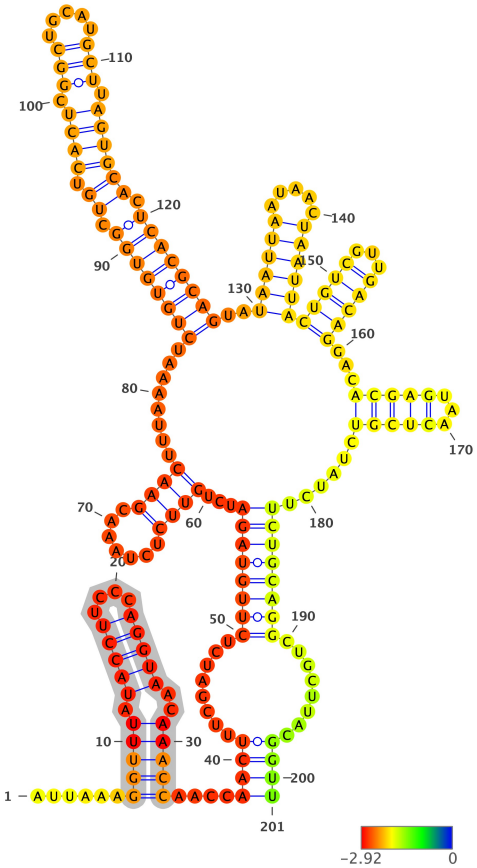
NC_045512.2 (forward strand): Structure number 1 from nt 7 to 33 (nt 7 to 33)

```
5'-GGUUUAUACCUUCCCAGGUAACAAACC-3'
5'-(((...(((((....)))))....)))-3'
Motif MFE = -7.0; z-score = -3.48; 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 = -2.74; 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(+)

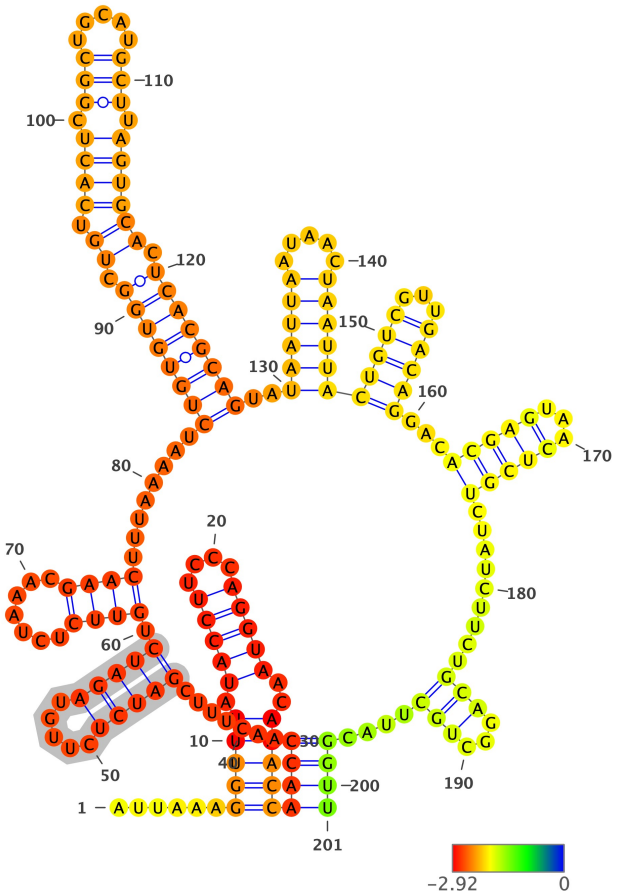
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 = -2.45; 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 = -2.98; 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(+)

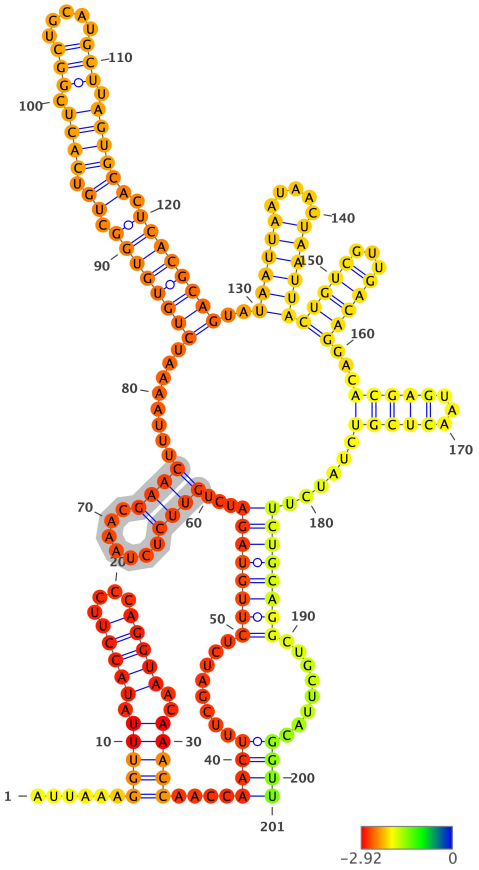
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 = -2.72; 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(+)

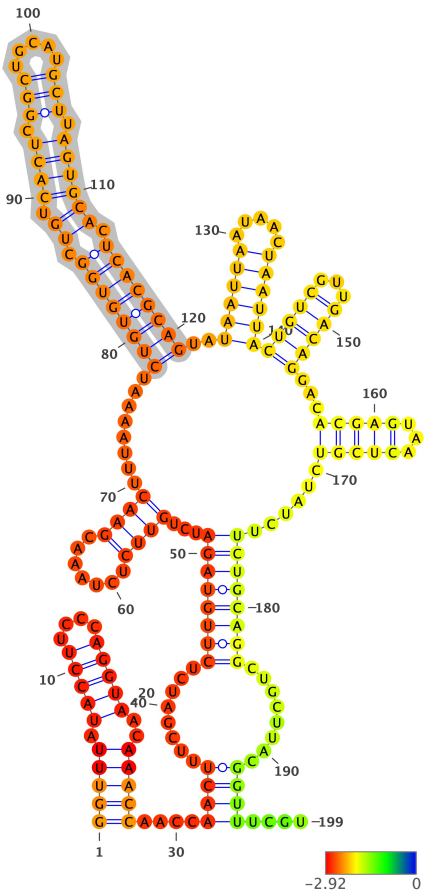
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 = -3.43; 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 = -2.89; 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(+)

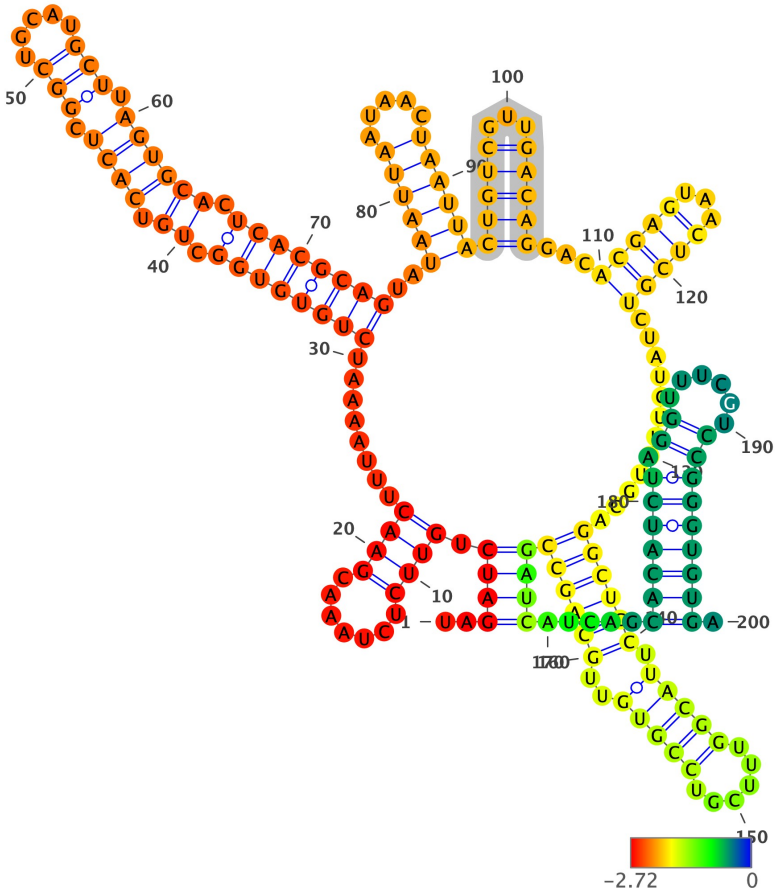
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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 147 to 159 (nt 94 to 106)

```
5'-CUGUCGUUGACAG-3'
5'-(((((...)))))-3'
Motif MFE = -3.4; z-score = -4.07; 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 54 to 253 (motif highlighted in silver):

```
5'-UAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACAC
GAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGA-3
5'-..((((.((((.......)))).........((((((((.((.((((.(((.....))).)))))).)))))))..((((((.....))))))(((((...)))))...((
(((...)))))............((((((.(((((......)))))..))))))))))).....(((((((.((......)))))))))).-3'
MFE = -66.3; z-score = -3.21; ED = 8.42
```

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(+)

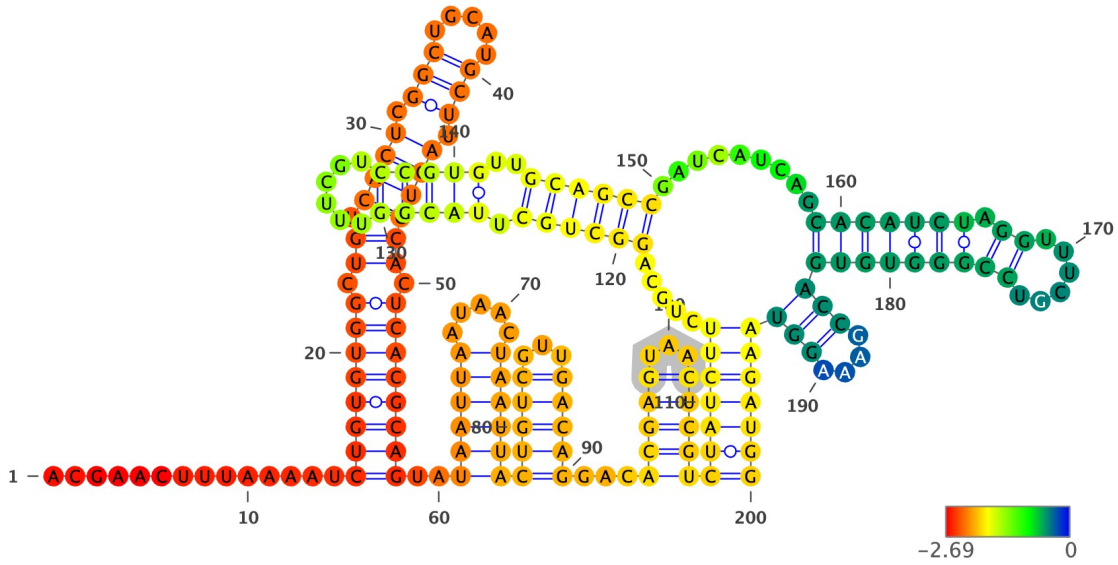
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--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 167 to 171 (nt 98 to 102)

```
5'-GUAAC-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 70 to 269 (motif highlighted in silver):

```
5'-ACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUC
UUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGG-3
5'-..............((((((((.((.((((.(((.....))).)))))).))))))))..((((((.....))))))(((((...)))))...(((((...)))))(((((
((.....((((((.(((((......)))))..))))))).........(((((((.((......)))))))))(((....)))))))))))-3'
MFE = -65.2; z-score = -2.9; ED = 18.03
```

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 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(+)

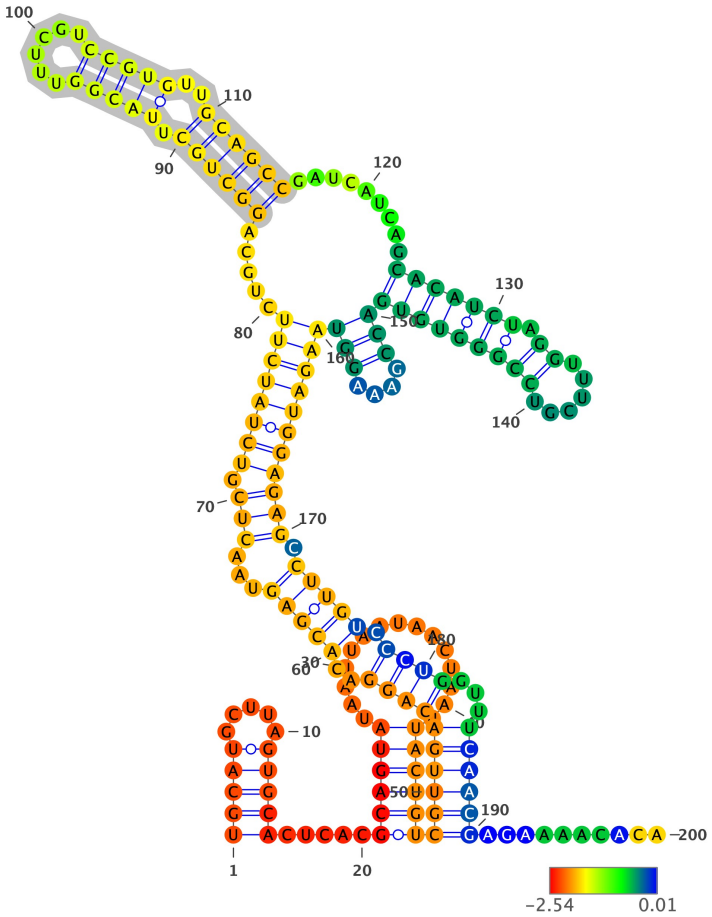
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 7 from nt 188 to 218 (nt 85 to 115)

```
5'-GGCUGCUUACGGUUUCGUCCGUGUUGCAGCC-3'
5'-((((((.(((((.....)))))..))))))-3'
Motif MFE = -17.2; z-score = -4.44; 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 = -2.75; 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(+)

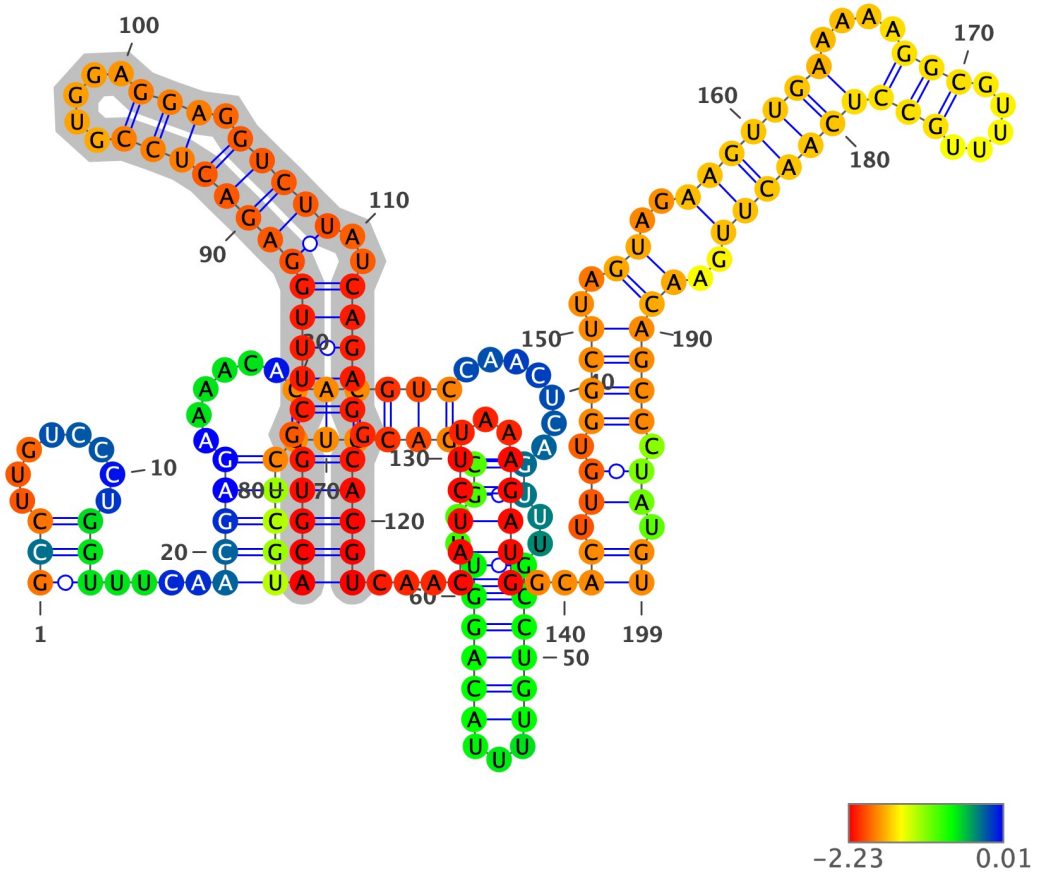
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 8 from nt 349 to 394 (nt 77 to 122)

```
5'-ACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGU-3'
5'-(((((.(((((((((((((.....))).)))))..)))))).)))))-3'
Motif MFE = -22.1; z-score = -4.43; ED = 3.03
```



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

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

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

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

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

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

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

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

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

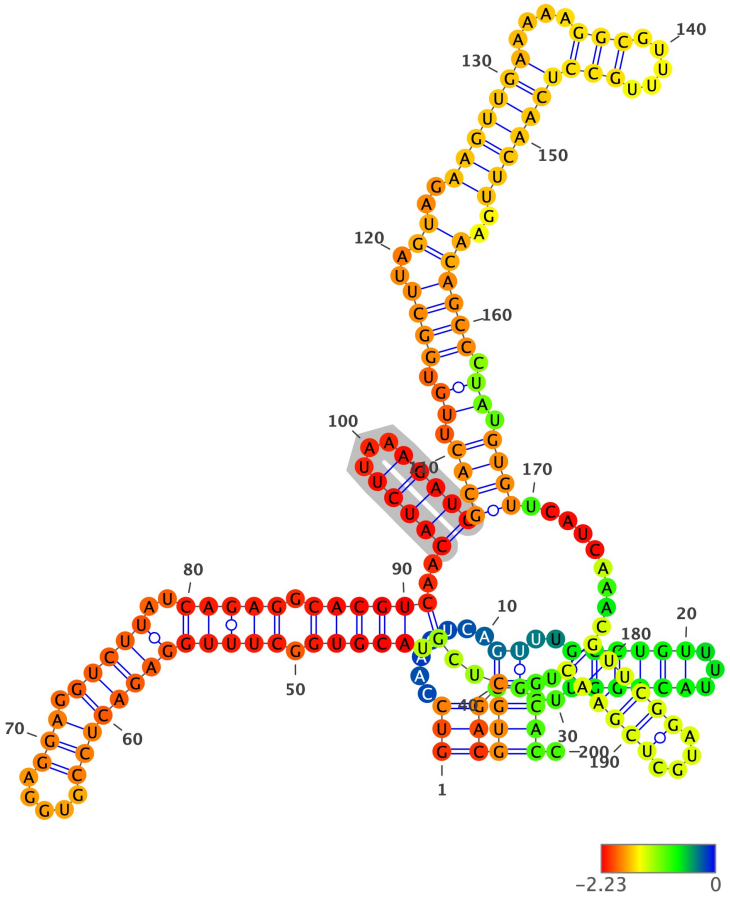
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 9 from nt 398 to 410 (nt 94 to 106)

```
5'-CAUCUUAAAGAUG-3'
5'-(((((...)))))-3'
Motif MFE = -1.8; z-score = -9.74; 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 = -2.21; 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(+)

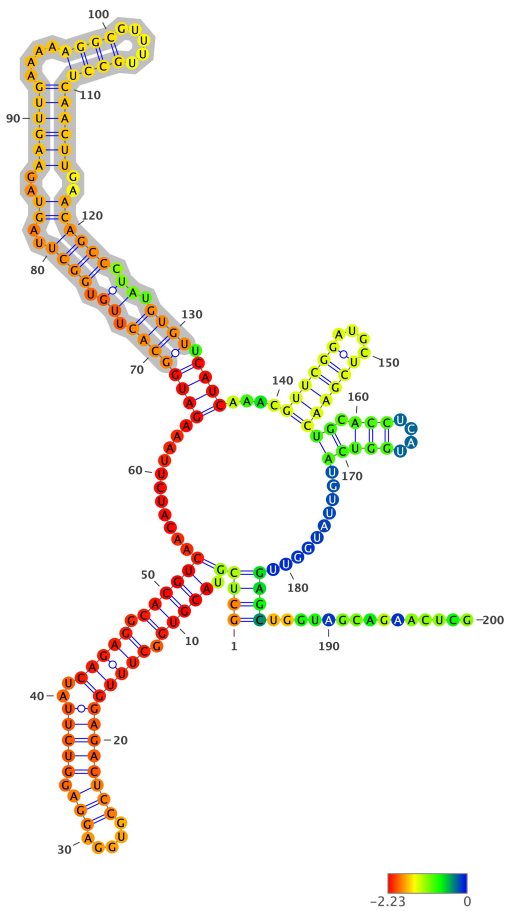
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 10 from nt 411 to 473 (nt 69 to 131)

```
5'-GCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGU-3'
5'-((((....((((..((..((((((....((((.....))))))))))..))))))....))))-3'
Motif MFE = -20.8; z-score = -3.15; ED = 3.51
```



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

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

```
5'-GCUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCA
ACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCG-3
5'-(((((.(((((.(((((((((((((.....))).)))))..)))))).))))))...........((((((((.((.((((..((..((((((....((((.....))))))
))))..)))))).)).)))).))))....((((((....))))))((.(((....)))))..........))))................-3'
MFE = -63.0; z-score = -1.57; ED = 26.91
```

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(+)

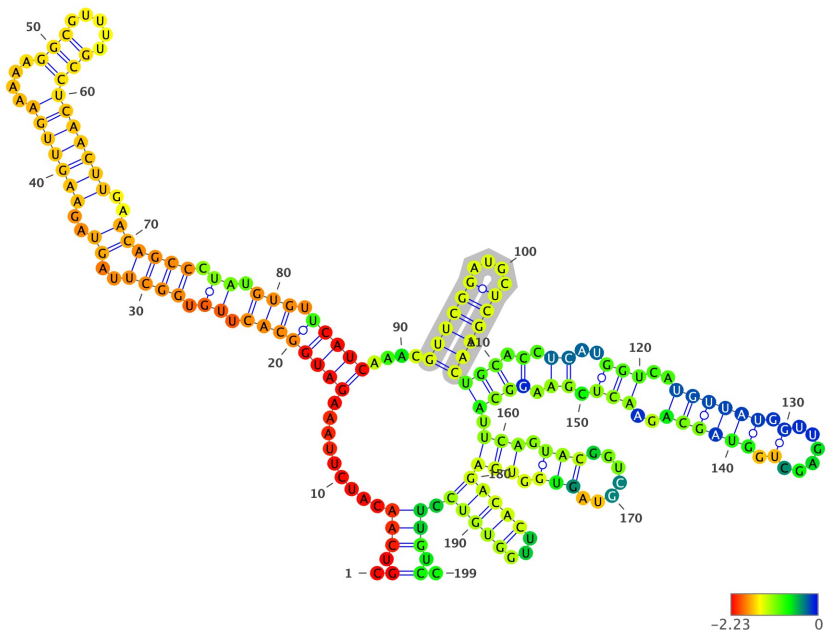
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 11 from nt 483 to 498 (nt 92 to 107)

```
5'-GUUCGGAUGCUCGAAC-3'
5'-((((((....))))))-3'
Motif MFE = -4.3; z-score = -2.22; 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 = -0.45; 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(+)

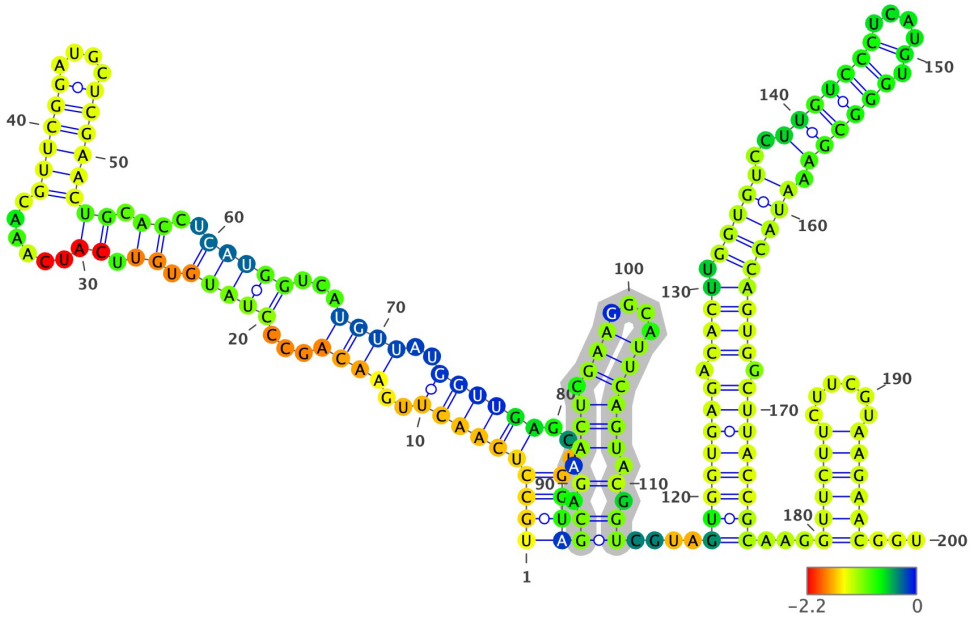
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 12 from nt 533 to 559 (nt 87 to 113)

```
5'-GCAGAACUCGAAGGCAUUCAGUACGGU-3'
5'-((...(((.(((....))))))...))-3'
Motif MFE = -2.0; z-score = 0.61; ED = 3.15
```



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 447 to 646 (motif highlighted in silver):

```
5'-UGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACG
GUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGU-3
5'-((((((((((..((((...(((((.((.((......((((((....))))))))).))..)))))...))))..))))))...))))((.(.(((.(((....))))))).).
))....((((((((.((((.(((((..(((((((....).))))))).)))))))))).))))))))...((((((......))))))...-3'
MFE = -59.0; z-score = -1.61; ED = 27.36
```

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

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

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

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

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

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

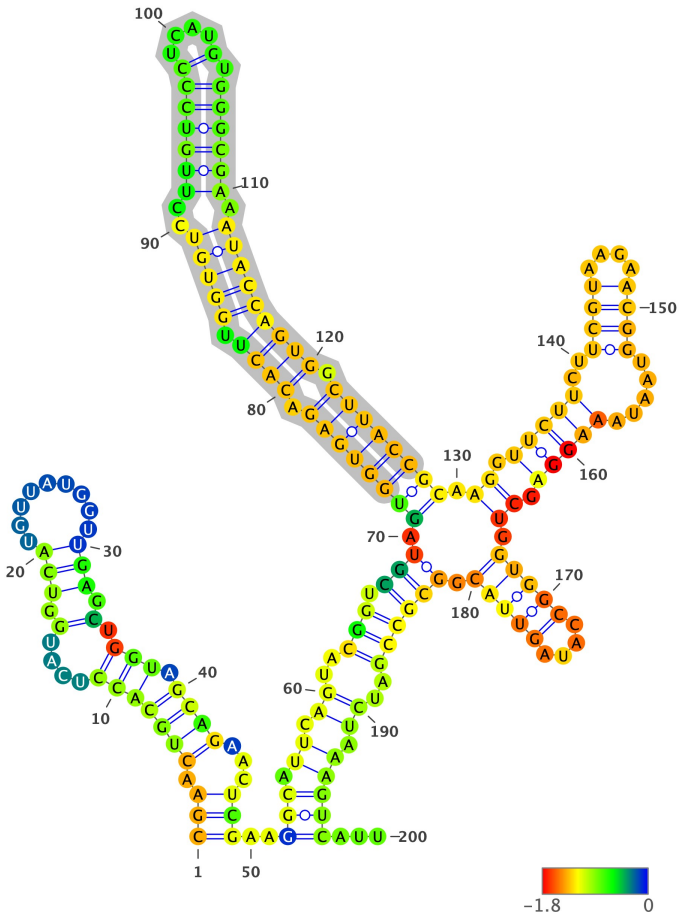
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 13 from nt 566 to 620 (nt 73 to 127)

```
5'-GGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACC-3'
5'-((((((.(((..(((((.....................)))))).))).))))))-3'
Motif MFE = -24.3; z-score = -3.43; ED = 5.02
```



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

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

```
5'-CGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAA
AUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUU-3
5'-(((.(((((((....(.(((.........))).).))).))))...)))..(((.((.((..(((.(((.((((((((.((((.(((((..(((((((....).))))))).
))))))))).)))))))).((.(((((..((((....)))).....))))).)).(((((....)))))).))))))..)).)))))...-3'
MFE = -59.2; z-score = -0.16; ED = 60.55
```

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

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

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

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

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

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

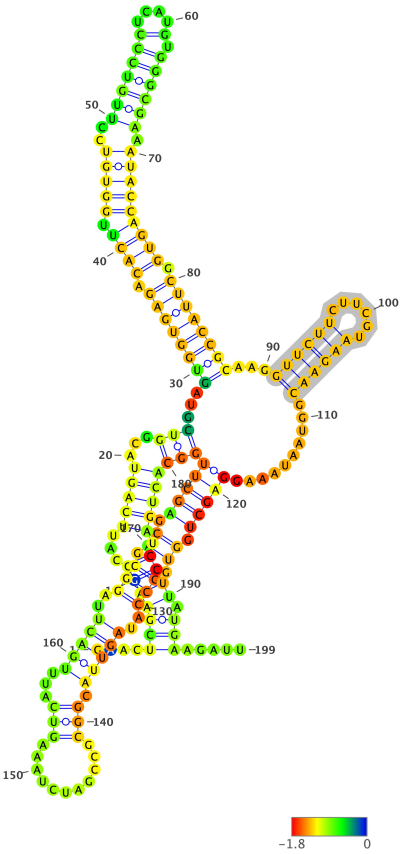
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 14 from nt 626 to 643 (nt 91 to 108)

```
5'-GUUCUUCUUCGUAAGAAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -3.05; 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 = -2.37; 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(+)

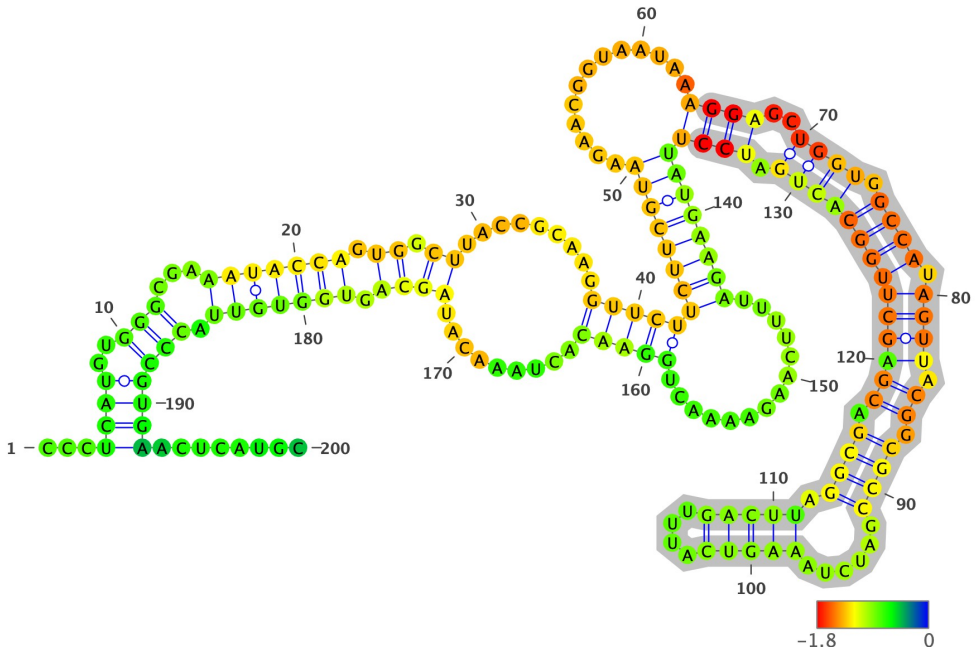
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 15 from nt 653 to 723 (nt 65 to 135)

```
5'-GGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUUAGGCGACGAGCUUGGCACUGAUCC-3'
5'-((........((((.(((..((.((((.....................)))).)).)))))))......))-3'
Motif MFE = -23.8; z-score = -1.41; ED = 6.33
```



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

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

```
5'-CCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUUUGACUU
AGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGC-3
5'-...((((..(((...(((((((.((.((.........((((((((((((.............((((..((((.((((.((((.((.((((......(((((....)))))
.)))).))))))))))))).))))))))))))..............)))))........)))).)))))))).)))))))........-3'
MFE = -52.6; z-score = -1.21; ED = 47.41
```

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

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

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

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

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

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

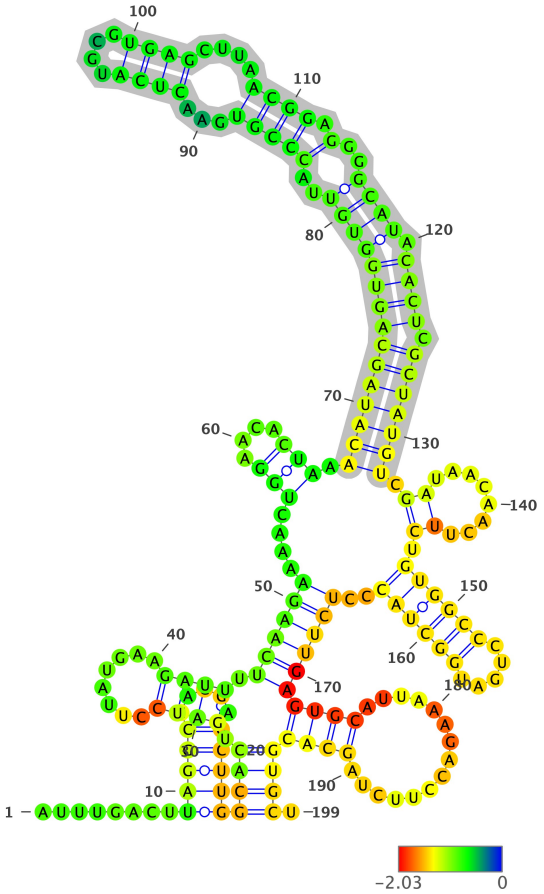
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 16 from nt 757 to 822 (nt 67 to 132)

```
5'-ACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGU-3'
5'-(((((((((((.........................................)))).)))))))-3'
Motif MFE = -26.1; z-score = -3.41; 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 = -0.59; 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(+)

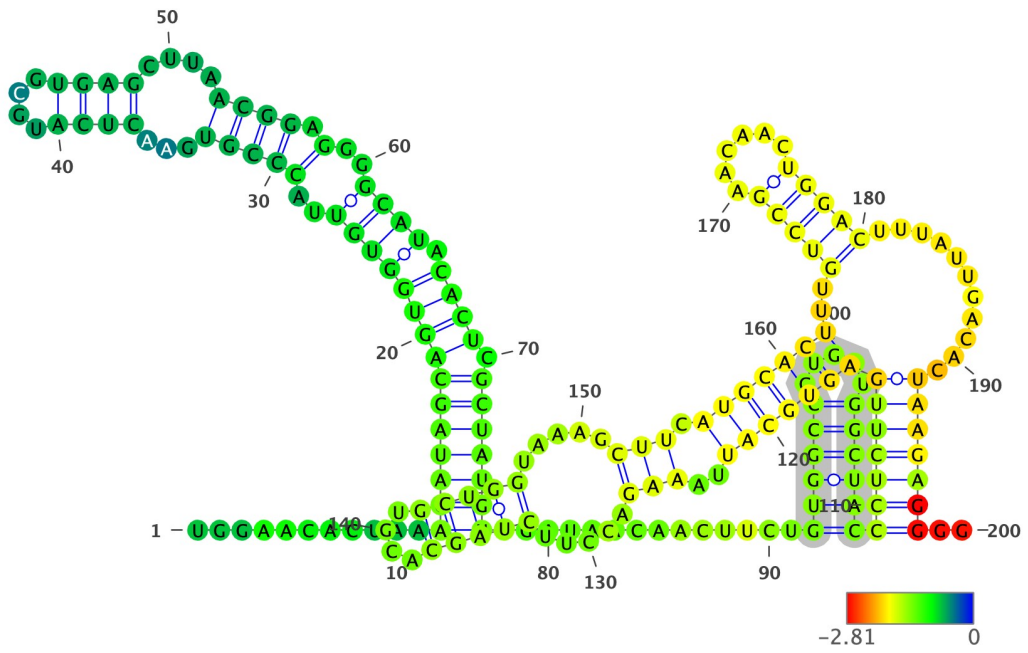
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 17 from nt 837 to 853 (nt 92 to 108)

```
5'-GUGGCCCUGAUGGCUAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.1; z-score = -3.13; 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 = -2.47; 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(+)

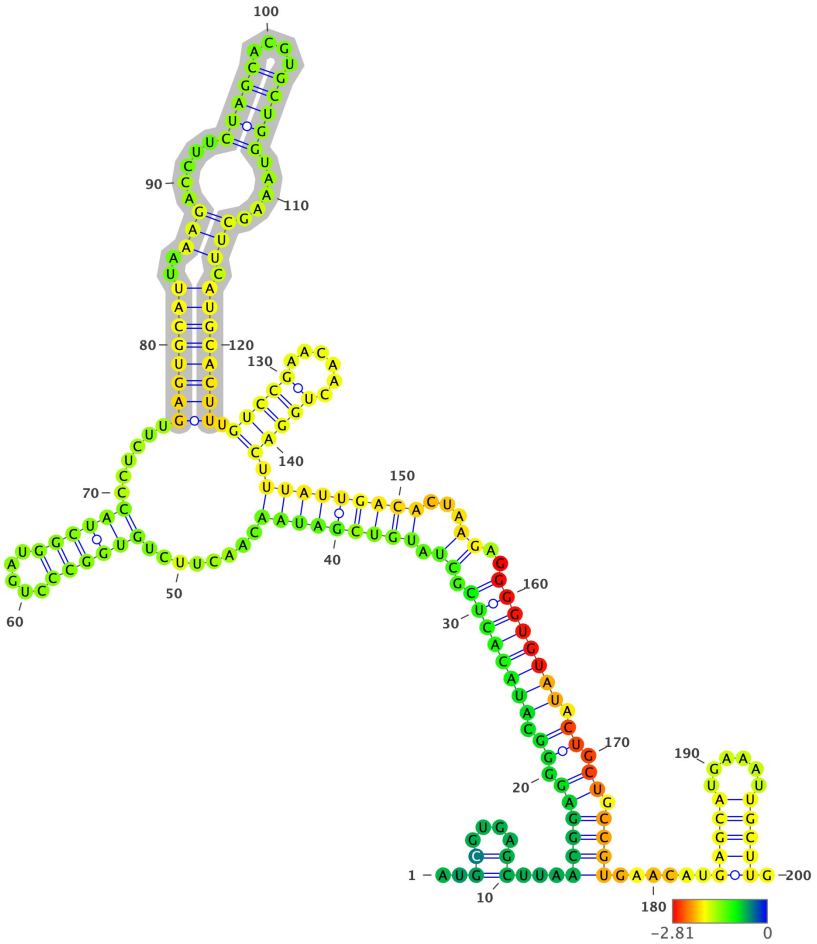
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 18 from nt 860 to 908 (nt 76 to 124)

