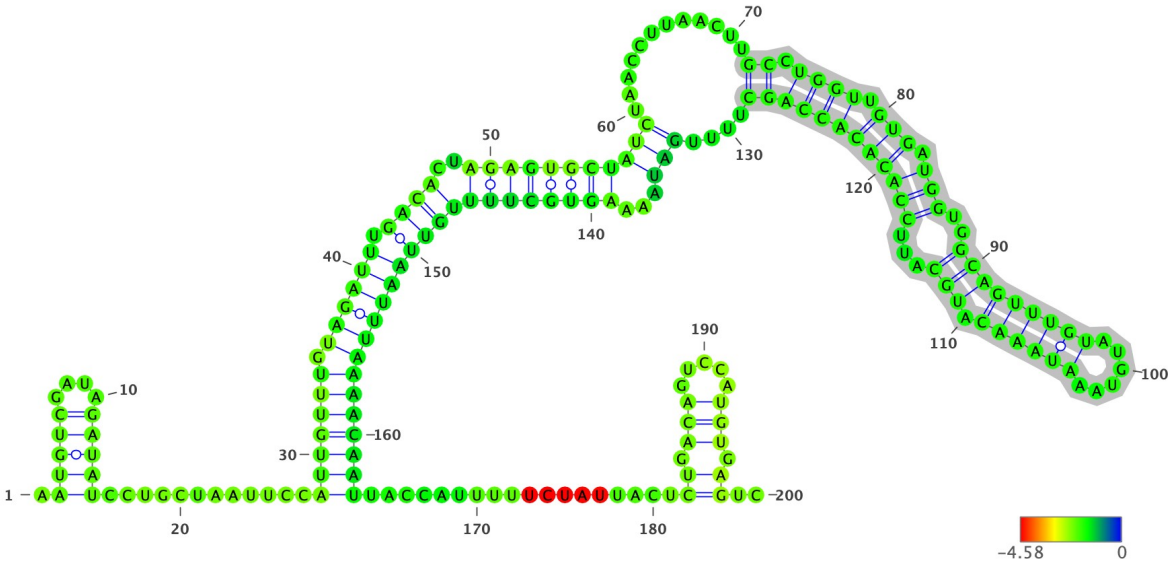
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 19272 to 19328 (nt 72 to 128)

```
5'-GCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGC-3'
5'-((.((((.(((.(((..((((((((((......))))))).)))...)))))))))))))-3'
Motif MFE = -20.3; z-score = -2.9; 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 = -0.85; 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(+)

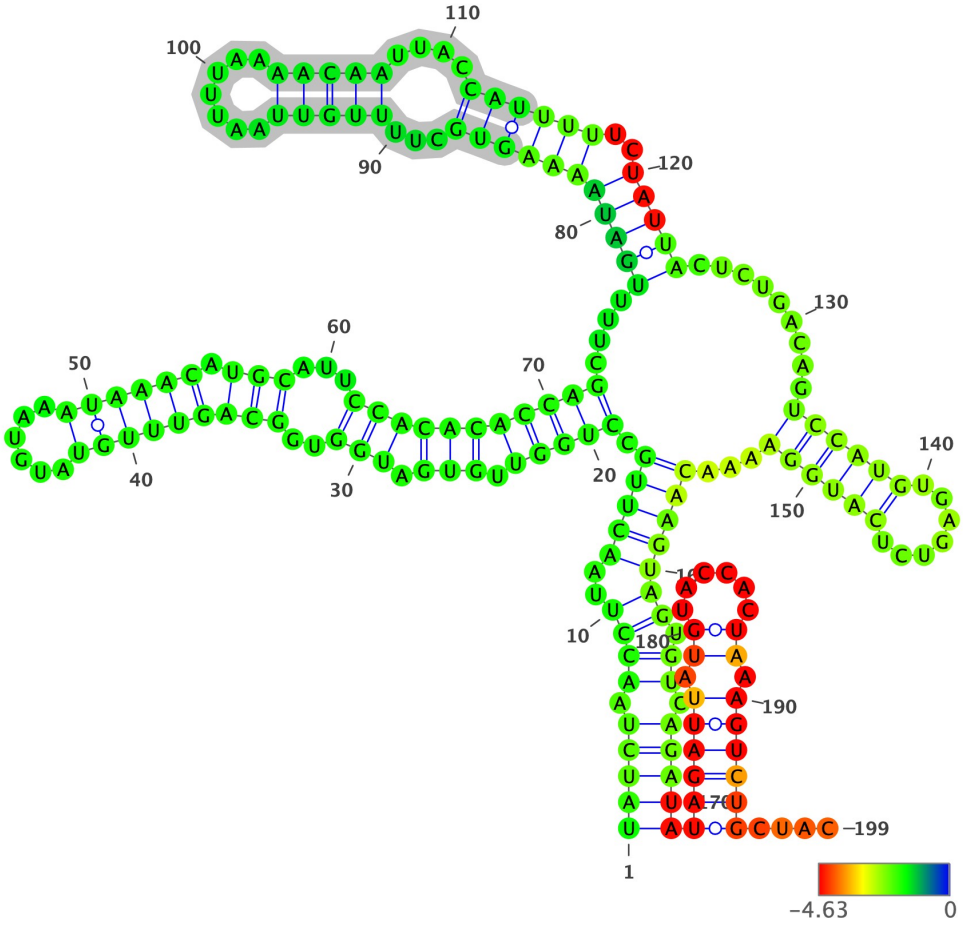
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 333 from nt 19340 to 19369 (nt 85 to 114)

```
5'-GUGCUUUUGUUAAUUUAAAACAAUUACCAU-3'
5'-(((...(((((.......)))))....)))-3'
Motif MFE = -0.9; z-score = 0.24; 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 = -1.87; 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(+)

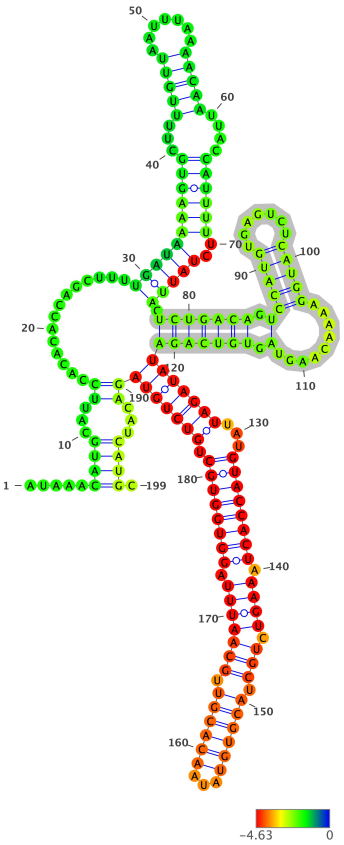
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 334 from nt 19381 to 19424 (nt 78 to 121)

```
5'-UCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGA-3'
5'-(((((((.((((((.......)))))).........).)))))))-3'
Motif MFE = -12.4; z-score = -2.57; ED = 5.92
```



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 19304 to 19502 (motif highlighted in silver):

```
5'-AUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAG
UAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGC-3
5'-.....((((...((.............((((((((((...(((((.......)))))....)))))))..)))))).(((((((.((((((.......)))))).........
.).)))))))((((((((...(((((((((.((((.(((.(((((((...)))))))..)))))))..)))))))).)))))))))...)))).-3'
MFE = -49.3; z-score = -3.33; ED = 35.75
```

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(+)

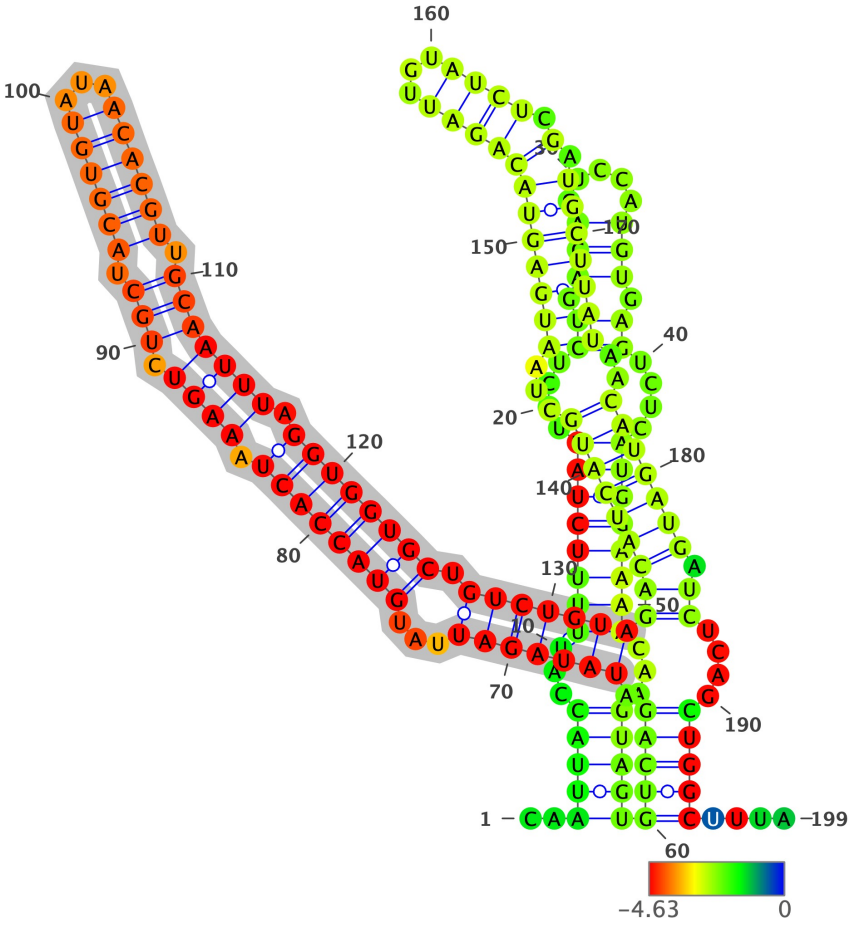
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 335 from nt 19425 to 19492 (nt 66 to 133)

```
5'-UAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUA-3'
5'-(((((((...((((((((.((((.(((.((((((...)))))).)))))))).))))))))).)))))))-3'
Motif MFE = -29.1; z-score = -5.53; 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 = -4.18; 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(+)

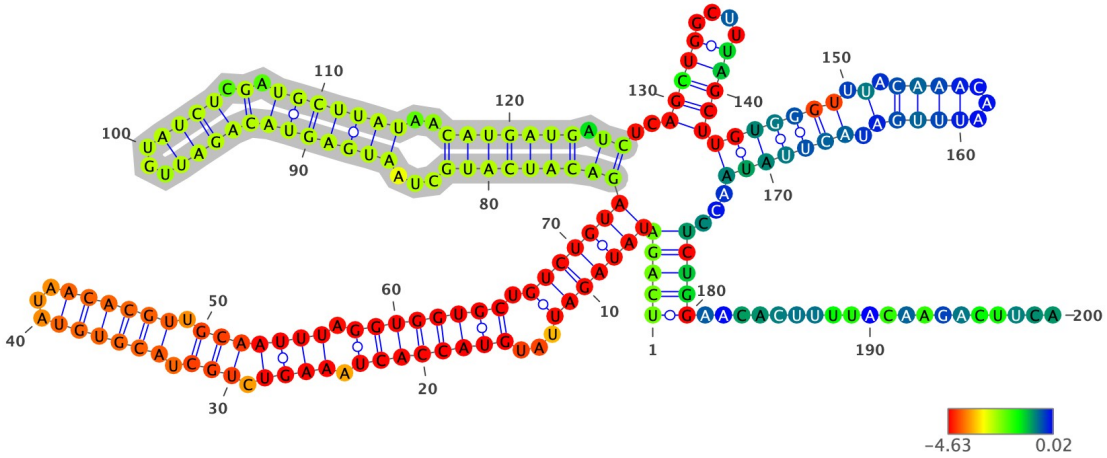
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 336 from nt 19493 to 19545 (nt 74 to 126)

```
5'-GACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUGAUC-3'
5'-(((((((((...(((((((((((...)))).).)))))))..)))))))).))-3'
Motif MFE = -14.1; z-score = -2.61; ED = 5.46
```



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 19420 to 19619 (motif highlighted in silver):

```
5'-UCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCU
UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUCA-3
5'-(((((((((((...((((((((.((((.((((.((((((...)))))).)))))))).))))))))).)))))))(((((((((...(((((((((((...)))).).))))
)))..)))))))).))..(((((....)))))(((((((.(.((((...)))))).)))))))...)))))...................-3'
MFE = -56.0; z-score = -3.77; ED = 14.42
```

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(+)

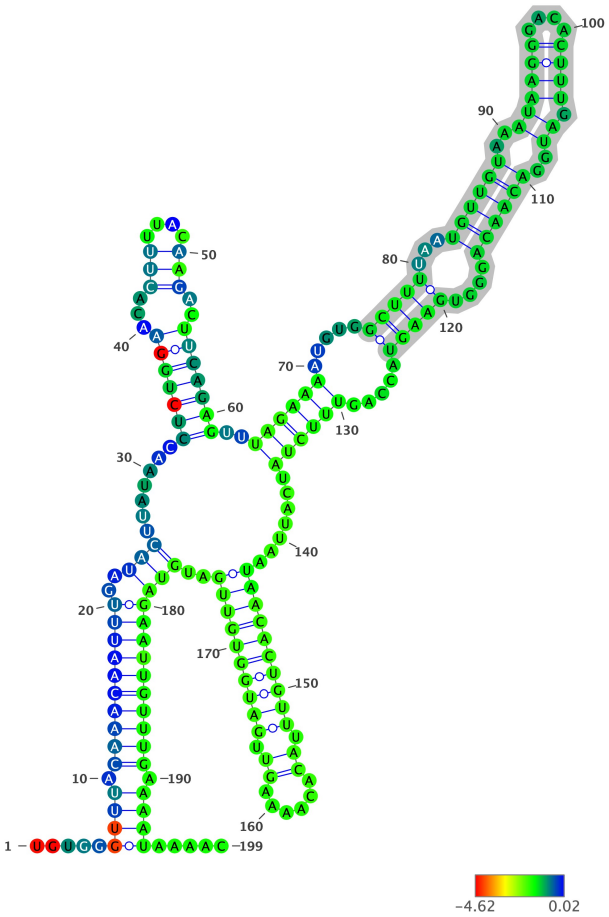
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 19636 to 19685 (nt 75 to 124)

```
5'-GCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGU-3'
5'-(...(...(((((((..(((((((....))))).))..)))))))....)...)-3'
Motif MFE = -11.6; z-score = -2.48; ED = 3.23
```



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 19562 to 19760 (motif highlighted in silver):

```
5'-UGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGAC
AACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAAC-3
5'-.....((((.((((((((((..(((.......(((((((...(((....)))..)))))))..(((((((.....((((((...(((((((..(((((((....))))).))..))
))))).....))))).....))))))).......((((((((((.((......)).))))))))))..))))))))))))).....-3'
MFE = -43.7; z-score = -1.89; ED = 17.09
```

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(+)

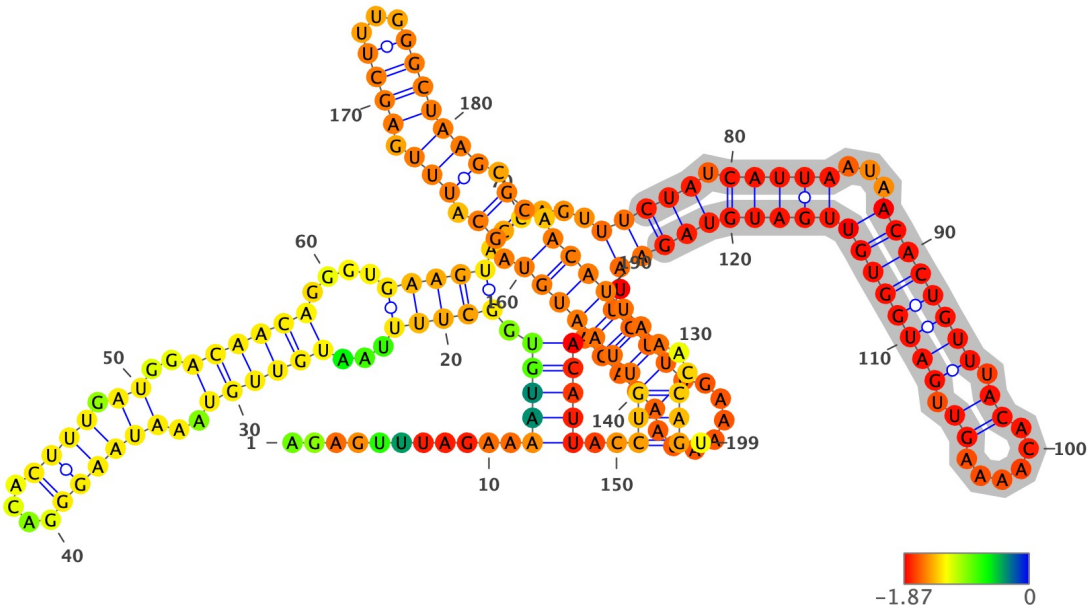
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 338 from nt 19694 to 19741 (nt 76 to 123)

```
5'-CUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAG-3'
5'-(((.(((((...(((((((((.((......)).)))))))))))))))))-3'
Motif MFE = -10.5; z-score = -1.79; ED = 5.3
```



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

Extracted structure model with flanking nucleotides 19619 to 19817 (motif highlighted in silver):

```
5'-AGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUG
GUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGU-3
5'-...........(((((.(((((...((((((..((((((....)))))..))..)))))))....)))))......(((((.(((((...(((((((((.((......)).))))
))))))))))))))).(((((.......)))))))))..((((((((((.((.(((.((((...)))))))).)).)))))))..))).-3'
MFE = -43.4; z-score = -1.37; 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(+)

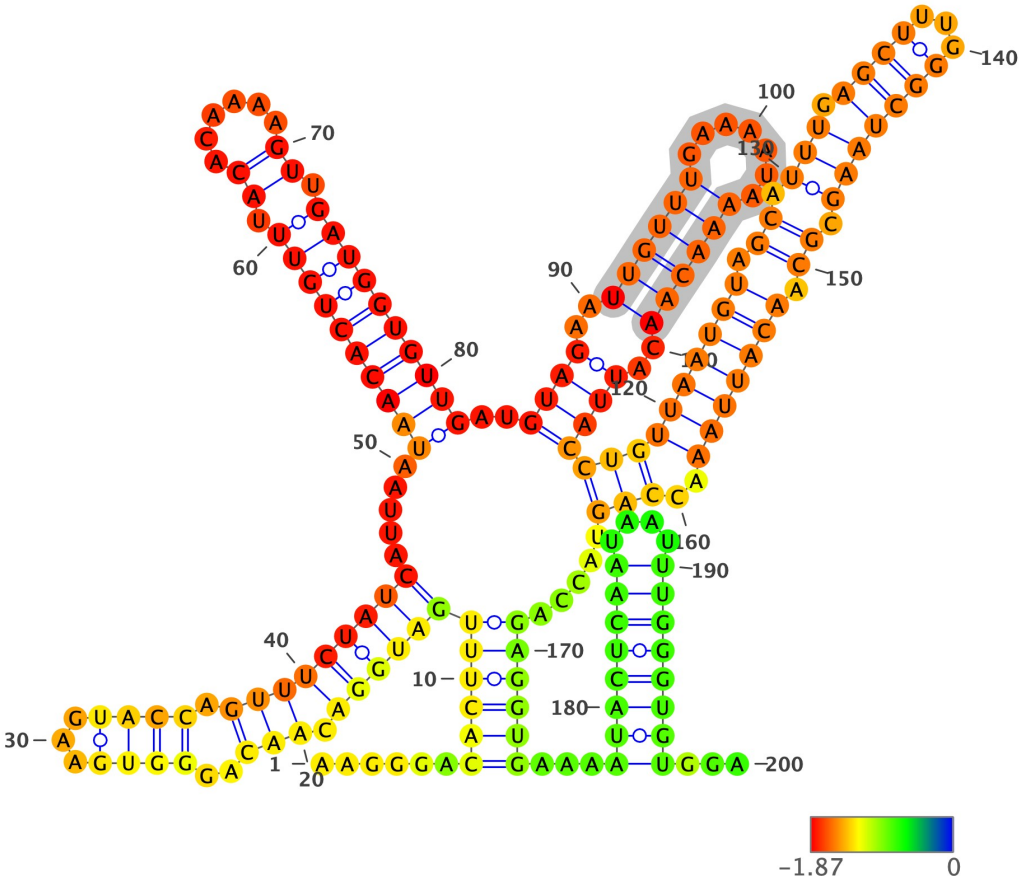
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 339 from nt 19744 to 19762 (nt 91 to 109)

```
5'-UUGUUUGAAAAUAAAACAA-3'
5'-((((((.......))))))-3'
Motif MFE = -2.1; z-score = -5.34; 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 19654 to 19853 (motif highlighted in silver):

```
5'-AAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACA
UUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGA-3
5'-......((((((((((((.((((..(((((...)))))..)))))))))).....((((((((((.((......)).)))))))))).((((..((((((.......))))))..
))))((((((((((.((.(((.(((((...)))))))).)).)))))))..)))).....)))))).((((((((....))))))))...-3'
MFE = -48.3; z-score = -2.31; ED = 33.3
```

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

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

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

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

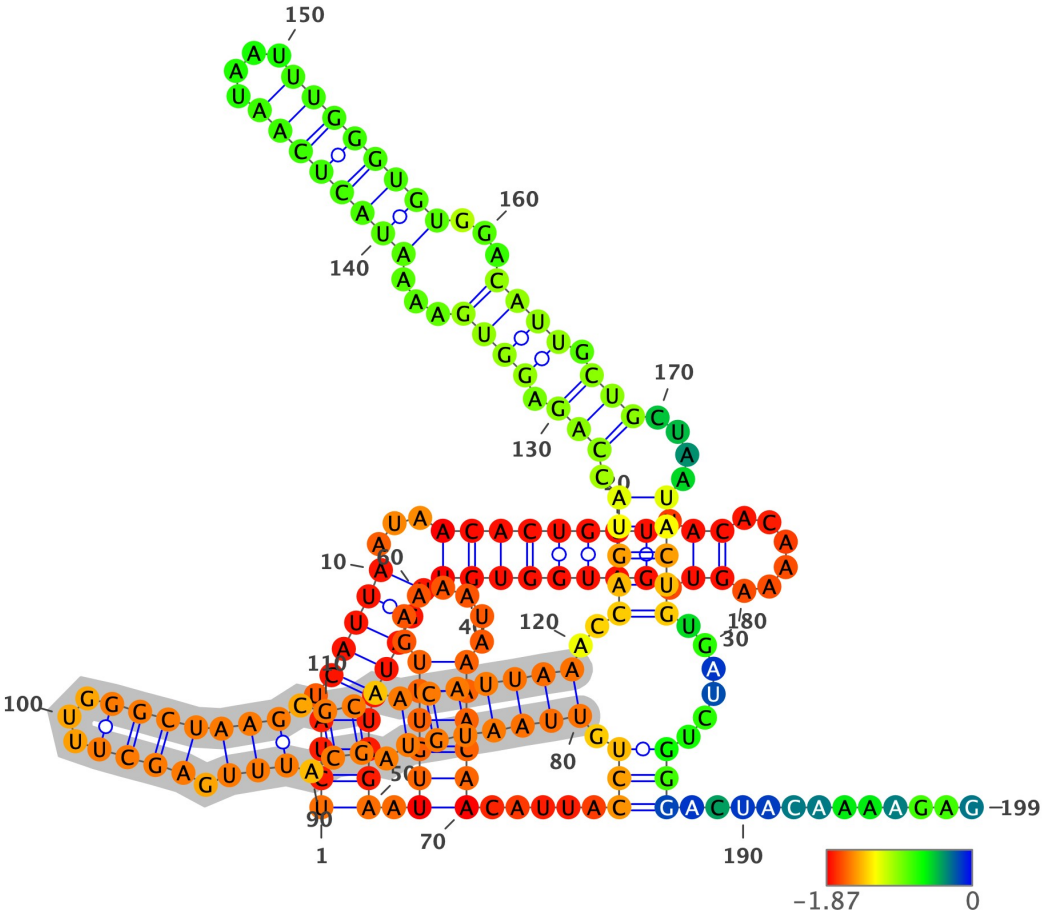
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 340 from nt 19772 to 19811 (nt 80 to 119)

```
5'-UUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAA-3'
5'-(((((((.((.(((.((((...)))))))).)).)))))))-3'
Motif MFE = -10.5; z-score = -2.35; 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 = -1.55; 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(+)

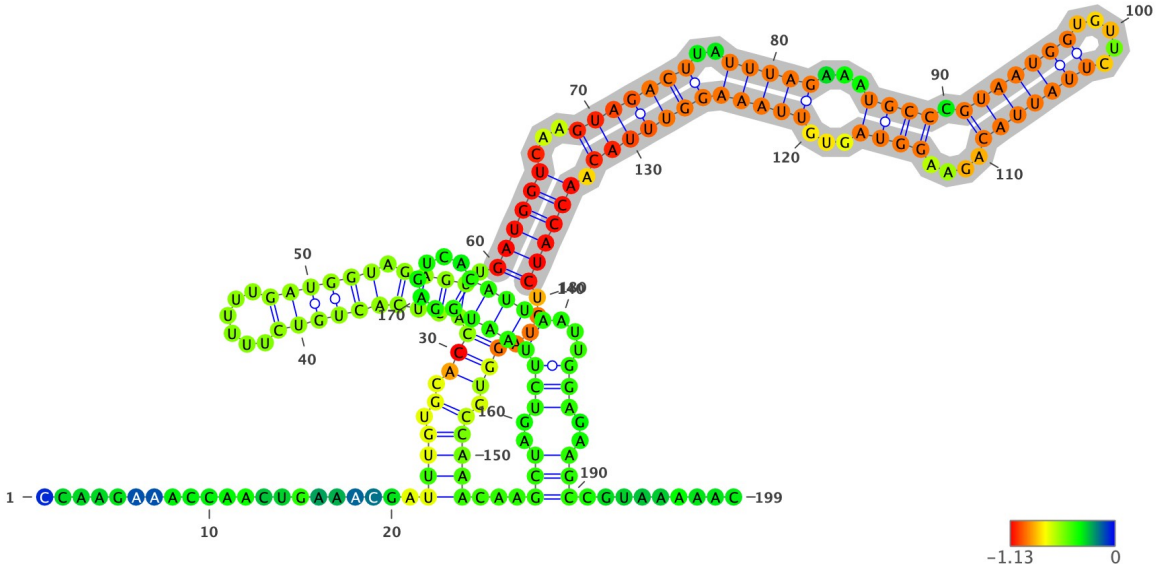
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 341 from nt 20002 to 20081 (nt 60 to 139)

```
5'-GAUGGUCAAGUAGACUUAUUUAGAAAUGCCCGUAAUGGUGUUCUUAUUACAGAAGGUAGUGUUAAAGGUUUACAACCAUC-3'
5'-((((((...((((.....................................................)))).))))))-3'
Motif MFE = -20.7; z-score = -2.4; 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 = -0.62; 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(+)

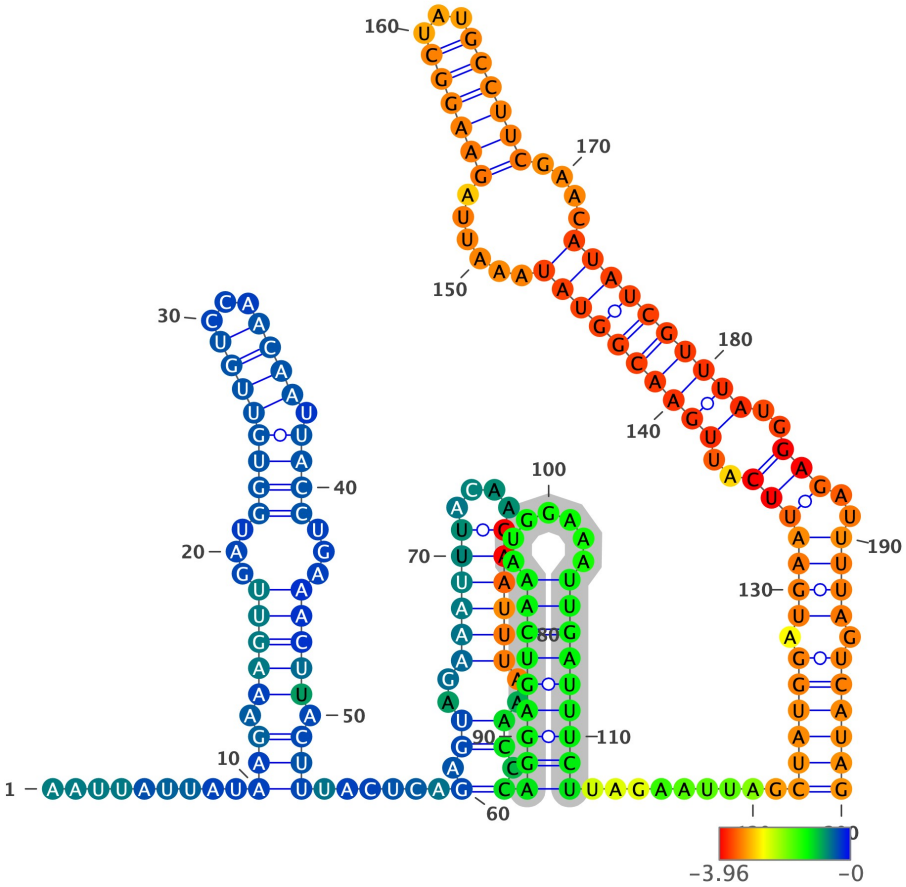
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 342 from nt 20236 to 20260 (nt 88 to 112)

```
5'-AGGAGUCAAAUGGAAAUUGAUUUCU-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.1; z-score = -4.25; 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 = -2.3; 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(+)

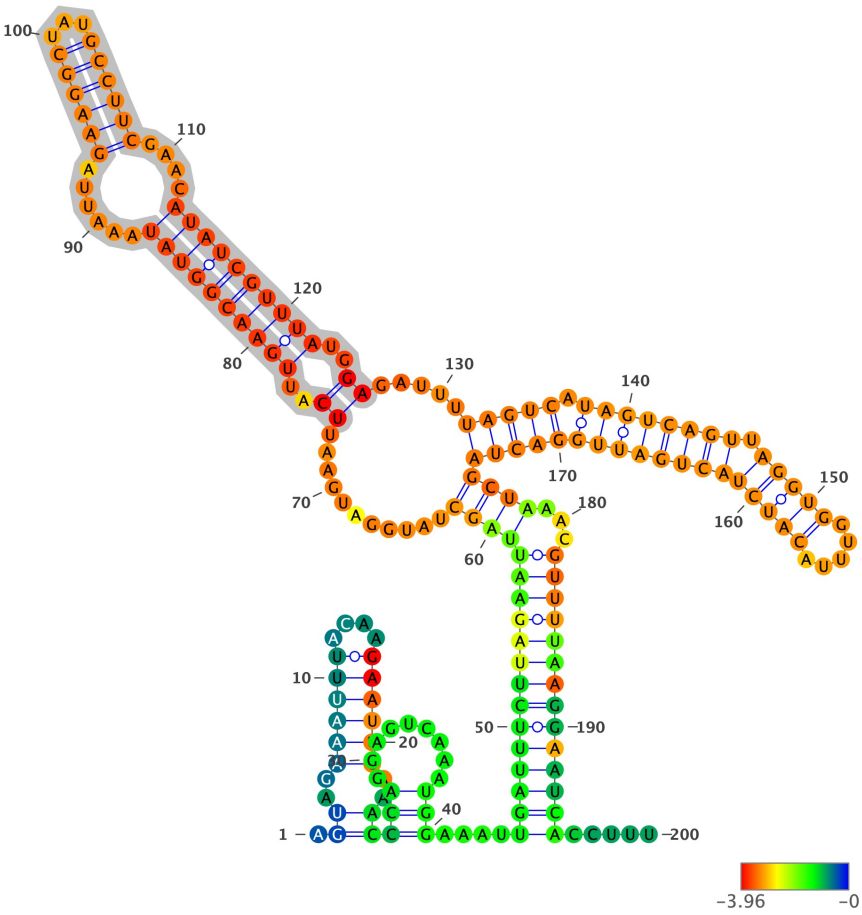
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 343 from nt 20282 to 20334 (nt 74 to 126)

```
5'-UCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGA-3'
5'-((..(((((((((((.....((((((...))))))....)))))))))))..))-3'
Motif MFE = -18.3; z-score = -4.28; 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 = -4.6; 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(+)

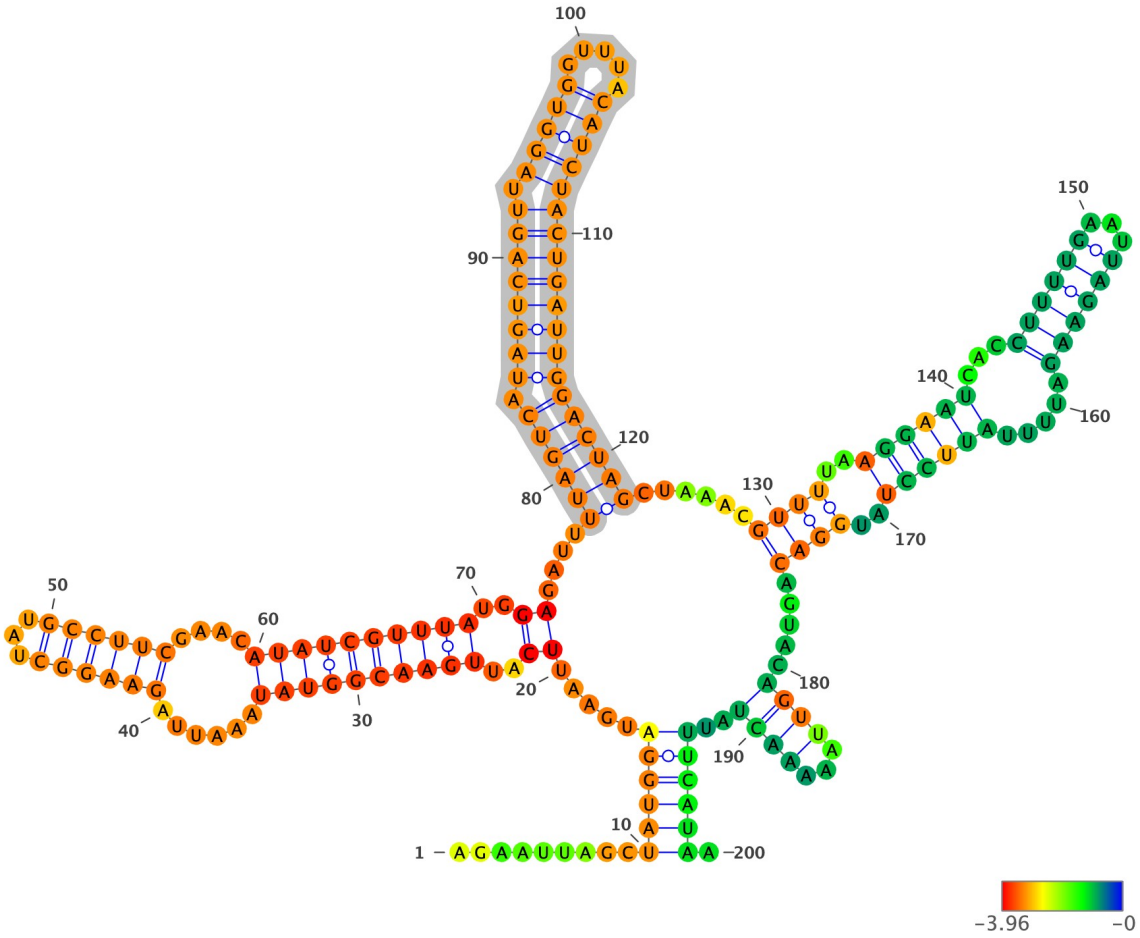
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 344 from nt 20339 to 20383 (nt 78 to 122)

```
5'-UUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAG-3'
5'-((((((.(((((((((.(((((.....)))))))))))))))))))-3'
Motif MFE = -20.0; z-score = -5.75; 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 = -3.68; 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(+)

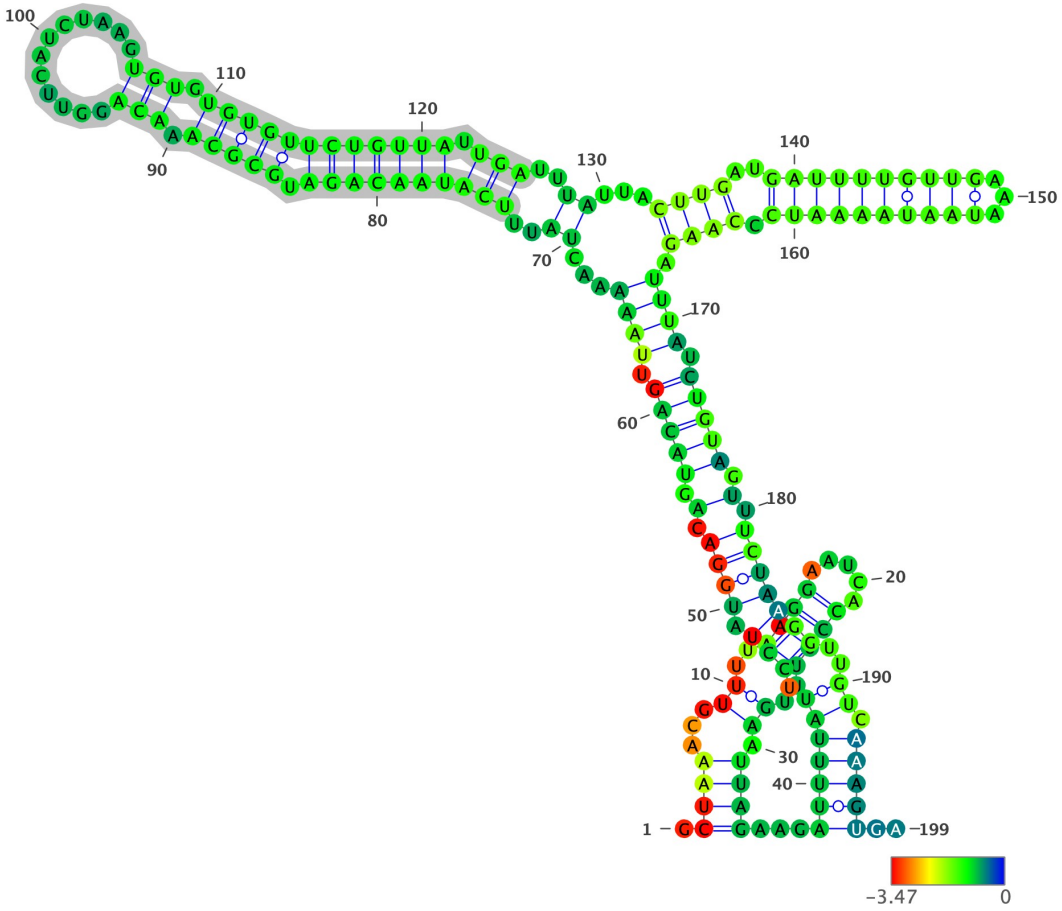
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 345 from nt 20456 to 20507 (nt 74 to 125)

```
5'-UCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGA-3'
5'-((((((((((.(((((.(((............))).))))))))))))).)))-3'
Motif MFE = -14.4; z-score = -2.38; ED = 12.78
```



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 20383 to 20581 (motif highlighted in silver):

```
5'-GCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUG
UGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGA-3
5'-.((((...((..((((.....))))..)).))))...(((((((.(((.((((.(.(((((.((((...((..((((((((((.(((((.(((............))).))
))))))))))).)))..))...((((..((((((((((...))))))))))).)))).)))).)))))).).)))))))..)).)))))..-3'
MFE = -39.1; z-score = -1.02; ED = 50.6
```

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(+)

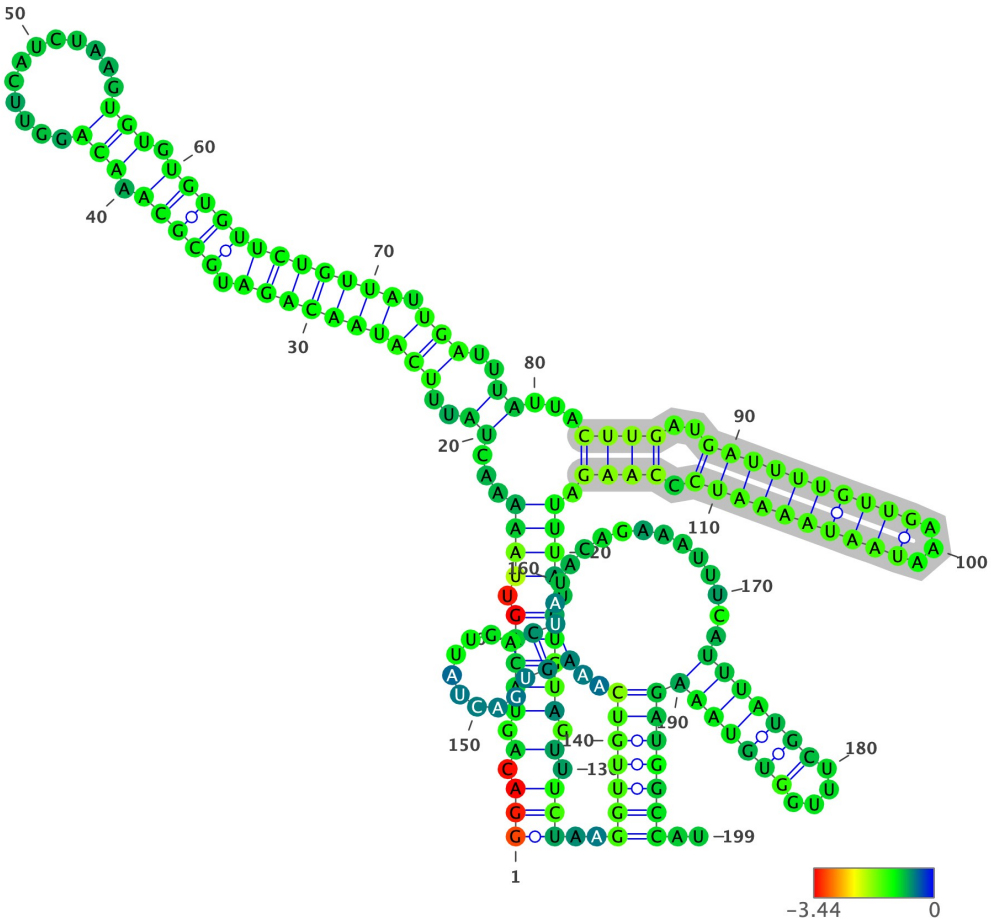
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 346 from nt 20515 to 20548 (nt 83 to 116)

```
5'-CUUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAAG-3'
5'-((((..((((((((((...)))))))))).))))-3'
Motif MFE = -7.4; z-score = -2.88; 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 = -1.83; 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(+)

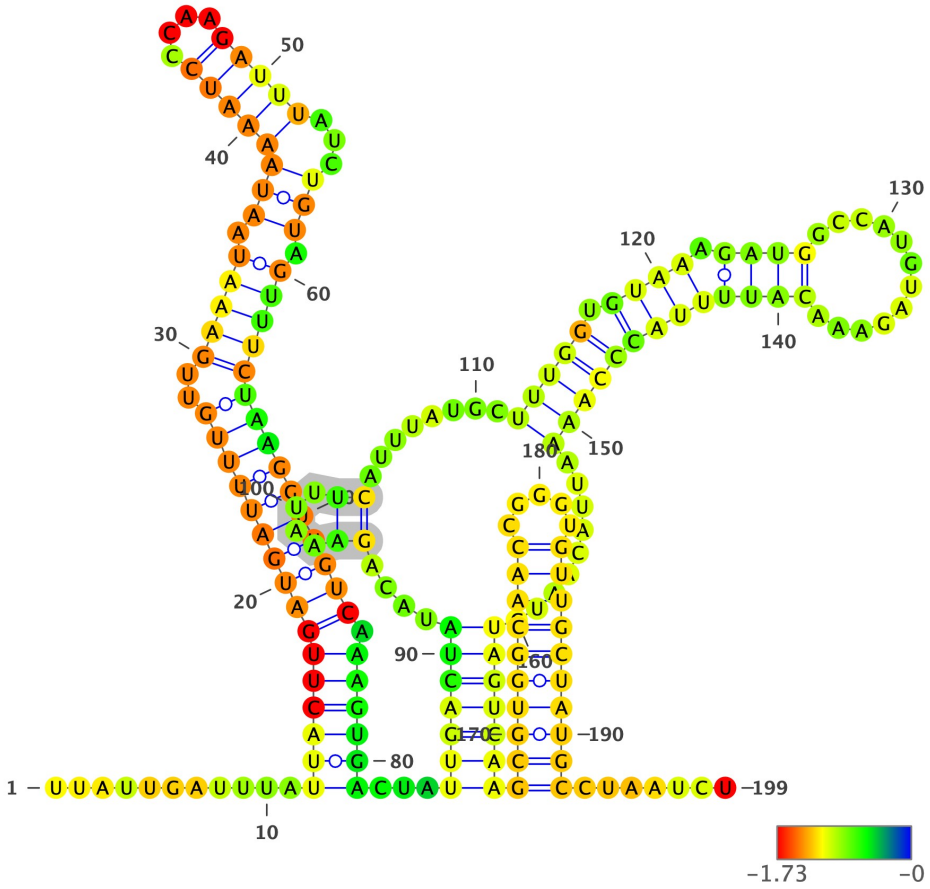
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 347 from nt 20596 to 20603 (nt 96 to 103)

```
5'-GAAAUUUC-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 = -1.46; 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(+)

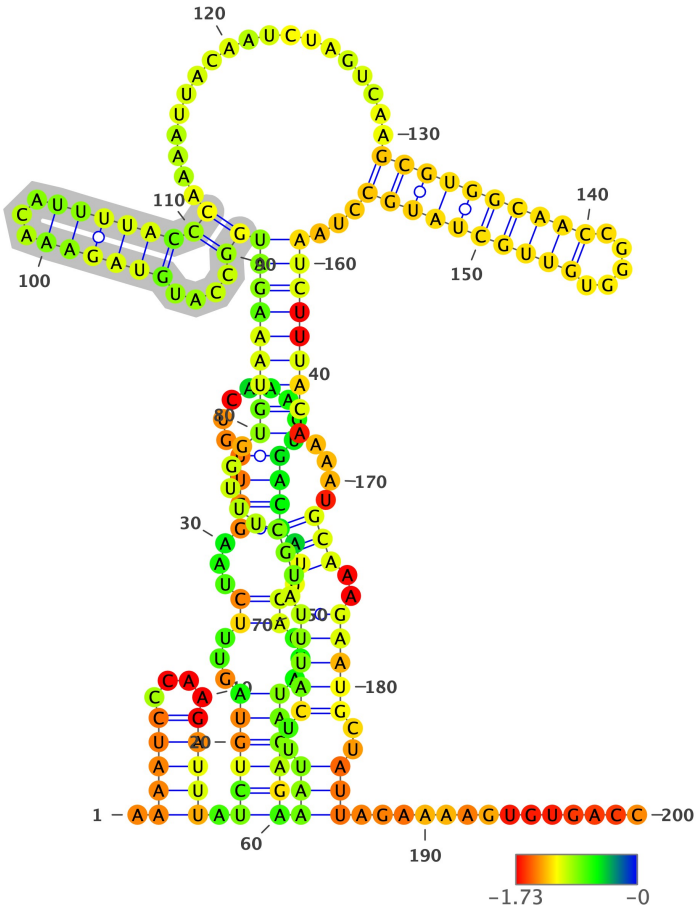
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 348 from nt 20626 to 20648 (nt 89 to 111)

```
5'-GGCCAUGUAGAAACAUUUUACCC-3'
5'-(......(((.......)))..)-3'
Motif MFE = -1.2; z-score = 0.12; 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 20538 to 20737 (motif highlighted in silver):

```
5'-AAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCC
AAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGUGUGACC-3
5'-.(((((....))))).((((((...((...((((........))))...))...))))))(((..(((((.(((.....((((((((((....((((((...))))))))
...................((((((((((.....)))))))))...))))))))))....)))..)))))..)))...............-3'
MFE = -38.8; z-score = -0.74; ED = 49.16
```

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(+)

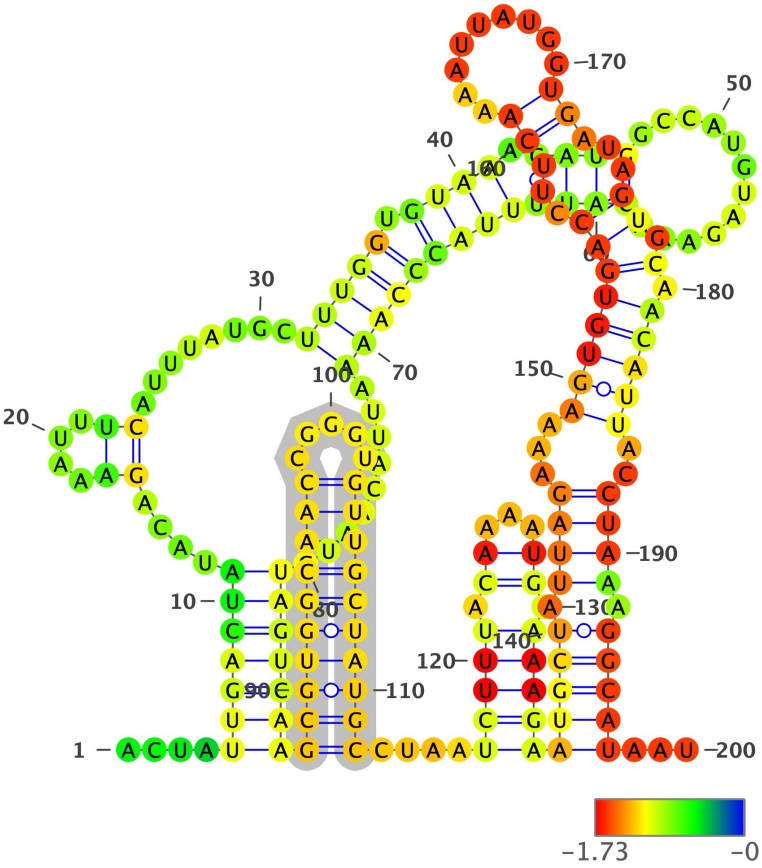
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 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 20668 to 20692 (nt 88 to 112)

```
5'-GCGUGGCAACCGGGUGUUGCUAUGC-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -13.0; z-score = -3.08; 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 = -1.07; 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(+)

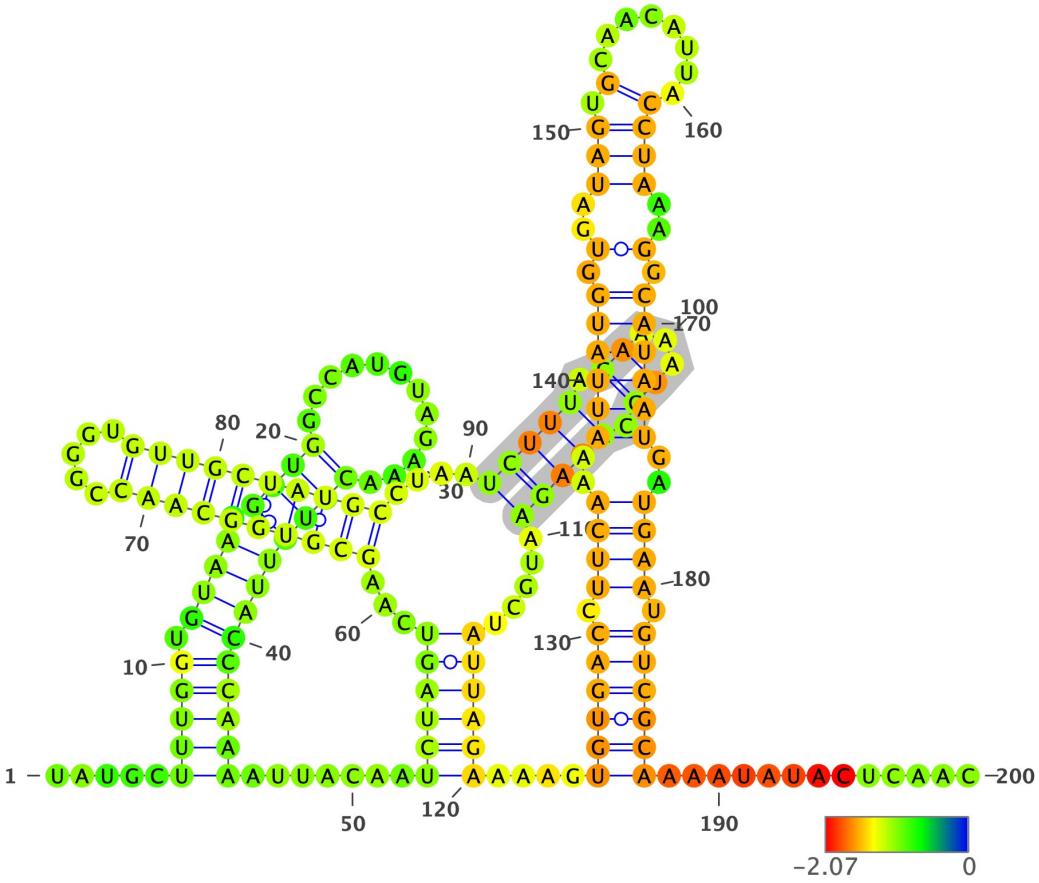
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 350 from nt 20697 to 20715 (nt 91 to 109)

```
5'-UCUUUACAAAAUGCAAAGA-3'
5'-((..(.(.....).)..))-3'
Motif MFE = -0.8; z-score = -1.59; ED = 2.12
```



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 20607 to 20806 (motif highlighted in silver):

```
5'-UAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAU
GCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAAC-3
5'-.....(((((.((((.((((.............)))))))))))))).......((((((...((((((((((.....)))))))))).....(((((.((...)).)))))..
...))))))....((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))..............-3'
MFE = -44.2; z-score = -2.27; ED = 20.91
```

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

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

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

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

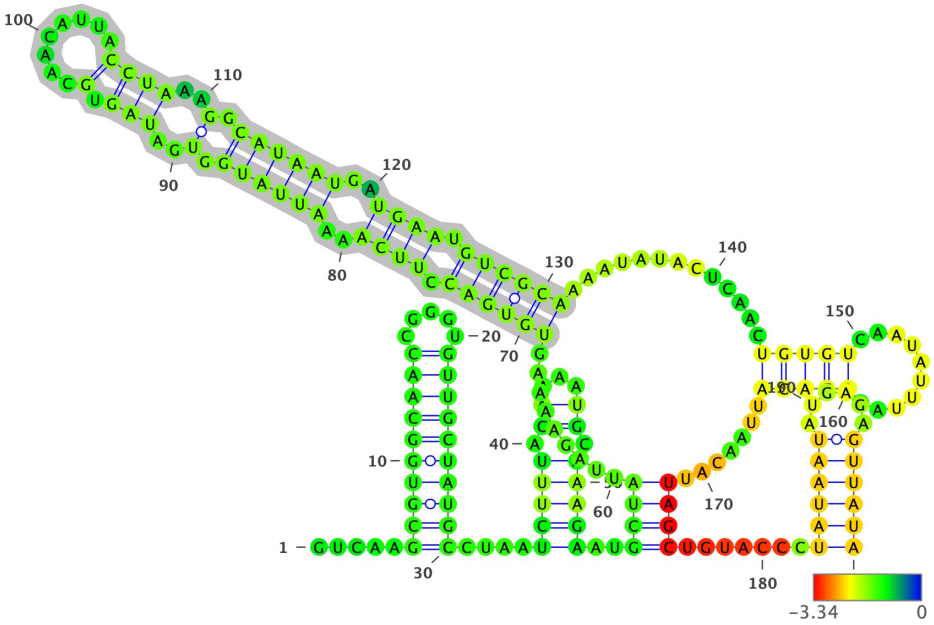
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 351 from nt 20731 to 20793 (nt 69 to 131)

```
5'-UGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCA-3'
5'-((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))-3'
Motif MFE = -17.6; z-score = -2.99; 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 = -1.4; 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(+)

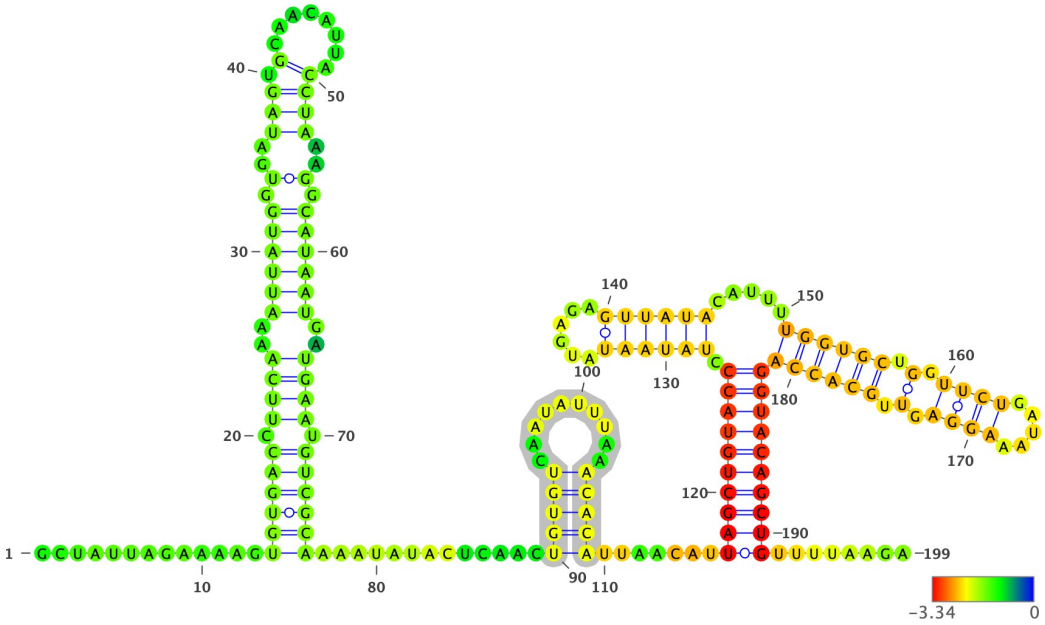
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 352 from nt 20807 to 20826 (nt 90 to 109)

```
5'-UGUGUCAAUAUUUAAACACA-3'
5'-(((((..........)))))-3'
Motif MFE = -1.8; z-score = -1.97; 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 = -3.56; 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(+)

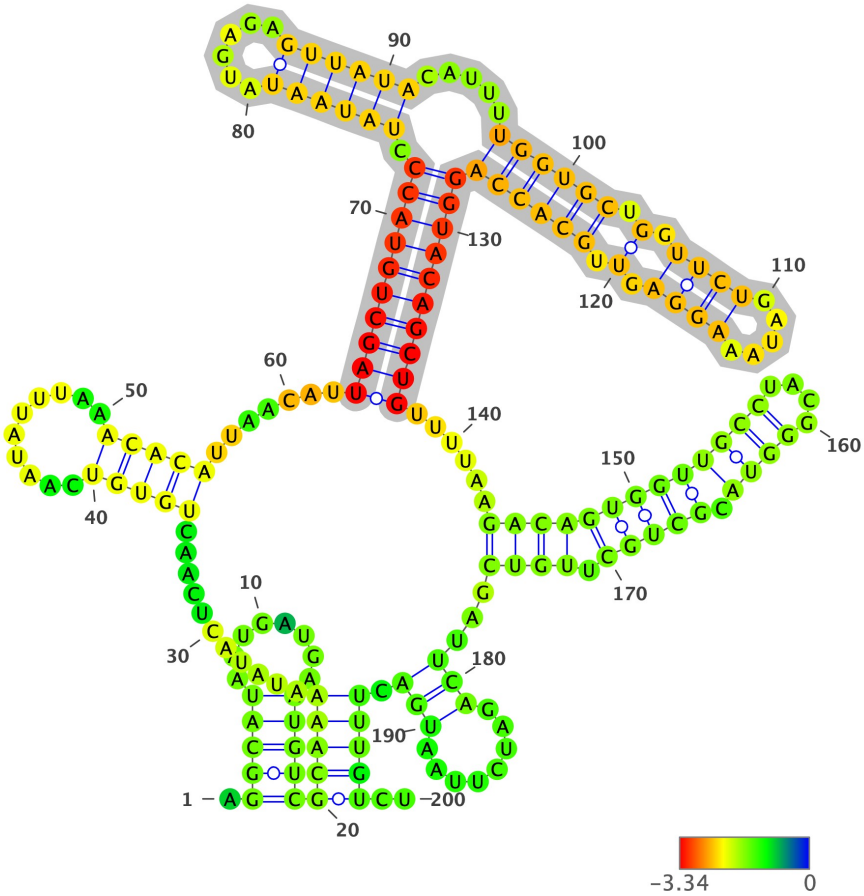
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 353 from nt 20834 to 20908 (nt 63 to 137)

```
5'-UAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUG-3'
5'-((((((((((.((((((......))))))).....((((((.(.((((.....)))).).))))))))))))))))-3'
Motif MFE = -28.8; z-score = -4.13; 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 = -2.48; 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(+)

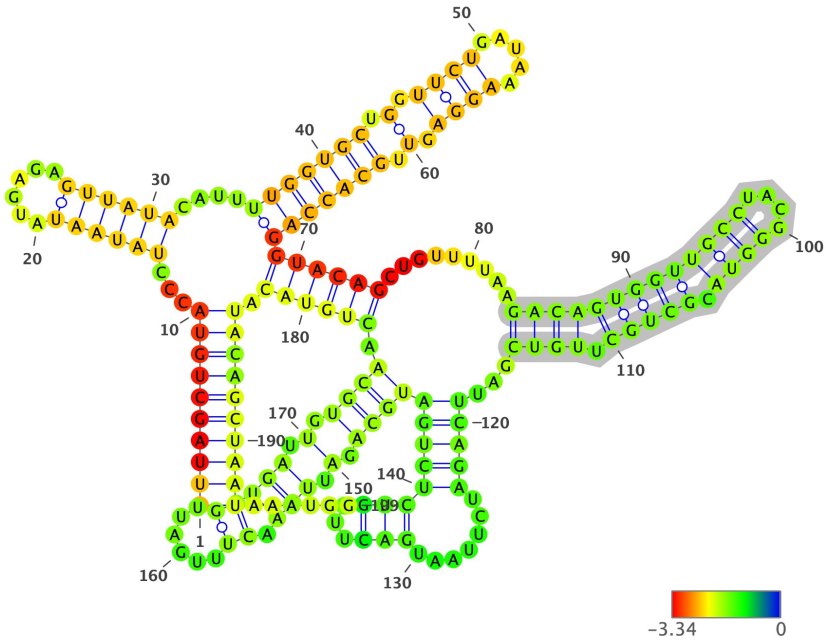
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 354 from nt 20915 to 20946 (nt 84 to 115)

```
5'-GACAGUGGUUGCCUACGGGUACGCUGCUUGUC-3'
5'-(((((((((((((....)))).))))).))))-3'
Motif MFE = -12.6; z-score = -2.4; 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 = -2.96; 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(+)

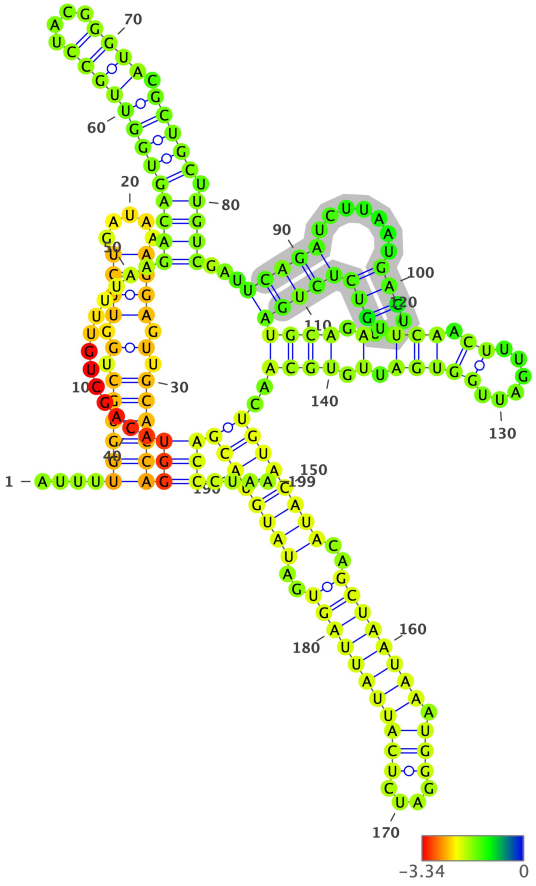
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 355 from nt 20951 to 20974 (nt 88 to 111)

```
5'-CAGAUCUUAAUGACUUUGUCUCUG-3'
5'-(.((.......((.....)))).)-3'
Motif MFE = -0.7; z-score = 0.42; ED = 6.81
```



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 20864 to 21062 (motif highlighted in silver):

```
5'-AUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUG
AUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAA-3
5'-....((((((.(.((((.....)))).).))))))(((.............((((((((((((....)))).))))).))))...(((((.......(((...)))))))
)((((.(.(((.((......))))).).))))..((((((((..((((((((.(((....)))))))))))..))))))))))....-3'
MFE = -58.3; z-score = -2.72; ED = 29.82
```

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

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

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

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

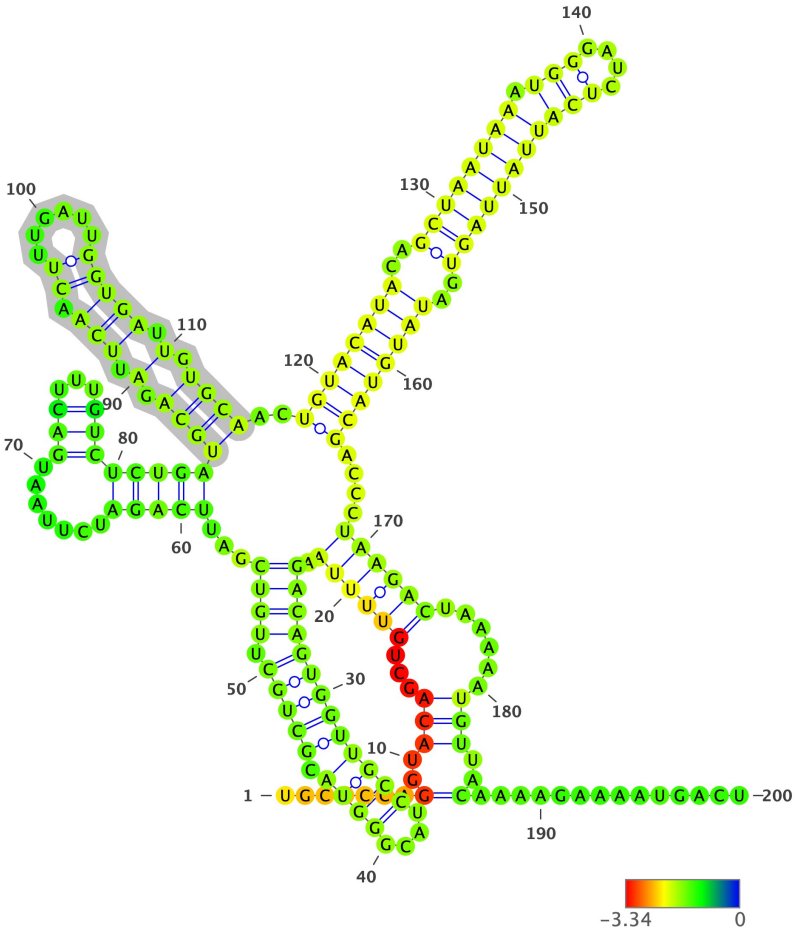
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 356 from nt 20976 to 21006 (nt 85 to 115)

```
5'-UGCAGAUUCAACUUUGAUUGGUGAUUGUGCA-3'
5'-((((.(.(((.((......))))).).))))-3'
Motif MFE = -7.1; z-score = -1.93; ED = 2.55
```