```
5'-GAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACUU-3'
5'-(((((((..(((.....(((((....)))))).....))).)))))))-3'
Motif MFE = -16.5; z-score = -3.26; ED = 2.89
```



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

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

```
5'-AUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAA
GCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUG-3
5'-..((....)).....((((((.((.(((((((((.(((((((.....)))))))).....((((((((..(((.....(((((....)))))).....
.))).)))))))).(((((.....)))))..))))))))...)).).))))))).))).))).))))).....(((((.....)))))).-3'
MFE = -65.6; z-score = -2.76; ED = 11.41
```

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

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

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

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

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

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

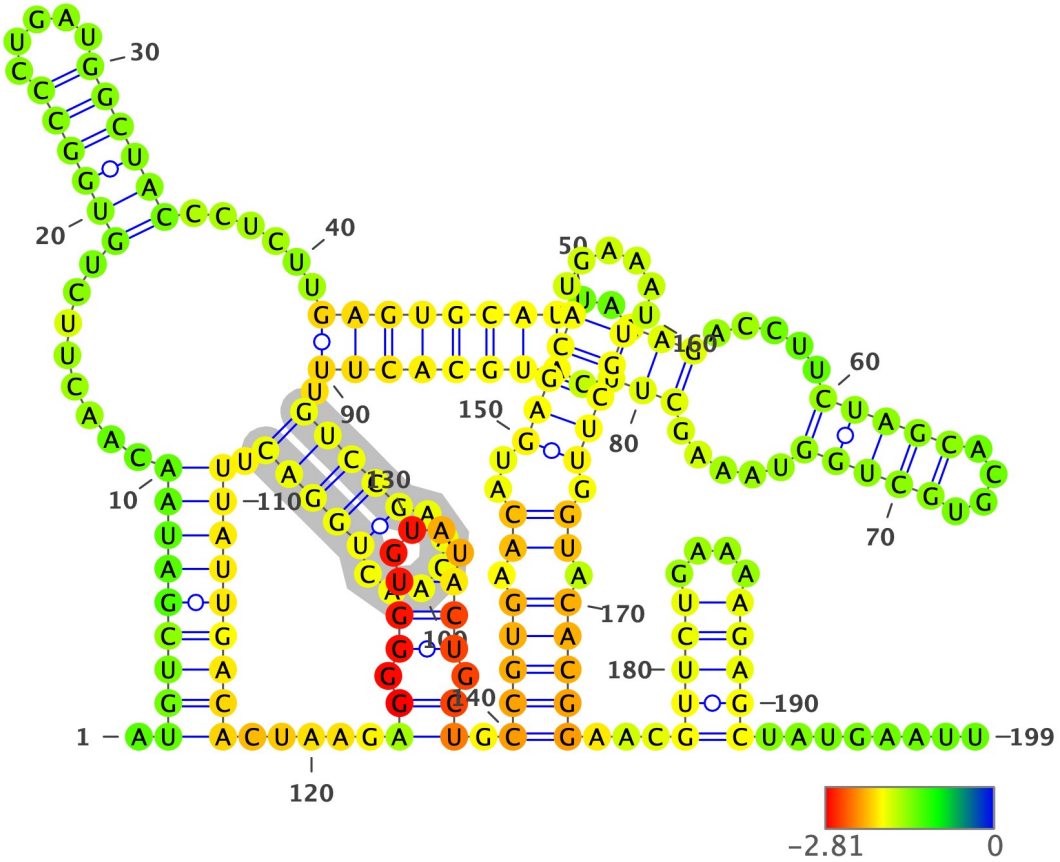
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 19 from nt 910 to 925 (nt 92 to 107)

```
5'-GUCCGAACAACUGGAC-3'
5'-((((........))))-3'
Motif MFE = -4.4; z-score = -3.16; 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 = -2.7; ED = 11.12
```

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

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

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

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

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

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

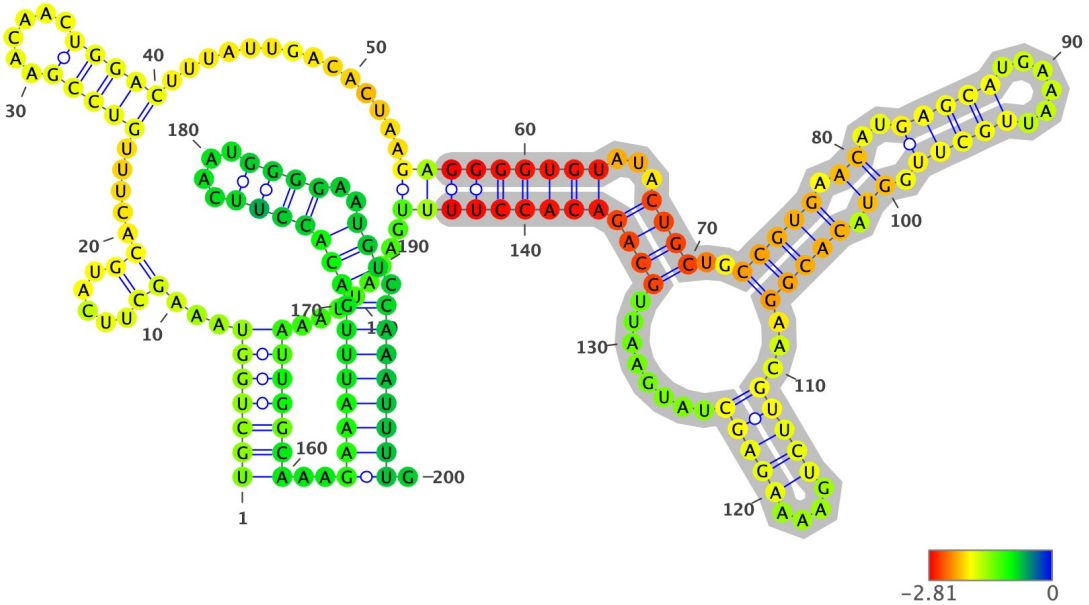
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 20 from nt 942 to 1028 (nt 57 to 143)

```
5'-GGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACGUUCUGAAAAGAGCUAUGAAUUGCAGACACCUU-3'
5'-(((((((...((((..(((((.((..(((((......))))).)).)))))...(((((....)))))........)))))))))))-3'
Motif MFE = -30.6; z-score = -3.71; ED = 1.96
```



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

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

```
5'-UGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACG
UUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUG-3
5'-(((((((...((.....)).....(((((......)))))..............(((((((((...((((..(((((.((..(((((......))))).)).)))))...(
((((....)))))........))))))))))))).........)))))))..((((((((((((((....))))..))).)))))))).-3'
MFE = -52.0; z-score = -1.81; ED = 16.45
```

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(+)

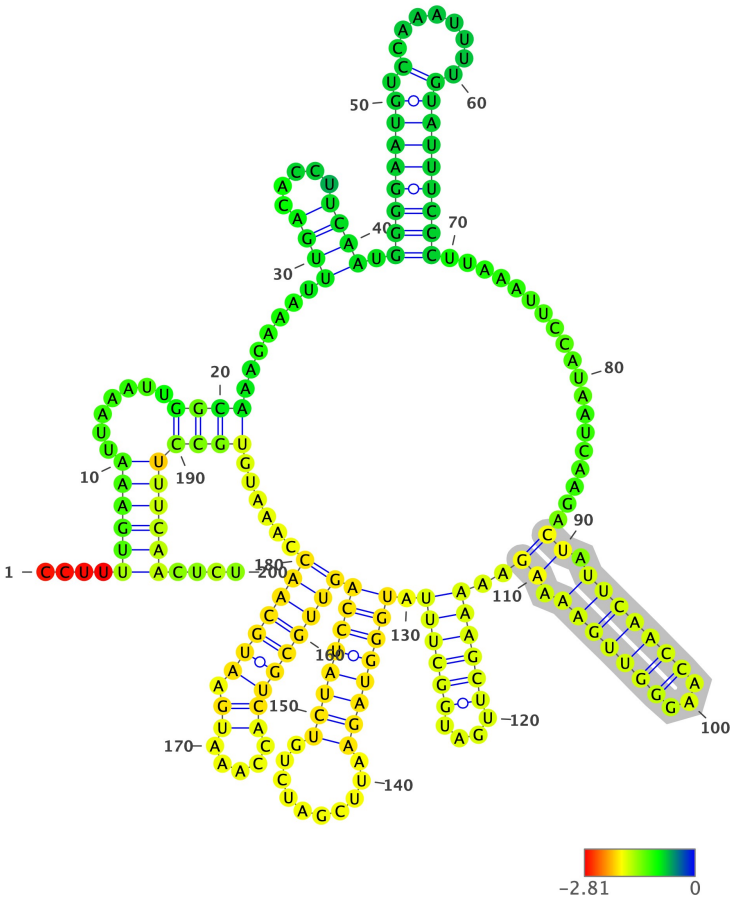
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 21 from nt 1113 to 1135 (nt 89 to 111)

```
5'-CUAUUCAACCAAGGGUUGAAAAG-3'
5'-((.((((((.....)))))).))-3'
Motif MFE = -6.7; z-score = -4.48; 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 = -2.52; 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(+)

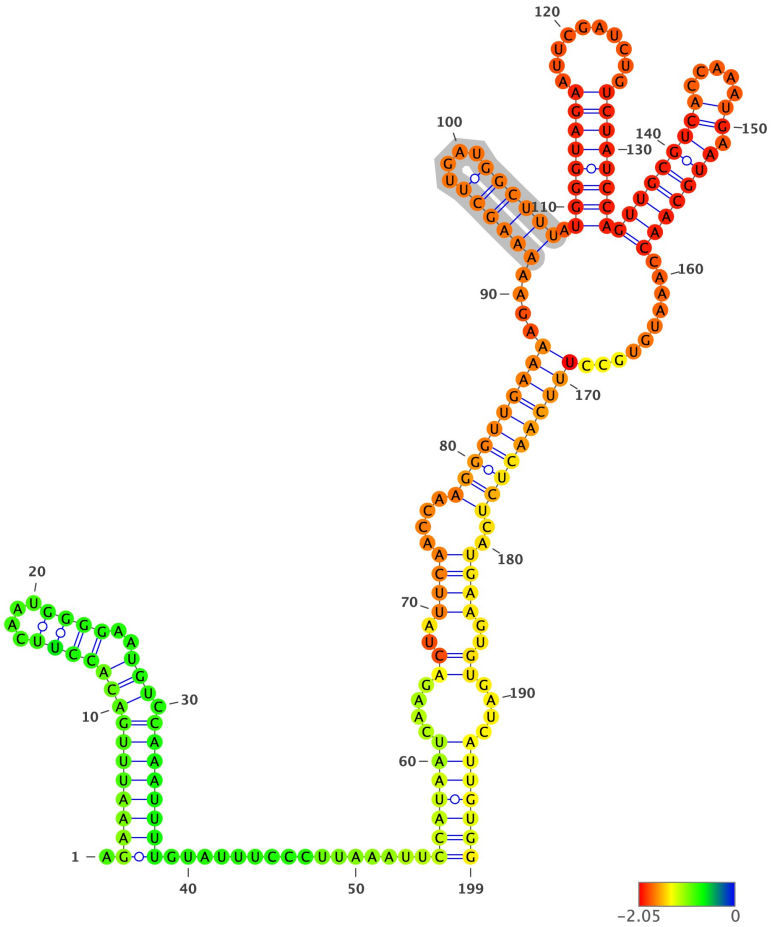
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 22 from nt 1138 to 1153 (nt 92 to 107)

```
5'-AAAGCUUGAUGGCUUU-3'
5'-((((((....))))))-3'
Motif MFE = -4.2; z-score = -3.73; 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 = -2.37; 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(+)

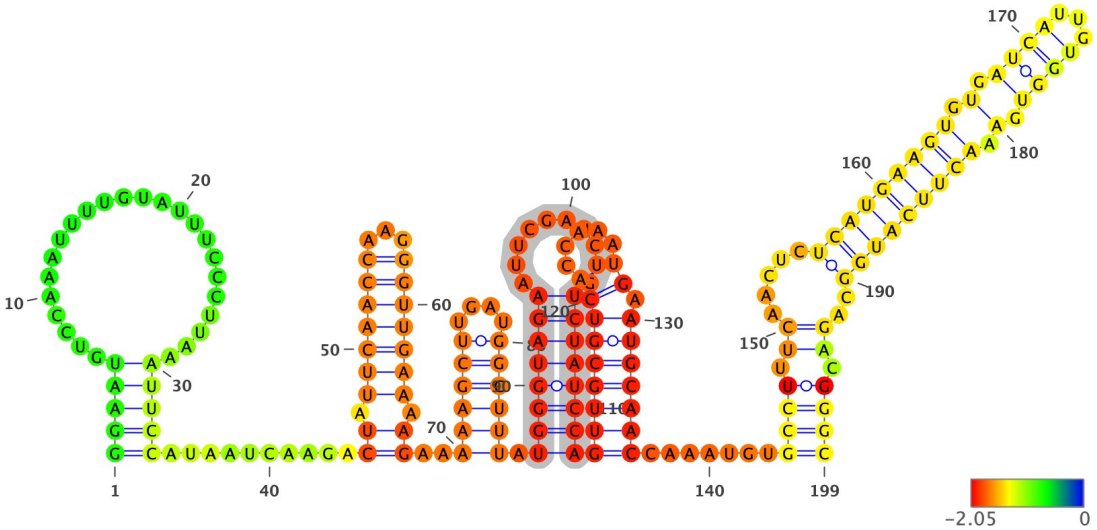
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 23 from nt 1155 to 1180 (nt 87 to 112)

```
5'-UGGGUAGAAUUCGAUCUGUCUAUCCA-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -7.4; z-score = -2.56; ED = 1.51
```



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

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

```
5'-GGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAGAAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCC
AGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGC-3
5'-(((((.......................)))))..........((.(((((((...)))))))).))..((((((....)))))).(((((((.........)))))))
)(((((((((.....)).)))))))......((((.((.....(((((((((.(.(((((...)))))).).)))))))))..)).)))-3'
MFE = -49.1; z-score = -1.58; 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(+)

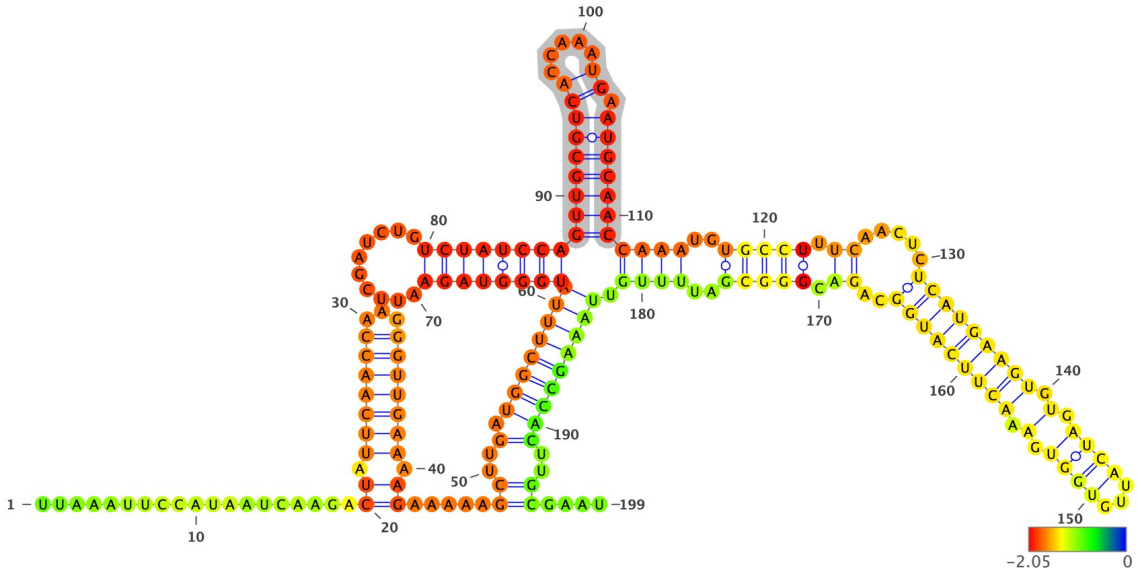
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 24 from nt 1181 to 1204 (nt 88 to 111)

```
5'-GUUGCGUCACCAAAUGAAUGCAAC-3'
5'-((((((((.......).)))))))-3'
Motif MFE = -6.5; z-score = -2.5; 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 = -3.64; 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(+)

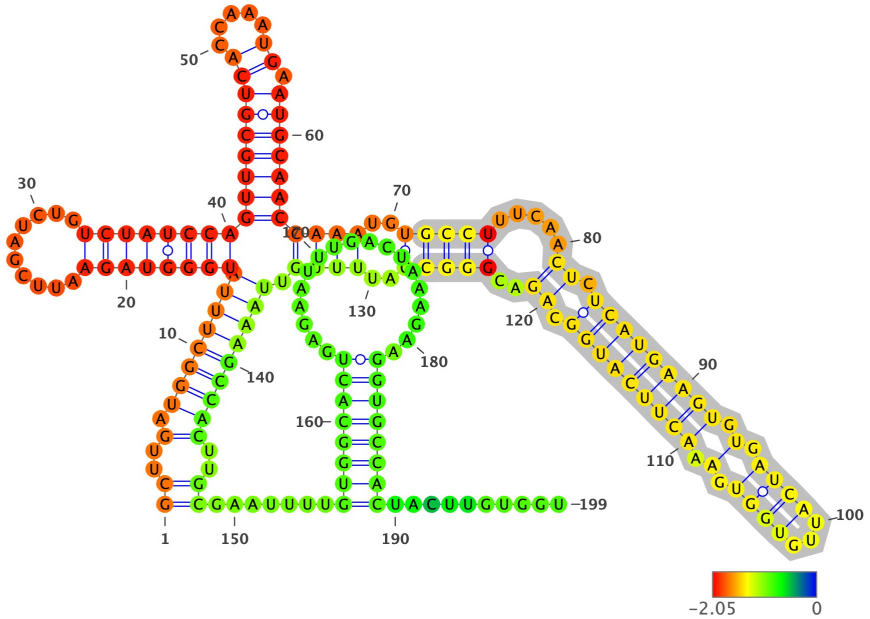
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 25 from nt 1212 to 1267 (nt 72 to 127)

```
5'-GCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGC-3'
5'-(((......((.(((((((((.................)))))))))).))...)))-3'
Motif MFE = -17.0; z-score = -1.96; ED = 4.35
```



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

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

```
5'-GCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAAC
UUCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGU-3
5'-((..(.((((((((((((((((.........))))))))(((((((((.....)).)))))))((((..(((((.....((.(((((((((.(.((((...)))).).))
)))))))).))..)))))..)))).)))))))))..))......((((((((.................))))))))..........-3'
MFE = -62.0; z-score = -2.67; ED = 10.67
```

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(+)

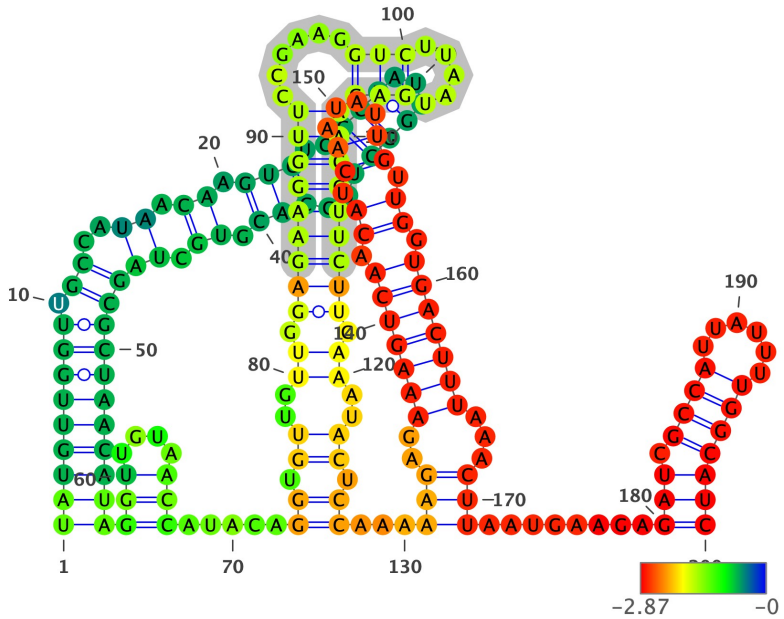
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 26 from nt 1586 to 1616 (nt 85 to 115)

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



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

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

```
5'-UAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAAC
CUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUC-3
5'-(((((((((.((..((.((.(((.((((...))))..))).)).))))))))))))(((....)))).....((.((..((.(((((((((......(((.....))))))
))))))).))..)).))...(((..(((((((.((.((....)).)).)))))))...))).........(((.((((......)))))))-3'
MFE = -51.5; z-score = -1.86; ED = 26.77
```

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

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

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

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

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

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

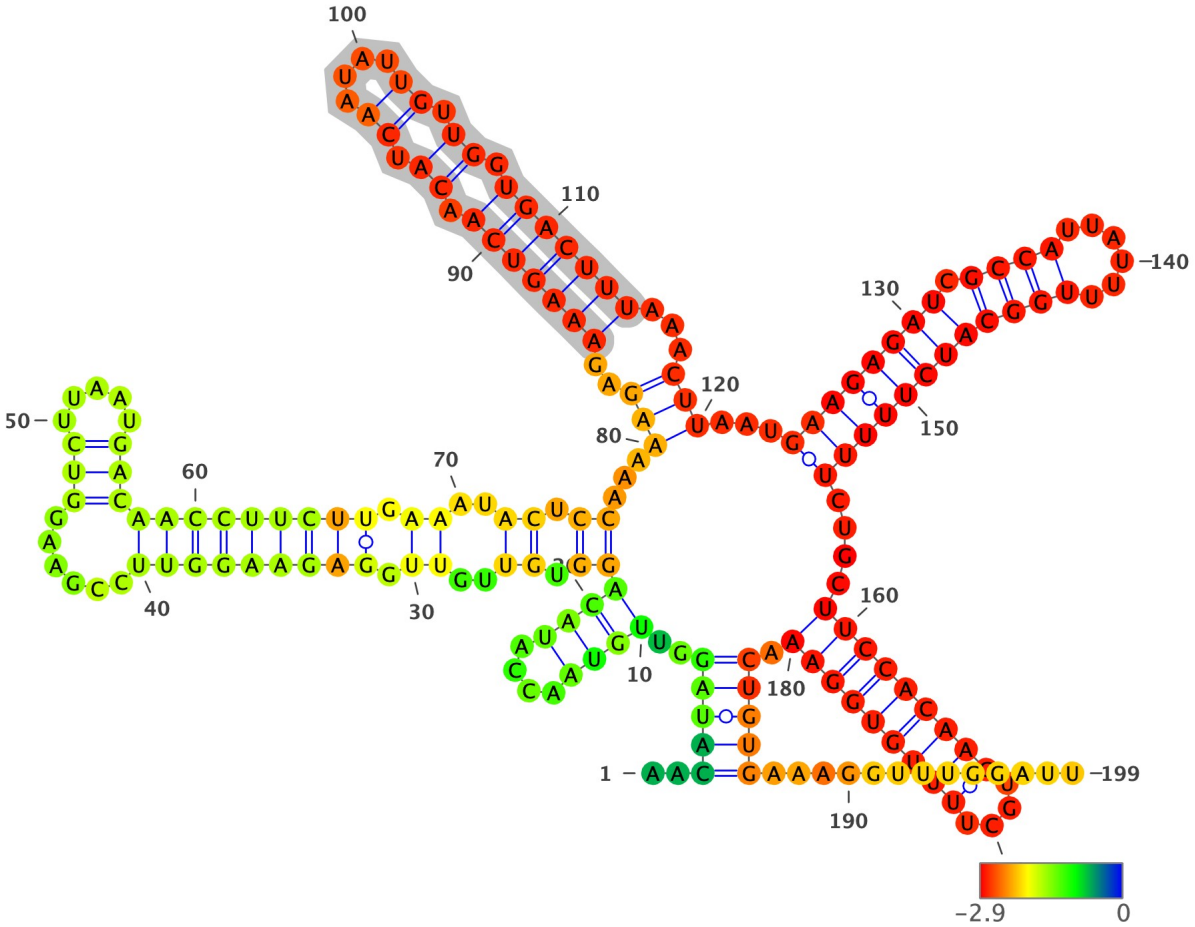
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 27 from nt 1637 to 1666 (nt 85 to 114)

```
5'-AAAGUCAACAUCAAUAUUGUUGGUGACUUU-3'
5'-(((((((.((.(......).)).)))))))-3'
Motif MFE = -7.2; z-score = -2.46; 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 = -3.22; 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(+)

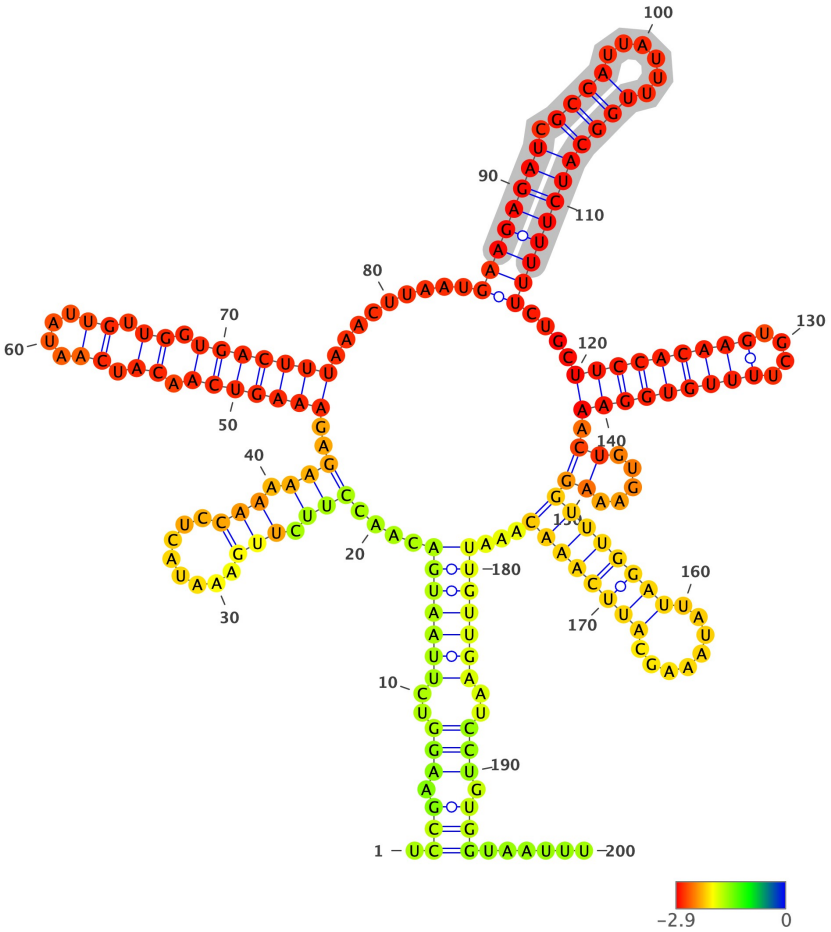
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 28 from nt 1678 to 1704 (nt 87 to 113)

```
5'-AGAGAUCGCCAUUAUUUUGGCAUCUUU-3'
5'-((((((.((((......))))))))))-3'
Motif MFE = -10.0; z-score = -5.12; ED = 0.79
```



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

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

```
5'-UCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCU
UUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUU-3
5'-.(((.(((..(((((((....(((.(((........))).)))..(((((((.((.((....)).)).)))))))..........((((((((.((((......))))))))
))))....((((((((((....)))))))))).((.....))((((((((........))))))))...)))))))..))).)))......-3'
MFE = -49.0; z-score = -3.16; ED = 44.52
```

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

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

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

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

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

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

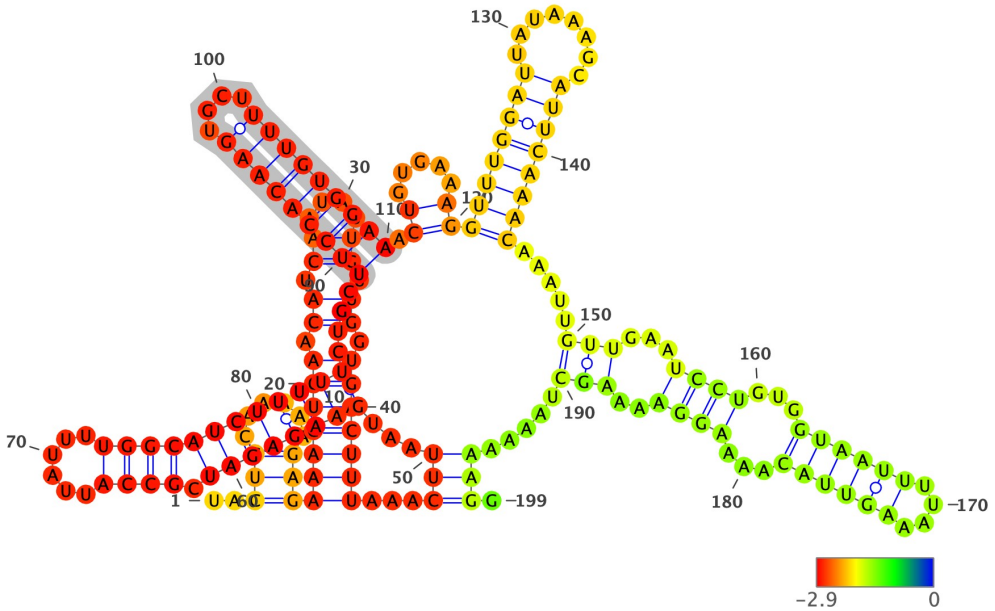
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 29 from nt 1711 to 1732 (nt 89 to 110)

```
5'-UUCCACAAGUGCUUUUGUGGAA-3'
5'-((((((((((....)))))))))-3'
Motif MFE = -9.5; z-score = -4.51; ED = 1.03
```



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

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

```
5'-UACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAA
CUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGG-3
5'-..(((......)))(((((((.((.((....)).)).)))))))...(((...((((((((.((((......)))))))))))....((((((((((....))))))))).
((.....))((((((((........))))))))).....(((...((((...((((((....))))))...))))..)))).....))).-3'
MFE = -48.5; z-score = -2.94; 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(+)

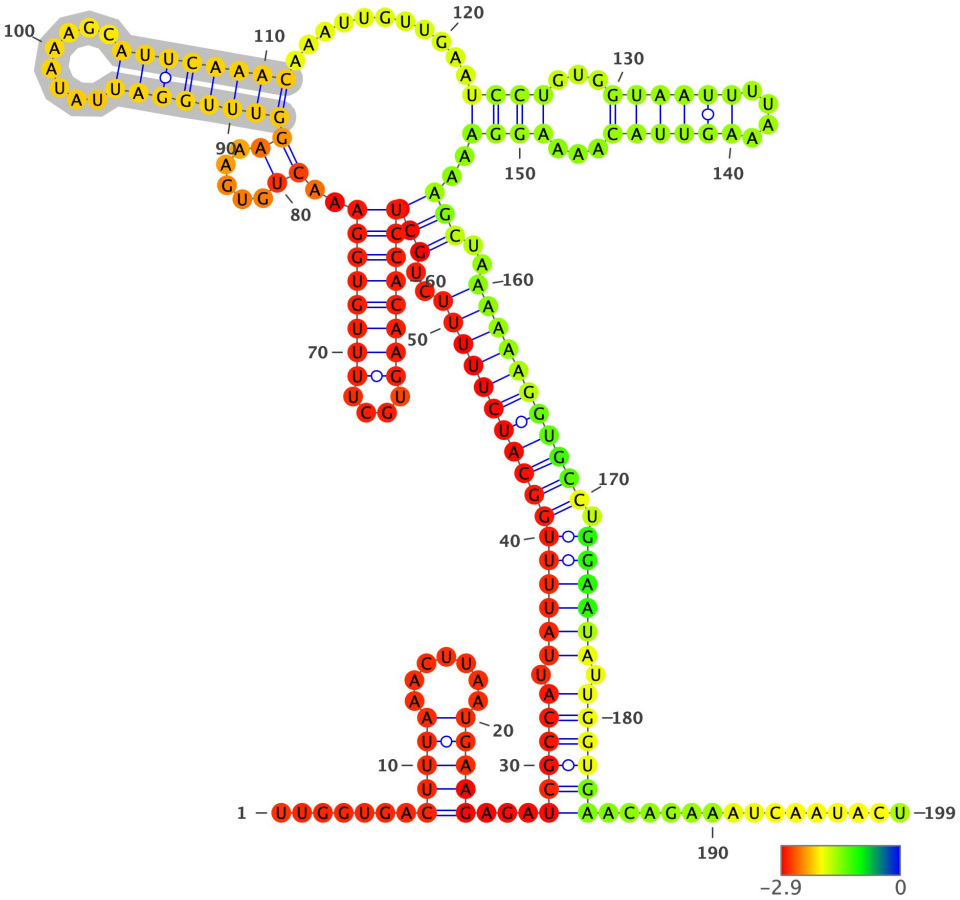
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 30 from nt 1743 to 1766 (nt 88 to 111)

```
5'-GUUUGGAUUAUAAAGCAUUCAAAC-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -4.6; z-score = -2.39; 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 = -3.93; 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(+)

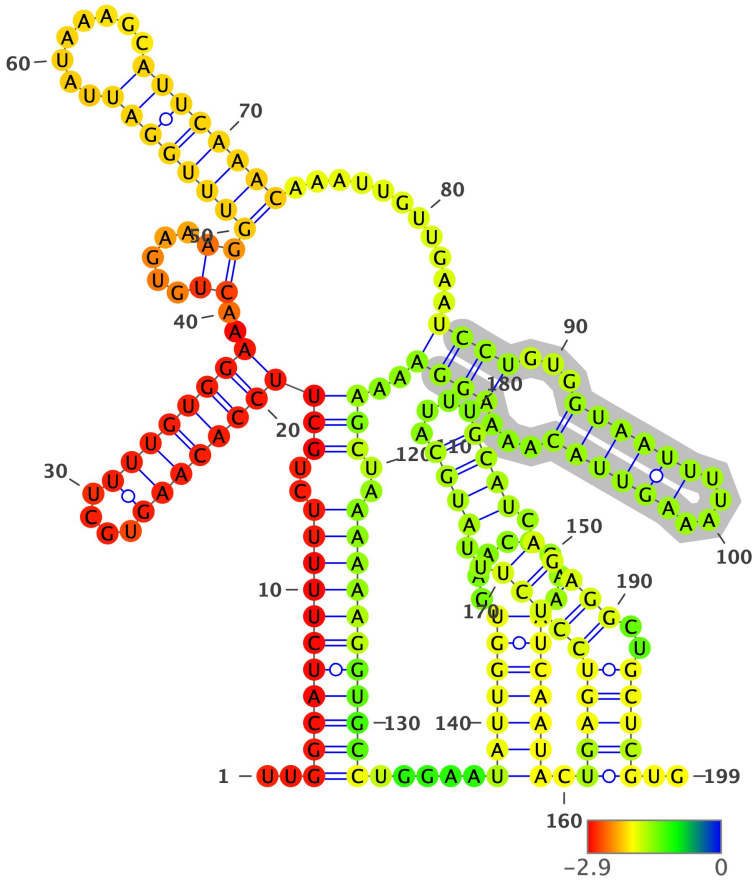
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 31 from nt 1779 to 1806 (nt 86 to 113)

```
5'-CCUGUGGUAAUUUUAAAGUUACAAAAGG-3'
5'-(((...((((((....)))))))...)))-3'
Motif MFE = -5.5; z-score = -2.18; ED = 0.85
```



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

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

```
5'-UUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAA
GGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUG-3
5'-..(((((((((((..((((((((((....)))))))))..((.....))(((((((((.......)))))))))...........((((...((((((....)))))))...)
)))..)))..))))))))))).....(((((((.......))))))).((((((((((..((((....)))).)))))..)))))..-3'
MFE = -60.5; z-score = -4.66; ED = 17.01
```

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(+)

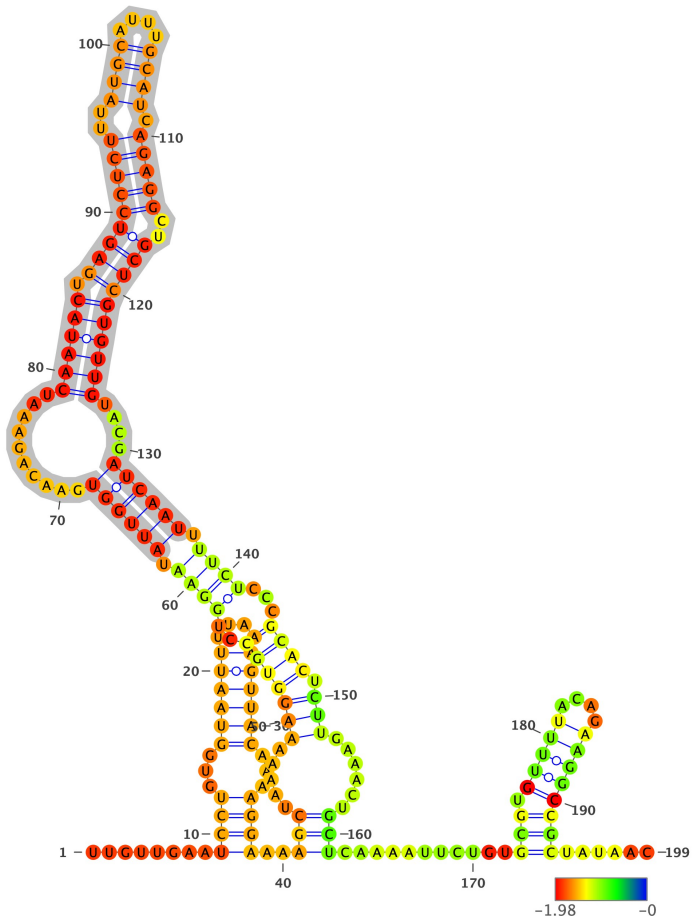
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 32 from nt 1832 to 1905 (nt 63 to 136)

```
5'-AUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUGUUGUACGAUCAAU-3'
5'-((((((..........((((((..(((((((((..((((....)))).)))))..))).))))))....))))))-3'
Motif MFE = -20.1; z-score = -2.41; ED = 7.62
```



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

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

```
5'-UUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAG
AGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAAC-3
5'-........((((...((((((....))))))...))))..(((.....(((((((..((((.((((((..........((((((.(((((((((..((((....)))).))
)))..))))))))))....)))))).))))...)))).)))......)))...........(((.(((((....))))))))......-3'
MFE = -48.9; z-score = -1.76; ED = 28.5
```

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

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

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

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

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

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

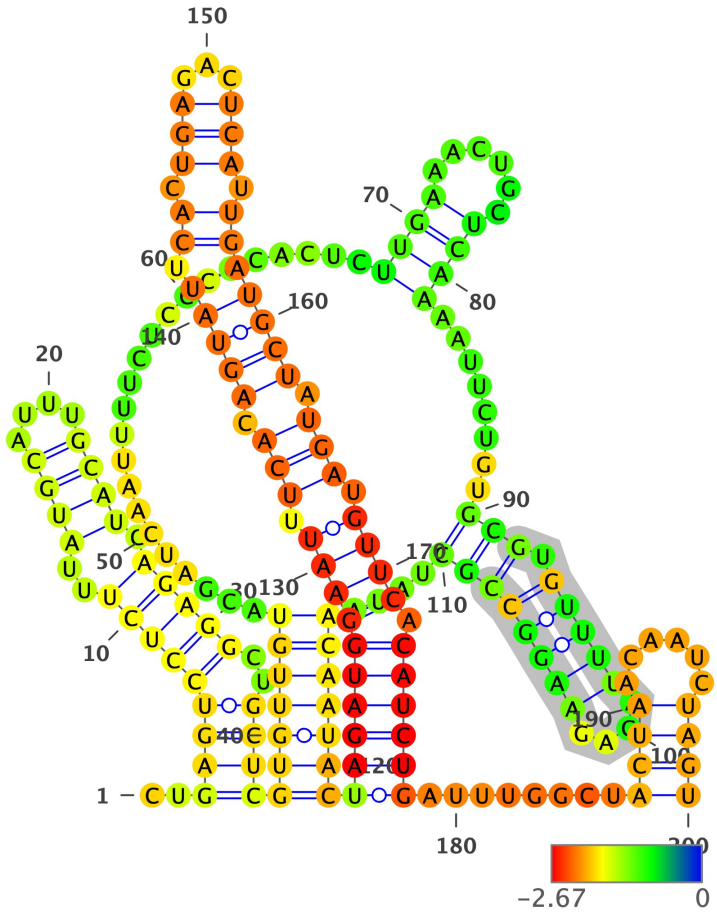
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 33 from nt 1944 to 1960 (nt 92 to 108)

```
5'-GUGUUUUACAGAAGGCC-3'
5'-(.....(....)....)-3'
Motif MFE = -0.8; z-score = 0.08; ED = 4.69
```



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 1853 to 2052 (motif highlighted in silver):

```
5'-CUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCU
AUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGU-3
5'-..(((((((((..((((....)))).)))))..))))(((((((.......................((((......))))........(((.(((((....)))))))).
...)))))))((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).))))))........((((......))))-3'
MFE = -44.8; z-score = -1.88; ED = 24.3
```

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(+)

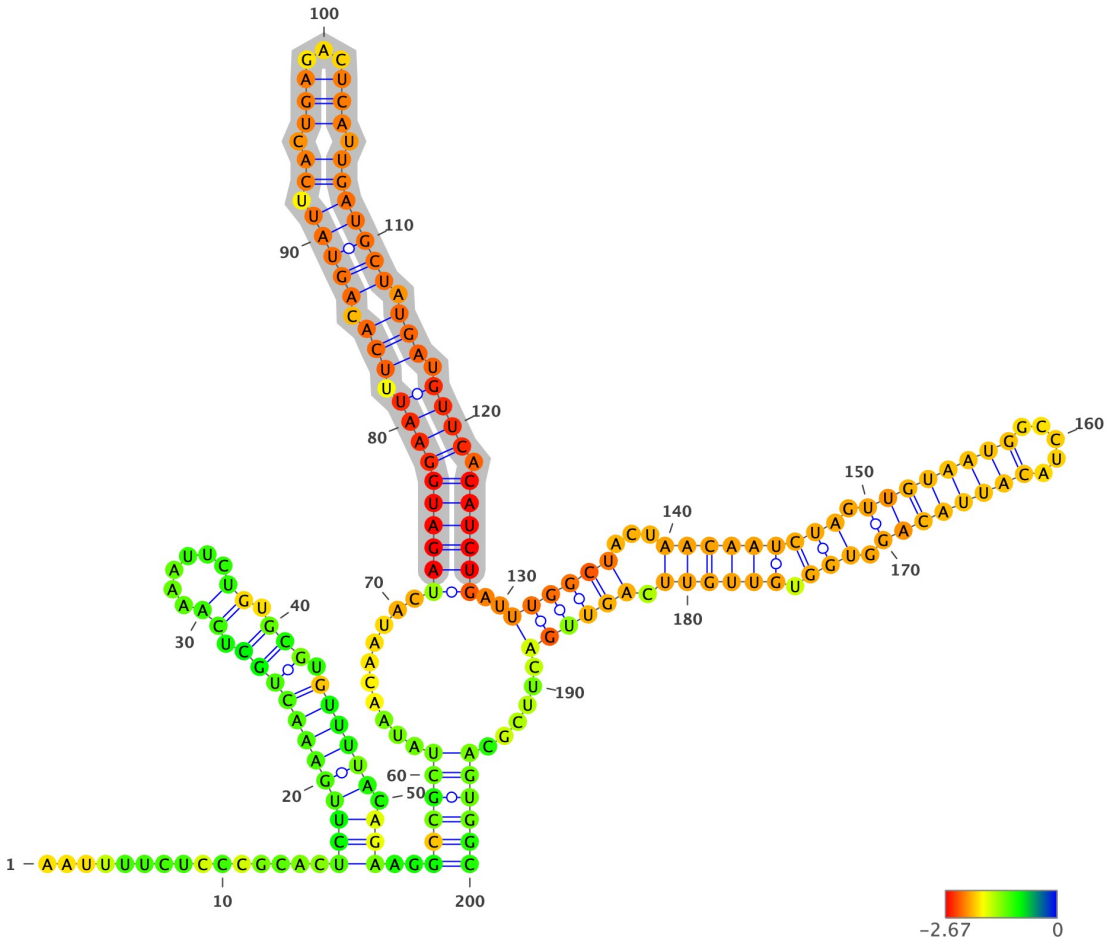
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 34 from nt 1975 to 2029 (nt 73 to 127)

```
5'-AGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCU-3'
5'-(((((((((.(((.(((((.((.(((...))).)))))))).))).)))).)))))-3'
Motif MFE = -16.5; z-score = -3.18; ED = 2.83
```



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

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

```
5'-AAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGC
UAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGC-3
5'-...............(((((((((((.((......)).))).)))))).)))..((((((..........(((((((((.(((.(((((.((.(((...))).))))))
).))).)))).)))))).((((((...(((((((((.((((((((.....)))))))).))).)))))).))))))......))))))-3'
MFE = -52.4; z-score = -2.27; 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(+)

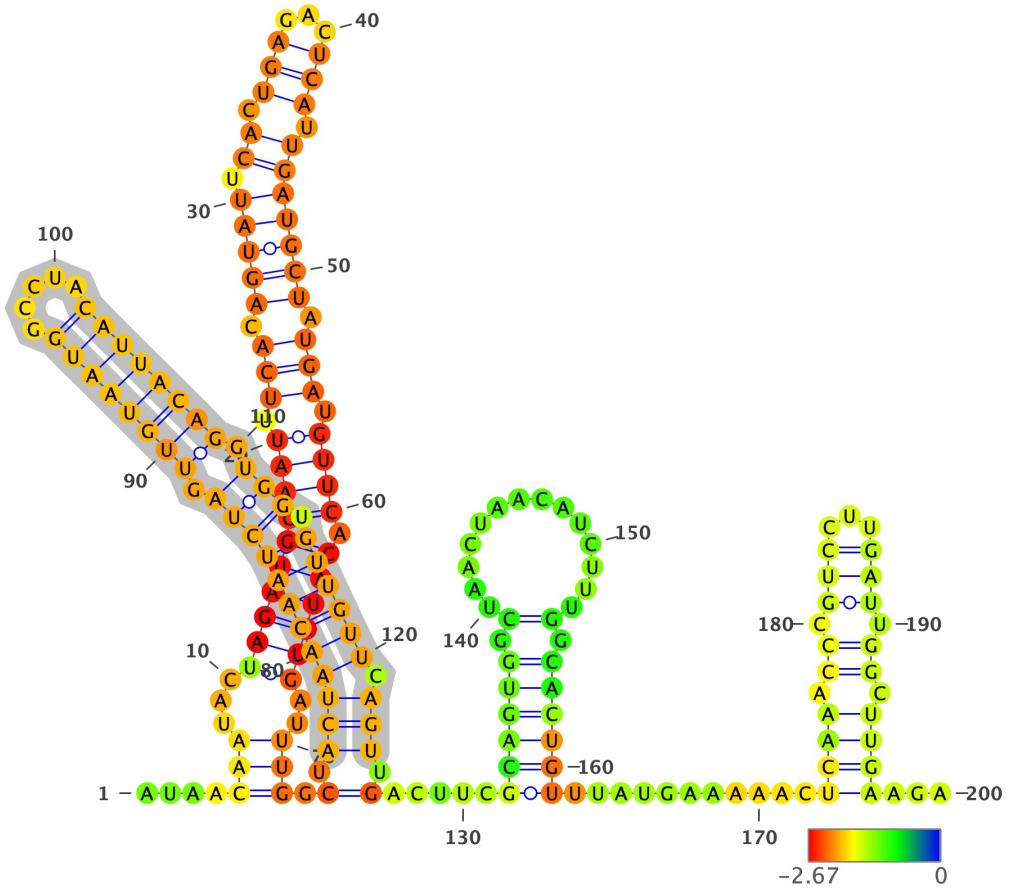
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 35 from nt 2039 to 2087 (nt 76 to 124)

```
5'-ACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGU-3'
5'-(((((((((((.((((((((.....)))))))).))).)))))).)))-3'
Motif MFE = -17.4; z-score = -4.0; ED = 1.42
```



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

Extracted structure model with flanking nucleotides 1964 to 2163 (motif highlighted in silver):

```
5'-AUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGU
GGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGA-3
5'-....(((...(((((((((((.(((.(((((.((.(((...))).)))))))).))).)))).))))))..))).(.(((((((((((((.((((((((.....)))))))).)
)).)))))).))).).....((((((.(..............).))))))...........((((.((.(((...))).)).))))...-3'
MFE = -50.7; z-score = -2.25; ED = 17.03
```

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(+)

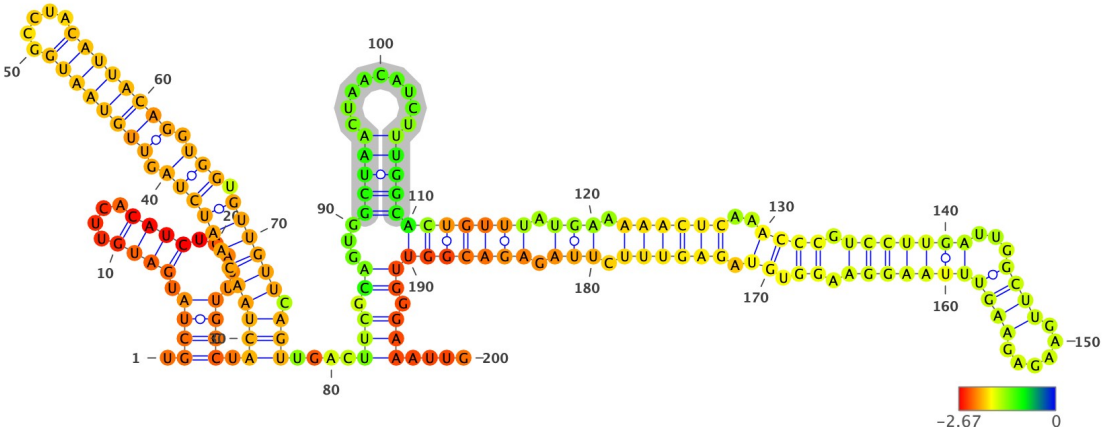
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 36 from nt 2101 to 2119 (nt 91 to 109)

```
5'-GCUAACUAACAUCUUUGGC-3'
5'-(((((.........))))-3'
Motif MFE = -1.2; z-score = -0.67; ED = 2.31
```



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

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

```
5'-UGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCAC
UGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUG-3
5'-.((((.((((....)))).....)))).((((((((((((.((((((((.....)))))))).))).)))))).))).....(((.((...(((((.........)))))))(
(((((.(((.(((((((..((((.(((((((...((((.....)))))))))))).)).)).)))))).))).)))))))).)).....-3'
MFE = -52.3; z-score = -2.53; ED = 31.48
```

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

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

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

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

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

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

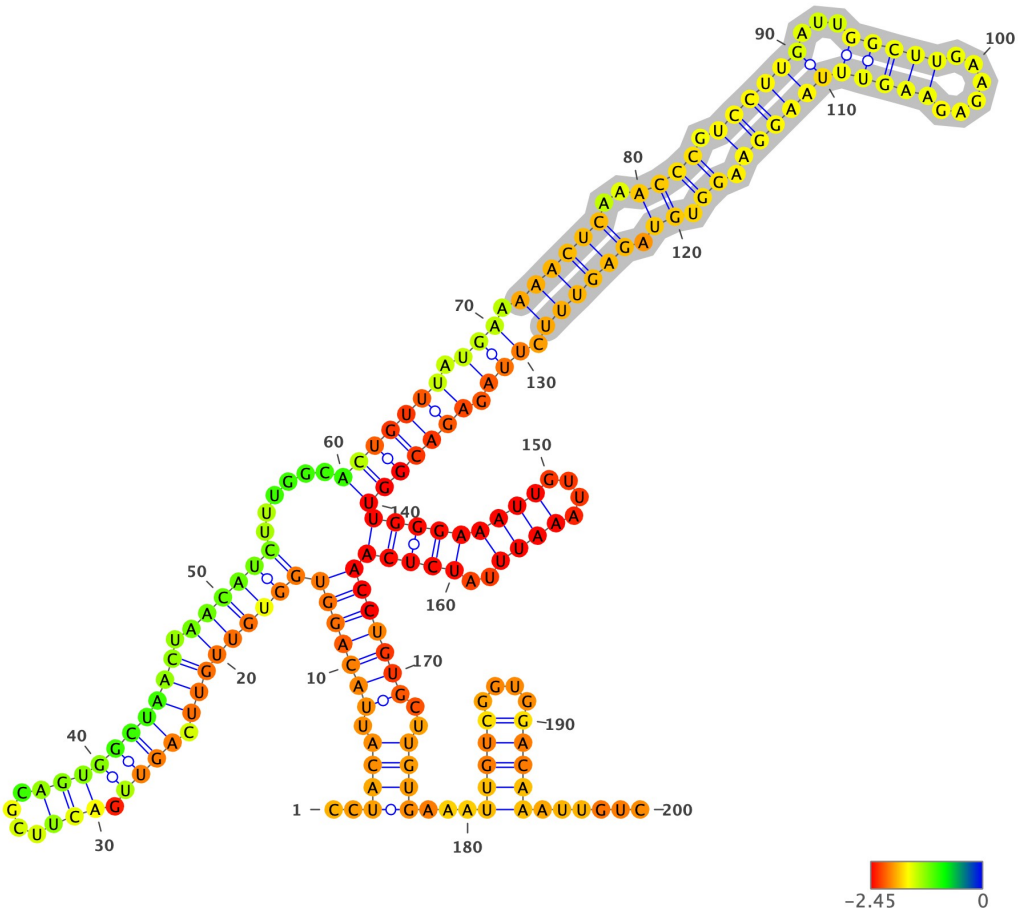
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 37 from nt 2132 to 2188 (nt 72 to 128)

```
5'-AAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUU-3'
5'-((((((..(((((.(((((....(((((......))))).))))).)).)).))))))-3'
Motif MFE = -17.2; z-score = -3.23; ED = 8.14
```



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 2061 to 2260 (motif highlighted in silver):

```
5'-CCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUA
AGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUC-3
5'-..((((.(((((((((((((((.((((.(((....)))))))))).))))))......(((((((.(((.((((((..((((.((((((...(((((......)))))))
)))).)).)).)))))).))).)))))))((((((((....))))..))))))))))))..))))...(((((....)))))......-3'
MFE = -53.5; z-score = -1.76; ED = 42.53
```

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

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

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

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

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

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

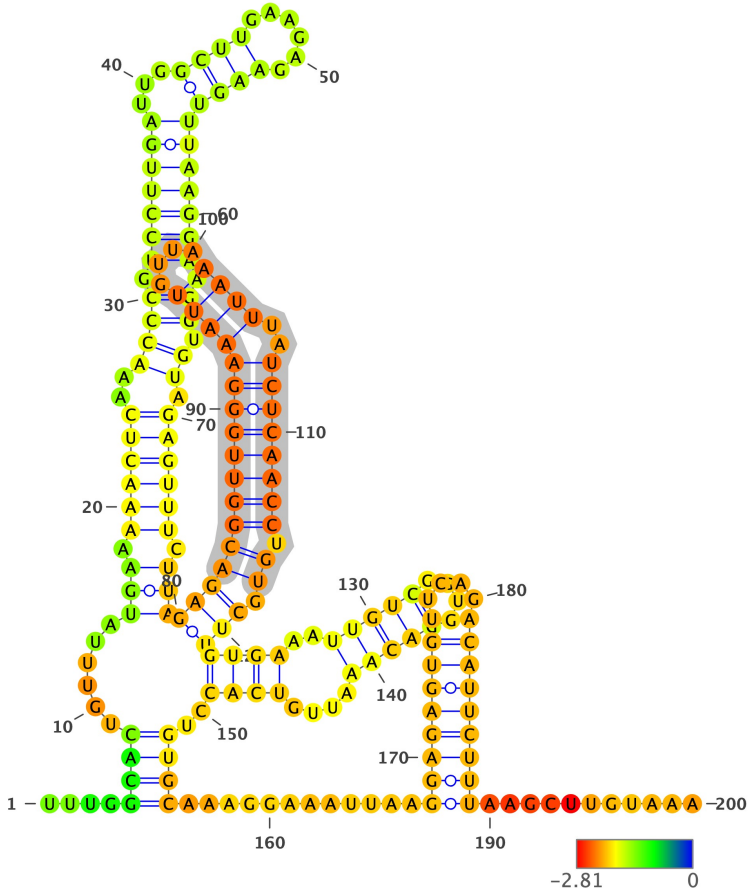
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 38 from nt 2196 to 2230 (nt 83 to 117)

```
5'-ACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGU-3'
5'-(((((((((((((....)))).))))))))).))-3'
Motif MFE = -10.9; z-score = -3.82; ED = 2.57
```



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 2114 to 2313 (motif highlighted in silver):

```
5'-UUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCA
ACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAA-3
5'-....((((......(((.((((((..((((.(((((((...((((......))))))))))).)).)).)))))).)))((((((((((((((((....)))).))))))
))).)).)))((((..(((((....)))))....)))).))))............(((((((((....)))))))))............-3'
MFE = -51.1; z-score = -3.69; ED = 41.91
```

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(+)

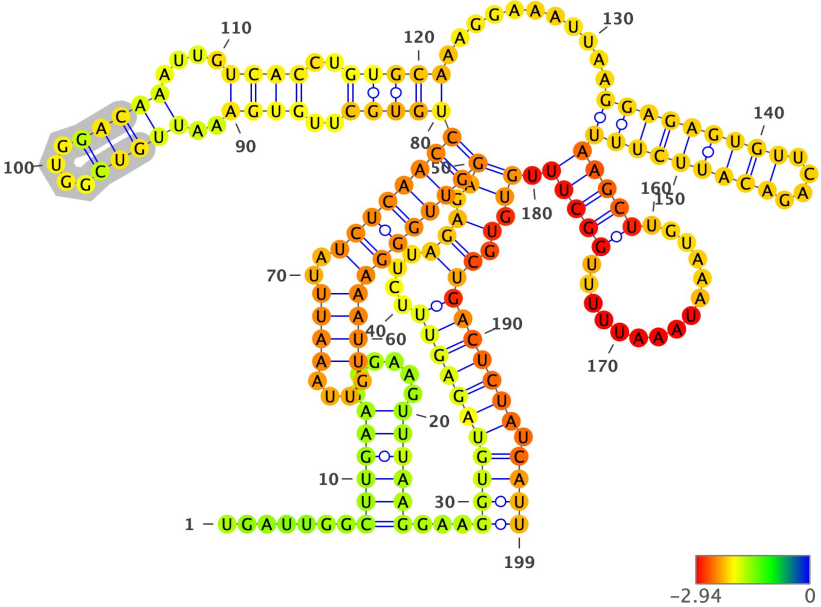
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 39 from nt 2243 to 2252 (nt 95 to 104)

```
5'-GUCGGUGGAC-3'
5'-((......))-3'
Motif MFE = -1.4; z-score = -5.47; ED = 0.57
```



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

Extracted structure model with flanking nucleotides 2149 to 2347 (motif highlighted in silver):

```
5'-UGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGU
CACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUU-3
5'-.......((((((......))))))...(((((((((((....(((.((((((((((((((....))))..))))))))(((((..((((..(((((....)))))....)
)))..)))))...........(((((((((....)))))))))(((((...............)))))).)).).))))))))).))))-3'
MFE = -47.8; z-score = -1.4; ED = 45.43
```

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(+)

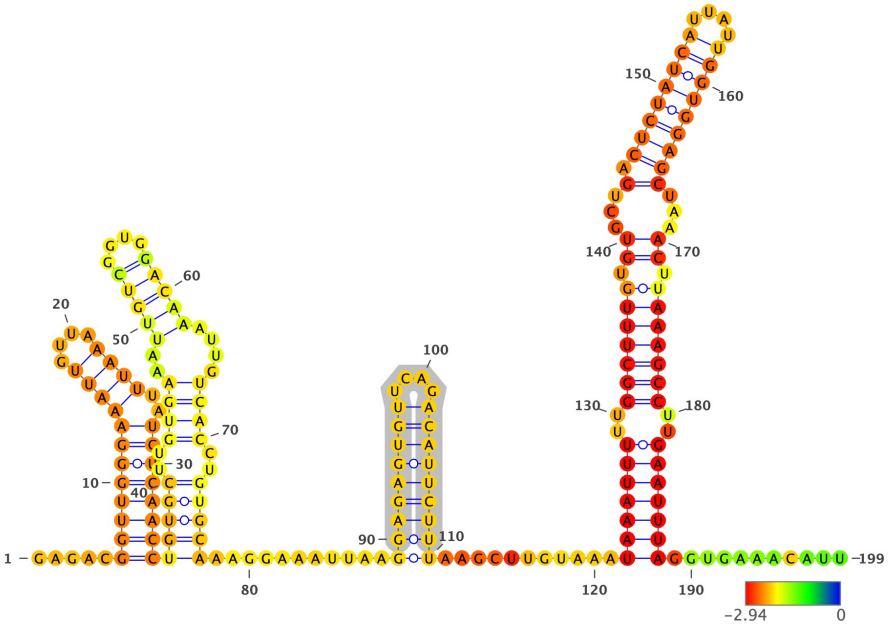
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 40 from nt 2282 to 2301 (nt 90 to 109)

```
5'-GAGAGUGUUCAGACAUUCUU-3'
5'-((((((((....))))))))-3'
Motif MFE = -6.2; z-score = -4.31; ED = 0.77
```



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

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

```
5'-GAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUA
AGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUU-3
5'-.....(((((((((((....))))..))))))))(((((..((((..(((((....)))))....))))..)))))...........((((((((....))))))))).
..........(((((((..(((((((.((...(.((((((((....)))))))))...)).)))))))..)))))))...........-3'
MFE = -57.6; z-score = -3.73; ED = 14.55
```

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

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

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

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

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

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

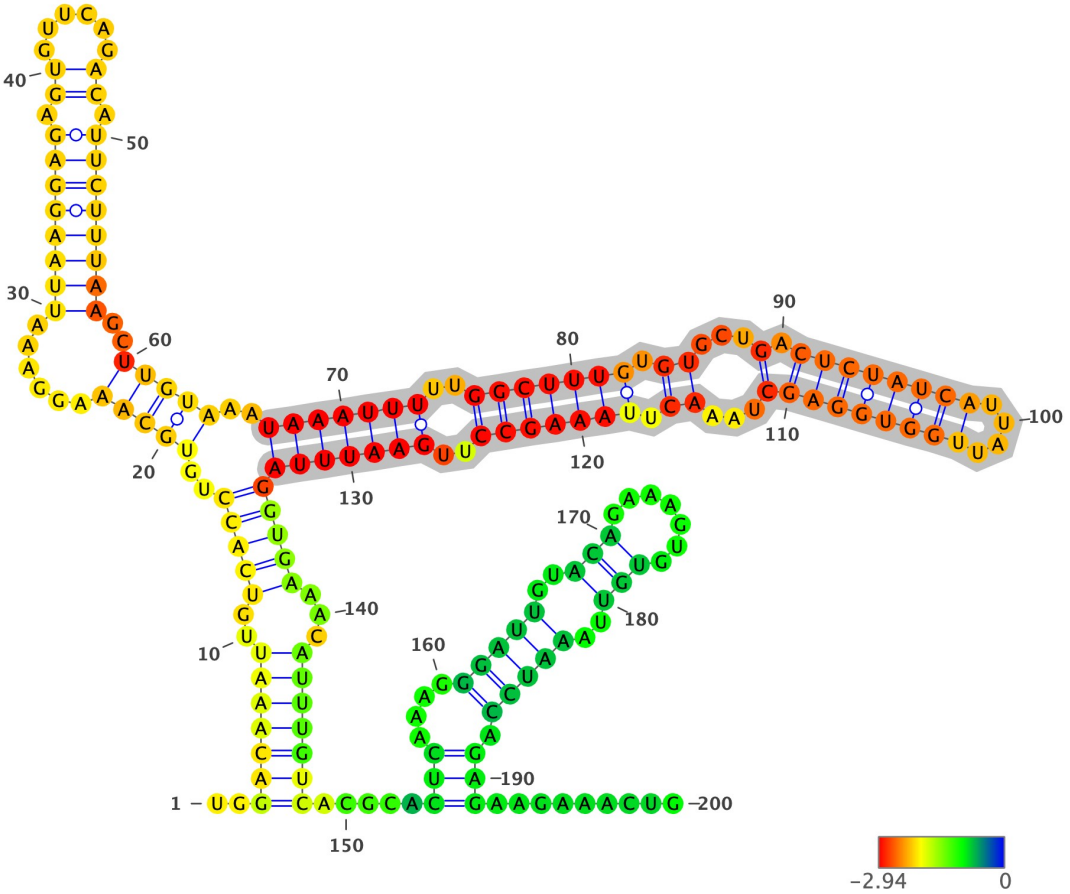
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 41 from nt 2314 to 2380 (nt 67 to 133)

```
5'-UAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUA-3'
5'-(((((((..((((((..((...(.(((((((.....))))))))...))..))))))..)))))))-3'
Motif MFE = -24.1; z-score = -5.22; 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 = -2.97; 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(+)

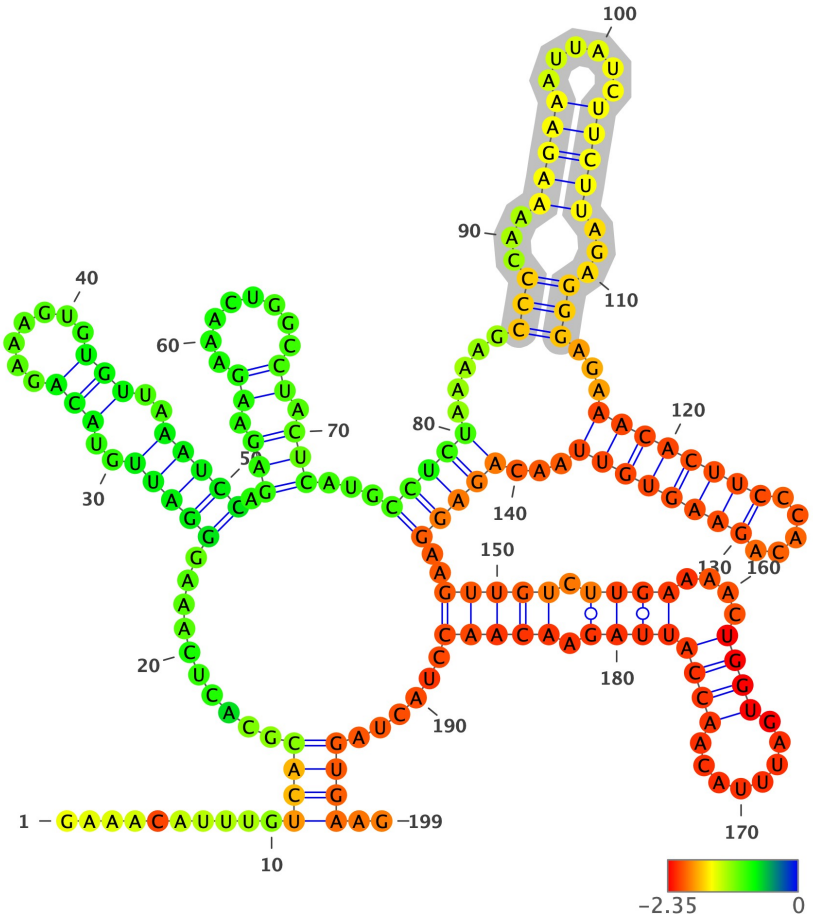
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 42 from nt 2469 to 2496 (nt 86 to 113)

```
5'-CCCCAAAAGAAAUUAUCUUCUUAGAGGG-3'
5'-(((...(((((......)))))...)))-3'
Motif MFE = -5.3; z-score = -1.79; ED = 3.98
```



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

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

```
5'-GAAACAUUUGUCACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAG
GGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAG-3
5'-..........((((..........(((((..(((.......)))..))))).(((.((........)).)))...(((((.....(((...(((((......)))))...)
))...(((((((.....)))))))...)))))..(((((.((((....((((........)))))))).)))))......))))..-3'
MFE = -42.6; z-score = -1.75; ED = 22.67
```

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

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

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

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

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

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

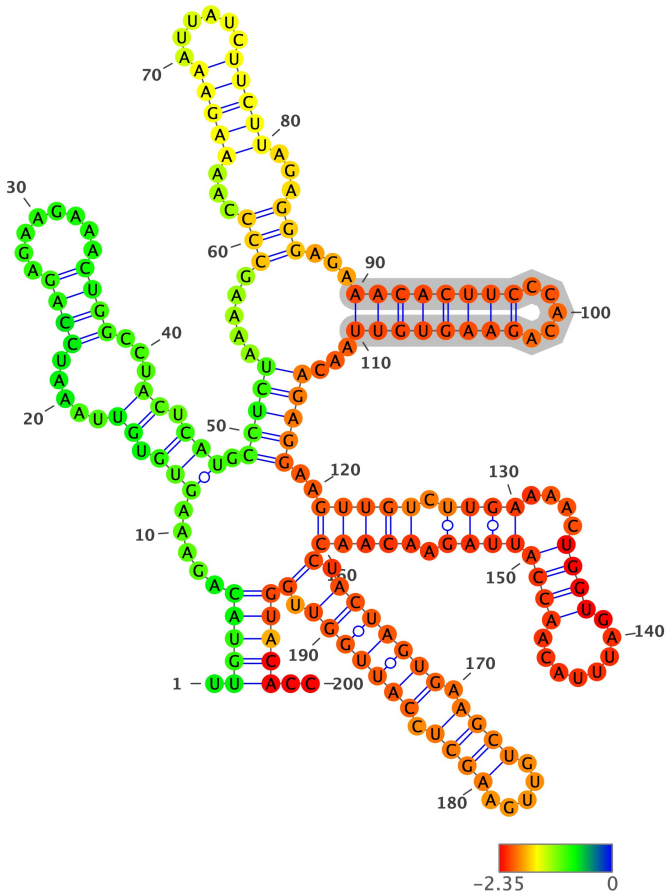
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 43 from nt 2500 to 2520 (nt 90 to 110)

```
5'-AACACUUCCCACAGAAGUGUU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.6; z-score = -5.49; ED = 0.62
```



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

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

```
5'-UUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUA
ACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACC-3
5'-.(((((.....(((.((.....((((........))))...)).))).(((((.....(((...(((((......)))))...)))...(((((((.....)))))))).
..)))))..(((((.((((....((((........)))))))).)))))(.(((((((.((((.....)))).))))))).)))))..-3'
MFE = -50.3; z-score = -2.72; ED = 26.56
```

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

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

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

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

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

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

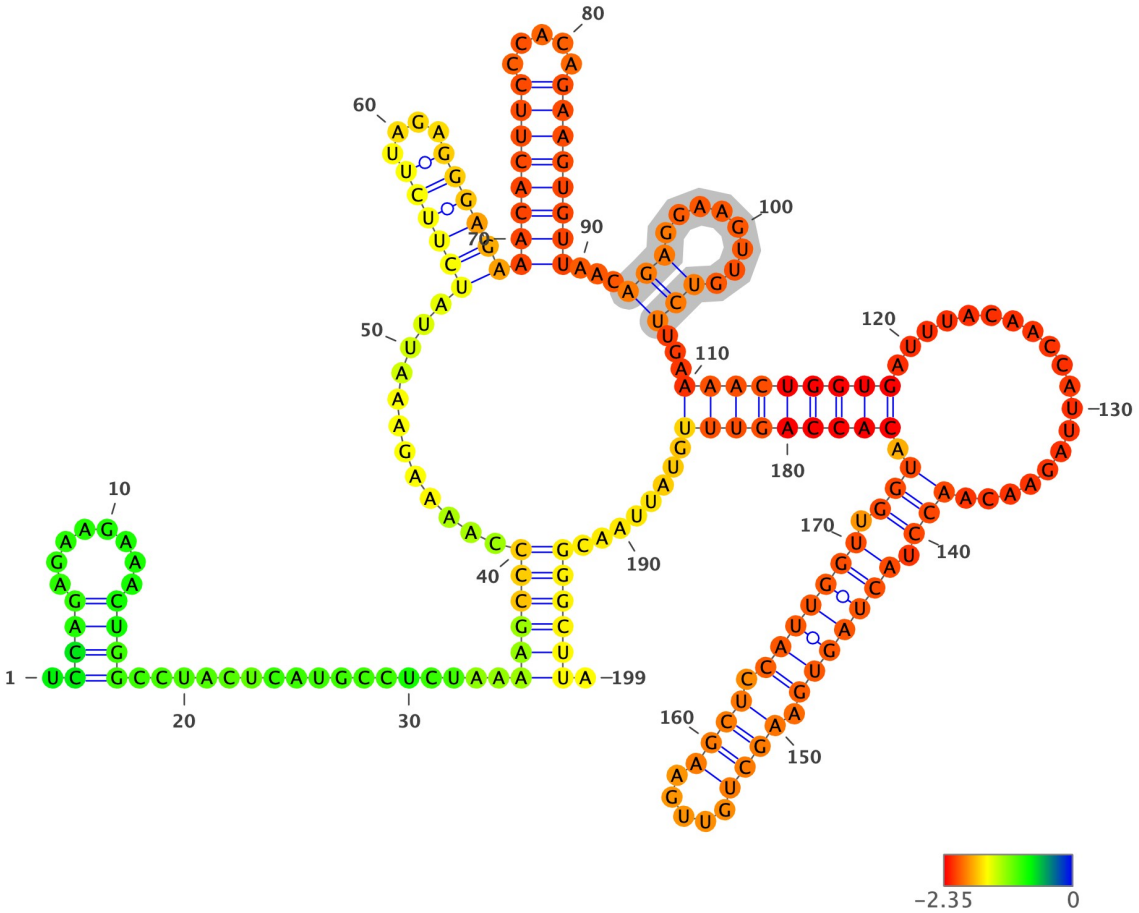
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 44 from nt 2524 to 2537 (nt 93 to 106)

```
5'-AGAGGAAGUUGUCU-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.29; ED = 2.55
```



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

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

```
5'-UCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAA
ACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUA-3
5'-.((((........))))..................((((((............((((((....))))))((((((((.....))))))))...(((........)))...((
(((((((...................(((.(((((((.((((.....)))).)))))))).))).))))))))).......))))))).-3'
MFE = -51.8; z-score = -2.84; 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(+)

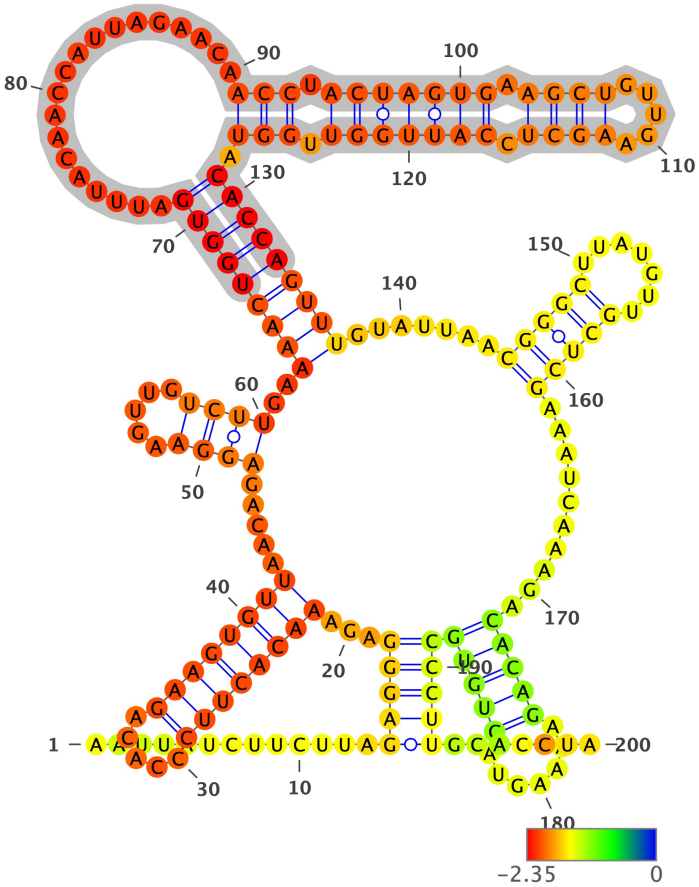
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 45 from nt 2545 to 2611 (nt 67 to 133)

```
5'-UGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCA-3'
5'-(((((...................(((.(((((((.((((.....)))).)))))))).))).)))))-3'
Motif MFE = -20.1; z-score = -2.74; ED = 4.88
```



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

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