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

Extracted structure model with flanking nucleotides 20892 to 21091 (motif highlighted in silver):

```
5'-UGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUG
UGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACU-3
5'-.......(..(((...((((((.((((((((((((....)))).))))).))))...(((((.......(((...))))))))((((.(.(((.((......))))).).
))))..((((((((..((((((((.(((....)))))))))))..))))))))....))))))......)))..)..............-3'
MFE = -47.3; z-score = -1.19; ED = 42.64
```

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(+)

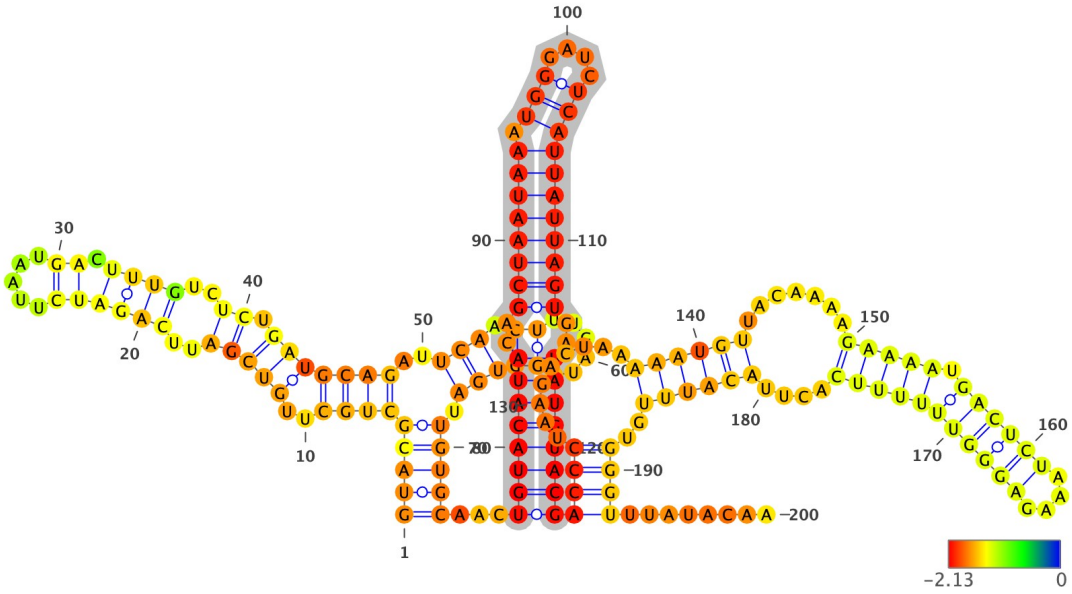
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 357 from nt 21009 to 21055 (nt 77 to 123)

```
5'-UGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACG-3'
5'-((((((((..((((((((.(((....)))))))))))..))))))))-3'
Motif MFE = -16.4; z-score = -4.63; 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 = -1.16; 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(+)

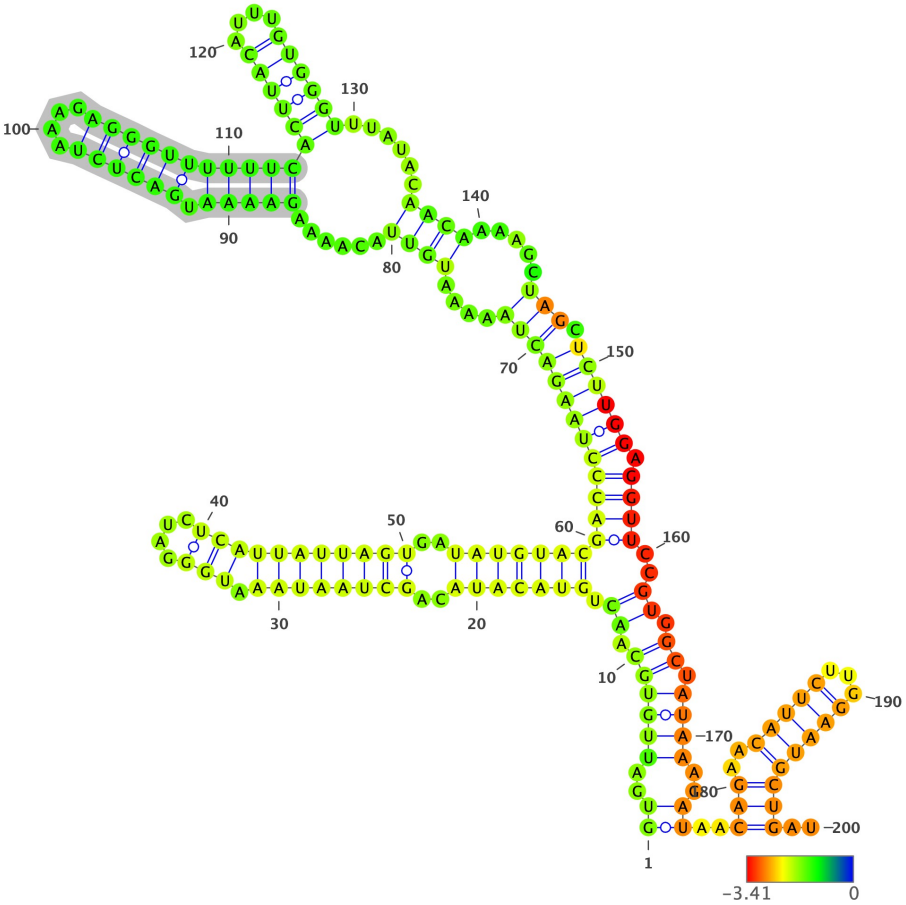
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 358 from nt 21082 to 21108 (nt 87 to 113)

```
5'-GAAAAUGACUCUAAAGAGGGUUUUUUC-3'
5'-(((((.((((((....)))))))))))-3'
Motif MFE = -6.0; z-score = -2.6; ED = 2.81
```



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

Extracted structure model with flanking nucleotides 20996 to 21195 (motif highlighted in silver):

```
5'-GUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUU
UCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU-3
5'-((..((((((.((.(((((((..((((((((.(((....)))))))))))..)))))))((((((((((((....((((......(((((.((((((....)))))))))
))((((((....))))))......))))).....))).)))))).))))..)).)).))))..))..(((..(((((...))))))))..-3'
MFE = -43.9; z-score = -1.53; ED = 49.81
```

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

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

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

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

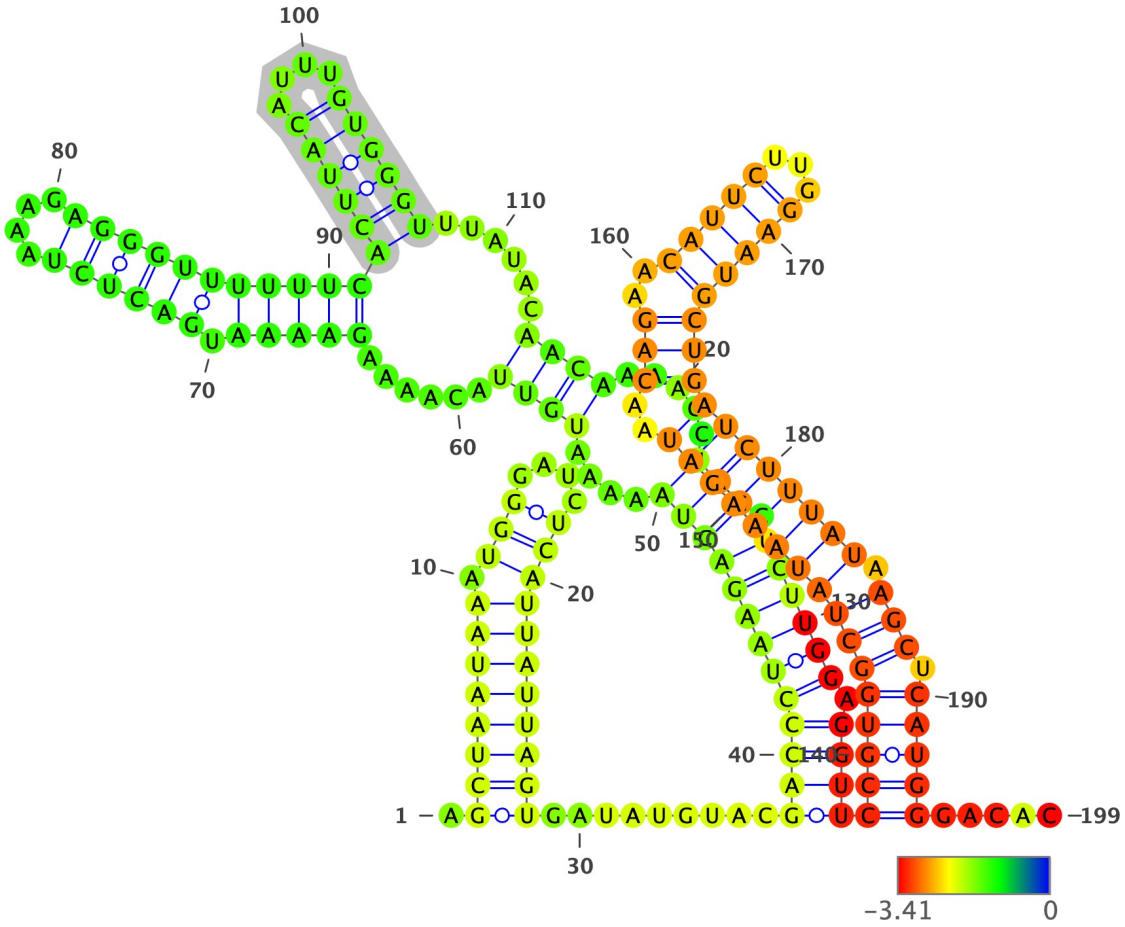
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 359 from nt 21109 to 21124 (nt 92 to 107)

```
5'-ACUUACAUUUGUGGGU-3'
5'-((((((....))))))-3'
Motif MFE = -3.4; z-score = -3.84; ED = 0.5
```



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 21018 to 21216 (motif highlighted in silver):

```
5'-AGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAU
ACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAUCUUUAUAAGCUCAUGGGACAC-3
5'-.((((((((.(((....)))))))))))).........(((((((((((((....((((......(((((.((((((....)))))))))))((((((....))))))....
..))))).....))).)))))).))))((((((((((((((((..(((..(((((...)))))))))))))))).))).)))))).....-3'
MFE = -49.8; z-score = -3.0; ED = 14.59
```

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(+)

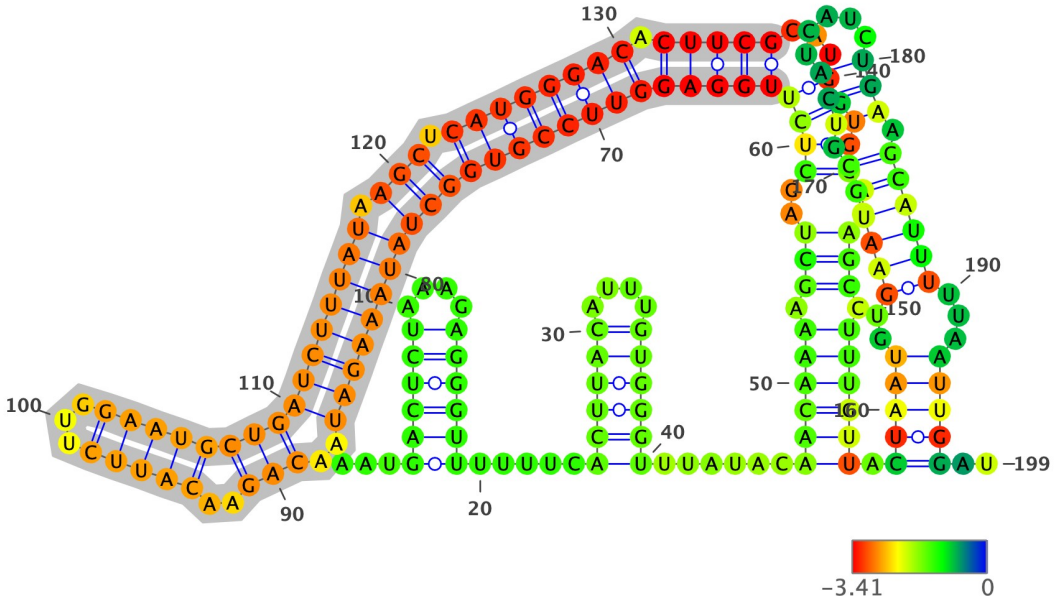
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 360 from nt 21147 to 21220 (nt 63 to 136)

```
5'-UGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAUCUUUAUAAGCUCAUGGGACACUUCG-3'
5'-(((((((((((((((((((((((..(((..(((((...))))))))))))))).))).))))))).)))))-3'
Motif MFE = -30.6; z-score = -4.78; 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 = -3.39; 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(+)

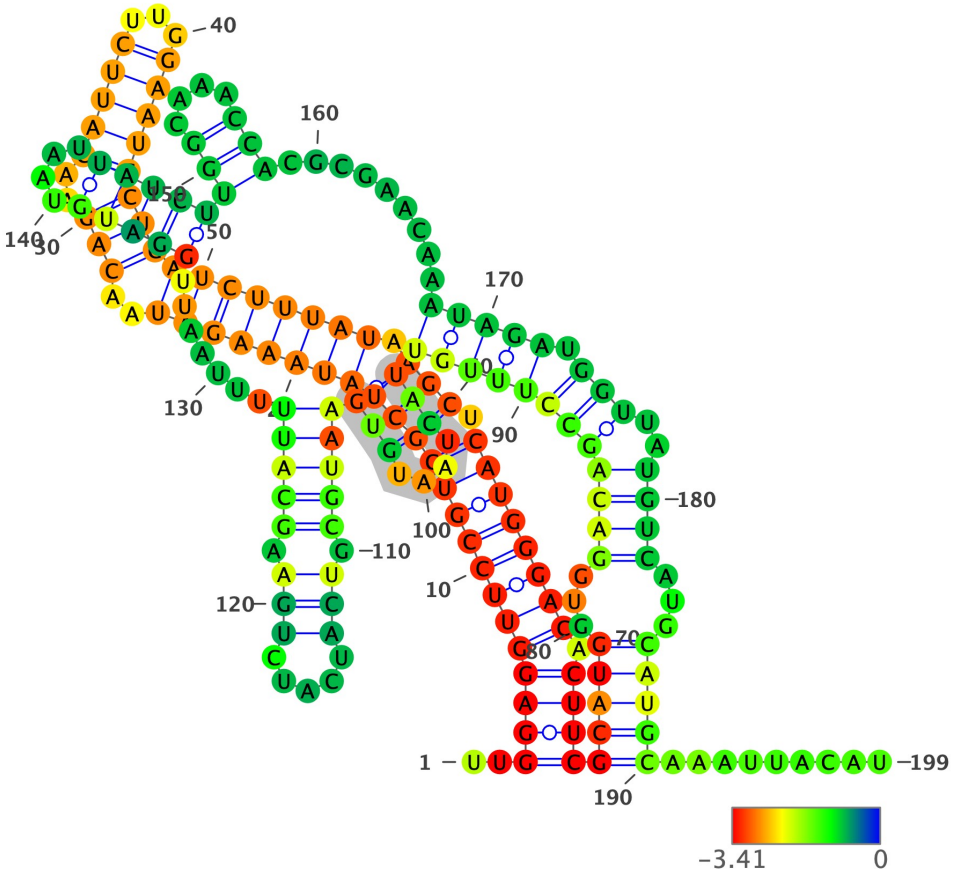
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 361 from nt 21240 to 21249 (nt 95 to 104)

```
5'-UACUAAUGUG-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.19
```



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

Extracted structure model with flanking nucleotides 21146 to 21344 (motif highlighted in silver):

```
5'-UUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAUCUUUAUAAGCUCAUGGGACACUUCGCAUGGUGGACAGCCUUUGUUACUAAUGUGAAUGCGU
CAUCAUCUGAAGCAUUUUUAAUUGGAUGUAAUUAUCUUGGCAAACCACGCGAACAAAUAGAUGGUUAUGUCAUGCAUGCAAAUUACAU-3
5'-..(((((((((((((((((((((((..(((..(((((...)))))))))))))))).))).)))))))).))))(((((...((((((((((((((....)))(((((.(
((.....))).)))))).......(((((....)))))(((....)))........)))))).)))..))))...)))))..........-3'
MFE = -56.2; z-score = -3.32; ED = 31.73
```

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

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

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

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

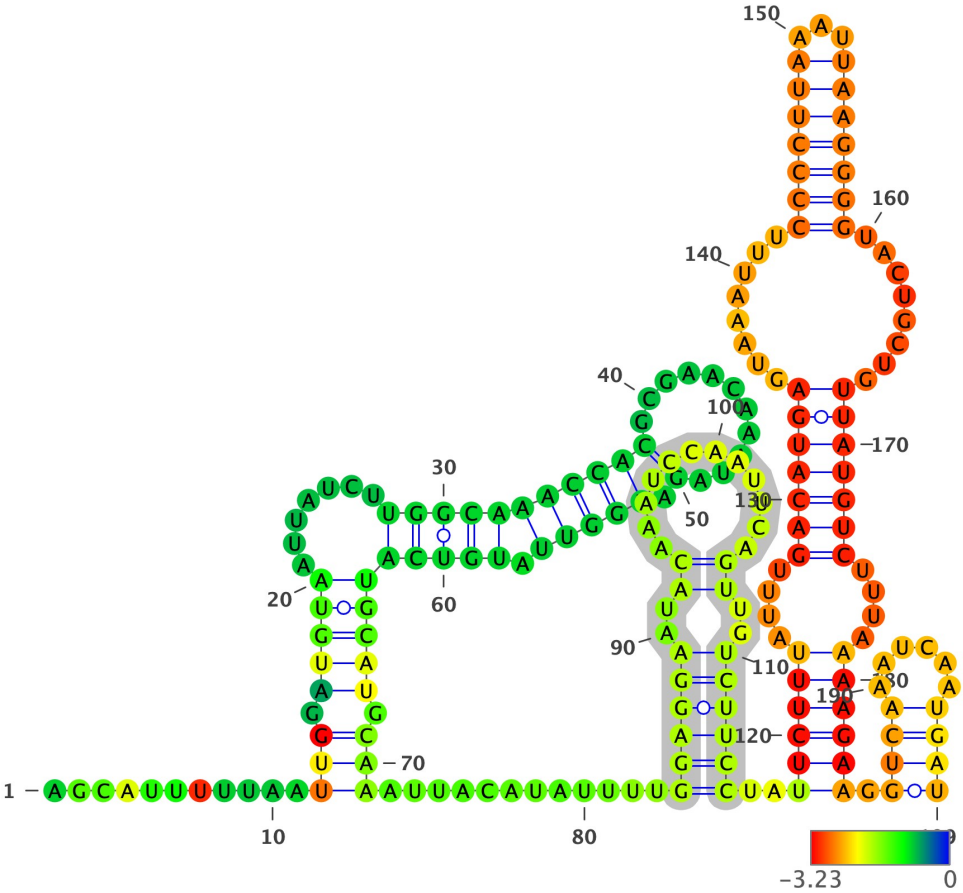
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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

NC_045512.2 (forward strand): Structure number 362 from nt 21350 to 21381 (nt 84 to 115)

```
5'-GGAGGAAUACAAAUCCAAUUCAGUUGUCUUCC-3'
5'-((((((..((............))..))))))-3'
Motif MFE = -6.4; z-score = -1.72; 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 = -1.86; 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(+)

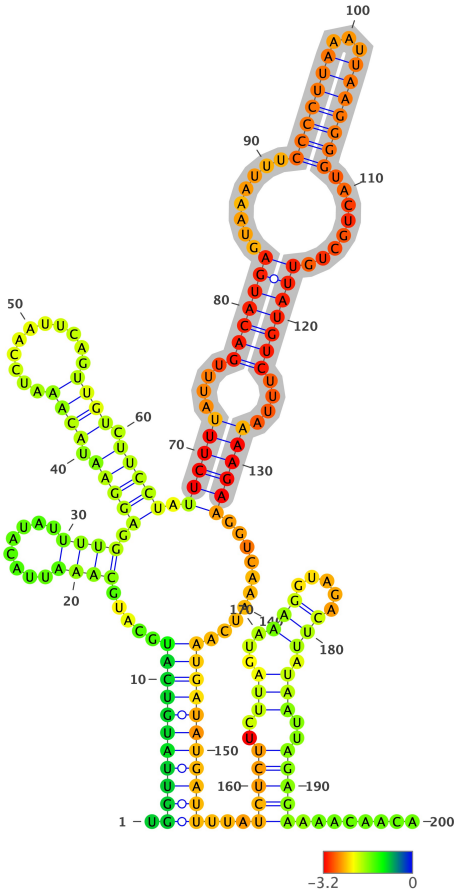
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 363 from nt 21385 to 21449 (nt 68 to 132)

```
5'-UCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGA-3'
5'-((((.....(((((((.........(((((((...)))))))........)))))))).....))))-3'
Motif MFE = -19.7; z-score = -4.23; 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 = -2.35; 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(+)

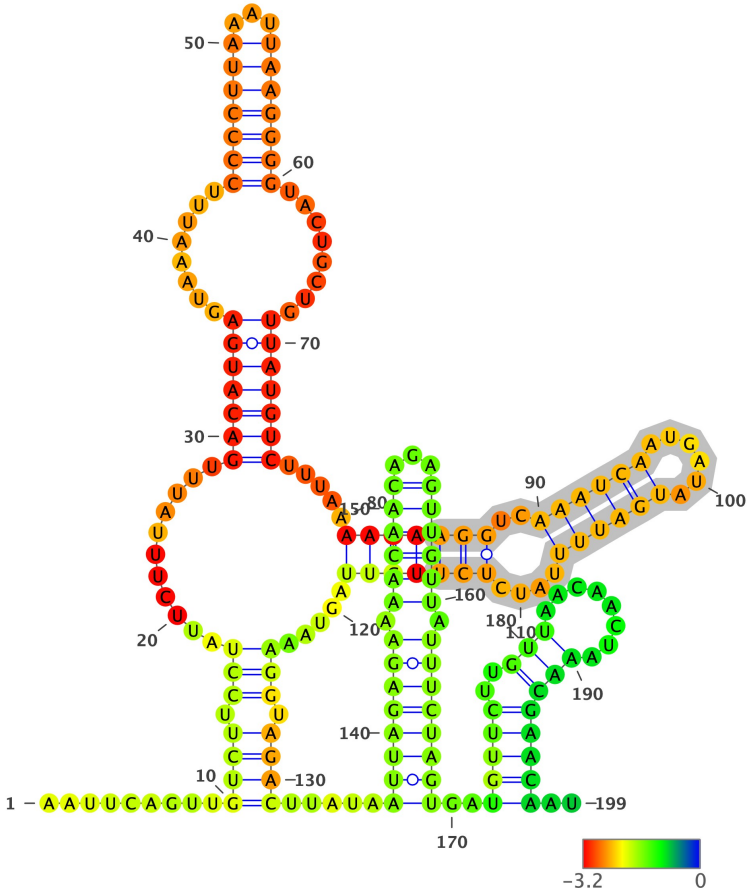
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 364 from nt 21450 to 21479 (nt 85 to 114)

```
5'-AGGUCAAAUCAAUGAUAUGAUUUUAUCUCU-3'
5'-(((..((((((......))))))....)))-3'
Motif MFE = -5.0; z-score = -2.49; 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 = -3.23; 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(+)

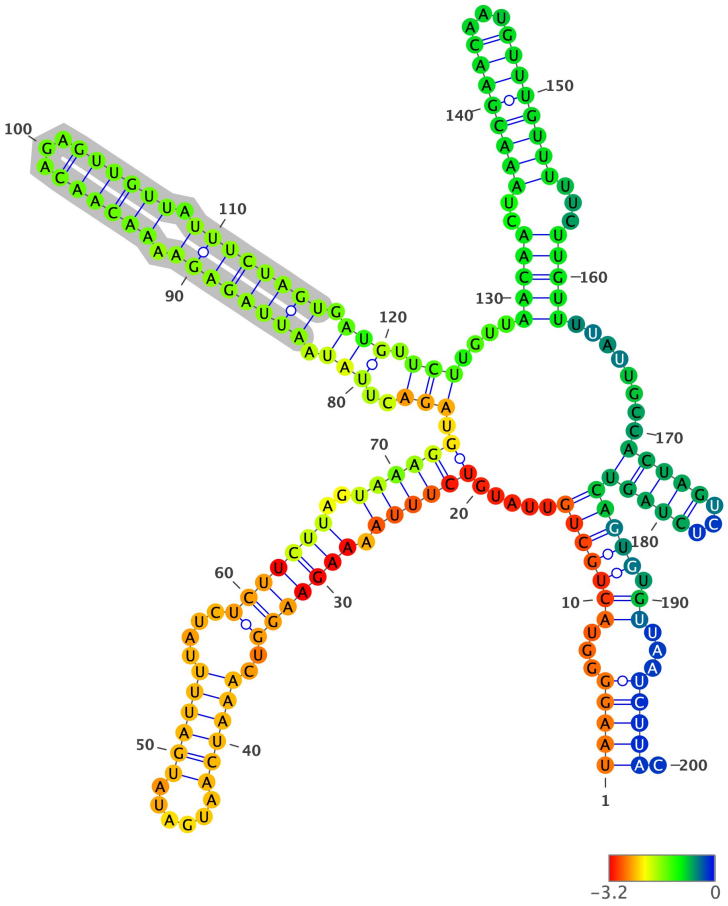
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 365 from nt 21502 to 21534 (nt 84 to 116)

```
5'-AUUAGAGAAAACAACAGAGUUGUUAUUUCUAGU-3'
5'-(((((((((.((((((...)))))).)))))))))-3'
Motif MFE = -10.2; z-score = -5.34; 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 = -0.97; 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(+)

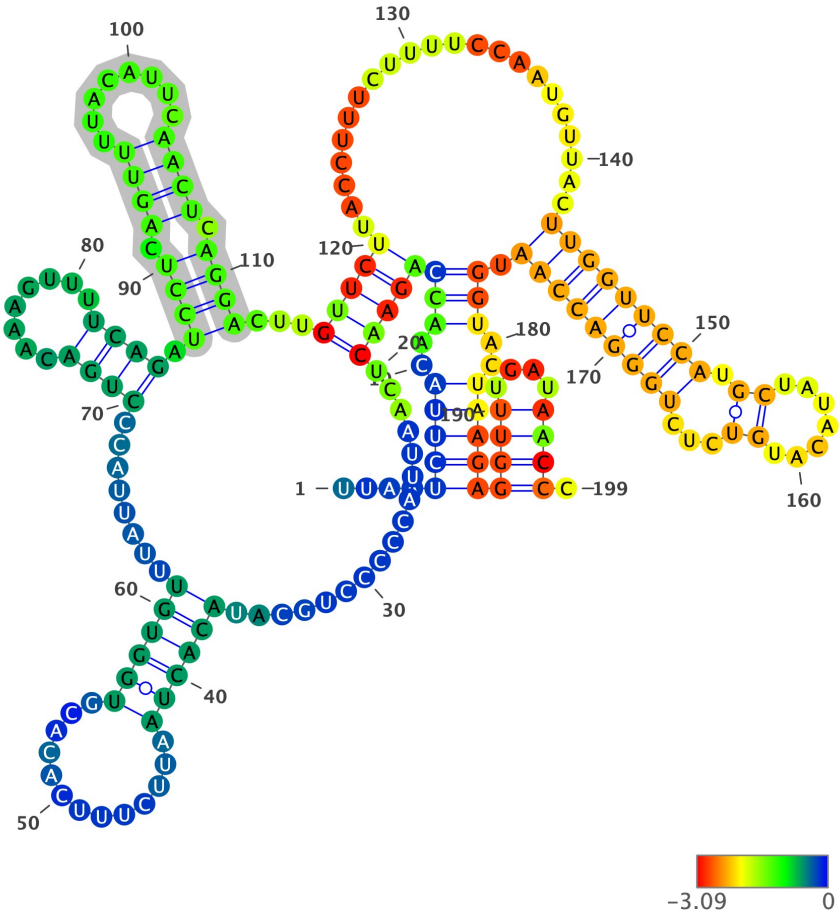
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 366 from nt 21695 to 21720 (nt 87 to 112)

```
5'-UCCUCAGUUUUACAUUCAACUCAGGA-3'
5'-((((.((((........)))).))))-3'
Motif MFE = -5.2; z-score = -3.38; 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 21609 to 21807 (motif highlighted in silver):

```
5'-UUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACGUGGUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGG
ACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCC-3
5'-....(((((..((((((((.................((((((.............))))))........((((........)))).((((.((((........)))).)))
)...)))))......................(((((((((.((.......))...)))))))))).)))..)))))((((....)))).-3'
MFE = -34.3; z-score = -1.77; ED = 31.2
```

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(+)

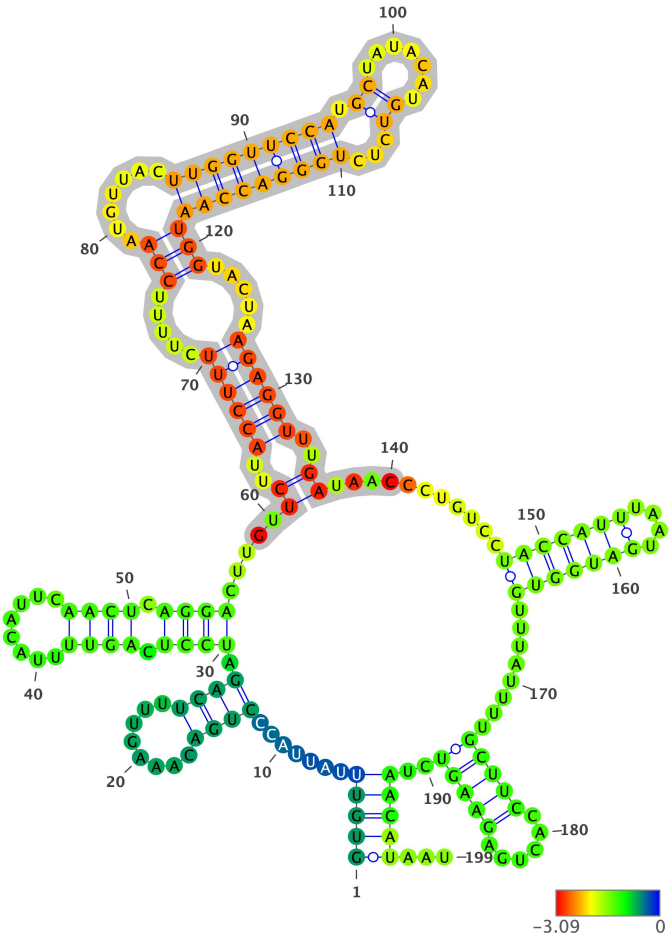
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 367 from nt 21724 to 21805 (nt 59 to 140)

```
5'-GUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAAC-3'
5'-(.((..(((((((.....(((.......(((((((((.(((.......)).)))))))))))))).....)))))))..)).)-3'
Motif MFE = -20.7; z-score = -2.72; 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 21666 to 21864 (motif highlighted in silver):

```
5'-GUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGGACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUG
GGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAU-3
5'-(((((.......((((........)))).(((((.((((........)))).)))).)))).....((..((((((.....(((.......(((((((((.(((.......)).)))
))))))))))).....))))))..)).....((((((.....)))))).(((((((....)))))))........(((((.....)))))..))))))...-3'
MFE = -42.3; z-score = -2.21; ED = 23.14
```

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_gp02, 21563-25384(+)

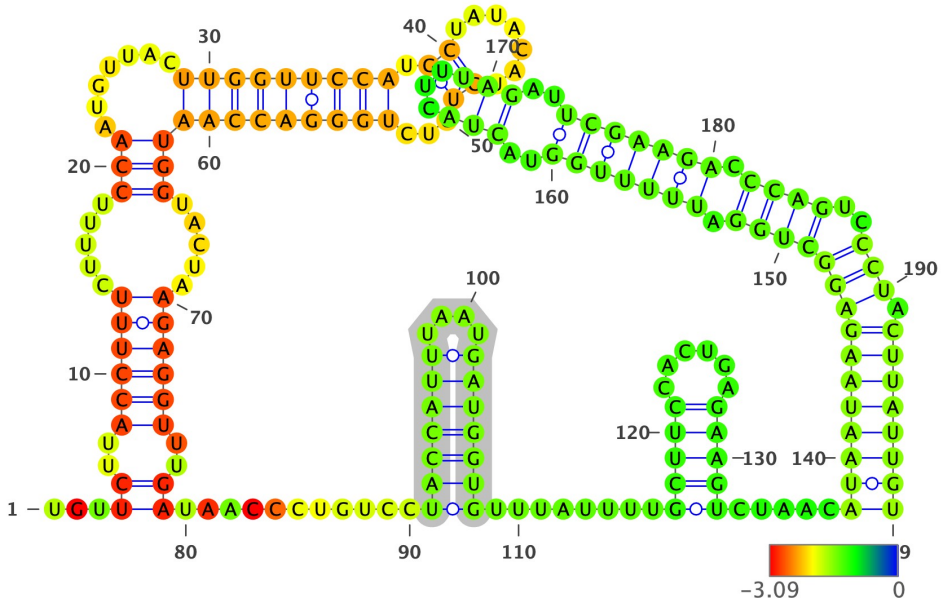
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 368 from nt 21813 to 21830 (nt 91 to 108)

```
5'-UACCAUUUAAUGAUGGUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.8; z-score = -5.61; 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 = -2.63; 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(+)

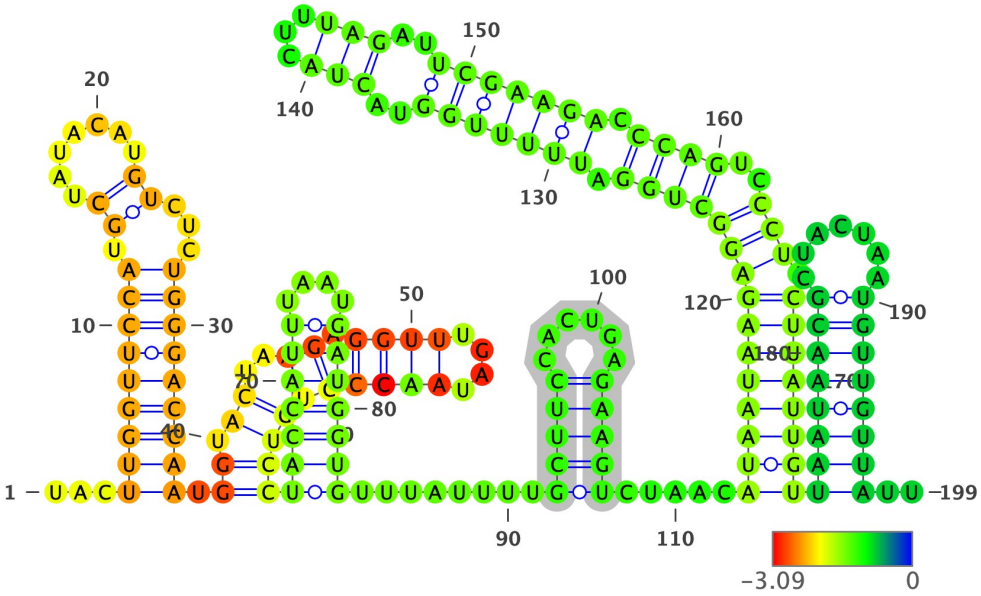
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 369 from nt 21839 to 21854 (nt 92 to 107)

```
5'-GCUUCCACUGAGAAGU-3'
5'-(((((......)))))-3'
Motif MFE = -3.0; z-score = -2.35; ED = 0.68
```



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

Extracted structure model with flanking nucleotides 21748 to 21946 (motif highlighted in silver):

```
5'-UACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAA
CAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUU-3
5'-...(((((((((.((.......))...))))))))).((.((..((.((((....)))))))))))(((((((....)))))))........(((((......)))))....
.((((((((((((((.(((((((..(((...)))..)))))))).))))..))).))))))))((((((((.......))))))))..-3'
MFE = -48.6; z-score = -2.52; 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(+)

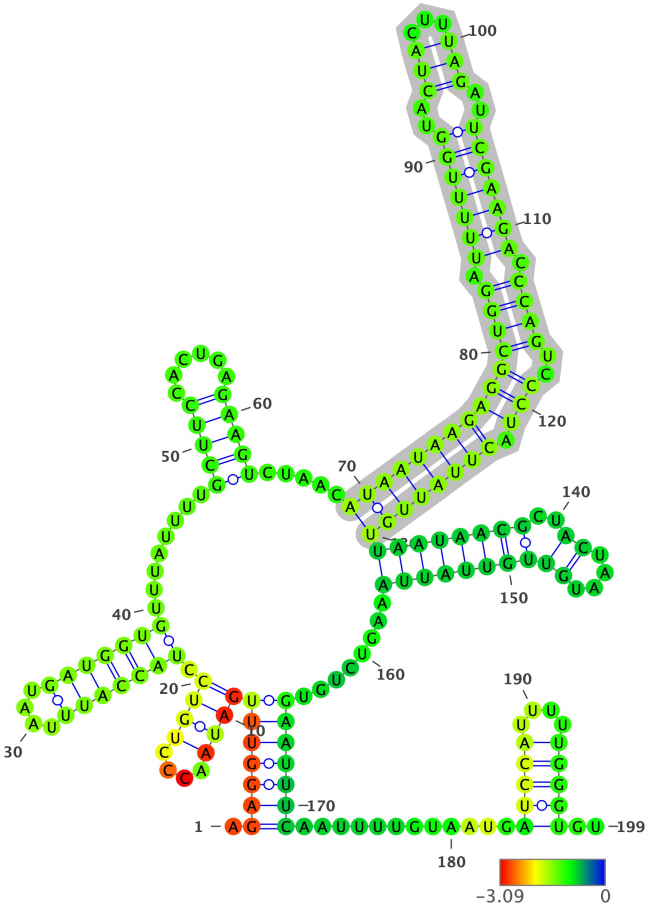
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 370 from nt 21860 to 21921 (nt 69 to 130)

```
5'-AUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGACCCAGUCCCUACUUAUUGU-3'
5'-(((((((((((((((.(((((((..(((...)))..)))))))).)))))..))))..)))))))))-3'
Motif MFE = -17.2; z-score = -2.96; ED = 6.02
```



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

Extracted structure model with flanking nucleotides 21792 to 21990 (motif highlighted in silver):

```
5'-AGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGA
CCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGU-3
5'-.((((((((((....)))).(((((((....)))))))).......(((((......))))).....((((((((((((((.(((((((..(((...)))..)))))))
.))))..))))..)))))))))(((((((..((....))))))))))........)))))))...........(((((....)))))..-3'
MFE = -42.5; z-score = -1.2; ED = 27.04
```

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_gp02, 21563-25384(+)

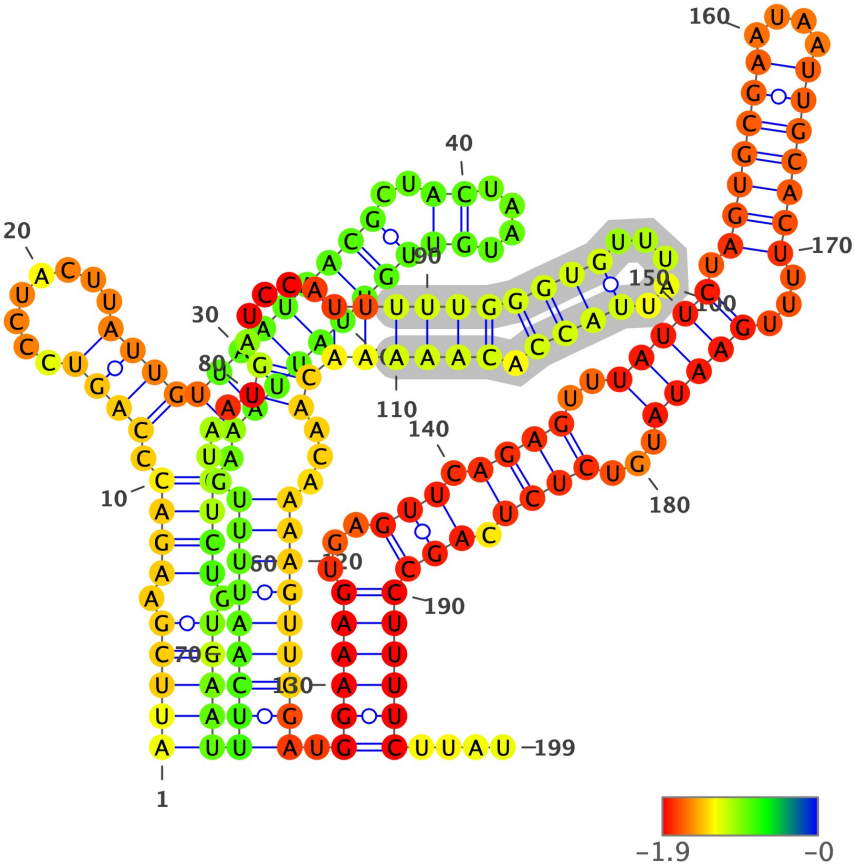
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 21982 to 22003 (nt 89 to 110)

```
5'-UUUGGGUGUUUAUUACCACAAA-3'
5'-((((((((.....)))).))))-3'
Motif MFE = -4.8; z-score = -3.02; 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 21894 to 22092 (motif highlighted in silver):

```
5'-AUUCGAAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAA
ACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAU-3
5'-(((((.((((.((((........))))((((((((..((....))))))))))).)))).)))))((((((((....((.....((((((((((.....)))).)))))
)))...))))))))).((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))....-3'
MFE = -40.5; z-score = -1.56; ED = 32.66
```

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_gp02, 21563-25384(+)

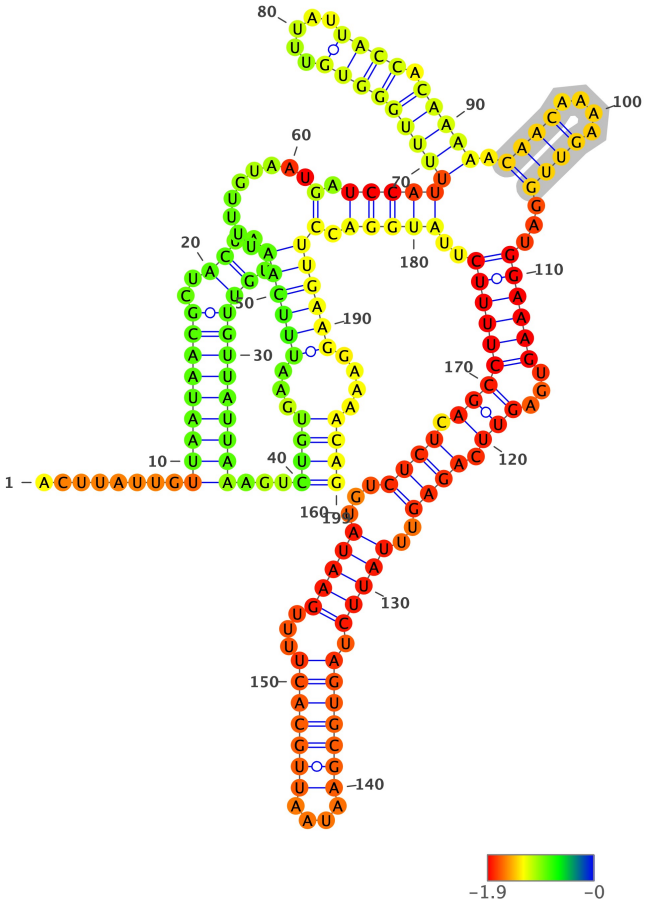
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 372 from nt 22006 to 22017 (nt 94 to 105)

```
5'-CAACAAAAGUUG-3'
5'-((((....))))-3'
Motif MFE = -1.1; z-score = -5.51; 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 21913 to 22111 (motif highlighted in silver):

```
5'-ACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAACAAAAGUUGGAUGGA
AAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAG-3
5'-.........((((((((((..((....))))))))))...((((...((((((.........(.((((((((((((((.....)))).)))))).((((....)))))...(((
(((...(((.(((((..((((((.(((((((....)))))))...))))))...)))))..)))))))))..))))))..)))))))....))))-3'
MFE = -42.2; z-score = -1.6; ED = 39.5
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

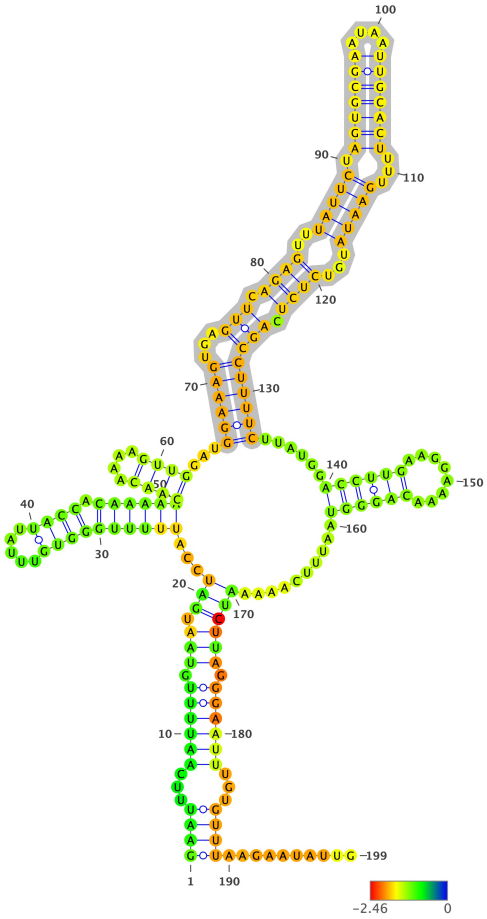
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 373 from nt 22021 to 22088 (nt 66 to 133)

```
5'-GGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUC-3'
5'-((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).)))))))))-3'
Motif MFE = -18.5; z-score = -2.67; 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 = -1.4; 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(+)

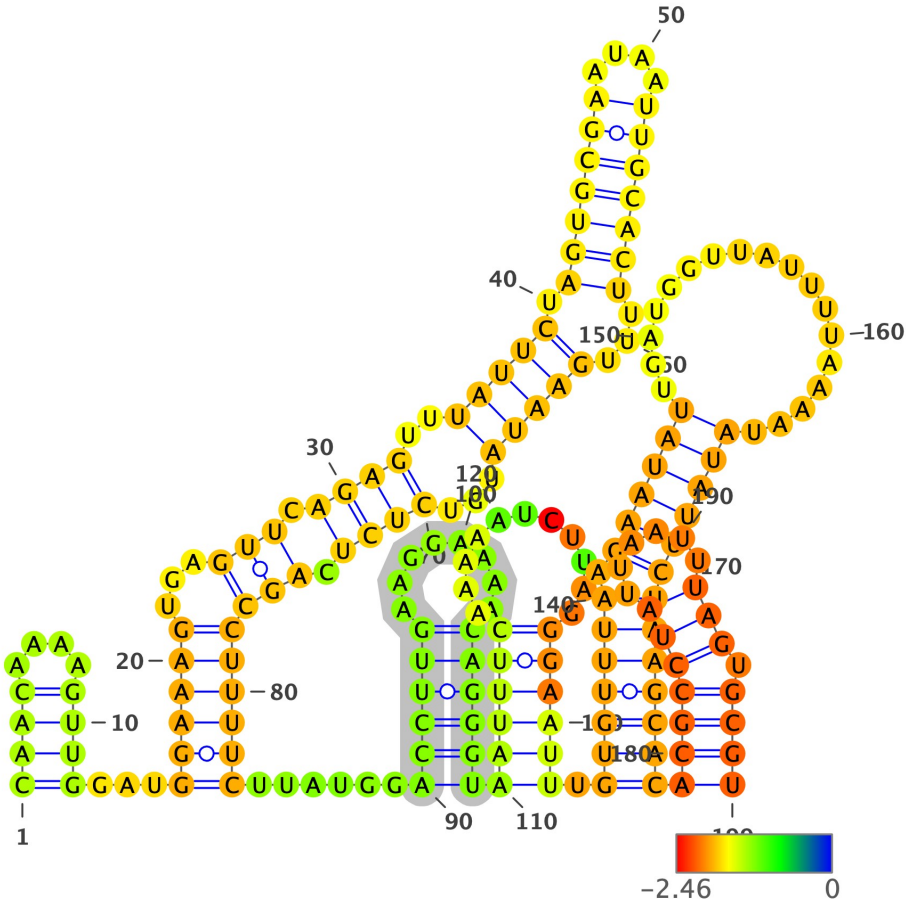
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 374 from nt 22095 to 22114 (nt 90 to 109)

```
5'-ACCUUGAAGGAAAACAGGGU-3'
5'-((((((........))))))-3'
Motif MFE = -5.4; z-score = -4.33; ED = 0.45
```



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

Extracted structure model with flanking nucleotides 22006 to 22204 (motif highlighted in silver):

```
5'-CAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAA
UUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGU-3
5'-((((....))))...((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))).....((((((........))))))((
((((...........)))))).(((((((.((((((.................))))))))))))))(((((((......))).))))-3'
MFE = -45.6; z-score = -1.83; 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(+)

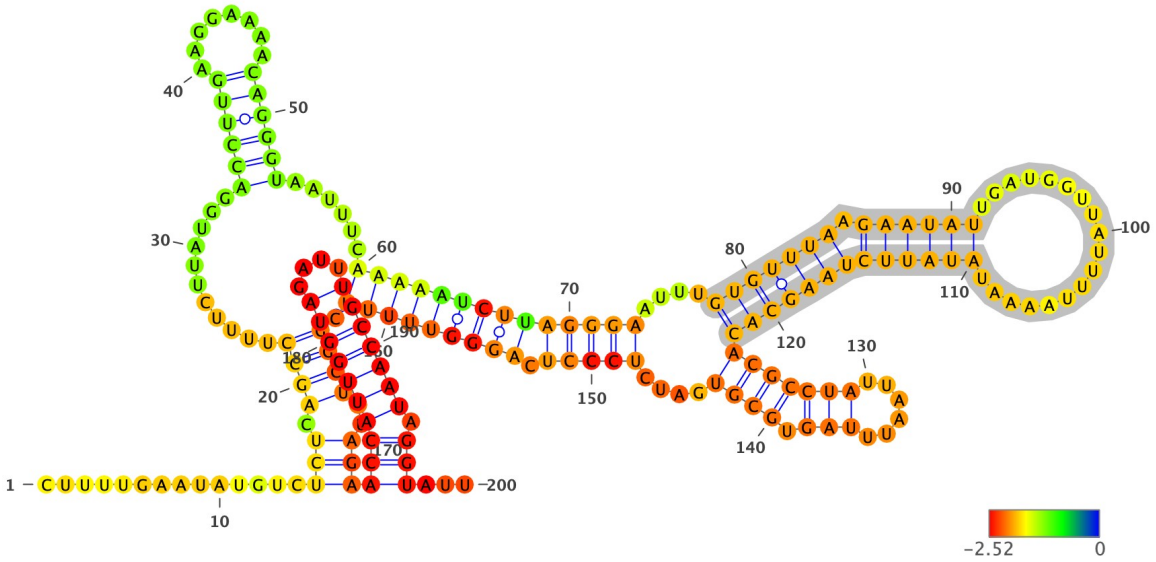
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 375 from nt 22139 to 22183 (nt 78 to 122)

```
5'-GUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCAC-3'
5'-(((((((.((((((.................)))))))))))))-3'
Motif MFE = -8.5; z-score = -1.88; ED = 5.04
```



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

Extracted structure model with flanking nucleotides 22062 to 22261 (motif highlighted in silver):

```
5'-CUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAU
AUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUU-3
5'-..............(((.((((...........((((((........))))))......((((((((((((((....(((((((.((((((.................))
))))))))))))(((((((......))).))))....))))).))))))))).))))..)))((((((((((....)))))))).)))...-3'
MFE = -50.3; z-score = -2.59; ED = 13.45
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

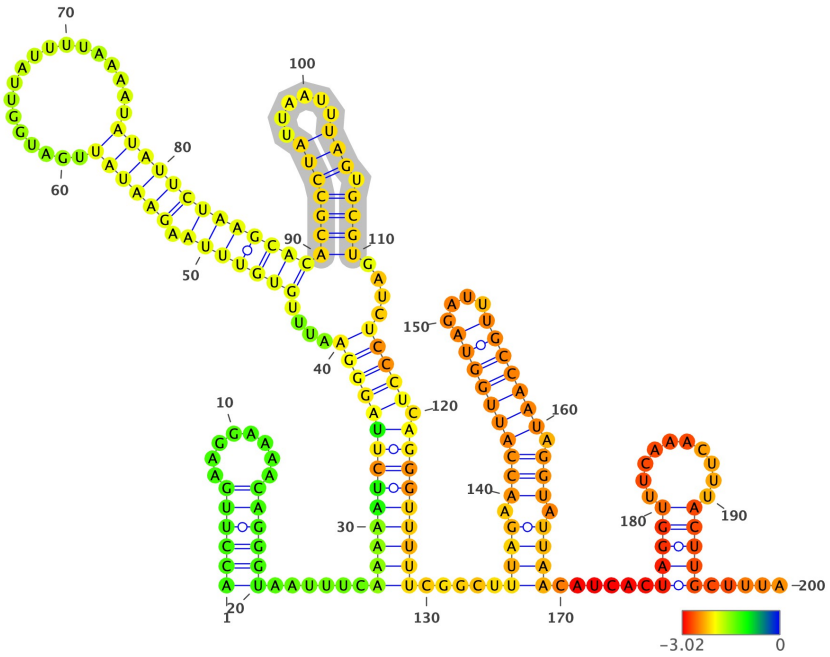
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 376 from nt 22184 to 22204 (nt 90 to 110)

```
5'-ACGCCUAUUAAUUUAGUGCGU-3'
5'-(((((((......))).))))-3'
Motif MFE = -6.2; z-score = -4.25; ED = 0.5
```



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 22095 to 22294 (motif highlighted in silver):

```
5'-ACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUG
AUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUA-3
5'-((((((........))))))......(((((((((((((....(((((((.((((((.................))))))))))))))(((((((......))).)))).
...))))).))))))))).....((((.((((((((((....)))))))).))).))))......(((((..........)))))).....-3'
MFE = -46.1; z-score = -1.95; ED = 22.69
```

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_gp02, 21563-25384(+)

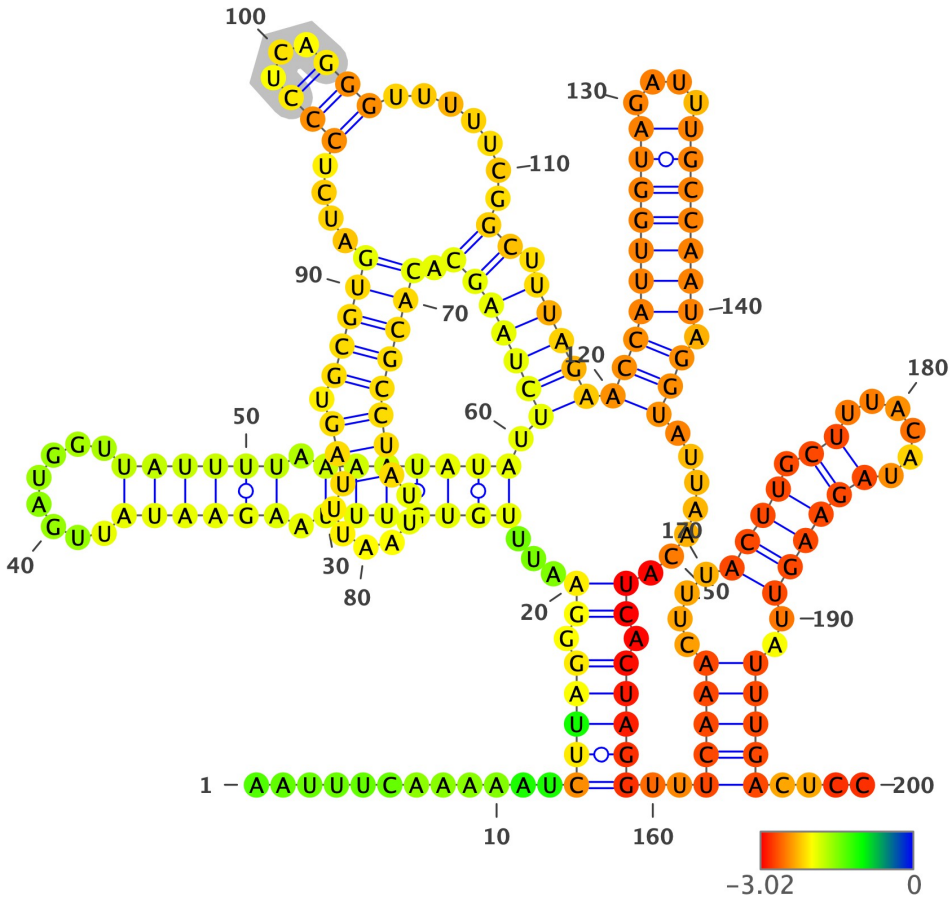
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22212 to 22216 (nt 98 to 102)

```
5'-CUCAG-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 22115 to 22314 (motif highlighted in silver):

```
5'-AAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCG
GCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCC-3
5'-............(((((.((...(((((((.((((((........))))))).)))))))).(((((((.((((((((......))).)))))....(((...)))........
)).)))))((((((((((....)))))))).)))........)).)))))..(((((....((((.((......))))))..)))))....-3'
MFE = -38.7; z-score = -2.98; ED = 51.03
```

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_gp02, 21563-25384(+)

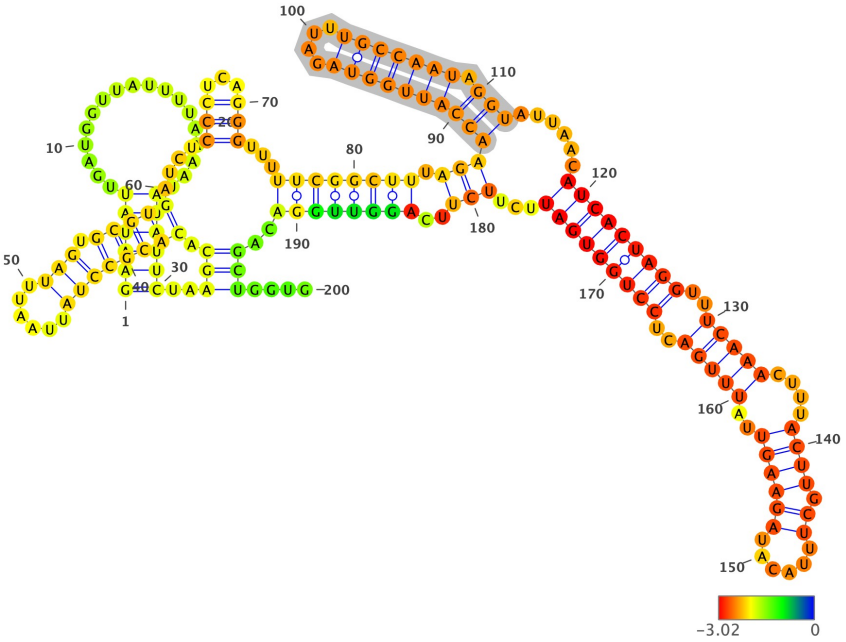
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 378 from nt 22234 to 22258 (nt 88 to 112)

```
5'-ACCAUUGGUAGAUUUGCCAAUAGGU-3'
5'-((((((((((....)))))))).)))-3'
Motif MFE = -9.1; z-score = -4.06; 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 22147 to 22346 (motif highlighted in silver):

```
5'-GAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGG
UAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUG-3
5'-((((((.................))))))..(((.((((((((......))).)))))....(((...)))...((((((((.((((((((((((....)))))))).))
).....((((((((..(((((....((((.((......))))))..)))))..)))))))))...)))..)))))))))..)))....-3'
MFE = -50.3; z-score = -2.7; ED = 27.04
```

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_gp02, 21563-25384(+)

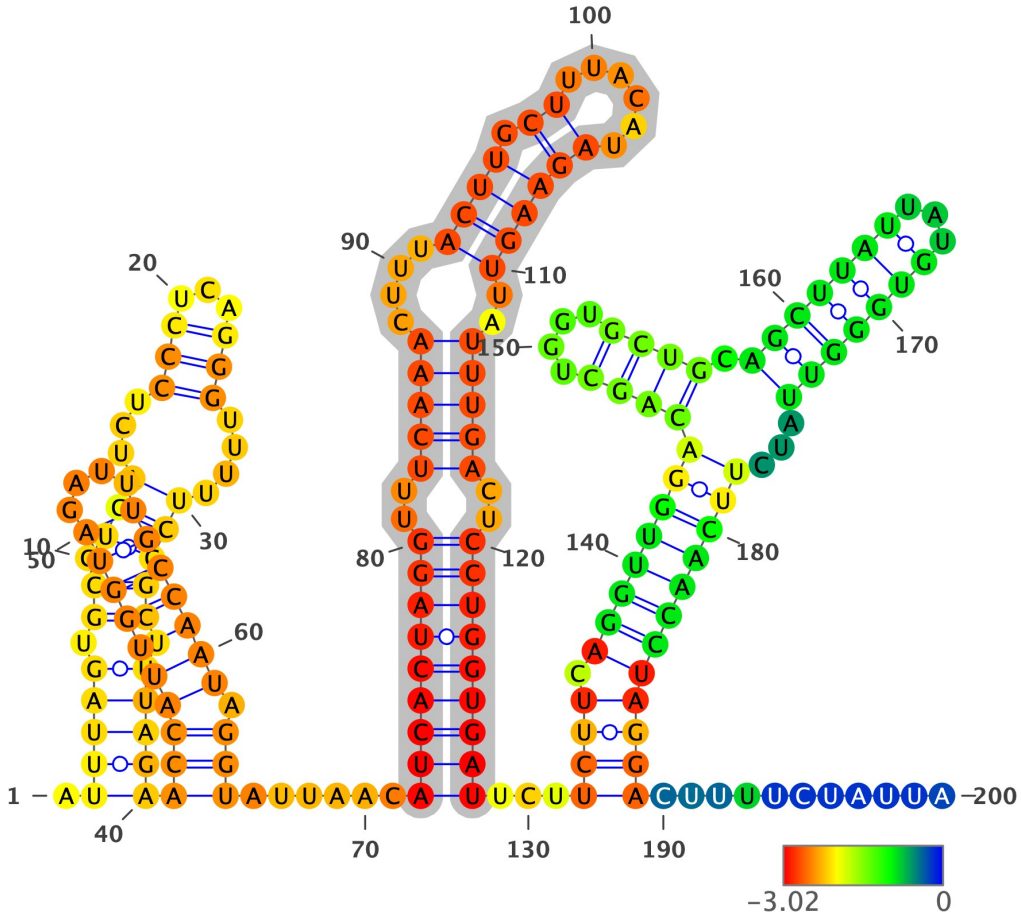
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 379 from nt 22265 to 22321 (nt 72 to 128)

```
5'-AUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAU-3'
5'-((((((((((..((((((....((((.((......))))))..))))))..))))))))))-3'
Motif MFE = -18.6; z-score = -5.19; 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 = -2.93; 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(+)

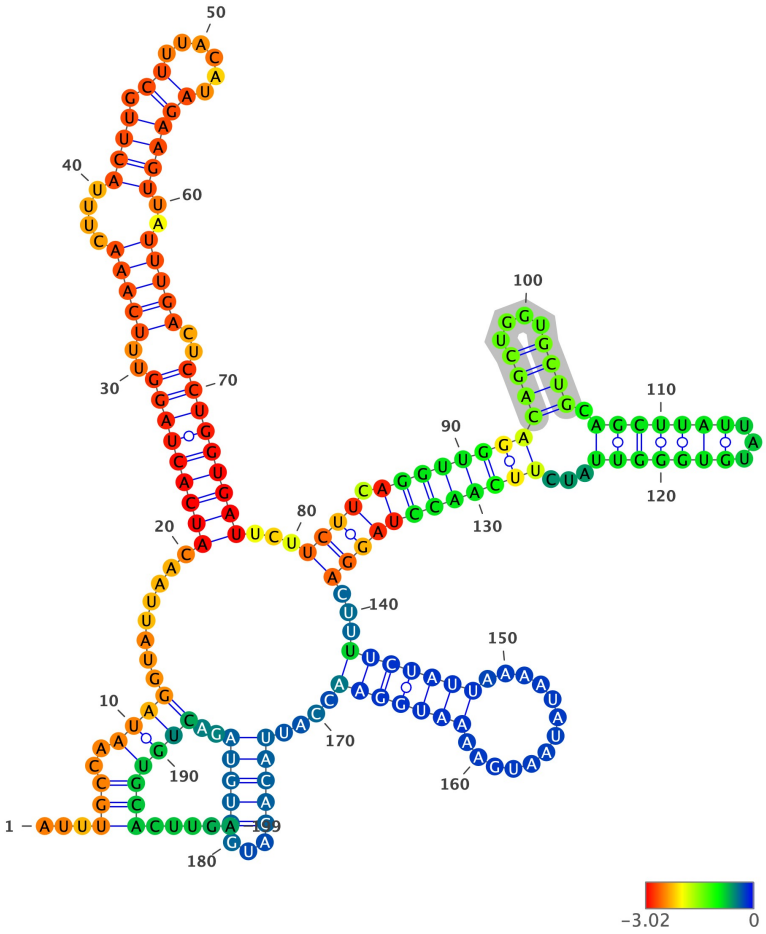
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 380 from nt 22338 to 22349 (nt 94 to 105)

```
5'-CAGCUGGUGCUG-3'
5'-((((....))))-3'
Motif MFE = -4.1; z-score = -3.67; 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 = -2.11; 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(+)