```
5'-AAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGA
AGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUA-3
5'-.............(((((...((((((((.....))))))))).....((((.....)))).((((((((((...................(((.(((((((.((((.....
)))).)))))))).))).))))))))).......(((((.......)))))..........(((((.......)))))))))).......-3'
MFE = -53.0; z-score = -2.83; ED = 27.49
```

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

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

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

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

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

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

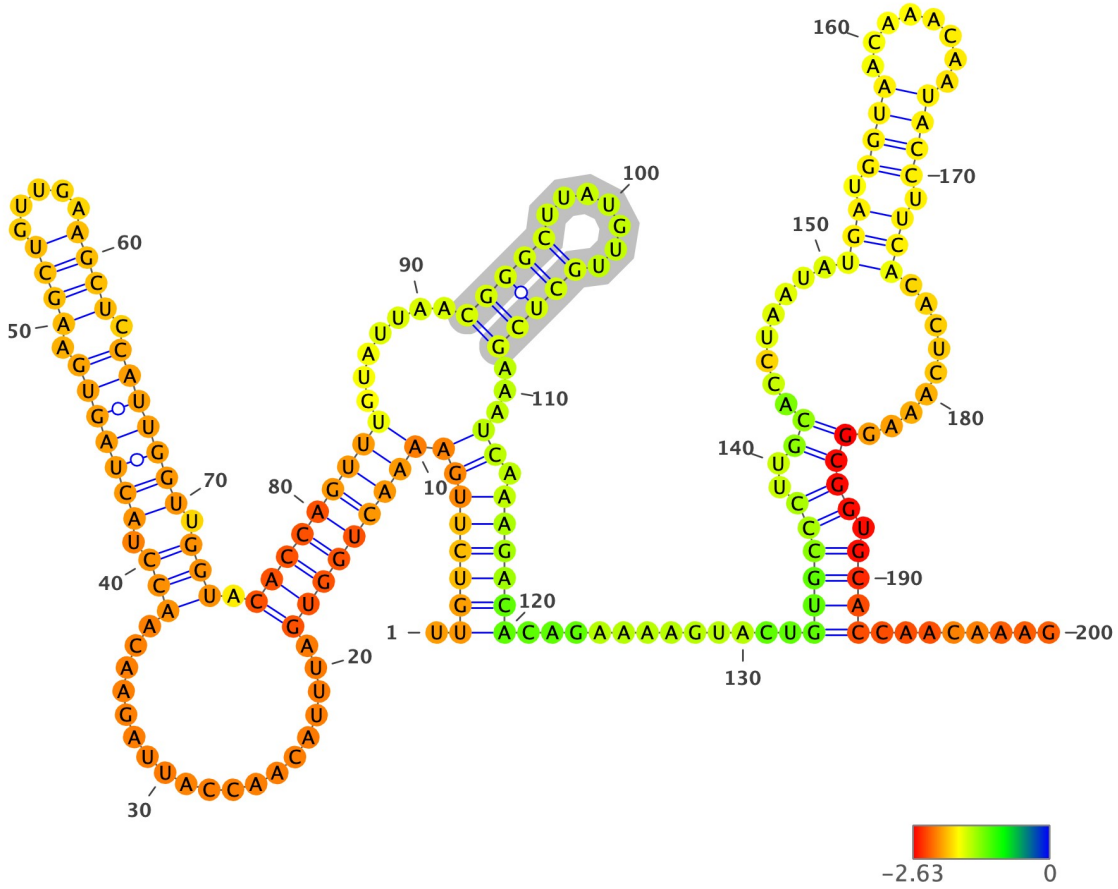
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 46 from nt 2623 to 2639 (nt 92 to 108)

```
5'-CGGGCUUAUGUUGCUCG-3'
5'-(((((.......)))))-3'
Motif MFE = -5.5; z-score = -2.18; 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 = -2.7; 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(+)

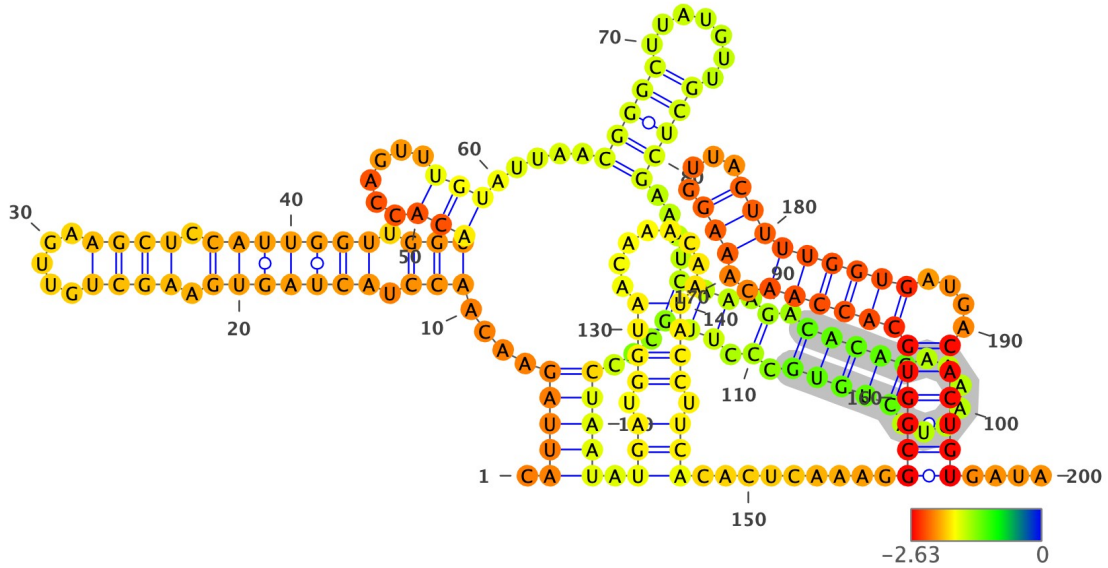
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 47 from nt 2650 to 2666 (nt 92 to 108)

```
5'-CACAGAAAAGUACUGUG-3'
5'-(((((.......)))))-3'
Motif MFE = -3.6; z-score = -4.44; 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 = -2.04; 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(+)

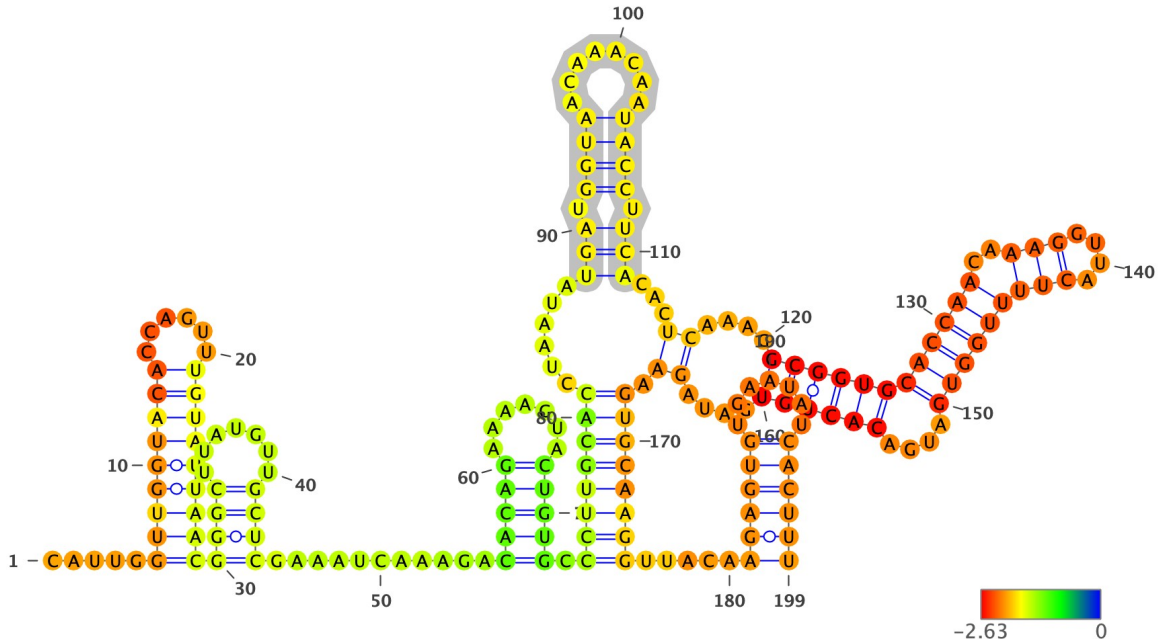
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 48 from nt 2682 to 2705 (nt 88 to 111)

```
5'-UGAUGGUAACAAACAAUACCUUCA-3'
5'-(((.((((.......)))).)))-3'
Motif MFE = -4.8; z-score = -4.83; 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
CACUCAAAGGCGGUGCACCAACAAAGGUUACUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUU-3
5'-.....(((((((((.....)))))))))((((.......)))).........(((((.......))))).((((((((.....(((.((((........)))).)))
...((....((((((((((..((((....)))))))))....)))))))....)).)))))))).....((((((.......))))))-3'
MFE = -52.2; z-score = -2.46; 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(+)

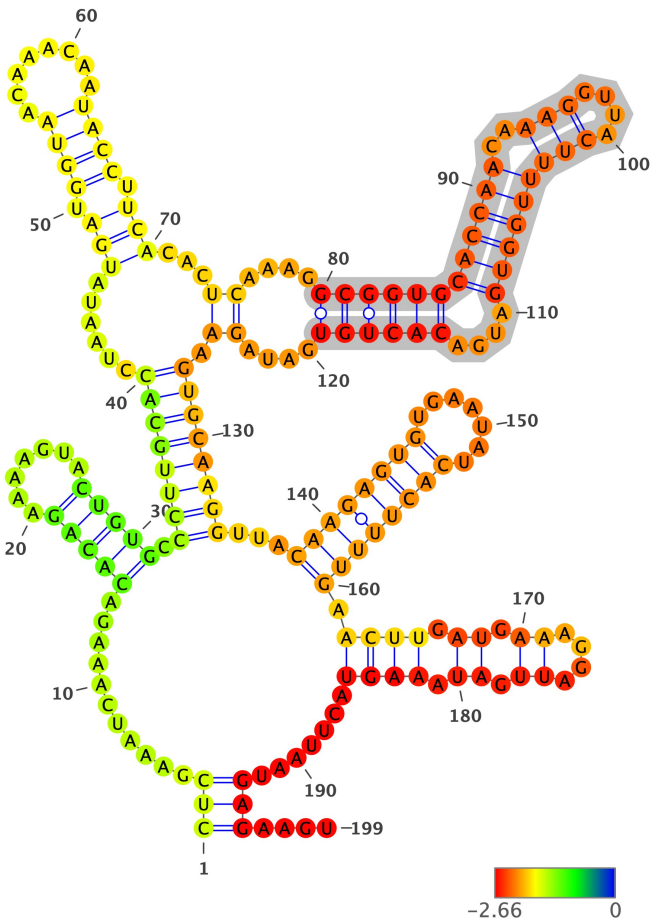
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 49 from nt 2715 to 2754 (nt 80 to 119)

```
5'-GCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGU-3'
5'-(((((((((((..(((....)))))))))....)))))))-3'
Motif MFE = -12.9; z-score = -2.8; ED = 3.61
```



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

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

```
5'-CUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAU
GACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGU-3
5'-(((...........(((((.......)))))).(((((((.....(((.((((........)))).))).))...((....((((((((((..(((....)))))))))..
..))))))....)).)))))))...(((((((.......)))))))).(((((.((.(((....)).)).)))).......)))....-3'
MFE = -47.4; z-score = -2.34; ED = 24.31
```

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

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

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

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

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

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

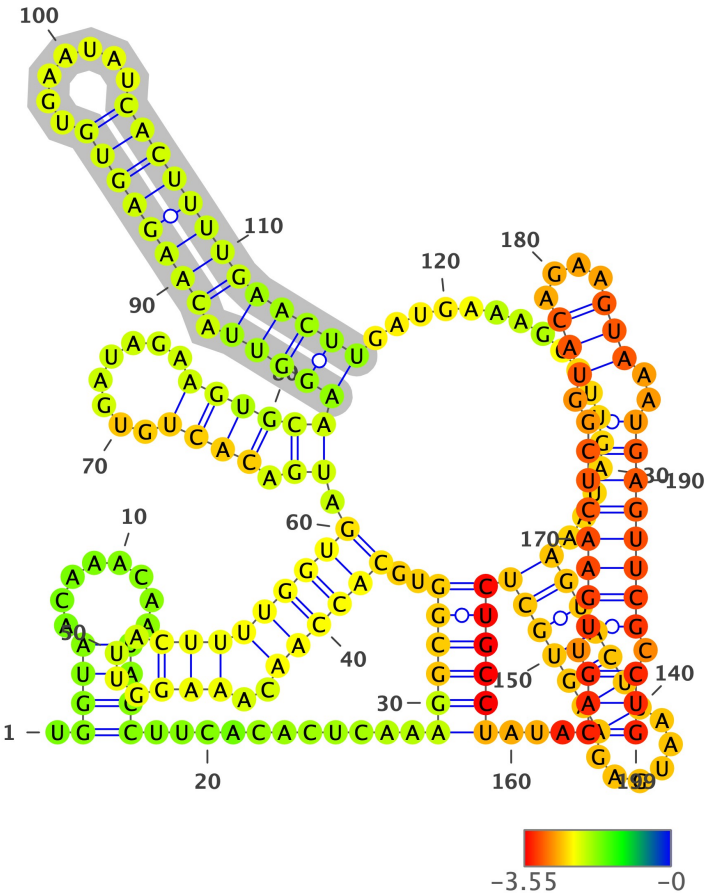
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 50 from nt 2767 to 2800 (nt 83 to 116)

```
5'-AGGUUACAAGAGUGUGAAUAUCACUUUUGAACUU-3'
5'-(((((.((((((((.......)))))))))))))-3'
Motif MFE = -10.9; z-score = -3.73; ED = 0.81
```



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

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

```
5'-UGGUAACAAACAAUACCUUCACACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUG
AACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUG-3
5'-.((((........))))...........((((((..((((((..(((....))))))))).((.((((........))))))(((((.((((((((.......))))))))
)))))).................(((((((......)))))))))))))...(((.((((((((.(((....)))..)))))))).)))-3'
MFE = -55.0; z-score = -3.24; 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(+)

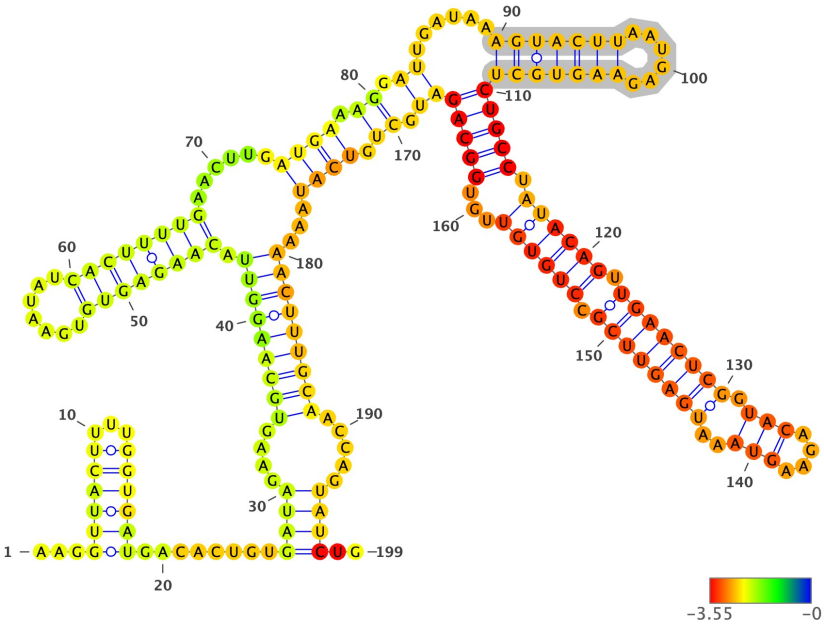
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 51 from nt 2818 to 2837 (nt 90 to 109)

```
5'-AGUACUUAAUGAGAAGUGCU-3'
5'-(((((((......)))))))-3'
Motif MFE = -5.4; z-score = -4.52; 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 = -3.45; 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(+)

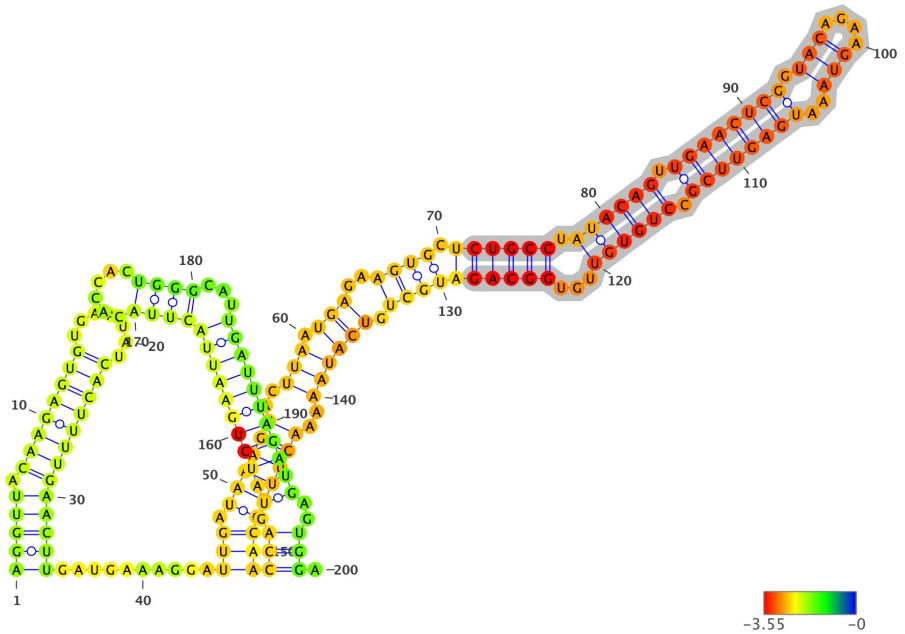
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 52 from nt 2838 to 2894 (nt 72 to 128)

```
5'-CUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAG-3'
5'-(((((...((((.(((((((..(((....)))...)))))))).)))).....)))))-3'
Motif MFE = -25.1; z-score = -4.67; ED = 1.38
```



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

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

```
5'-AGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUU
CGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGA-3
5'-(((((.((((((((.......)))))))))))))..........(((.((((((..(((.(((..((((.((((((.((((((.((((((((.(((....)))..))))))
)).))))))...)))))))))).))))))..)))))))))(((.((((((((((((((.......))))...)))))))))))..))).-3'
MFE = -60.4; z-score = -4.66; ED = 19.72
```

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(+)

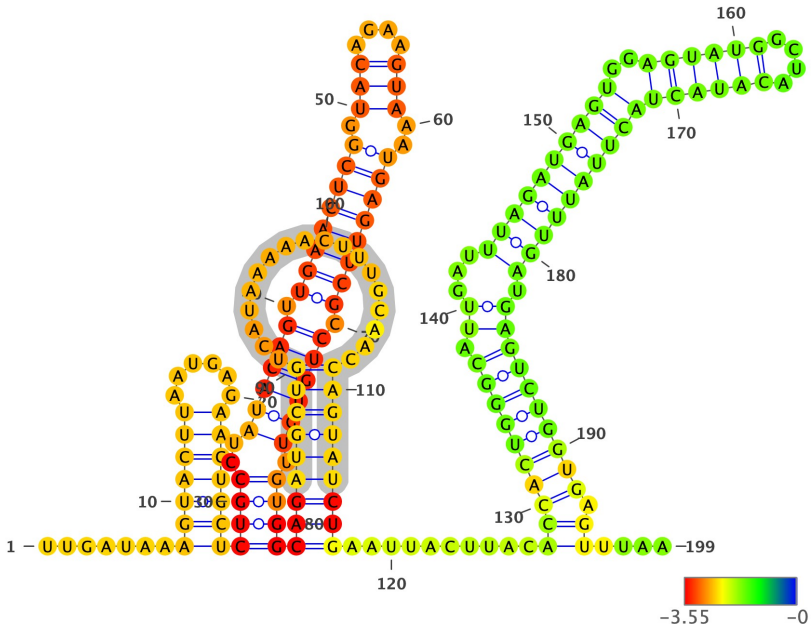
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 53 from nt 2895 to 2924 (nt 85 to 114)

```
5'-AUGCUGUCAUAAAAACUUUGCAACCAGUAU-3'
5'-((((((..................))))))-3'
Motif MFE = -2.2; z-score = -0.66; 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 = -4.11; ED = 19.81
```

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

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

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

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

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

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

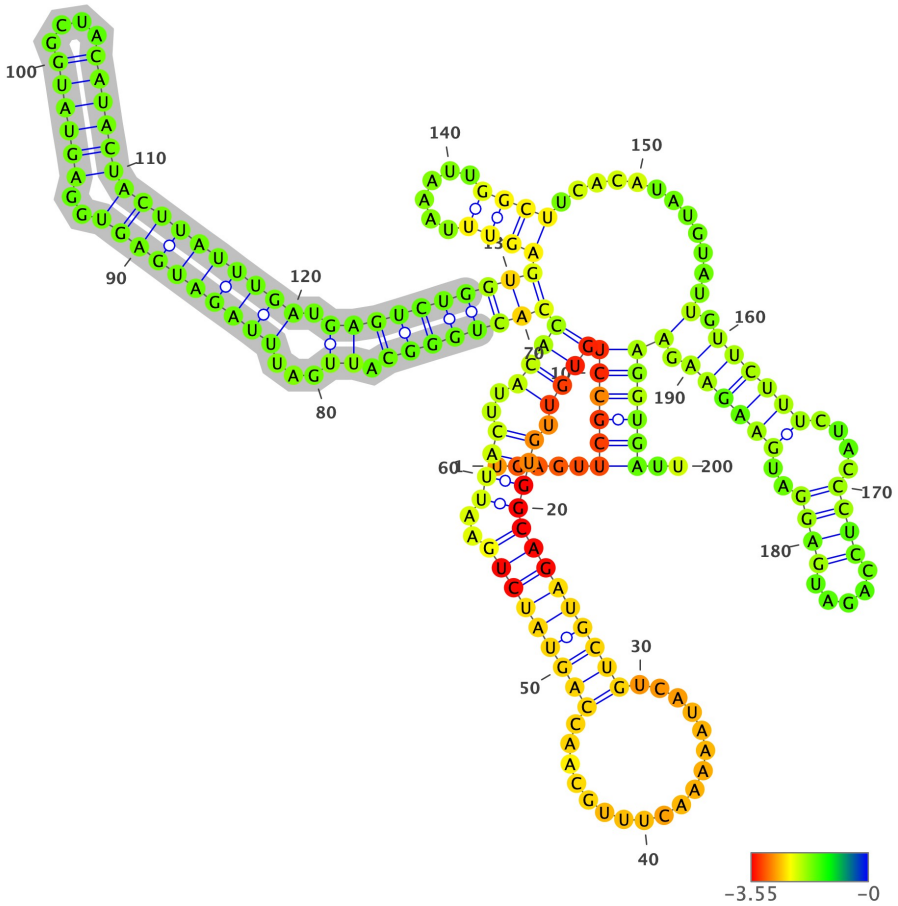
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 54 from nt 2943 to 2999 (nt 72 to 128)

```
5'-UGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUG-3'
5'-(.((.......((((((((((..((((((....)))))))))))))))))....)).)-3'
Motif MFE = -16.1; z-score = -2.98; 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 2872 to 3071 (motif highlighted in silver):

```
5'-UGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUA
CUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUU-3
5'-.....((((((((((.(((((((((((((.................)))))))))..))))..))))(((((((((.((...((((((((((..((((((....)))))))
)))))))))).))))))))))(((.....))))............(.((((((....((((.....)))))..)))))).)))))))..-3'
MFE = -54.6; z-score = -2.13; ED = 23.07
```

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, 266-13468(+)

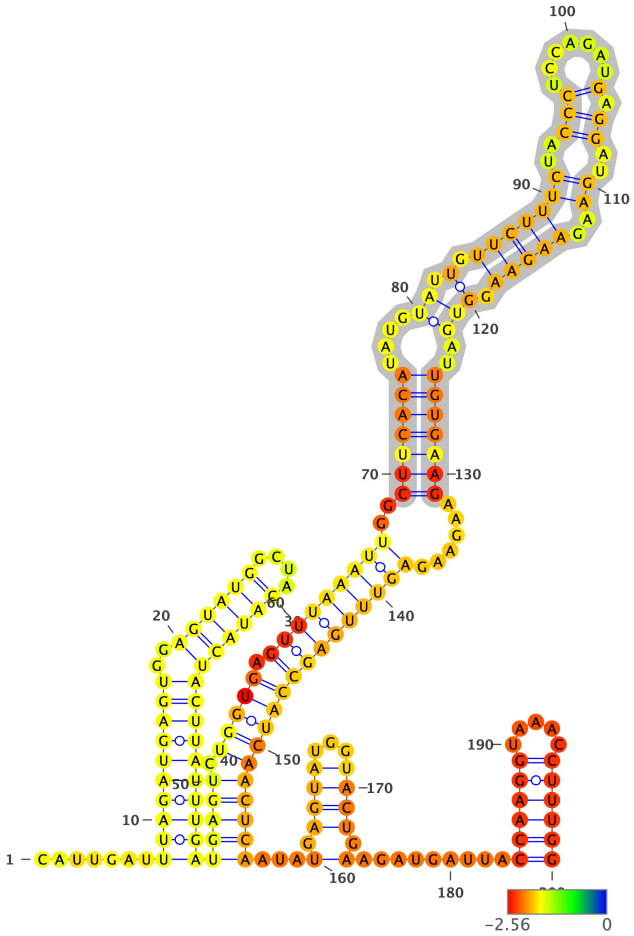
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 3015 to 3077 (nt 69 to 131)

```
5'-CUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAG-3'
5'-((.((((.......(.(((((((..(((.......).))..))..))))))..)....)))).))-3'
Motif MFE = -17.5; z-score = -2.9; ED = 8.76
```



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

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

```
5'-CAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGA
AGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGG-3
5'-.......((((((((((..((((((....)))))))))))))))))(((((.(((((.(((((((((..(((((((....((.(.(((((((..(((.......).)).))..))
..)))))).)))..)))))))).....))))))))))))))))))...(.((((...)))).).........((((((.....))))))-3'
MFE = -48.3; z-score = -3.29; ED = 21.25
```

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

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

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

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

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

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

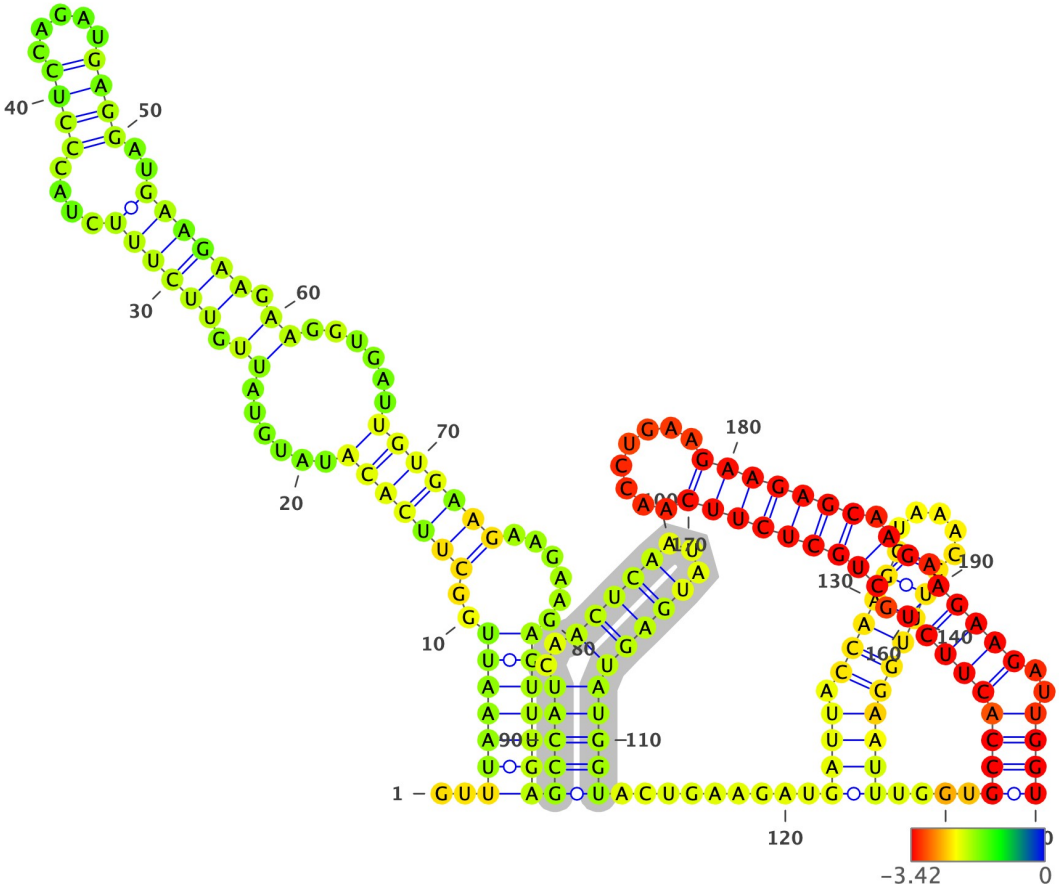
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 56 from nt 3091 to 3115 (nt 88 to 112)

```
5'-GCCAUCAACUCAAUAUGAGUAUGGU-3'
5'-(((((..((((.....)))))))))-3'
Motif MFE = -7.6; z-score = -2.94; ED = 1.38
```



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

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

```
5'-GUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGG
UACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGU-3
5'-..(((((((..(((((((......((.((((((....((((.....))))..))))))).))......)))))))......)))))))(((((..(((((...)))))))))
).........((((.((((((.....)))))))))....((((((((((.(((((((((.........)))))))).)).)))))..))))-3'
MFE = -55.6; z-score = -3.63; ED = 28.76
```

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

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

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

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

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

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

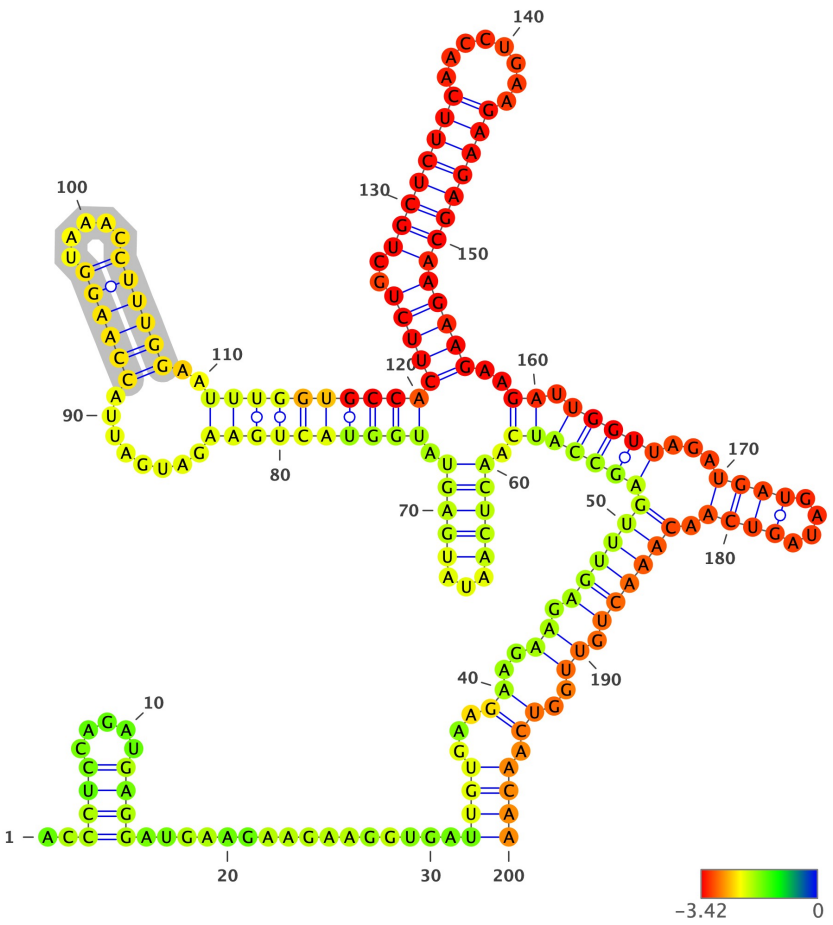
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 57 from nt 3130 to 3146 (nt 92 to 108)

```
5'-CCAAGGUAAACCUUUGG-3'
5'-((((((.....))))))-3'
Motif MFE = -4.3; z-score = -2.38; ED = 3.55
```



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

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

```
5'-ACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAU
UUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAA-3
5'-..((((.....))))................((((...((..((.(((((((((((((.(((((...))))).((((((((((.........((((((.....))))))..)
))))))))))(((((..((((((((.........)))))))))))))..)).)))))...((((....)))).)))))).))..)).))))-3'
MFE = -51.1; z-score = -2.84; ED = 39.98
```

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

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

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

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

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

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

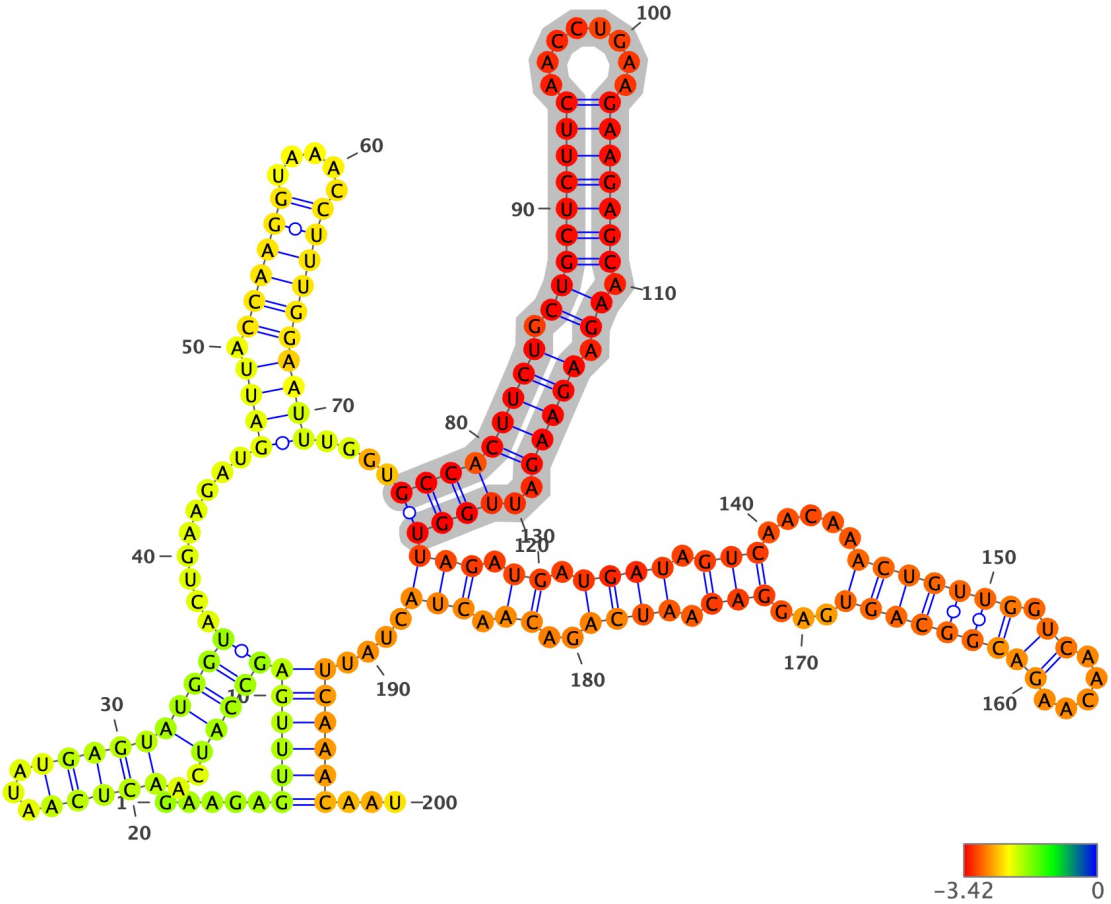
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 58 from nt 3155 to 3203 (nt 76 to 124)

```
5'-GCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGU-3'
5'-(((.(((((.(((((((((........)))))))).)).)))))...)))-3'
Motif MFE = -20.1; z-score = -4.05; ED = 2.9
```



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

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

```
5'-GAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAA
GAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAU-3
5'-.....(((((((((((..(((((...)))))))))).........((((.((((((.....)))))))))).....(((((((((.(((((((((........)))))))).)
).)))))..))))(((.((.((((.(((.....(((((((.((.....)))))))))...))).))))..)).)))....))))))...-3'
MFE = -57.7; z-score = -4.57; ED = 17.56
```

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

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

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

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

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

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

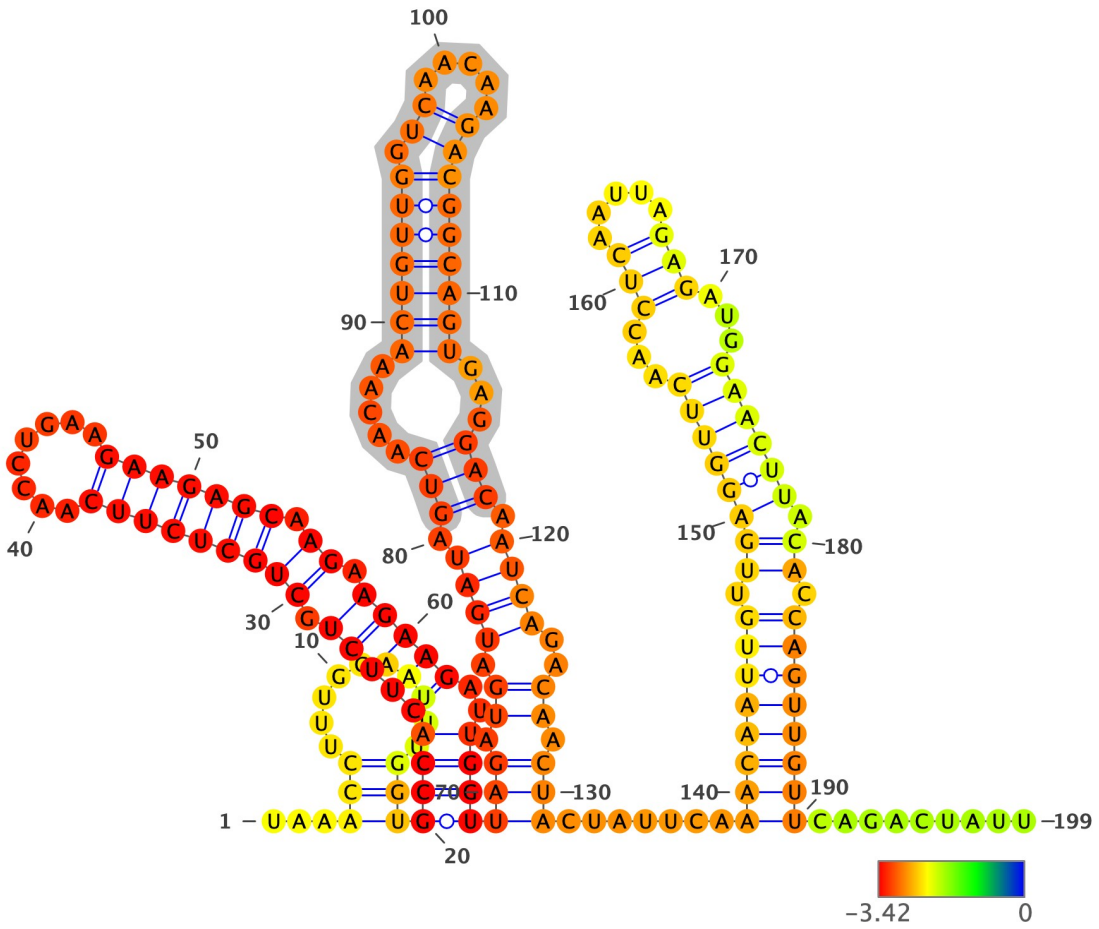
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 59 from nt 3216 to 3253 (nt 81 to 118)