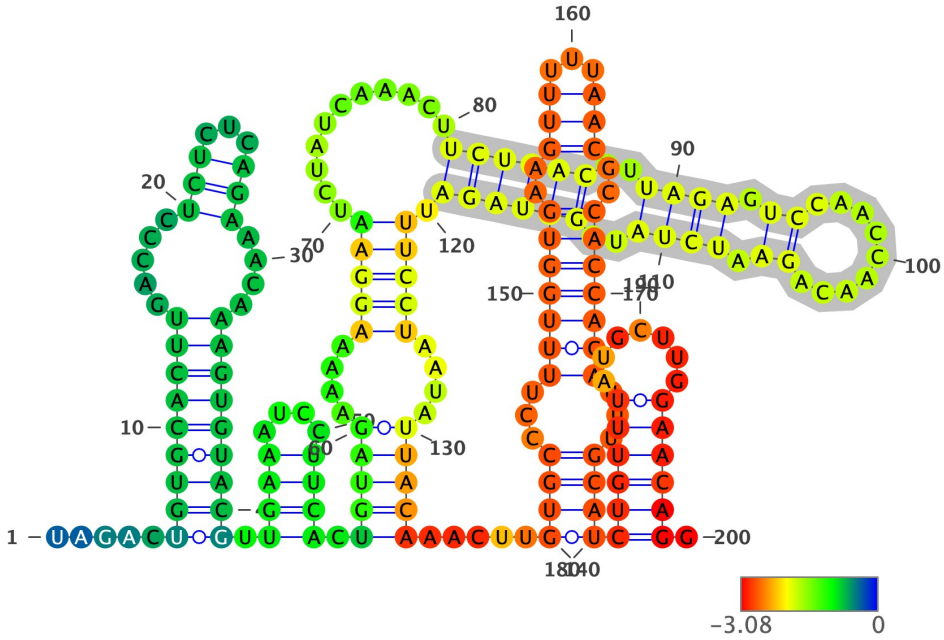
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 381 from nt 22508 to 22546 (nt 81 to 119)

```
5'-UCUAACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGA-3'
5'-((((((..(((((.(((.........))).))))).)))))))-3'
Motif MFE = -9.2; z-score = -3.51; 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 = -2.3; 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(+)

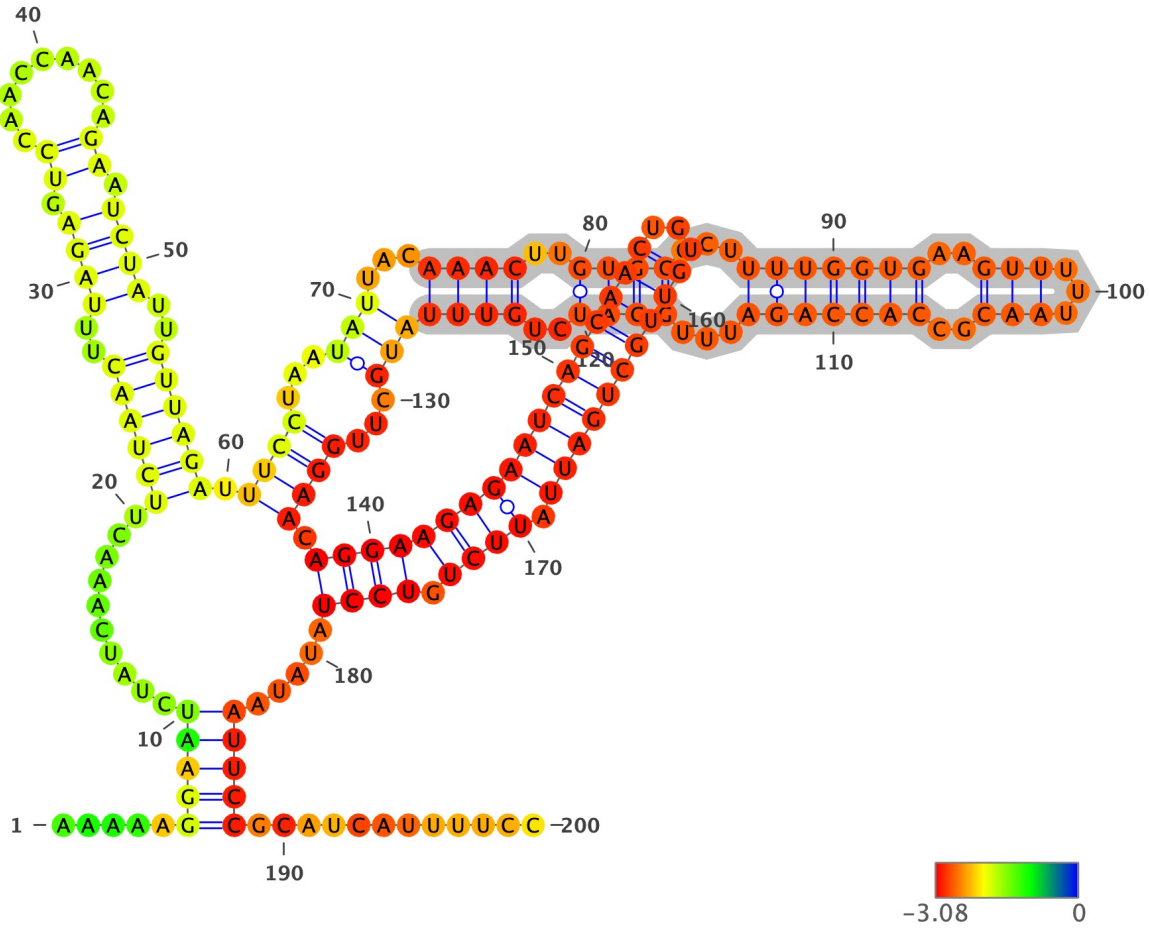
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 382 from nt 22561 to 22613 (nt 74 to 126)

```
5'-AAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUU-3'
5'-((((..((((...(((((((..(((...)))..)))))))...))))..))))-3'
Motif MFE = -15.2; z-score = -2.81; 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 = -4.14; 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(+)

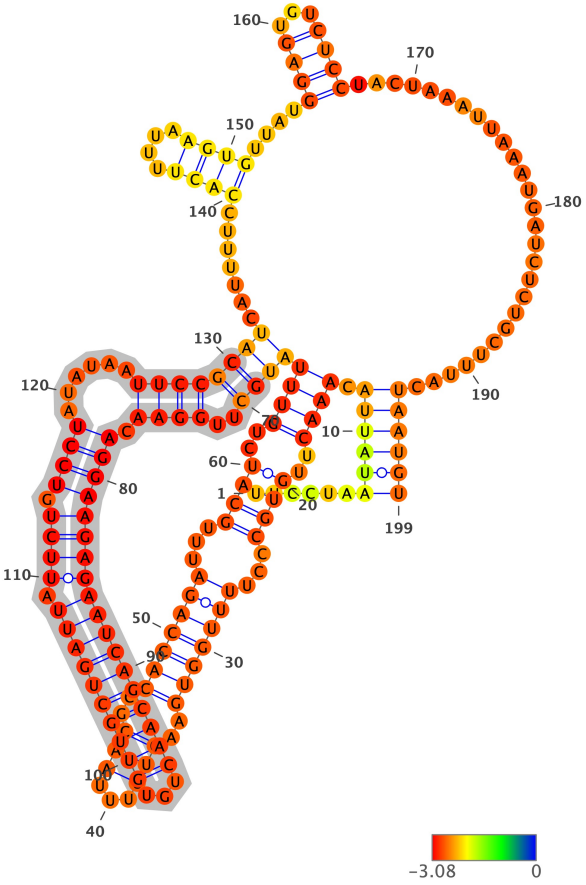
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 383 from nt 22616 to 22677 (nt 69 to 130)

```
5'-GCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGC-3'
5'-(...((((.((((((((((((((((((...)))))))))).)))).)))).....))))).)-3'
Motif MFE = -21.0; z-score = -3.42; 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 22548 to 22746 (motif highlighted in silver):

```
5'-UUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUU
CUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGU-3
5'-......((((((.((((..((((...(((((((..(((...)))..)))))))...))))..))))((((..((((.((((((((((((((((((...)))))))))).))
)).))))......))))))))).......((((....))))....((((...))))..........................))))))-3'
MFE = -45.7; z-score = -2.81; ED = 22.97
```

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(+)

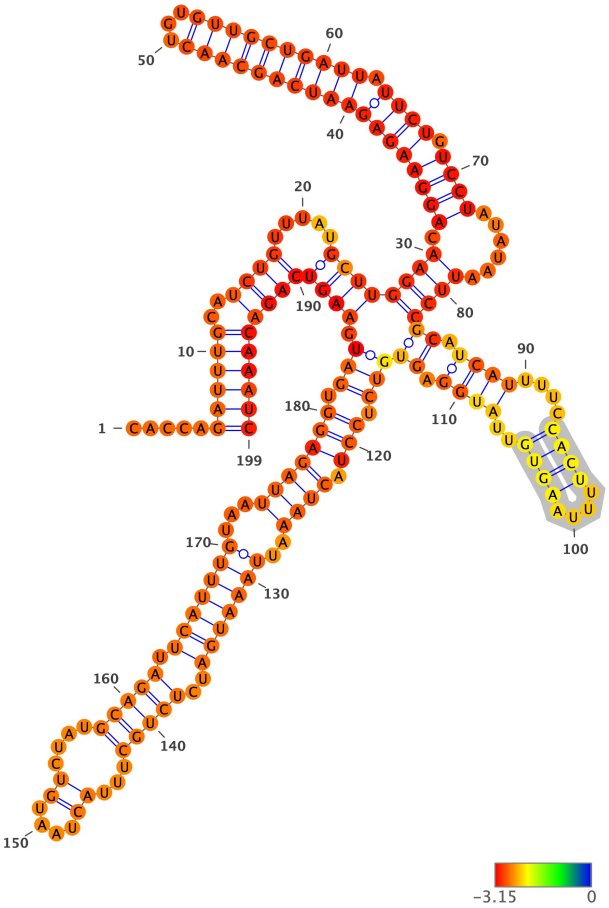
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 384 from nt 22687 to 22698 (nt 94 to 105)

```
5'-CACUUUUAAGUG-3'
5'-((((....))))-3'
Motif MFE = -1.0; z-score = -4.62; ED = 1.19
```



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

Extracted structure model with flanking nucleotides 22594 to 22792 (motif highlighted in silver):

```
5'-CACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGG
AGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUC-3
5'-.....((((((..((((.....((((((((.((((((((((((((((((...)))))))))).)))).))))......))))((.((((....((((....))))..))))
.))(((.(((.((((..(((((((..(((((...((....))....))))).)))))))...)))))))).))).)))))))))))))-3'
MFE = -52.5; z-score = -3.79; ED = 30.91
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

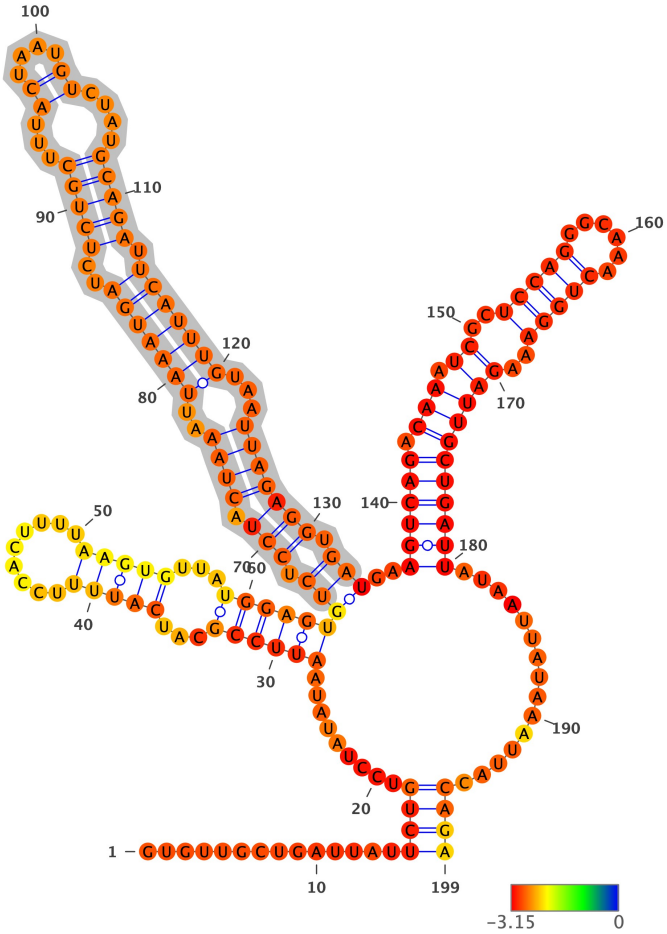
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 385 from nt 22709 to 22776 (nt 66 to 133)

```
5'-UCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGA-3'
5'-((.((..(((((..(((((((..(((((...((....)).....)))))).)))))))...)))))..)).))-3'
Motif MFE = -17.9; z-score = -4.17; ED = 3.87
```



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 22644 to 22842 (motif highlighted in silver):

```
5'-GUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAG
AUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGA-3
5'-..............((((.........((((((...(((((.........)))))...))))))))(((.(((.(((((..(((((((..((((((...((....)).....))))
).)))))))...)))))))..)))..((((((.(((.((..(((((......)))))..))))))))))).............))))-3'
MFE = -46.3; z-score = -2.73; ED = 29.94
```

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_gp02, 21563-25384(+)

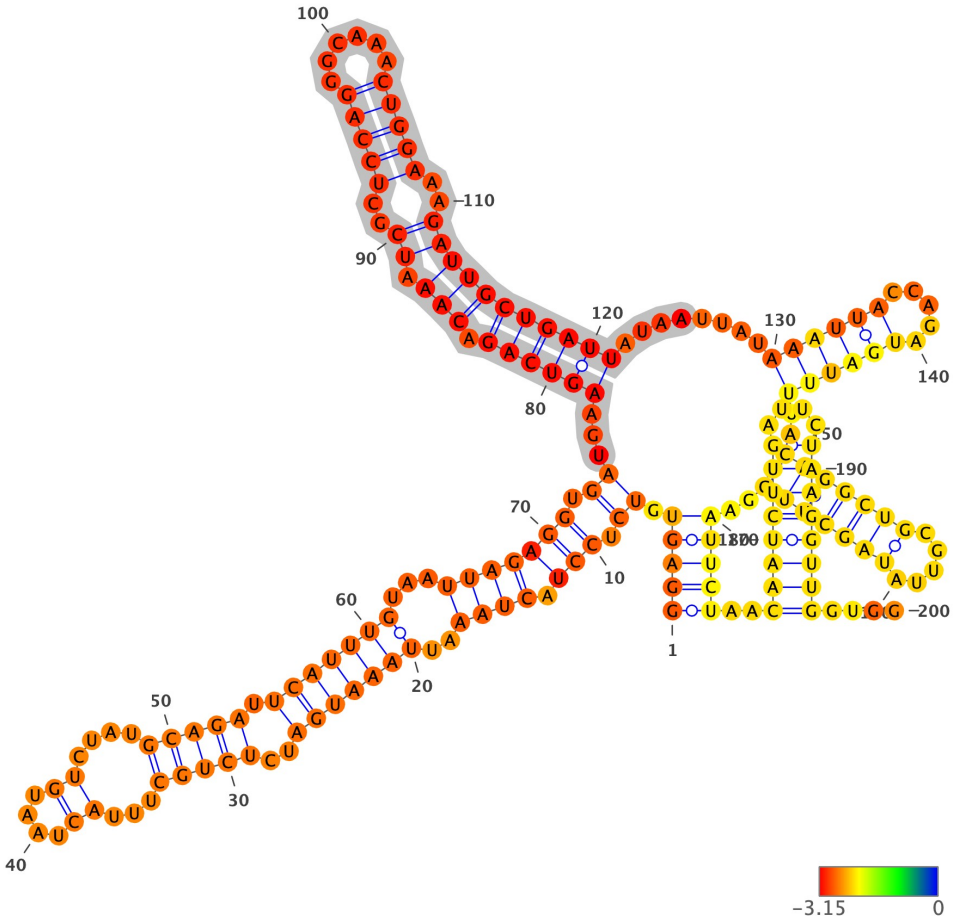
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 386 from nt 22777 to 22827 (nt 75 to 125)

```
5'-UGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAA-3'
5'-(..(((((((.(((.((..(((((.....)))))..))))))))))...)-3'
Motif MFE = -17.5; z-score = -3.74; 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 22703 to 22902 (motif highlighted in silver):

```
5'-GGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAG
AUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUGG-3
5'-(((((.((.(((.((((..(((((((..(((((...((....))....))))).)))))))...)))))))).))...((((((.(((.((..(((((.....)))))..)
))))))))))........((((((.....))))))..(((((((.....)))))))..))))))..((((((((....))))))))....-3'
MFE = -51.8; z-score = -3.19; ED = 28.03
```

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_gp02, 21563-25384(+)

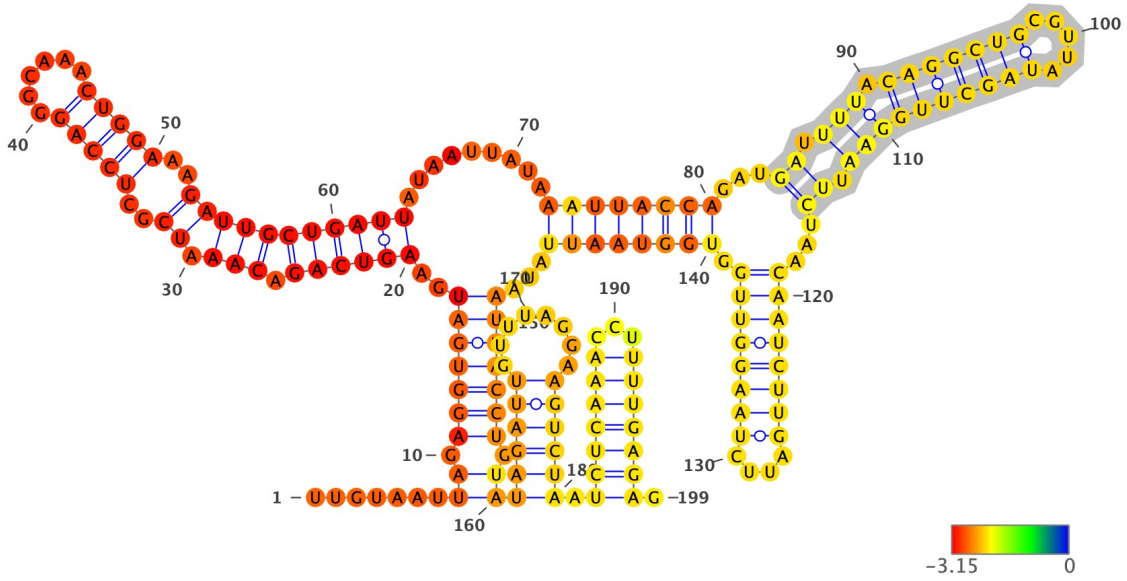
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 387 from nt 22844 to 22875 (nt 84 to 115)

```
5'-GAUUUUACAGGCUGCGUUAUAGCUUGGAAUUC-3'
5'-((.(((.(((((((.....)))))))))).))-3'
Motif MFE = -7.3; z-score = -1.76; 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 = -3.87; 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(+)

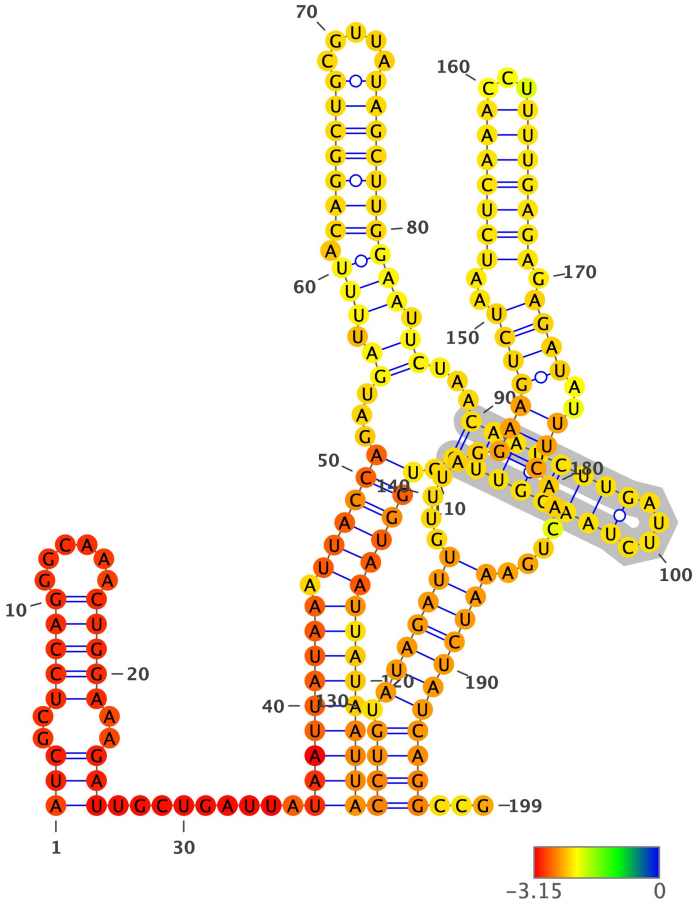
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 388 from nt 22879 to 22898 (nt 90 to 109)

```
5'-CAAUCUUGAUUCUAAGGUUG-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -4.8; z-score = -2.65; 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 = -3.9; 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(+)

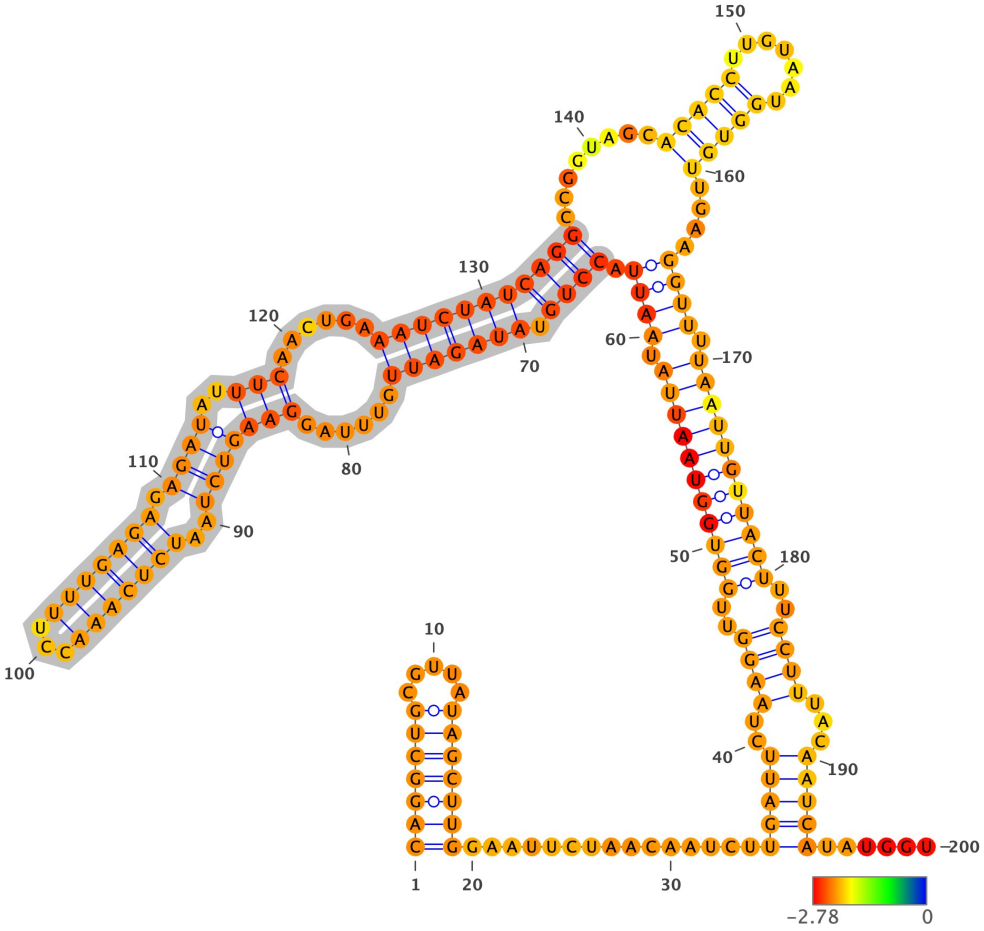
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 389 from nt 22915 to 22985 (nt 65 to 135)

```
5'-CCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGG-3'
5'-((((.(((((((.....(((((((..(((((((...)))))))).))))..)))......)))))))))))-3'
Motif MFE = -21.1; z-score = -3.88; 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 = -2.62; 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(+)

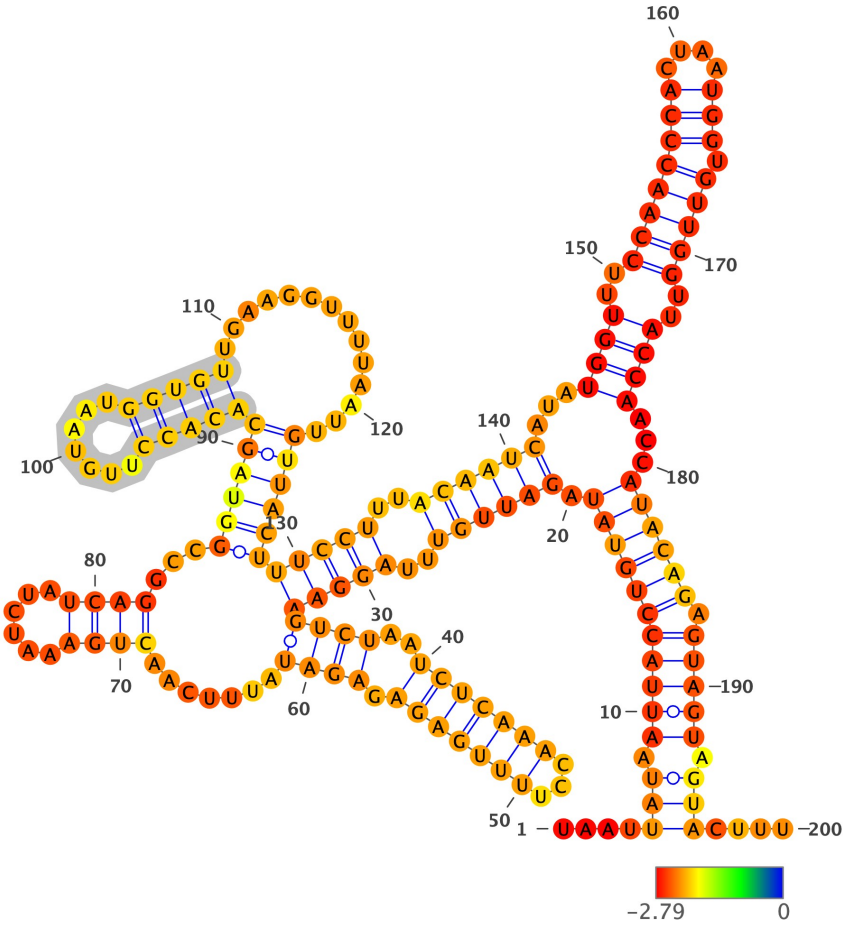
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 390 from nt 22994 to 23010 (nt 92 to 108)

```
5'-ACACCUUGUAAUGGUGU-3'
5'-(((((.......)))))-3'
Motif MFE = -5.4; z-score = -4.37; ED = 0.44
```



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

Extracted structure model with flanking nucleotides 22903 to 23102 (motif highlighted in silver):

```
5'-UAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGA
AGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUU-3
5'-....(((.(((((((((((.((((((..((((((((((..(((((((...)))))))).))))).......((((......))))...(((((((((((.......)))))...
...........))))))))))))..))))))...((((..((((((((....))).)))))..))))...))))))).)))))).)))....-3'
MFE = -57.3; z-score = -5.07; 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(+)

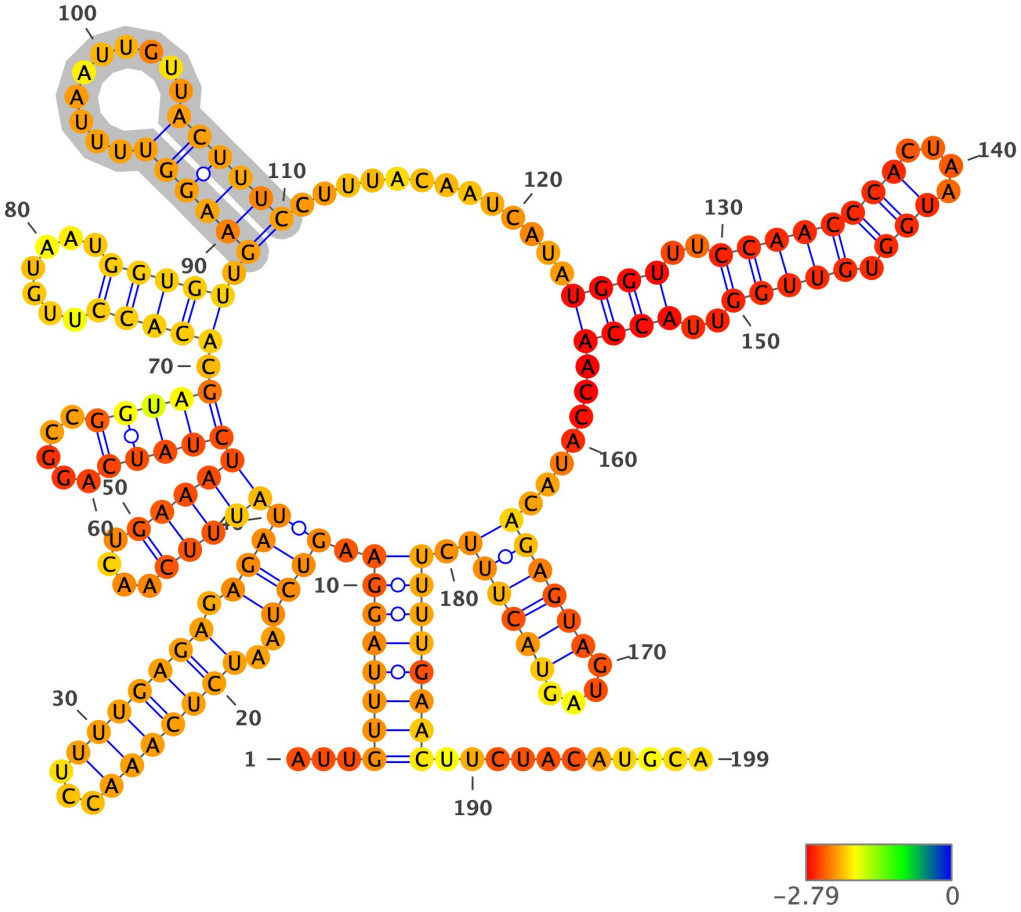
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 391 from nt 23012 to 23033 (nt 89 to 110)

```
5'-GAAGGUUUUAAUUGUUACUUUC-3'
5'-(..(((..........)))..)-3'
Motif MFE = -2.6; z-score = -2.0; 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 22924 to 23122 (motif highlighted in silver):

```
5'-AUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCC
UUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCA-3
5'-...((((((((.((((..(((((((...)))))))).))))(((((....)))))(((((.....))))).(((((.......))))).((((((..........)))))).
............((((..((((((((....))).)))))..)))).......((((((....)))))).))))))))...........-3'
MFE = -47.9; z-score = -2.91; ED = 40.47
```

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_gp02, 21563-25384(+)

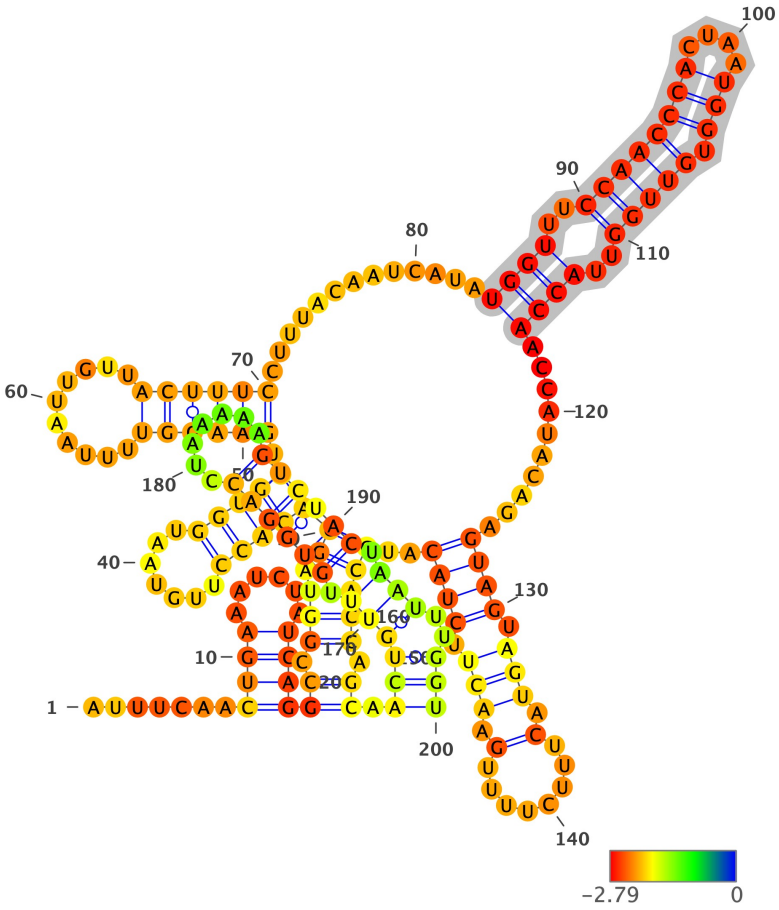
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23047 to 23079 (nt 84 to 116)

```
5'-UGGUUUCCAACCCACUAAUGGUGUUGGUUACCA-3'
5'-((((..((((((((....))).)))))..))))-3'
Motif MFE = -14.7; z-score = -5.0; 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 = -2.95; 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(+)

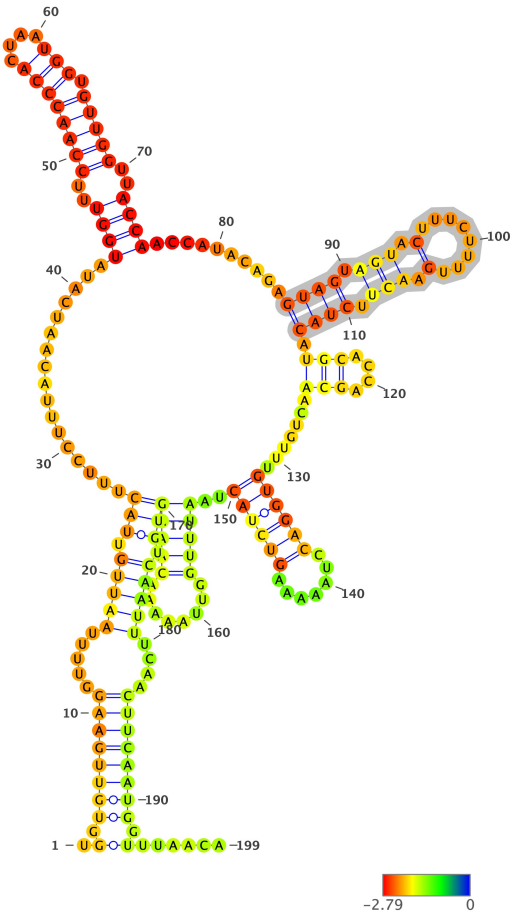
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 393 from nt 23090 to 23117 (nt 86 to 113)

```
5'-GUAGUAGUACUUUCUUUUGAACUUCUAC-3'
5'-((((.....(........).....))))-3'
Motif MFE = -4.1; z-score = -1.7; 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 = -2.78; ED = 29.28
```

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_gp02, 21563-25384(+)

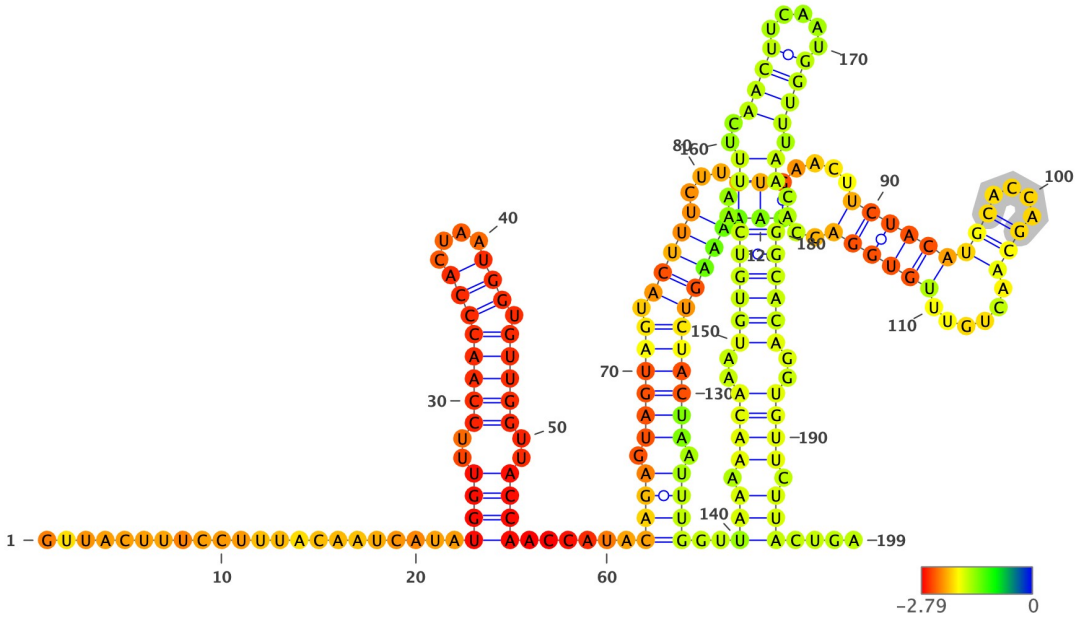
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 394 from nt 23121 to 23126 (nt 97 to 102)

```
5'-CACCAG-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 23025 to 23223 (motif highlighted in silver):

```
5'-GUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUU
GUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGA-3
5'-.....((((..(((((((((....))).))))))..))))......((((.((((((.((((((...(((....(((((((((....))).....)
))))))..))))))))))))))).))))..(((.((((..((((((..((..((((.....)))))..))..))))))..)))))..)))....-3'
MFE = -43.5; z-score = -2.61; ED = 35.62
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

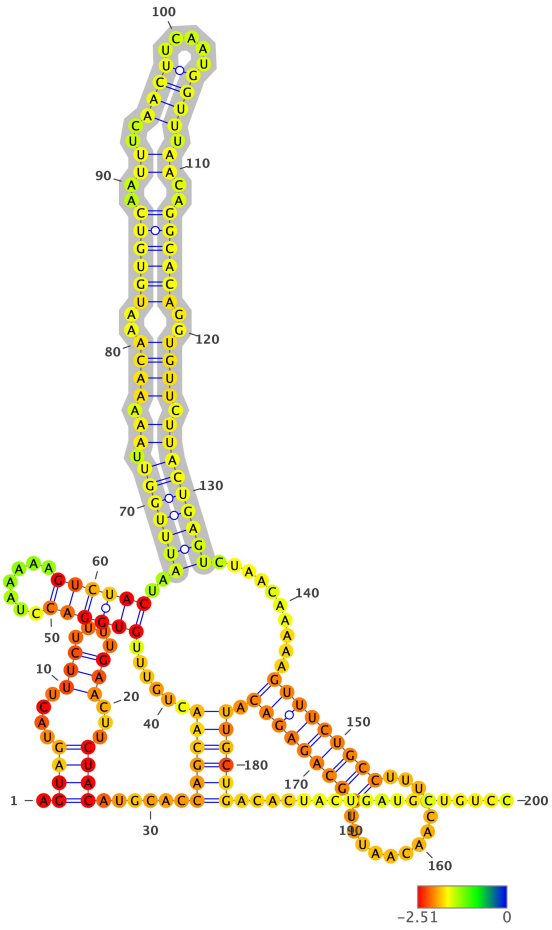
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 395 from nt 23157 to 23225 (nt 66 to 134)

```
5'-AUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGU-3'
5'-(((((((.((.(((((..(((((((..((..((((.....)))))..))..)))))))..)))))..)))))))))-3'
Motif MFE = -14.5; z-score = -1.72; ED = 5.5
```



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 23092 to 23291 (motif highlighted in silver):

```
5'-AGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAAC
AGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCC-3
5'-.((((....(((....)))...)))).....((((((.....((((((.......)))))).(((((((.((.(((((..((((((..((..((((.....)))))..)).
.))))))..)))))..)))))))))).........(((((((((.............)))))))))..))))))..................-3'
MFE = -46.1; z-score = -2.23; ED = 29.58
```

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_gp02, 21563-25384(+)

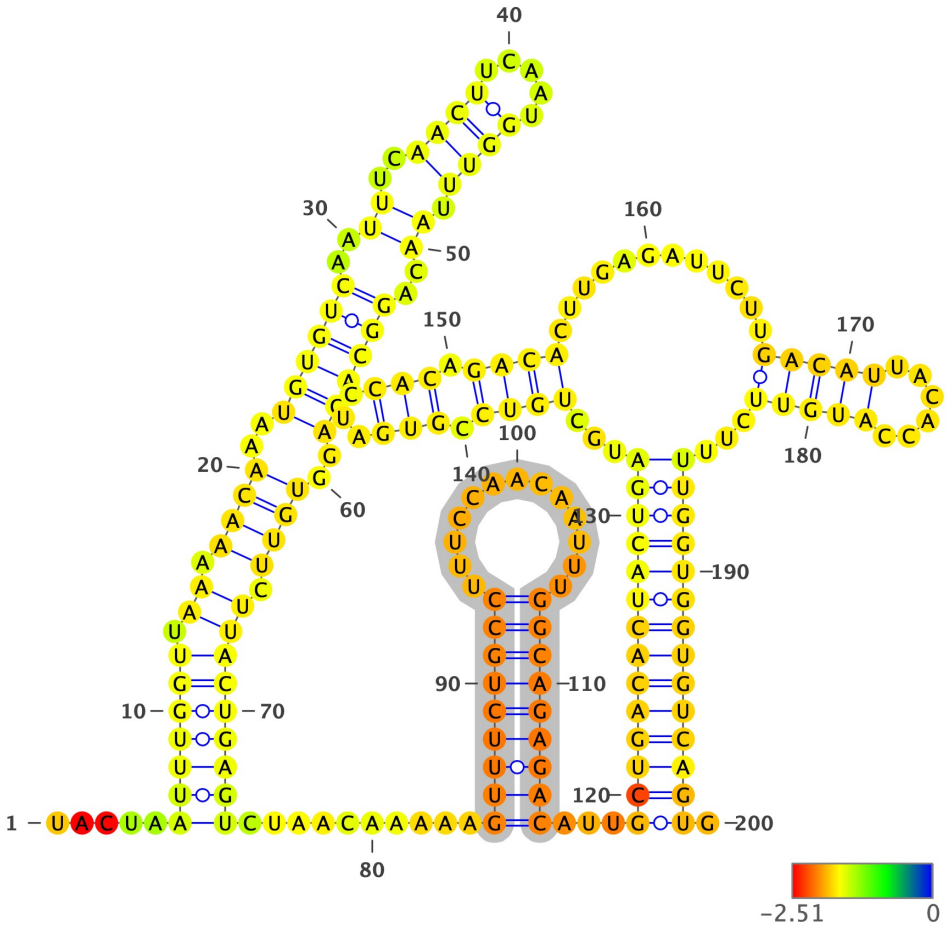
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 396 from nt 23236 to 23266 (nt 85 to 115)

```
5'-GUUUCUGCCUUUCCAACAAUUUGGCAGAGAC-3'
5'-(((((((((.............)))))))))-3'
Motif MFE = -12.7; z-score = -4.48; ED = 0.2
```



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 23152 to 23351 (motif highlighted in silver):

```
5'-UACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAG
AGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUG-3
5'-.....(((((((.((.((((..(((((((..((..((((.....)))).))..))))))..)))).))))))))).........(((((((((.............)))))
))))...((((((((((((((...((((.(((...))).))))............(((((......)))))...))))))))))))).-3'
MFE = -54.1; z-score = -3.24; ED = 19.51
```

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(+)

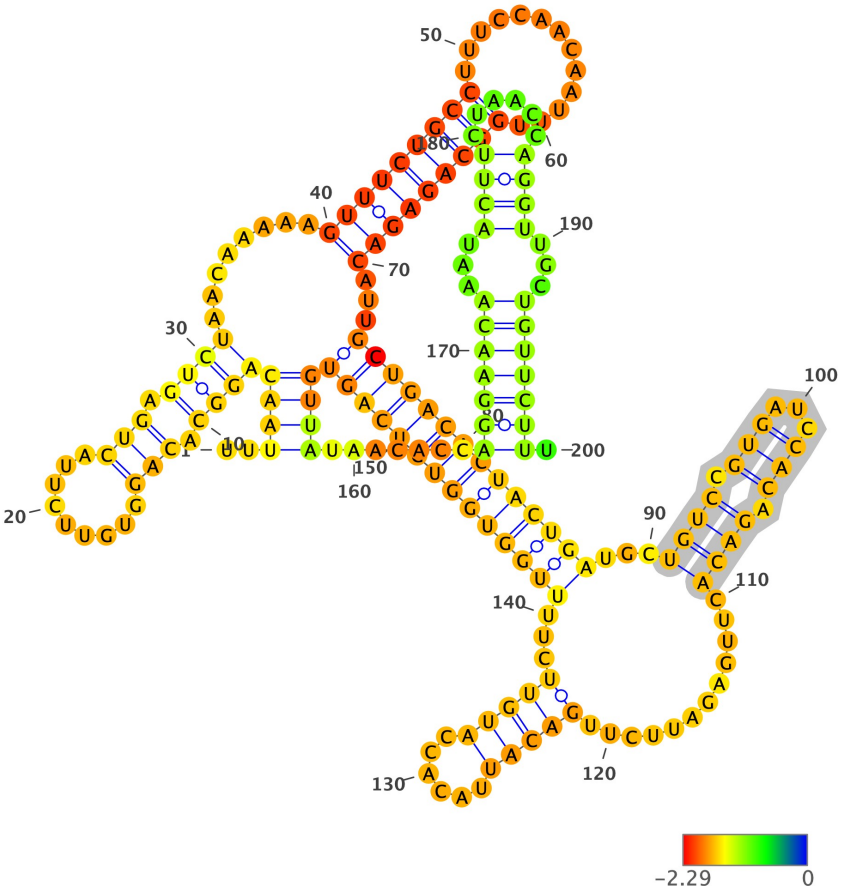
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 397 from nt 23287 to 23305 (nt 91 to 109)

```
5'-UGUCCGUGAUCCACAGACA-3'
5'-((((.(((...))).))))-3'
Motif MFE = -4.6; z-score = -2.6; 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 = -2.62; 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(+)

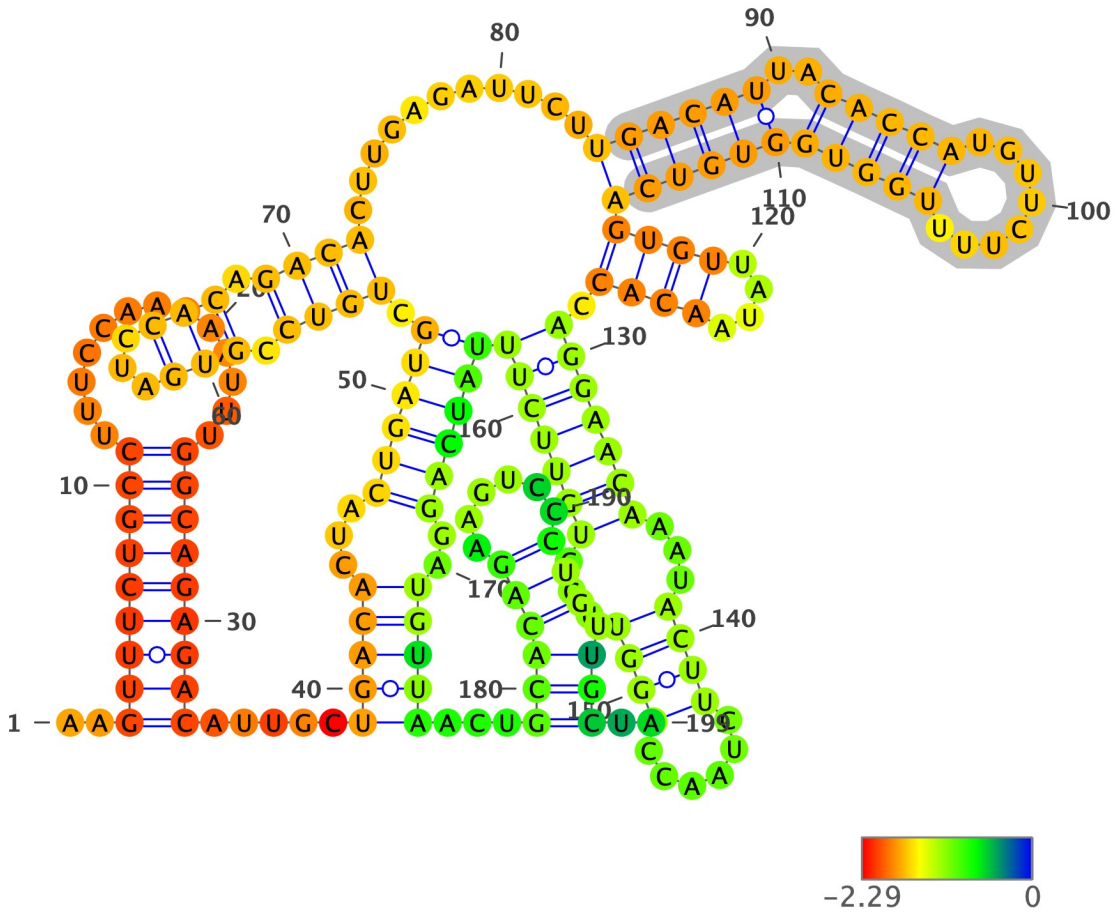
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 398 from nt 23318 to 23347 (nt 85 to 114)

```
5'-GACAUUACACCAUGUUCUUUUGGUGGUGUC-3'
5'-((((((..(((((........)))))))))))-3'
Motif MFE = -10.2; z-score = -3.37; 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 23234 to 23432 (motif highlighted in silver):

```
5'-AAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGU
GUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUA-3
5'-..((((((((((.............))))))))).....((((((...(((((((.((((.(((...))).)))).)))).....((((((..(((((........)))))))
))))))(((....)))).(((((((...((((......))))...)))))))))))))..))))))...((((((.....))).))))..-3'
MFE = -56.1; z-score = -3.0; ED = 15.54
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

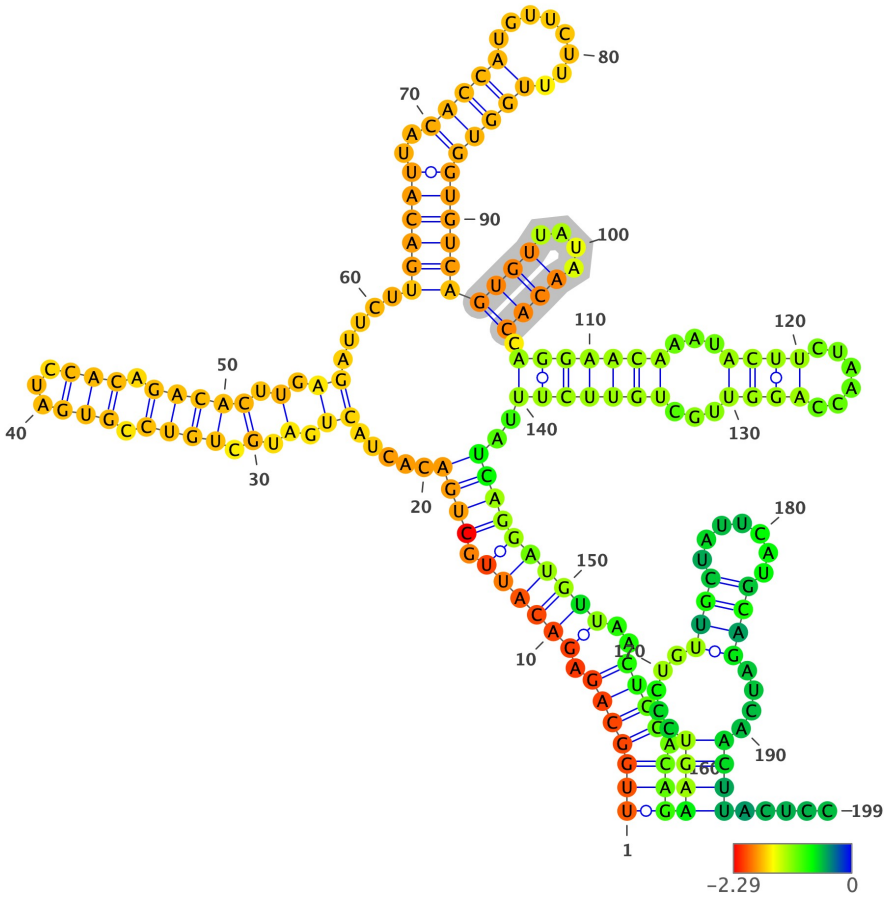
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 399 from nt 23349 to 23360 (nt 94 to 105)

```
5'-GUGUUAUAACAC-3'
5'-((((....))))-3'
Motif MFE = -1.1; z-score = -7.44; 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 23256 to 23454 (motif highlighted in silver):

```
5'-UUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAA
CAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCC-3
5'-(((((((.((((((.((((.....((.(.(.((((.(((...))).))))).).)).....((((((..(((((........)))))))))))((((....)))).(((((
((...((((......)))...)))))))..))))))))))..)))).)))((((.....((((.......)))).....)))).....-3'
MFE = -48.3; z-score = -1.27; 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 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

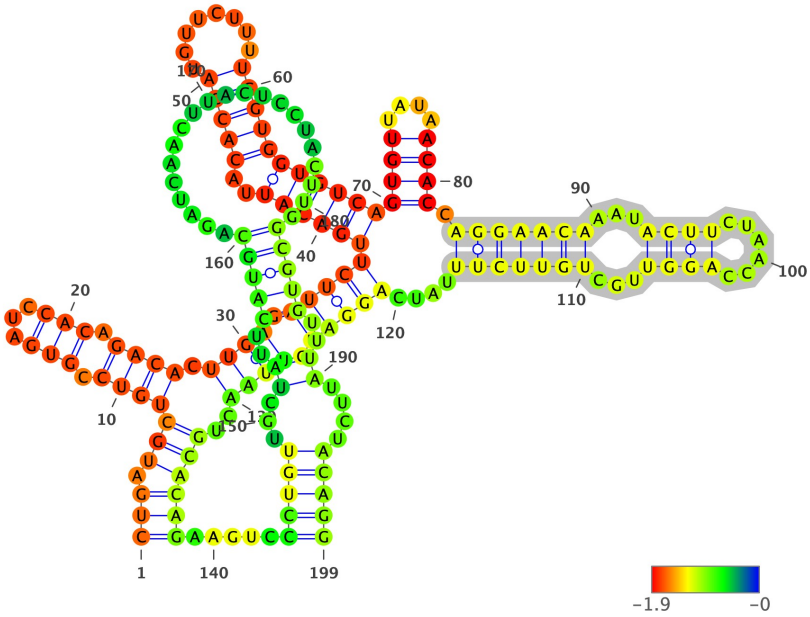
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 400 from nt 23362 to 23395 (nt 83 to 116)

```
5'-AGGAACAAAUACUUCUAACCAGGUUGCUGUUCUU-3'
5'-(((((((...((((......))))...)))))))-3'
Motif MFE = -6.7; z-score = -2.12; 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 = -0.98; 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(+)

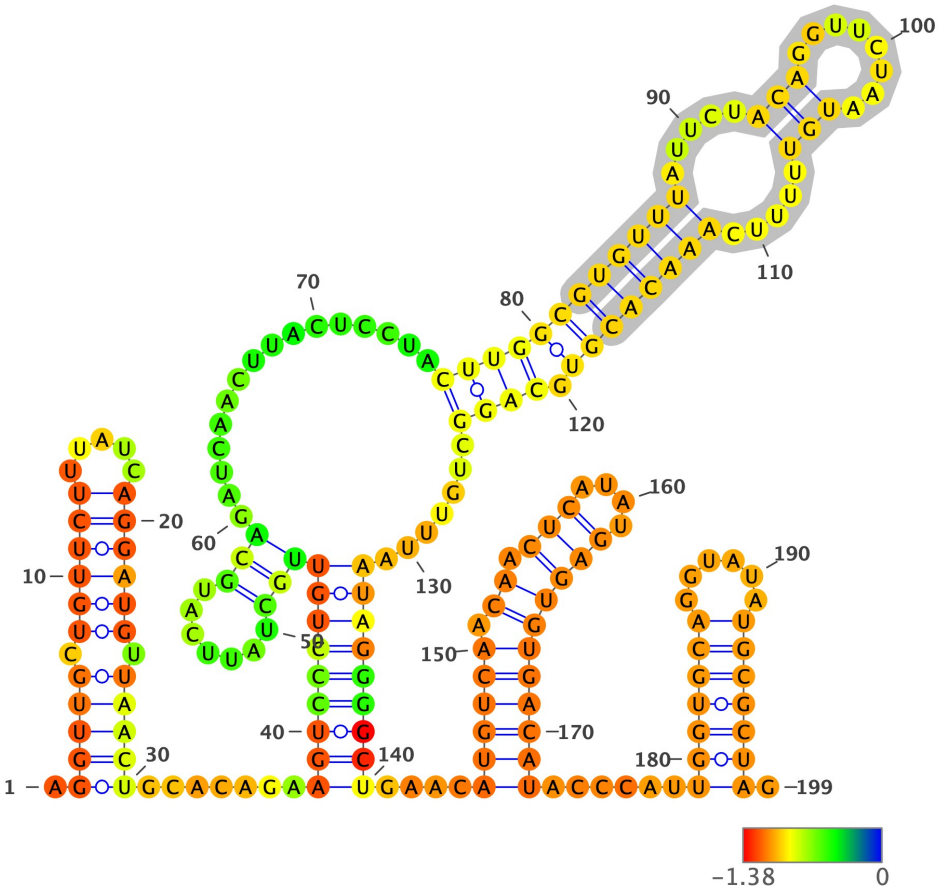
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 401 from nt 23463 to 23498 (nt 82 to 117)

```
5'-GUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACAC-3'
5'-(..............................)-3'
Motif MFE = -5.0; z-score = -1.76; 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 23382 to 23580 (motif highlighted in silver):

```
5'-AGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUC
AAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAG-3
5'-.((((((.((((((.....)))))).)))))).....(((((((((((.......))).................(((((((((((.....(((........))).....
))))))))).))))).....)))))))))....((((((.((.(((....)))))))))))......(((((((.....))))))).-3'
MFE = -50.0; z-score = -0.88; ED = 32.66
```

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_gp02, 21563-25384(+)

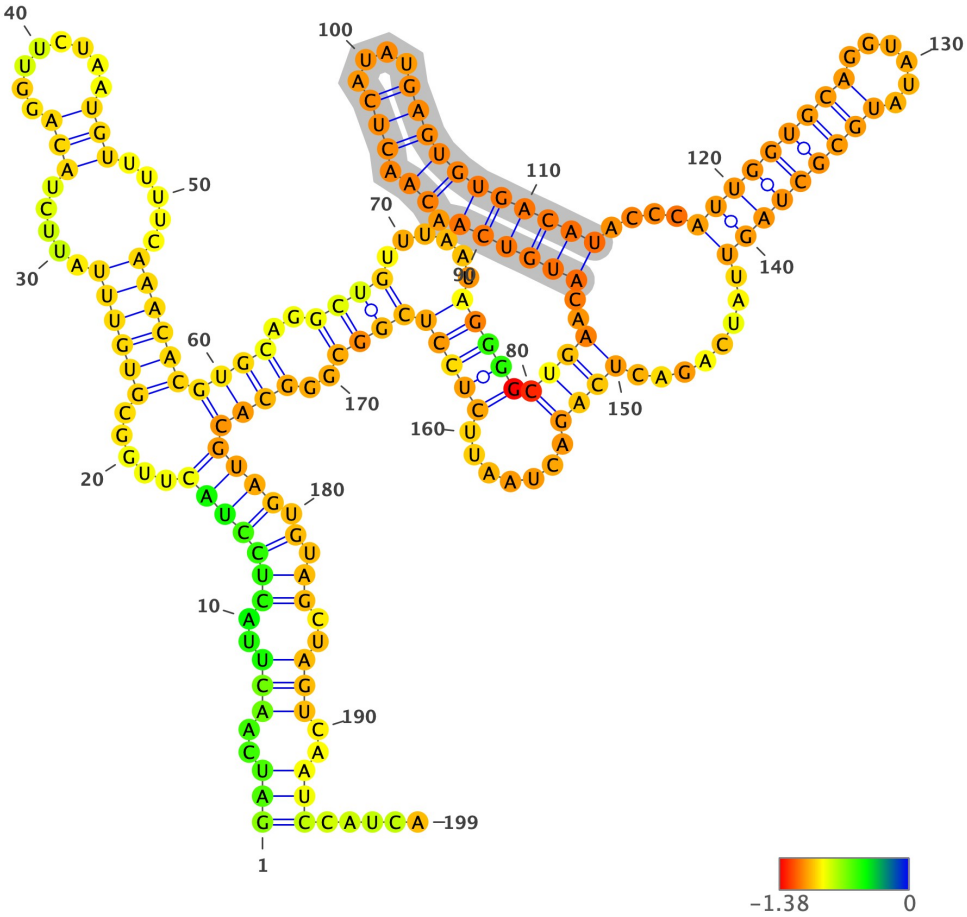
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23526 to 23553 (nt 86 to 113)

```
5'-AUGUCAACAACUCAUAUGAGUGUGACAU-3'
5'-((((((.((.(((....)))))))))))-3'
Motif MFE = -8.7; z-score = -4.2; 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 = -0.68; 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(+)

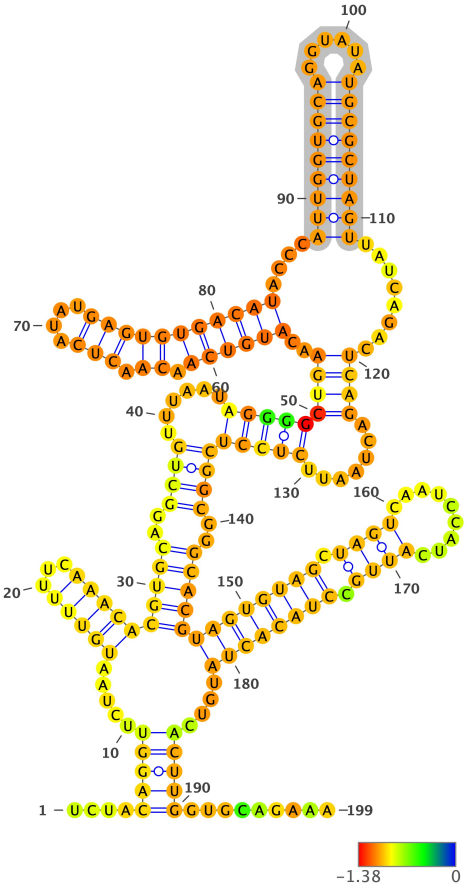
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 403 from nt 23558 to 23581 (nt 88 to 111)

```
5'-AUUGGUGCAGGUAUAUGCGCUAGU-3'
5'-(((((((((......)))))))))-3'
Motif MFE = -9.8; z-score = -4.24; 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 = -0.76; 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(+)

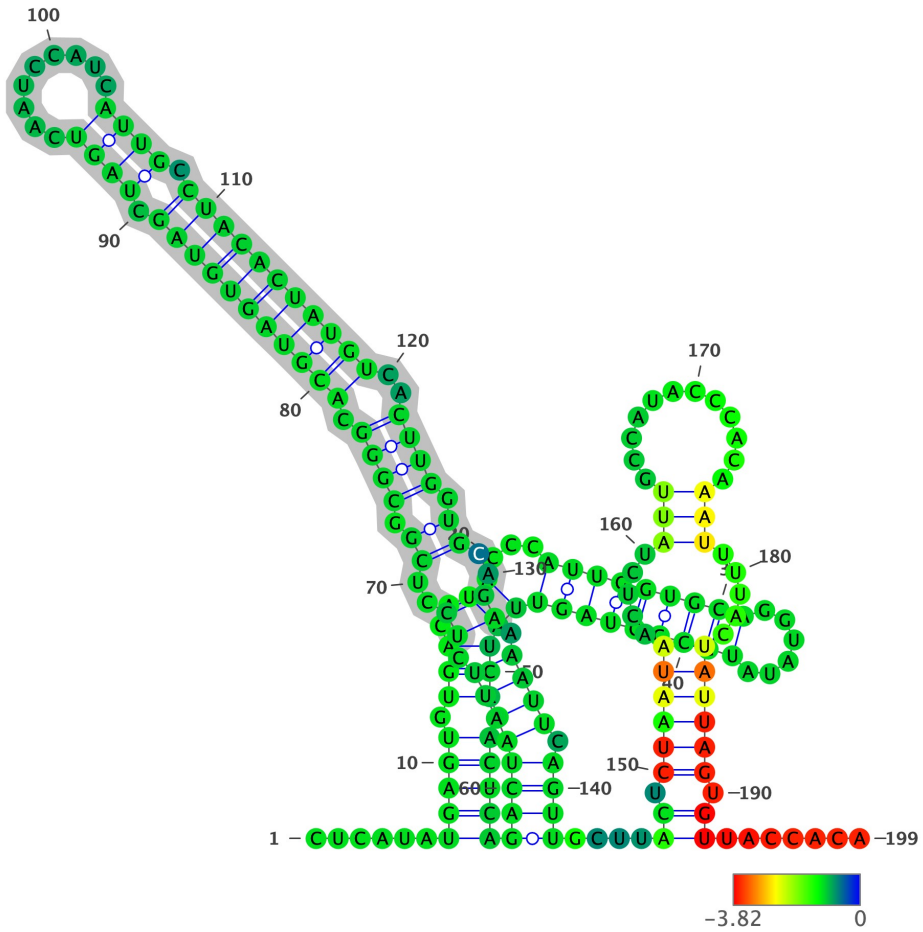
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 404 from nt 23602 to 23667 (nt 67 to 132)

```
5'-UCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACUUGGUGCAGA-3'
5'-(...((.((((.(((((((((((.((((.........)))).))))))))))..)))).))...)-3'
Motif MFE = -19.8; z-score = -1.87; ED = 7.01
```



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 23536 to 23734 (motif highlighted in silver):

```
5'-CUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUA
CACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACA-3
5'-......(((((.(((..((...(((((((((.....)))))))))))))).)))))((((((((.((..((.((((.(((((((((((.((((.........)))).)))
))))))))..)))).))..)).)))).)))).....((.((((((.....(((.............)))).....)))))).)).......-3'
MFE = -43.4; z-score = -1.24; ED = 35.34
```

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_gp02, 21563-25384(+)

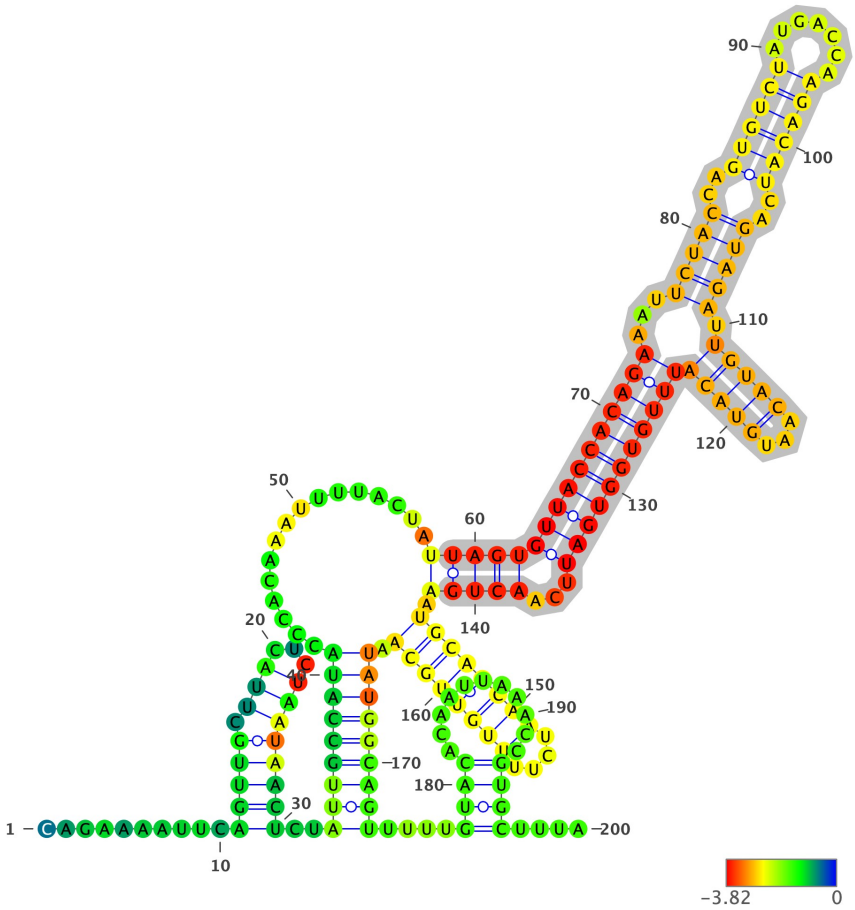
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 405 from nt 23722 to 23804 (nt 59 to 141)

```
5'-UAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUG-3'
5'-(((((((((((((((...(((((..((((((.......))))))..))))).(((((...)))))))))))))))...))))-3'
Motif MFE = -25.8; z-score = -4.0; 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 23664 to 23863 (motif highlighted in silver):

```
5'-CAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUU
GUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUUUA-3
5'-..........(((((.(((...))))))))..(((((((((.................(((((((((((((((...(((((..((((((.......))))))..))))).(
((((...)))))))))))))))...))))).((((((((....))))))))).))))))))....((((...........))))....-3'
MFE = -48.1; z-score = -3.93; ED = 16.41
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

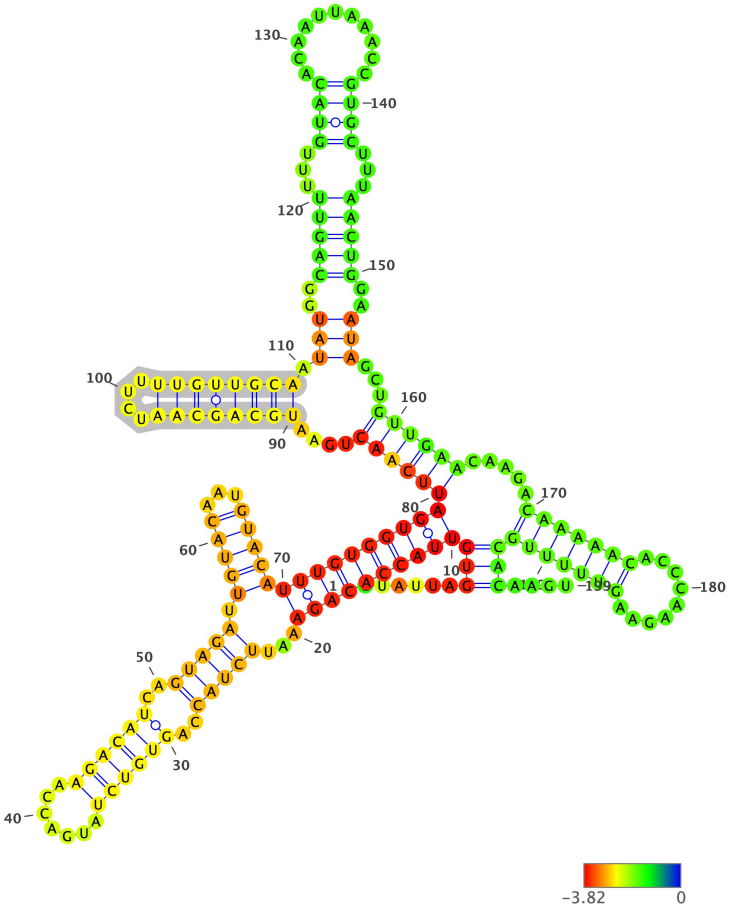
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 406 from nt 23807 to 23826 (nt 90 to 109)

```
5'-UGCAGCAAUCUUUUGUUGCA-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.8; z-score = -5.51; 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 = -3.41; 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(+)

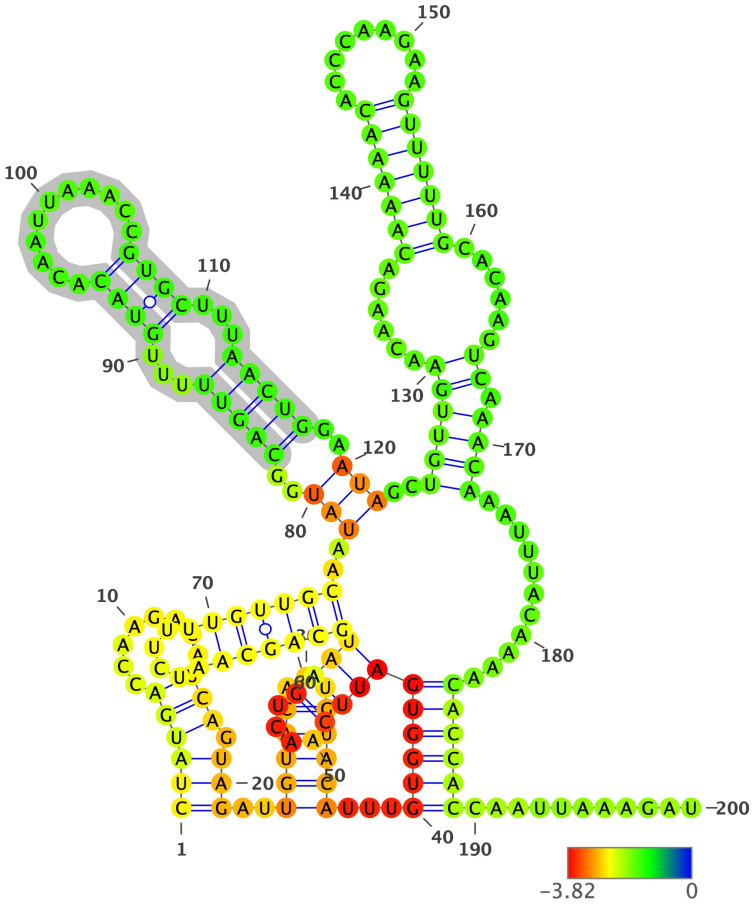
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 407 from nt 23833 to 23867 (nt 83 to 117)

```
5'-CAGUUUUUGUACACAAUUAAACCGUGCUUUAACUG-3'
5'-(((((...((((...........))))...)))))-3'
Motif MFE = -6.4; z-score = -2.14; 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 = -1.64; 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(+)

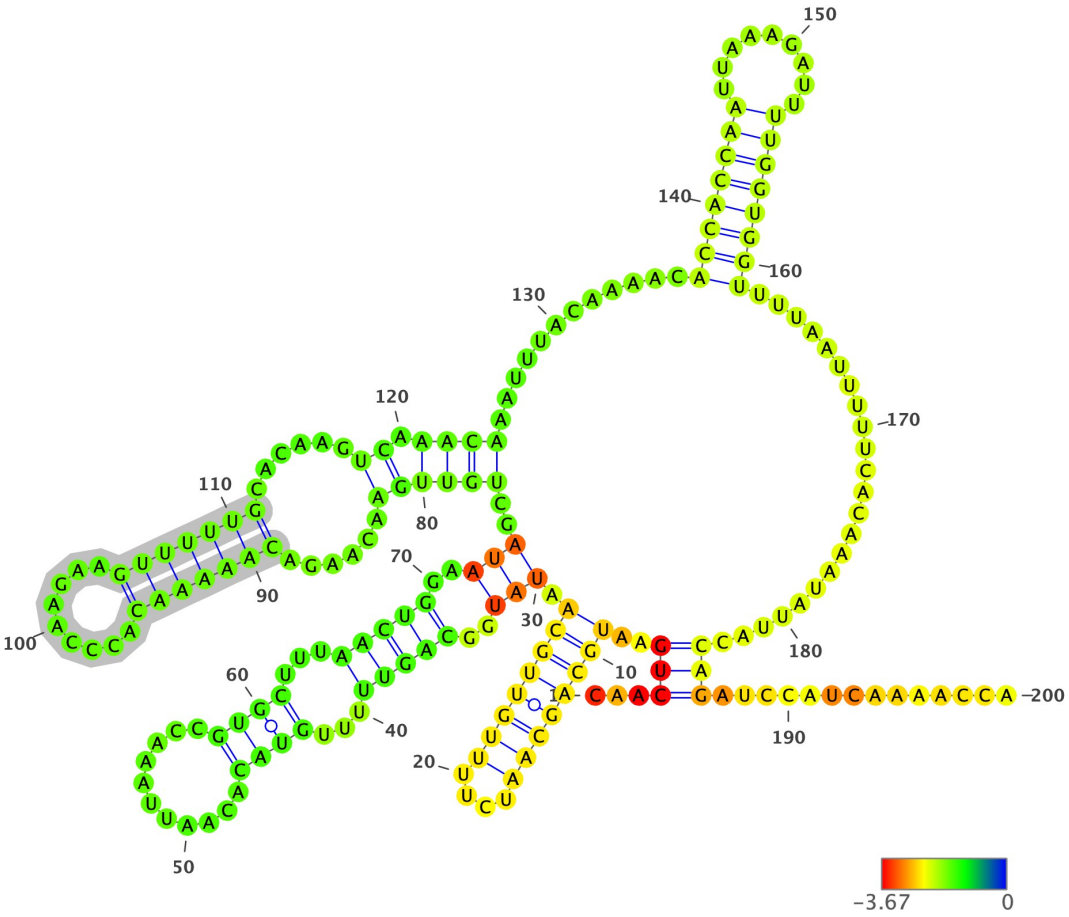
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 408 from nt 23887 to 23909 (nt 89 to 111)

```
5'-CAAAAACACCCAAGAAGUUUUUG-3'
5'-(((((((.........)))))))-3'
Motif MFE = -3.0; z-score = -2.2; 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(+)

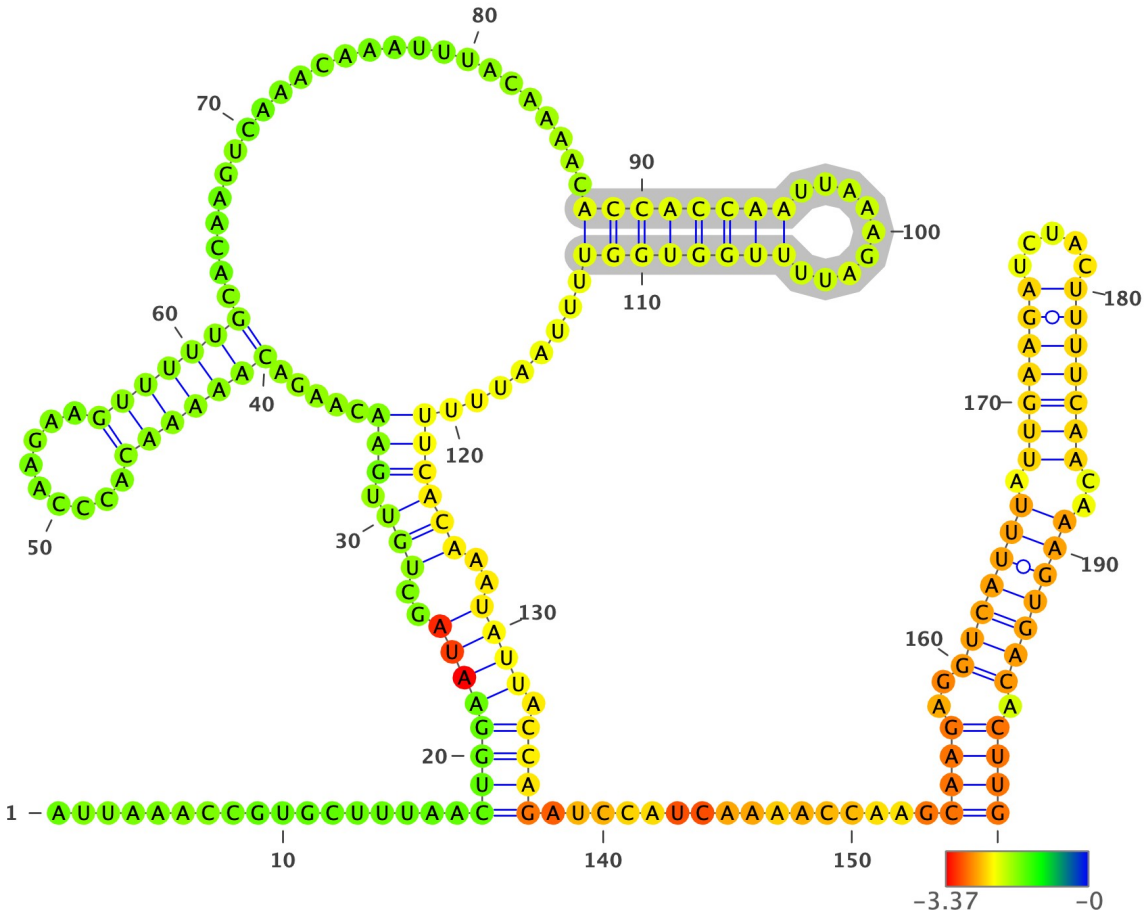
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 409 from nt 23935 to 23959 (nt 88 to 112)

```
5'-ACCACCAAUUAAAGAUUUUGGUGGU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -10.4; z-score = -4.48; 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 = -2.6; 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(+)

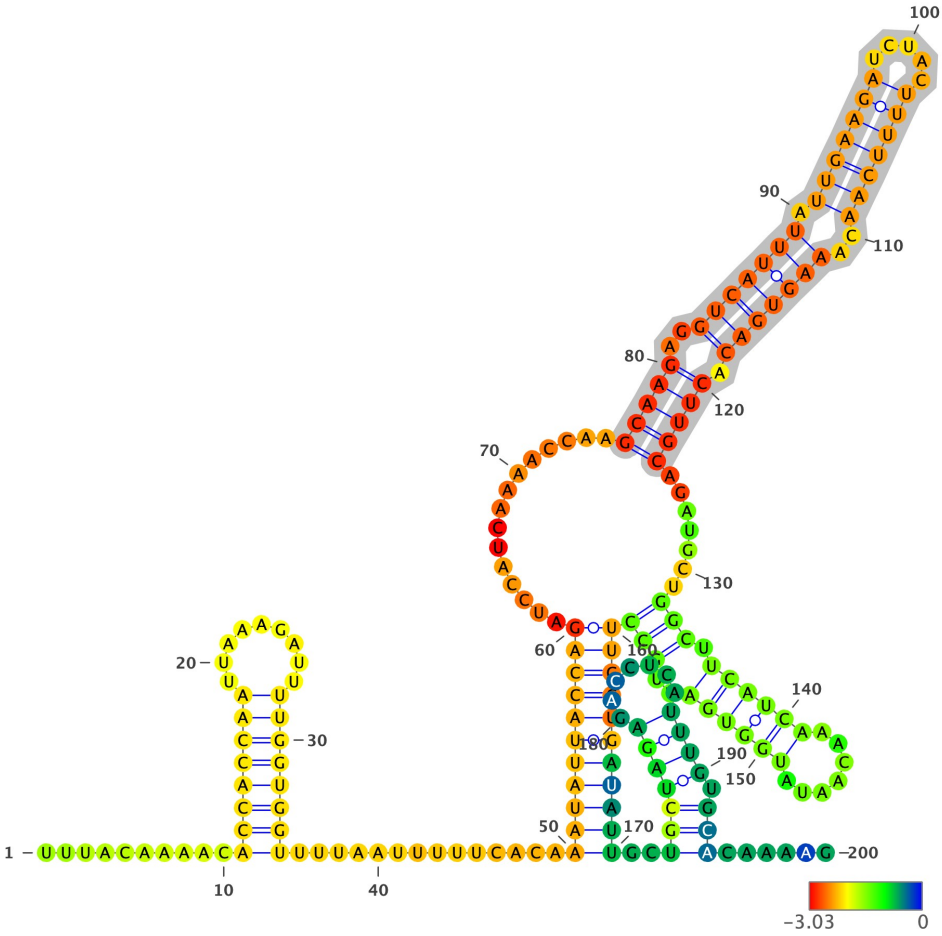
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 410 from nt 24000 to 24048 (nt 76 to 124)

```
5'-GCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUGC-3'
5'-((((((..(((((((.(((((((.....)))))))..)))))))..))))))-3'
Motif MFE = -16.1; z-score = -4.4; ED = 1.88
```



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

Extracted structure model with flanking nucleotides 23925 to 24124 (motif highlighted in silver):

```
5'-UUUACAAAACACCACCAAUUAAAGAUUUUGGUGGUUUUAAUUUUUCACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACA
AAGUGACACUUGCAGAUGCUGGCUUCAUCAAACAAUAUGGUGAUUGCCUUGGUGAUAUUGCUGCUAGAGACCUCAUUUGUGCACAAAAG-3
5'-.........(((((((((........)))))))).............((((((((((.............((((..(((((((.(((((((.....)))))))..
)))))))).)))))).......(((.((((((.......))))))..)))))))))))..(((((((.......)))).))).....-3'
MFE = -49.6; z-score = -3.77; 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(+)

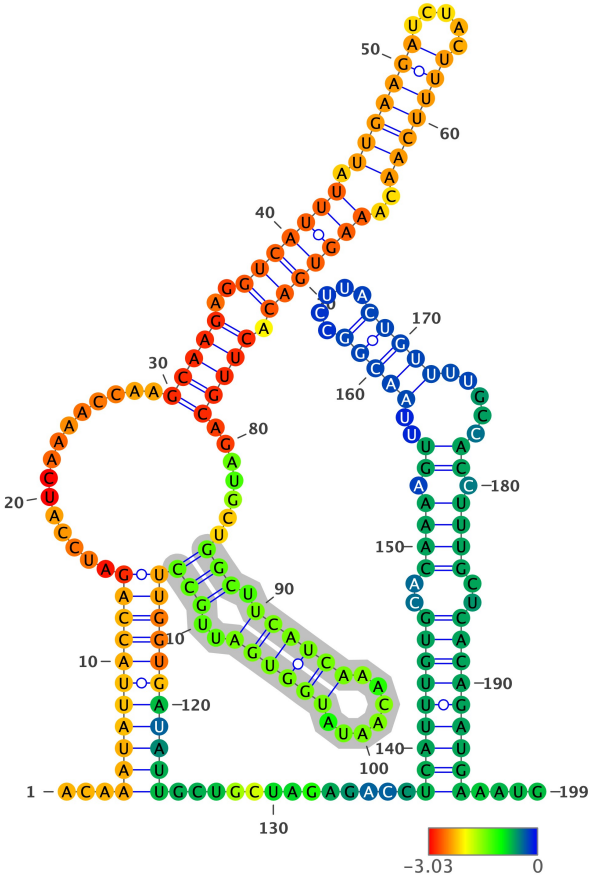
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 411 from nt 24056 to 24083 (nt 86 to 113)

```
5'-GGCUUCAUCAAACAAUAUGGUGAUUGCC-3'
5'-(((.((((((.......)))))).)))-3'
Motif MFE = -8.3; z-score = -3.05; 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 23971 to 24169 (motif highlighted in silver):

```
5'-ACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUGCAGAUGCUGGCUUCAUCAAACAAUAUGGUGAUUG
CCUUGGUGAUAUUGCUGCUAGAGACCUCAUUUGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUG-3
5'-...((((((((((.............((((((..(((((((.(((((((.....)))))))..)))))))).)))))).......(((.((((((.......)))))))..)
))))))))))))).............(((((((((..((((.((..(((((.....))))).....)).)))))..)))))))))....-3'
MFE = -52.1; z-score = -3.05; ED = 12.78
```

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(+)

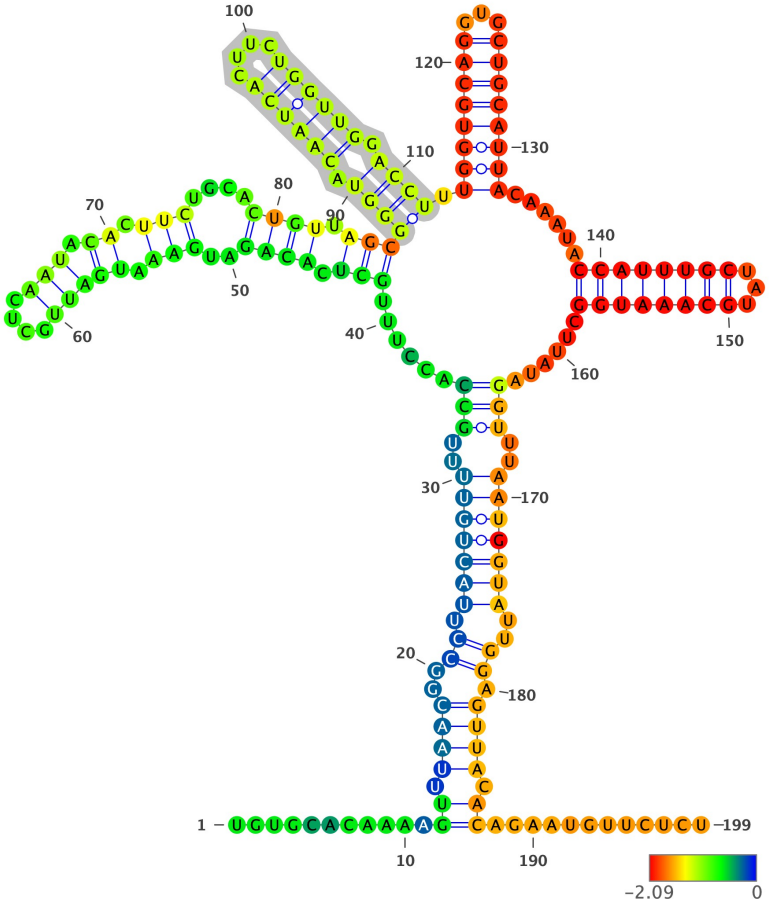
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 412 from nt 24199 to 24224 (nt 87 to 112)

```
5'-GGGUACAAUCACUUCUGGUUGGACCU-3'
5'-((((.((((((....)))))).))))-3'
Motif MFE = -8.5; z-score = -2.48; 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 = -0.87; 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(+)

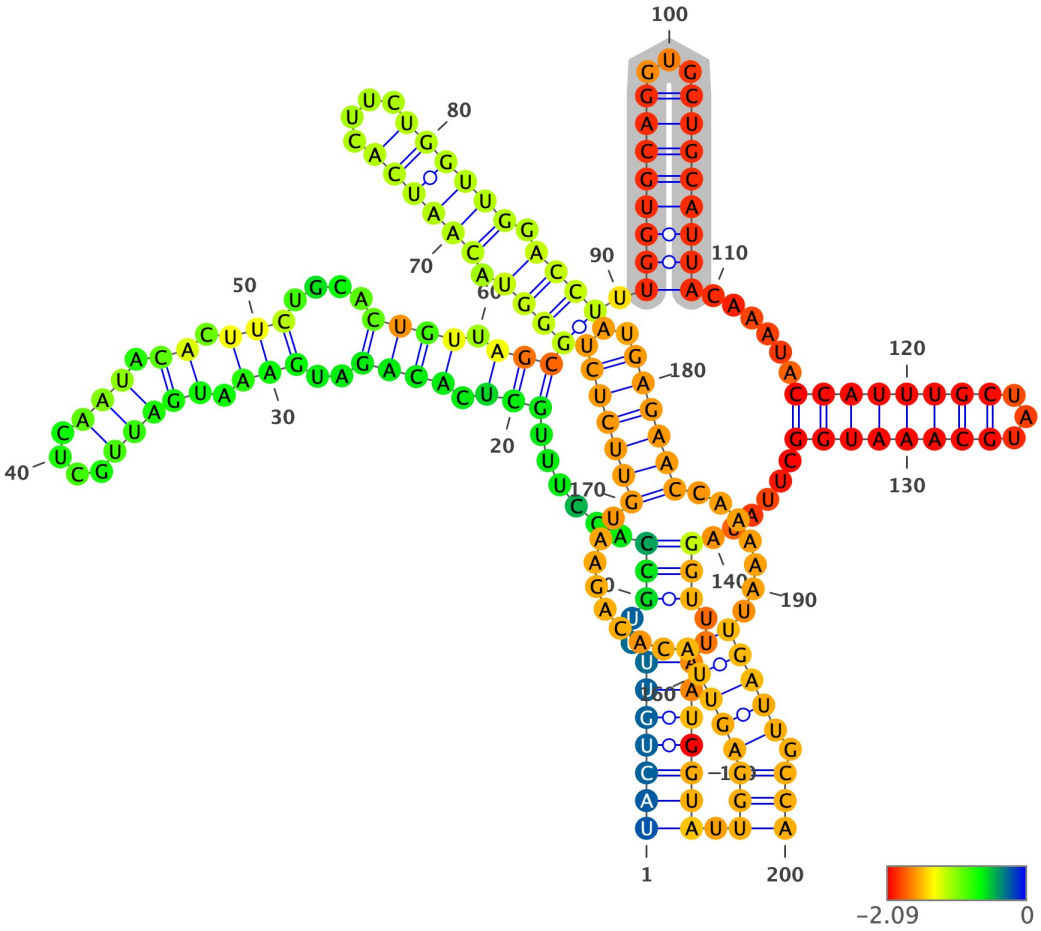
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 413 from nt 24226 to 24244 (nt 91 to 109)

```
5'-UGGUGCAGGUGCUGCAUUA-3'
5'-((((((((...))))))))-3'
Motif MFE = -6.7; z-score = -3.56; 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 = -1.78; 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(+)

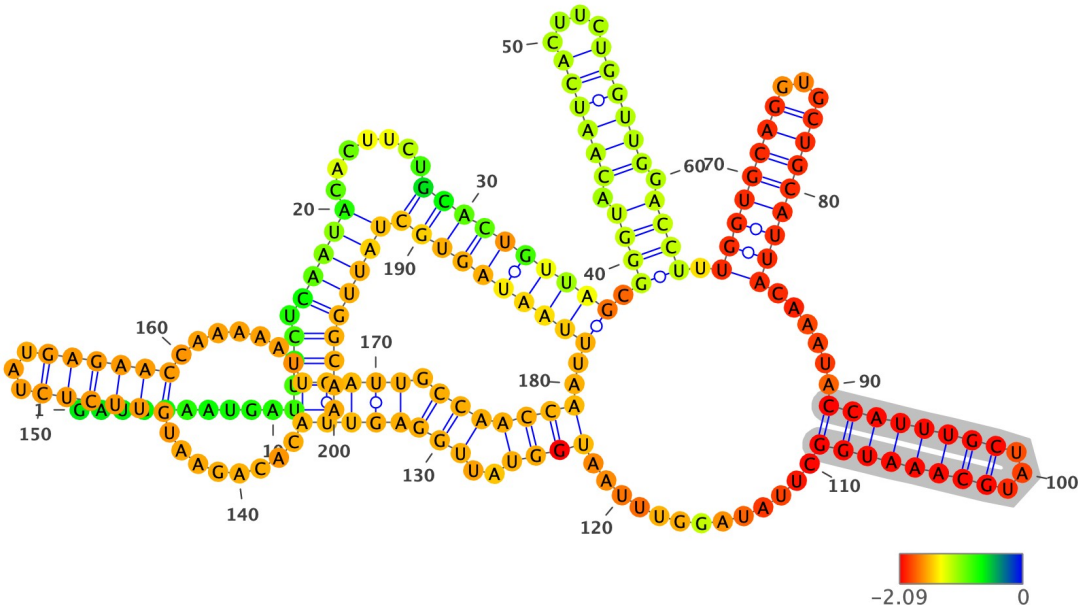
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 414 from nt 24251 to 24269 (nt 91 to 109)

```
5'-CCAUUUGCUAUGCAAAUGG-3'
5'-(((((((((...)))))))))-3'
Motif MFE = -8.4; z-score = -5.44; 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
UAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3
5'-.........((((.(((((.......((((((((((.(((((.((((((....)))))).)))))..(((((((((...)))))))))......(((((((((...)))))))))..
..........((((..(((((((((........((((((...))))))).......)))))).)))))))..))))))))))))))))))))-3'
MFE = -55.2; z-score = -2.93; 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(+)

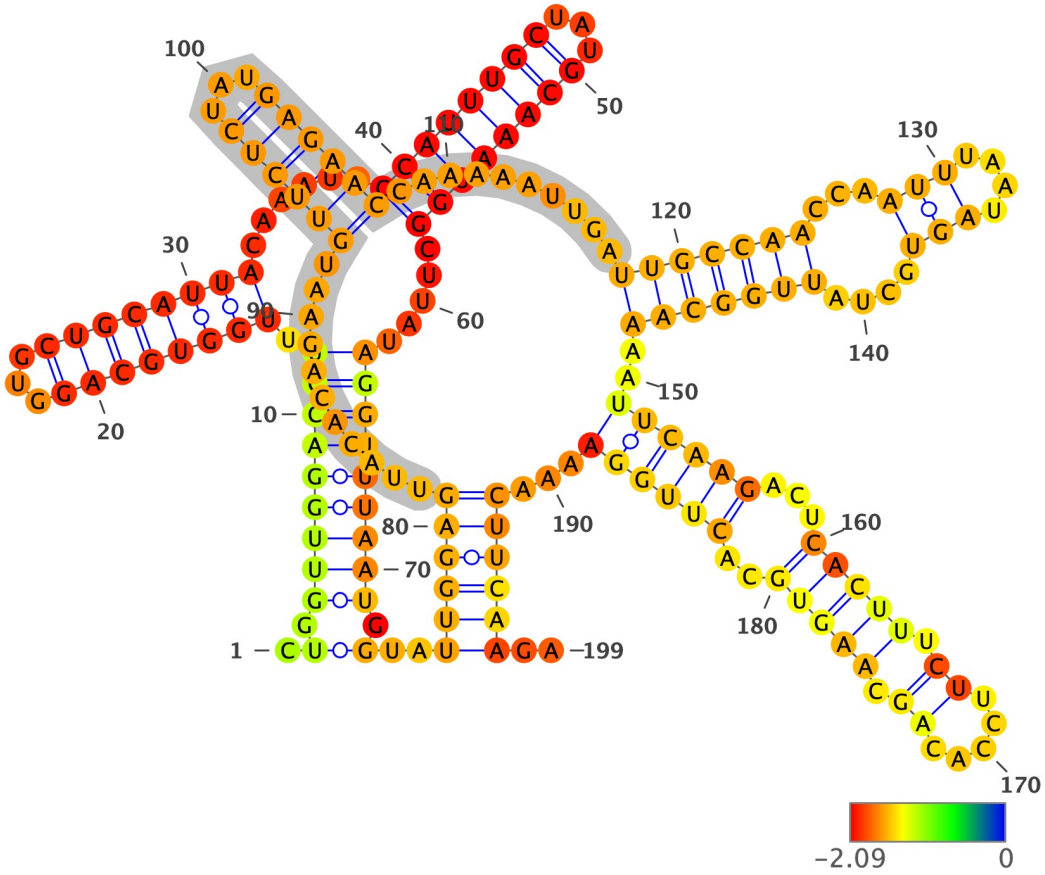
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 415 from nt 24294 to 24329 (nt 82 to 117)

```
5'-UUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGA-3'
5'-(((........((((((...))))))).......)))-3'
Motif MFE = -5.4; z-score = -1.67; 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 24213 to 24411 (motif highlighted in silver):

```
5'-CUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAA
AAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGA-3
5'-.(.(((((((((.(((((((((...)))))))))......(((((((((...)))))))))).....))))))))).)..((((((...........((((((...))))))....
......(((((((...(((....)))....)))))))..((((((...(((((.((.....)).)))))..))))))...))))))..-3'
MFE = -48.4; z-score = -2.63; ED = 15.51
```

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(+)

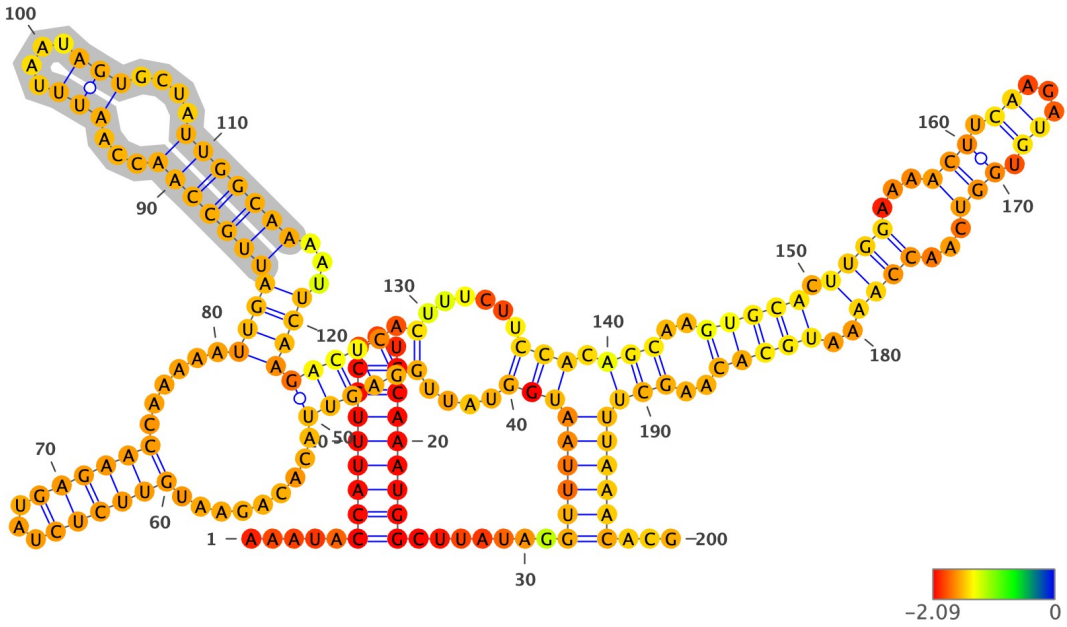
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 416 from nt 24330 to 24360 (nt 85 to 115)

```
5'-UUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3'
5'-(((((((...(((....))).....)))))))-3'
Motif MFE = -6.5; z-score = -2.48; ED = 3.02
```



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

Extracted structure model with flanking nucleotides 24246 to 24445 (motif highlighted in silver):

```
5'-AAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUG
GCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACG-3
5'-.....(((((((((...)))))))).......((((((((((....((((((.........((((((...))))))......((((((((((...(((....))).....)))
))))...))))))))).).......))).(((..((((((.((((...(((.((...)).))).....)))))..))))))..)))))))))...-3'
MFE = -42.9; z-score = -2.21; ED = 40.05
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

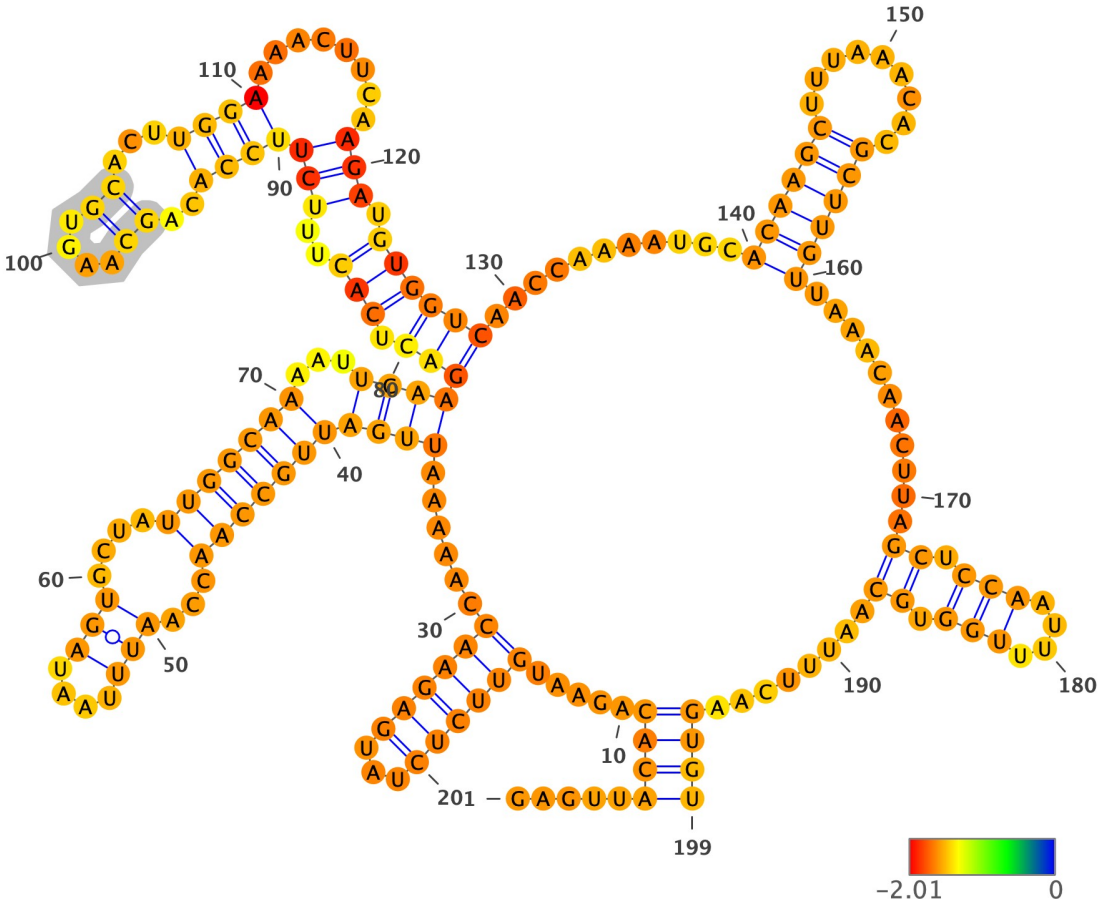
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 417 from nt 24386 to 24393 (nt 96 to 103)

```
5'-GCAAGUGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 24291 to 24489 (motif highlighted in silver):

```
5'-GAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAA
AACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGU-3
5'-.....((((.....((((((...))))))......((((((((((...(((....)))....)))))))...))))))(((.(((..(((((((..((....))...))))).
.......))).))))))..........((((((.........))))))..........((.(((....))).)).........))))-3'
MFE = -39.0; z-score = -2.58; ED = 33.85
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

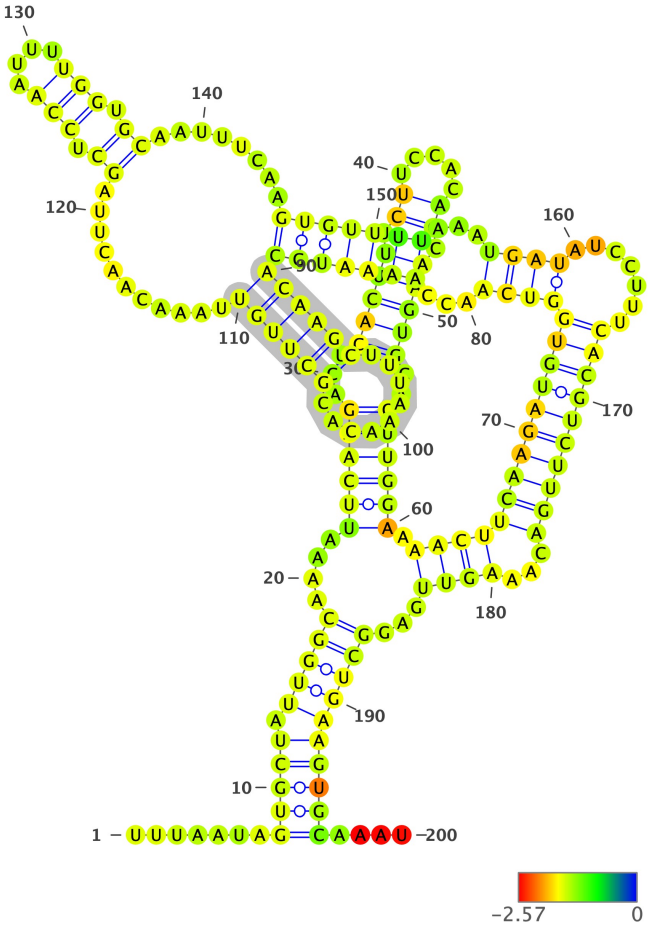
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24430 to 24450 (nt 90 to 110)

```
5'-ACAAGCUUUAAACACGCUUGU-3'
5'-((((((.........))))))-3'
Motif MFE = -5.2; z-score = -4.05; ED = 0.59
```



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 24341 to 24540 (motif highlighted in silver):

```
5'-UUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUU
AAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAU-3
5'-.......(((((.(((((....((((((...(((((.((.....)).)))))..)))))).((((((((((((((((((...((((((((((((((.........))))))).
..........((.(((....))).))........)))))))...))))).......))))))))))...))))...))))))))))....-3'
MFE = -43.2; z-score = -2.15; ED = 42.09
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

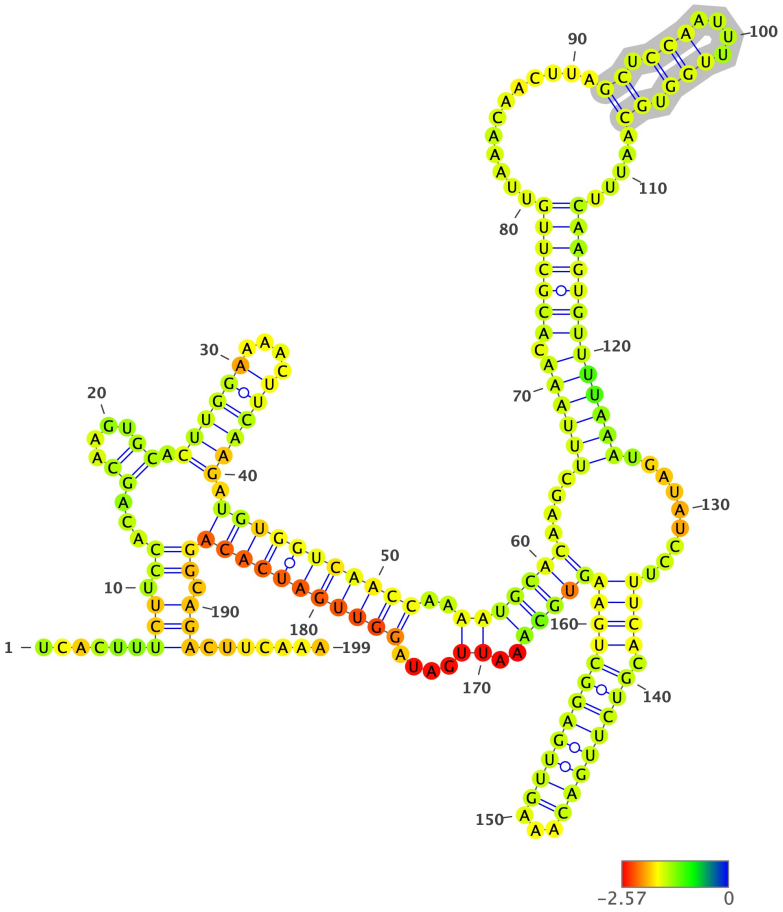
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24462 to 24477 (nt 92 to 107)

```
5'-GCUCCAAUUUUGGUGC-3'
5'-((.(((....))).))-3'
Motif MFE = -3.8; z-score = -2.98; 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 24371 to 24569 (motif highlighted in silver):

```
5'-UCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUU
UCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAA-3
5'-......(((.((...((....)).((((((....)))))).((((((((((..(((((((....(((((((.(((((((.............((.((....)))).)).....
.)))))))))))))).........((((.(((((((((...))))))))))))))))..)).....))))))))))))).))).....-3'
MFE = -47.9; z-score = -2.58; ED = 23.91
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

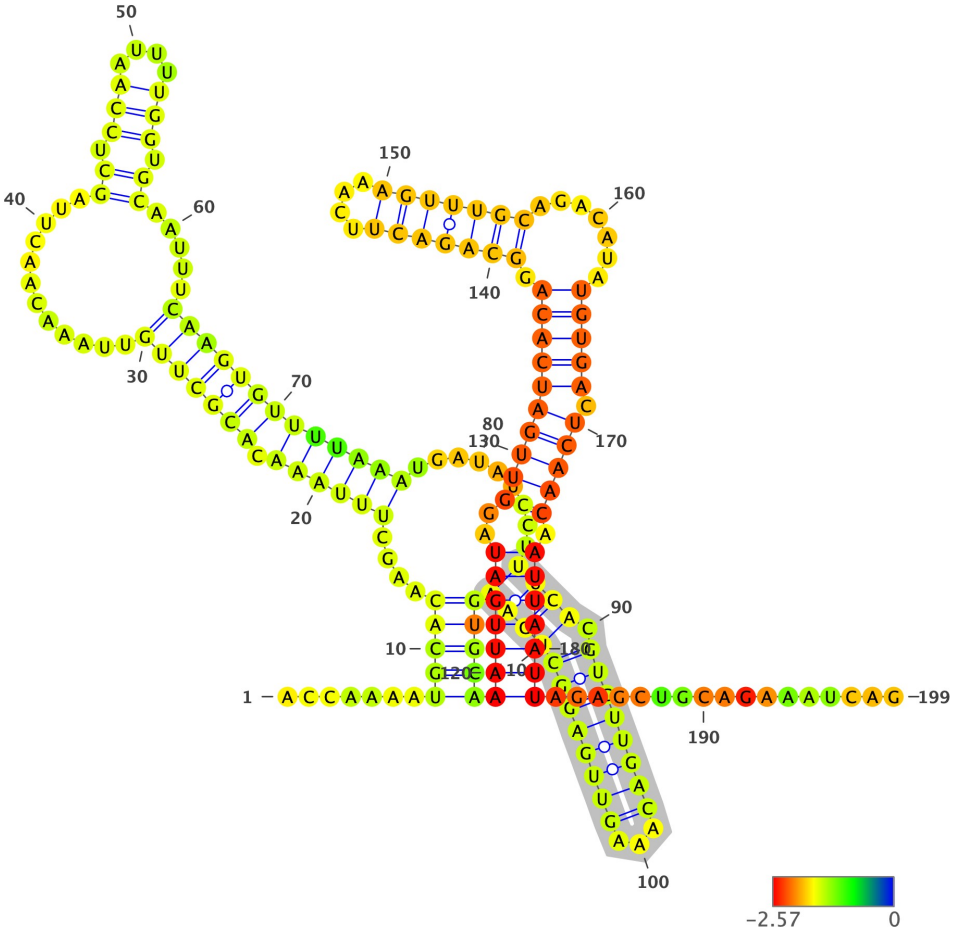
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 420 from nt 24505 to 24532 (nt 86 to 113)

```
5'-UUCACGUCUUGACAAAGUUGAGGCUGAA-3'
5'-((((.(((((((((...))))))))))))-3'
Motif MFE = -8.5; z-score = -2.29; 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 = -2.03; 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(+)

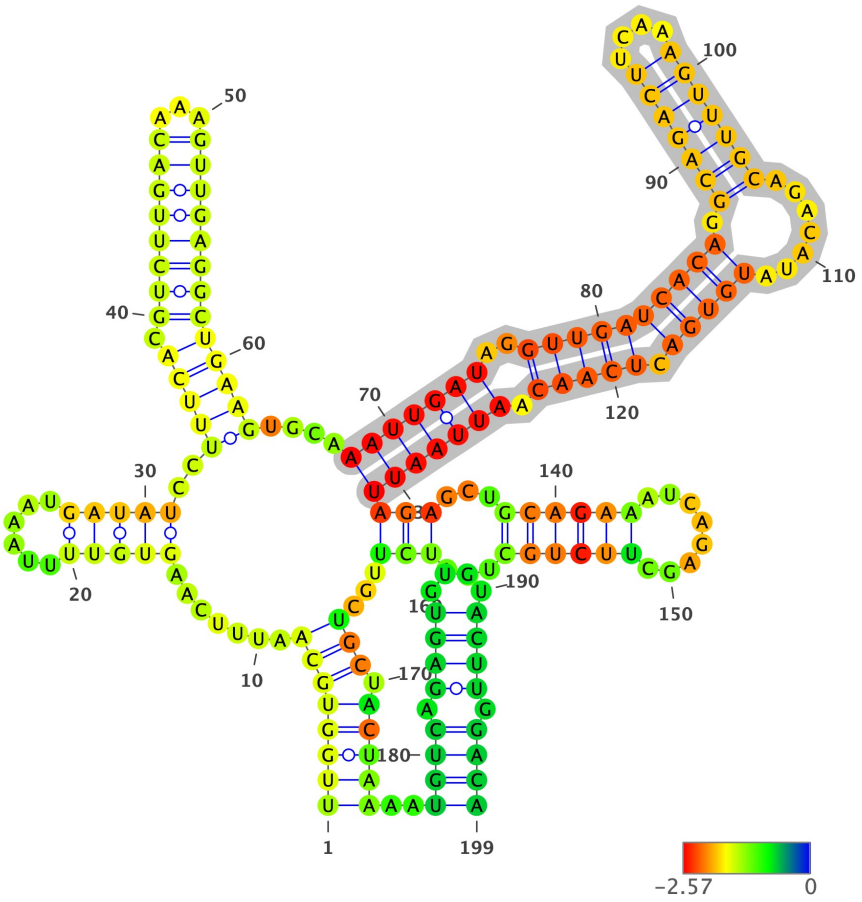
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 421 from nt 24538 to 24601 (nt 68 to 131)

```
5'-AAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUU-3'
5'-(((((((..((((((((((.(((((((....)))))))).......))))).)))))).)))))))-3'
Motif MFE = -17.9; z-score = -3.76; 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 = -1.89; 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(+)

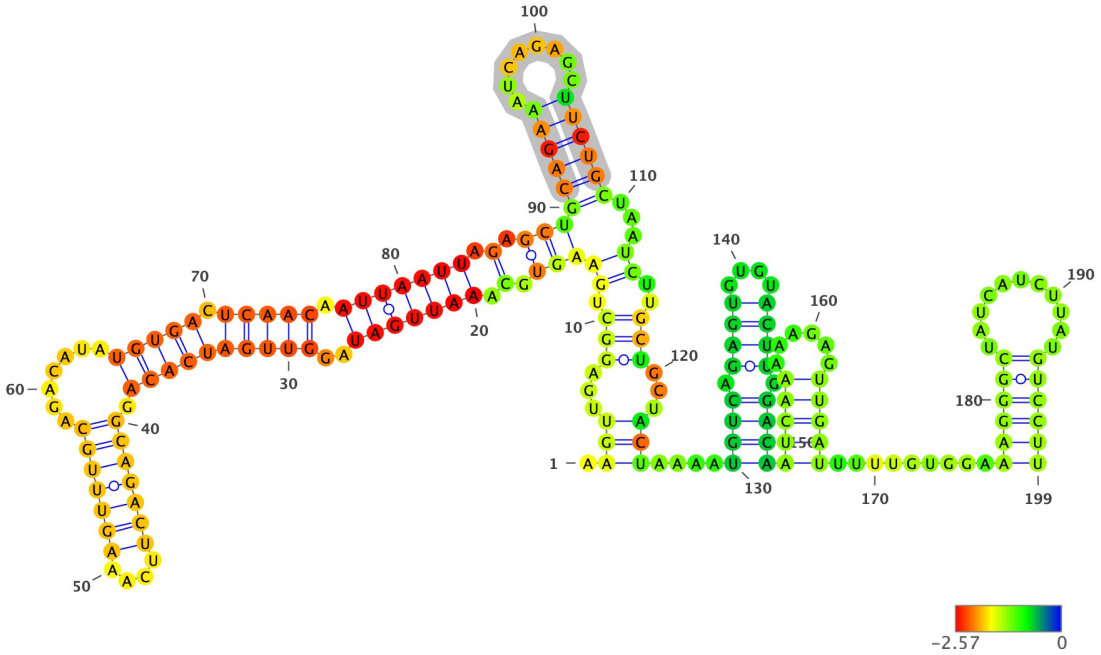
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 422 from nt 24609 to 24626 (nt 91 to 108)

```
5'-CAGAAAUCAGAGCUUCUG-3'
5'-((..............))-3'
Motif MFE = -2.5; z-score = -1.15; 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 24519 to 24717 (motif highlighted in silver):

```
5'-AAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUA
AUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU-3
5'-.(((...(((.(((((.(.(((((((..((((((((((.(((((((....)))))))).......))))).))))).)))))))).).)))((((((........))))))..
.))..)))...)))....((((.((((....)))).))))(((((......)))))..........((((((...........))))))-3'
MFE = -44.9; z-score = -1.25; ED = 40.15
```

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_gp02, 21563-25384(+)

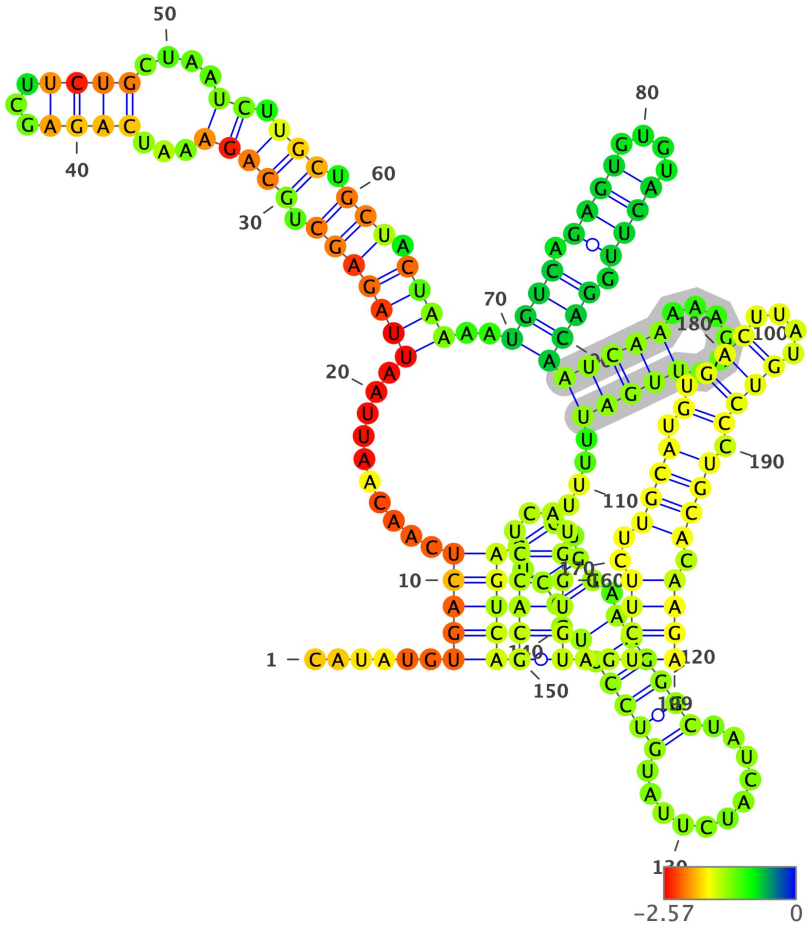
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24670 to 24685 (nt 92 to 107)

```
5'-AUCAAAAAGAGUUGAU-3'
5'-(((((......)))))-3'
Motif MFE = -0.9; z-score = -4.18; 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 24579 to 24777 (motif highlighted in silver):

```
5'-CAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUU
GUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGA-3
5'-......(((((..........(((((((.(((((...((((...))))....)).))).))).))))..((((.((((....)))).))))(((((......)))))....
(.((.((((((...........)))))).)).))))))(((((....)))))..((((..((((.(.(((....)))).)))).))))-3'
MFE = -48.9; z-score = -1.56; ED = 37.74
```

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_gp02, 21563-25384(+)

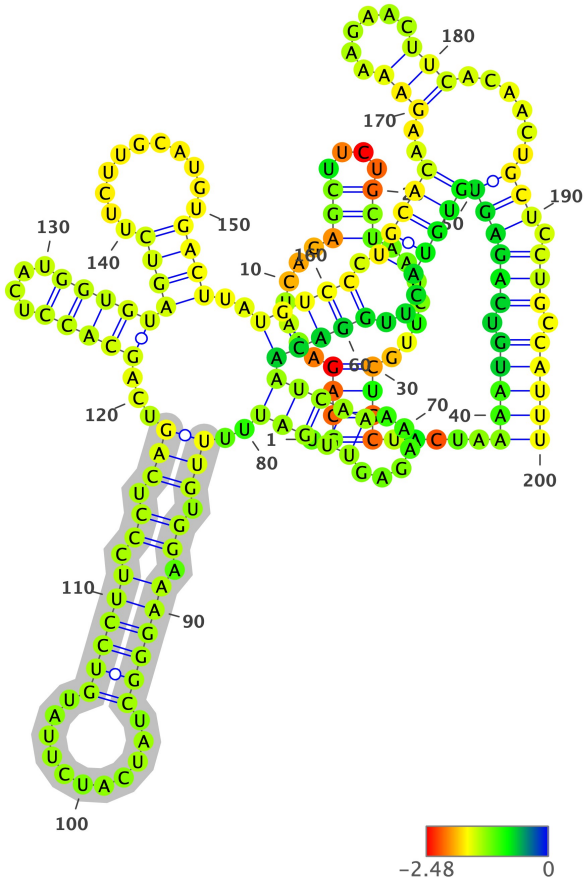
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 424 from nt 24688 to 24724 (nt 82 to 118)

```
5'-UUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAG-3'
5'-(((.((.((((((...........))))))).)).)))-3'
Motif MFE = -10.6; z-score = -2.34; ED = 4.23
```



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 24607 to 24806 (motif highlighted in silver):

```
5'-UGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU
CCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUU-3
5'-.((((.......(((....)))........))))).....(((((.(((((((((((...((((((((((......)))))..(((.((.((((((...........))))))
.)).)))...(((((....)))))((((...........))))..)))))).)))))..(((......)))......))).))).)))))-3'
MFE = -47.6; z-score = -1.4; ED = 38.93
```

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(+)

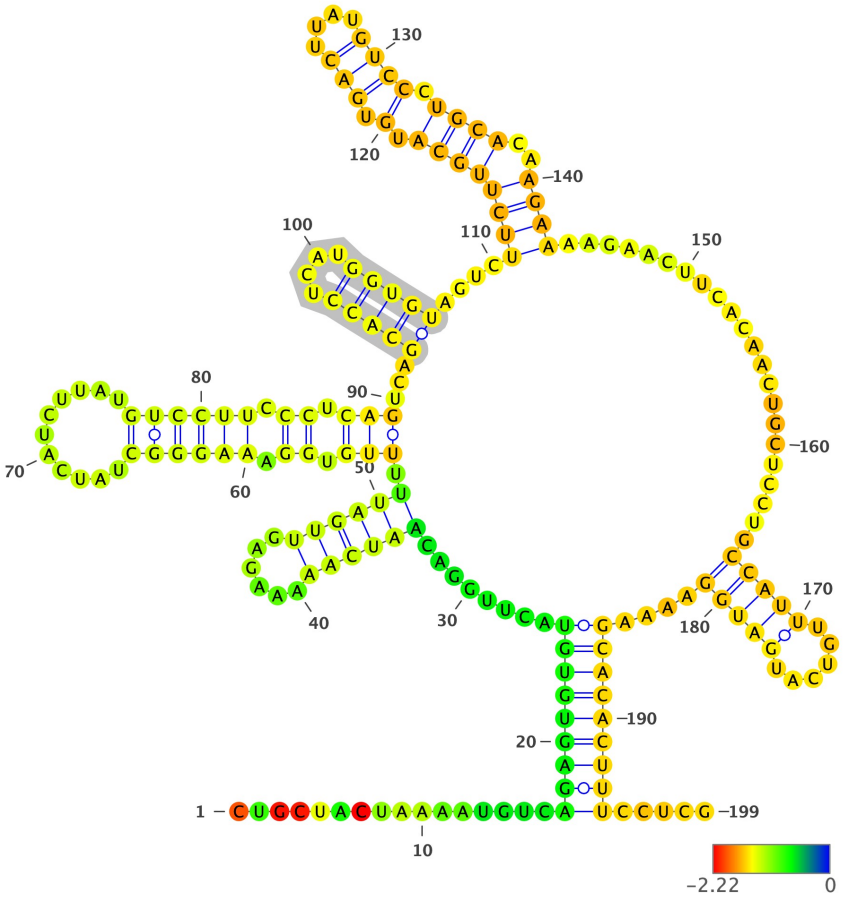
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 425 from nt 24728 to 24741 (nt 93 to 106)

```
5'-GCACCUCAUGGUGU-3'
5'-(((((....)))))-3'
Motif MFE = -6.1; z-score = -4.38; ED = 0.32
```



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

Extracted structure model with flanking nucleotides 24636 to 24834 (motif highlighted in silver):

```
5'-CUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCU
UCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCG-3
5'-................(((((((((.........((((((......)))))).(((.((.((((((...........)))))).)).)))...(((((....)))))....(
(((((((.(.(((....)))).)))).)))).....................(((((......)))))....))))))))).....-3'
MFE = -45.8; z-score = -0.87; ED = 39.36
```

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

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

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

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

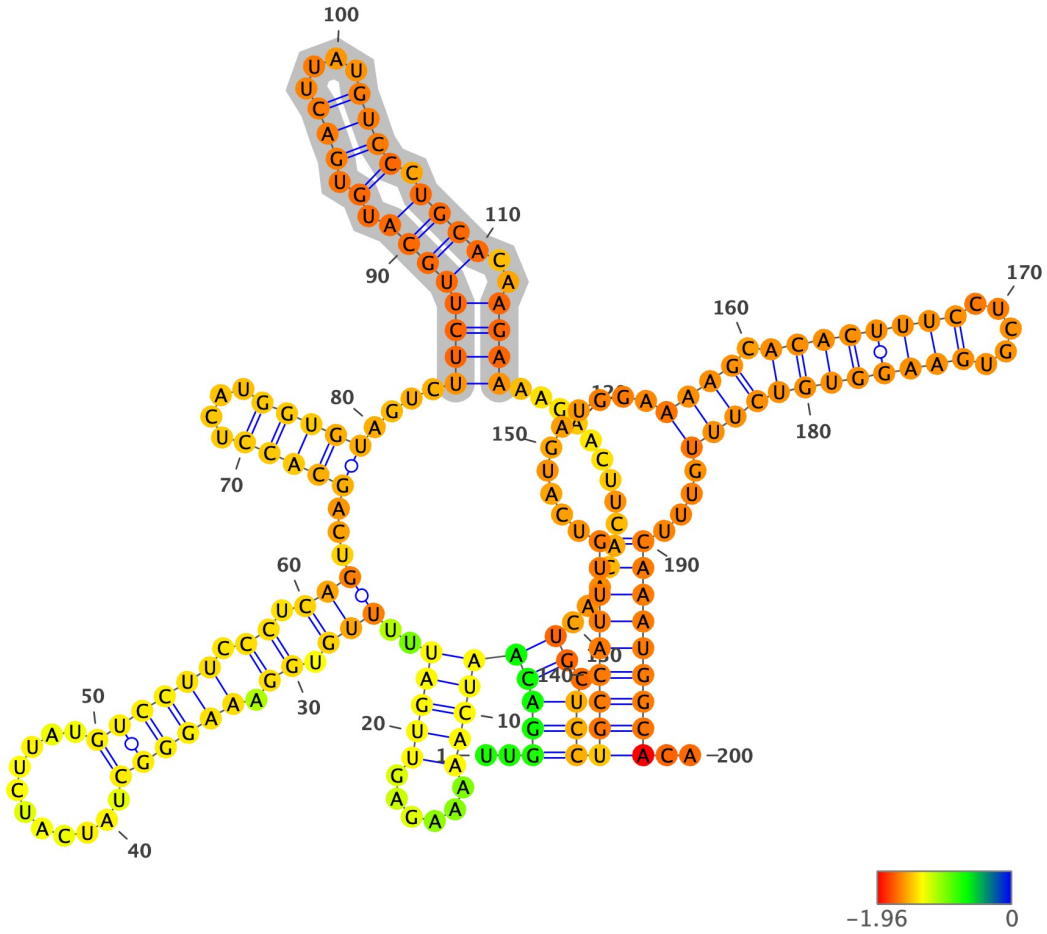
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 426 from nt 24746 to 24778 (nt 84 to 116)

```
5'-UUCUUGCAUGUGACUUAUGUCCCUGCACAAGAA-3'
5'-(((((((((.(.(((....)))))..))))..)))))-3'
Motif MFE = -8.2; z-score = -2.3; ED = 3.79
```



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 24663 to 24862 (motif highlighted in silver):

```
5'-UUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCAC
AAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACA-3
5'-..((((((((((.....))))))..(((.((.((((((.........))))))..)).)))...(((((....)))))....(((((((((.(.((((....)))).)))))
.))))..............)).)))(((((((((.........((((.(((((((((.....)))))))))))))....)))))))))..-3'
MFE = -52.9; z-score = -2.12; ED = 34.44
```

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_gp02, 21563-25384(+)

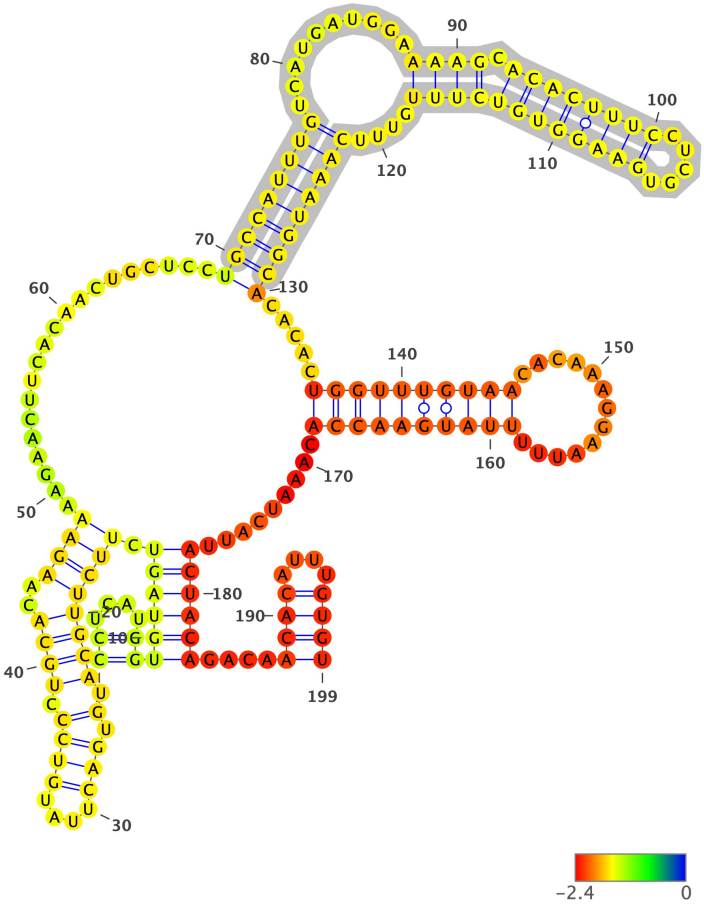
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 427 from nt 24800 to 24859 (nt 70 to 129)

```
5'-GCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGC-3'
5'-((((((((.........((((.((((((((.....)))))))))))....))))))))-3'
Motif MFE = -18.9; z-score = -3.11; ED = 10.4
```