```
5'-GUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGAC-3'
5'-(((.....((((((............))))))...)))-3'
Motif MFE = -9.6; z-score = -2.09; ED = 3.91
```



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

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

```
5'-UAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAG
UGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUU-3
5'-...(((..........)))(((((((((.((((((((((........)))))))).)).)))))..))))(((.((.((((.(((.....(((((((.((.....))))))))
)...))).))))..)).)))......((((((((.((((((((...(((.....)))...)))))).)).))))))))).........-3'
MFE = -56.1; z-score = -3.85; ED = 44.94
```

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(+)

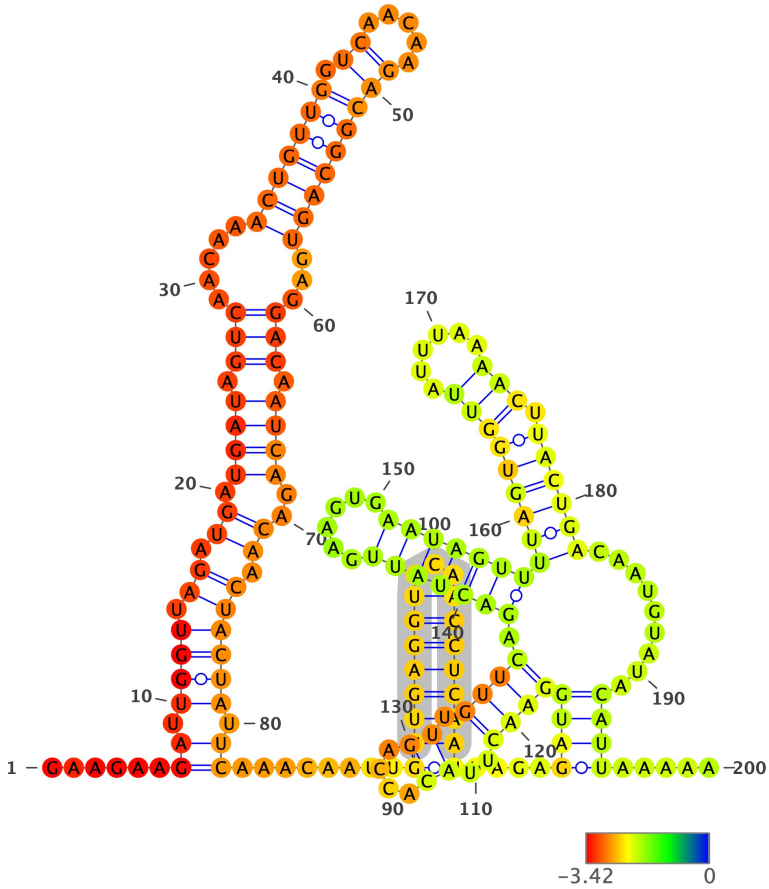
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 60 from nt 3282 to 3298 (nt 92 to 108)

```
5'-UUGAGGUUCAACCUCAA-3'
5'-((((((.....))))))-3'
Motif MFE = -6.7; z-score = -6.14; ED = 0.96
```



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

Extracted structure model with flanking nucleotides 3191 to 3390 (motif highlighted in silver):

```
5'-GAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUA
GAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAA-3
5'-......((.((((.((.((.((((.(((.....(((((((.((.....)))))))))...))).)))).)).)).)))))).)).........((((((((...)))))))).
..(((((((..((....)).)))).(((((((.....)))))))((((((((.....))).)))))).........)))).....-3'
MFE = -42.3; z-score = -3.7; ED = 42.62
```

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(+)

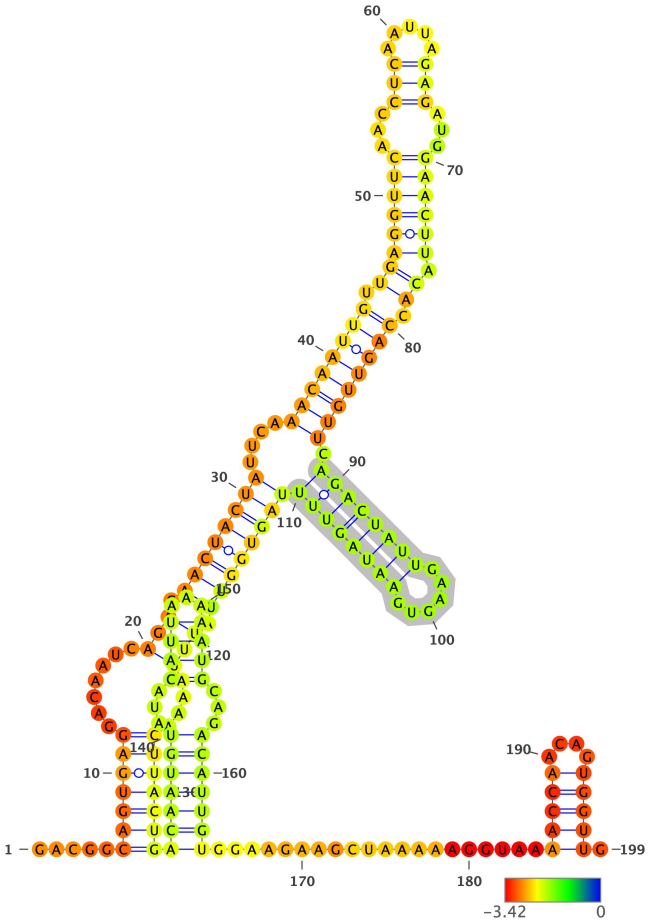
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 61 from nt 3327 to 3348 (nt 89 to 110)

```
5'-AGACUAUUGAAGUGAAUAGUUU-3'
5'-(((((.((......)).)))))-3'
Motif MFE = -5.2; z-score = -5.5; 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 = -3.03; 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(+)

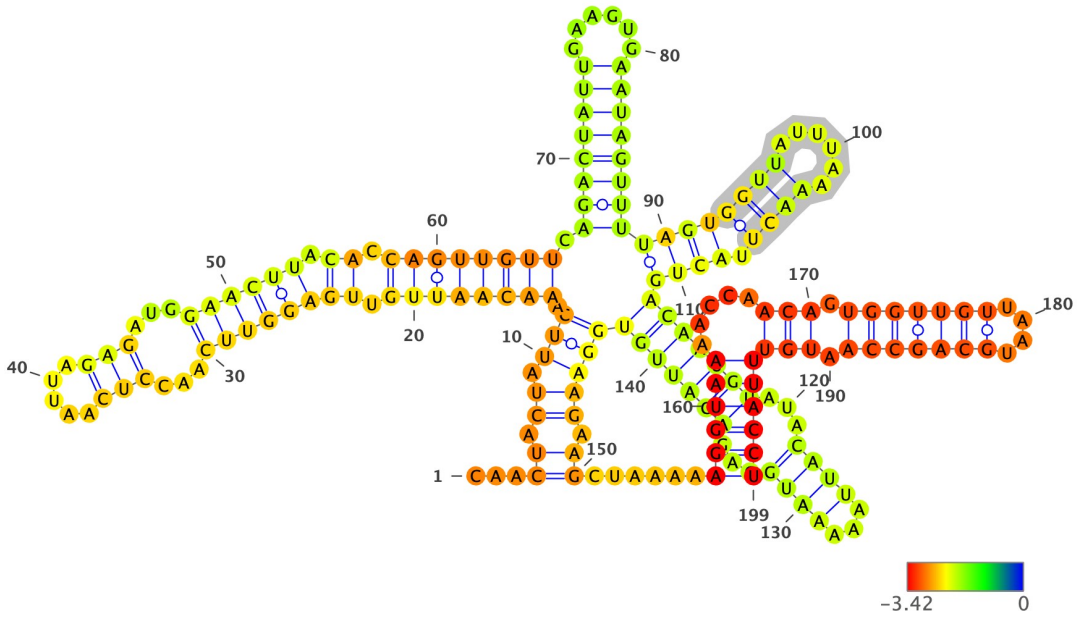
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 62 from nt 3353 to 3366 (nt 93 to 106)

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



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

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

```
5'-CAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUG
ACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCU-3
5'-...((.((.(((.((((((((.((((((((...(((.....)))...)))))).)).))))))))).((((((((......))))))))((((((((......)))).))))
(((((((...((((...))))...)))))))))))).)).....((((((.....(((.(((((((....)))))))).)))))))))-3'
MFE = -49.9; z-score = -4.22; ED = 19.31
```

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(+)

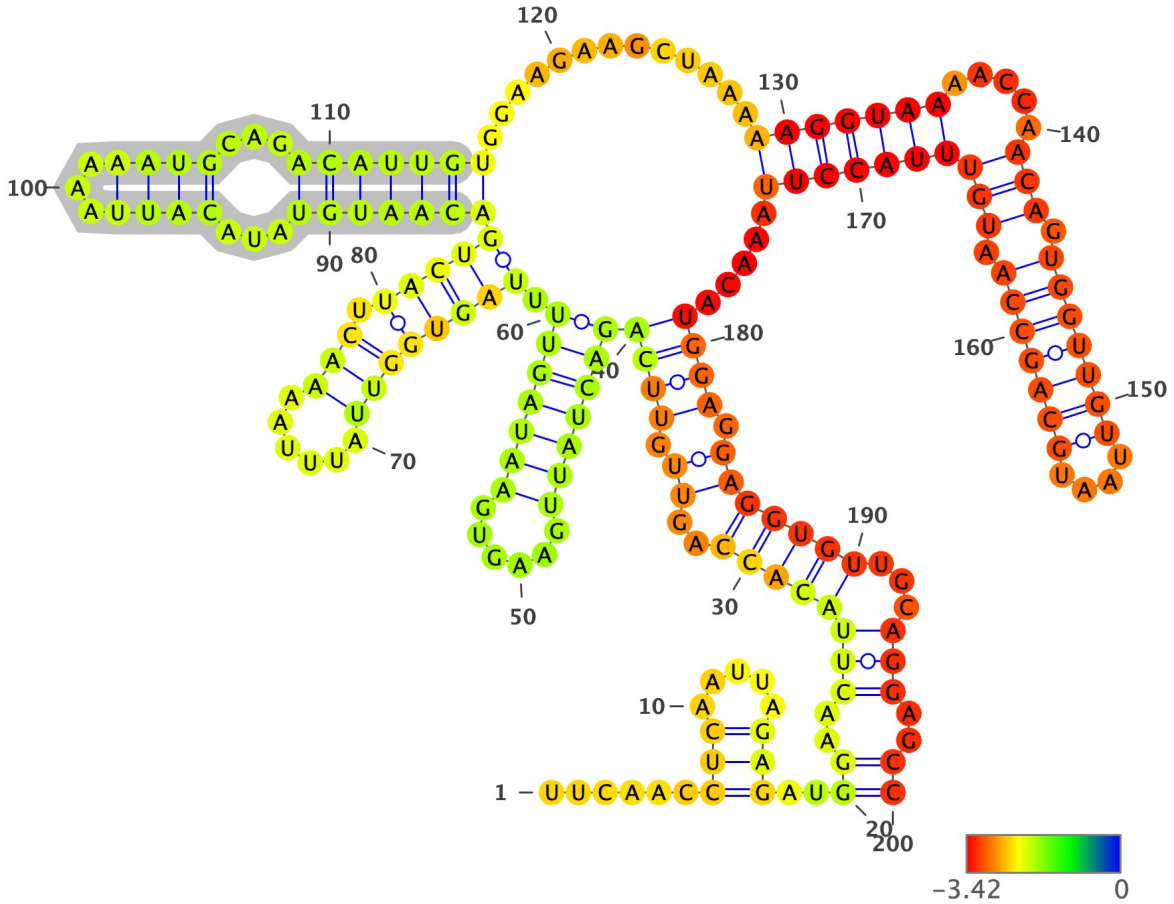
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 63 from nt 3373 to 3401 (nt 86 to 114)

```
5'-CAAUGUAUACAUUAAAAAUGCAGACAUUG-3'
5'-((((((...(((.....)))...))))))-3'
Motif MFE = -4.7; z-score = -2.73; ED = 1.16
```



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

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

```
5'-UUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACA
UUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCC-3
5'-......(((.....)))..((..((((((((..((.(((((((((((.....)))))))).((((((((.....))).)))))(((((((...((((...))))...)))
))))).............(((((((.....(((.(((((((....)))))))).))))))))))).....)))).)))))))...)))..))-3'
MFE = -45.5; z-score = -1.88; ED = 38.66
```

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(+)

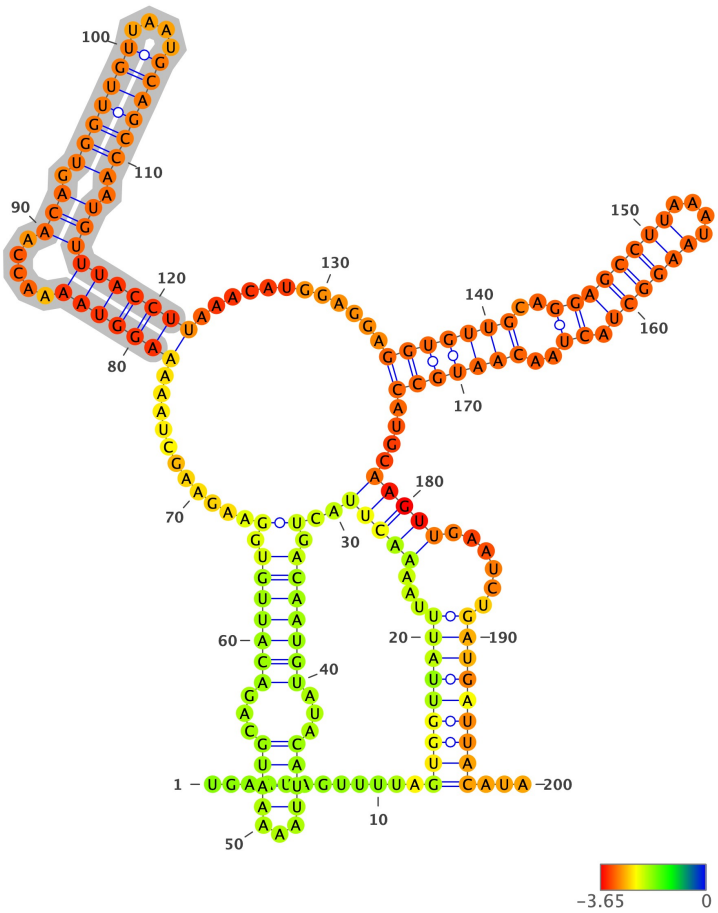
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 64 from nt 3417 to 3459 (nt 79 to 121)

```
5'-AGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCU-3'
5'-((((((.....(((.(((((((....)))))))).)))))))))-3'
Motif MFE = -15.1; z-score = -4.16; ED = 2.8
```



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

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

```
5'-UGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCA
AUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUA-3
5'-............((((((((((...(((((..(.(((((((...((((...))))...)))))))).)...........(((((((.....(((.(((((((....)))))))
.))))))))))............(((((((..((((((((....)))))).))..)))))))....)))))......))))))))...-3'
MFE = -50.2; z-score = -3.64; ED = 29.93
```

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

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

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

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

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

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

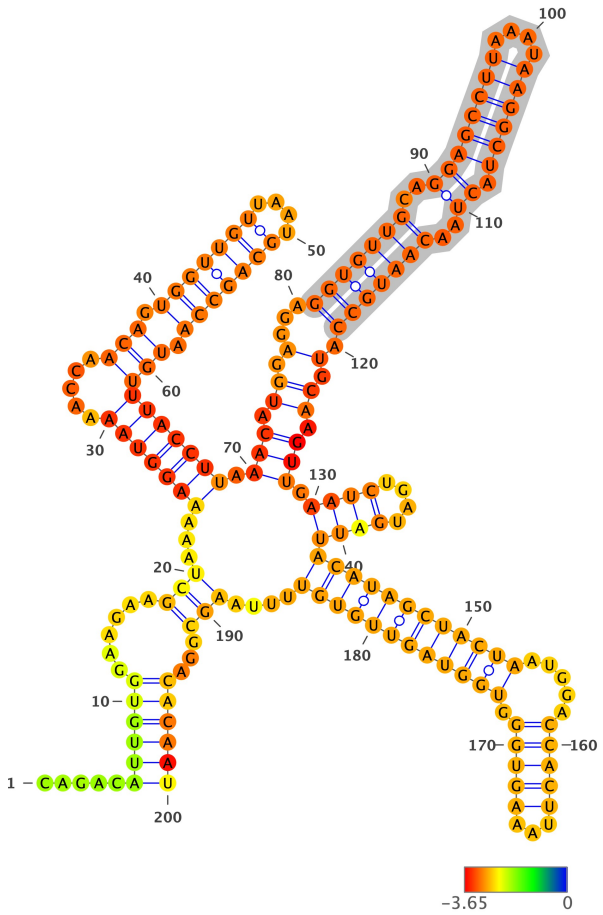
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 65 from nt 3473 to 3511 (nt 81 to 119)

```
5'-GGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCC-3'
5'-(((((((..(((((((((....)))))))).))..)))))))-3'
Motif MFE = -15.6; z-score = -4.1; 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 = -4.69; 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(+)

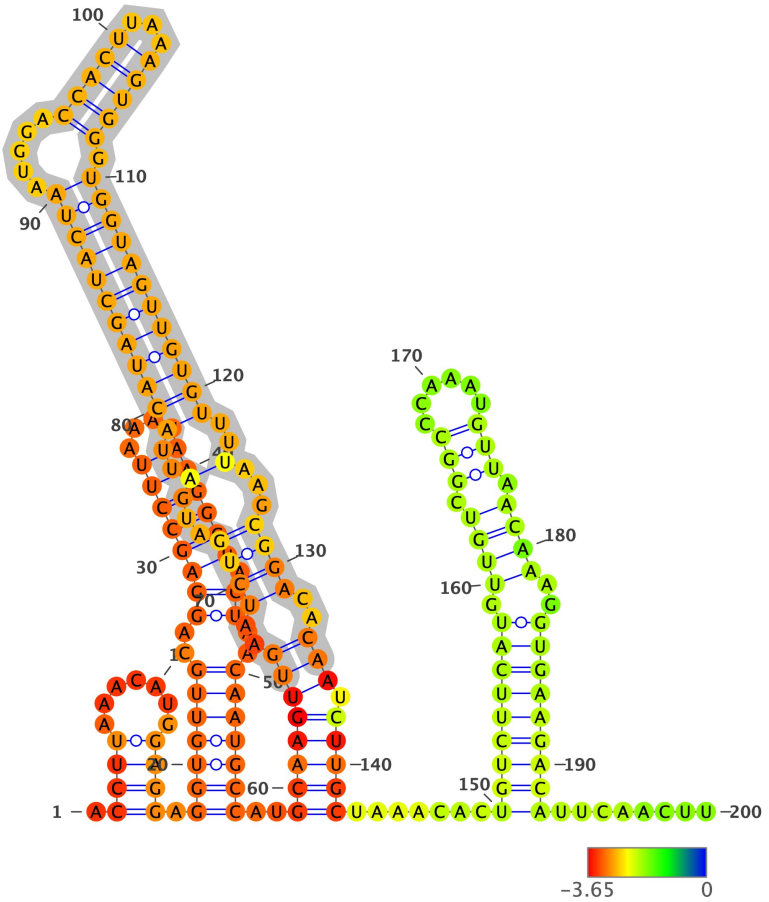
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 66 from nt 3520 to 3590 (nt 65 to 135)

```
5'-UGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACA-3'
5'-((..((........((((((((((((.....(((((...))))).))))))))))))........))..))-3'
Motif MFE = -21.3; z-score = -3.29; ED = 4.11
```



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 3456 to 3655 (motif highlighted in silver):

```
5'-ACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUG
GUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUU-3
5'-.((((.......)))).(((((((..((((((((....))))))).))..)))))))..((((((((..((((...(..(((((((((((.....(((((...))))).))
))))))))))..)...))))..))).)))))).......(((((((((.((((.(((......))).))))..)))))))))........-3'
MFE = -64.9; z-score = -4.68; 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(+)

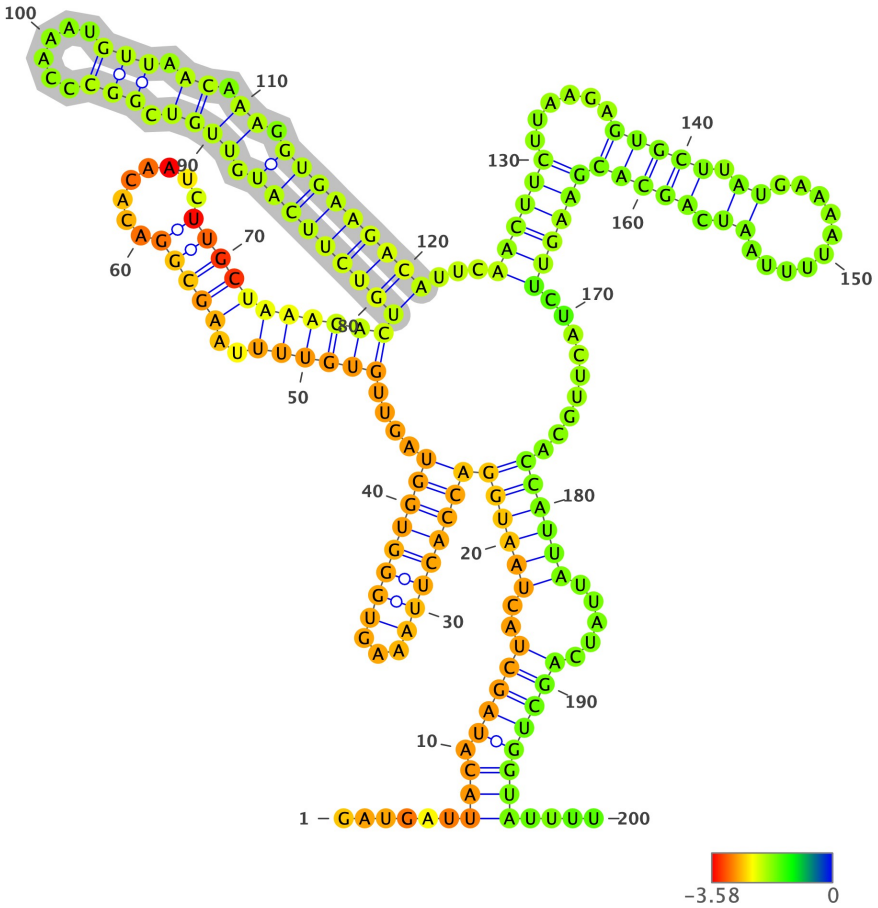
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 67 from nt 3605 to 3647 (nt 79 to 121)

```
5'-UGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACA-3'
5'-(((((((((.((((.(((......))).)).)).)))))))))-3'
Motif MFE = -14.2; z-score = -3.84; ED = 2.86
```



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

Extracted structure model with flanking nucleotides 3527 to 3726 (motif highlighted in silver):

```
5'-GAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAA
GGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUU-3
5'-......(((.(((((..((((((((((((((...))))))))....((((((..(((((........)))))))))))(((((((((.((((.(((......))).)).))
.)))))))))...((((((......(((((.((..........)).))))))))))).........))))))).....))))))))....-3'
MFE = -49.3; z-score = -2.35; ED = 33.14
```

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

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

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

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

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

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

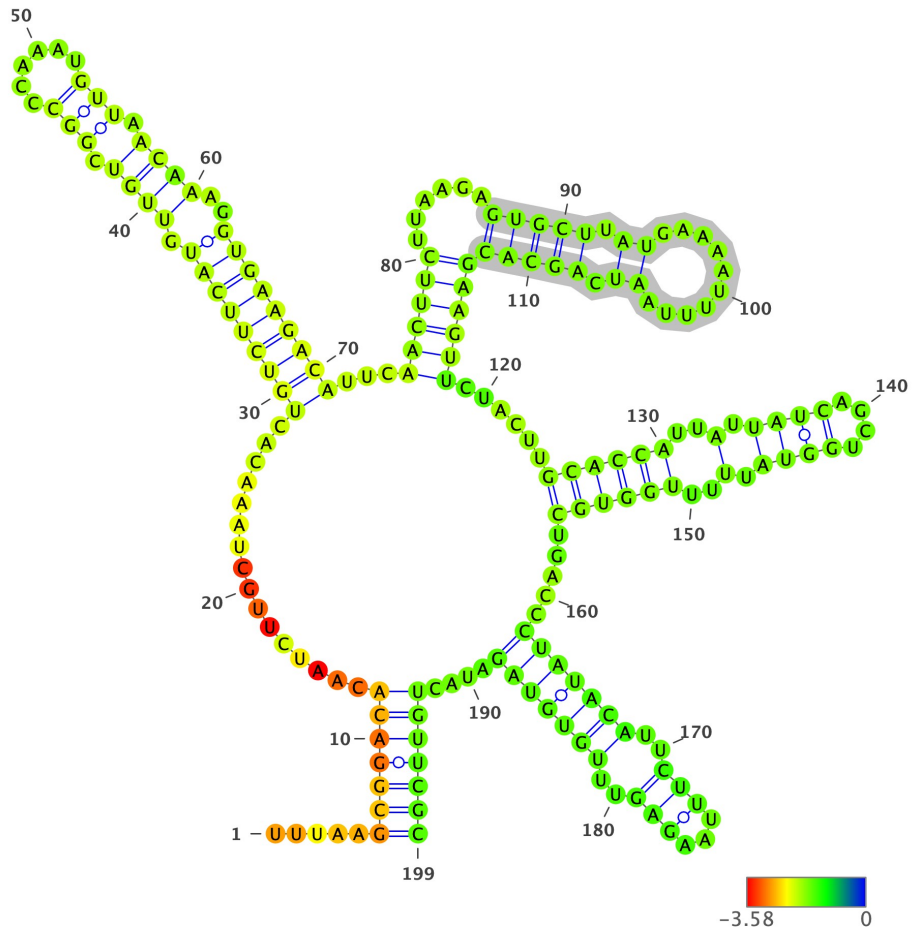
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 68 from nt 3663 to 3688 (nt 87 to 112)

```
5'-GUGCUUAUGAAAAUUUUAAUCAGCAC-3'
5'-(((((.((..........)).)))))-3'
Motif MFE = -4.0; z-score = -1.67; ED = 3.63
```



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

Extracted structure model with flanking nucleotides 3577 to 3775 (motif highlighted in silver):

```
5'-UUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCA
CGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGC-3
5'-.....(((((((.................(((((((((.((((.(((......))).))))..)))))))))...((((((......(((((.((..........)).))))
)))))))......((((((..(.((((....)))).)..))))))).....(((((((..(((...)))..)))))))....)))))))-3'
MFE = -53.2; z-score = -3.73; ED = 19.46
```

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(+)

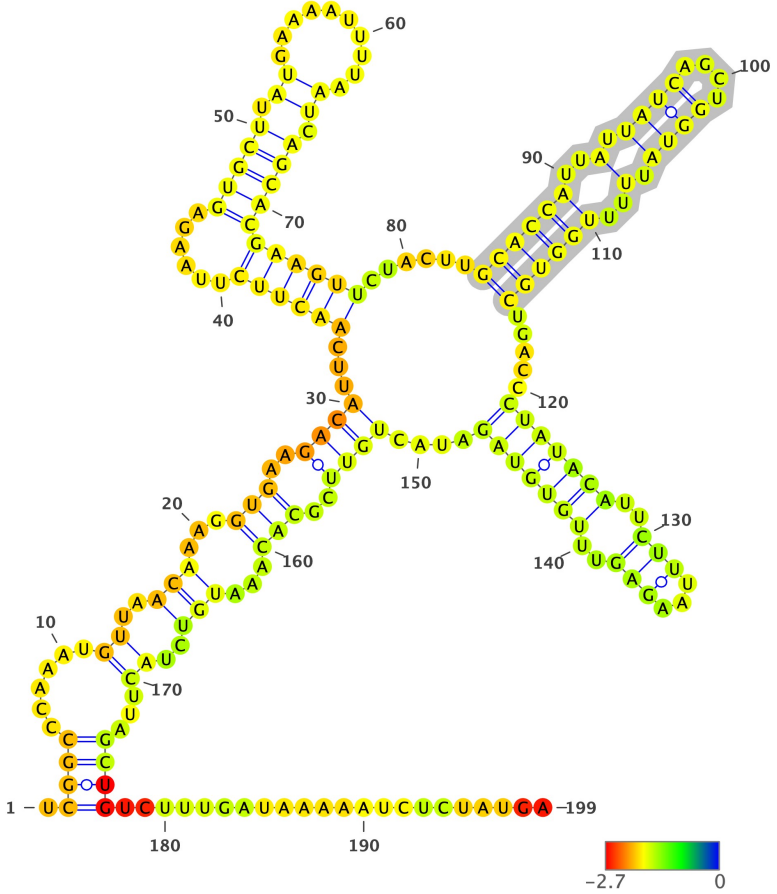
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 69 from nt 3701 to 3732 (nt 84 to 115)

```
5'-GCACCAUUAUUAUCAGCUGGUAUUUUUGGUGC-3'
5'-((((((..(.((((....)))).)..))))))-3'
Motif MFE = -11.2; z-score = -3.78; 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 = -1.23; ED = 36.24
```

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

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

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

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

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

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

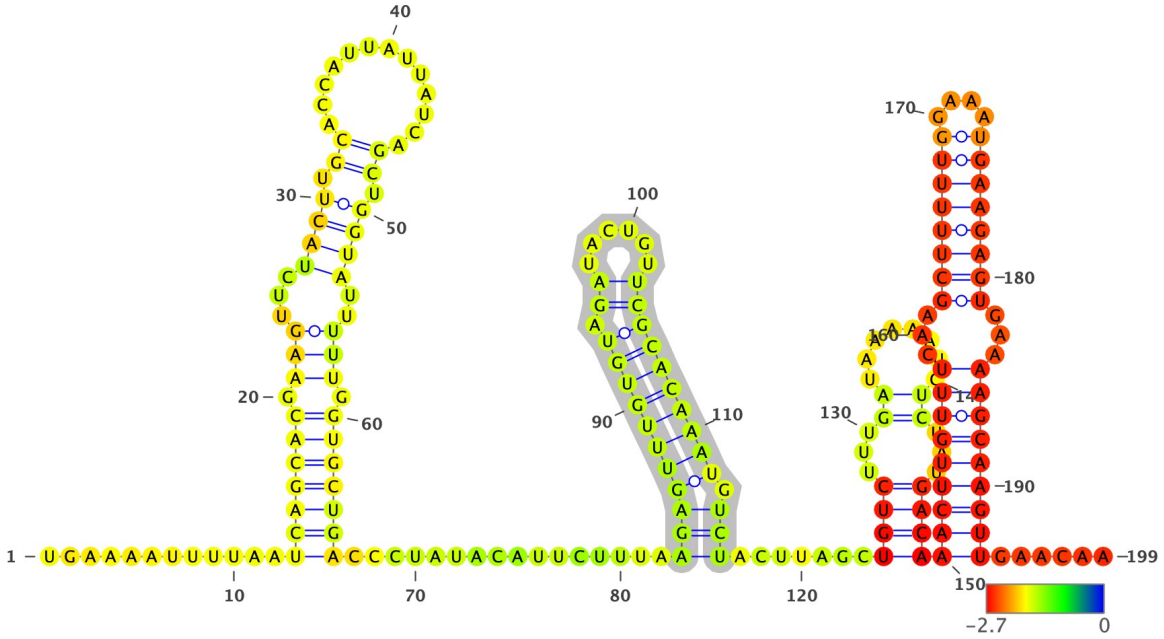
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 70 from nt 3752 to 3785 (nt 83 to 116)

```
5'-AGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCU-3'
5'-(((.(((((((.((......)))))))))..)))-3'
Motif MFE = -8.7; z-score = -2.02; ED = 3.36
```



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

Extracted structure model with flanking nucleotides 3670 to 3868 (motif highlighted in silver):

```
5'-UGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAA
UGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAA-3
5'-............(((((((.(((...((((.((.............)).)))).)))).)))))))................(((((((((((.((......)))))))))
).)))........((((...((........))...))))((((((((((...((((((((....)))))))))...))))))))).......-3'
MFE = -43.7; z-score = -2.64; ED = 27.76
```

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

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

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

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

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

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

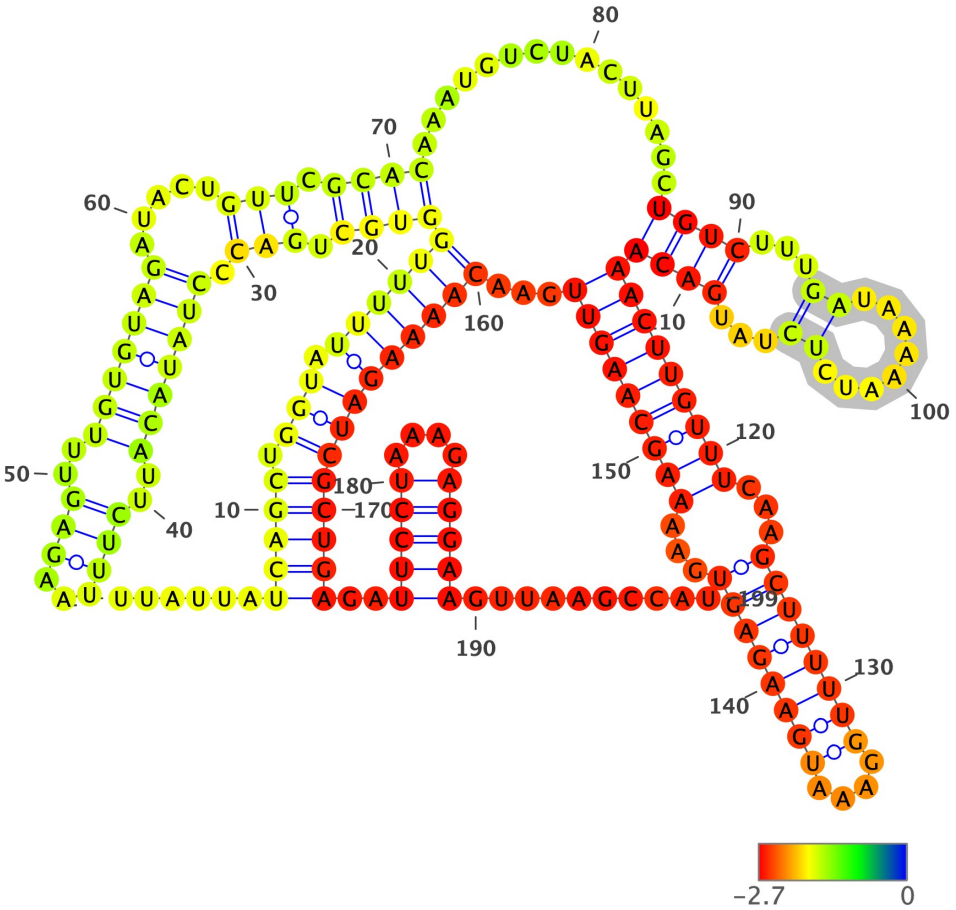
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 71 from nt 3800 to 3811 (nt 94 to 105)

```
5'-GAUAAAAAUCUC-3'
5'-((........))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.4
```



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

Extracted structure model with flanking nucleotides 3707 to 3905 (motif highlighted in silver):

```
5'-UUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGAC
AAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAU-3
5'-......(((((.(((.(((((((((((.(((.(((((((..(((...)))..)))))))).....))).))))...............((((...((........))...)))
)(((((((((...((((((((....))))))))...))))))))))...))))))))))))))..(((((....)))))..........-3'
MFE = -46.9; z-score = -2.29; ED = 37.63
```

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(+)

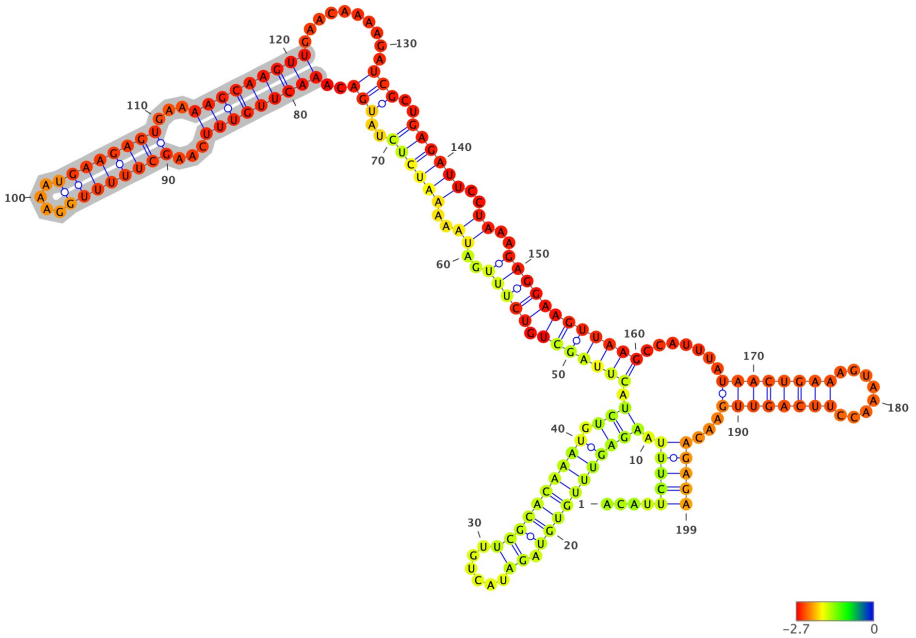
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 72 from nt 3819 to 3862 (nt 78 to 121)

```
5'-AACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUU-3'
5'-((((((((((...(((((((.....)))))))...)))))))))-3'
Motif MFE = -13.1; z-score = -4.08; ED = 3.73
```