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

Extracted structure model with flanking nucleotides 24731 to 24929 (motif highlighted in silver):

```
5'-CCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGU
GUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGU-3
5'-((....))((((((.((((((((.(.(((....)))).))))..))))...................(((((((((.........((((.((((((((.....))))))
))))))....)))))))))).....((((((((((.............))))))))))).........))))))....((((....))))-3'
MFE = -44.1; z-score = -1.77; ED = 32.79
```

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 199--gene, gene-GU280_gp02, 21563-25384(+)

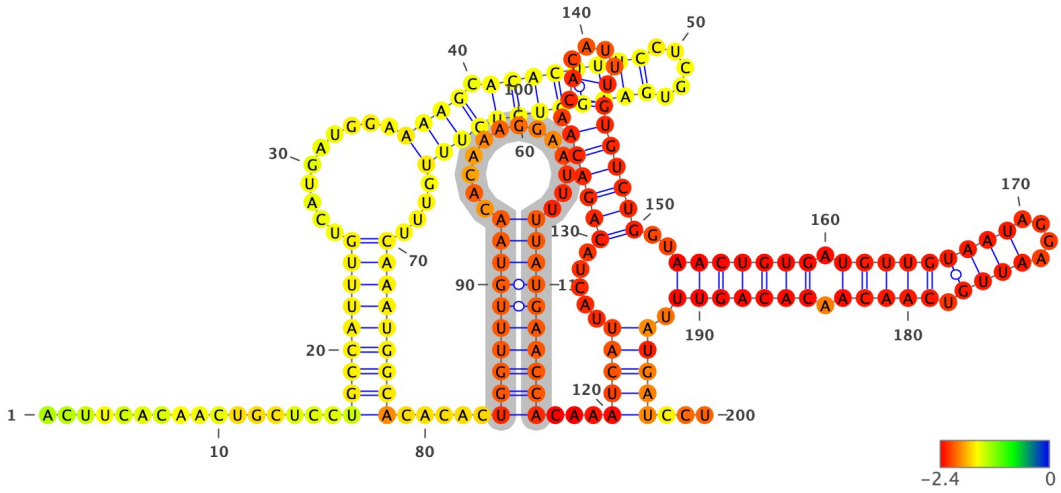
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 428 from nt 24866 to 24898 (nt 84 to 116)

```
5'-UGGUUUGUAACACAAAGGAAUUUUUAUGAACCA-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -6.0; z-score = -1.91; 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 = -3.02; 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(+)

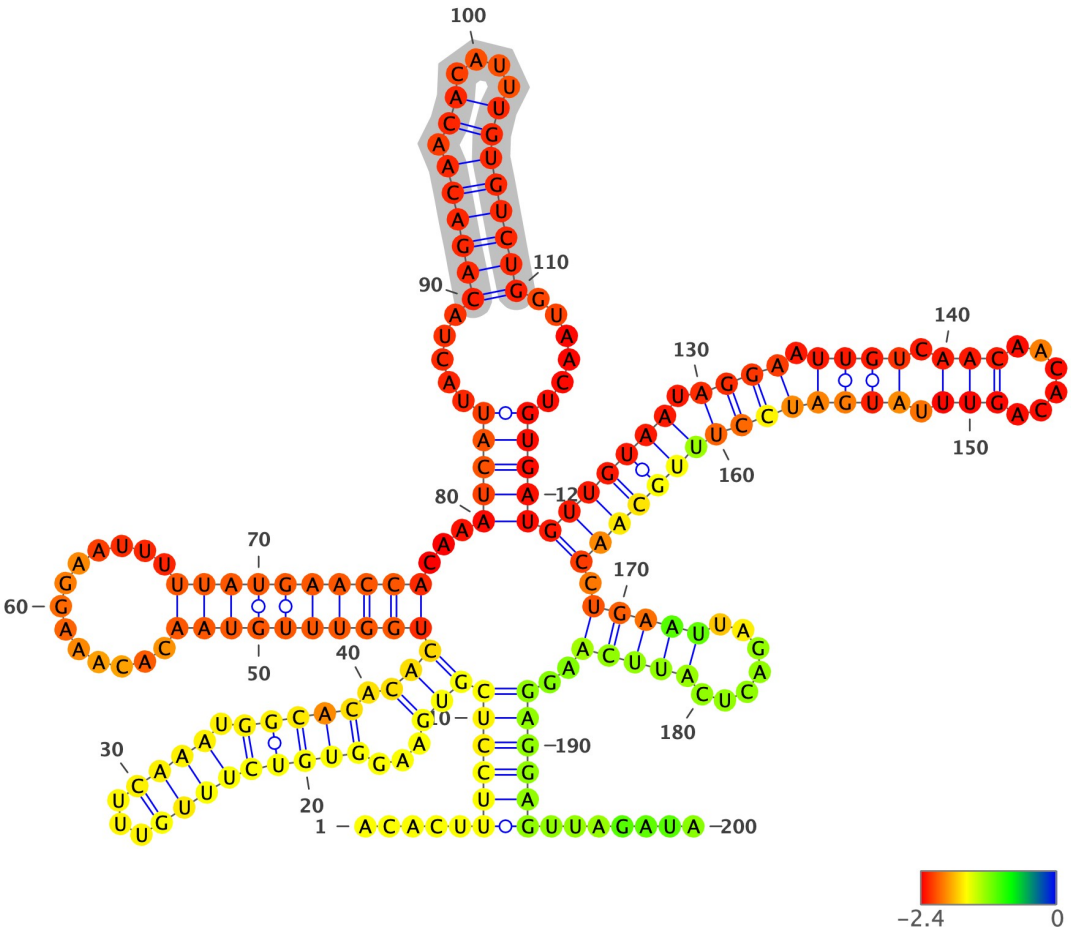
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 429 from nt 24912 to 24932 (nt 90 to 110)

```
5'-CAGACAACACAUUUGUGUCUG-3'
5'-((((((.((....)))))))))-3'
Motif MFE = -6.0; z-score = -3.65; 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 = -2.15; 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(+)

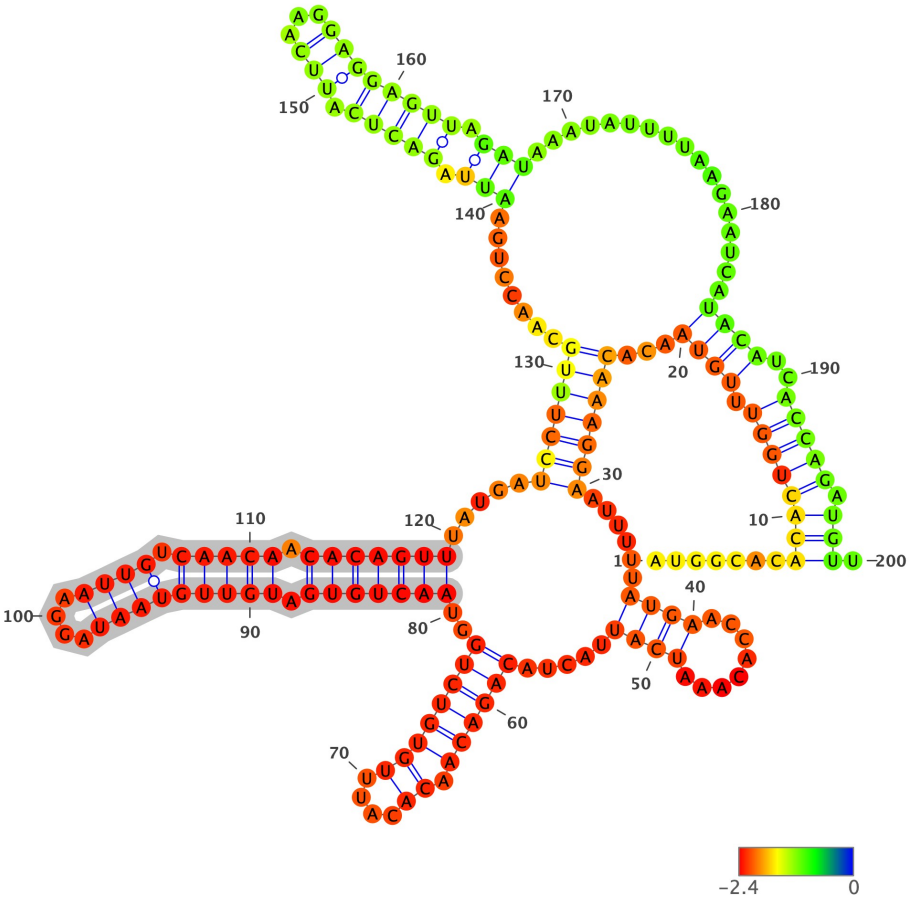
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 430 from nt 24935 to 24973 (nt 81 to 119)

```
5'-AACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUU-3'
5'-(((((((.((((((((((....)))))).))))))..)))))))-3'
Motif MFE = -13.8; z-score = -5.26; 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 = -2.29; 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(+)

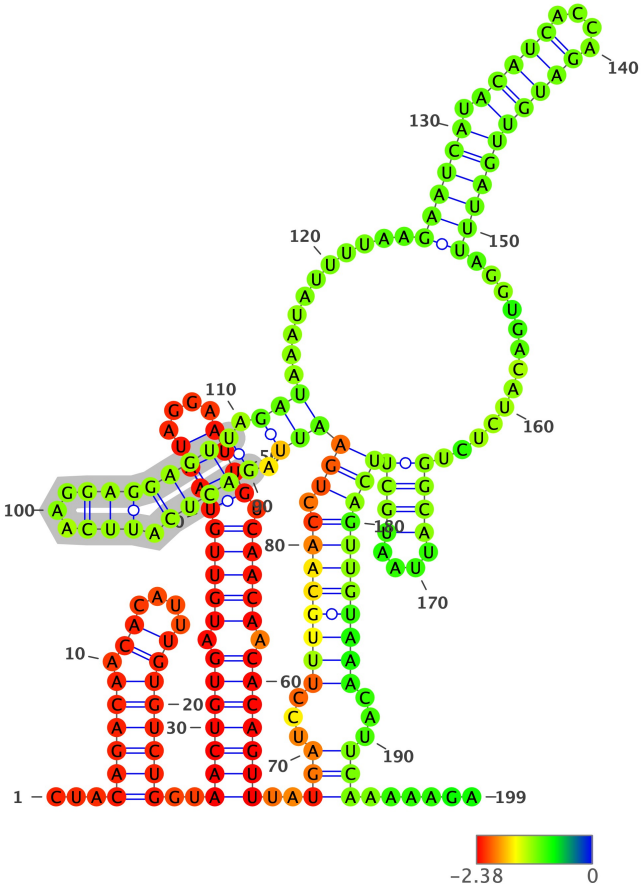
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 431 from nt 24998 to 25017 (nt 90 to 109)

```
5'-GACUCAUUCAAGGAGGAGUU-3'
5'-(((((.(((...))))))))-3'
Motif MFE = -3.4; z-score = -1.33; 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 24909 to 25107 (motif highlighted in silver):

```
5'-CUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAG
AUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGA-3
5'-...((((((.((....))))))))..(((((((.(((((((((....)))).))))).)))))))..(((...((((((((.((((((.(((((.(((...))))))))).)
)).........((((((.(((((....)))))))))))).............((((....)))))))))))))))...)))......-3'
MFE = -48.1; z-score = -3.02; ED = 20.43
```

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_gp02, 21563-25384(+)

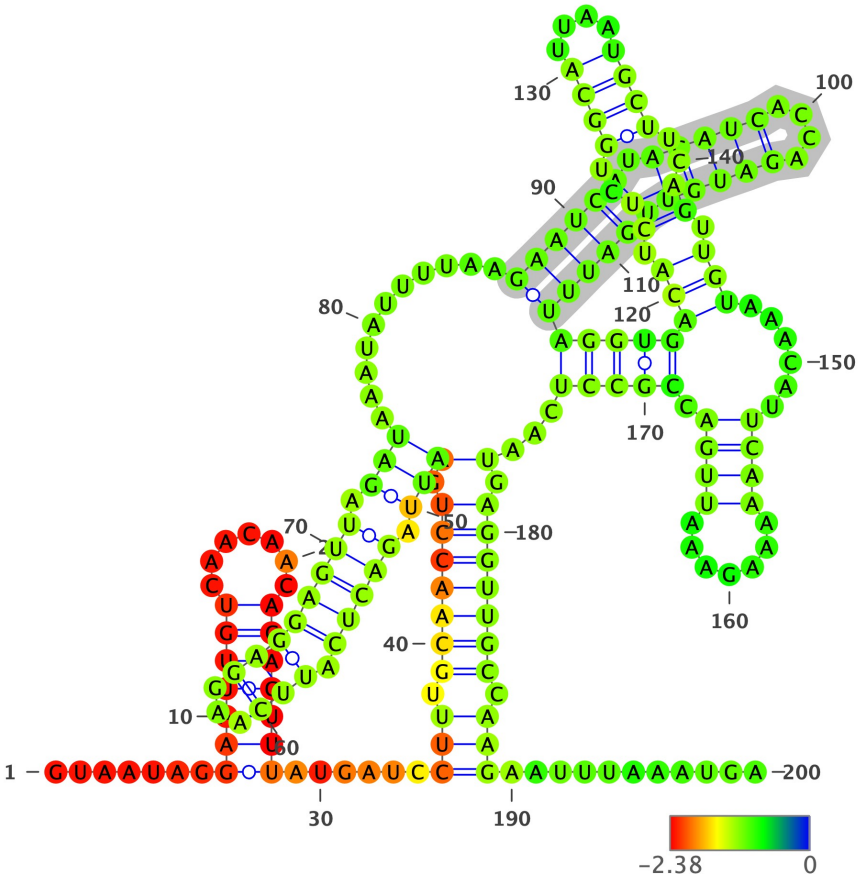
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 432 from nt 25033 to 25059 (nt 87 to 113)

```
5'-GAAUCAUACAUCACCAGAUGUUGAUUU-3'
5'-((((((.(((((....)))))))))))-3'
Motif MFE = -8.1; z-score = -3.82; 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 = -1.13; 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(+)

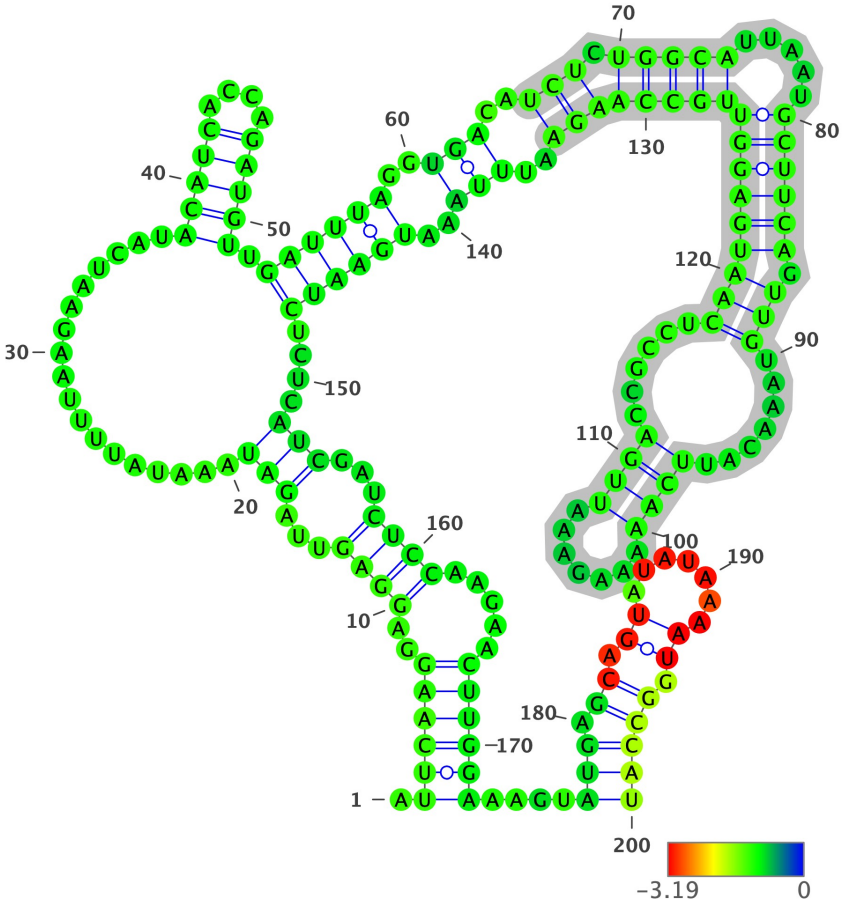
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 433 from nt 25068 to 25136 (nt 66 to 134)

```
5'-UCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGA-3'
5'-(((.(((((.....((((((.(((.......((((.......)))).....)))))))))))))))))-3'
Motif MFE = -13.2; z-score = -1.21; ED = 16.17
```



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

Extracted structure model with flanking nucleotides 25003 to 25202 (motif highlighted in silver):

```
5'-AUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGA
CCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAU-3
5'-.((((((..((((...(((.................((((((....)))))).((((((..((((..((((.(((((.....((((((.(((.......((((.......))))
.....))))))))))))))))))..)))..))))))....)))...)))).....)))))))....(((.((.((.......)).)))))-3'
MFE = -34.4; z-score = -0.24; ED = 43.0
```

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_gp02, 21563-25384(+)

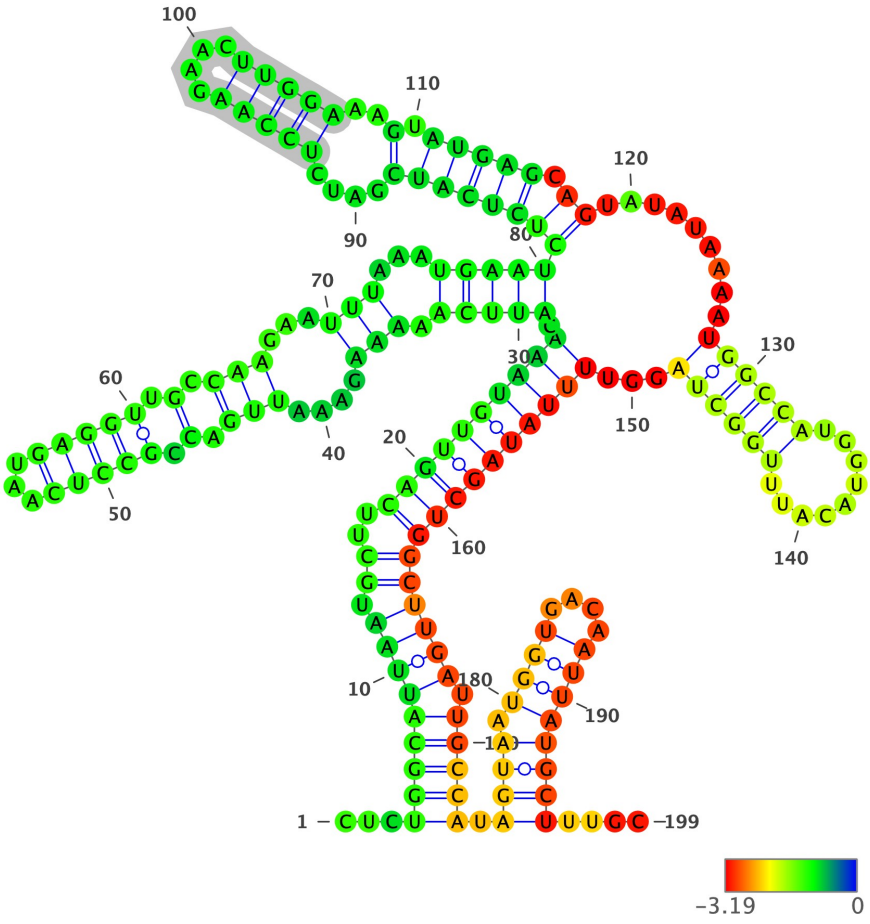
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 434 from nt 25161 to 25174 (nt 93 to 106)

```
5'-UCCAAGAACUUGGA-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 = -0.66; 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(+)

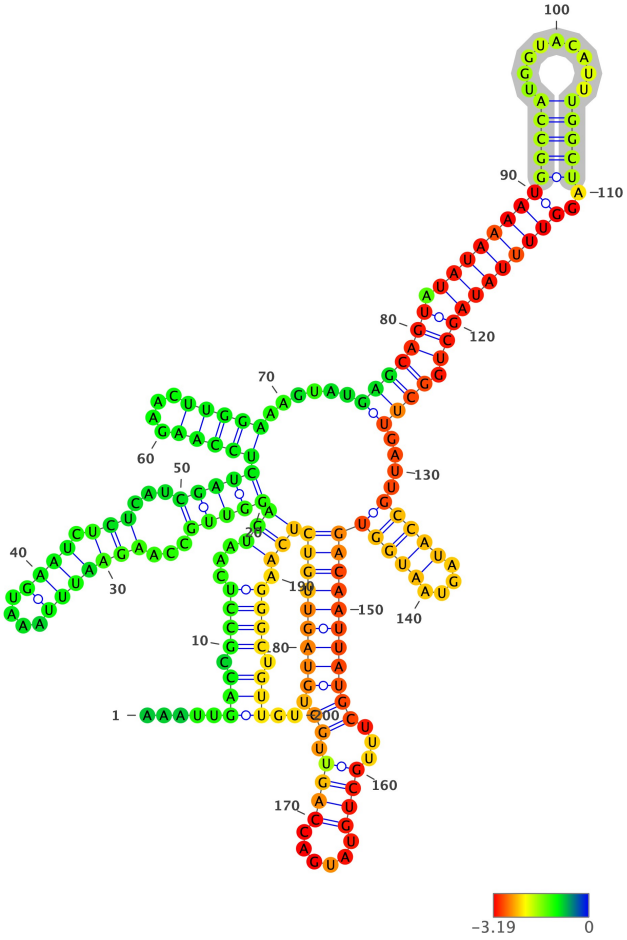
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 435 from nt 25197 to 25215 (nt 91 to 109)

```
5'-GGCCAUGGUACAUUUGGCU-3'
5'-(((((.........)))))-3'
Motif MFE = -5.2; z-score = -1.8; ED = 1.07
```



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

Extracted structure model with flanking nucleotides 25107 to 25306 (motif highlighted in silver):

```
5'-AAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAG
GUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGU-3
5'-.....(((.((((...((((((((...(((((((....)))).)))...)))))(((((....)))))......(((((((.((((((((((((.........)))))..
)))))))))))).))))....(((((....)))))((((((((((...((((......)))).)).))))))))))))).)))).)))..-3'
MFE = -51.6; z-score = -1.28; ED = 62.32
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

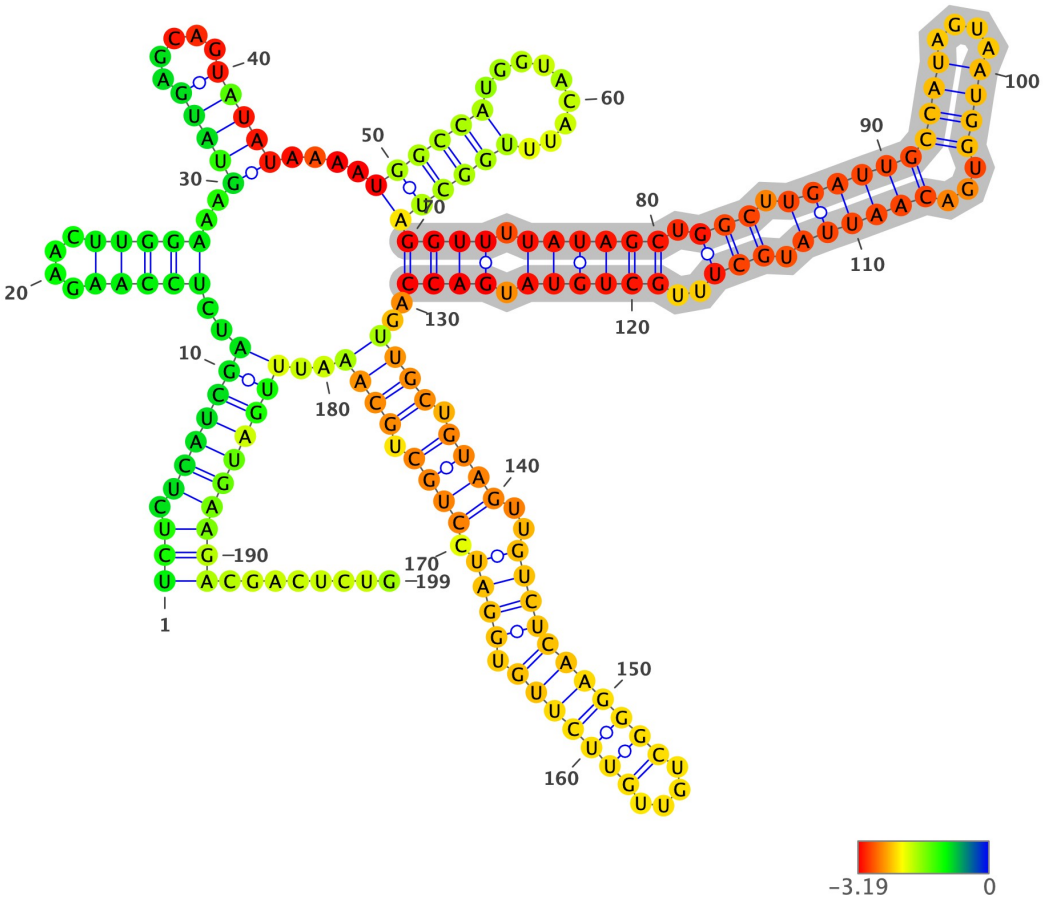
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 436 from nt 25217 to 25276 (nt 70 to 129)

```
5'-GGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACC-3'
5'-((((.((((((.(((.((((((((((....))))...)))))).)))..)))))).))))-3'
Motif MFE = -21.5; z-score = -4.01; ED = 5.07
```



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 25148 to 25346 (motif highlighted in silver):

```
5'-UCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUU
AUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUG-3
5'-(((.(((((((..(((((....))))).(((((.....))))).....((((((.........))))))((((.((((((.(((.((((((((((....))))...)))))
).)))..)))))).))))..((((.((((..((((((((((....)))))))).)))).)))).))))..))))))))))........-3'
MFE = -61.3; z-score = -2.85; ED = 16.7
```

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_gp02, 21563-25384(+)

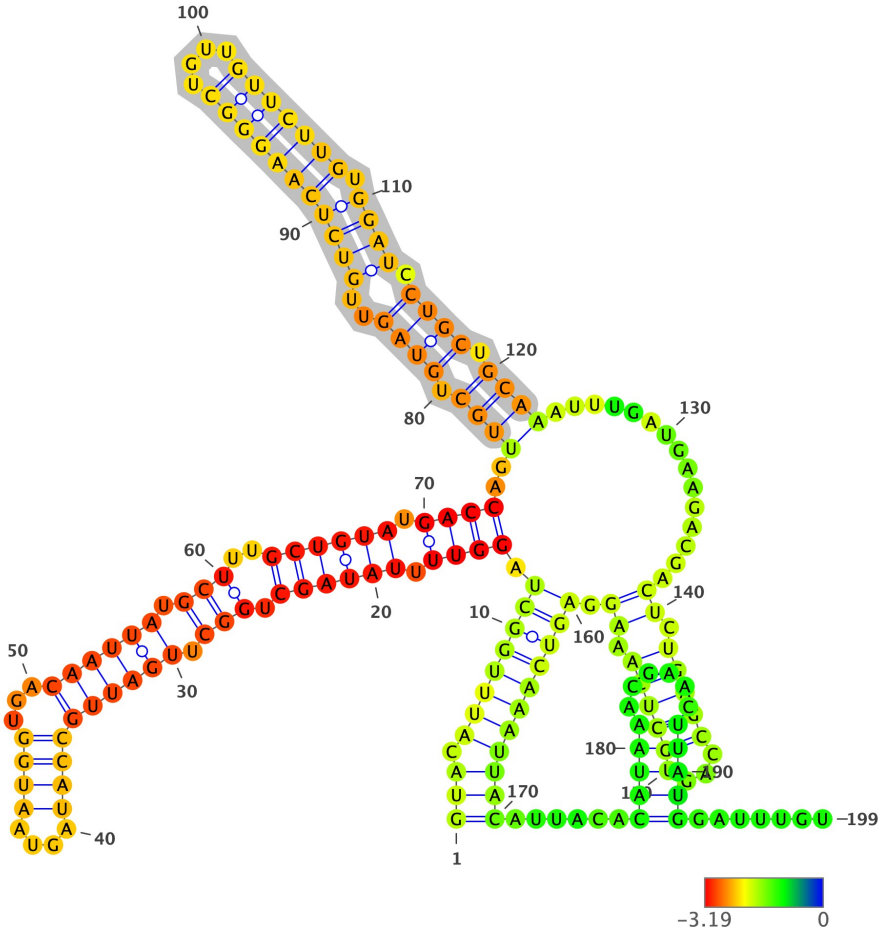
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 437 from nt 25280 to 25325 (nt 77 to 122)

```
5'-UGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCA-3'
5'-(((.((((..(((((((((((....)))))))).)))).)))).)))-3'
Motif MFE = -16.9; z-score = -3.06; 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 25204 to 25402 (motif highlighted in silver):

```
5'-GUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGG
AUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGU-3
5'-(((.((((((((.((((.((((((.(((.(((((((((((....))))...)))))).)))..)))))).))))..((((.((((..(((((((((((....)))))))).))
)).)))).))))...............((.(((((....))))).)).))))))))))).....(((((......)))))........-3'
MFE = -59.0; z-score = -3.07; ED = 27.75
```

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 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(+)

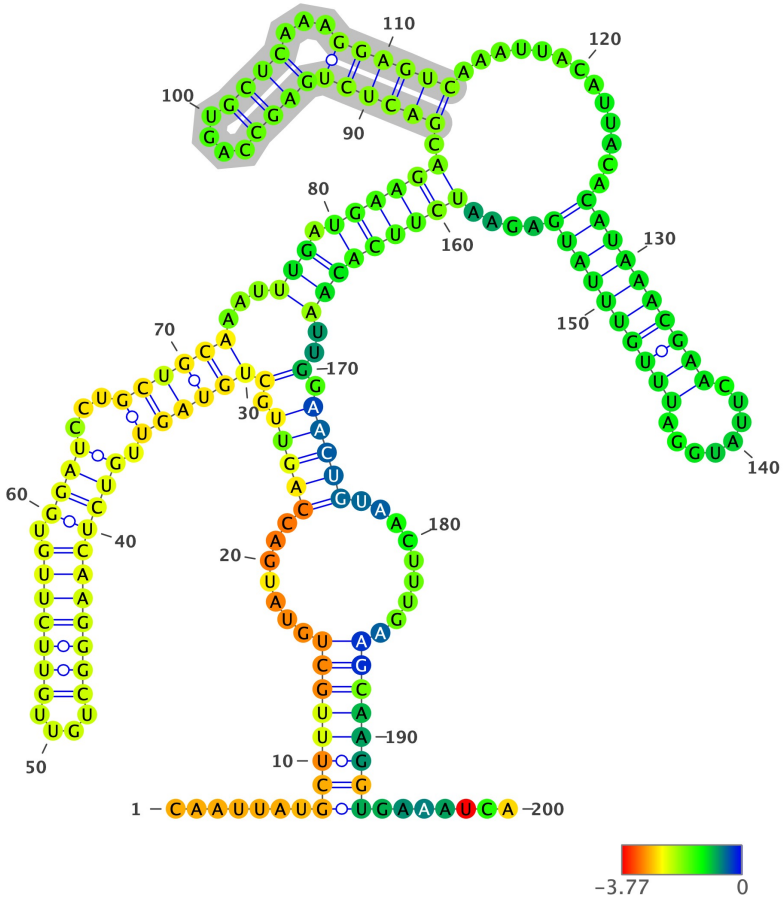
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 438 from nt 25340 to 25366 (nt 87 to 113)

```
5'-GACUCUGAGCCAGUGCUCAAAGGAGUC-3'
5'-((((((((((....))))...))))))-3'
Motif MFE = -10.6; z-score = -2.76; ED = 1.16
```



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

Extracted structure model with flanking nucleotides 25254 to 25453 (motif highlighted in silver):

```
5'-CAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAG
UCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUAUGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCA-3
5'-.......((((((((.......(((((.(((((((.((((((((((....)))))))).))))...))))))...(((.((((((.((((((((((....))))...))))
)).............((((((((((........))))))))))....))))))))))..).)))))..........))))))))........-3'
MFE = -55.1; z-score = -2.78; ED = 19.57
```

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

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

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

2-- nt 1 to 131--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 131--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 140 to 200--gene, gene-GU280_gp03, 25393-26220(+)

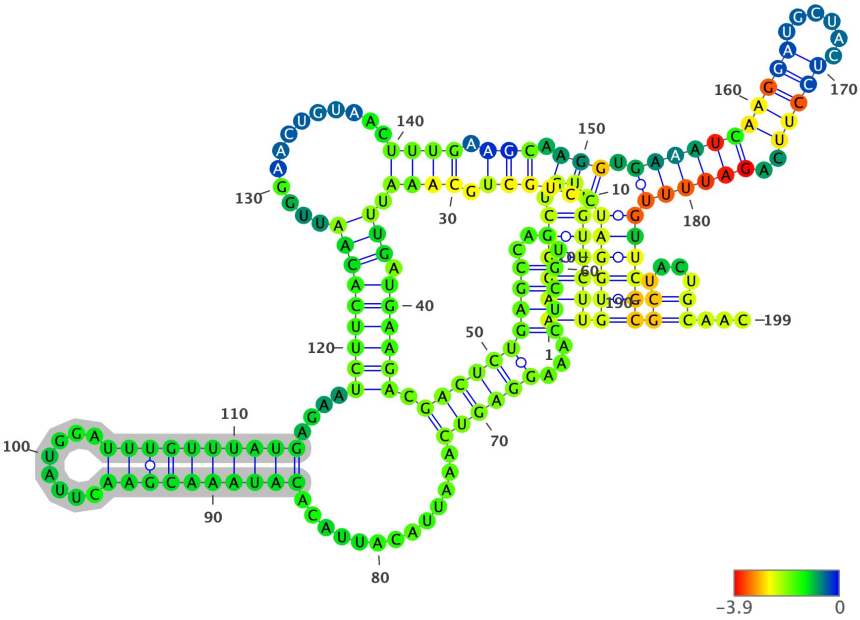
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 140 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 439 from nt 25380 to 25407 (nt 86 to 113)

```
5'-CAUAAACGAACUUAUGGAUUUGUUUAUG-3'
5'-((((((((((........))))))))))-3'
Motif MFE = -6.7; z-score = -2.59; 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 25295 to 25493 (motif highlighted in silver):

```
5'-AAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUA
UGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAAC-3
5'-((((((....))))))((((((((((((.((((.(((.((((((.((((((((((....)))))...))))))).............((((((((((........))))))))))
))....))))))))).............))))).))).))).(((((((((((.....))))))..)))))))))))((....))...-3'
MFE = -45.8; z-score = -0.68; 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']

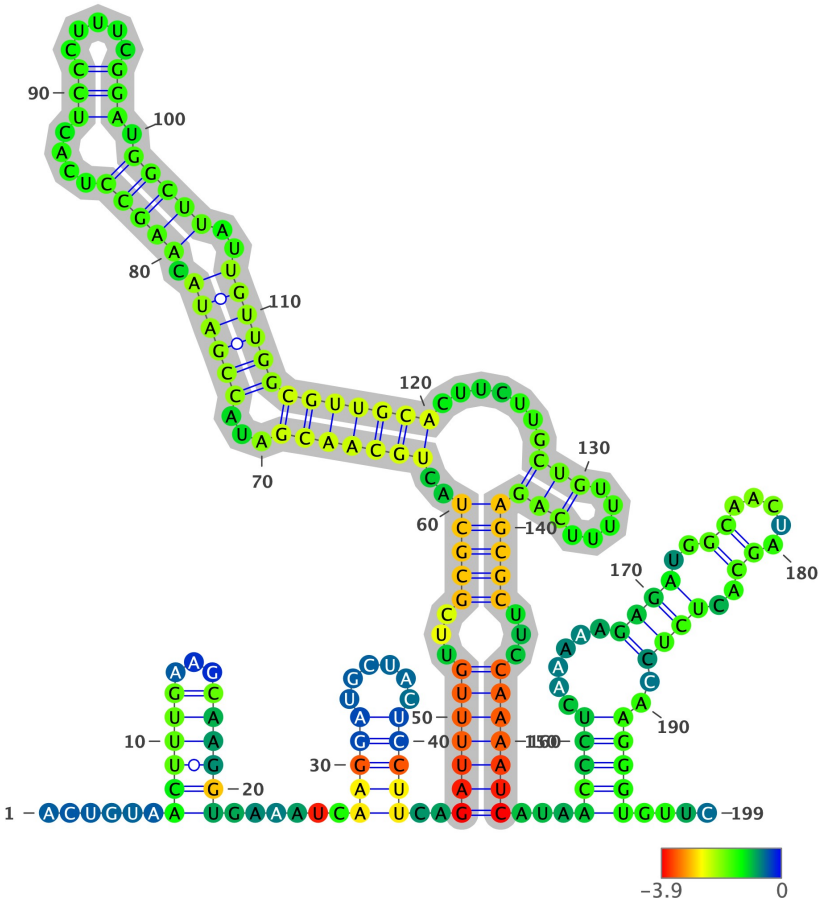
5-- nt 99 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

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 440 from nt 25471 to 25578 (nt 46 to 153)

```
5'-GAUUUUGUUCGCGCUACUGCAACGAUACCGAUACAAGCCUCACUCCCUUUCGGAUGGCUUAUUGUUGGCGUUGCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUC-3'

5'-(((((((...(((((..(((((((...((((((.(((((....(((.....))).)))))..))))))))))))).......(((.....))))))))...)))))))-3'
Motif MFE = -34.1; z-score = -3.4; 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 = -2.45; 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(+)

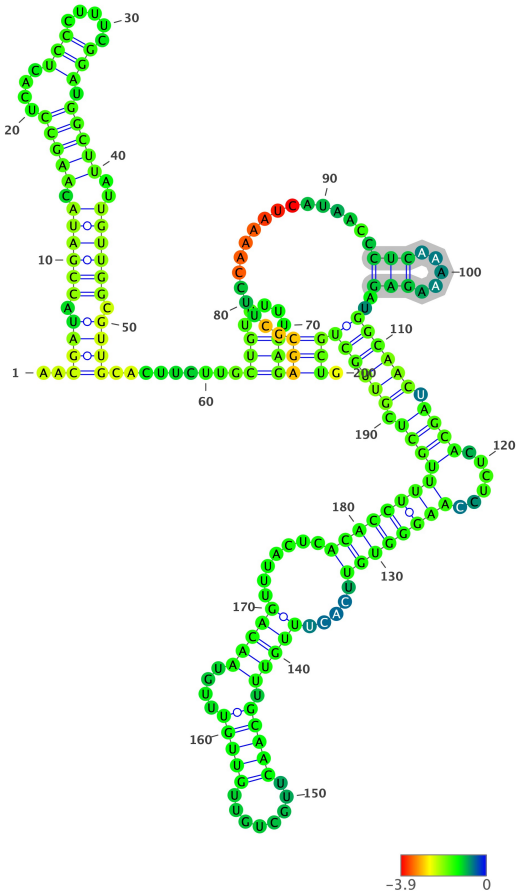
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 441 from nt 25585 to 25595 (nt 95 to 105)

```
5'-CUCAAAAAGAG-3'
5'-(((.....)))-3'
Motif MFE = -0.3; z-score = -3.46; 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 25491 to 25690 (motif highlighted in silver):

```
5'-AACGAUACCGAUACAAGCCUCACUCCCUUUCGGAUGGCUUAUUGUUGGCGUUGCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCA
ACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUG-3
5'-..(((((.((((((.((((((....(((.....))).)))))..))))))).))))).........(((.....)))(((.................(((.....))))..((((
((.((((......(((((((((.....(((((.(((((.........)))))....)))))).......))))))))))).)))))))).-3'
MFE = -44.9; z-score = -0.54; ED = 28.37
```

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_gp03, 25393-26220(+)

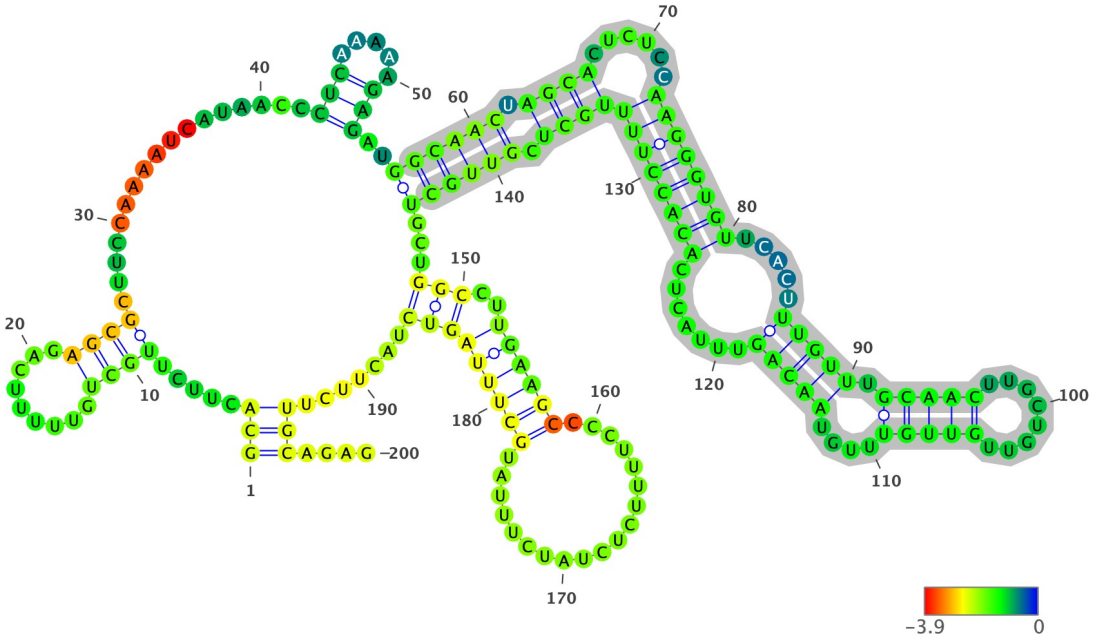
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 442 from nt 25599 to 25685 (nt 57 to 143)

```
5'-GCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGC-3'
5'-((.....((..........(.(((.....(((((.(((((........)))))....)))))).......))).)....)).....))-3'
Motif MFE = -23.2; z-score = -3.1; ED = 11.11
```



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 25543 to 25742 (motif highlighted in silver):

```
5'-GCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUU
GUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAG-3
5'-(((.....((((.........))))..................(((.....)))..((((((.((((......((((((((.....(((((.(((((........)))))..
..)))))).......))))))))))))).))))))...(((..((((((...................))))))))).......))).....-3'
MFE = -36.4; z-score = 0.29; ED = 33.67
```

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_gp03, 25393-26220(+)

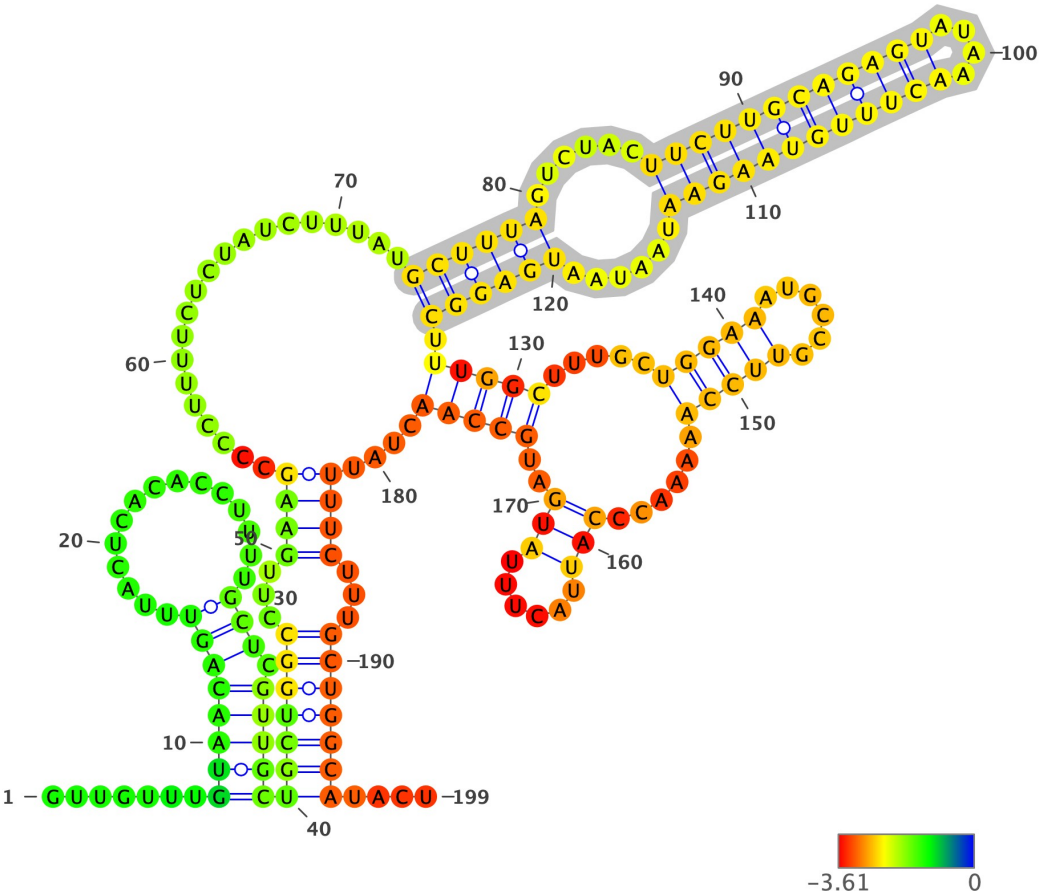
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 443 from nt 25720 to 25771 (nt 74 to 125)

```
5'-GCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGC-3'
5'-((((((......((((((((((((....))))))))))))......))))))-3'
Motif MFE = -18.3; z-score = -4.35; 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 25647 to 25845 (motif highlighted in silver):

```
5'-GUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAG
AAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACU-3
5'-.......(((((((((.............))).)))))(((((((...((((.....................((((((.....((((((((((....))))))))))
))).....))))))).(((((.....(((((.....)))))).....(((.....)))..)))))....)))))...)))))))....-3'
MFE = -42.2; z-score = -1.46; ED = 39.26
```

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_gp03, 25393-26220(+)

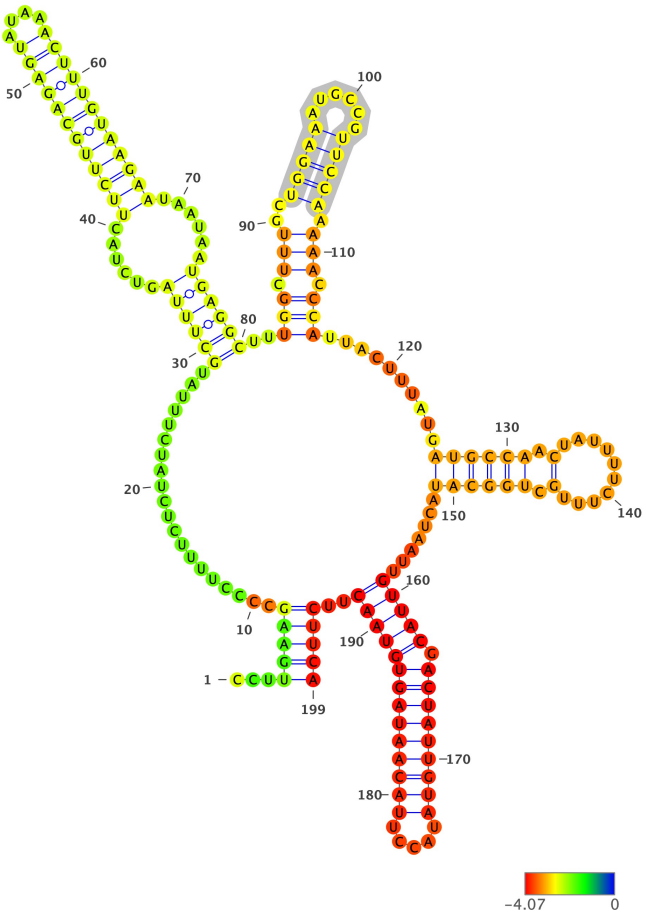
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 444 from nt 25783 to 25798 (nt 92 to 107)

```
5'-UGGAAAUGCCGUUCCA-3'
5'-(((((......)))))-3'
Motif MFE = -3.1; z-score = -2.59; 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 = -4.94; 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(+)

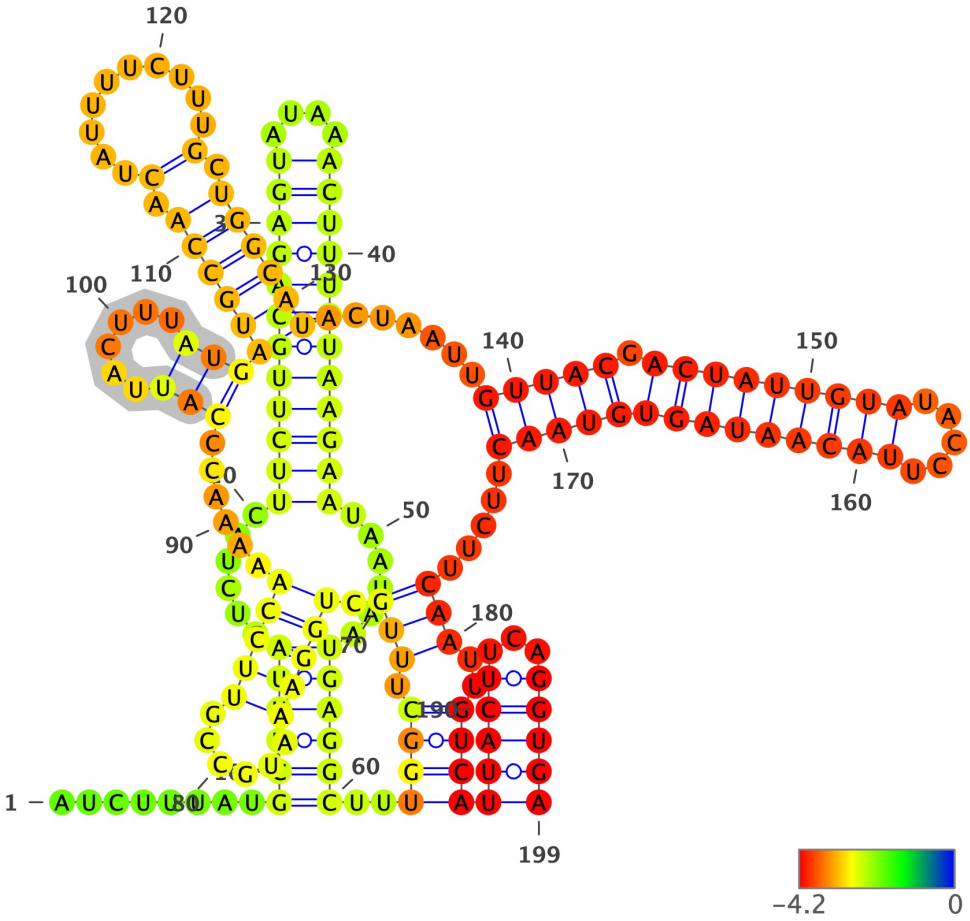
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 445 from nt 25806 to 25815 (nt 95 to 104)

```
5'-AUUACUUUAU-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.02
```



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 25712 to 25910 (motif highlighted in silver):

```
5'-AUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCA
ACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGA-3
5'-........((((((......(((((((((((....)))))))))))).....))))))..((((.(((.(((((......)))))......(((......)))((((((
.(..........).))))))).......(((((.((((((((.....)))))))))))))).....)))..))))(((((...)))))-3'
MFE = -49.0; z-score = -3.53; ED = 25.81
```

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_gp03, 25393-26220(+)

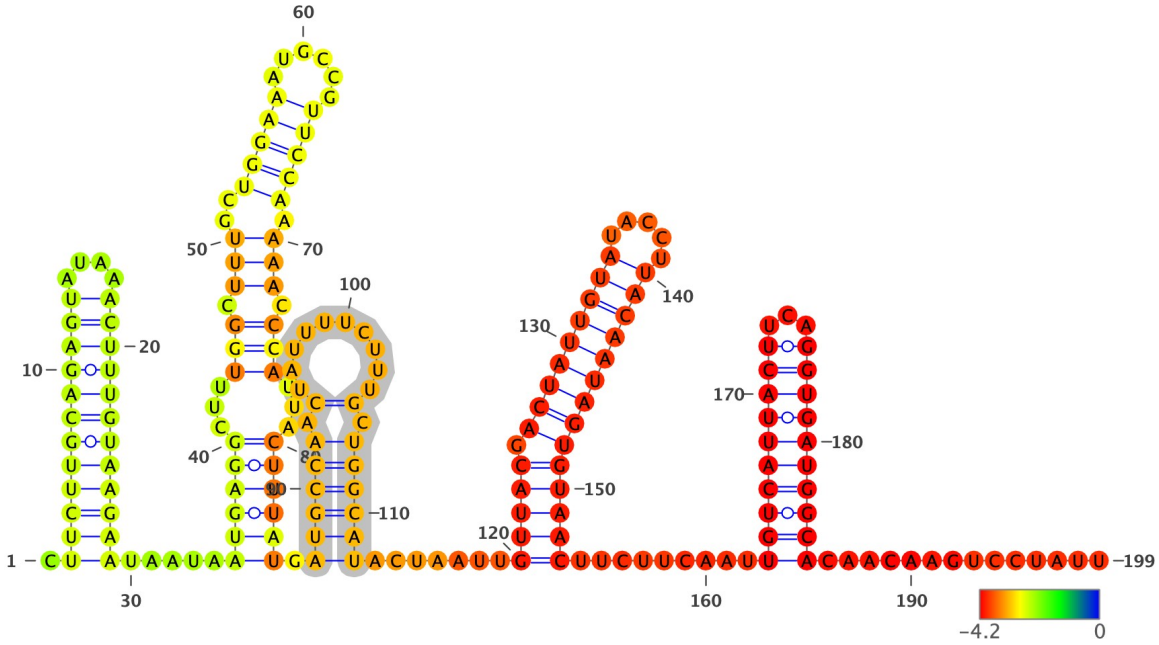
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 446 from nt 25817 to 25842 (nt 87 to 112)

```
5'-AUGCCAACUAUUUUCUUUGCUGGCAU-3'
5'-((((((.(.........).)))))))-3'
Motif MFE = -5.9; z-score = -4.01; 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 = -5.31; 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(+)

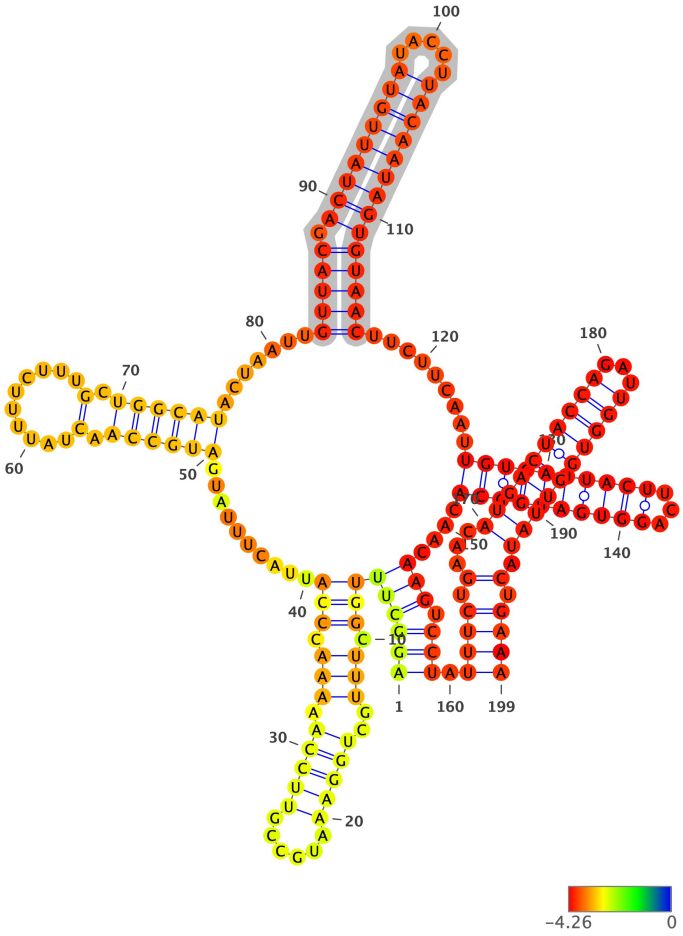
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 447 from nt 25850 to 25883 (nt 83 to 116)

```
5'-GUUACGACUAUUGUAUACCUUACAAUAGUGUAAC-3'
5'-(((((.(((((((((.....)))))))))))))))-3'
Motif MFE = -13.6; z-score = -5.75; ED = 1.1
```



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

Extracted structure model with flanking nucleotides 25768 to 25966 (motif highlighted in silver):

```
5'-AGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGU
GUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAA-3
5'-(((((((((.(((..(((((.....))))).))).))).........((((((.(..........).))))))).......(((((.(((((((((.....)))))))))
))))).........((((((((((...)))))))))....))).))).((((.(...((((((((((...)))))))))).).))))-3'
MFE = -53.8; z-score = -3.56; 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(+)

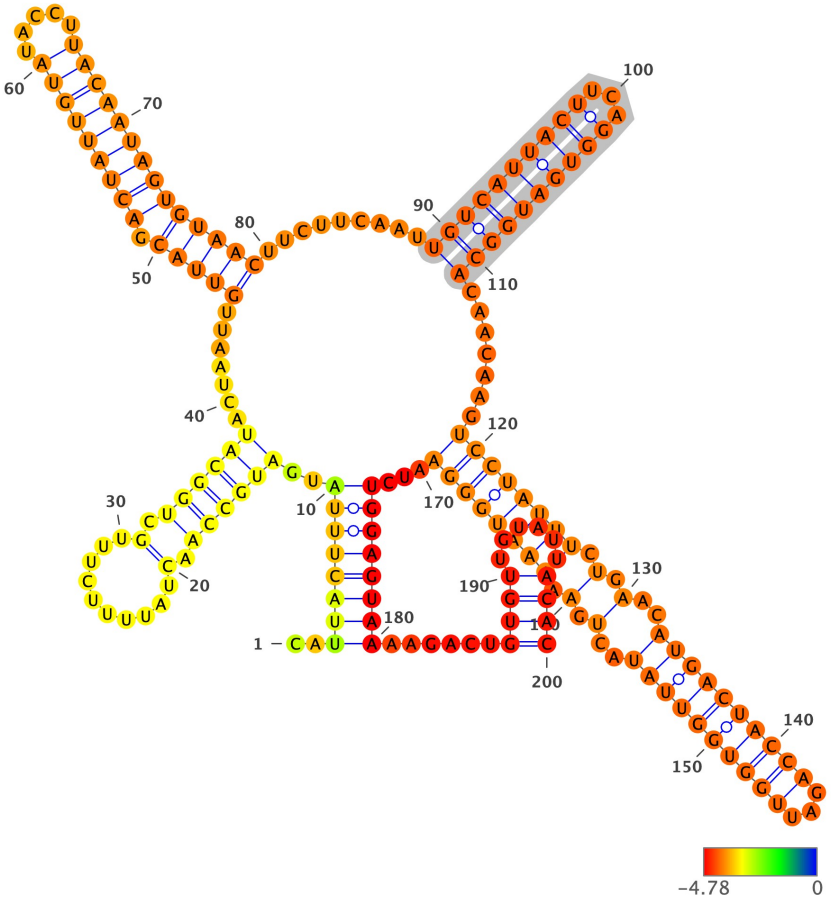
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 448 from nt 25893 to 25915 (nt 89 to 111)

```
5'-UGUCAUUACUUCAGGUGAUGGCA-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -9.5; z-score = -3.61; 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 = -4.47; 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(+)

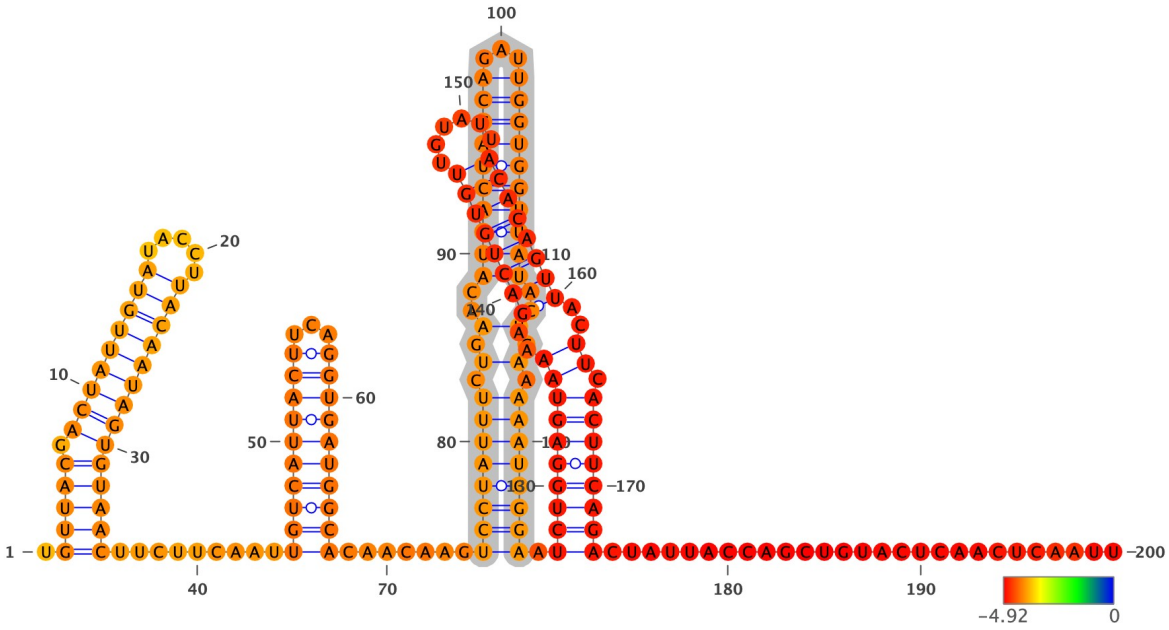
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 449 from nt 25923 to 25973 (nt 75 to 125)

```
5'-UCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGA-3'
5'-(((((((((.(.(..((((((((((...)))))))))).).).)))))))))-3'
Motif MFE = -17.8; z-score = -3.51; 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 = -5.82; 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(+)

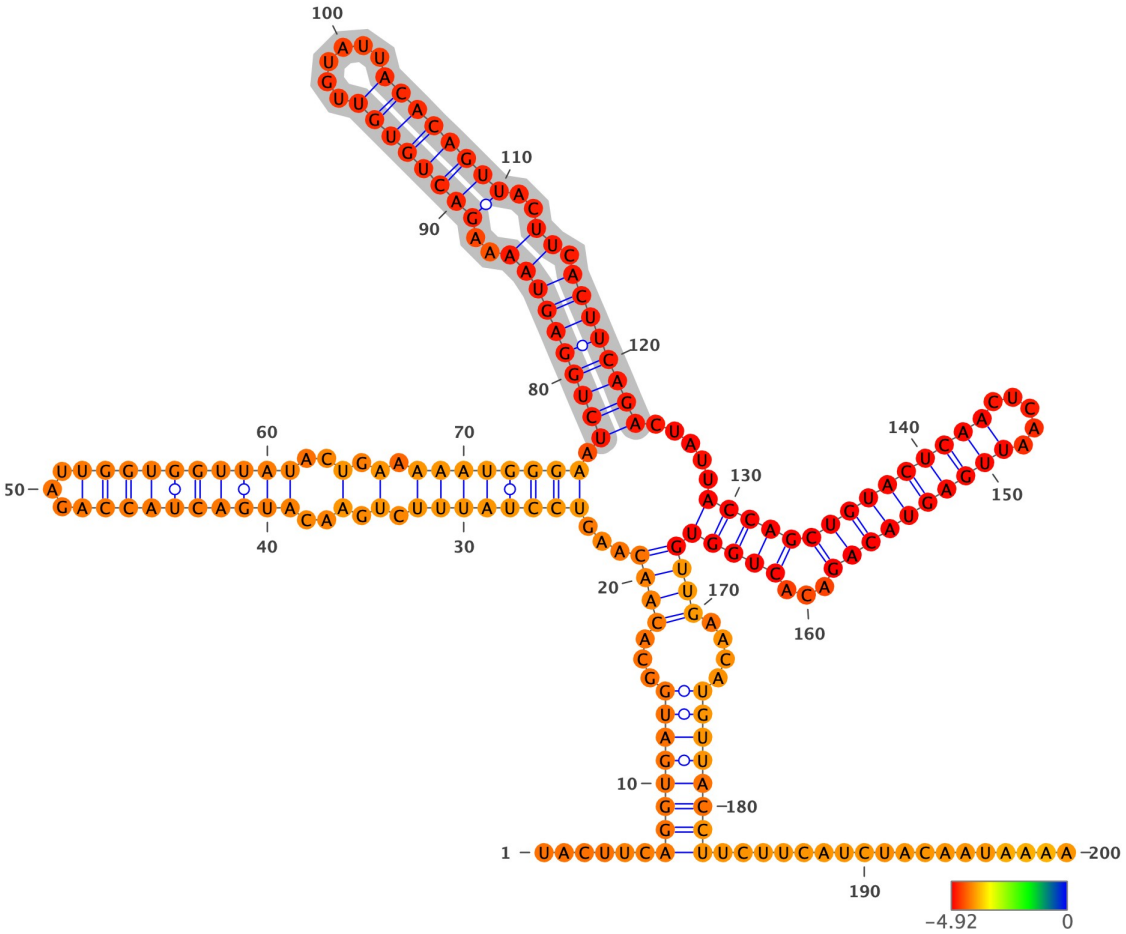
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 450 from nt 25975 to 26021 (nt 77 to 123)

```
5'-UCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGA-3'
5'-((((((((((..((((((((.....))))))))..)).))))))))-3'
Motif MFE = -19.0; z-score = -4.72; ED = 2.84
```