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

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

```
5'-ACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGA
AAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGA-3
5'-....(((((.((((((((((((.((.....)))))))))).))).(((((((.(((((..((..((((((..(((..(((((((((...((((((((....))))))))..
.)))))))))..........)))..))))))..))..))))))))))))).......((((((((........))))))))...)))))-3'
MFE = -47.3; z-score = -3.1; 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(+)

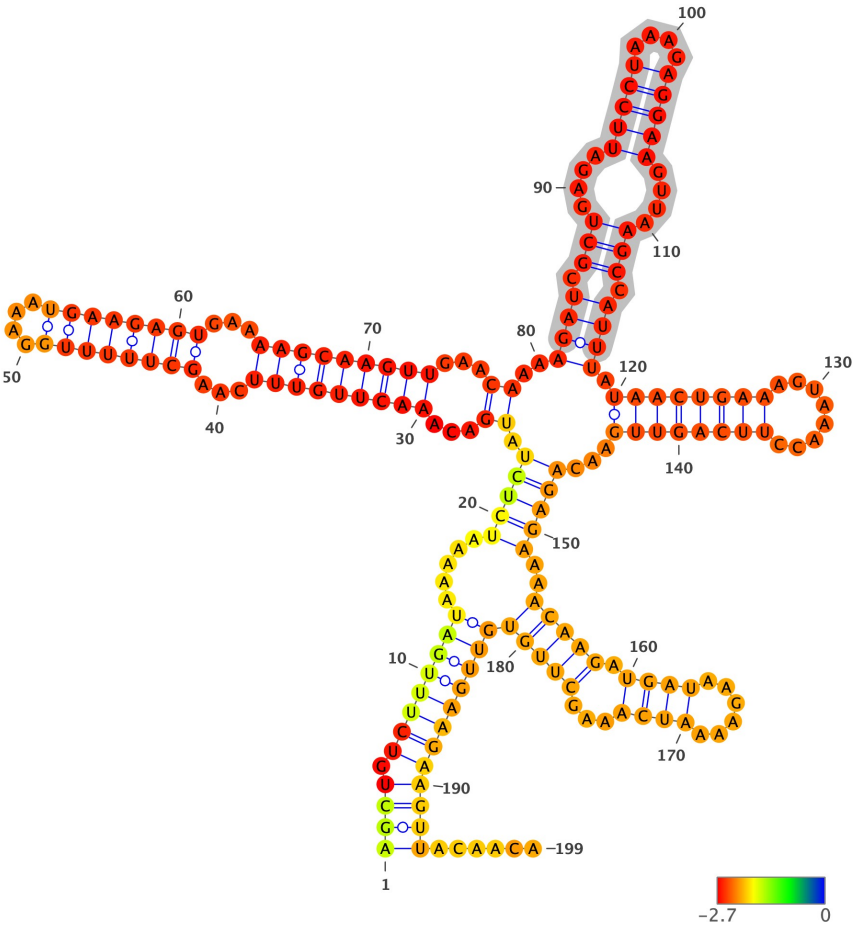
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 73 from nt 3871 to 3906 (nt 82 to 117)

```
5'-GAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUU-3'
5'-(((.(((....((((......)))).....))).)))-3'
Motif MFE = -8.5; z-score = -2.4; ED = 2.8
```



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

Extracted structure model with flanking nucleotides 3790 to 3988 (motif highlighted in silver):

```
5'-AGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAA
GCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACA-3
5'-((((.((((((((.....(((((.((...((((((((((...((((((((....))))))))...))))))))))...))..((((.(((....(((((....)))))....)
)).)))).((((((((.........))))))))...)))))..(((((.((((......))))...))))))))))))))))).....-3'
MFE = -45.2; z-score = -3.51; ED = 13.48
```

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

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

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

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

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

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

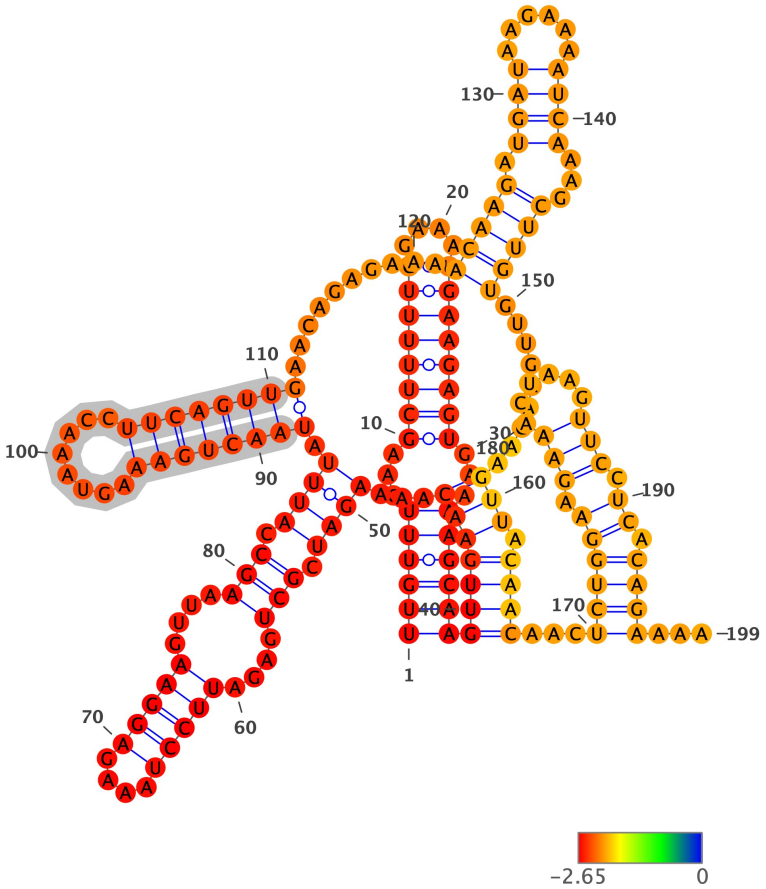
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 74 from nt 3910 to 3931 (nt 89 to 110)

```
5'-AACUGAAAGUAAACCUUCAGUU-3'
5'-(((((((........)))))))-3'
Motif MFE = -5.1; z-score = -3.63; ED = 1.95
```



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

Extracted structure model with flanking nucleotides 3822 to 4020 (motif highlighted in silver):

```
5'-UUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUG
AACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAA-3
5'-((((((...((((((((....))))))))...))))))(((((((...((((.(((....(((((....)))))....))).)))).((((((((........))))))))
..........(((((.((((......))))...)))))..........))).))))...((((((.(((......))).)).))))...-3'
MFE = -40.6; z-score = -3.47; ED = 28.09
```

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

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

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

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

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

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

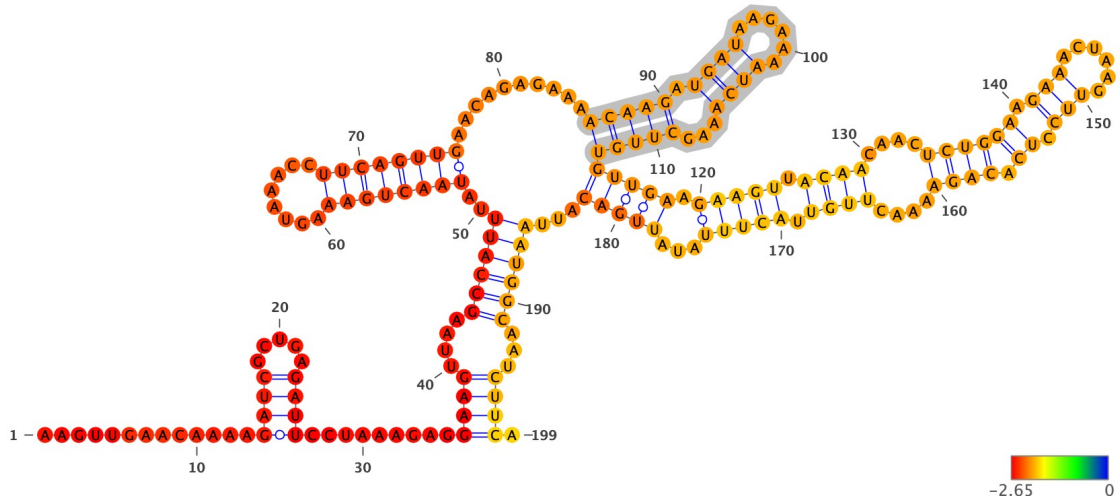
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 75 from nt 3943 to 3970 (nt 86 to 113)

```
5'-ACAAGAUGAUAAGAAAAUCAAAGCUUGU-3'
5'-(((((.((((......))))...)))))-3'
Motif MFE = -4.5; z-score = -3.34; 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 = -2.36; 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(+)

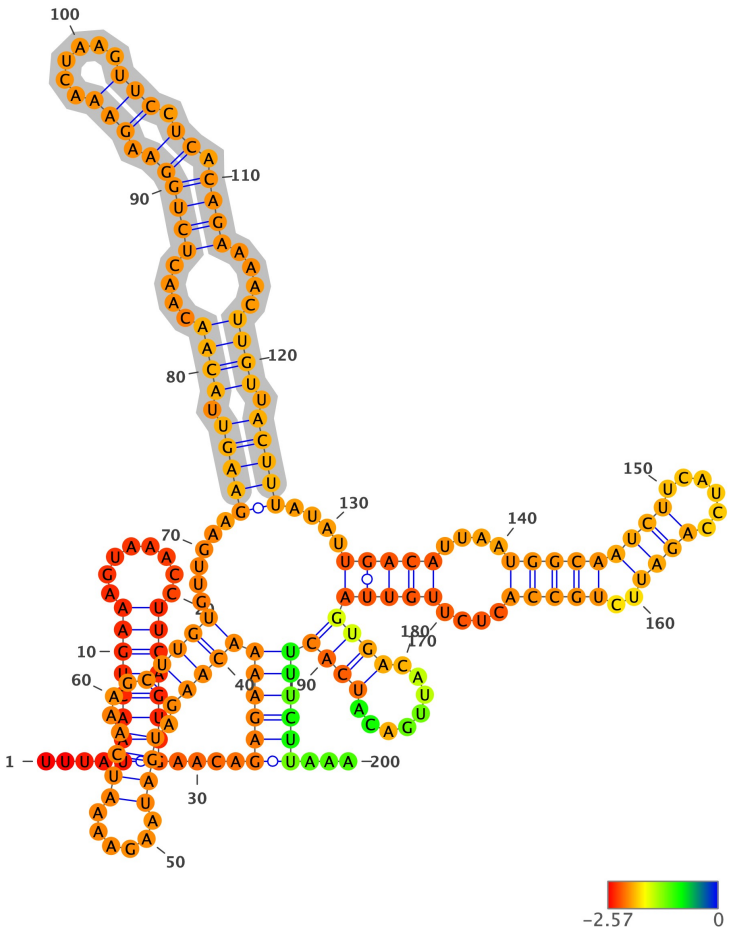
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 76 from nt 3978 to 4030 (nt 74 to 126)

```
5'-AAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUU-3'
5'-((((.((((....((((((.(((......))).)).)))).....)))).))))-3'
Motif MFE = -10.0; z-score = -2.64; 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 = -2.79; 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(+)

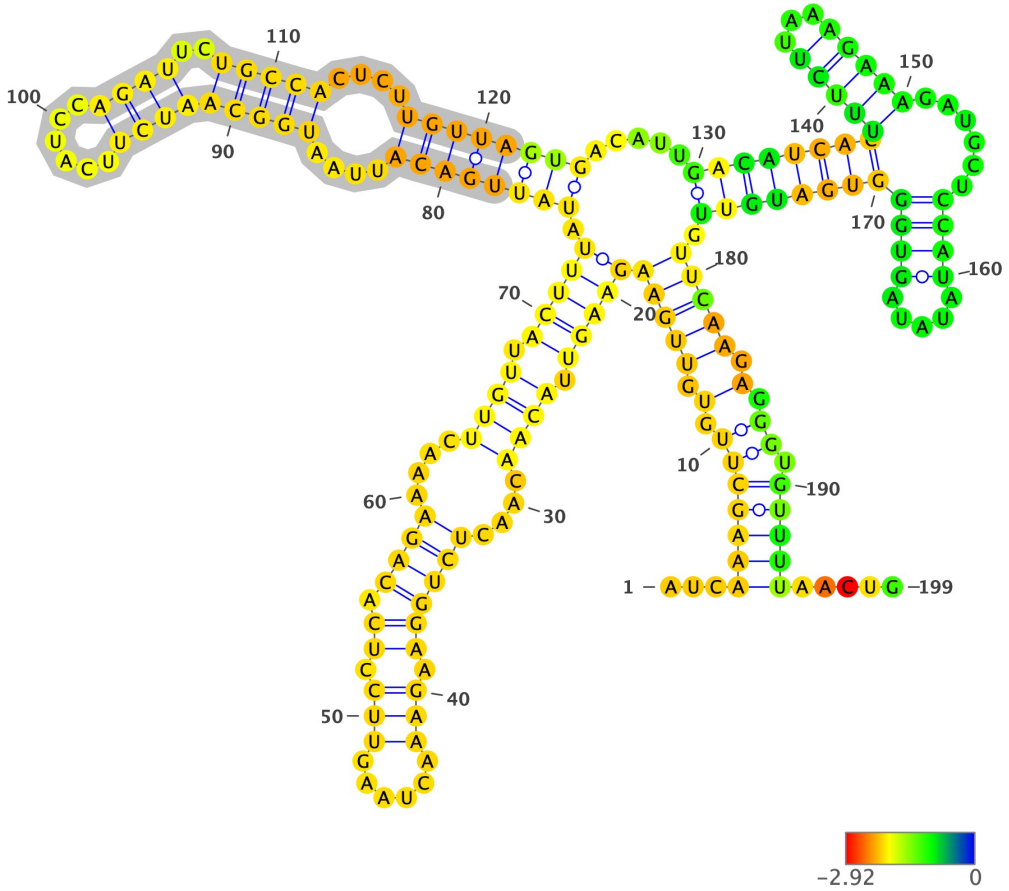
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 77 from nt 4036 to 4079 (nt 78 to 121)

```
5'-UGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUCUUGUUA-3'
5'-(((((....(((((((((.....)))).)).)))))....)))))-3'
Motif MFE = -10.4; z-score = -2.91; 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 3959 to 4157 (motif highlighted in silver):

```
5'-AUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCC
ACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUG-3
5'-...(((((((.(.((((((((((.((((....((((((.(((.....))).)).)))).....)))).)))))).(((((((((....(((((((((.....)))))..))))
)....)))))))).....((((((((((((...)))))).....(((.....)))))))))))).)))))).)).)))))).....-3'
MFE = -44.4; z-score = -1.51; ED = 34.17
```

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(+)

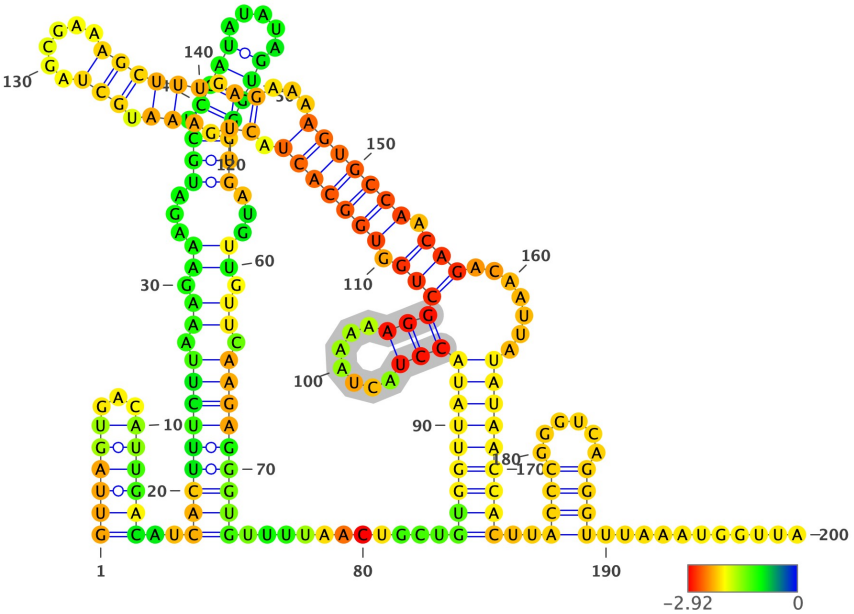
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 78 from nt 4169 to 4181 (nt 94 to 106)

```
5'-CCUACUAAAAAGG-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.13; 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 = -2.49; 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(+)

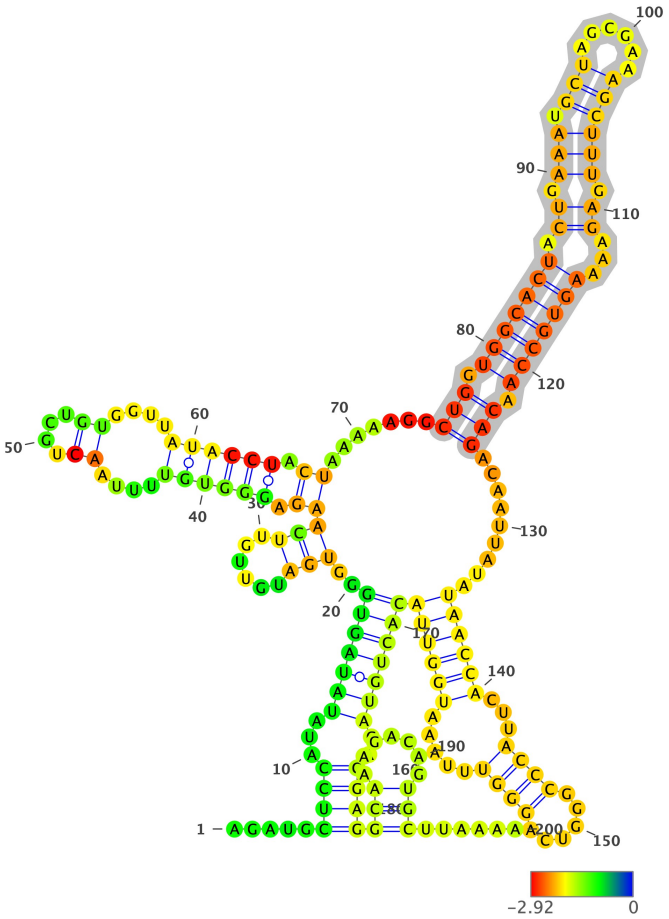
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 79 from nt 4182 to 4232 (nt 75 to 125)

```
5'-CUGGUGGCACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAG-3'
5'-(((.(((((((.((.(((.(((......)))))).))...))))))).)))-3'
Motif MFE = -18.7; z-score = -4.02; 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 = -2.47; 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(+)

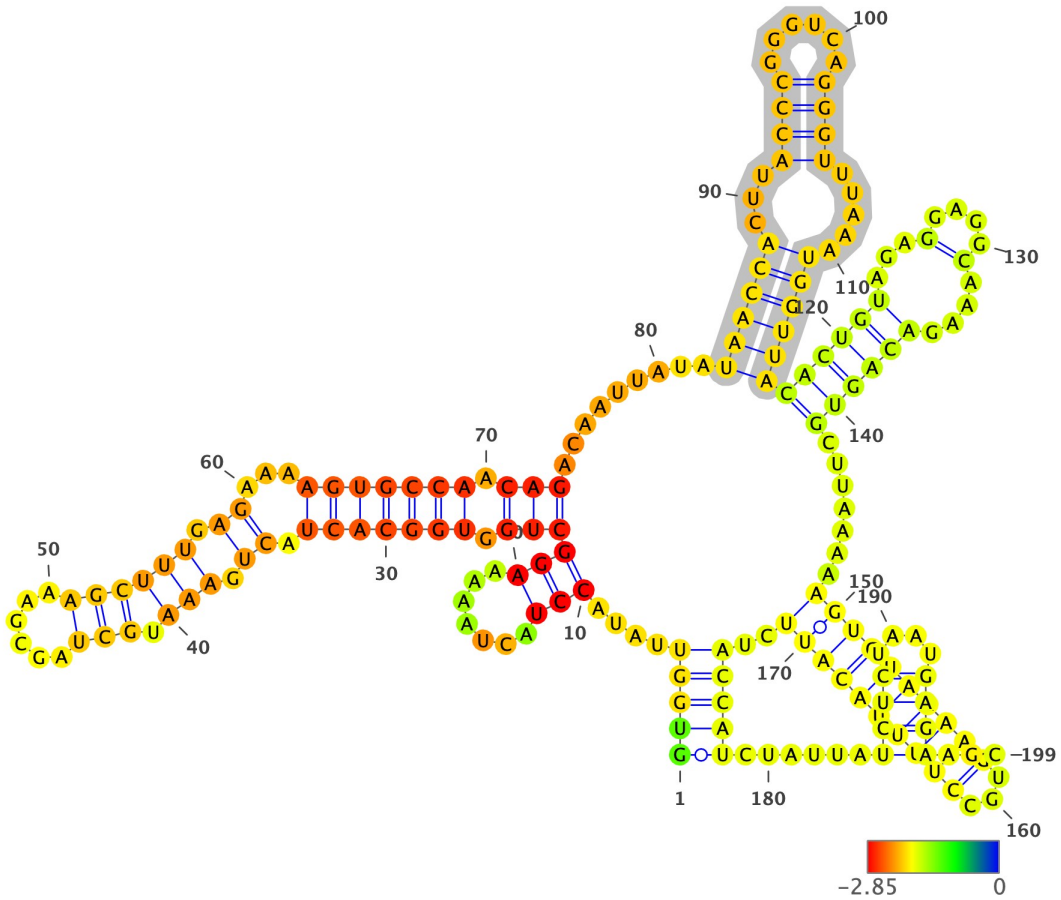
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 80 from nt 4242 to 4275 (nt 83 to 116)

```
5'-UAACCACUUACCCGGGUCAGGGUUUAAAUGGUUA-3'
5'-((((((...((((......))))).....))))))-3'
Motif MFE = -10.7; z-score = -3.53; 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 = -3.97; 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(+)

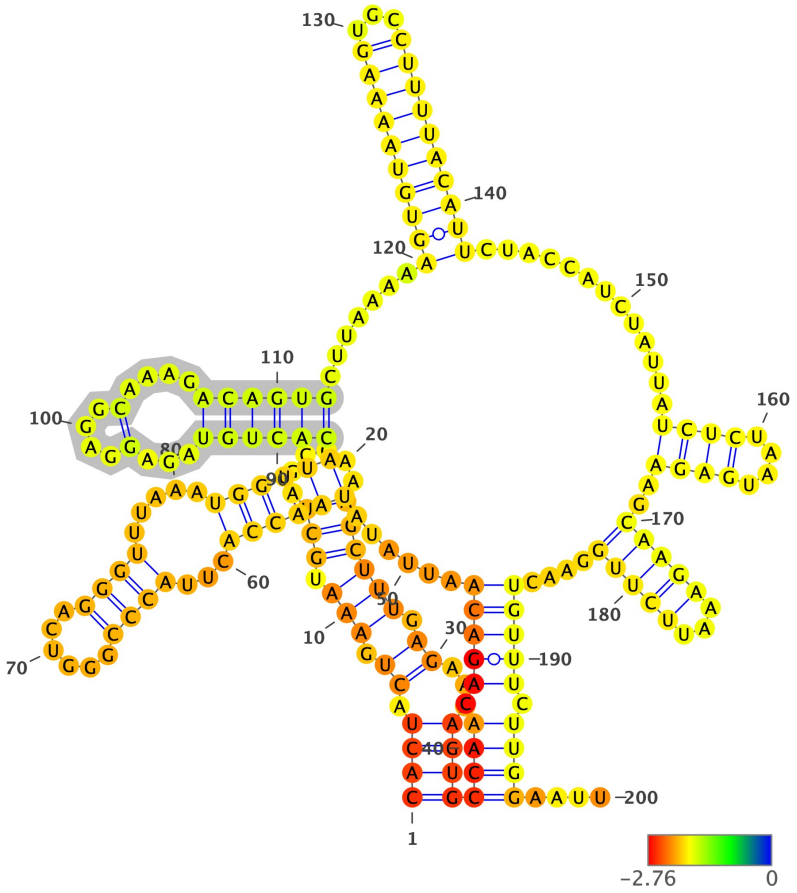
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 81 from nt 4276 to 4300 (nt 88 to 112)

```
5'-CACUGUAGAGGAGGCAAAGACAGUG-3'
5'-((((((...(....)....))))))-3'
Motif MFE = -4.7; z-score = -1.51; ED = 0.96
```



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

Extracted structure model with flanking nucleotides 4189 to 4388 (motif highlighted in silver):

```
5'-CACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGU
GCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUU-3
5'-((((.((.(((.(((......))))))).))...))))((((.(((((......((((((...((((......))))).....))))))((((((...(....)....)))))
).......((((((((((...))))))))))).............((((....))))..(((((...)))))....)))))).))))....-3'
MFE = -46.8; z-score = -2.32; ED = 9.79
```

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(+)

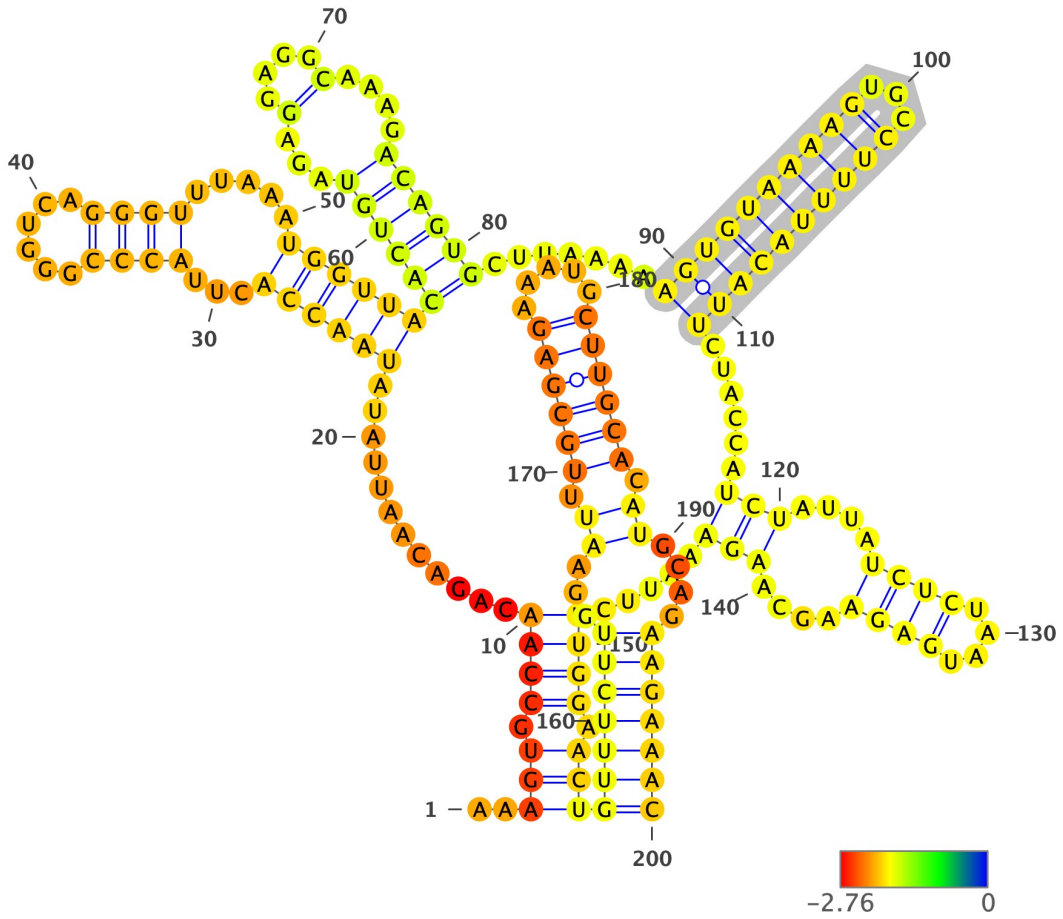
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 82 from nt 4308 to 4330 (nt 89 to 111)

```
5'-AGUGUAAAAGUGCCUUUUACAUU-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -6.6; z-score = -4.42; 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 4220 to 4419 (motif highlighted in silver):

```
5'-AAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUU
CUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAAC-3
5'-..(((.((((............((((((...((((......))))).....))))))((((((...(....)....))))))).......((((((((((...))))))))))
......(((....((((....))))....)))).....)))).)))(((((((...((.((((((.....)))))).))....)))))))-3'
MFE = -46.6; z-score = -2.26; ED = 31.61
```

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

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

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

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

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

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

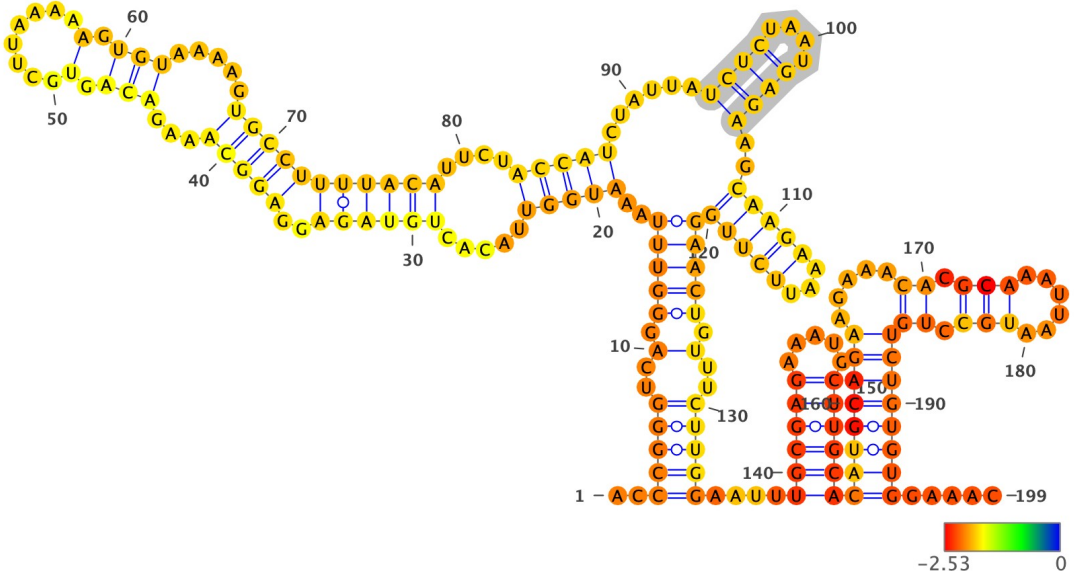
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 4344 to 4355 (nt 94 to 105)

```
5'-UCUCUAAUGAGA-3'
5'-((((....))))-3'
Motif MFE = -2.9; z-score = -9.48; 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 = -1.86; 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(+)

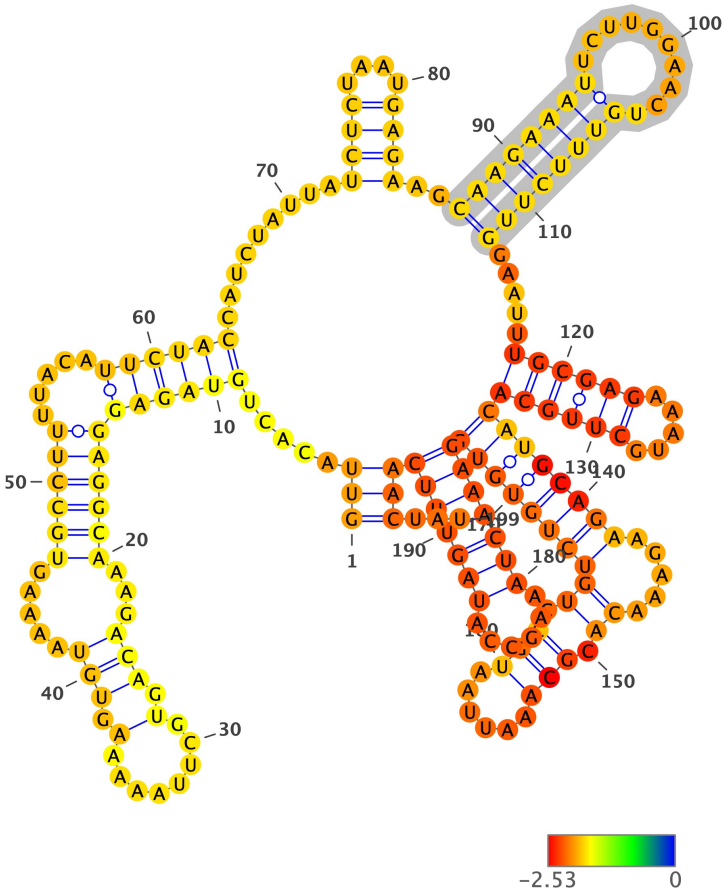
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 84 from nt 4358 to 4383 (nt 87 to 112)

```
5'-CAAGAAAUUCUUGGAACUGUUUCUUG-3'
5'-((((((((..........))))))))-3'
Motif MFE = -5.1; z-score = -2.2; 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 4272 to 4470 (motif highlighted in silver):

```
5'-GUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUU
GGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAU-3
5'-(((.....(((((((((((...(((.(........).)))).....))))))).....))))))..........((((....))))..((((((((..........)))))))
).....((((((.....))))))((((((((.....((.(((......))).))))))))))(((((((......)))))))))...-3'
MFE = -49.0; z-score = -2.99; ED = 43.34
```

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

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

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

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

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

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

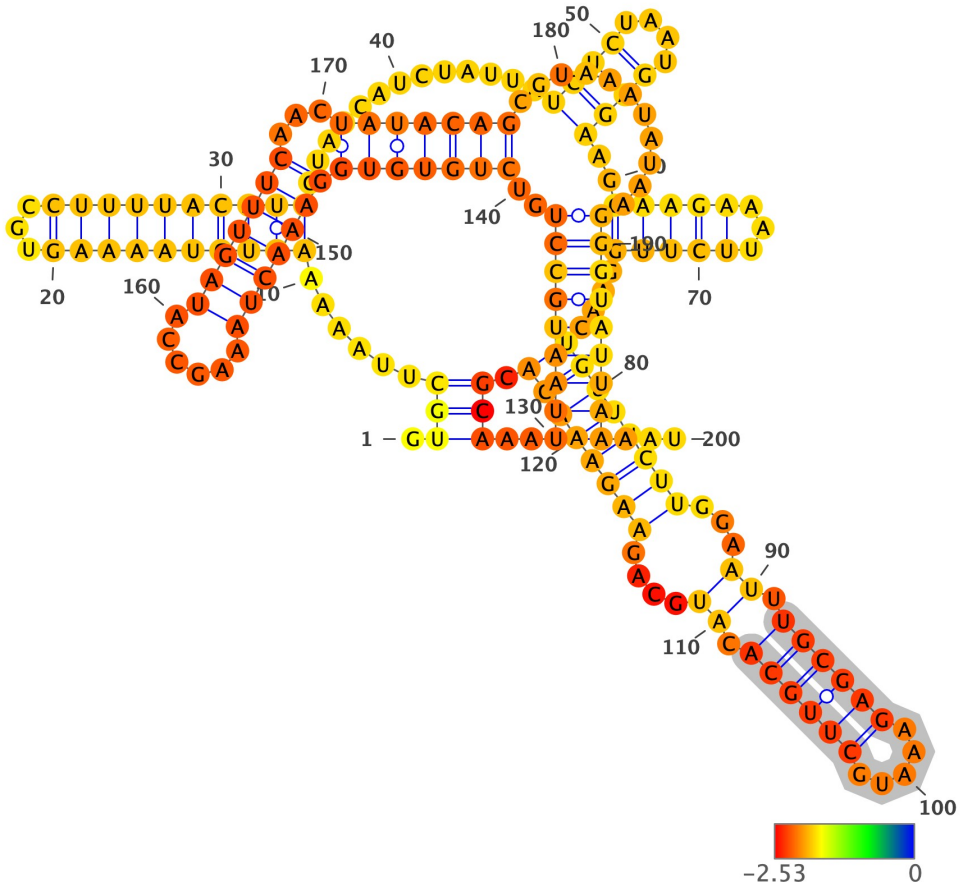
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 4389 to 4405 (nt 92 to 108)

```
5'-UGCGAGAAAUGCUUGCA-3'
5'-((((((.....))))))-3'
Motif MFE = -5.4; z-score = -3.65; ED = 0.52
```



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

Extracted structure model with flanking nucleotides 4298 to 4497 (motif highlighted in silver):

```
5'-GUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAU
GCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAU-3
5'-.(((......((((((((((...)))))))))).............((((....)))).((((((...)))))....((((((((...((.((((((.....)))))).))
....)))))))).))).((((((((..((((((((((((((.....)))))))...)))))))).........))))))))...-3'
MFE = -49.7; z-score = -3.32; ED = 12.9
```

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(+)

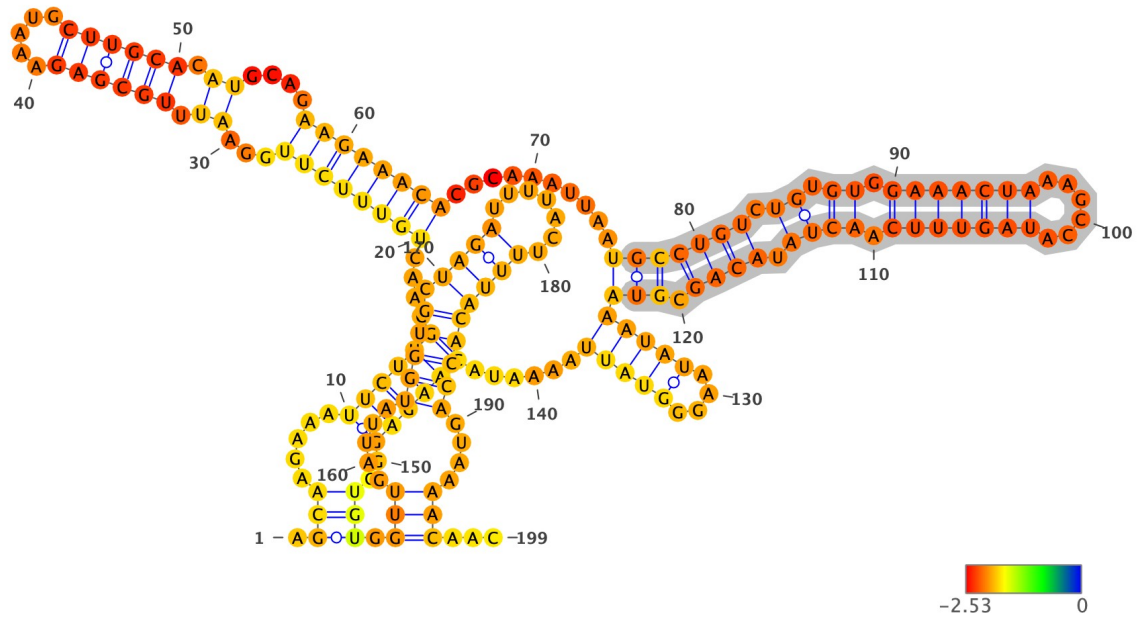
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 86 from nt 4432 to 4477 (nt 77 to 122)

```
5'-GCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGU-3'
5'-(.((((.......(((((((......)))))))......))))..)-3'
Motif MFE = -12.1; z-score = -2.05; ED = 8.39
```