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

Extracted structure model with flanking nucleotides 25899 to 26098 (motif highlighted in silver):

```
5'-UACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUA
CUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAA-3
5'-......((((((((...((((...((((((((.(.(..((((((((((...)))))))))))..).).))))))))).((((((((((..((((((((......))))))))).
.)).))))))))).....((((((((((((((.....)))))))))))...)))))))))....))))))))).................-3'
MFE = -66.5; z-score = -5.23; ED = 11.75
```

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

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

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

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

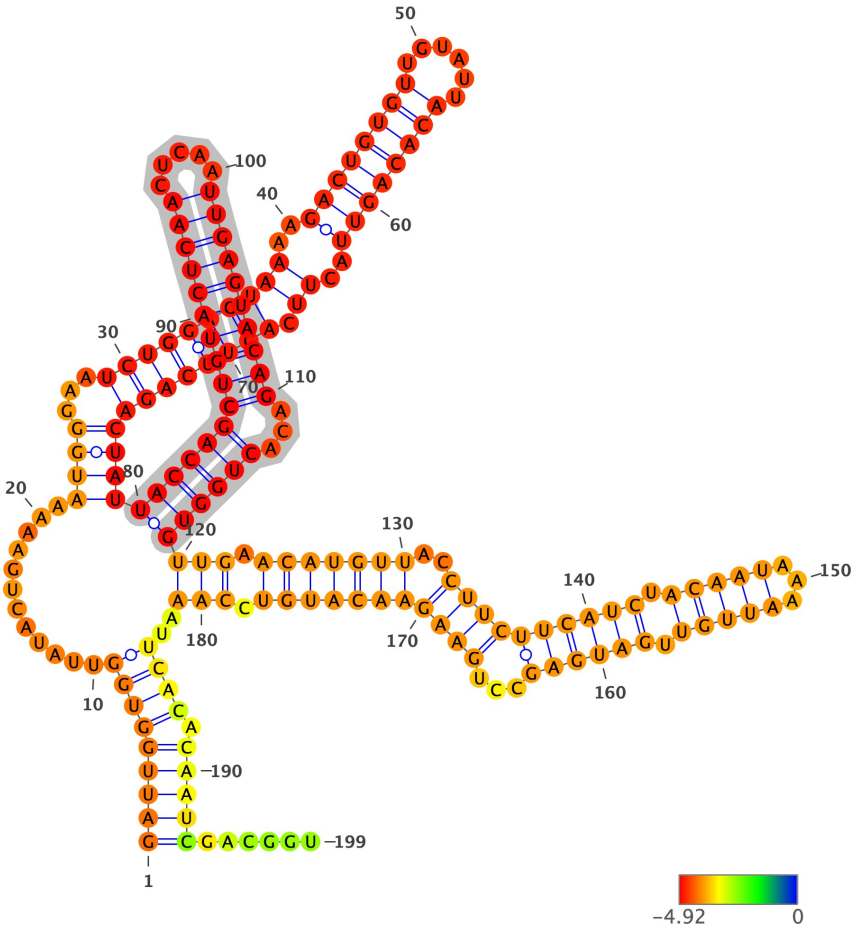
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 451 from nt 26026 to 26065 (nt 80 to 119)

```
5'-UACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUG-3'
5'-(((((((((((((((.....)))))))))...))))))-3'
Motif MFE = -18.8; z-score = -4.95; 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 25947 to 26145 (motif highlighted in silver):

```
5'-GAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGA
CACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGU-3
5'-(((((((((.............((((...(((((((((((..((((((((.....)))))))))..)).))))))))))))((((((((((((((((.....)))))))))).
..))))))(((.(((((((..((((((((((.(((((...))))).))))))...))))))))))).)))..)))).)))))......-3'
MFE = -66.4; z-score = -5.48; ED = 11.94
```

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(+)

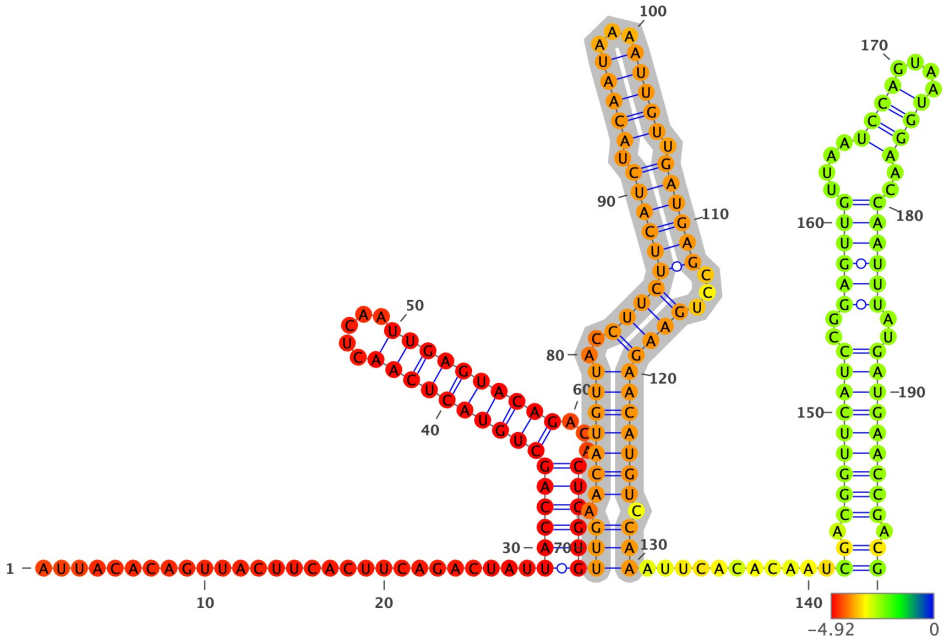
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 452 from nt 26066 to 26127 (nt 69 to 130)

```
5'-UUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAA-3'
5'-(((.(((((((..((((((((((.(((((...))))).)))))))...)))))))))))).)))-3'
Motif MFE = -18.2; z-score = -4.71; 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 = -4.94; 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(+)

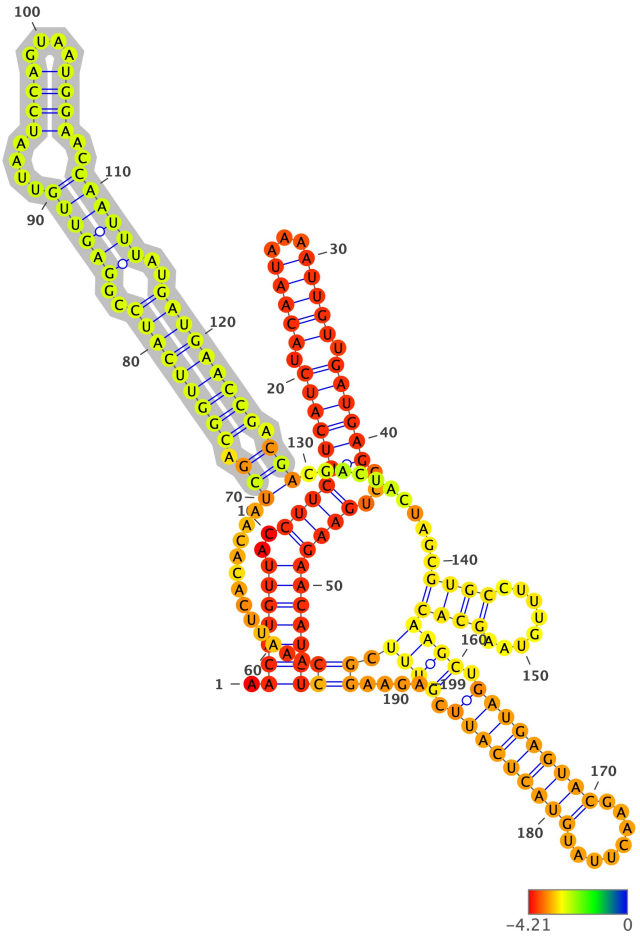
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 453 from nt 26139 to 26196 (nt 71 to 128)

```
5'-CGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACG-3'
5'-(..(((((((((..((((((....((((....)))).)))))).)))))))))..)-3'
Motif MFE = -21.2; z-score = -3.45; 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 = -4.38; 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(+)

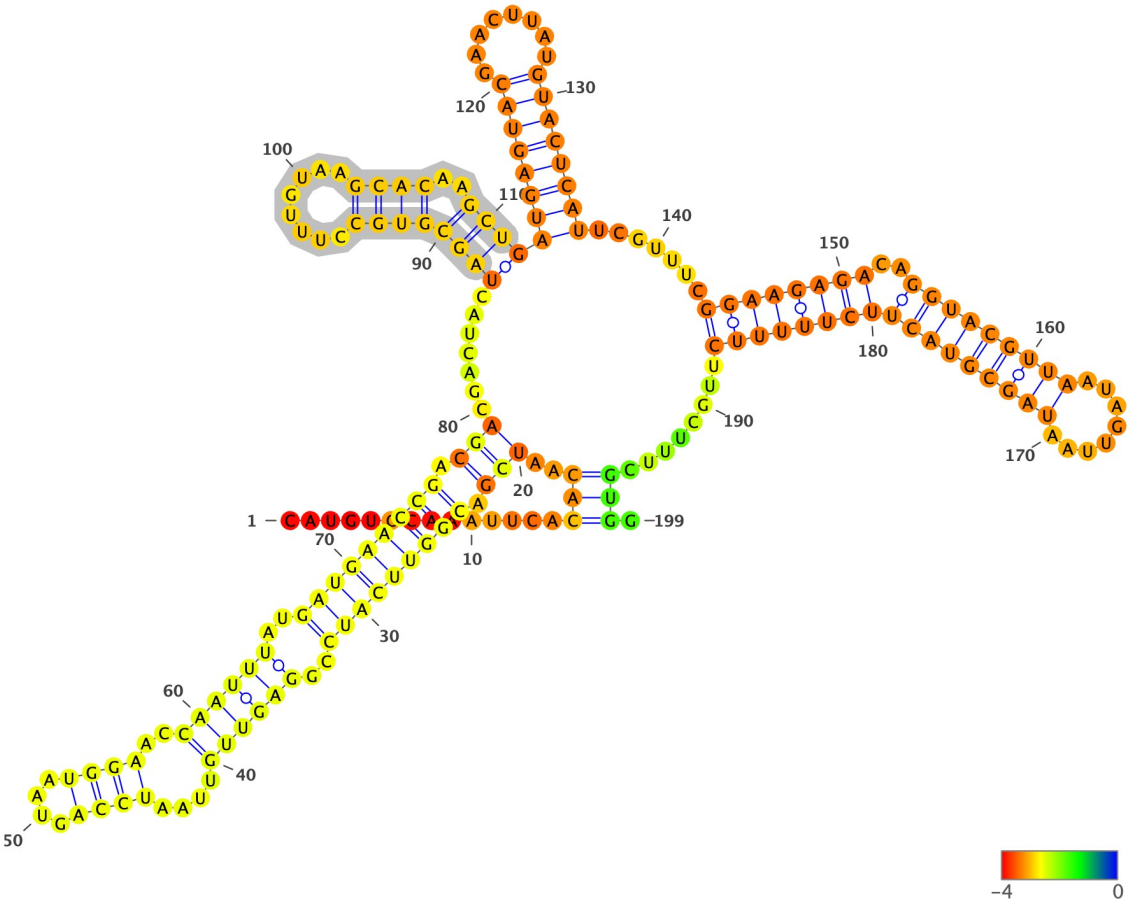
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 454 from nt 26206 to 26229 (nt 88 to 111)

```
5'-AGCGUGCCUUUGUAAGCACAAGCU-3'
5'-(((((((........)))))..)))-3'
Motif MFE = -5.4; z-score = -1.61; ED = 1.83
```



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

Extracted structure model with flanking nucleotides 26119 to 26317 (motif highlighted in silver):

```
5'-CAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCU
GAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGG-3
5'-..............(((..((((.((((((((((..((((((....((((....))))..))))))..))))))))).)))).......(((((((........)))))..)))
)(((((((((........)))))))).......(((((((..(((((((((........)))))))))))))))))........))).-3'
MFE = -60.4; z-score = -4.17; ED = 20.01
```

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

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

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

2-- nt 1 to 102--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 102--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 127 to 199--gene, gene-GU280_gp04, 26245-26472(+)

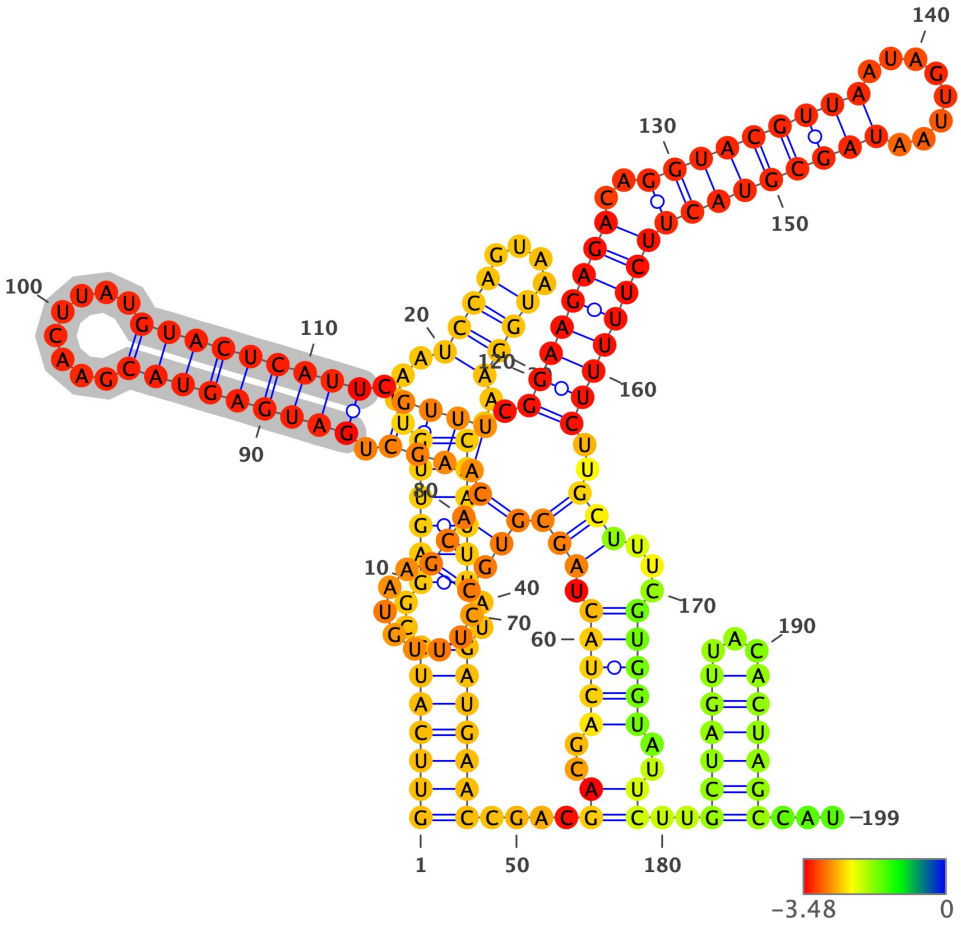
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 127 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 455 from nt 26230 to 26255 (nt 87 to 112)

```
5'-GAUGAGUACGAACUUAUGUACUCAUU-3'
5'-(((((((((........)))))))))-3'
Motif MFE = -10.2; z-score = -4.77; 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 26144 to 26342 (motif highlighted in silver):

```
5'-GUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAU
UCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAU-3
5'-(((((((..((((((....((((....))))..))))))..)))))))....((..(((((.(((((((........))))((((.(((((((((........))))))))
).)))).((((((((..(((((((((........)))))))))))))))))..)))...)))))..))..((((((...))))))...-3'
MFE = -63.5; z-score = -4.38; ED = 17.03
```

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 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(+)

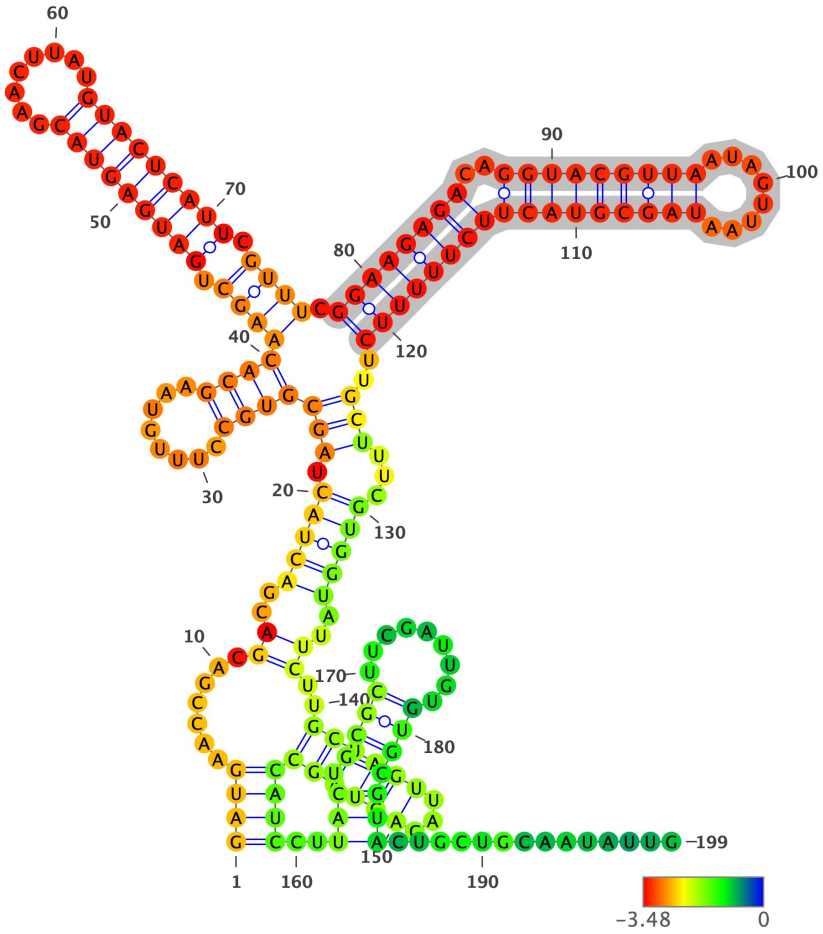
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 456 from nt 26262 to 26305 (nt 78 to 121)

```
5'-GGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUC-3'
5'-(((((((((..((((((((((........))))))))))))))))))-3'
Motif MFE = -15.7; z-score = -3.86; ED = 1.57
```



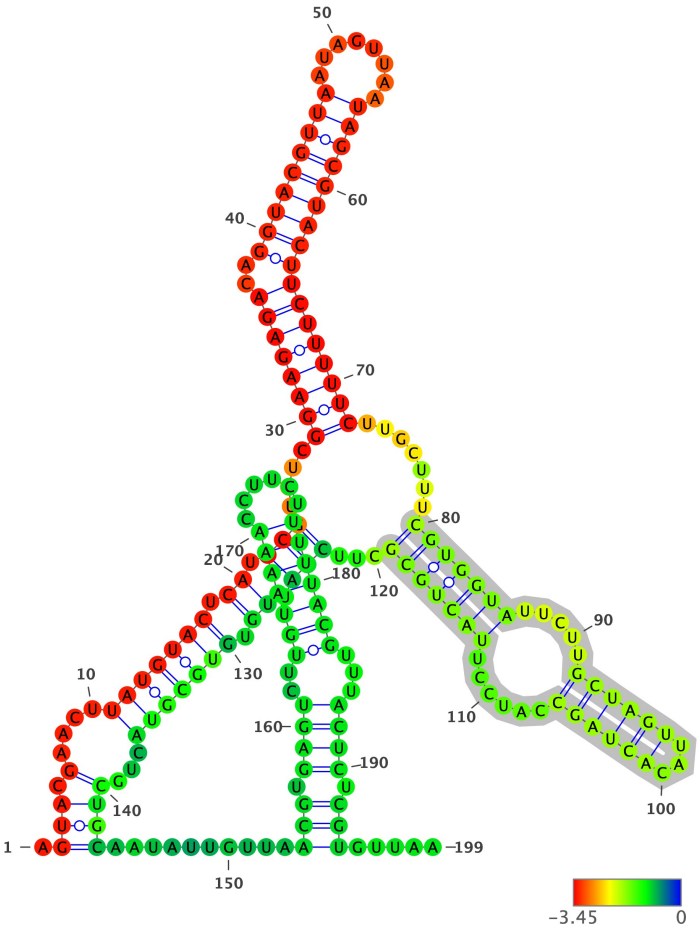
Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26185 to 26383 (motif highlighted in silver):

```
5'-GAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUA
CUUCUUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUG-3
5'-((((.......((..((((((.(((((((........)))))(((((.(((((((((........)))))))))))))))))))
```

NC_045512.2 (forward strand): Structure number 457 from nt 26313 to 26352 (nt 80 to 119)

```
5'-CGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCG-3'
5'-(((((((.....((((((...)))))).....)))))))-3'
Motif MFE = -12.1; z-score = -2.77; 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 26234 to 26432 (motif highlighted in silver):

```
5'-AGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCC
UUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAA-3
5'-.(((.(....(((((((.((.(((....(((((((..(((((((((........)))))))))))))))))).......(((((((.....((((((...)))))).....
.)))))))...))).)).)))))))...))))..........(((.(((((..(((((((.....)))))))...)))))..))).....-3'
MFE = -50.8; z-score = -2.73; ED = 26.89
```

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

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

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

2-- nt 12 to 199--gene, gene-GU280_gp04, 26245-26472(+)

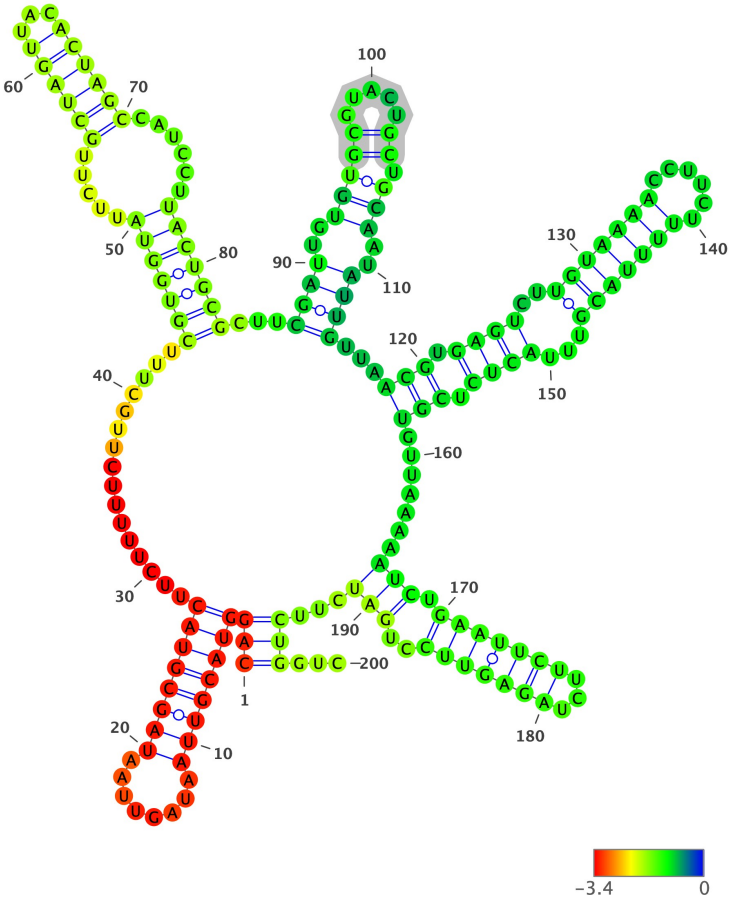
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 458 from nt 26365 to 26373 (nt 96 to 104)

```
5'-GCGUACUGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.18; 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 26270 to 26469 (motif highlighted in silver):

```
5'-CAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUA
UUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUC-3
5'-(((((((((((.........))))))))).................(((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..)
)))...(((.((((..(((((((......)))))))...)))).))).......(((.(((((((...)))))))..)))...)))...-3'
MFE = -45.3; z-score = -2.47; ED = 25.48
```

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_gp04, 26245-26472(+)

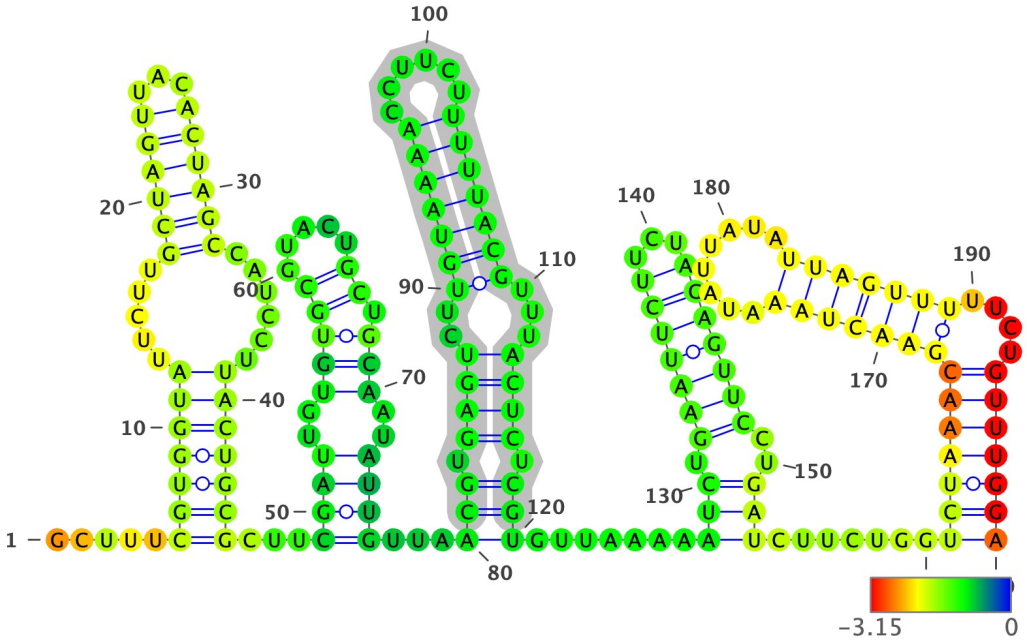
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 200--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 459 from nt 26388 to 26426 (nt 81 to 119)

```
5'-CGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCG-3'
5'-((.((((..(((((((.....)))))))...)))).))-3'
Motif MFE = -7.9; z-score = -2.51; ED = 1.66
```



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

Extracted structure model with flanking nucleotides 26308 to 26507 (motif highlighted in silver):

```
5'-GCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUU
UACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGA-3
5'-.....(((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..))))...(((.((((..(((((((.....)))))))..
.)))).)))......(((.(((((((...)))))))..)))......((((((((((((((.......)))))))....)))))))-3'
MFE = -42.5; z-score = -1.62; ED = 21.12
```

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

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

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

2-- nt 1 to 165--gene, gene-GU280_gp04, 26245-26472(+)

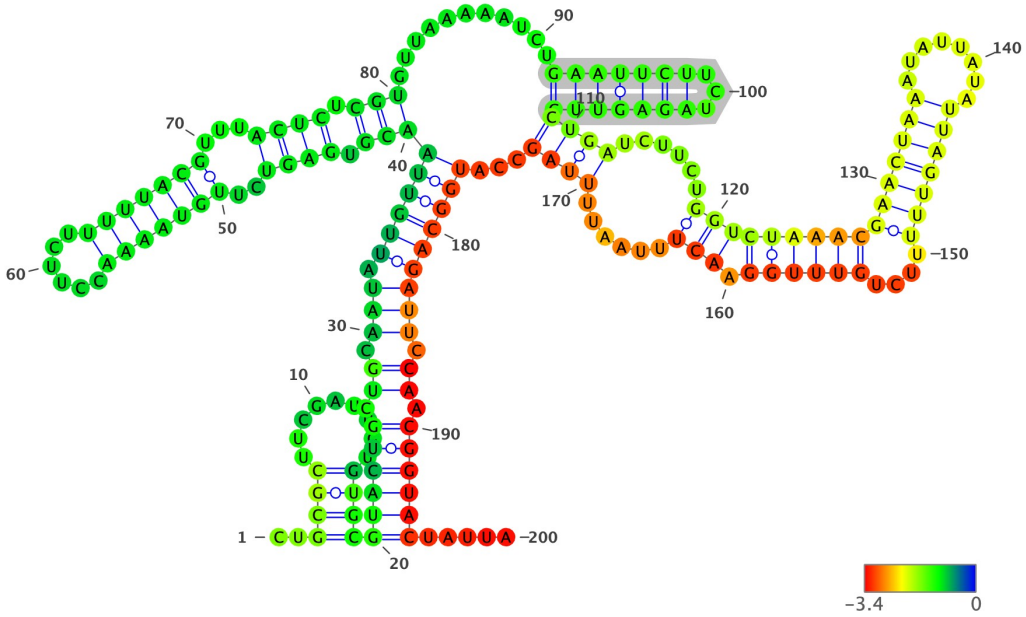
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 165--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 460 from nt 26439 to 26455 (nt 92 to 108)

```
5'-GAAUUCUUCUAGAGUUC-3'
5'-(((((((...)))))))-3'
Motif MFE = -3.9; z-score = -3.57; ED = 0.43
```



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

Extracted structure model with flanking nucleotides 26348 to 26547 (motif highlighted in silver):

```
5'-CUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUG
AUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUA-3
5'-..((((.........))))((((((.((.(((.(((((((((.((((..(((((((.......)))))))...)))).))).........(((((((...)))))))(((
(......((((((((((((((((.........)))))))....)))))).)))......))))...)))))))))).)).))))))).....-3'
MFE = -42.6; z-score = -1.92; ED = 30.5
```

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

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

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

2-- nt 1 to 125--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 125--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 176 to 200--gene, gene-GU280_gp05, 26523-27191(+)

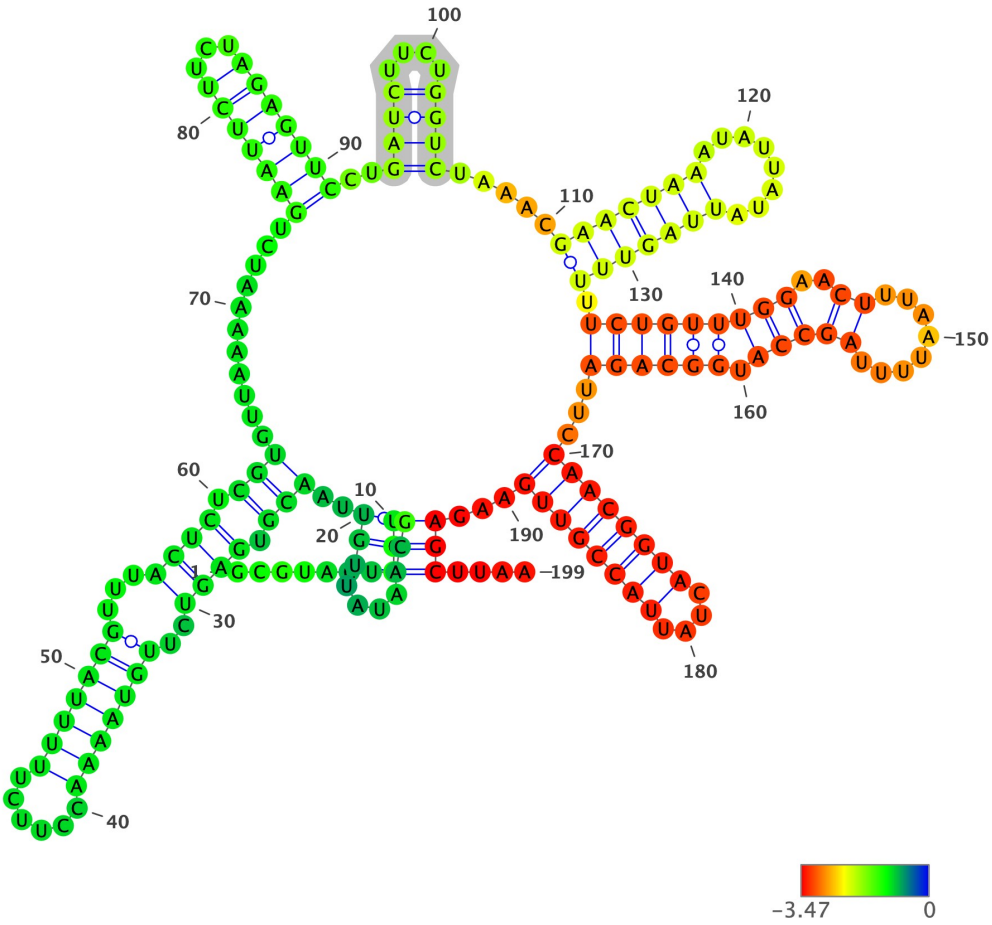
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 176 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 461 from nt 26458 to 26469 (nt 94 to 105)

```
5'-GAUCUUCUGGUC-3'
5'-((((....))))-3'
Motif MFE = -1.8; z-score = -3.22; ED = 0.48
```



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 26365 to 26563 (motif highlighted in silver):

```
5'-GCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACG
AACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAA-3
5'-.......((((((....)))..(((.((((..(((((((.....)))))))...)))))..)))..........(((((((...)))))))..((((....)))).....(
((((((........)))))))..(((((((((..((........))))).)))))))...(((((((((....)))))))))...)))....-3'
MFE = -44.1; z-score = -2.31; 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 108--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 108--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 159 to 199--gene, gene-GU280_gp05, 26523-27191(+)

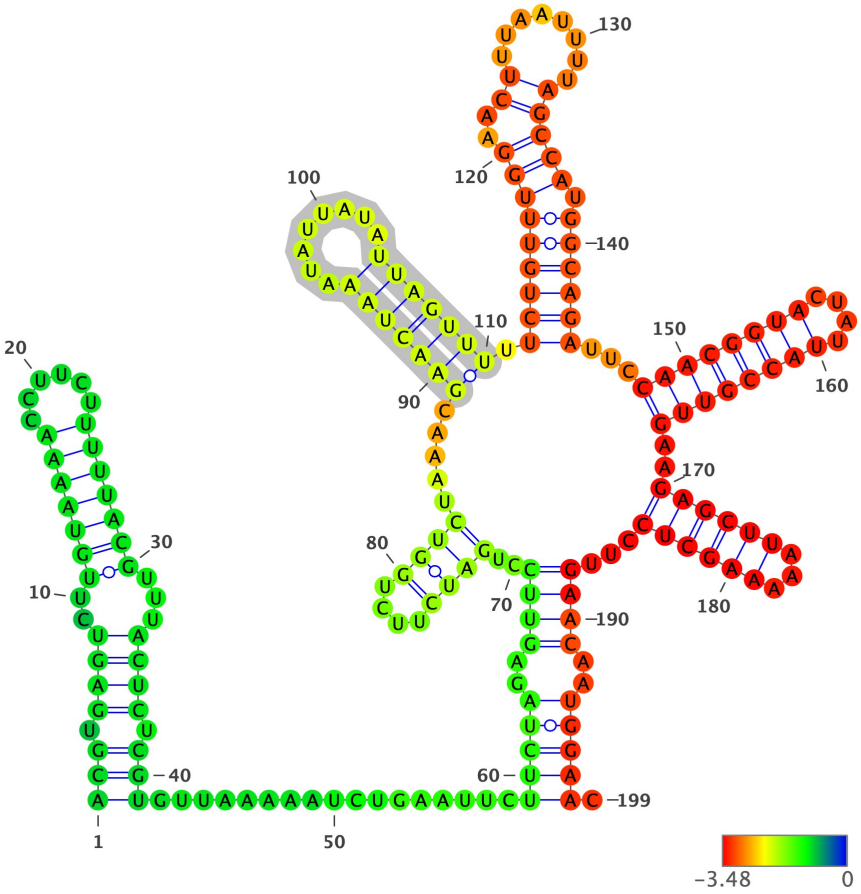
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 159 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 462 from nt 26475 to 26496 (nt 89 to 110)

```
5'-GAACUAAAUAUUAUAUUAGUUU-3'
5'-(((((((........)))))))-3'
Motif MFE = -3.0; z-score = -2.88; 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 26387 to 26585 (motif highlighted in silver):

```
5'-ACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUU
UCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAAC-3
5'-(((.((((..(((((((......)))))))...)))).))).................(((((..((((..((((....))))).....(((((((........)))))))).
((((((((..((........))))).))))))...((((((((....))))))))..((((((...))))))...))))..))))).-3'
MFE = -48.5; z-score = -3.65; ED = 23.59
```

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 86--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 86--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 137 to 199--gene, gene-GU280_gp05, 26523-27191(+)

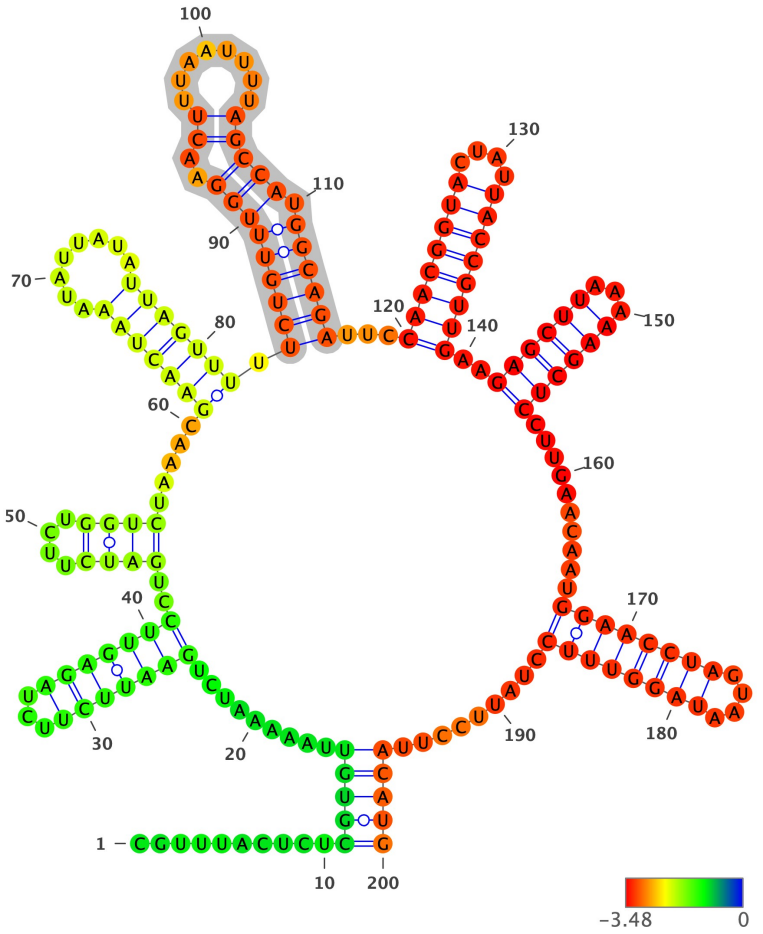
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 137 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 463 from nt 26498 to 26530 (nt 84 to 116)

```
5'-UCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGA-3'
5'-((((((((((..((........))))))).))))))-3'
Motif MFE = -6.0; z-score = -1.18; ED = 2.55
```



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

Extracted structure model with flanking nucleotides 26415 to 26614 (motif highlighted in silver):

```
5'-CGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUG
GCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUG-3
5'-.........(((((.........(((((((...)))))))..((((....)))).....(((((((........)))))))..((((((((..((........)))))).)
)))))...(((((((((....)))))))))..(((((((...)))))).........(((((((((....)))))))))........)))))-3'
MFE = -48.7; z-score = -3.52; ED = 18.46
```

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 58--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 58--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 109 to 200--gene, gene-GU280_gp05, 26523-27191(+)

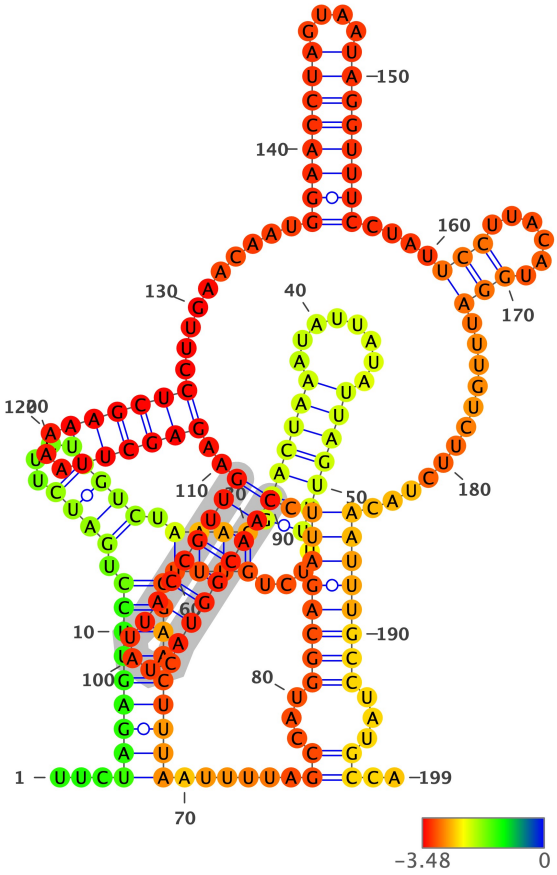
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 109 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 464 from nt 26534 to 26553 (nt 90 to 109)

```
5'-CAACGGUACUAUUACCGUUG-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -9.0; z-score = -5.43; 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 = -5.02; 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(+)

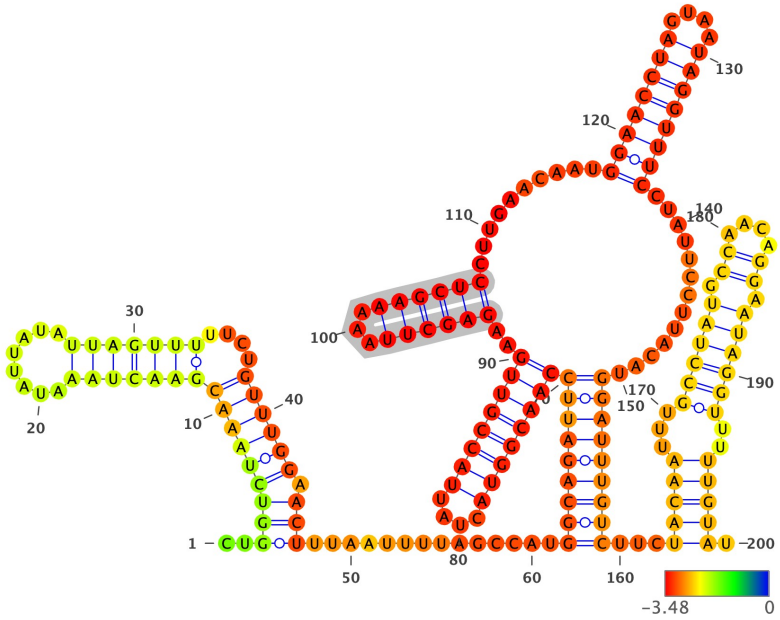
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 465 from nt 26556 to 26570 (nt 93 to 107)

```
5'-GAGCUUAAAAAGCUC-3'
5'-((((((...))))))-3'
Motif MFE = -5.0; z-score = -8.13; 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 = -4.35; 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(+)

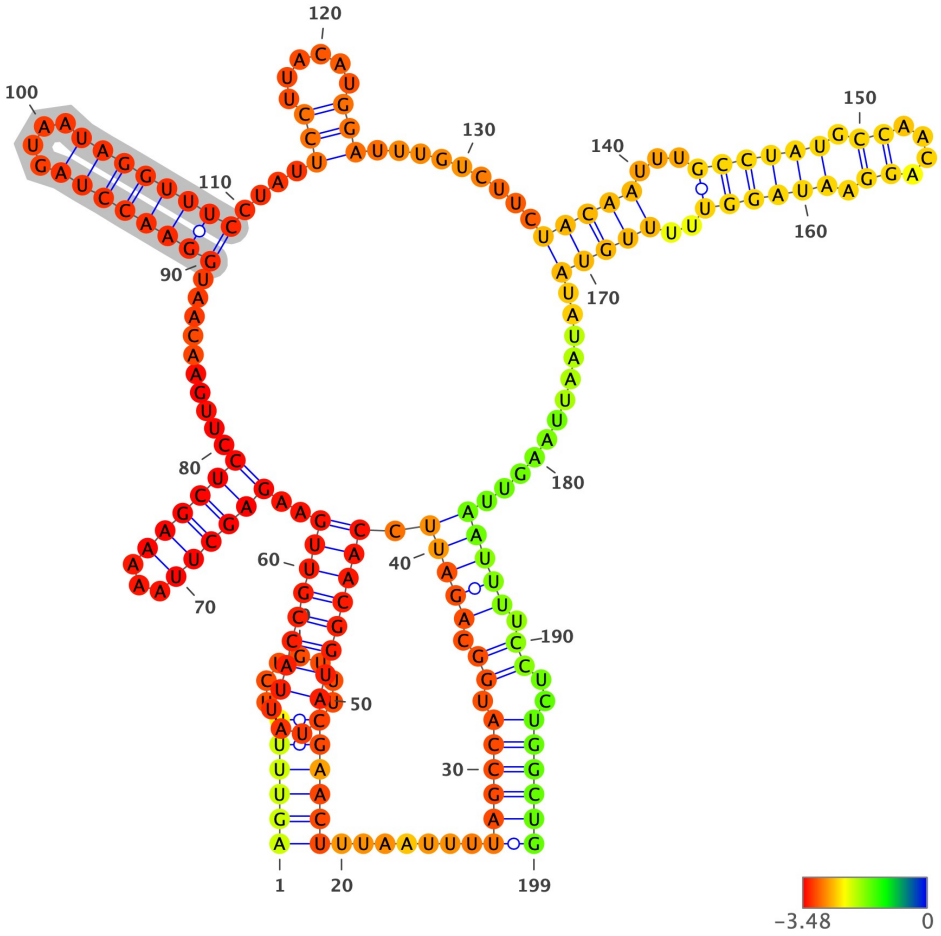
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 466 from nt 26581 to 26600 (nt 90 to 109)

```
5'-GGAACCUAGUAAUAGGUUUC-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.2; z-score = -5.2; ED = 0.38
```



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

Extracted structure model with flanking nucleotides 26492 to 26690 (motif highlighted in silver):

```
5'-AGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCU
AUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUG-3
5'-((((((.......))))))........((((((.((.(((((.((((((((....))))))))..((((((...))))))..........((((((((....))))))))..
..(((......)))..........(((((...((((((.((....)).))))))..)))))............)))))..))..))))))-3'
MFE = -52.9; z-score = -3.19; 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(+)

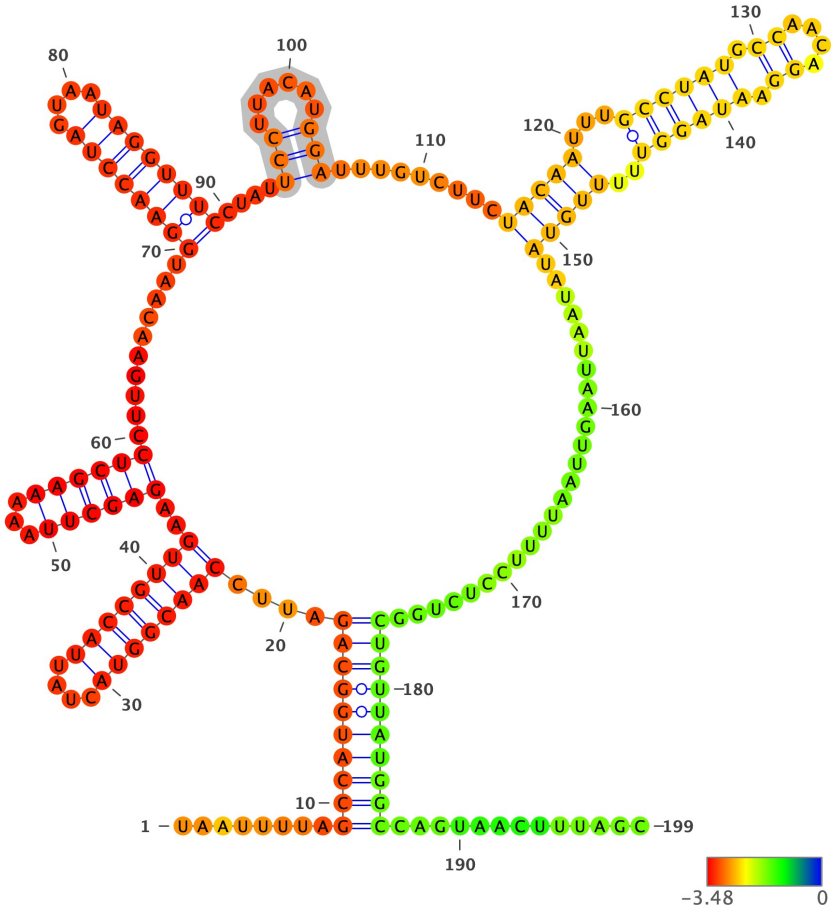
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 467 from nt 26605 to 26616 (nt 94 to 105)

```
5'-UCCUUACAUGGA-3'
5'-(((......)))-3'
Motif MFE = -1.9; z-score = -5.76; 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 = -4.33; 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(+)

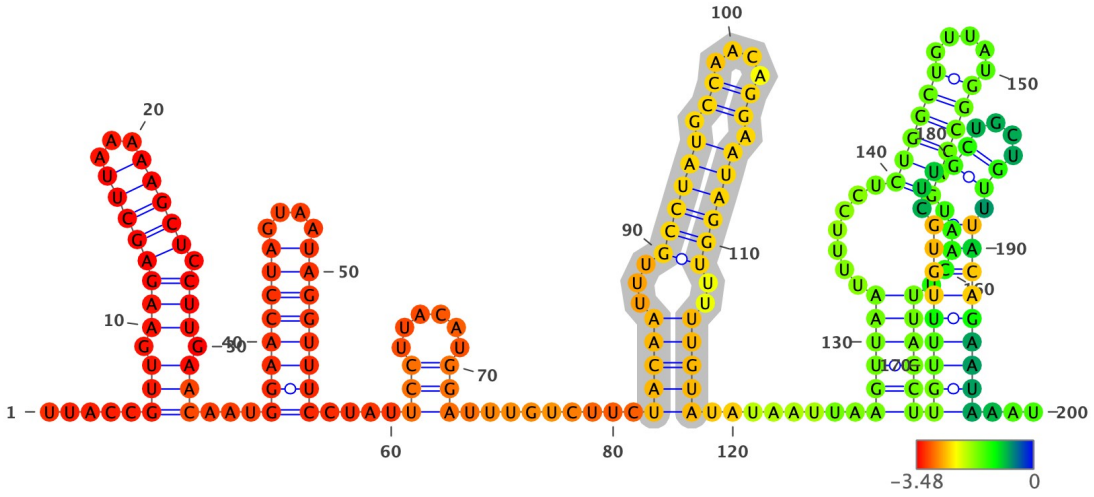
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 468 from nt 26626 to 26662 (nt 82 to 118)

```
5'-UACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUA-3'
5'-(((((...((((((.((....)).))))))..)))))-3'
Motif MFE = -10.9; z-score = -3.27; 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 = -3.02; 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(+)

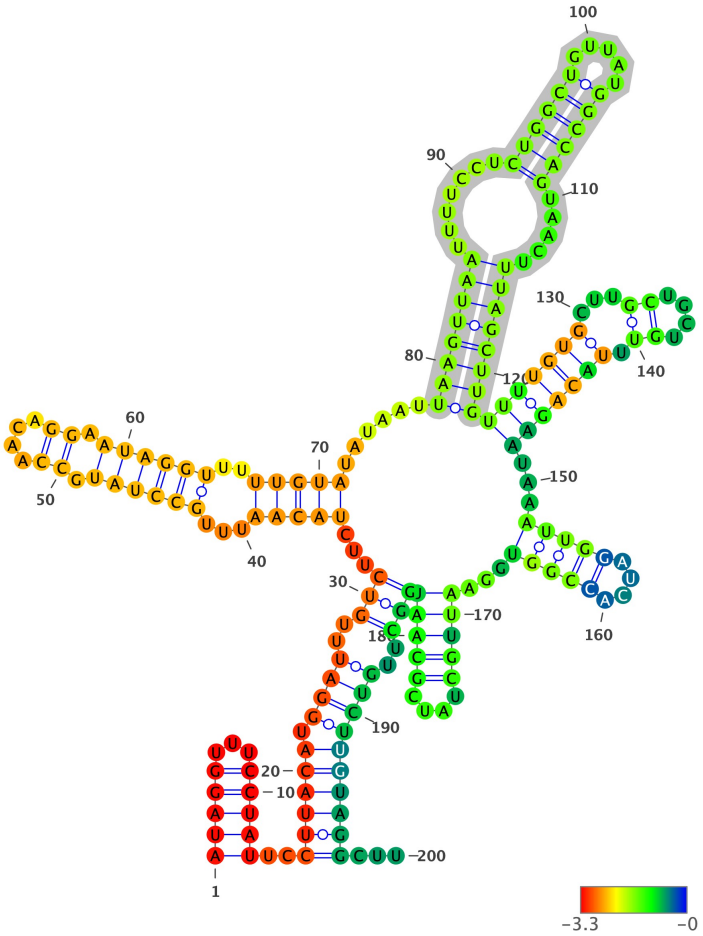
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 469 from nt 26669 to 26713 (nt 78 to 122)

```
5'-UAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCUUG-3'
5'-(((((((((.......((((((.....))))))).....)))))))))-3'
Motif MFE = -13.0; z-score = -3.23; 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 = -2.58; 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']

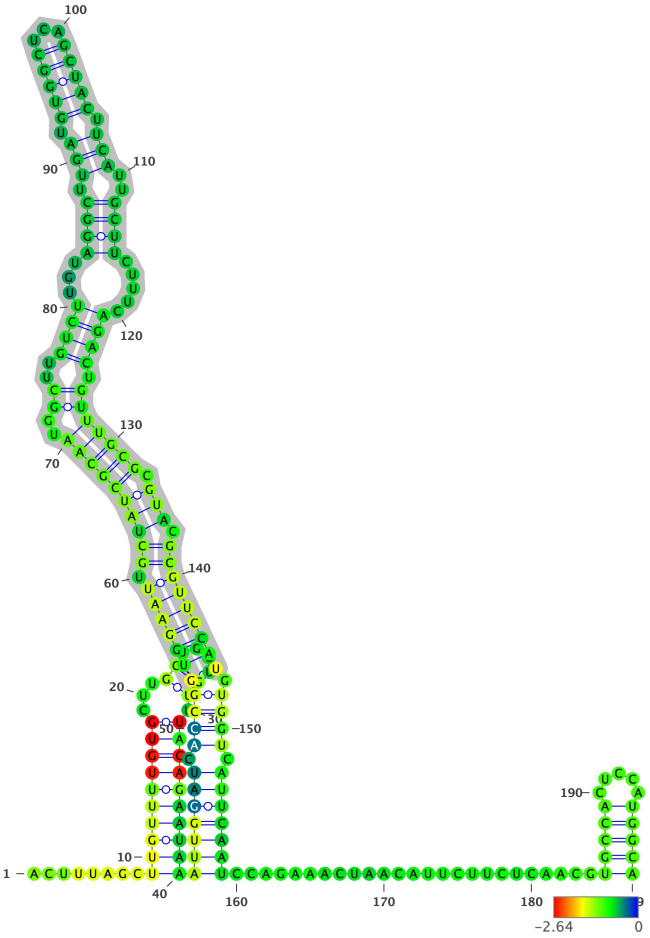
3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

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 470 from nt 26755 to 26848 (nt 53 to 146)

5'-GUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUUGCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAU-3'

5'-(..((((.((.(((((((...(...).))))))..))..)))))))..)-3'
Motif MFE = -29.4; z-score = -2.87; ED = 11.16



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 26703 to 26901 (motif highlighted in silver):

5'-ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUU
GCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCA-3
5'-........((((((((((...((....)).)))))))))).(((((((.((((((((((.((((((((((..((..(((((...((((.(((.((((((...)))))).)))).
))))).....)))).)))))))).))))..)))))))))).))))).)))))).....................(((((.....)))))-3'
MFE = -52.0; z-score = -1.4; ED = 18.27

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_gp05, 26523-27191(+)

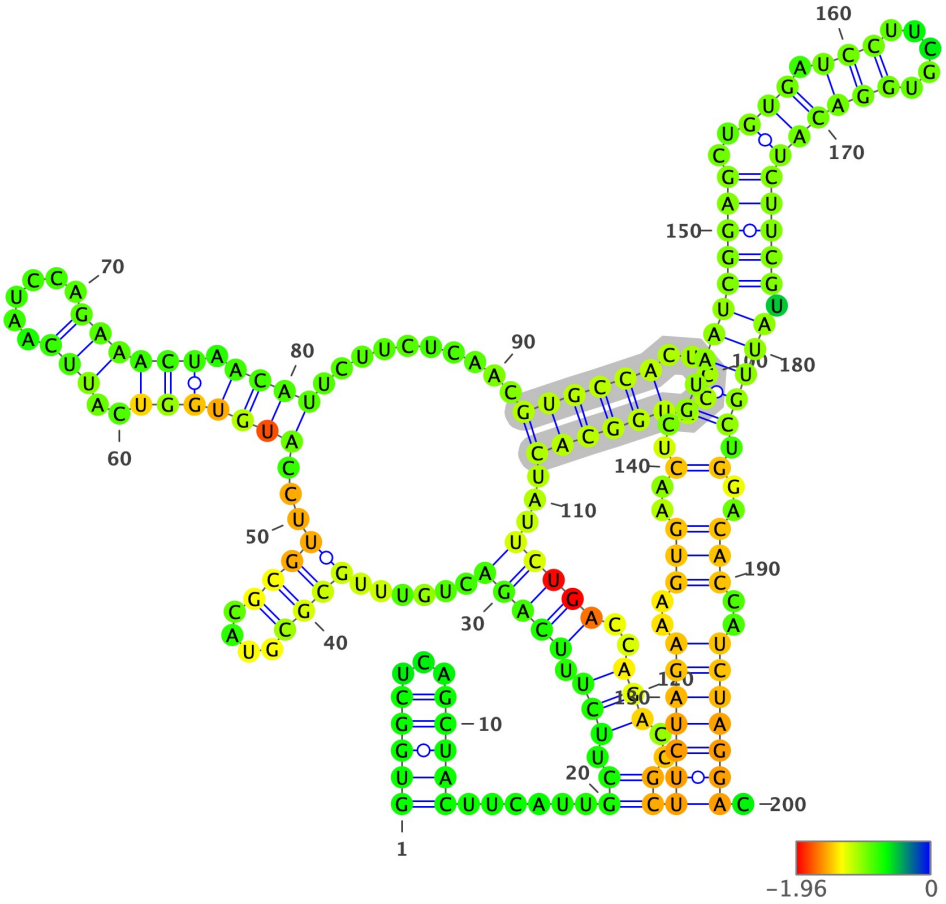
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 471 from nt 26886 to 26902 (nt 92 to 108)

```
5'-GUGCCACUCCAUGGCAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.5; z-score = -3.86; ED = 0.38
```



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

Extracted structure model with flanking nucleotides 26795 to 26994 (motif highlighted in silver):

```
5'-GUGGCUCAGCUACUUCAUUGCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAU
UCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGAC-3
5'-(((((...))))).....((.(((.(((((.....((((....)))))...(((((((..(((......)))))).)))).........((((((.....)))))))...
))))))..))))..))(((((((..((((..(..((((((((((..(((.(((.....)))))))))))).)))))).)..))))..)))))))).-3'
MFE = -50.5; z-score = -1.2; 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(+)

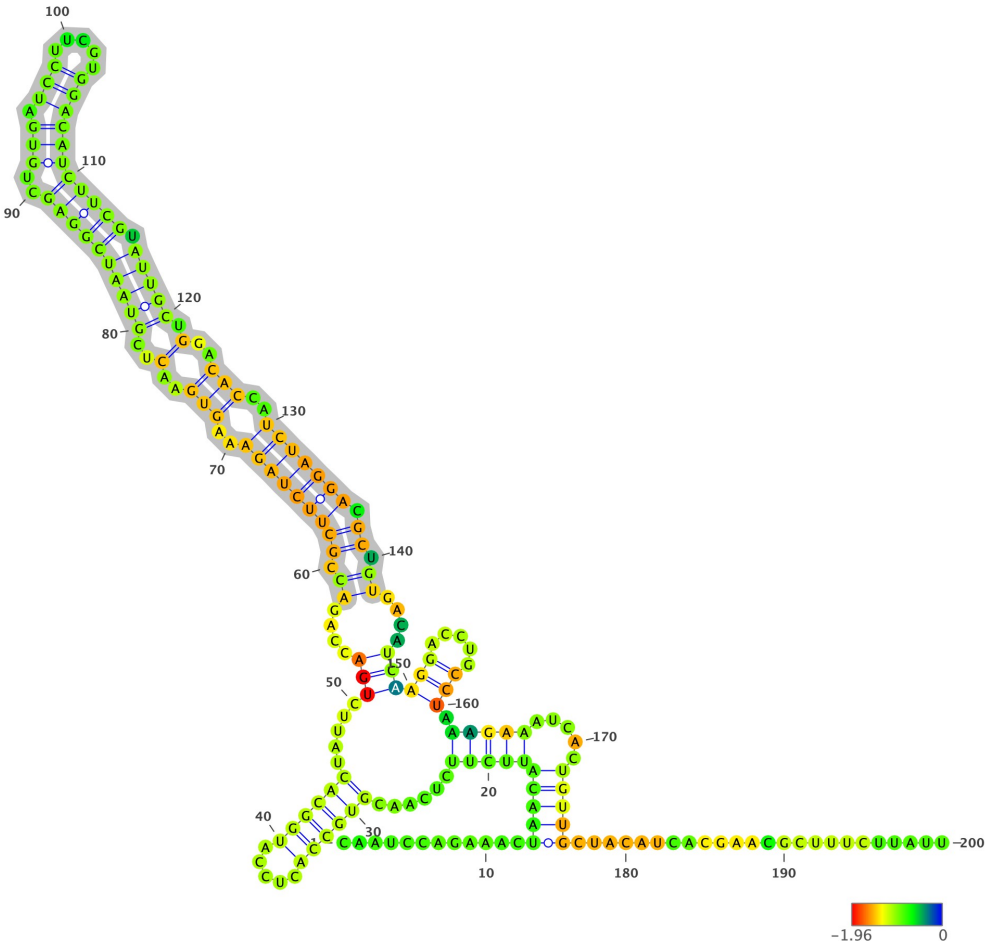
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 472 from nt 26915 to 26999 (nt 58 to 142)

```
5'-ACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGCUGU-3'
5'-(..((((((((((..(((..(..(((((.............................))))))..)..))))..)))))))).))..)-3'
Motif MFE = -27.3; z-score = -2.07; ED = 5.03
```



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 26858 to 27057 (motif highlighted in silver):

```
5'-CAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAUUCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCU
UCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUU-3
5'-...........((((((((((.....((((((.....))))))).....(((....((.((((((((((..(((..(..((((((((((..(((.(((.....)))))))))
)))).)))))).)..)))..)))))))).)).))....)))(((.....))).)))))).....))))).....................-3'
MFE = -42.5; z-score = -0.93; ED = 26.38
```

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_gp05, 26523-27191(+)

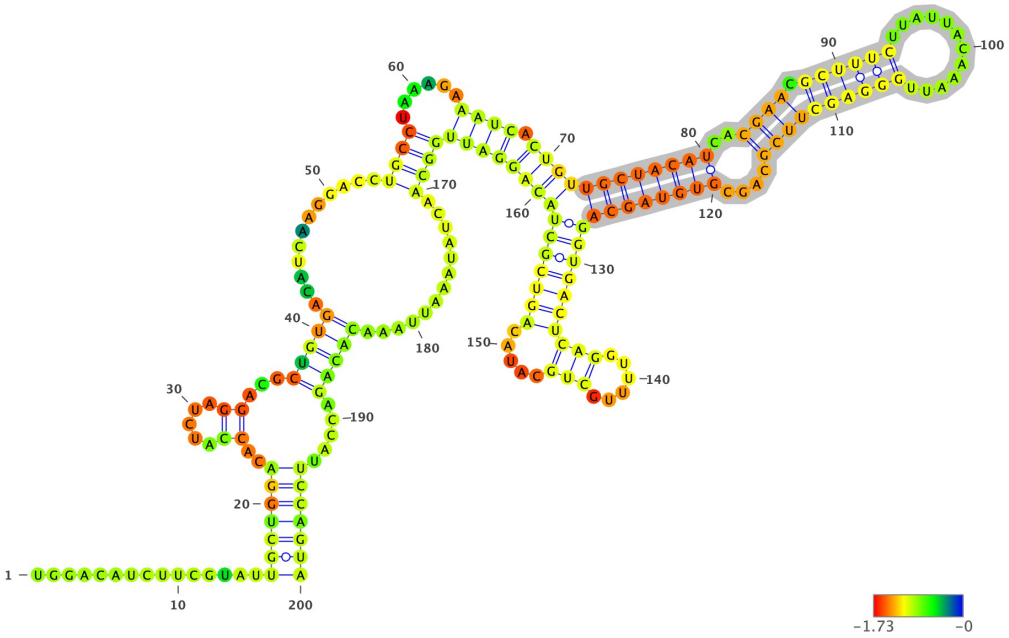
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 473 from nt 27032 to 27086 (nt 73 to 127)

```
5'-UGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAGCUUCGCAGCGUGUAGCA-3'
5'-((((((((..((((.((((((............))))))))))....))))))))-3'
Motif MFE = -18.4; z-score = -2.91; 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 26960 to 27159 (motif highlighted in silver):

```
5'-UGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAGC
UUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUA-3
5'-...............(((((((..((.....))...(((((.............((((......((((.(((((((((((..((((.((((((.............))))))
))))....))))))))((((((((((......)))).....))))))))))))))))))).............)))))).....)))))))-3'
MFE = -48.6; z-score = -0.83; ED = 40.02
```

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_gp05, 26523-27191(+)

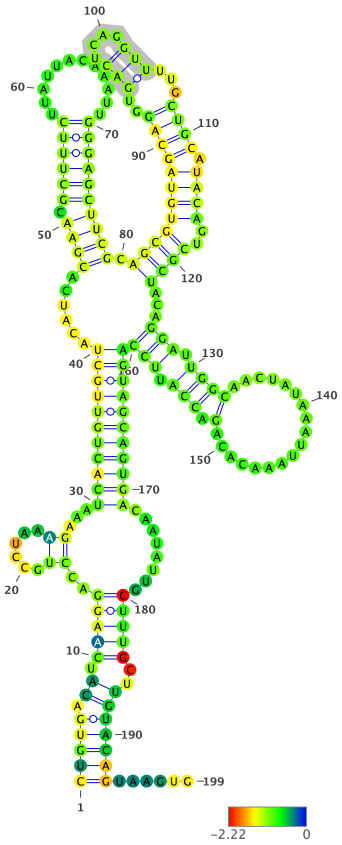
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 474 from nt 27090 to 27099 (nt 95 to 104)

```
5'-GACUCAGGUU-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = 0.14; 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 26996 to 27194 (motif highlighted in silver):