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 4356 to 4554 (motif highlighted in silver):

```
5'-AGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAA
CUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAAC-3
5'-.(((.....((((((....((((((((...((.((((((.....)))))).))....))))))))..........(((((((.((.((.(((((((......)))))))).)
))).)))).)))(((((....)))))......)))))).))).(((.....(((((.((((.......)))))))))....)))...-3'
MFE = -41.4; z-score = -2.51; ED = 42.83
```

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(+)

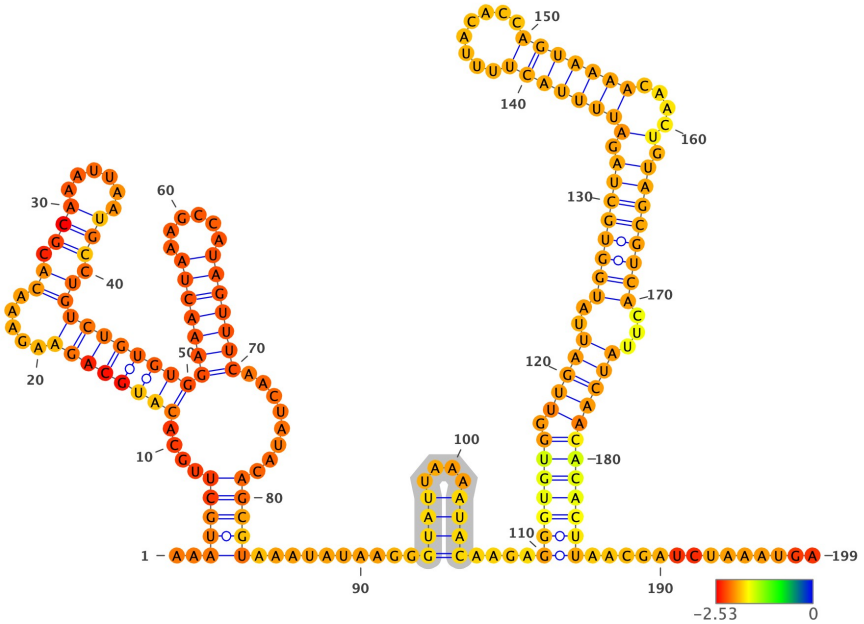
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 87 from nt 4488 to 4499 (nt 94 to 105)

```
5'-GUAUUAAAAUAC-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 1.48
```



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

Extracted structure model with flanking nucleotides 4395 to 4593 (motif highlighted in silver):

```
5'-AAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGG
GUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGA-3
5'-..(((((....((((((((.....((.(((......))).))))))))))(((((((......)))))))........)))))..........((((....))))....((
(((((.(((((..((((((((.((((((((........)))))))....).)))))))))...))))))))))))..............-3'
MFE = -42.1; z-score = -2.01; ED = 33.98
```

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

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

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

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

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

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

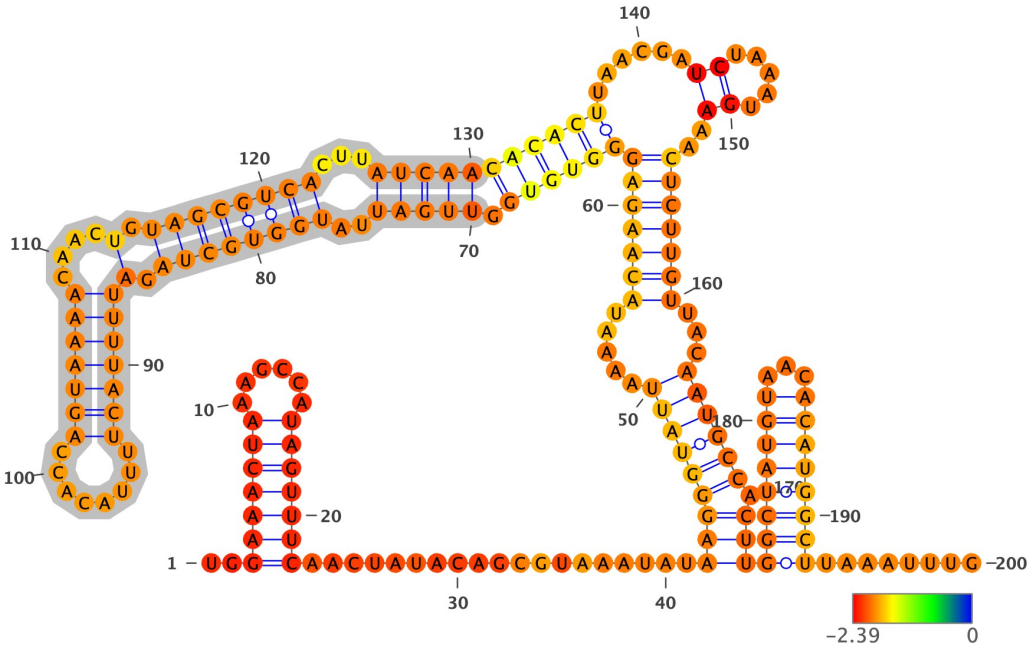
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 88 from nt 4512 to 4572 (nt 70 to 130)

```
5'-UUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAA-3'
5'-(((((..(((((((((..(((((((.......)))))))).....)))))))))...)))))-3'
Motif MFE = -11.9; z-score = -1.65; ED = 9.59
```



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

Extracted structure model with flanking nucleotides 4443 to 4642 (motif highlighted in silver):

```
5'-UGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAA
CUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUG-3
5'-..(((((((.....)))))))...................(((((((((.....(((((((((((((.(((((..(((((((((.(((((((.......)))))))...
.).))))))))...))))))))))).....((.....)).)))))))...)))))).)))((((((((((...)))))))))........-3'
MFE = -49.0; z-score = -3.31; ED = 22.11
```

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(+)

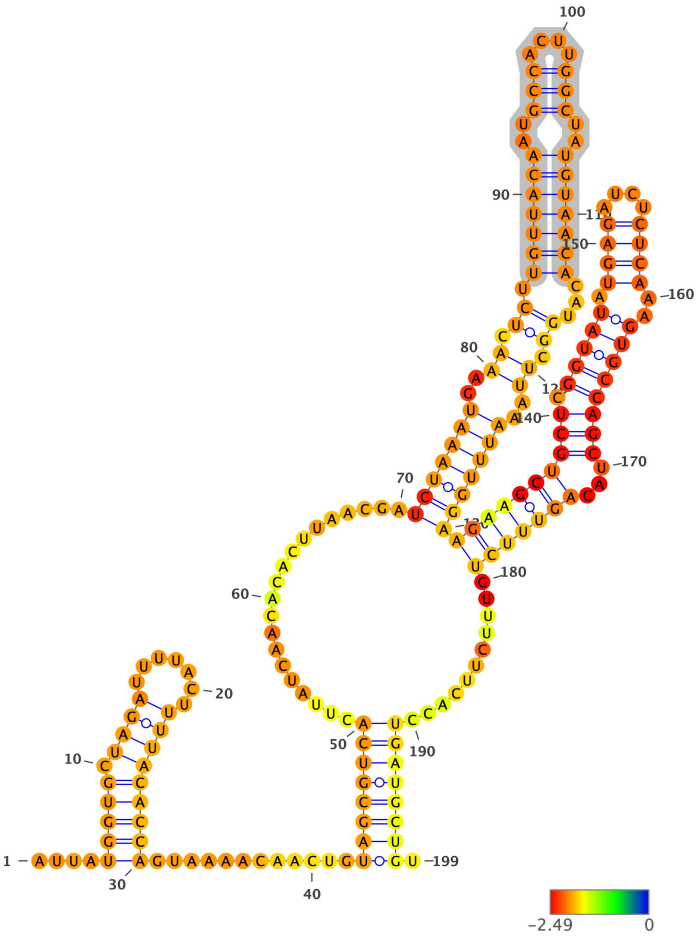
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 89 from nt 4600 to 4627 (nt 86 to 113)

```
5'-UGUUACAAUGCCACUUGGCUAUGUAACA-3'
5'-(((((((..(((....)))..)))))))-3'
Motif MFE = -11.1; z-score = -4.68; 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 4515 to 4713 (motif highlighted in silver):

```
5'-AUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAACUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAA
CACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGU-3
5'-....(((((.((((.......)))))))))............((((((((.....................(((((((..((.((.(((((((..(((....)))..)))))
))...)).))..)))))))((((((((((.(((((.((((....))))..)))))))))...)))))))...........))))))).-3'
MFE = -48.7; z-score = -3.07; ED = 16.91
```

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(+)

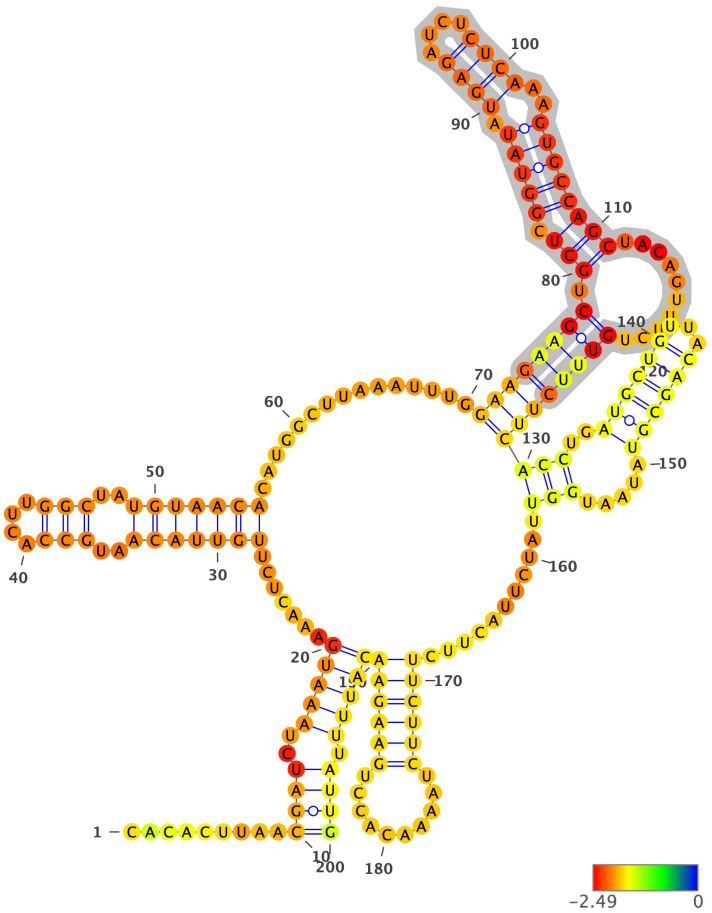
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 90 from nt 4646 to 4698 (nt 74 to 126)

```
5'-GAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUC-3'
5'-(.....(((.(((((.((((....)))).)))))))).............)-3'
Motif MFE = -16.8; z-score = -2.84; 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 4573 to 4772 (motif highlighted in silver):

```
5'-CACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGC
UACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUG-3
5'-.........((((..(((((.......(((((((..(((....)))..)))))))).............((((((((.(((.(((((.((((....)))).)))))))
..........))))))))(((..((((((...))))))).....))).........((((((..........))))))))))).))))-3'
MFE = -43.2; z-score = -2.3; ED = 27.69
```

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

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

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

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

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

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

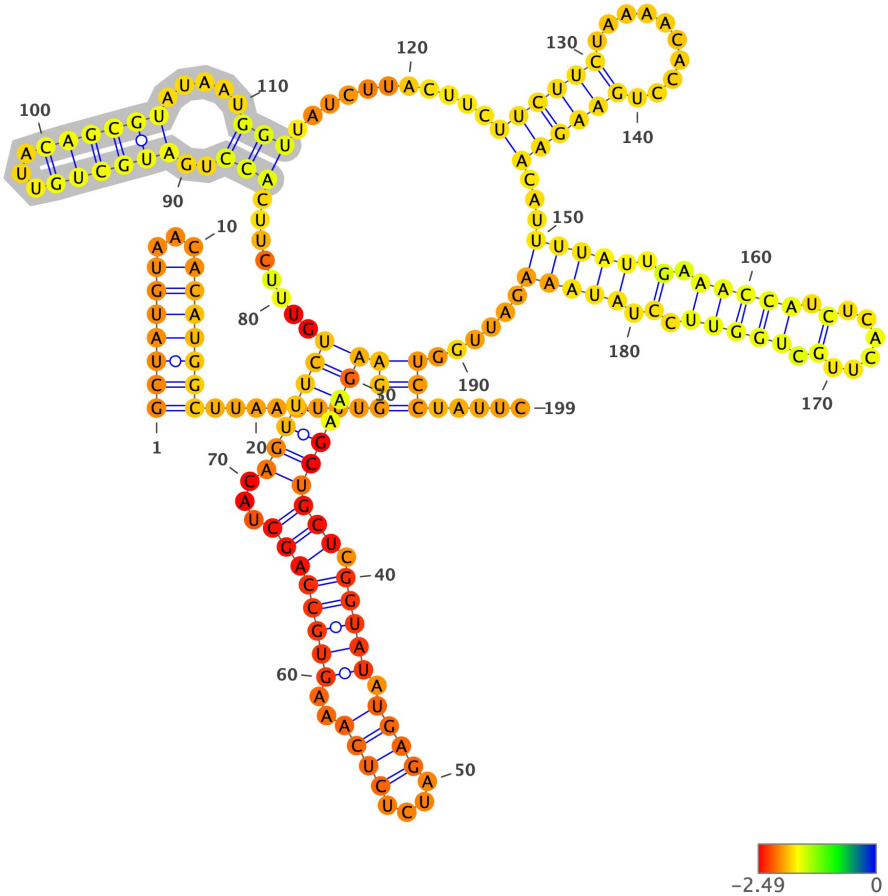
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 91 from nt 4702 to 4729 (nt 86 to 113)

```
5'-ACCUGAUGCUGUUACAGCGUAUAAUGGU-3'
5'-(((..((((((...))))))).....)))-3'
Motif MFE = -5.3; z-score = -1.16; ED = 2.2
```



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

Extracted structure model with flanking nucleotides 4617 to 4815 (motif highlighted in silver):

```
5'-GCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUG
GUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUC-3
5'-(((((((...)))))))........(((((((((((((.(((((.((((....))))..))))))))...)))))))........(((..((((((...))))))).....)
)).........((((((.........))))))...(((((.(.(((((.(......).))))).).)))))......)))).....-3'
MFE = -44.6; z-score = -1.84; ED = 22.67
```

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

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

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

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

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

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

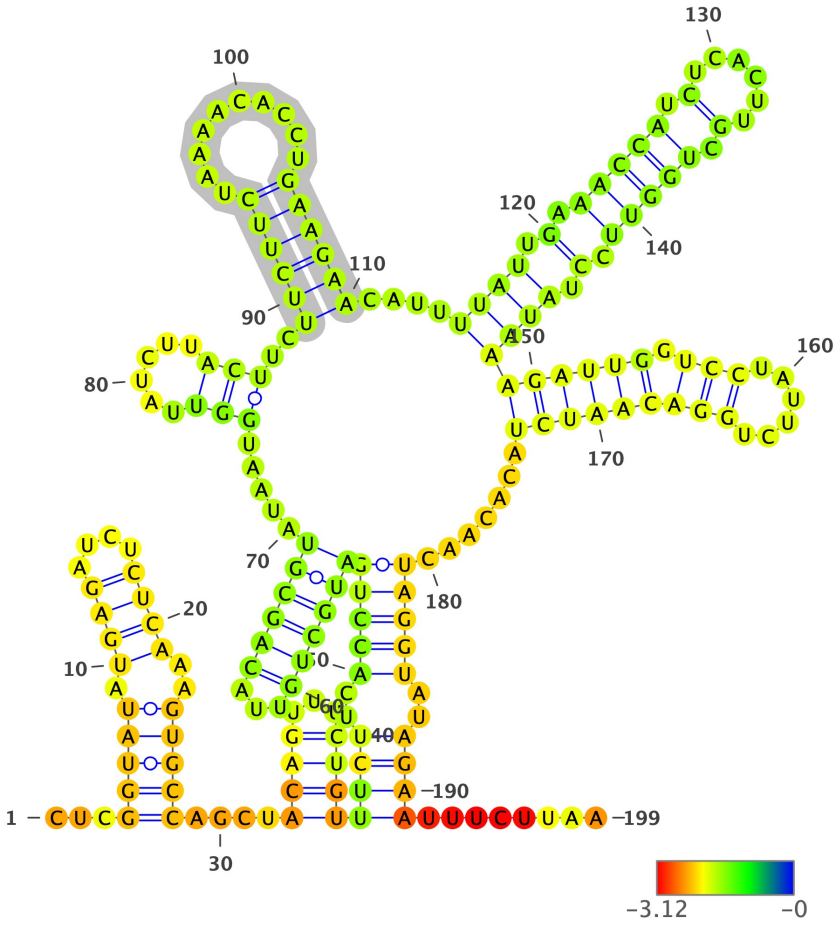
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 92 from nt 4741 to 4762 (nt 89 to 110)

```
5'-UUCUUCUAAAACACCUGAAGAA-3'
5'-((((((..........))))))-3'
Motif MFE = -3.9; z-score = -4.46; ED = 0.65
```



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

Extracted structure model with flanking nucleotides 4653 to 4851 (motif highlighted in silver):

```
5'-CUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAAC
AUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAA-3
5'-...(((((.((((....)))).)))))....((((...))))((((..(((((((((((...))))))).....(((......))).((((((..........)))))).
...((((.(.(((((.(......).)))))).).))))((((((.(((......)))))))))).......)))))..))))........-3'
MFE = -42.2; z-score = -2.44; ED = 28.37
```

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

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

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

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

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

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

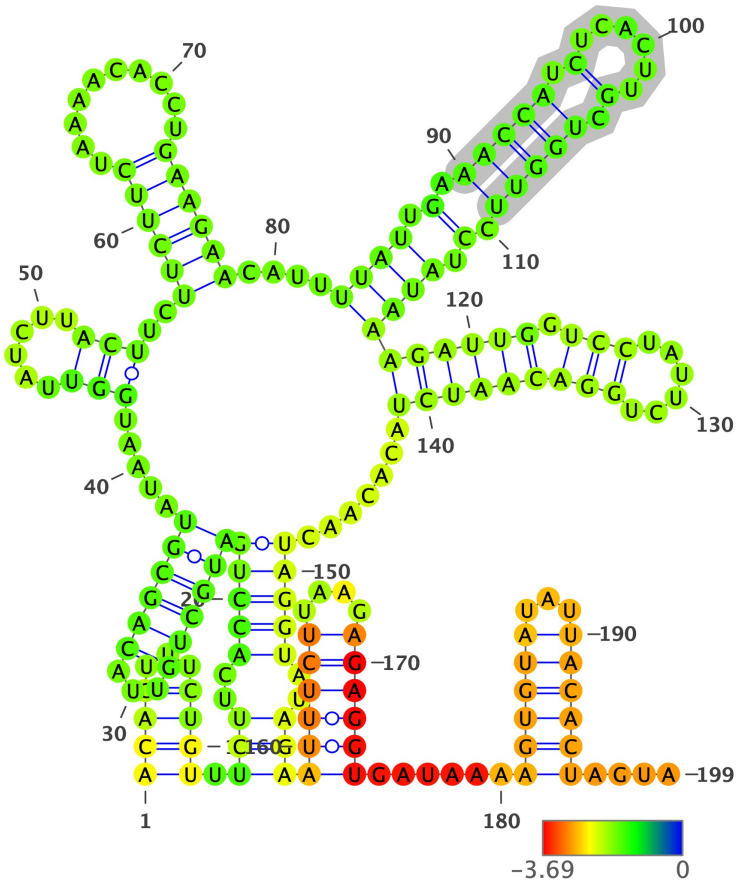
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 93 from nt 4774 to 4793 (nt 90 to 109)

```
5'-AACCAUCUCACUUGCUGGUU-3'
5'-(((((.(......).)))))-3'
Motif MFE = -3.5; z-score = -2.15; ED = 0.87
```



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

Extracted structure model with flanking nucleotides 4685 to 4883 (motif highlighted in silver):

```
5'-ACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCC
UAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUA-3
5'-((((...)))).(((..((((((((((((...))))))).....(((......))).((((((..........))))))....((((.(.(((((.(......).)))))).)
.))))((((((.(((......)))))))))).......)))))..)))((((((....))))))......((((((...))))))....-3'
MFE = -39.3; z-score = -1.76; ED = 38.69
```

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

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

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

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

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

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

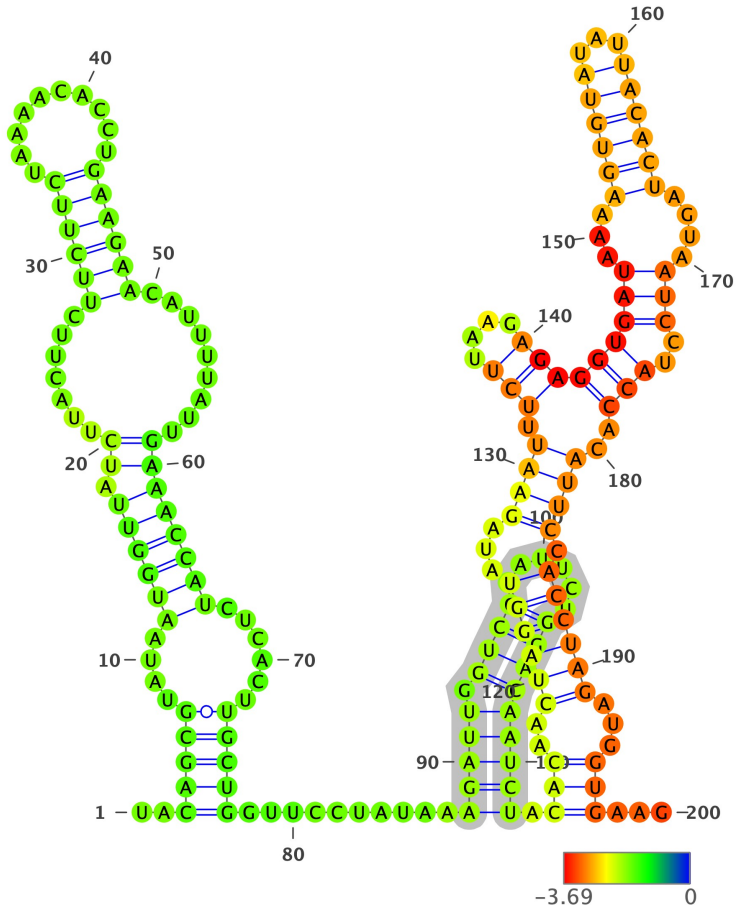
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 94 from nt 4801 to 4825 (nt 88 to 112)

```
5'-AGAUUGGUCCUAUUCUGGACAAUCU-3'
5'-(((((.((((......)))))))))-3'
Motif MFE = -8.9; z-score = -3.68; 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 = -2.15; ED = 36.31
```

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(+)

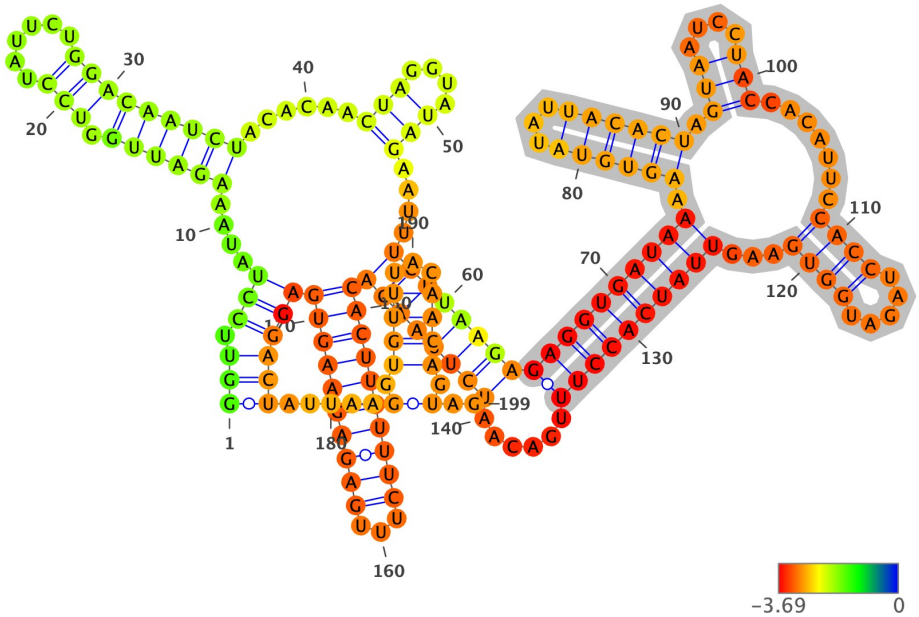
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 95 from nt 4854 to 4923 (nt 65 to 134)

```
5'-GAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUU-3'
5'-((((((((((..((((.....)))).....................((((.....))))...))))))))))-3'
Motif MFE = -20.2; z-score = -3.39; ED = 8.37
```



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

Extracted structure model with flanking nucleotides 4790 to 4988 (motif highlighted in silver):

```
5'-GGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCAC
CUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAG-3
5'-(((.(((....((((((.(((......)))))))))......(((....)))....((((((((((((((((((.((((((...)))))).(((....)))........(((
(.....))))...))))))))))......))))))))((((((((((...)))))))))))))))))).....(.((((...)))).)..-3'
MFE = -54.2; z-score = -4.02; ED = 19.48
```

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(+)

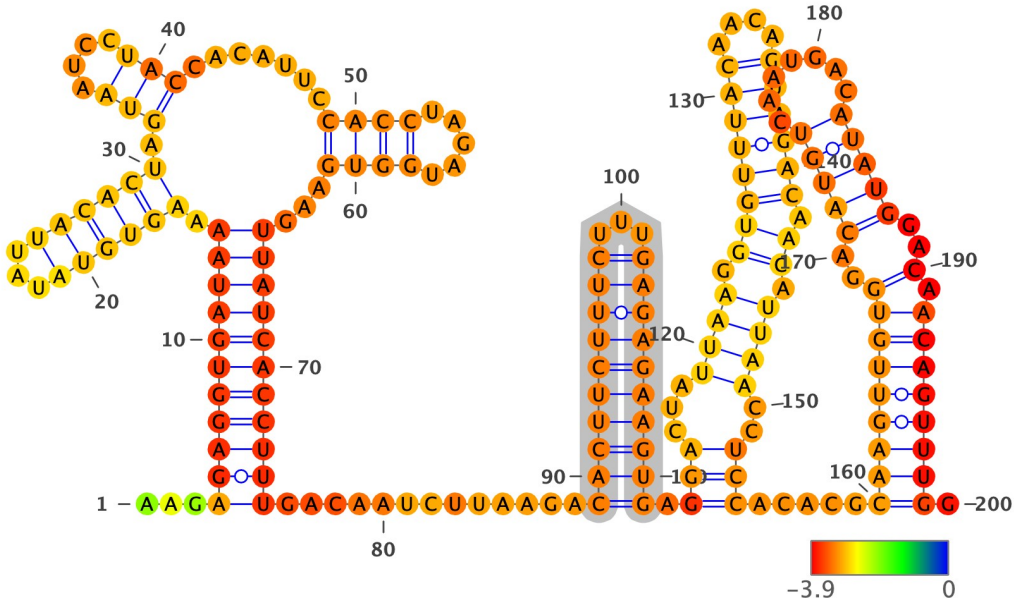
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 96 from nt 4938 to 4960 (nt 89 to 111)

```
5'-CACUUCUUUCUUUGAGAGAAGUG-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -10.7; z-score = -5.67; 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 = -3.21; 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(+)

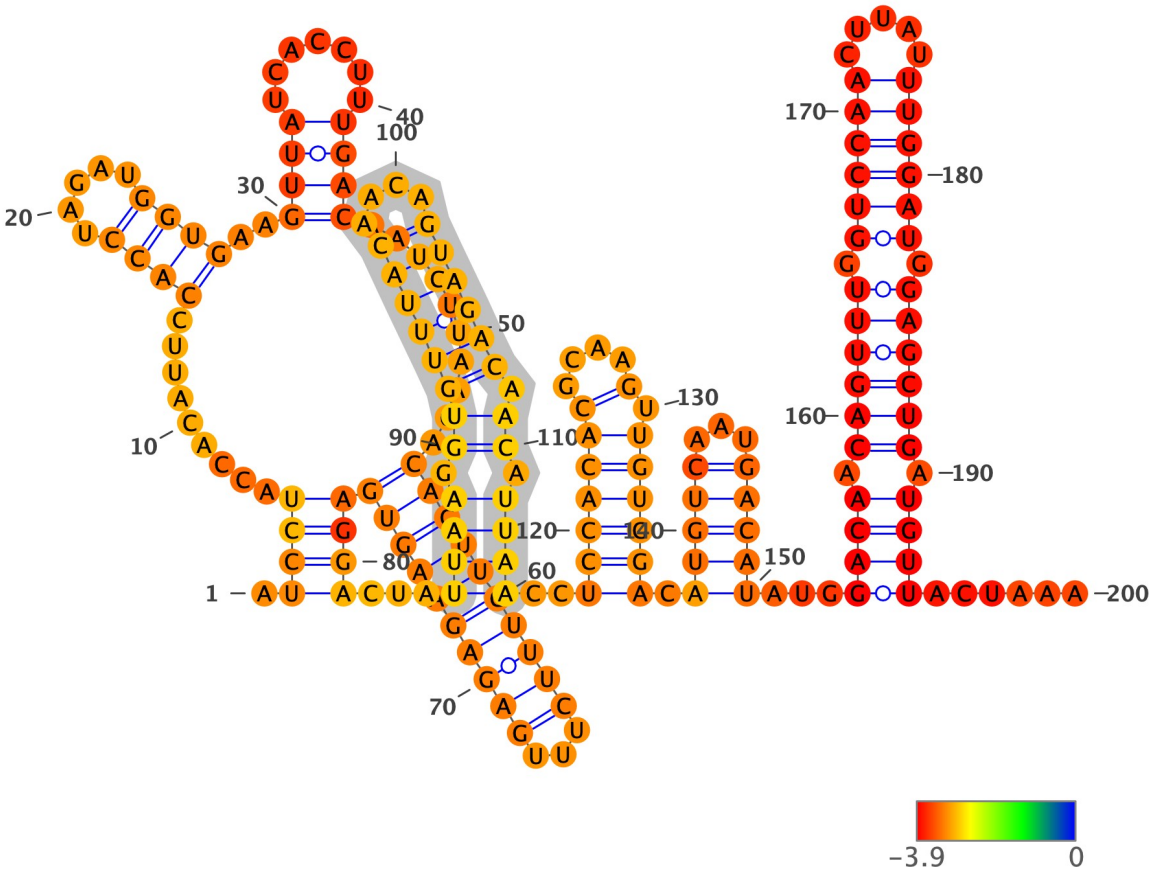
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 97 from nt 4968 to 4998 (nt 85 to 115)

```
5'-UUAAGGUGUUUACAACAGUAGACAACAUUAA-3'
5'-((((.((((((((....)))))).)).))))-3'
Motif MFE = -5.9; z-score = -2.2; 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 4884 to 5083 (motif highlighted in silver):

```
5'-AUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACA
UUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAA-3
5'-.((((.........((((.....))))..((((.......))))..........((((((((((...)))))))))))))...((((.((((((((....)))))).)).
))))..((((((((....).)))))).(((((...)))))...((((.((((((.((((((.....)))))).)))))).)))).....-3'
MFE = -56.3; z-score = -4.01; ED = 28.81
```

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(+)

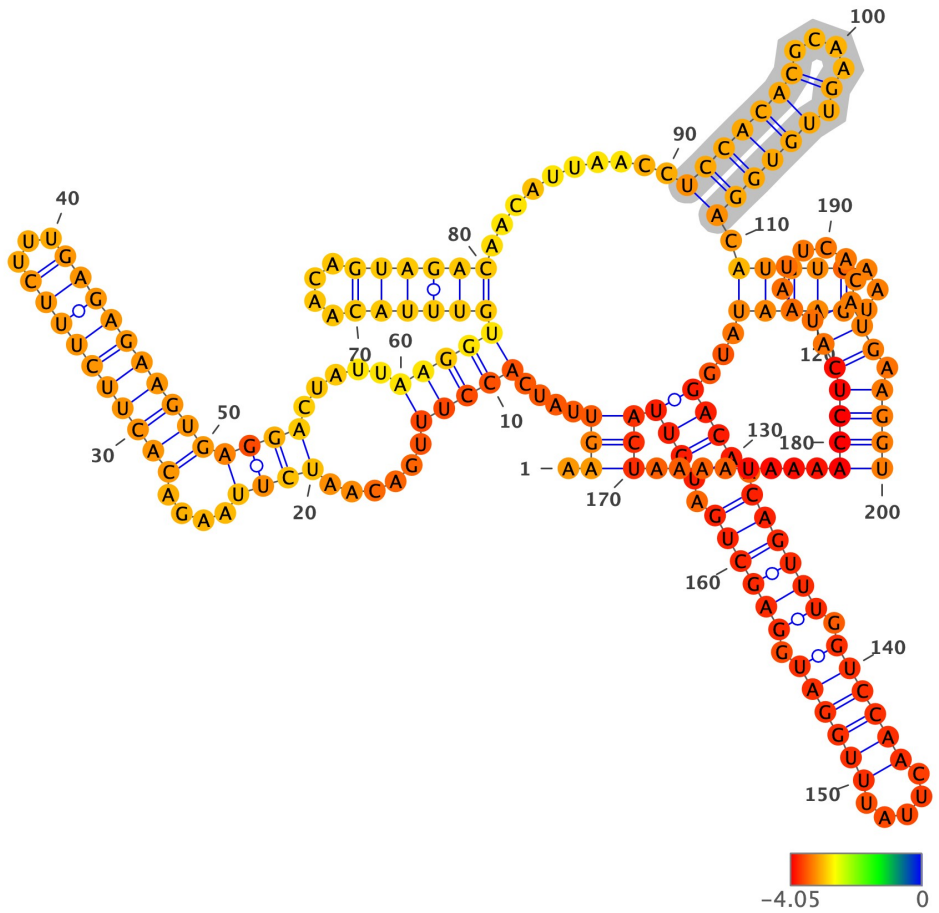
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 98 from nt 5001 to 5019 (nt 91 to 109)

```
5'-UCCACACGCAAGUUGUGGA-3'
5'-(((((((....).))))))-3'
Motif MFE = -6.7; z-score = -3.55; 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 = -4.61; 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(+)

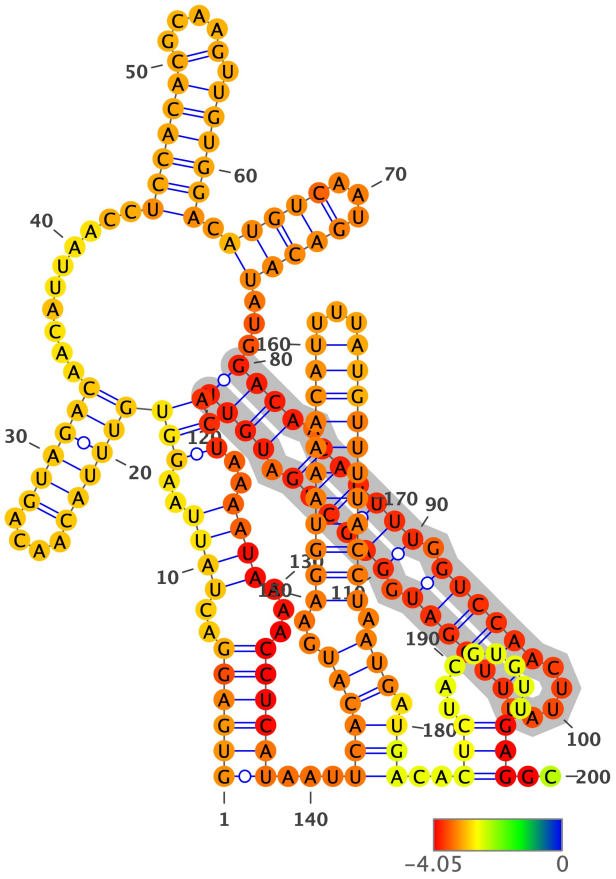
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 99 from nt 5037 to 5077 (nt 80 to 120)

```
5'-GACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUU-3'
5'-((((.((((((.((((((.....)))))).)))))).))))-3'
Motif MFE = -17.8; z-score = -4.53; 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 = -5.09; 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(+)

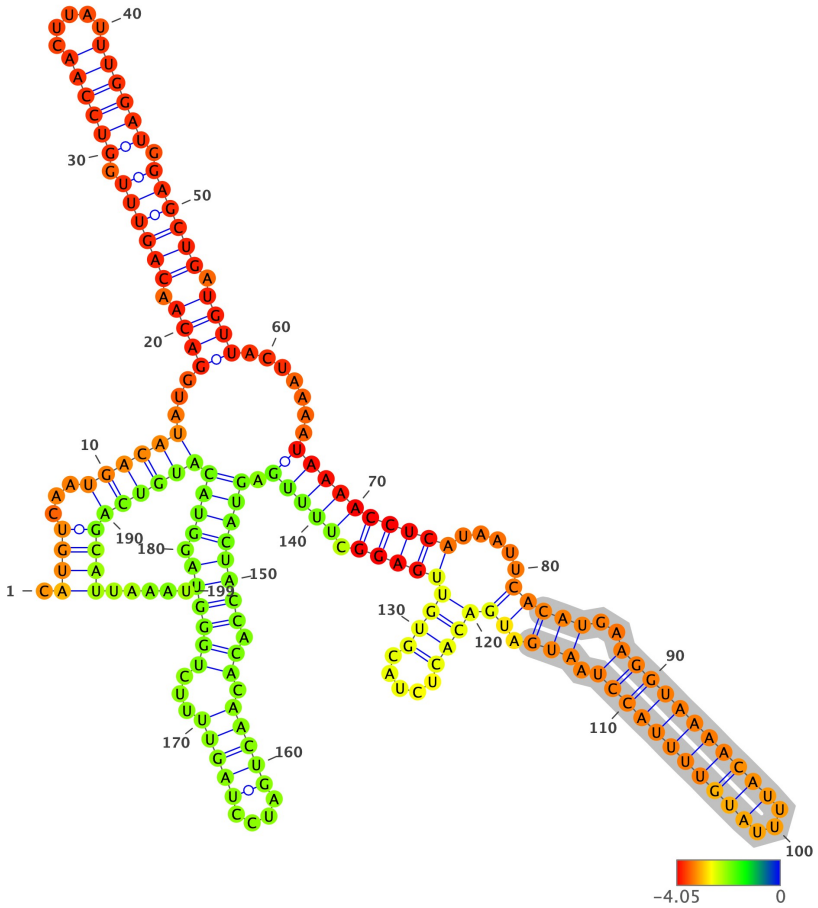
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 100 from nt 5102 to 5135 (nt 83 to 116)

```
5'-CAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUG-3'
5'-(((..(((((((((.........)))))))))..)))-3'
Motif MFE = -11.7; z-score = -5.27; 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 5020 to 5218 (motif highlighted in silver):