```
5'-CUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAGCUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGC
AUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUAGCAGUGACAAUAUUGCUUUGCUUGUACAGUAAGUG-3
5'-(((((.((.(((((..((......))...((((((((((.....((((.((((((.............)))))))))).((((((((((((..(((....)))...))))
.))))..))))...(((.((((.................).))).))))))))))))))).........)))))..)))))))......-3'
MFE = -49.6; z-score = -1.64; ED = 27.21
```

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 196--gene, gene-GU280_gp05, 26523-27191(+)

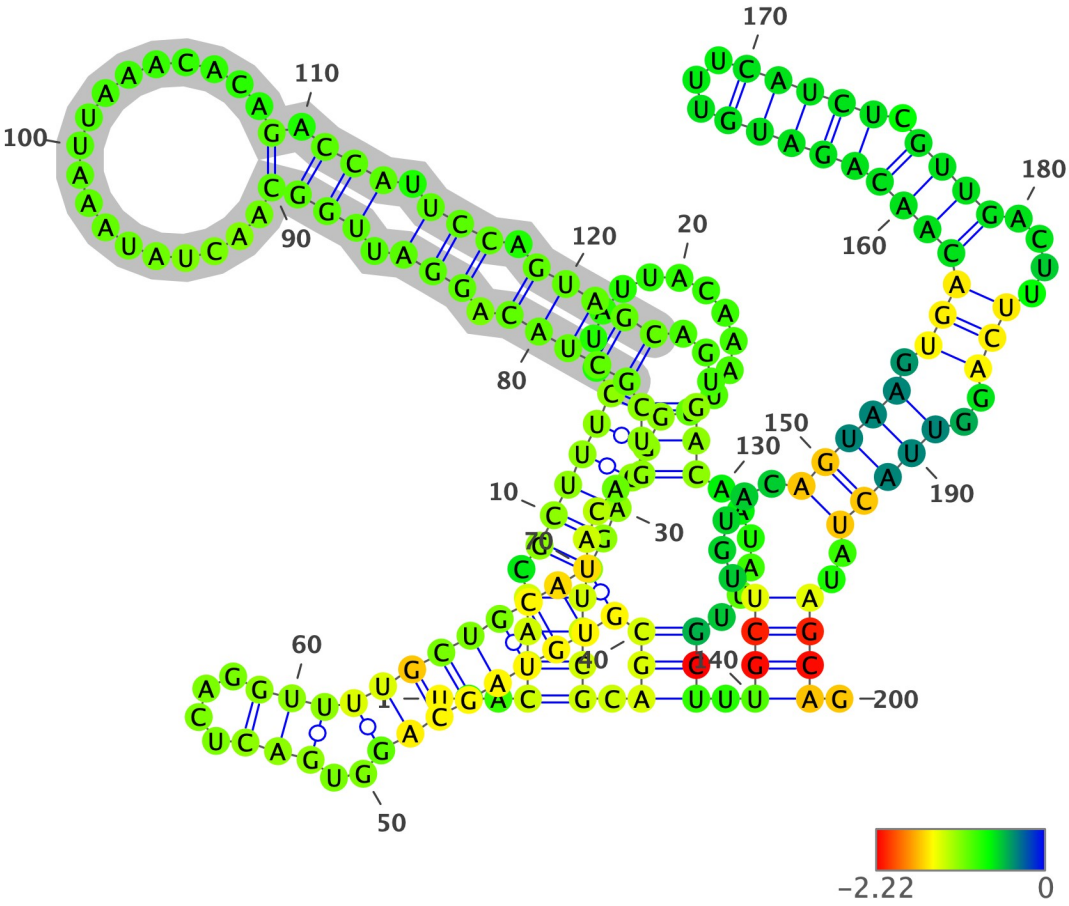
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 196--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 475 from nt 27115 to 27161 (nt 77 to 123)

```
5'-GCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUAGC-3'
5'-(((((.(.................................).)))))-3'
Motif MFE = -12.0; z-score = -4.21; 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 = -1.14; 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(+)

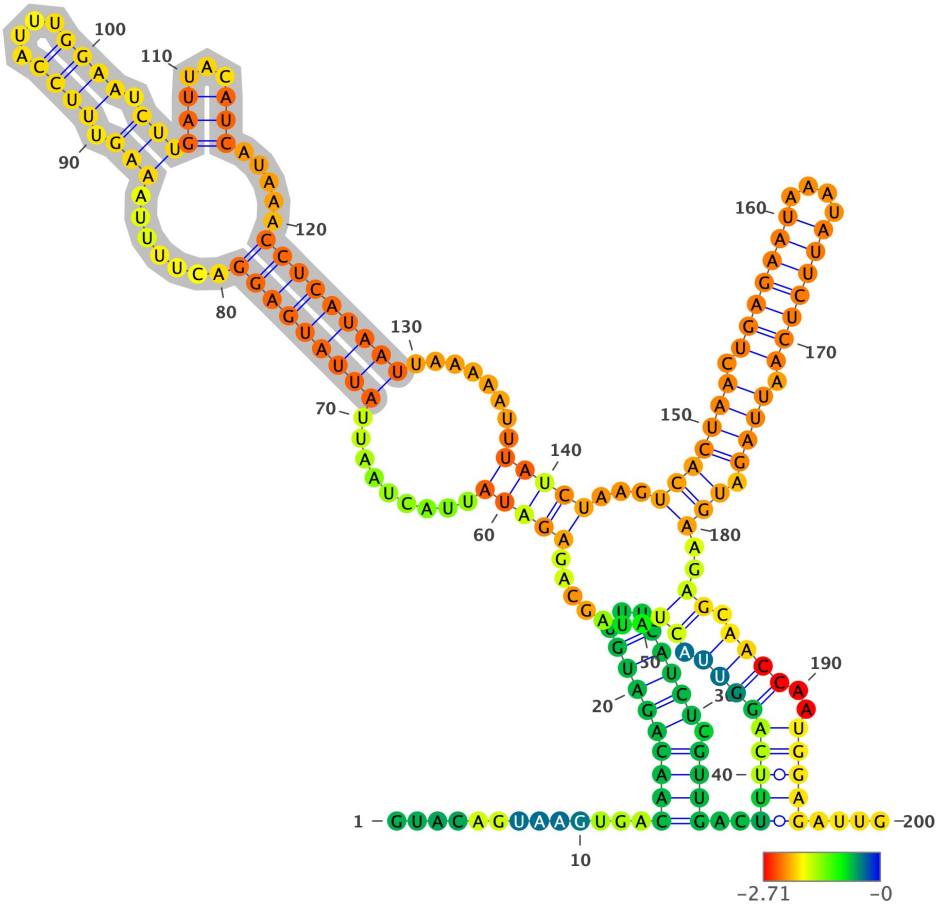
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

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 476 from nt 27253 to 27311 (nt 71 to 129)

```
5'-AUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUACAUCAUAAACCUCAUAAU-3'
5'-(((((((((.......(((.((((....)))).)))(((...))).....)))))))))-3'
Motif MFE = -12.7; z-score = -3.1; ED = 6.58
```



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

Extracted structure model with flanking nucleotides 27183 to 27382 (motif highlighted in silver):

```
5'-GUACAGUAAGUGACAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAGAGAUAUUACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUA
CAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUG-3
5'-.............(((((((((...))))).))))..(((((((((.((.......(((((.........(((((((((.......(((.((((....)))).)))(((..
.)))).....))))))))).......))))).....(((((((.(((((((....)))))))).)))).)))..)).))))..)))))....-3'
MFE = -39.0; z-score = -2.14; ED = 25.67
```

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 9--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 9--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

4-- nt 20 to 200--gene, gene-GU280_gp06, 27202-27387(+)

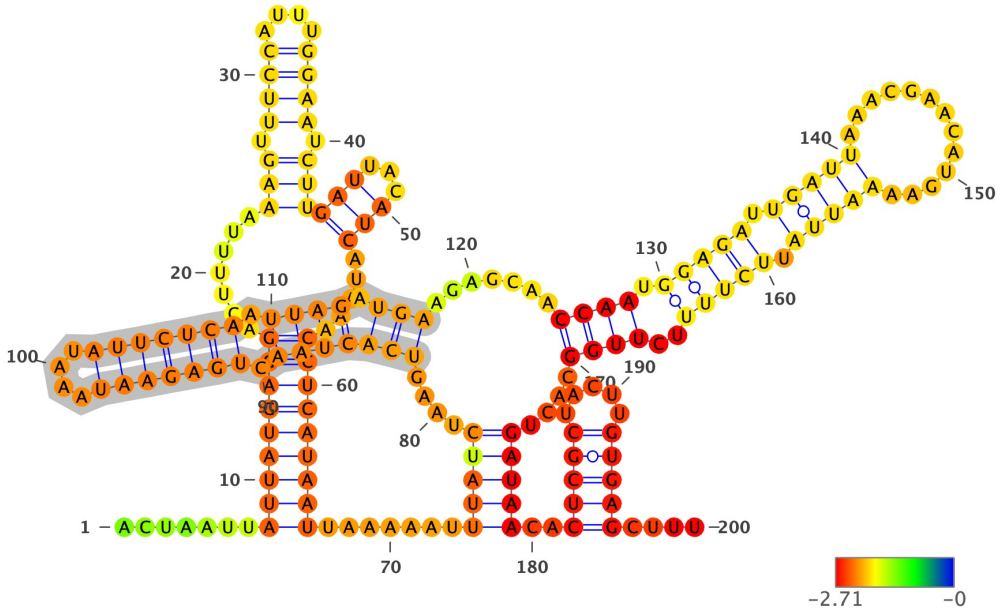
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 20 to 200--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

NC_045512.2 (forward strand): Structure number 477 from nt 27328 to 27362 (nt 83 to 117)

```
5'-UCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGA-3'
5'-(((((((.(((((((....))))))).))))).)))-3'
Motif MFE = -10.5; z-score = -4.76; 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 = -2.5; 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(+)

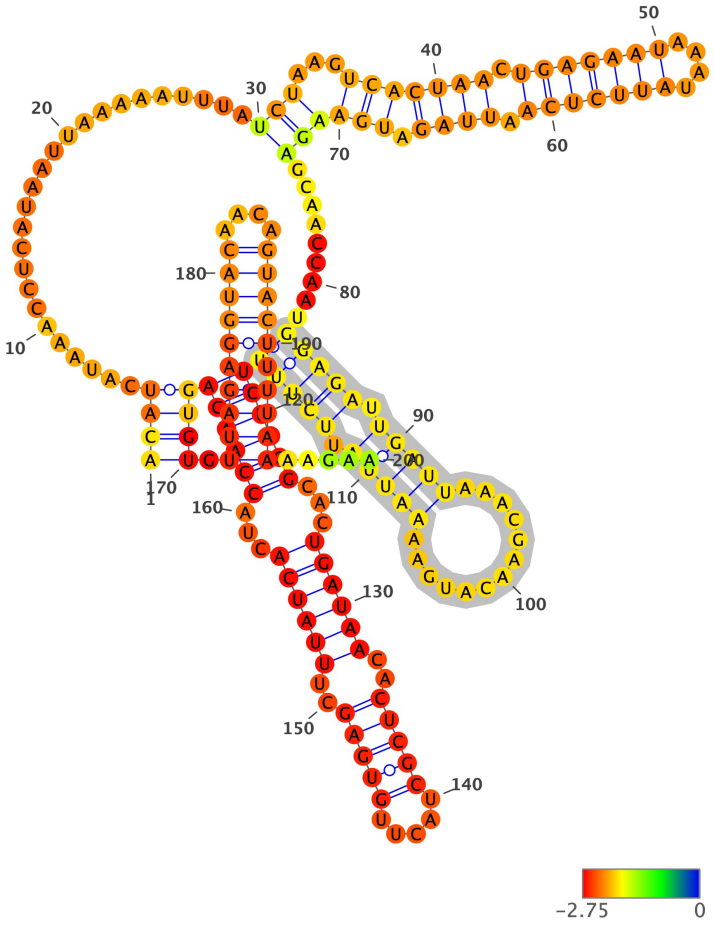
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 478 from nt 27375 to 27409 (nt 83 to 117)

```
5'-GGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUU-3'
5'-(((((.(((((.............))))).))))).-3'
Motif MFE = -2.8; z-score = -0.25; 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 = -3.75; 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(+)

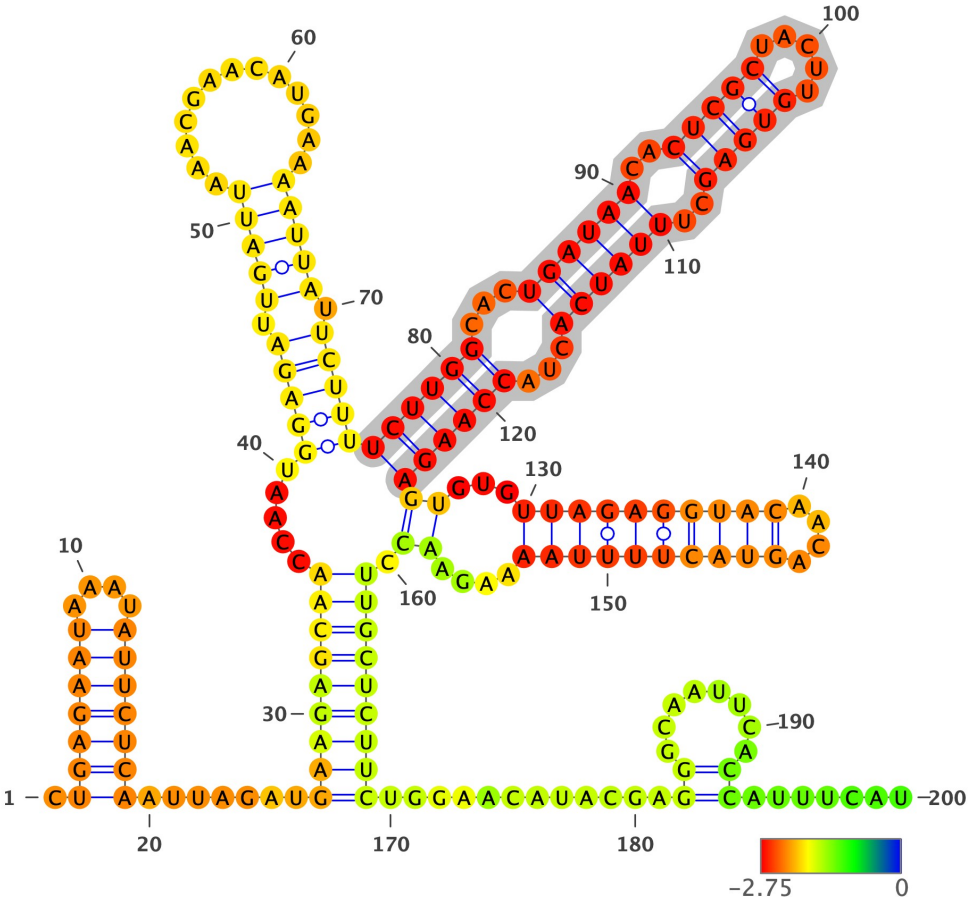
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 479 from nt 27410 to 27458 (nt 76 to 124)

```
5'-UCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGA-3'
5'-((((((...((((((..(((((.....)))))..))))))...))))))-3'
Motif MFE = -18.5; z-score = -5.33; 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 = -3.33; 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(+)

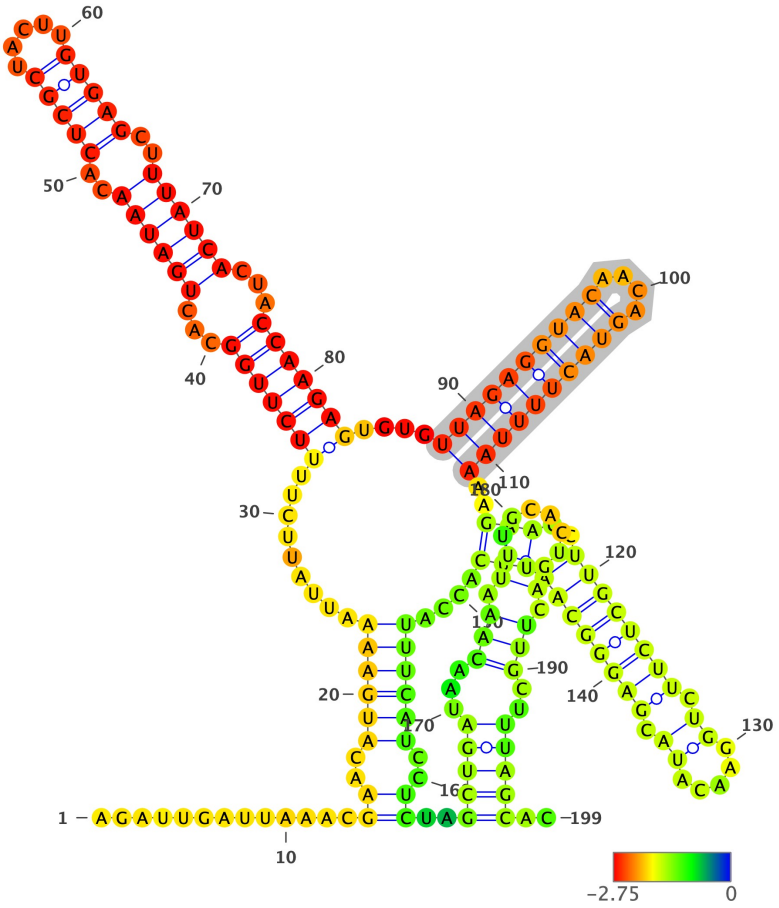
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 480 from nt 27464 to 27487 (nt 88 to 111)

```
5'-UUAGAGGUACAACAGUACUUUUAA-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -8.0; z-score = -4.64; 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 = -2.14; 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(+)

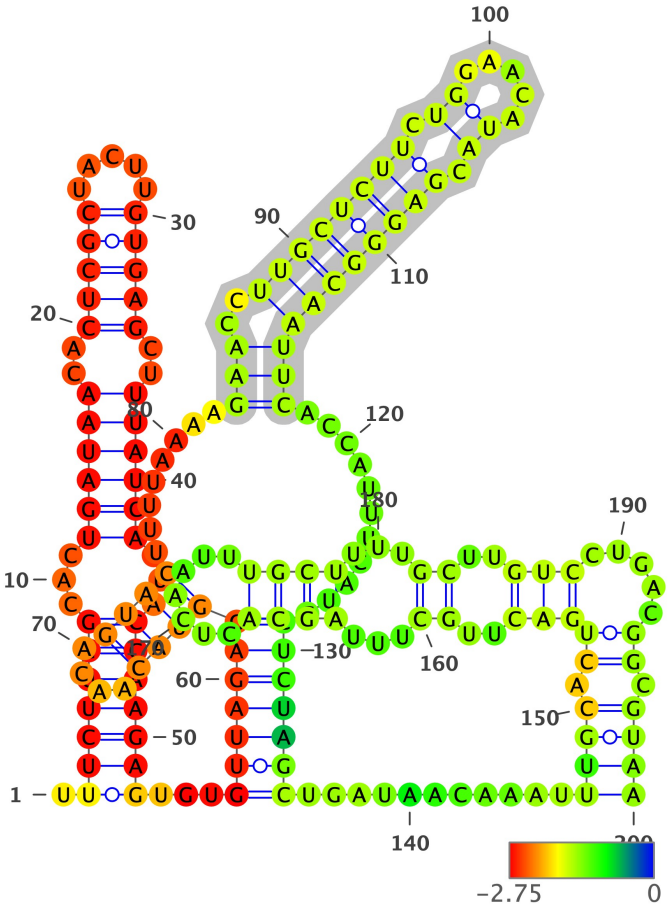
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 481 from nt 27490 to 27524 (nt 83 to 117)

```
5'-GAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUC-3'
5'-(((..(((((((((.((.....)).)))))))))))-3'
Motif MFE = -8.1; z-score = -1.28; ED = 4.7
```



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

Extracted structure model with flanking nucleotides 27408 to 27607 (motif highlighted in silver):

```
5'-UUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGG
CAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAA-3
5'-.(((((((...((((((..(((((.....)))))..))))))...)))))))...((((((((((....))))).......(((..(((((((.((.....)).)))))
))))))).........)))))))..........((((.((((((..((...((((.......))))...))..)))).....)).))))-3'
MFE = -49.0; z-score = -2.35; ED = 27.04
```

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_gp07, 27394-27759(+)

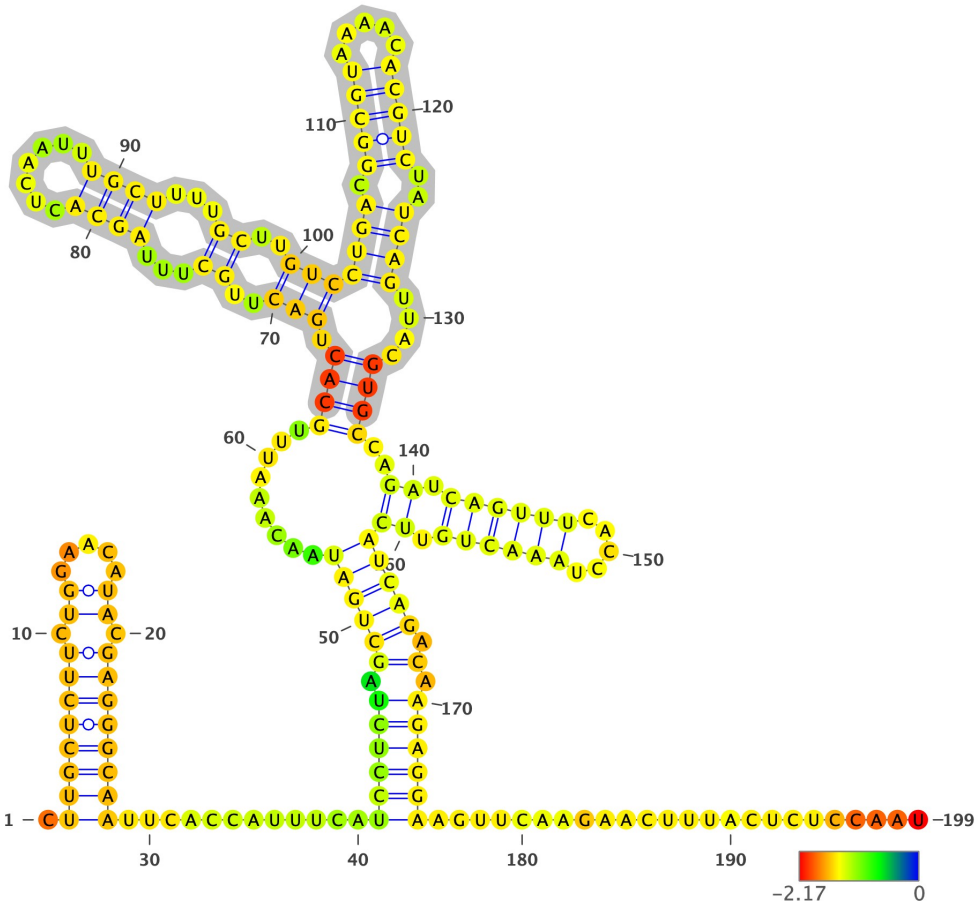
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 482 from nt 27557 to 27628 (nt 64 to 135)

```
5'-CACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAAAACACGUCUAUCAGUUACGUG-3'
5'-(((.(((..((...((((.......))))...))..)))((((.(((((.....)))))..))))....)))-3'
Motif MFE = -17.3; z-score = -1.72; 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 27494 to 27692 (motif highlighted in silver):

```
5'-CUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCG
UAAAACACGUCUAUCAGUUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAU-3
5'-.((((((((.((.....)).)))))))).............((((((.((((((.........((((.(((..((...((((.......))))...))..)))((((.((((
(.....)))))..))))....))))..((.((((((.....)))))).)))))))).).))))))........................-3'
MFE = -46.7; z-score = -2.44; ED = 15.3
```

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_gp07, 27394-27759(+)

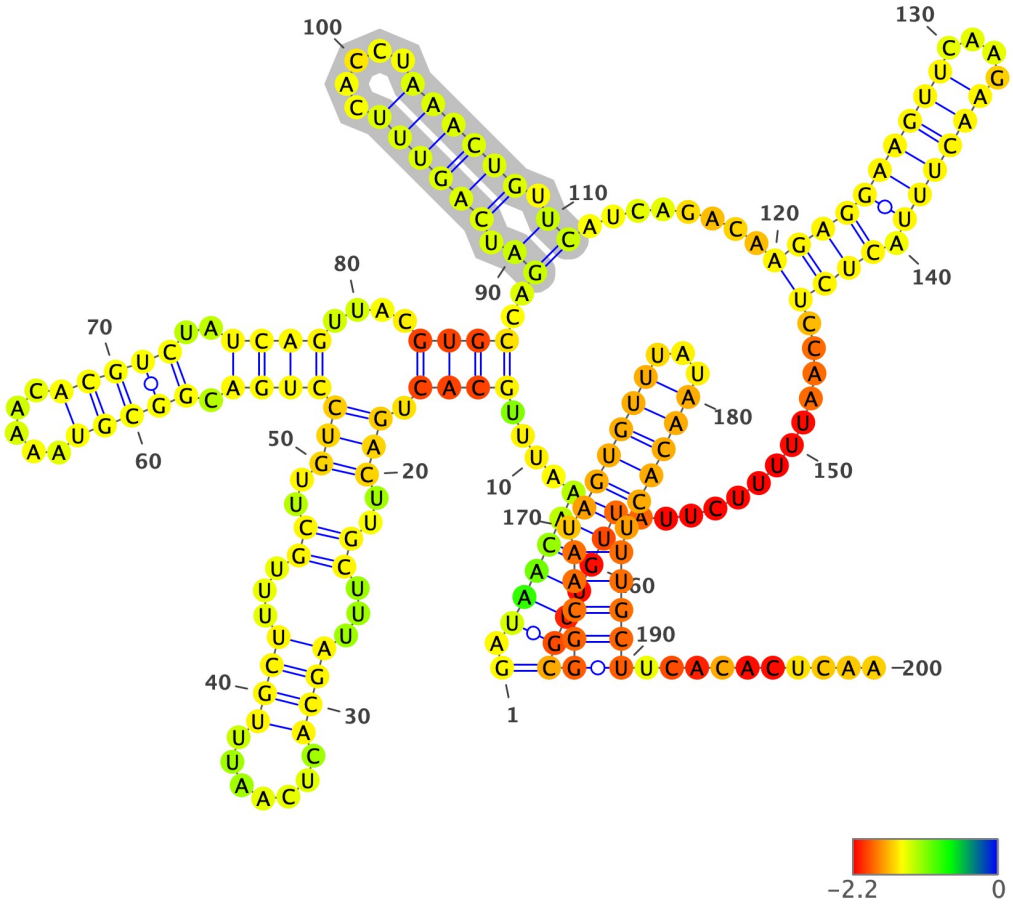
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 483 from nt 27632 to 27654 (nt 89 to 111)

```
5'-GAUCAGUUUCACCUAAACUGUUC-3'
5'-((.(((((((.....)))))))).))-3'
Motif MFE = -4.1; z-score = -2.88; 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 = -2.83; 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(+)

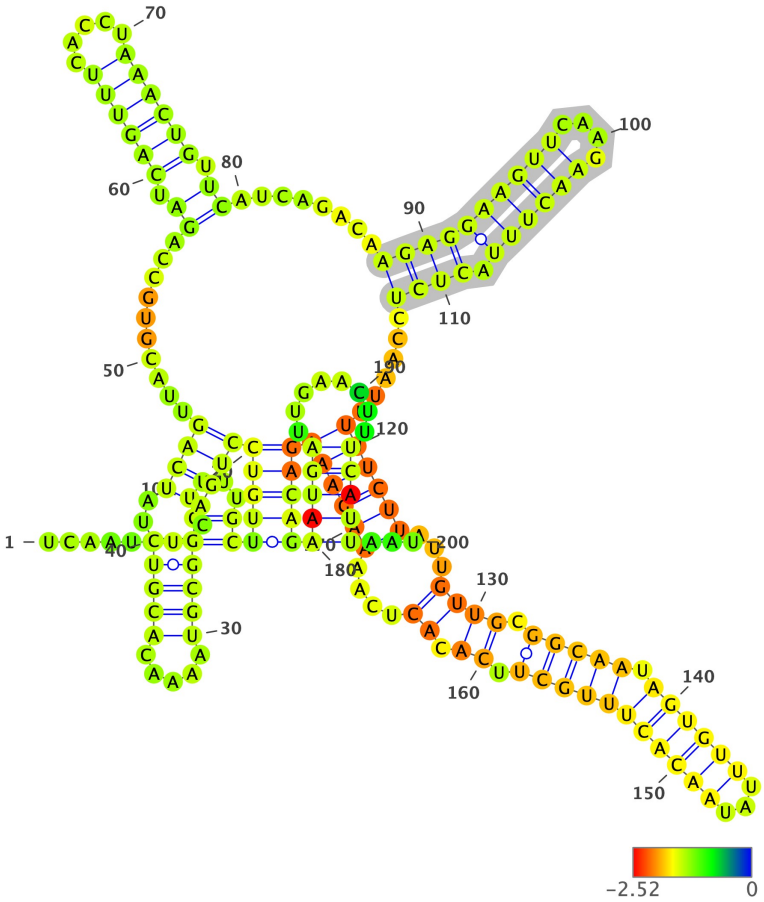
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 484 from nt 27663 to 27687 (nt 88 to 112)

```
5'-AGAGGAAGUUCAAGAACUUUACUCU-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -5.8; z-score = -2.91; 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 = -2.57; ED = 34.67
```

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 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(+)

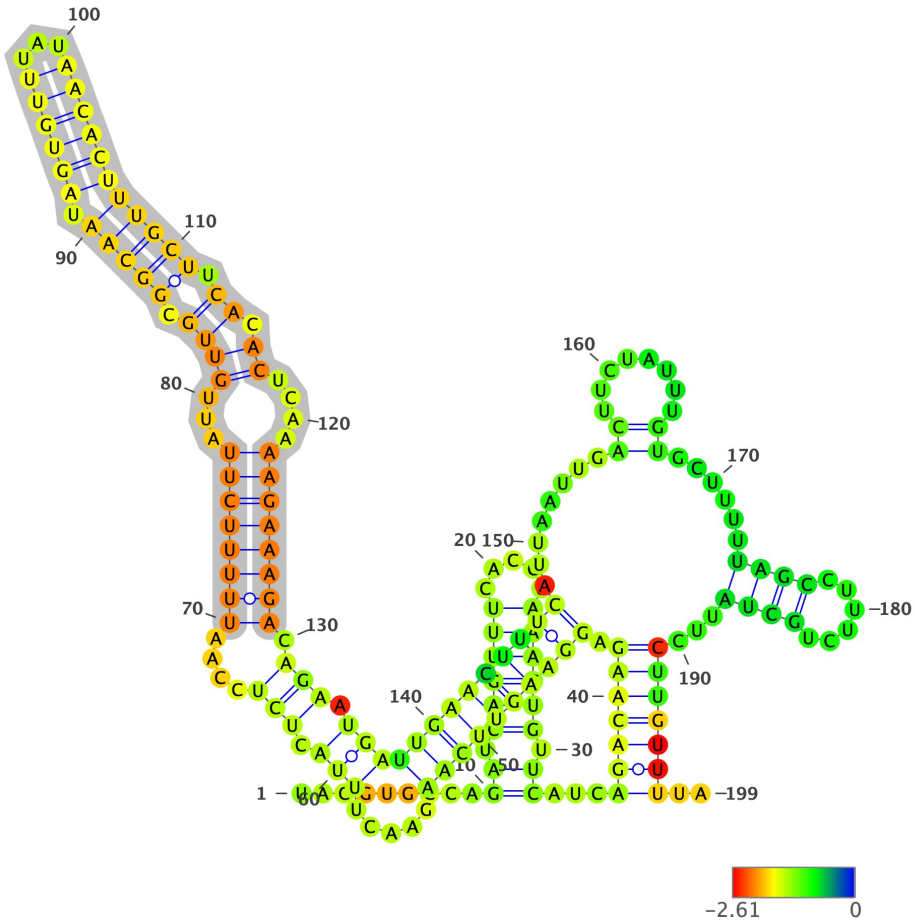
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 485 from nt 27692 to 27751 (nt 70 to 129)

```
5'-UUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCUUCACACUCAAAAGAAAGA-3'
5'-(((((((((...((((.(((((.(((((((...)))))))))))).)).))....))))))))-3'
Motif MFE = -15.2; z-score = -3.18; 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 = -2.34; 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(+)

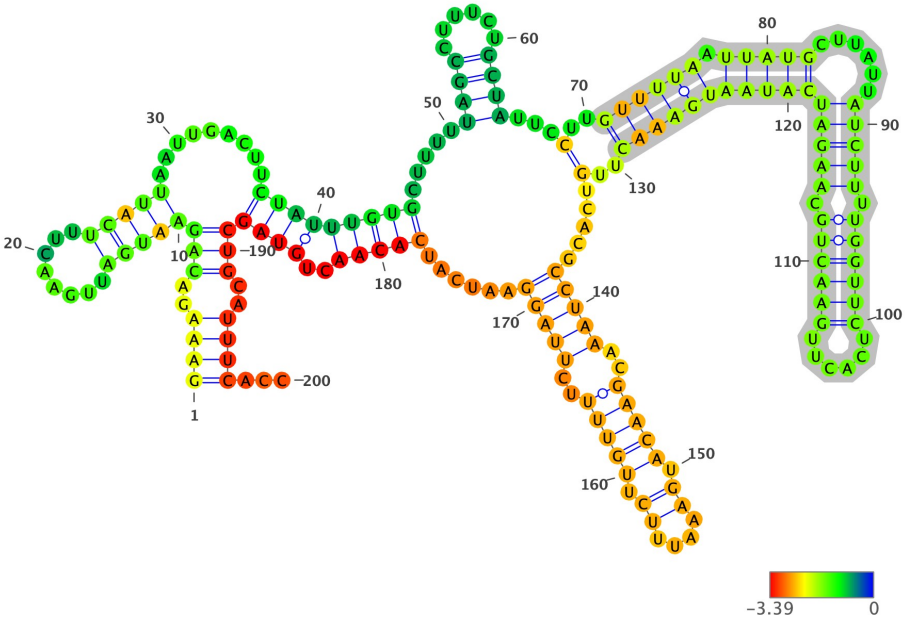
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 486 from nt 27816 to 27874 (nt 71 to 129)

```
5'-GUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAAC-3'
5'-(..(((.(((((.....(((((.((((((.....)))))).)))))))))))))..)-3'
Motif MFE = -12.7; z-score = -3.33; ED = 3.59
```



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 27746 to 27945 (motif highlighted in silver):

```
5'-GAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACU
GCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACC-3
5'-((((..(((((((((........)))))).........(((((((((.....((((......)))))...(..((((((.(((((......(((((.(((((((.....)))))
).)))))))))))))))..).....(((((..((((((.((....)).)))))..)))))).....)))))..)))))))..)))).--3'
MFE = -36.5; z-score = -1.83; ED = 17.06
```

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 14--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 14--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 11 to 142--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 11 to 142--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 149 to 200--gene, gene-GU280_gp09, 27894-28259(+)

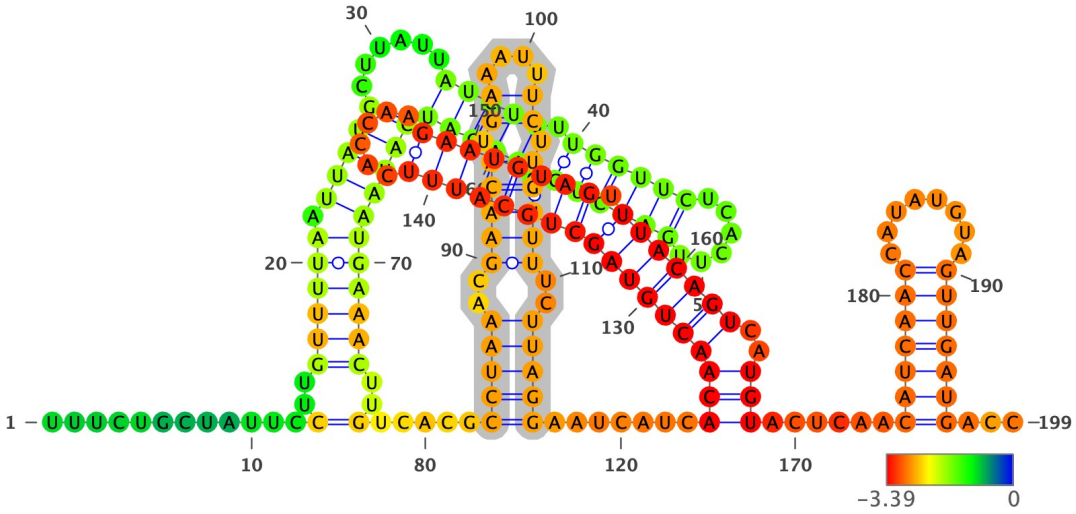
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 149 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 487 from nt 27883 to 27916 (nt 83 to 116)

```
5'-CCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGG-3'
5'-(((((..(((((.((....)).)))))..)))))-3'
Motif MFE = -8.0; z-score = -2.64; 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 = -4.24; 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(+)

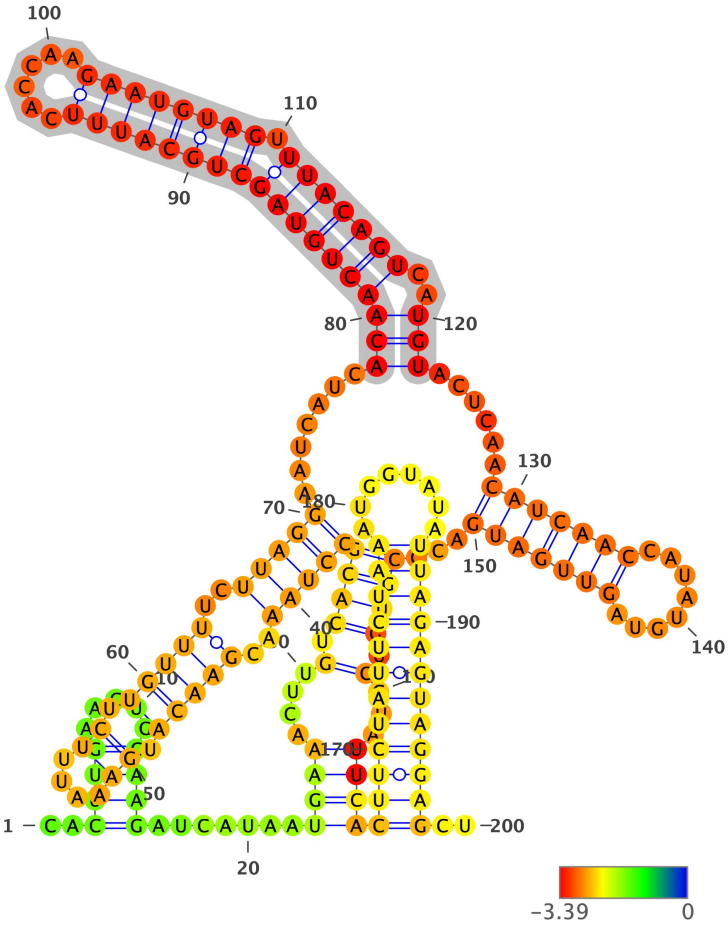
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 488 from nt 27924 to 27968 (nt 78 to 122)

```
5'-ACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGU-3'
5'-(((((((((((((((((.....)))))))).)))))))..)))-3'
Motif MFE = -15.2; z-score = -4.1; 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 = -3.83; 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(+)

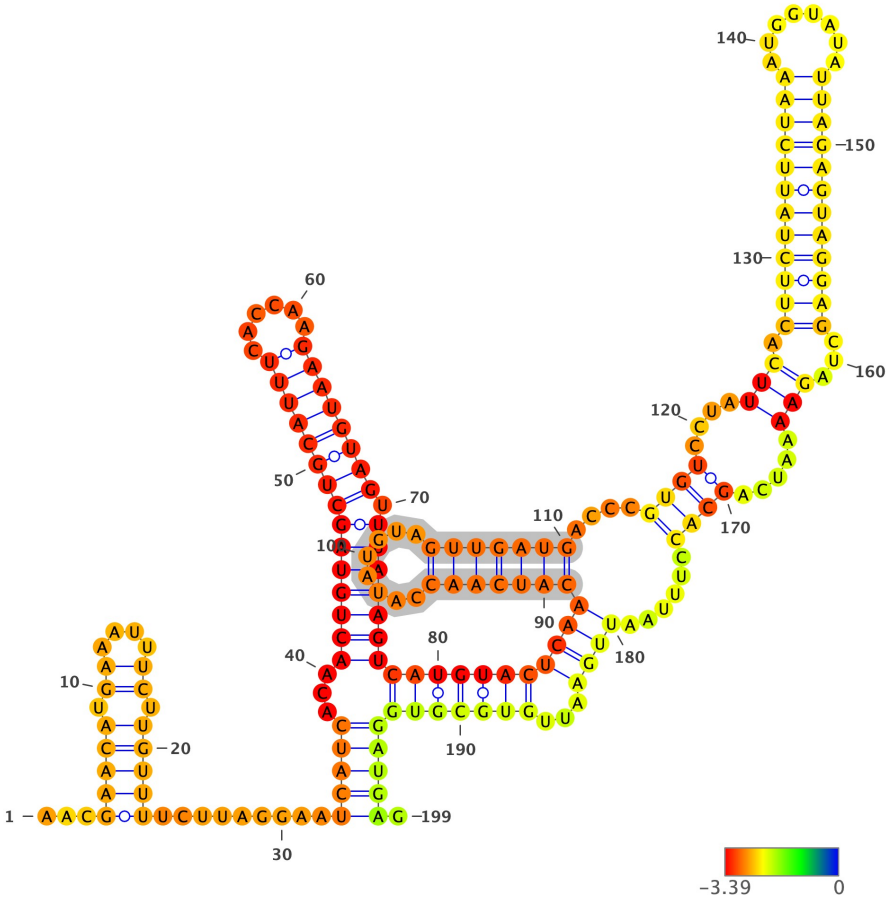
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 489 from nt 27975 to 27996 (nt 89 to 110)

```
5'-CAUCAACCAUAUGUAGUUGAUG-3'
5'-(((((((........)))))))-3'
Motif MFE = -6.3; z-score = -3.19; 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 = -3.9; 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(+)

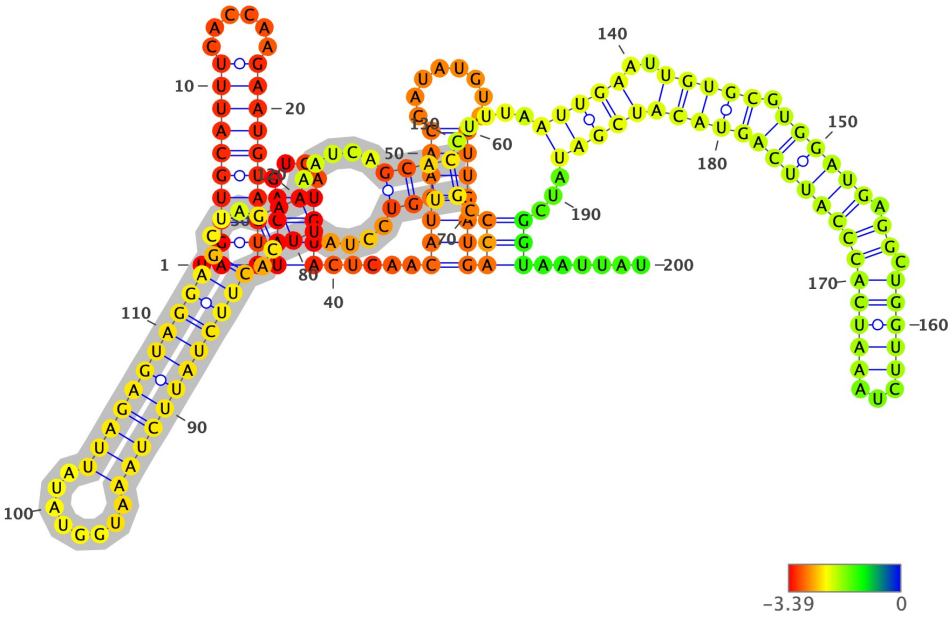
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 490 from nt 28001 to 28059 (nt 71 to 129)

```
5'-GUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCAC-3'
5'-(.........(.(((((((((((.........)))))))))))...).........)-3'
Motif MFE = -15.2; z-score = -2.95; ED = 4.7
```



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 27931 to 28130 (motif highlighted in silver):

```
5'-UAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAG
GAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAUAUCGGUAAUUAU-3
5'-.((((((((((.....))))))))))(((....)))).....(((((((........)))))))(((.((((....(((.((((((((((.........)))))))))
)))...)))).....)))).....(((((..(((((.((((((.((.(((((...)))))))))))))))))))))...))).......-3'
MFE = -52.9; z-score = -3.4; ED = 12.7
```

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_gp09, 27894-28259(+)

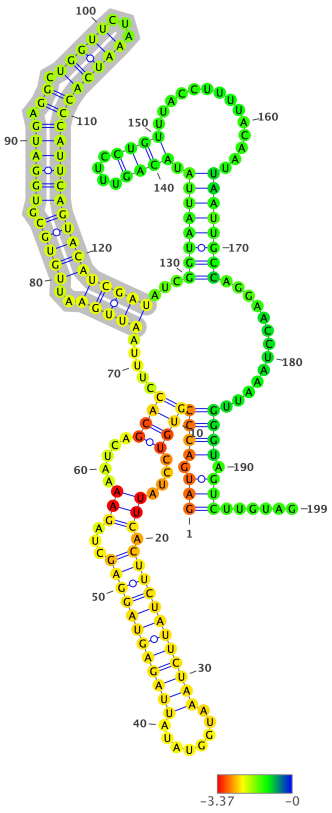
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 491 from nt 28065 to 28118 (nt 73 to 126)

```
5'-AUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAU-3'
5'-((((((..((((((.(((((((.((.((((((...))))))))))))))))))))))))))-3'
Motif MFE = -17.3; z-score = -2.72; 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 = -2.12; 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(+)

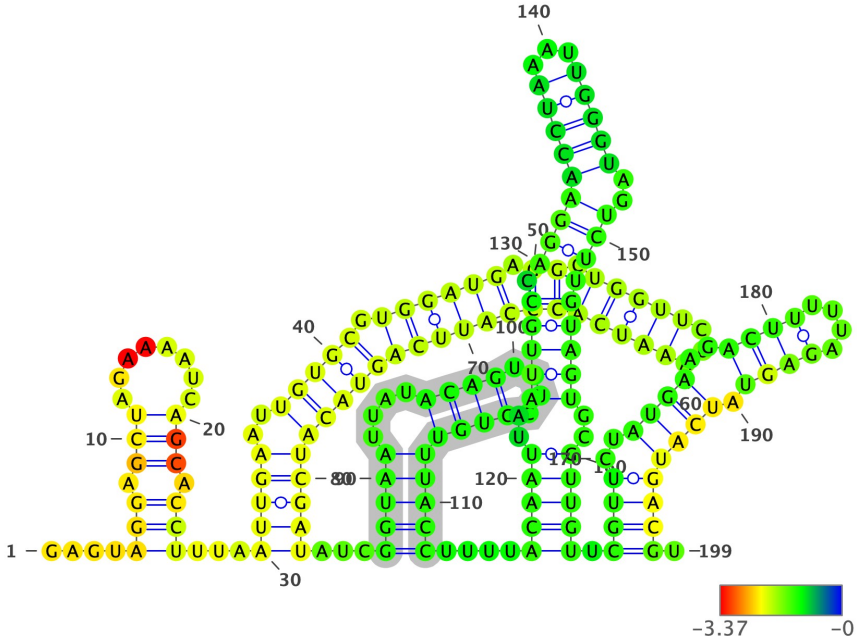
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 492 from nt 28122 to 28147 (nt 87 to 112)

```
5'-GGUAAUUAUACAGUUUCCUGUUUACC-3'
5'-(((((....((((....)))))))))-3'
Motif MFE = -4.9; z-score = -2.46; 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 28036 to 28234 (motif highlighted in silver):

```
5'-GAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUAC
CUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGU-3
5'-....(((.(((........))).)))...(((((..(((((.((((((.((.(((((...)))))))))))))))))))))))...(((((....((((....))))))))
)....(((((..(((((.((((((((...)))))..)))))))))..))))).((((..((((..((((....)))).)))))))).-3'
MFE = -47.5; z-score = -0.96; ED = 15.82
```

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_gp09, 27894-28259(+)

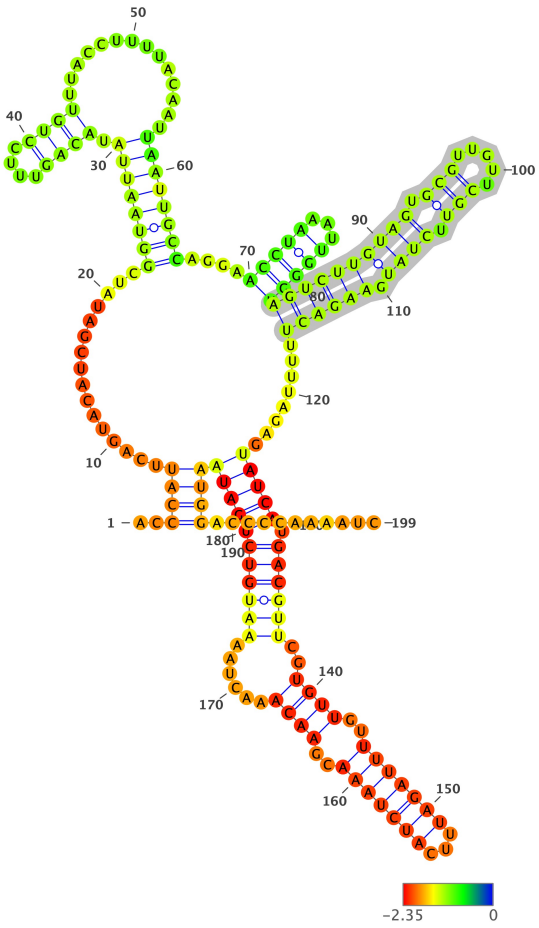
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 493 from nt 28182 to 28215 (nt 83 to 116)

```
5'-AGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACU-3'
5'-((((((((((.(((.....))).)))))).)))))))-3'
Motif MFE = -11.3; z-score = -3.19; ED = 2.02
```



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

Extracted structure model with flanking nucleotides 28100 to 28298 (motif highlighted in silver):

```
5'-ACCCAUUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGA
AGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUC-3
5'-..((((.................((((((((.((((....)))).............))))))))....(((((...)))))((((((((((.(((.....))).)))))
))))).......(((((.(((((((..(((((..(((((((...)))))))..))))).....))))))))))))))).....-3'
MFE = -40.9; z-score = -1.62; ED = 44.73
```

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

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

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 160--gene, gene-GU280_gp09, 27894-28259(+)

Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

3-- nt 1 to 160--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

4-- nt 175 to 199--gene, gene-GU280_gp10, 28274-29533(+)

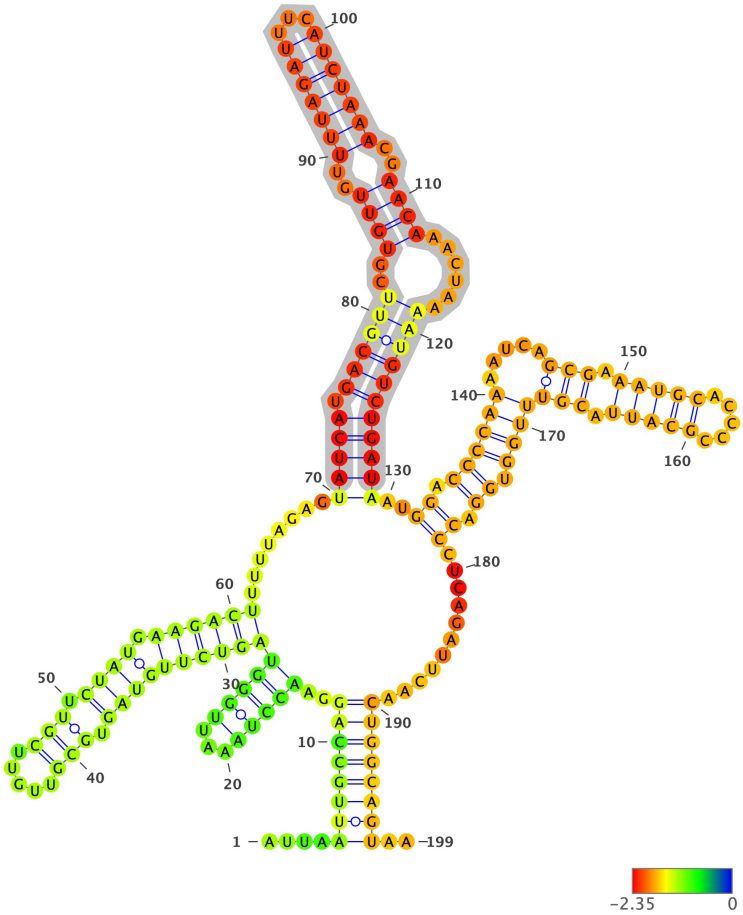
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 175 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 494 from nt 28225 to 28282 (nt 71 to 128)

```
5'-AUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAU-3'
5'-((((.(((.....((((..(((((((...)))))))..))))).........)))))))-3'
Motif MFE = -13.4; z-score = -2.67; ED = 9.4
```



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 28155 to 28353 (motif highlighted in silver):

```
5'-AUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAAC
AAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAA-3
5'-....(((((((((..((((((...))))))((((((((((.(((.....))).)))))..))))))........(((((.((((((..((((..(((((((...)))))))..)))
).....))))))))))))..((.((((((.....(((.(((((.....)))))).)))))))..)).))..........)))))))..-3'
MFE = -57.2; z-score = -3.59; ED = 16.23
```

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 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(+)

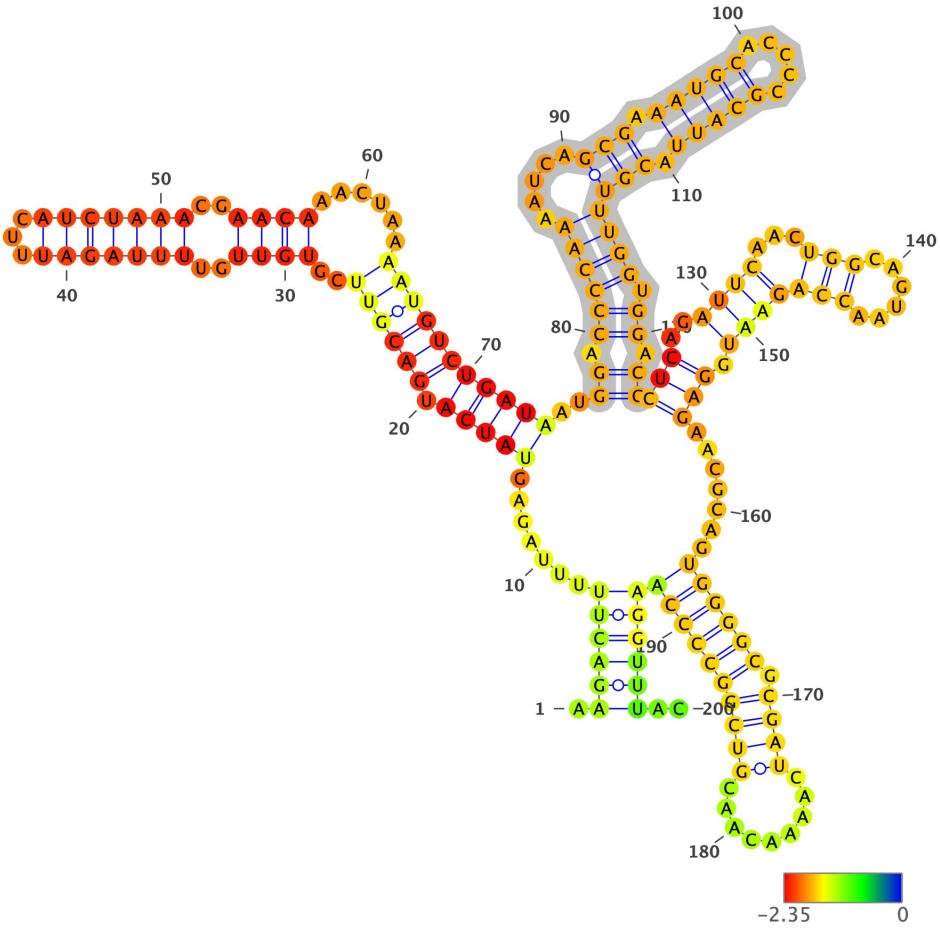
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 495 from nt 28286 to 28332 (nt 77 to 123)

```
5'-GGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACC-3'
5'-((.((((((.....(((.(((((.....))))).)))))))).)).))-3'
Motif MFE = -13.6; z-score = -2.2; 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 = -2.03; 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(+)

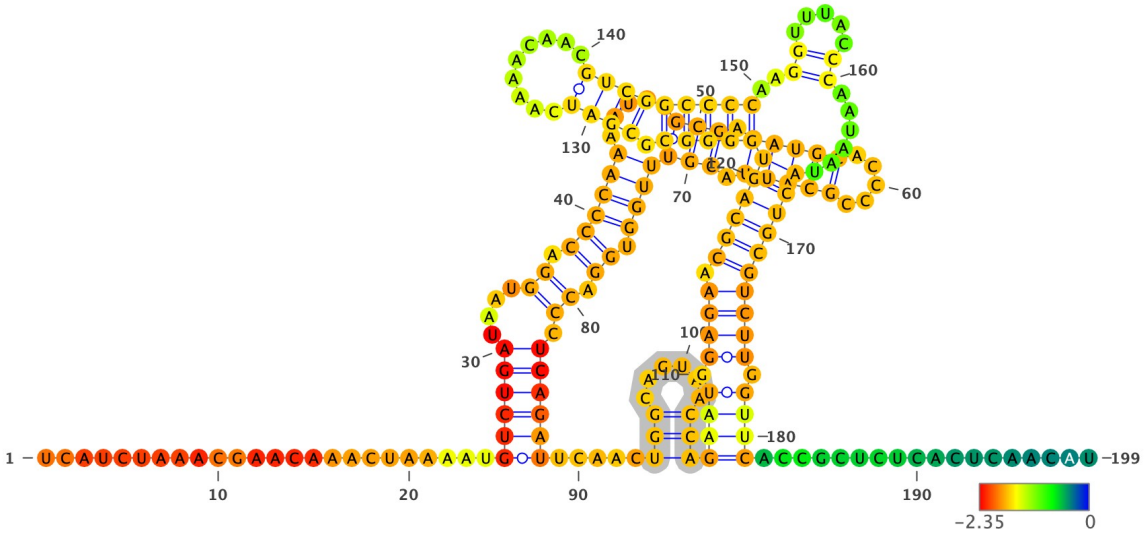
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 496 from nt 28345 to 28356 (nt 94 to 105)

```
5'-UGGCAGUAACCA-3'
5'-(((......)))-3'
Motif MFE = -0.6; z-score = -1.15; ED = 1.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28252 to 28450 (motif highlighted in silver):

```
5'-UCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGG
AGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAU-3
5'-.......................((((((....((.((((((.....(((.(((((.....)))))..)))))))..)).)).))))))).....(((......)))(((((.(
(((.((((((((((.((((.........)))))))))..((.....)).....)))))))))).))))..................-3'
MFE = -52.4; z-score = -2.66; 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(+)

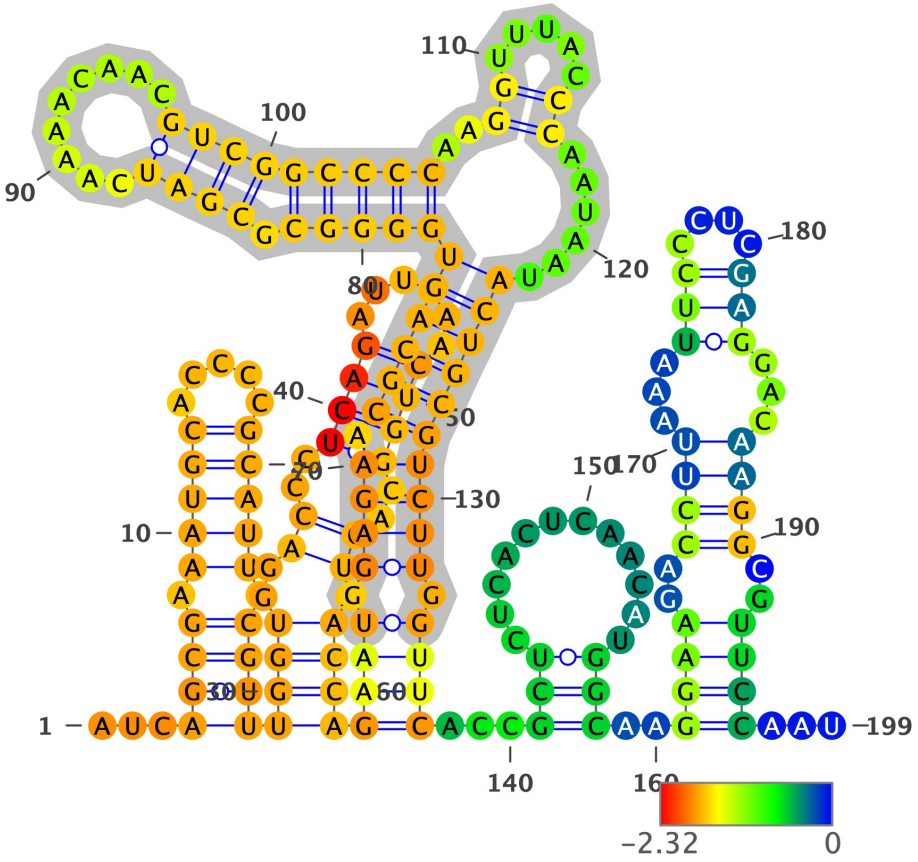
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 497 from nt 28360 to 28429 (nt 65 to 134)

```
5'-UGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGG-3'
5'-(.((((.(((((((((((.((((.........)))))))))..((.....)).....))))))))))).)-3'
Motif MFE = -24.7; z-score = -2.53; ED = 5.77
```



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 28296 to 28494 (motif highlighted in silver):

```
5'-AUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUU
UACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAU-3
5'-...((((.(((((.....))))).))))((((..((..((((.....))))..)).))))((((.((((.(((((((((((.((((.........)))))))))..((..
...)).....))))))))))).))))...(((.............)))..((((..((((...(((....)))...))))..))))...-3'
MFE = -56.6; z-score = -2.22; ED = 17.4
```

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(+)

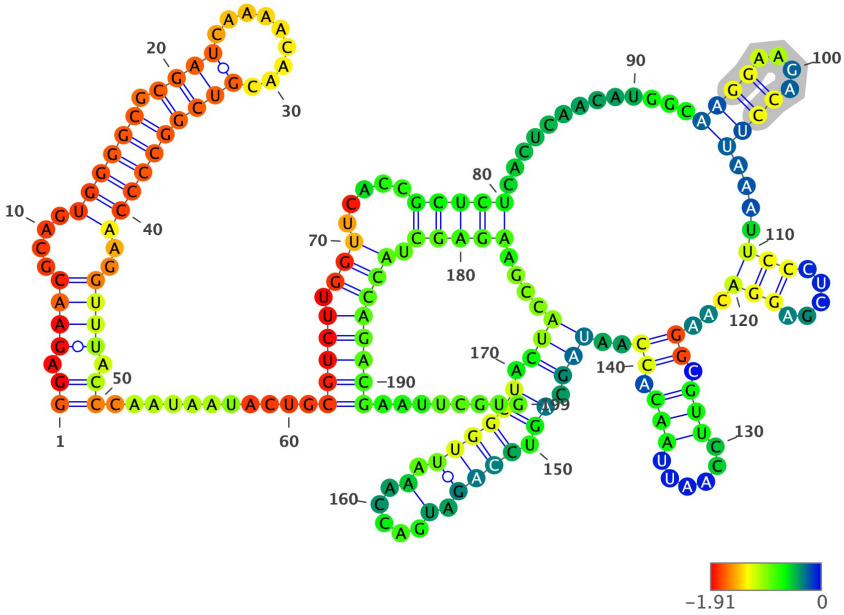
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 498 from nt 28456 to 28463 (nt 96 to 103)

```
5'-GGAAGACC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 28361 to 28559 (motif highlighted in silver):

```
5'-GGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUC
CCUCGAGGACAAGGCGUUCCAAUUAACACCAAUAGCAGUCCAGAUGACCAAAUUGGCUACUACCGAAGAGCUACCAGACGAAUUCGUG-3
5'-((.((((....((((((.((((.........))))))))))..)))).))...........(((((.(((.....(((((.............((((....))))....((
(.....)))...((.(((......))).))..(((.((.((((.(.....).)))))).)))....))))).))))))))........-3'
MFE = -44.2; z-score = -0.37; ED = 40.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

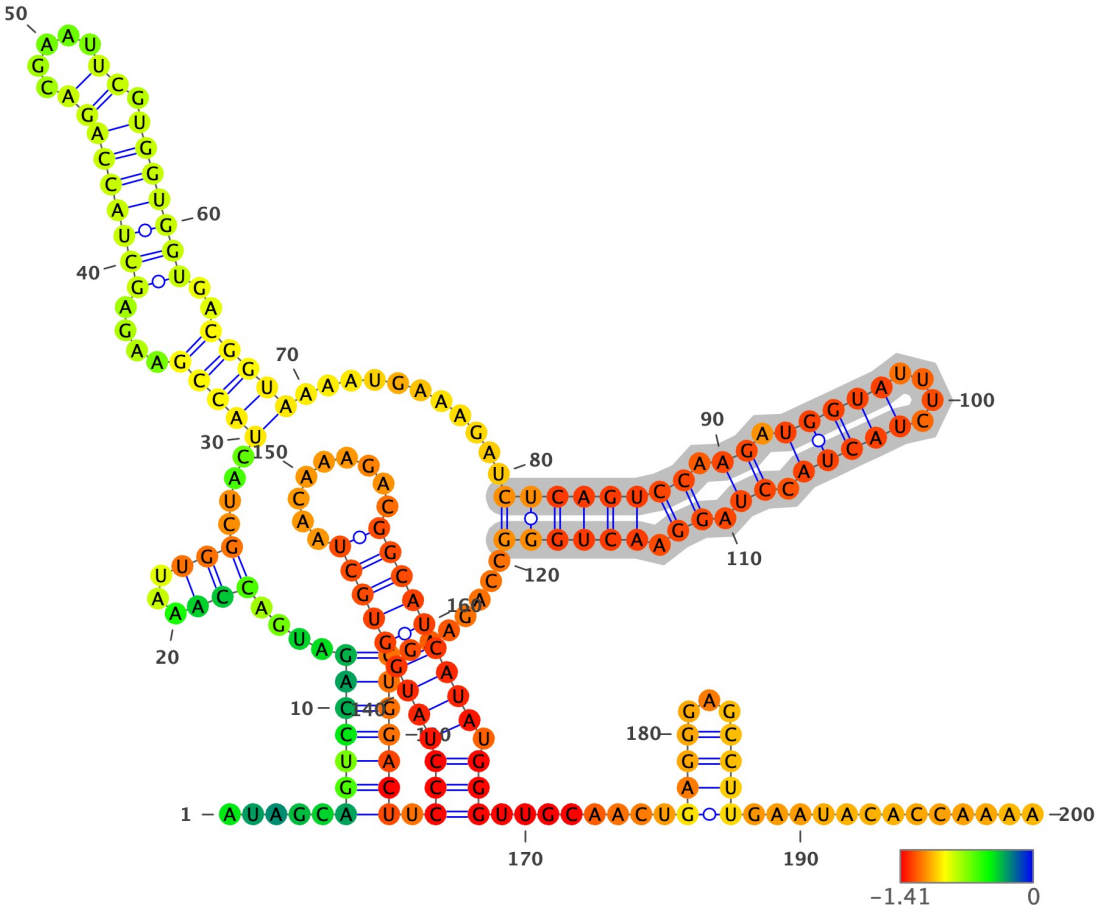
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 499 from nt 28583 to 28621 (nt 81 to 119)

```
5'-CUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGG-3'
5'-((((((((.((.(((((....))))).)).)).))))))-3'
Motif MFE = -12.9; z-score = -2.9; 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 = -2.52; 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(+)

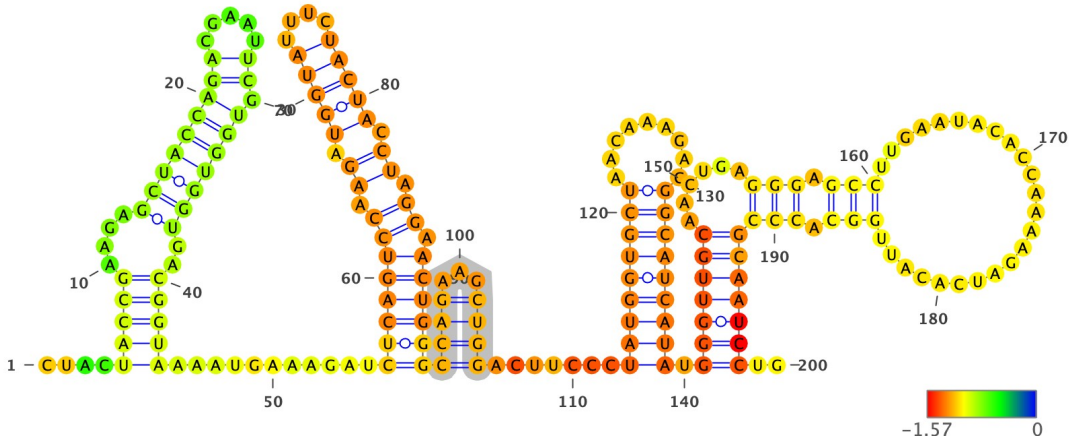
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 500 from nt 28622 to 28632 (nt 95 to 105)

```
5'-CCAGAAGCUGG-3'
5'-((((...))))-3'
Motif MFE = -2.1; z-score = -2.91; ED = 0.41
```



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 28528 to 28727 (motif highlighted in silver):

```
5'-CUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCC
CUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUG-3
5'-....(((((....((((((((((.....)).)))))))..)))))..........(((((((((.((.(((((....)))))).)).)).)))))))(((...))))......
.(((((((((.........)))))))).(((((((.....(((.(((.........................))).))))))))))..-3'
MFE = -57.7; z-score = -2.03; ED = 16.68
```

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_gp10, 28274-29533(+)

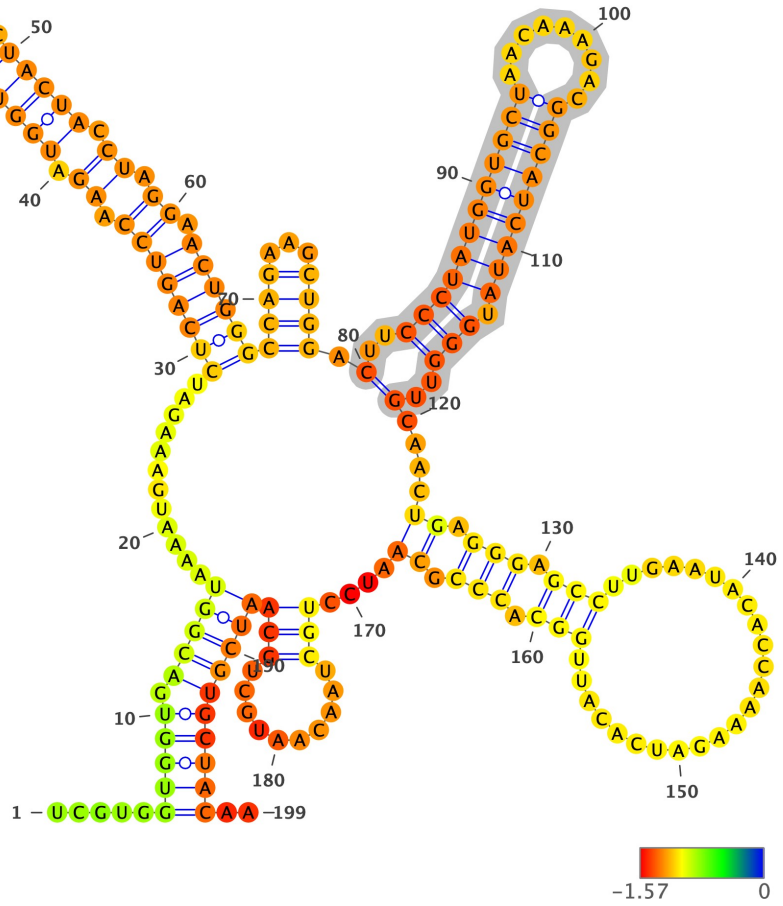
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 501 from nt 28634 to 28673 (nt 80 to 119)

```
5'-CUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUG-3'
5'-(..((((((((((((.........))))))))).)))..)-3'
Motif MFE = -14.5; z-score = -3.18; 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 28555 to 28753 (motif highlighted in silver):

```
5'-UCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAU
AUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAA-3
5'-.....(((((.(((((............((((((((.((.(((((....))))).)).)).))))))((((...)))).(..((((((((((((.........))))))))
).)))..)....((.(((.(((.........................))).))).)).....(((..........)))))))))))))..-3'
MFE = -54.2; z-score = -1.51; ED = 24.14
```

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_gp10, 28274-29533(+)

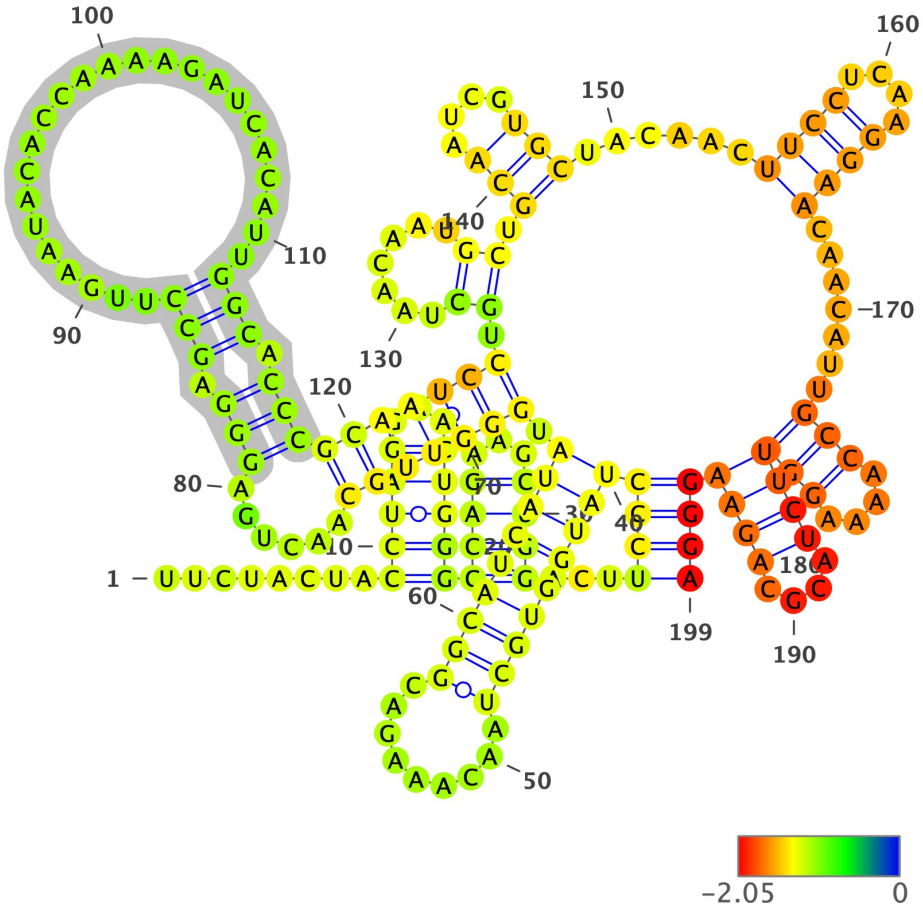
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 502 from nt 28681 to 28718 (nt 81 to 118)

```
5'-GGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCC-3'
5'-(((.(((.....................))).)))-3'
Motif MFE = -7.1; z-score = -0.98; 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 = -1.19; 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(+)

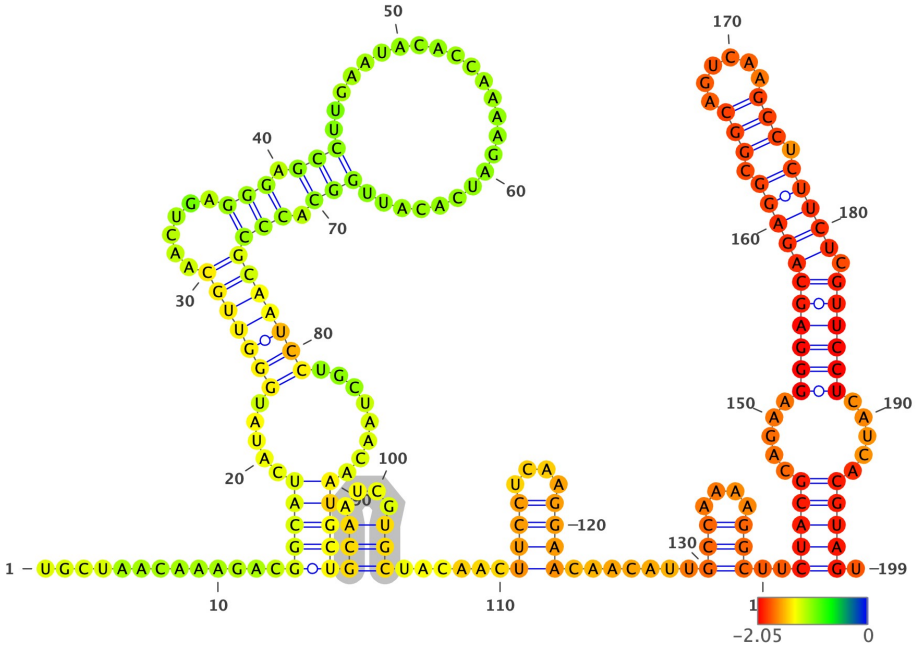
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 503 from nt 28739 to 28748 (nt 95 to 104)

```
5'-GCAAUCGUGC-3'
5'-(((....)))-3'
Motif MFE = -0.2; z-score = -0.6; 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 28645 to 28843 (motif highlighted in silver):

```
5'-UGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACU
UCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAGU-3
5'-.............(((((.....(((((((......(((.(((.......................))).))))))))))........)))))(((....)))......(
(((....))))......(((....)))..(((((.....((((((((((.(((......))).))))).))))))).....))))).-3'
MFE = -51.7; z-score = -2.05; ED = 30.44
```

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_gp10, 28274-29533(+)

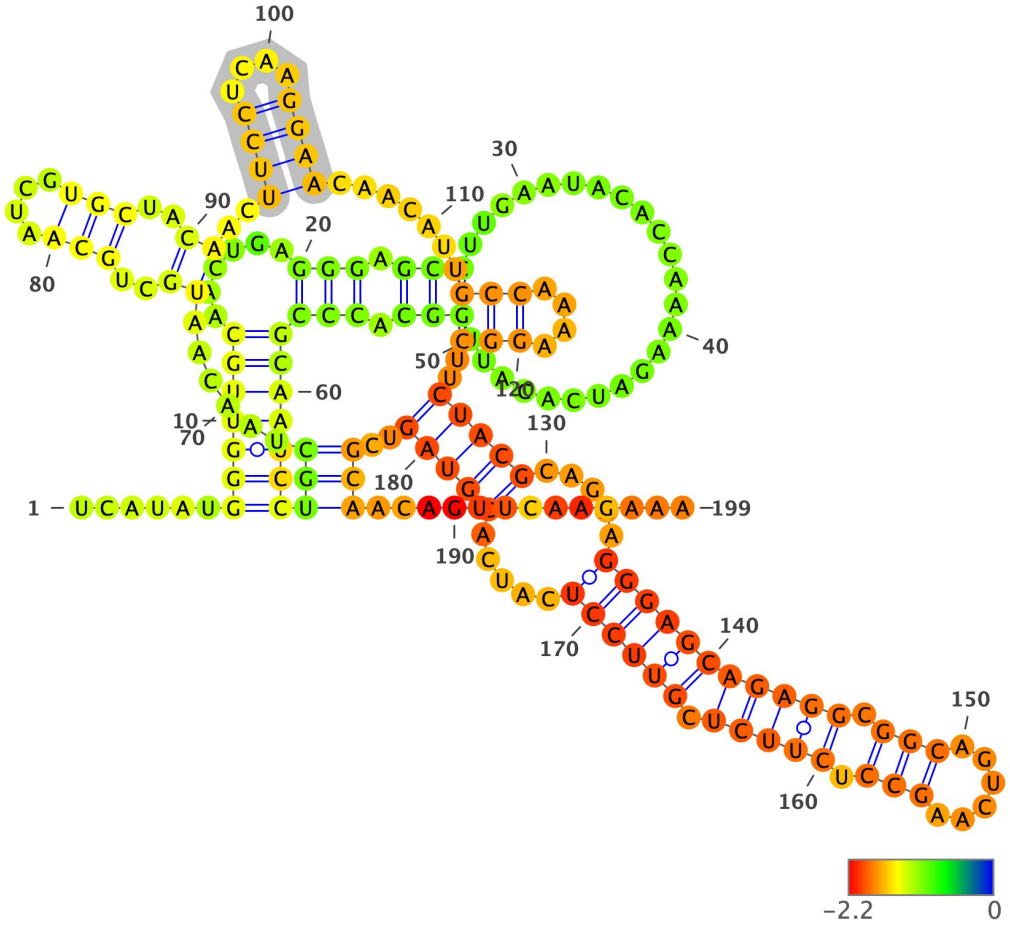
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 504 from nt 28755 to 28766 (nt 94 to 105)

```
5'-UUCCUCAAGGAA-3'
5'-((((....))))-3'
Motif MFE = -1.6; z-score = -6.95; 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 = -1.54; 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(+)

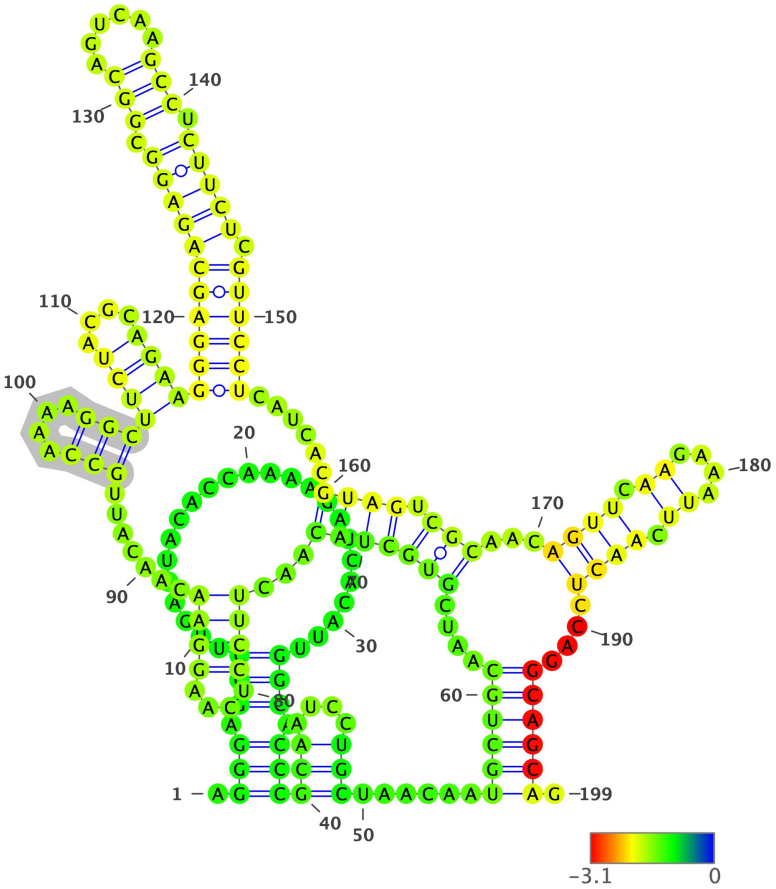
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 505 from nt 28774 to 28783 (nt 95 to 104)

```
5'-GCCAAAAGGC-3'
5'-(((....)))-3'
Motif MFE = -2.6; z-score = -7.22; 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 = -2.35; 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(+)

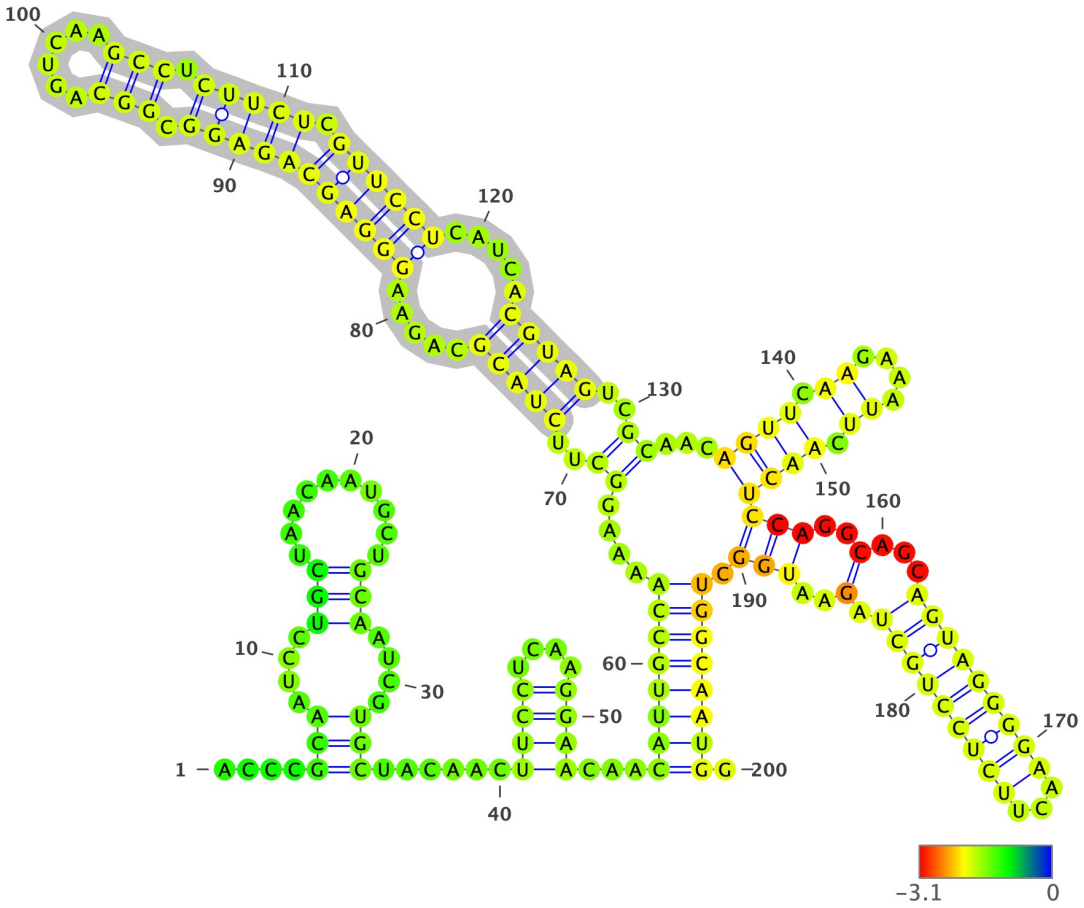
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 506 from nt 28786 to 28842 (nt 72 to 128)

```
5'-CUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAG-3'
5'-(((((.....((((((((((.(((......))).))))).))))))).....)))))-3'
Motif MFE = -24.0; z-score = -3.41; 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 = -2.84; 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(+)

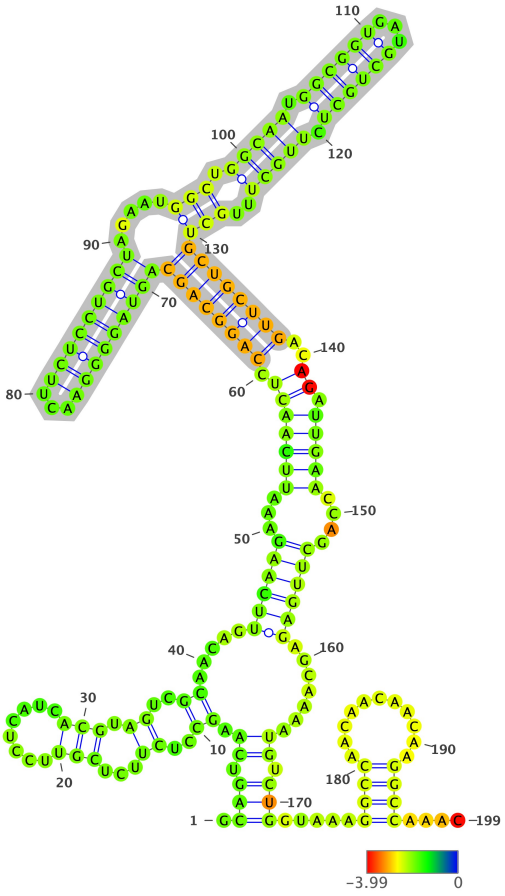
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 507 from nt 28869 to 28946 (nt 61 to 138)

```
5'-CAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUG-3'
5'-((((((((((((((((...))))))))).....(((.(((((.(((((((...))))))).))))))..)))))))))))-3'
Motif MFE = -37.9; z-score = -3.78; 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 = -1.96; 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(+)

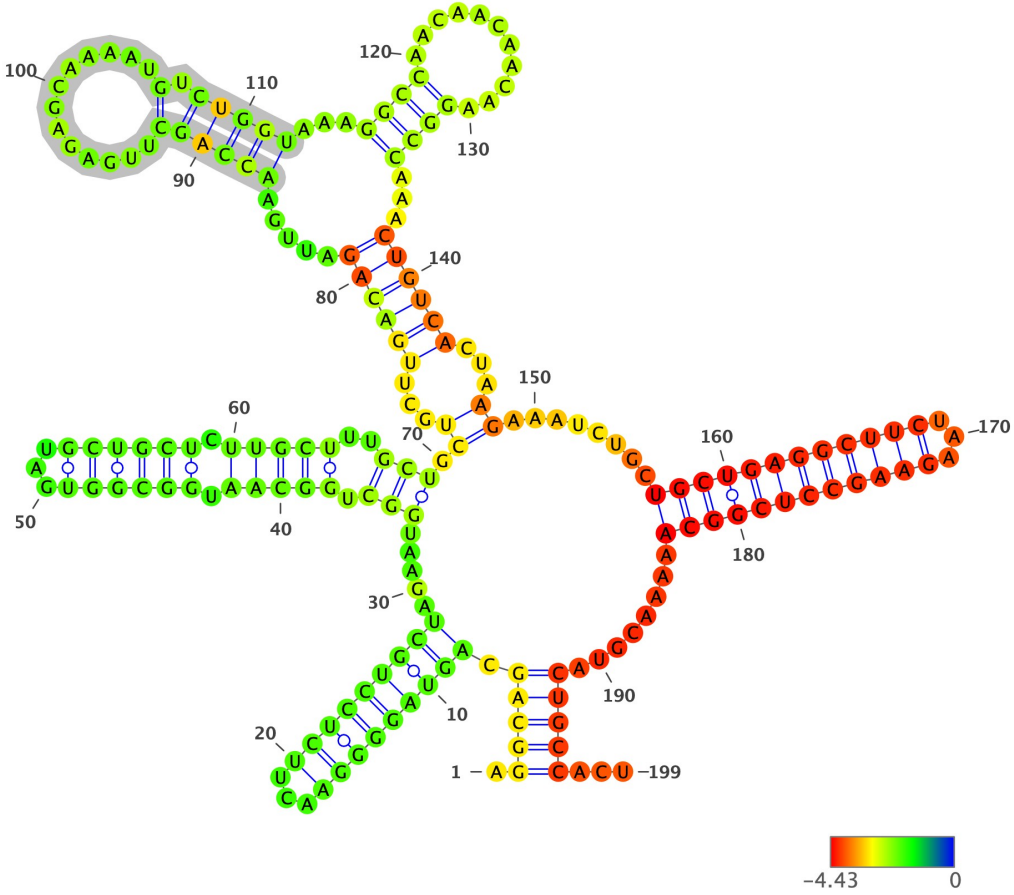
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 508 from nt 28956 to 28981 (nt 87 to 112)

```
5'-ACCAGCUUGAGAGCAAAAUGUCUGGU-3'
5'-(.(.((.............).).).)-3'
Motif MFE = -4.1; z-score = -0.96; ED = 3.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28870 to 29068 (motif highlighted in silver):

```
5'-AGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGG
UAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACU-3
5'-.(((((.((((((((((...)))))))))).....(((.(((((.((((((...)))))).)))))..))).((...((((((.....((((((.............).))))
)...((((...........))))...)))))))...)).......((((((((((((...))))))))))))........))))))...-3'
MFE = -74.5; z-score = -3.9; ED = 15.99
```

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_gp10, 28274-29533(+)

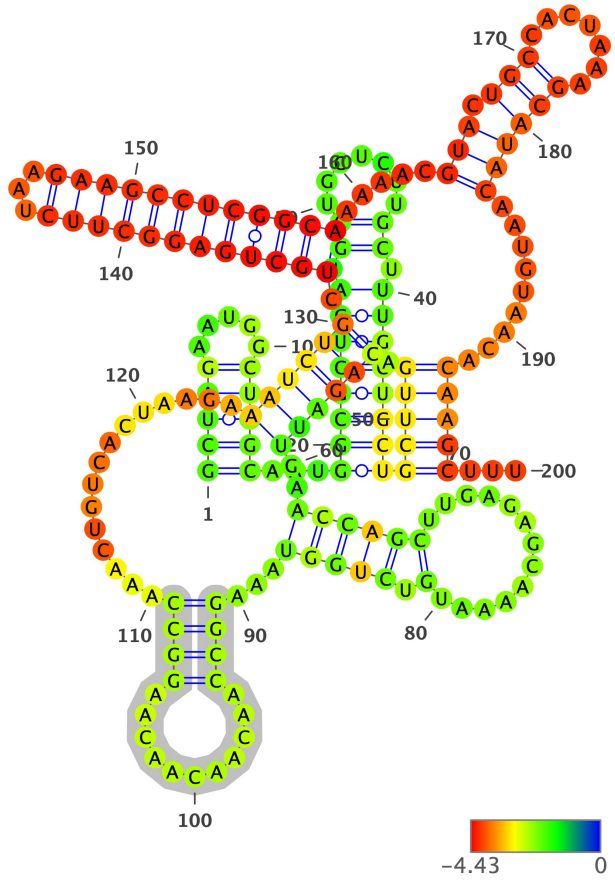
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 509 from nt 28985 to 29003 (nt 91 to 109)

```
5'-GGCCAACAACAACAAGGCC-3'
5'-((((...........))))-3'
Motif MFE = -4.9; z-score = -4.63; ED = 0.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28895 to 29094 (motif highlighted in silver):

```
5'-GCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAA
ACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUU-3
5'-(((((.....)))))...((((((((.((.......)).))))))))(((((.((((((..((((((.............).)))))...((((...........))))..
.............)))))).((((((((((((...)))))))))))).....(((.(((.......))))))..........)))))...-3'
MFE = -61.2; z-score = -3.29; 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(+)

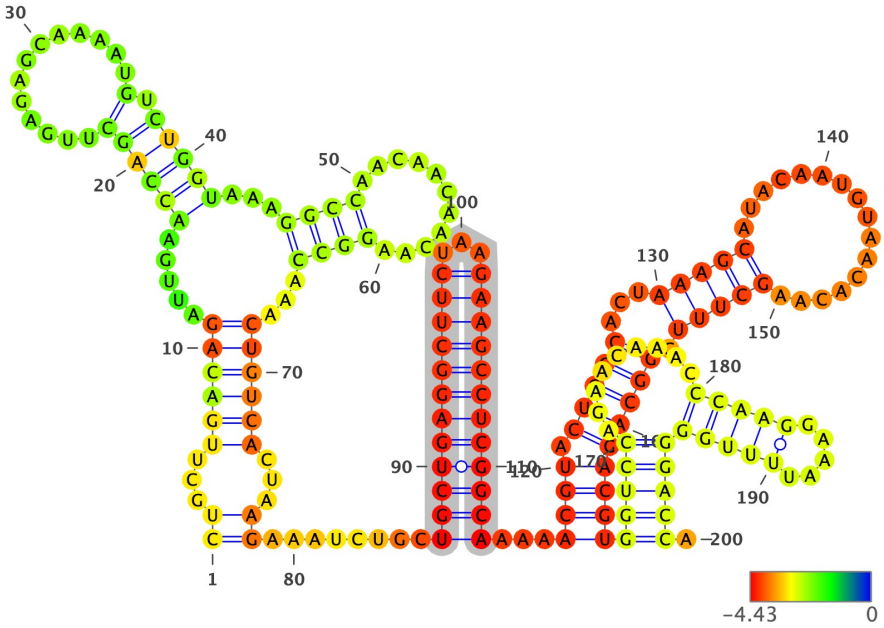
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 510 from nt 29026 to 29052 (nt 87 to 113)

```
5'-UGCUGAGGCUUCUAAGAAGCCUCGGCA-3'
5'-(((((((((((...)))))))))))-3'
Motif MFE = -19.7; z-score = -5.49; 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 = -5.07; 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(+)

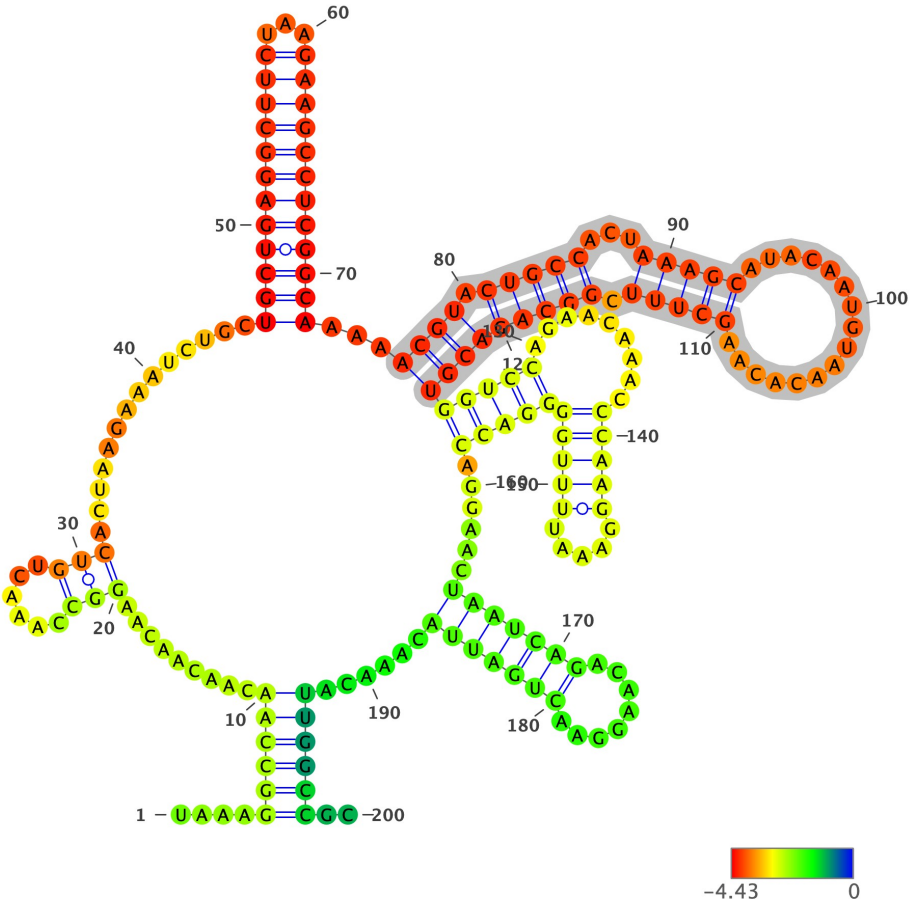
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 511 from nt 29056 to 29104 (nt 76 to 124)

```
5'-ACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGU-3'
5'-((((.(((((...(((((.................))))).)))))))))-3'
Motif MFE = -14.6; z-score = -3.94; 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 = -5.44; 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(+)

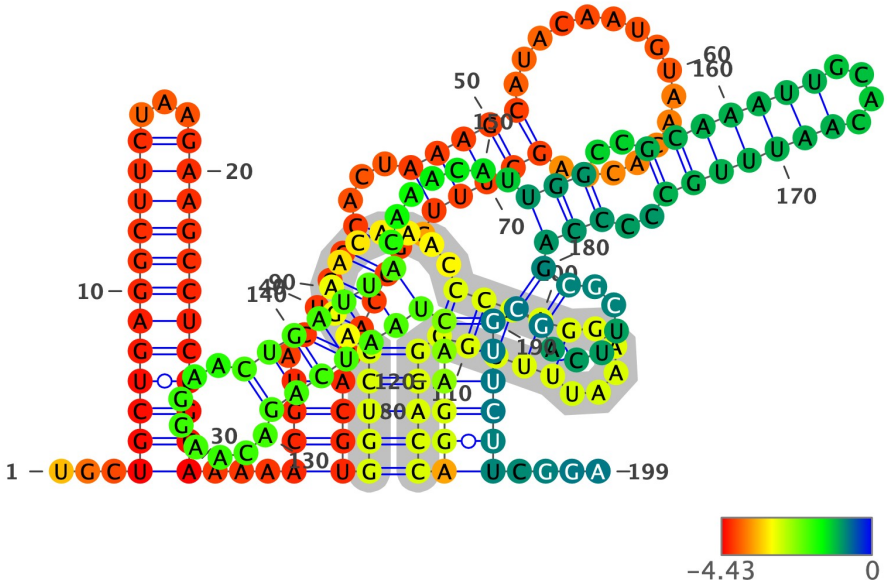
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 512 from nt 29105 to 29138 (nt 83 to 116)

```
5'-GGUCCAGAACAAACCCAAGGAAAUUUUGGGGACC-3'
5'-(((((.........(((((.....)))))))))-3'
Motif MFE = -8.1; z-score = -2.08; ED = 3.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29023 to 29221 (motif highlighted in silver):

```
5'-UGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGG
GGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGA-3
5'-...(((((((((((...)))))))))))...((((.(((((...(((((.................))))).)))))))))(((((.........(((((.....)))))
)))))((((((((((((.......))))))).......(((..(((((((....)))))))..)))((......)))))))....-3'
MFE = -66.0; z-score = -4.79; ED = 11.58
```

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_gp10, 28274-29533(+)

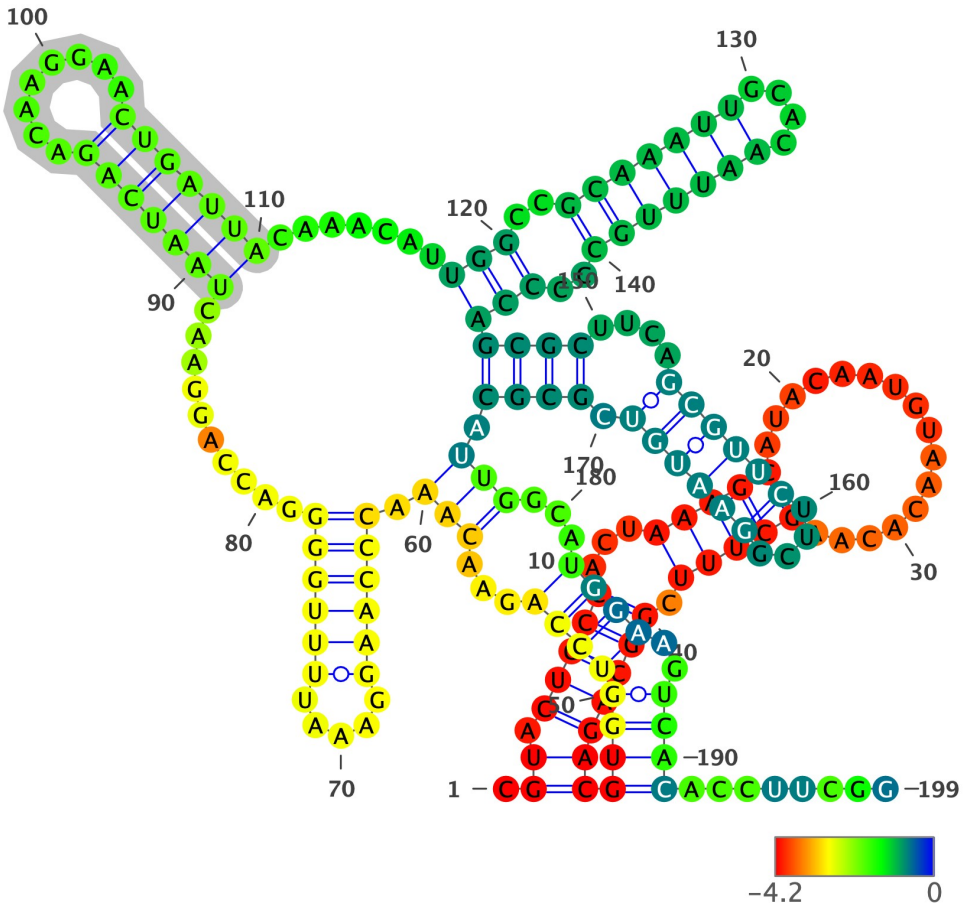
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 513 from nt 29145 to 29166 (nt 89 to 110)

```
5'-UAAUCAGACAAGGAACUGAUUA-3'
5'-(((((((........)))))))-3'
Motif MFE = -5.0; z-score = -5.1; 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 29057 to 29255 (motif highlighted in silver):

```
5'-CGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUAC
AAACAUUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGG-3
5'-.((.(((((...(((((.................))))).)))))))((((((((...(((.((((((.....))))))..........(((((((........)))))))).
......(((..(((((((....)))))))..)))((((....((((((....))))))).)))).)))...))))..))))........-3'
MFE = -53.1; z-score = -1.56; ED = 28.2
```

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_gp10, 28274-29533(+)

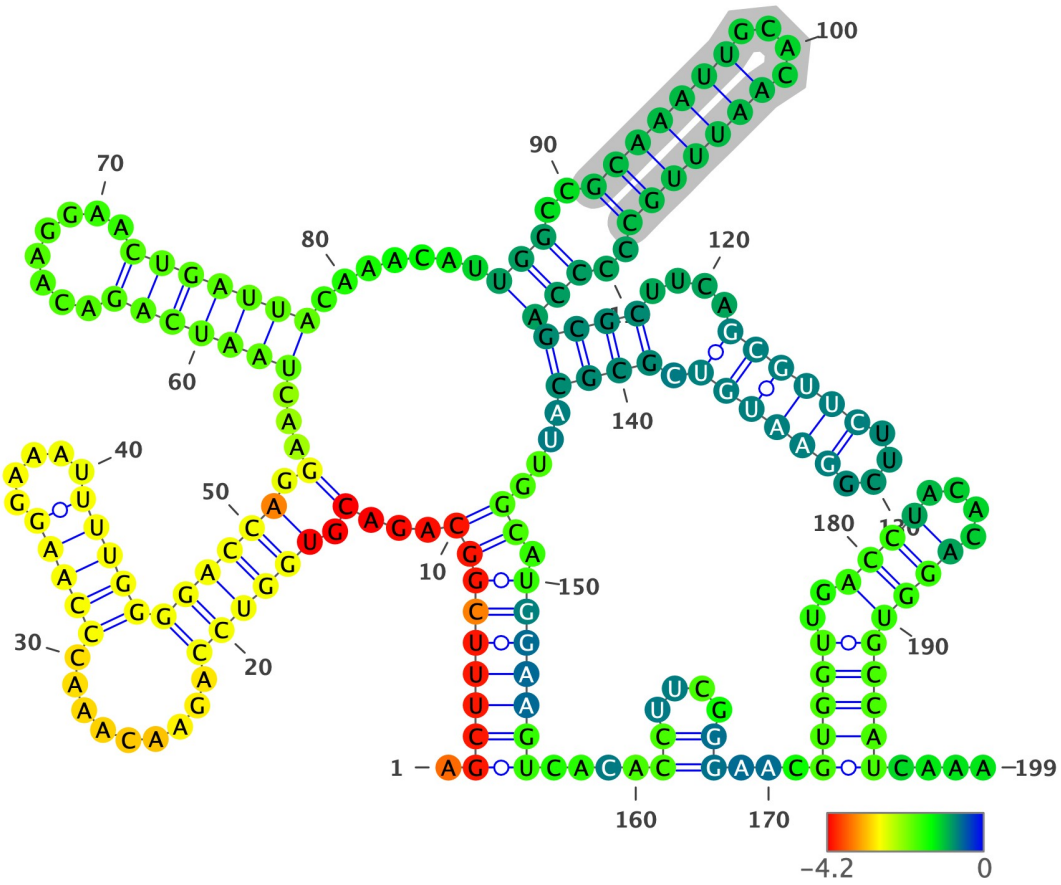
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 514 from nt 29179 to 29196 (nt 91 to 108)

```
5'-GCAAAUUGCACAAUUUGC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.0; z-score = -4.07; ED = 0.78
```



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 29089 to 29287 (motif highlighted in silver):

```
5'-AGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUUUGCCCC
CAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAUCAAA-3
5'-.((((((((((...(.((((((.........(((((.....)))))))))))).)...(((((((........)))))))).......(((..(((((((....)))))))..)
))))((....((((((....)))))).))))....)).)))))))....((....))...((((..((((....))))))))).....-3'
MFE = -54.9; z-score = -0.96; ED = 42.84
```

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_gp10, 28274-29533(+)

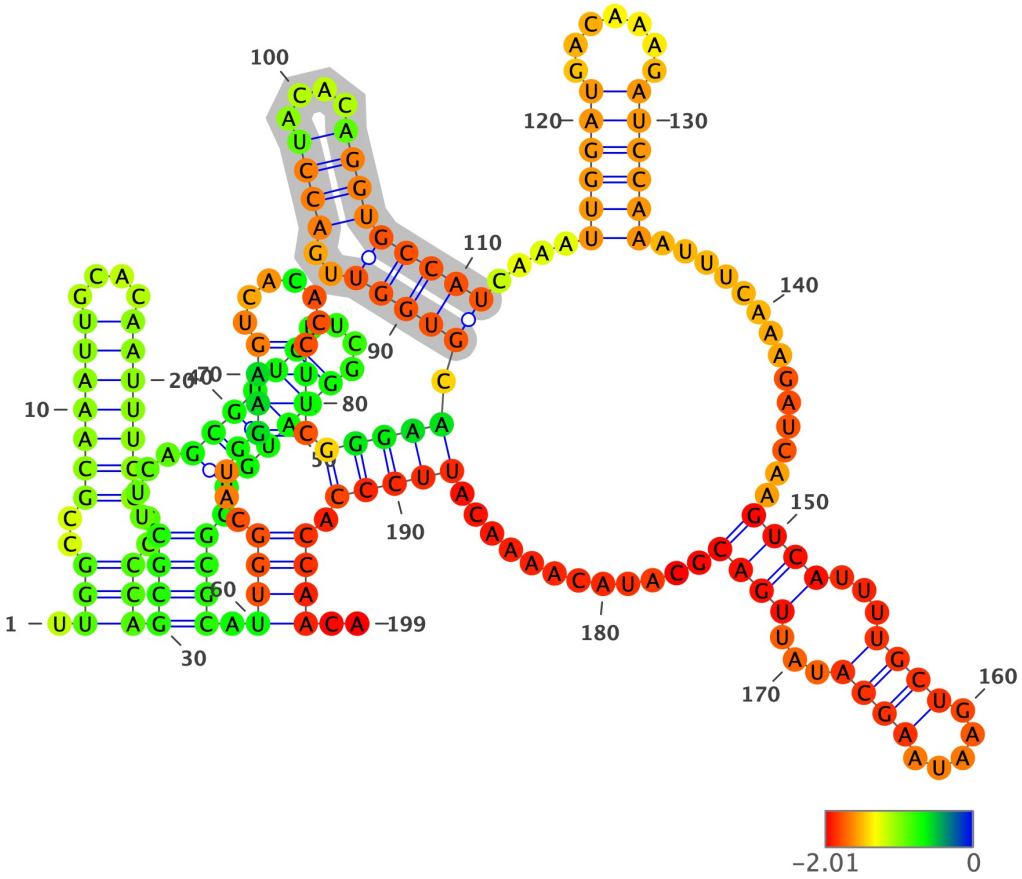
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 515 from nt 29260 to 29283 (nt 88 to 111)

```
5'-GUGGUUGACCUACACAGGUGCCAU-3'
5'-((((((..(((.....)))))))))-3'
Motif MFE = -7.3; z-score = -1.62; 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 = -2.19; ED = 21.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

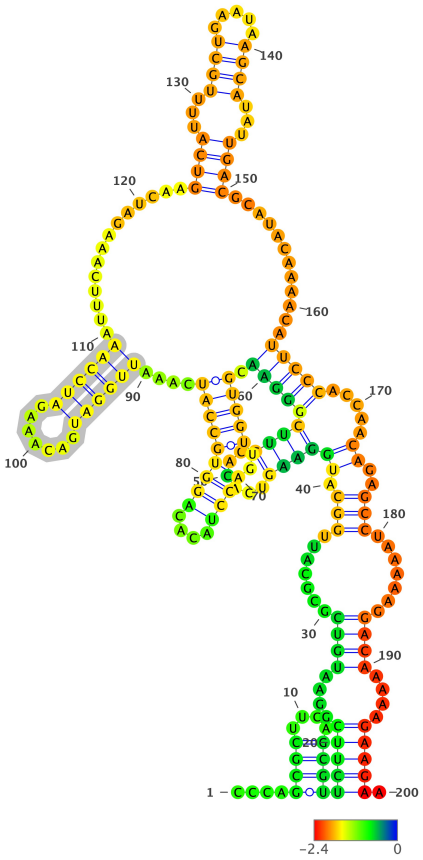
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 516 from nt 29288 to 29306 (nt 91 to 109)

```
5'-UUGGAUGACAAAGAUCCAA-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -4.62; 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 = -2.41; 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(+)

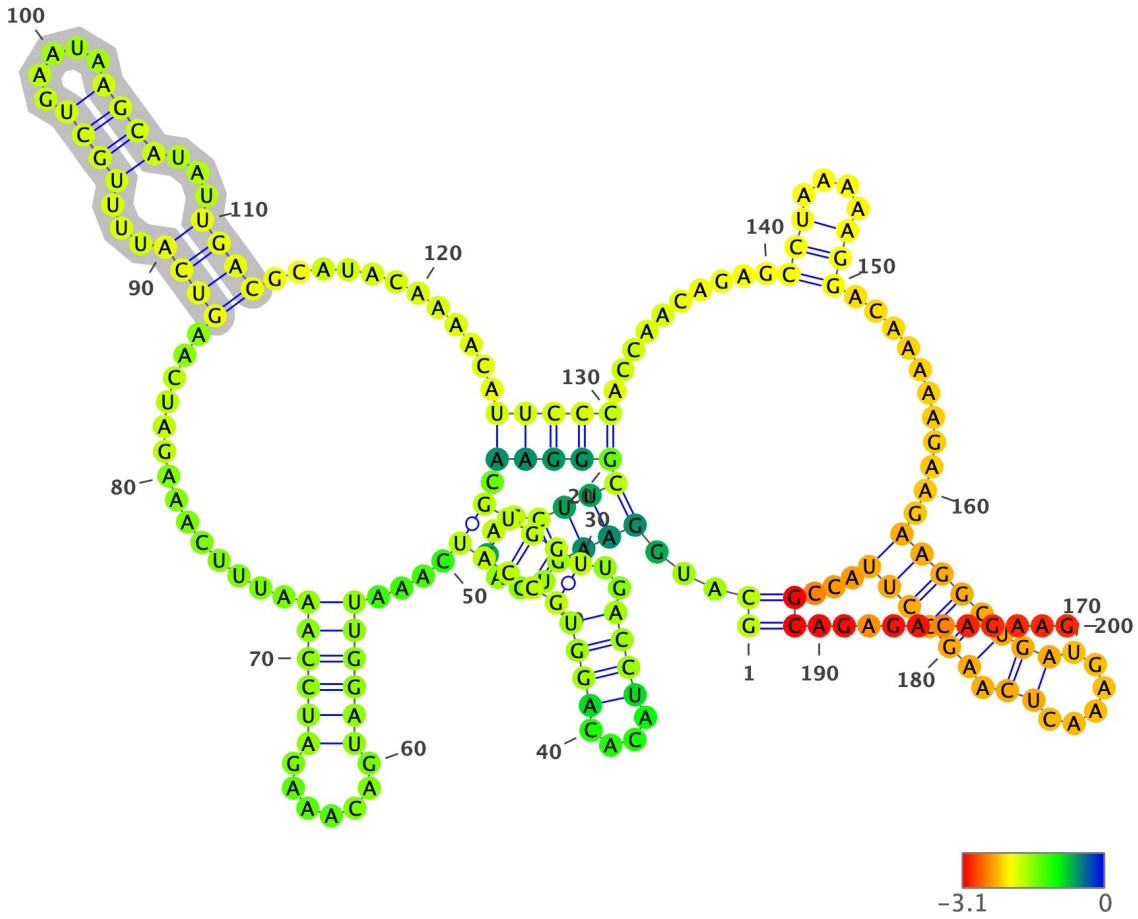
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 517 from nt 29321 to 29347 (nt 87 to 113)

```
5'-GUCAUUUUGCUGAAUAAGCAUAUUGAC-3'
5'-((((...((((.....))))...))))-3'
Motif MFE = -7.9; z-score = -3.43; 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 = -2.07; 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(+)

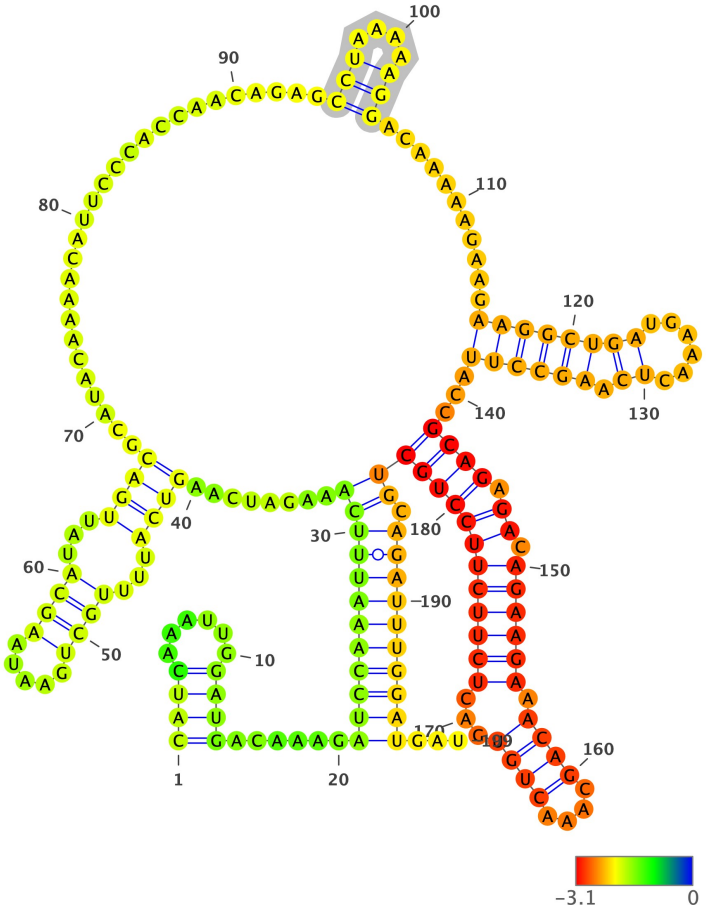
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 518 from nt 29375 to 29384 (nt 95 to 104)

```
5'-CCUAAAAAGG-3'
5'-(((....)))-3'
Motif MFE = -0.3; z-score = -10.1; 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 = -4.59; 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(+)

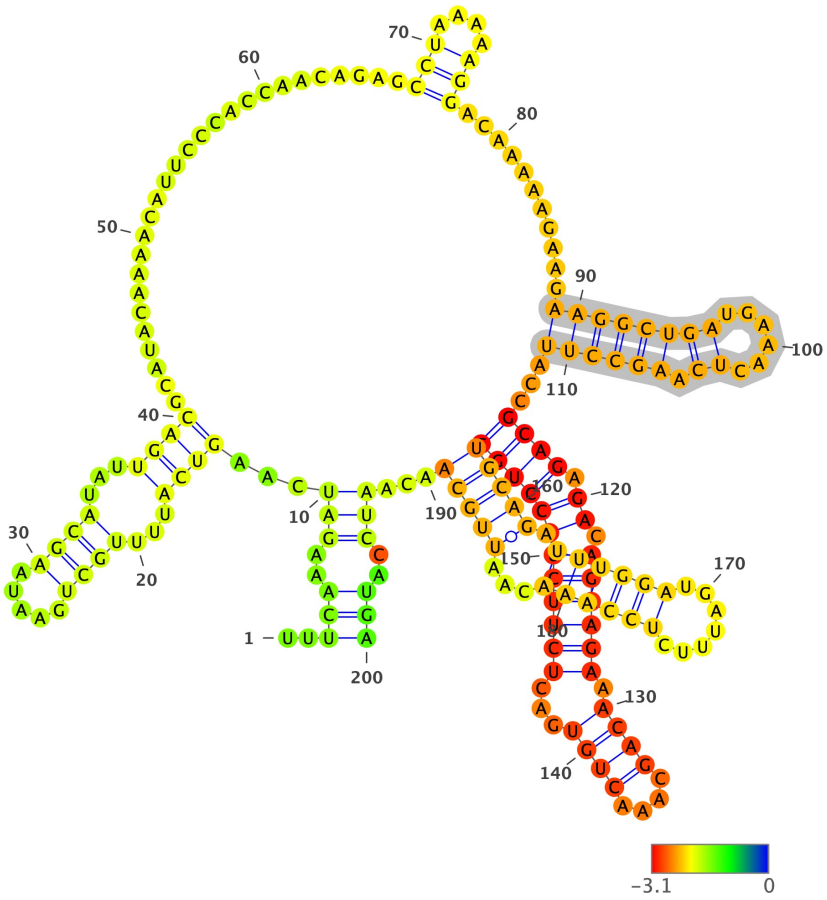
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 519 from nt 29396 to 29418 (nt 89 to 111)

```
5'-AAGGCUGAUGAAACUCAAGCCUU-3'
5'-((((((((......)).))))))-3'
Motif MFE = -6.9; z-score = -3.18; 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 = -3.68; 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(+)

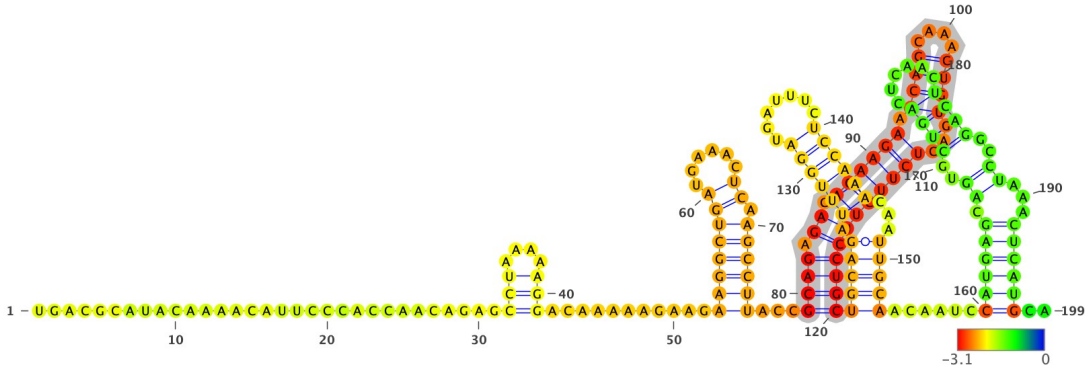
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 520 from nt 29422 to 29463 (nt 79 to 120)

```
5'-GCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGC-3'
5'-((((.((.(((((((.((((....))))...))))))))))))-3'
Motif MFE = -14.7; z-score = -4.09; 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 = -3.31; 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(+)

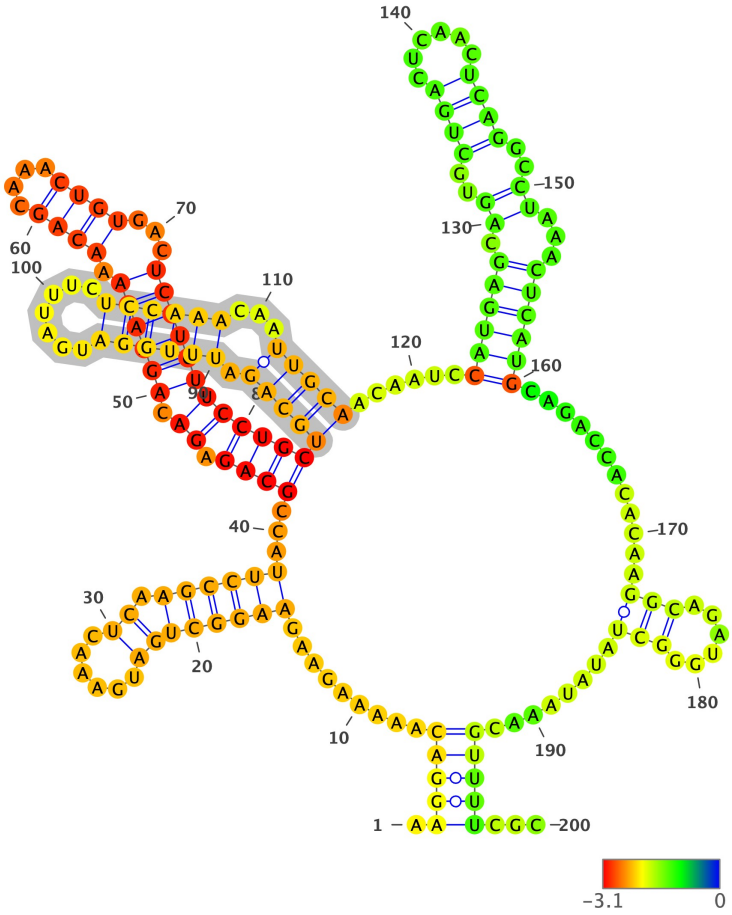
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 521 from nt 29464 to 29496 (nt 84 to 116)

```
5'-UGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCA-3'
5'-(((((.((((((.......))))))...)))))-3'
Motif MFE = -7.9; z-score = -2.78; 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 = -2.75; 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(+)

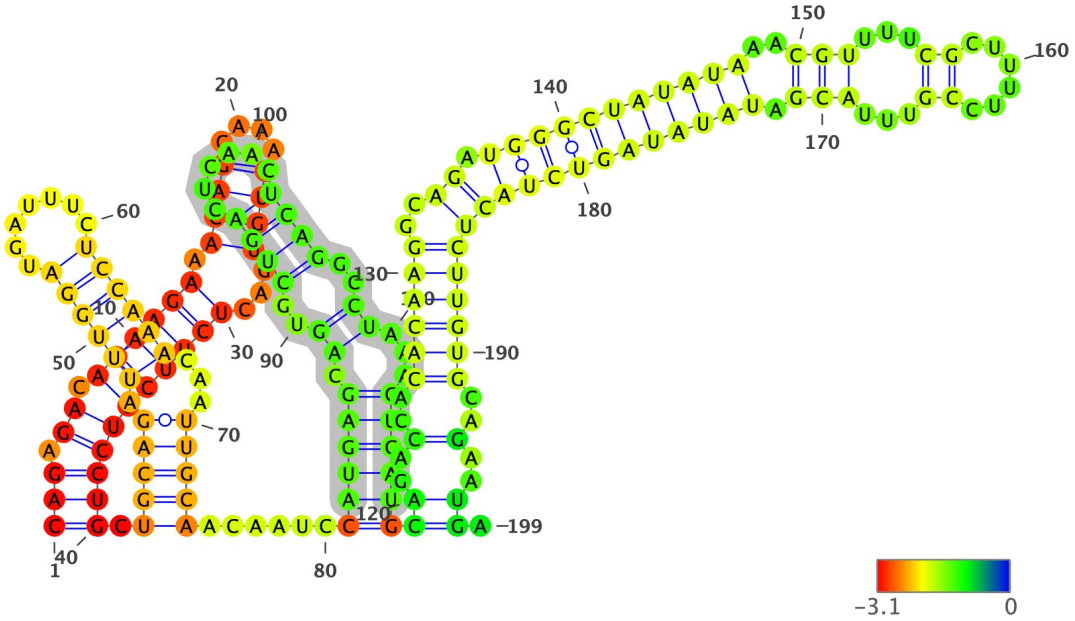
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

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 522 from nt 29504 to 29539 (nt 82 to 117)

```
5'-AUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAU-3'
5'-(((((.((..((((.....)))))..))...)))))-3'
Motif MFE = -8.1; z-score = -1.83; ED = 2.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29423 to 29621 (motif highlighted in silver):

```
5'-CAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAA
ACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGA-3
5'-(((.((.((((((.((((....)))).)...)))))))))).(((((.((((((.......))))))...)))))......((((((.((..((((......)))).))..))..
.)))))))((..(..(((((((..((.((((((((((..(((...((......))...)))).)))))))))))))))))..)..)).-3'
MFE = -53.2; z-score = -2.9; 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(+)

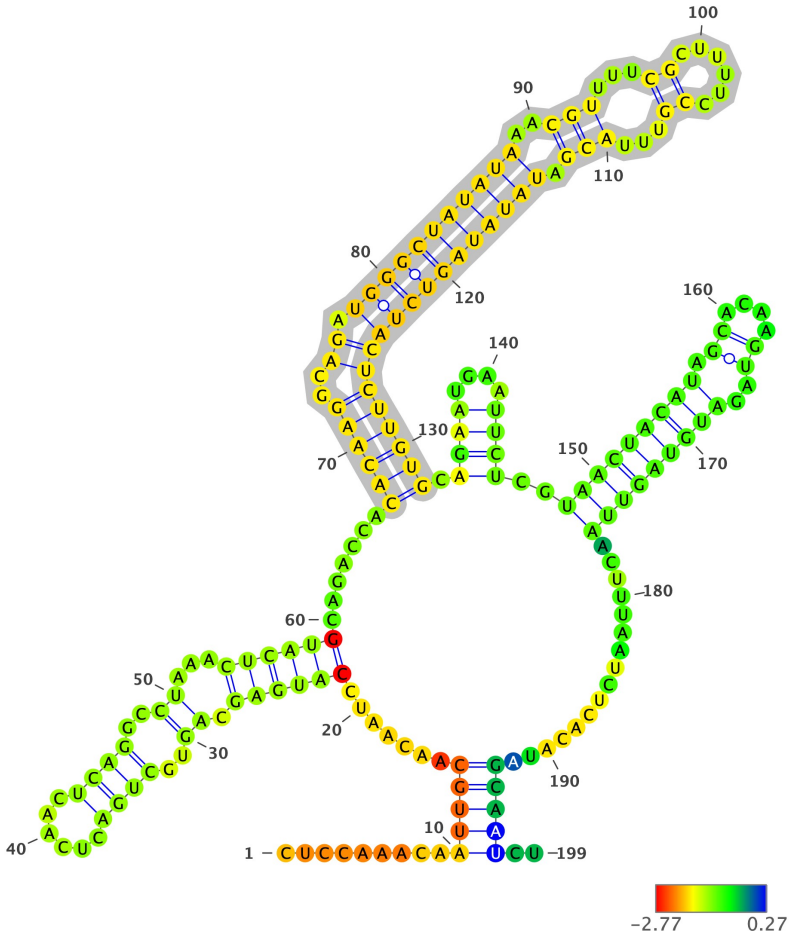
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

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 523 from nt 29548 to 29613 (nt 67 to 132)

```
5'-CACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUG-3'
5'-((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))-3'
Motif MFE = -19.7; z-score = -2.87; 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 = -3.18; 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(+)

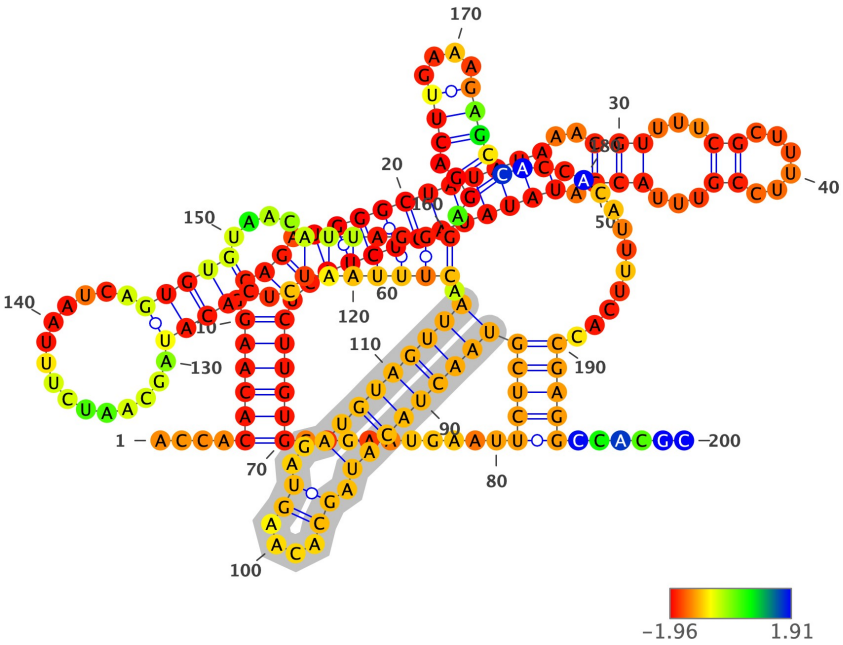
Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

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 524 from nt 29629 to 29657 (nt 86 to 114)

```
5'-UAACUACAUAGCACAAGUAGAUGUAGUUA-3'
5'-((((((((((.((....))..)))))))))-3'
Motif MFE = -8.5; z-score = -3.2; 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 = -1.1; ED = 35.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 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"]