```
5'-CAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACC
UAAUGAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAU-3
5'-.((((...((((((...((((.((((((.((((((.....)))))).)))))).)))).......((((((((((.....(((((..((((((((((...)))))))))))
).))).))((((.....)))))))))).)))))).((((((((.((.((((((....)))))...)))))).))))))))))))))).....-3'
MFE = -57.9; z-score = -4.2; ED = 15.8
```

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

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

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

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

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

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

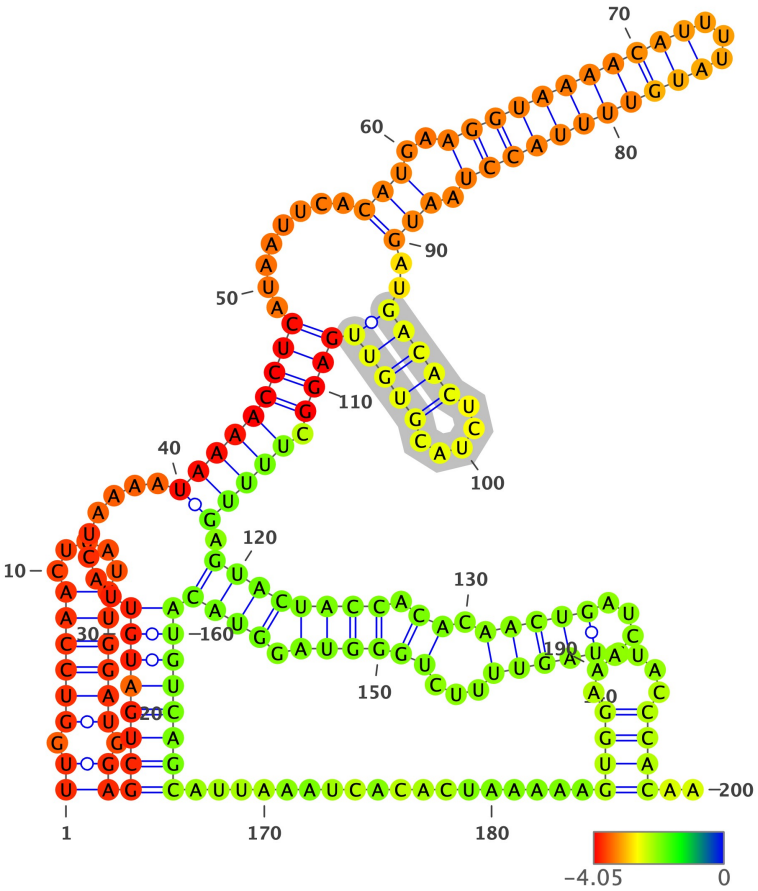
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 101 from nt 5138 to 5152 (nt 93 to 107)

```
5'-GACACUCUACGUGUU-3'
5'-(((((.....)))))-3'
Motif MFE = -3.0; z-score = -3.27; 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 5046 to 5245 (motif highlighted in silver):

```
5'-UUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGG
CUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAA-3
5'-((.(((((((.....)))))).))(((((((((.......((((((((((.......)))))))))..((..((((((((((...)))))))))))).)))..(((((.....)))))))))
.)))))..((((((((.((.(((((....)))))...)))))).)))))))))))).................((((......))))..-3'
MFE = -52.1; z-score = -3.75; ED = 19.11
```

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(+)

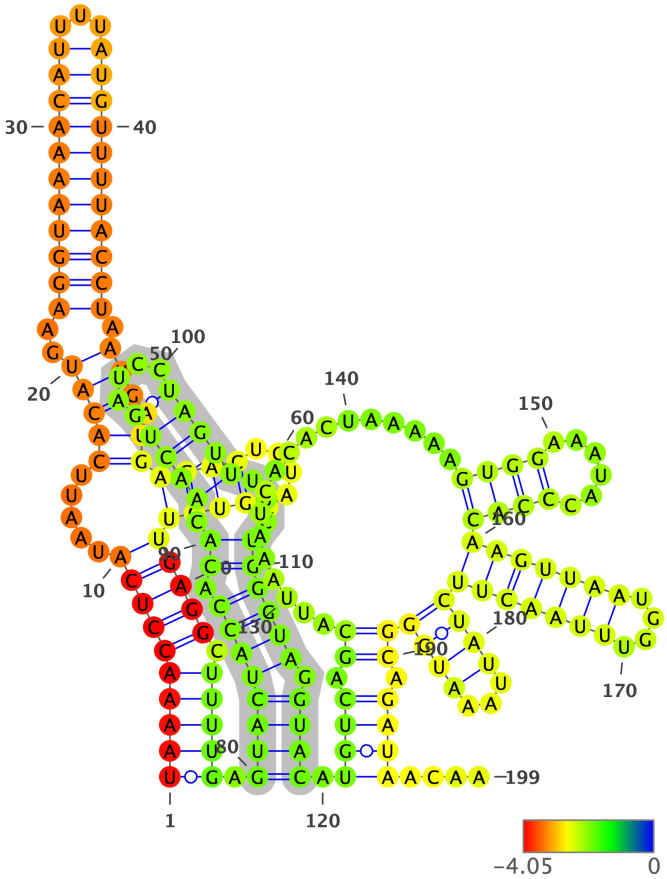
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 102 from nt 5164 to 5203 (nt 80 to 119)

```
5'-GUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUAC-3'
5'-((((((((.((.((((......))))...)))))).))))-3'
Motif MFE = -9.8; z-score = -2.23; 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 = -3.34; ED = 36.56
```

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

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

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

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

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

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

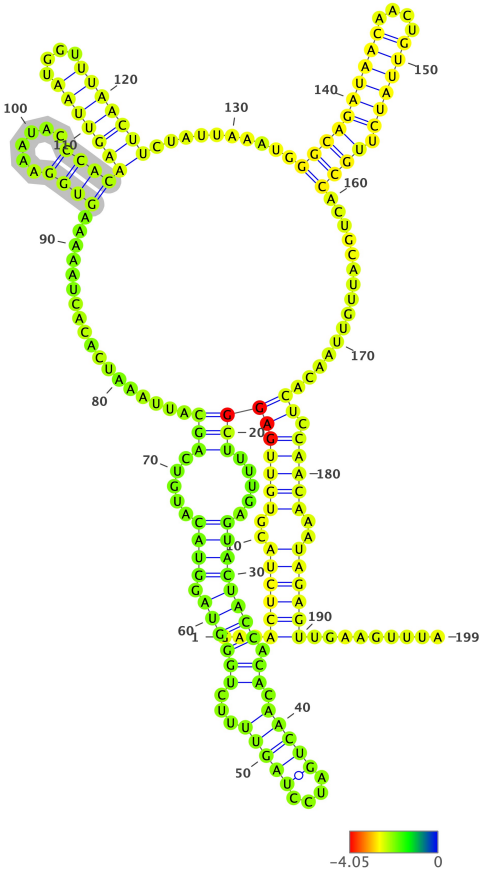
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 103 from nt 5230 to 5243 (nt 93 to 106)

```
5'-GUGGAAAUACCCAC-3'
5'-((((......))))-3'
Motif MFE = -3.7; z-score = -5.11; 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 = -2.33; 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(+)

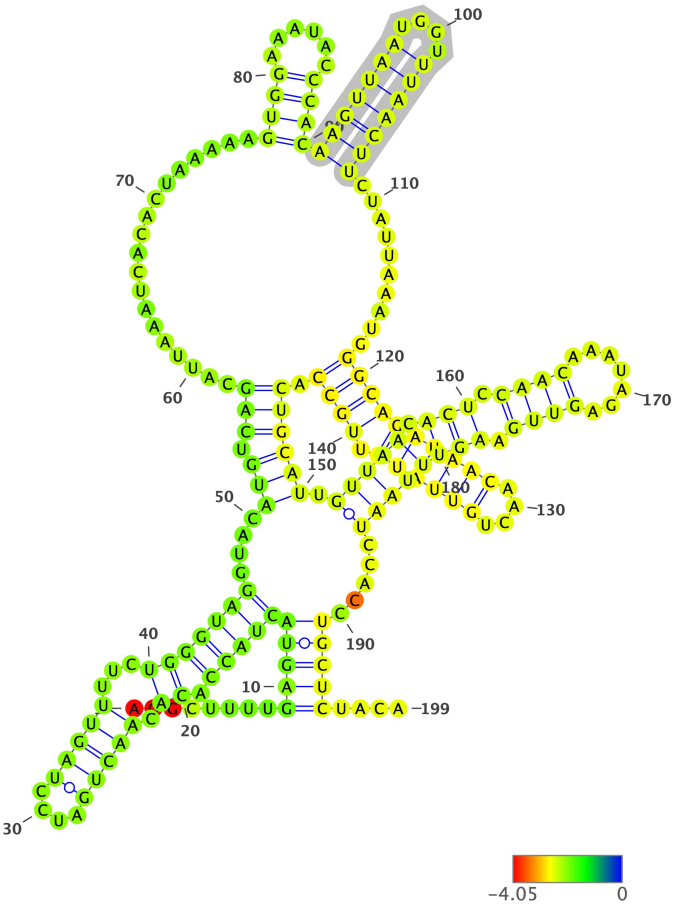
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 104 from nt 5244 to 5261 (nt 91 to 108)

```
5'-AAGUUAAUGGUUUAACUU-3'
5'-(((((((....)))))))-3'
Motif MFE = -3.4; z-score = -5.41; 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 = -2.48; 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(+)

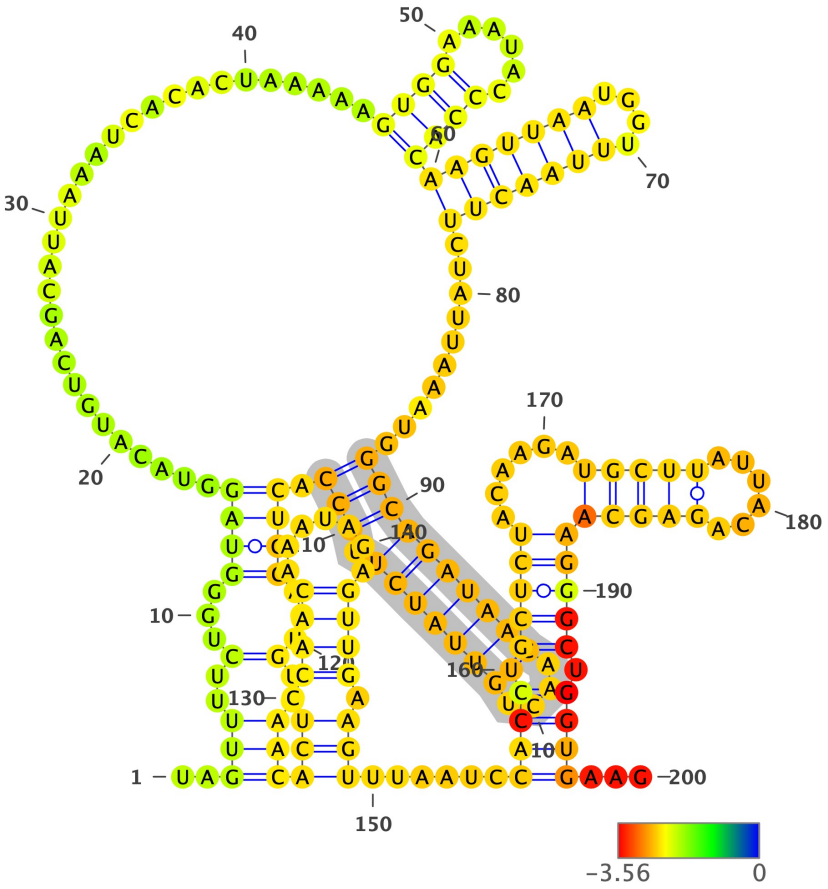
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 105 from nt 5272 to 5296 (nt 88 to 112)

```
5'-GGCAGAUAACAACUGUUAUCUUGCC-3'
5'-((((((((((....)))))))).)))-3'
Motif MFE = -10.9; z-score = -4.27; 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 = -2.15; 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(+)

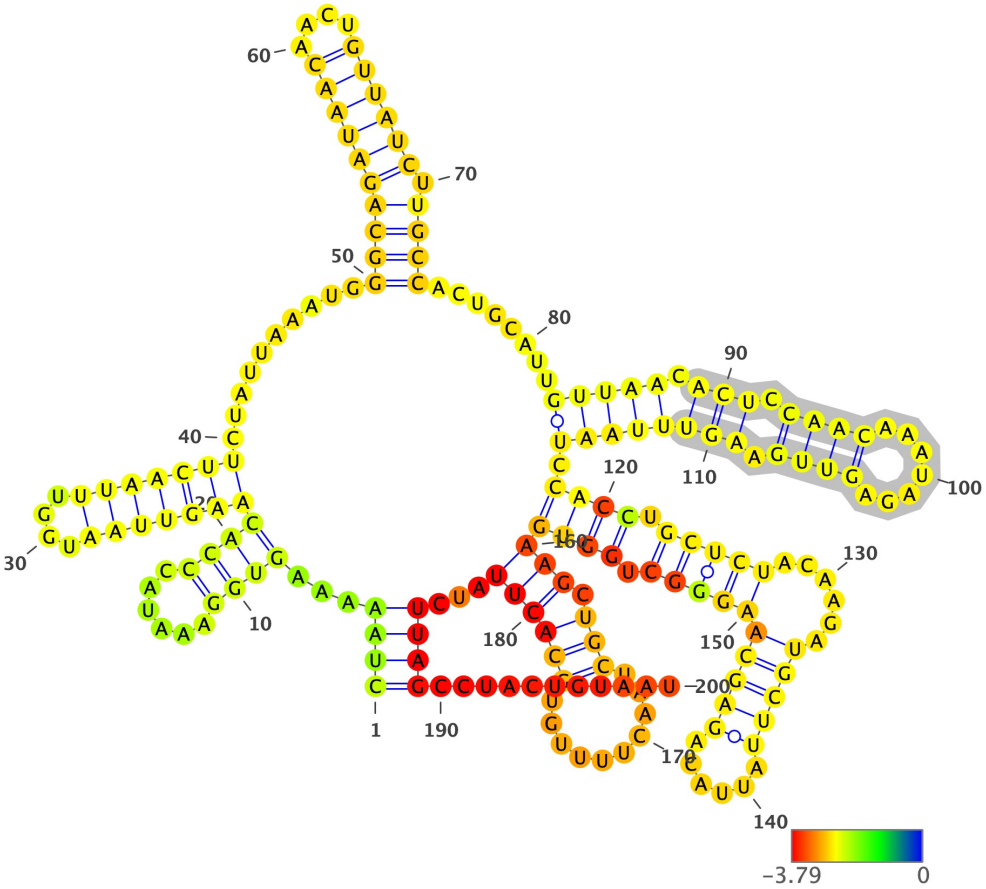
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 106 from nt 5311 to 5333 (nt 89 to 111)

```
5'-ACUCCAACAAAUAGAGUUGAAGU-3'
5'-(((.................)))-3'
Motif MFE = -3.3; z-score = -1.61; ED = 1.36
```



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

Extracted structure model with flanking nucleotides 5223 to 5422 (motif highlighted in silver):

```
5'-CUAAAAAGUGGAAAUACCCACAAGUUAAUGGUUUAACUUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGU
UUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAU-3
5'-((((...((((......))))(((((((....)))))))..........((((((((((....))))))).))))........(((((.(((.((((.......)))).)))
))))).((((.(((((......(((((......)))))))))).))))(((.(((..........))))))...))))...........-3'
MFE = -48.6; z-score = -3.27; ED = 38.61
```

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

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

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

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

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

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

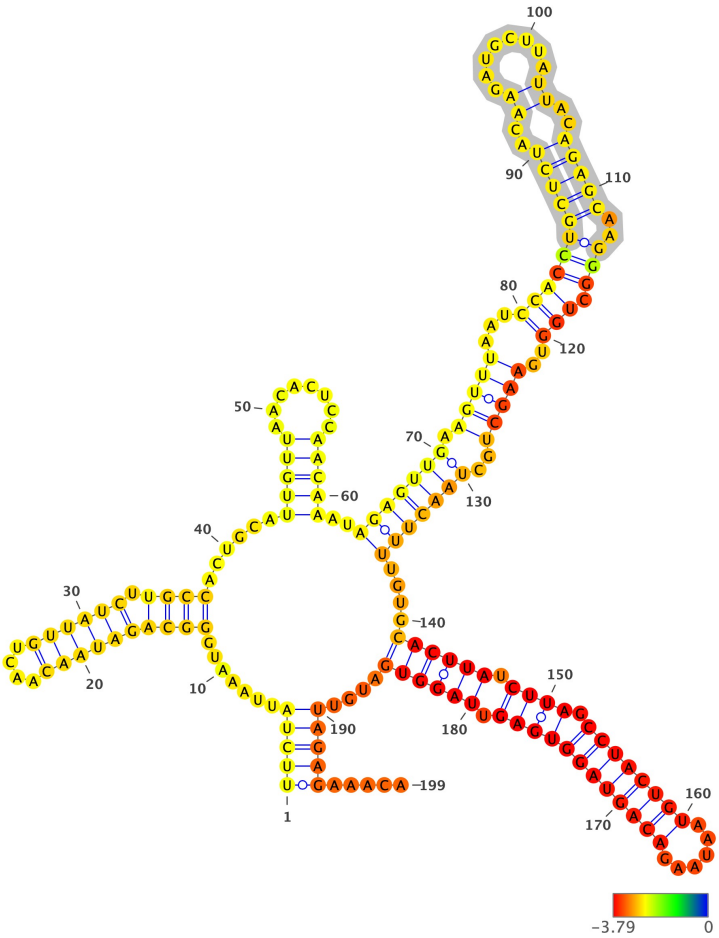
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 5344 to 5373 (nt 85 to 114)

```
5'-UGCUCUACAAGAUGCUUAUUACAGAGCAAG-3'
5'-((((((................)))))..)-3'
Motif MFE = -6.2; z-score = -2.05; ED = 3.04
```



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 5260 to 5458 (motif highlighted in silver):

```
5'-UUCUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGC
AAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACA-3
5'-(((((.......((((((((((....)))))).))))......(((((........)))))..(((((((.(((((...((((((((((..((........))..)))))
..))).)))..)))))..)))))))....((((((.((((.((((((((......)))))))))))).))))))....)))))).....-3'
MFE = -56.5; z-score = -4.5; ED = 26.81
```

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(+)

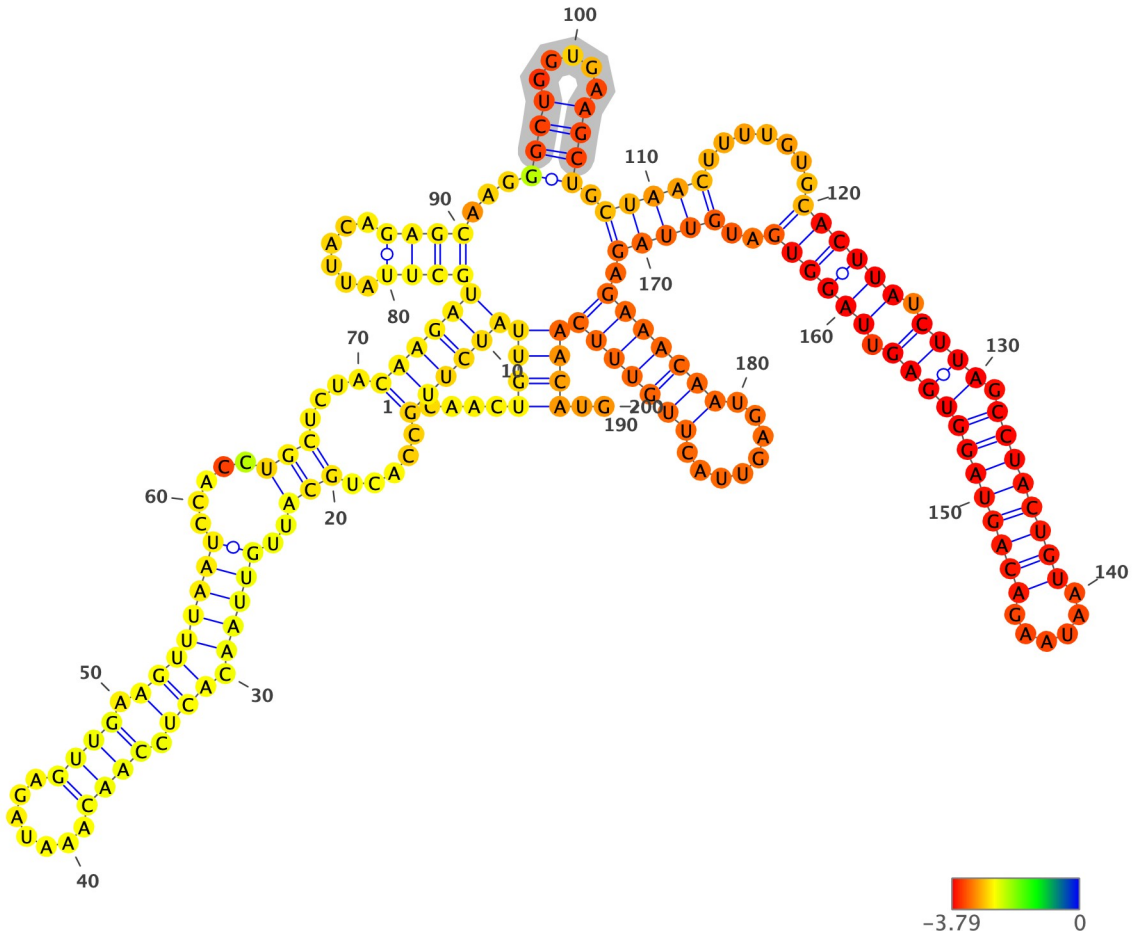
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 108 from nt 5375 to 5385 (nt 95 to 105)

```
5'-GCUGGUGAAGC-3'
5'-(((.....)))-3'
Motif MFE = -1.3; z-score = -3.44; ED = 0.64
```



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

Extracted structure model with flanking nucleotides 5281 to 5480 (motif highlighted in silver):

```
5'-CAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAA
CUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUG-3
5'-....((((((((((.....(((..(((((.(((.((((.......)))).))))))))).....)))....))))))((((......))))...((((.....)))).((((
(.......((((((.((((.((((((((.......)))))))))))).))))))..))))).(((((((.........)))))))))))..-3'
MFE = -51.3; z-score = -3.3; ED = 39.46
```

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

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

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

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

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

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

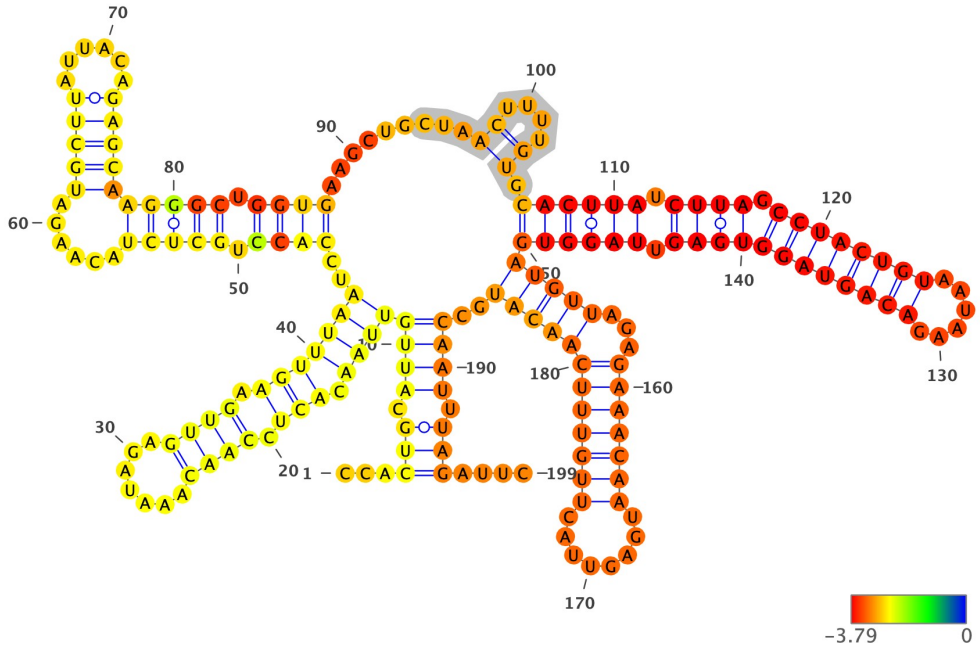
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 109 from nt 5388 to 5399 (nt 94 to 105)

```
5'-CUAACUUUUGUG-3'
5'-(..........)-3'
Motif MFE = 0.0; z-score = 0.13; ED = 0.79
```



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

Extracted structure model with flanking nucleotides 5295 to 5493 (motif highlighted in silver):

```
5'-CCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUA
UCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUC-3
5'-...(((.((((((((.(((.((((.......)))).)))))))..((((.(((((......(((((......)))))))))).))))..........((....)).((((((
.((((.((((((((......)))))))))))).))))))(((((...(((((((........)))))))))))..)))).)))....-3'
MFE = -52.8; z-score = -3.35; ED = 52.95
```

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(+)

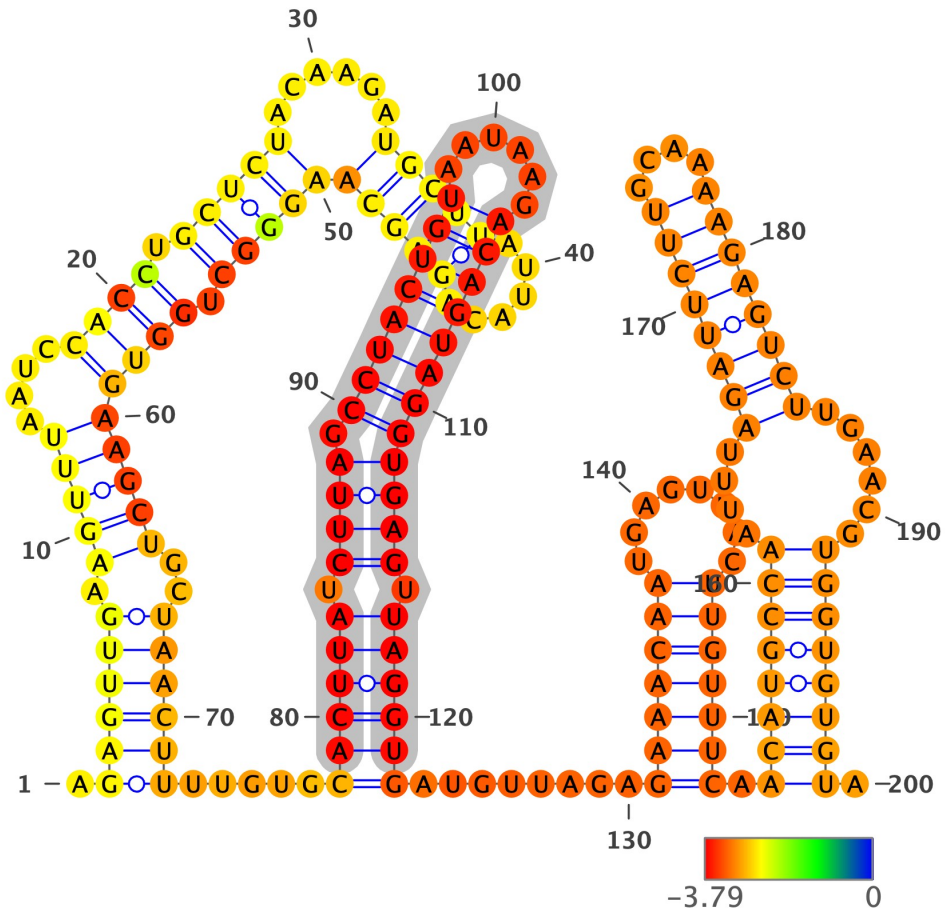
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 110 from nt 5401 to 5443 (nt 79 to 121)

```
5'-ACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGU-3'
5'-(((((.((((.(((((((((.....)))))))))))).)))))-3'
Motif MFE = -18.1; z-score = -4.86; ED = 2.13
```



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

Extracted structure model with flanking nucleotides 5323 to 5522 (motif highlighted in silver):

```
5'-AGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGG
UGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUA-3
5'-.((((((.(((((....((((.(((((.....(((((.....)))))))))).)))))))))..)))))).....((((((.((((.(((((((((.....)))))))))
))))).)))))).......(((((((.......)))))))).(((((((((....(((((((((....)))))))))).....)))))))).-3'
MFE = -67.6; z-score = -5.08; ED = 10.95
```

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(+)

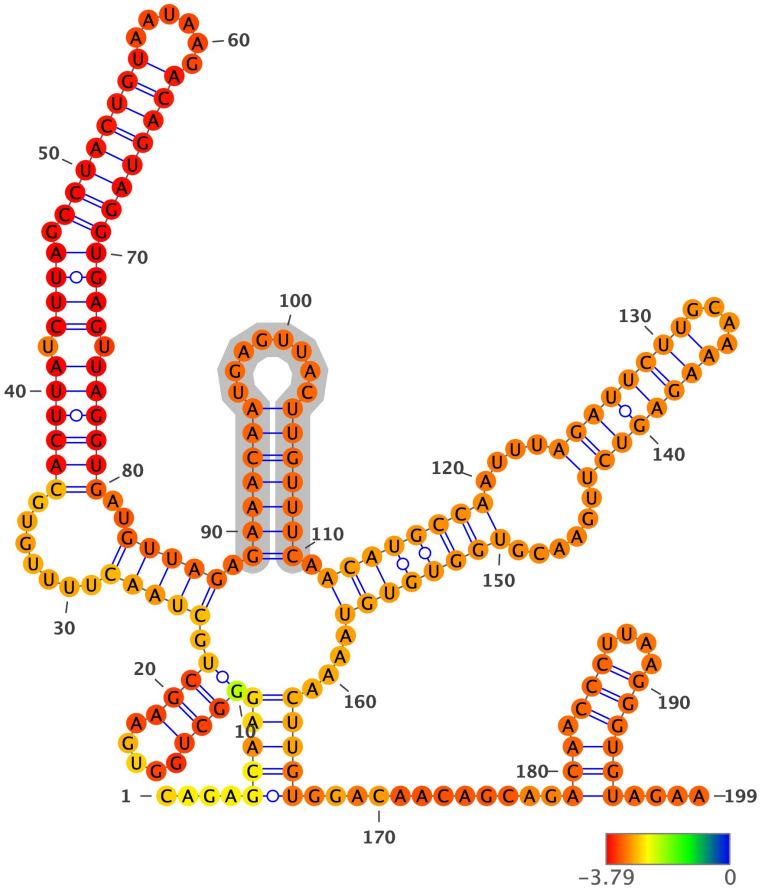
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-GAAACAAUGAGUUACUUGUUUC-3'
5'-(((((((........)))))))-3'
Motif MFE = -4.2; z-score = -2.26; 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 = -4.4; ED = 29.05
```

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

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

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

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

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

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

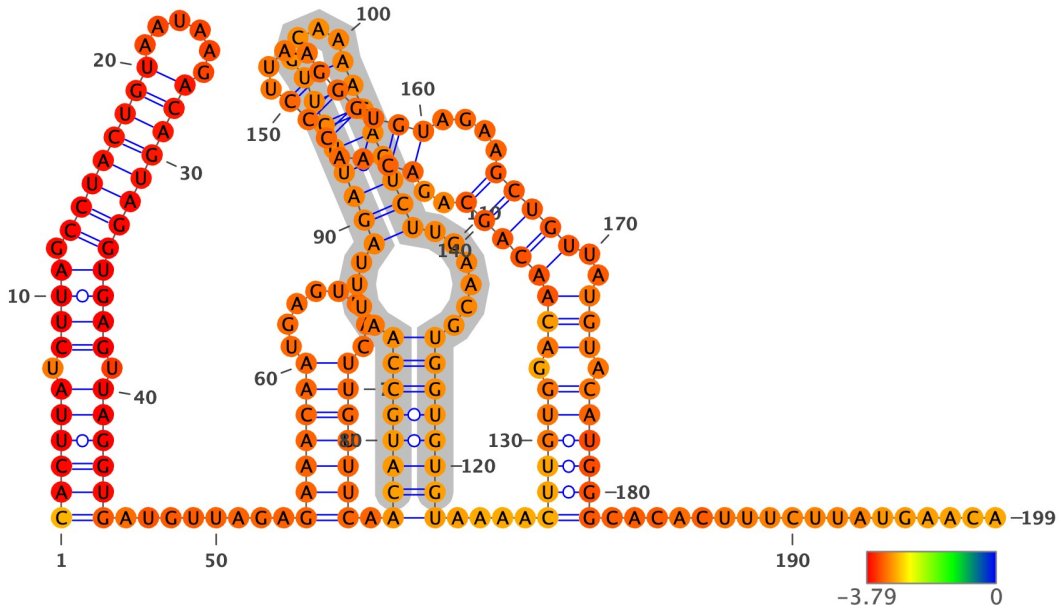
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 112 from nt 5477 to 5520 (nt 78 to 121)

```
5'-CAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUG-3'
5'-(((((((....((((((((....)))))))).....)))))))-3'
Motif MFE = -15.2; z-score = -3.88; ED = 3.07
```



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

Extracted structure model with flanking nucleotides 5400 to 5598 (motif highlighted in silver):

```
5'-CACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGA
ACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACA-3
5'-((((((.((((.(((((((((.....)))))))))))).)))))).......(((((((.......)))))))).(((((((((....(((((((((....)))))))))...
...)))))))))....((((((.(((((((((..(((.(((....)))))).....)))))..)))).)))))).................-3'
MFE = -63.0; z-score = -4.88; ED = 25.04
```

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

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

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

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

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

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

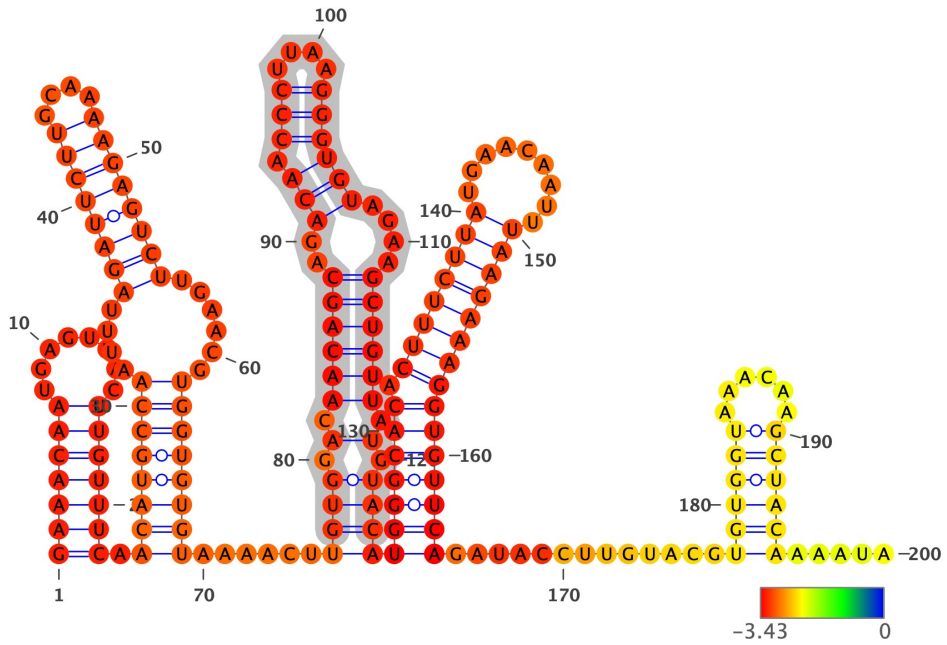
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 113 from nt 5529 to 5575 (nt 77 to 123)

```
5'-GUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUAC-3'
5'-(((.(.(((((((..(((.(((....)))))).....)))))).).)))-3'
Motif MFE = -14.3; z-score = -2.62; ED = 3.52
```



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 5453 to 5652 (motif highlighted in silver):

```
5'-GAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAA
GCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUA-3
5'-(((((((........)))))))..(((((((((....(((((((((....)))))))))).....)))))))).....((((.(.((((((..(((.(((....)))))))....
))))))).).))))(((((((.(((((((((.........)))))))))))))))).............((((((......)))))).....-3'
MFE = -61.9; z-score = -4.53; ED = 15.43
```

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

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

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

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

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

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

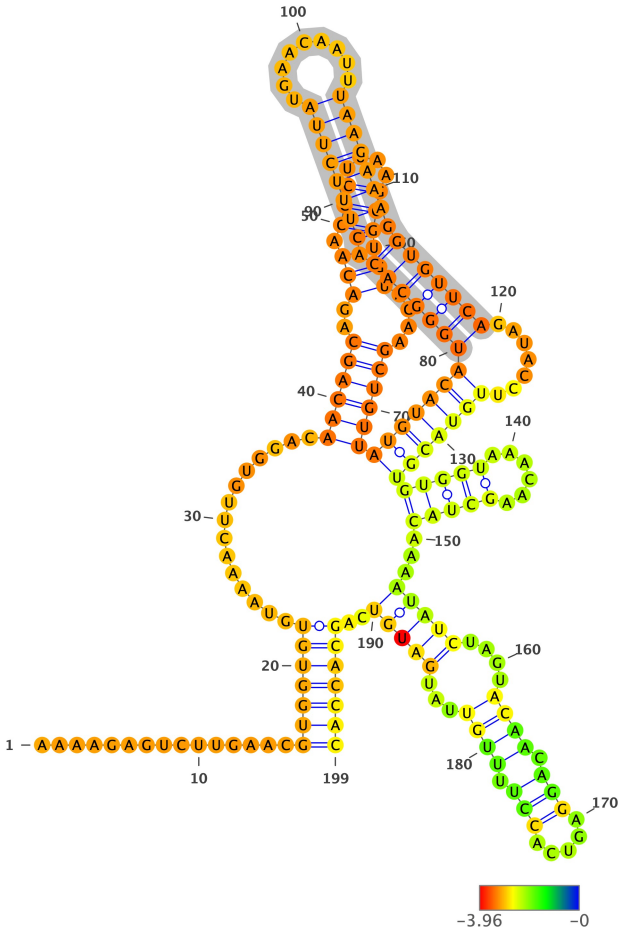
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 114 from nt 5577 to 5616 (nt 80 to 119)

```
5'-UGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCA-3'
5'-(((((((.((((((((.........)))))))))))))))-3'
Motif MFE = -15.3; z-score = -3.91; 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 = -3.48; 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(+)

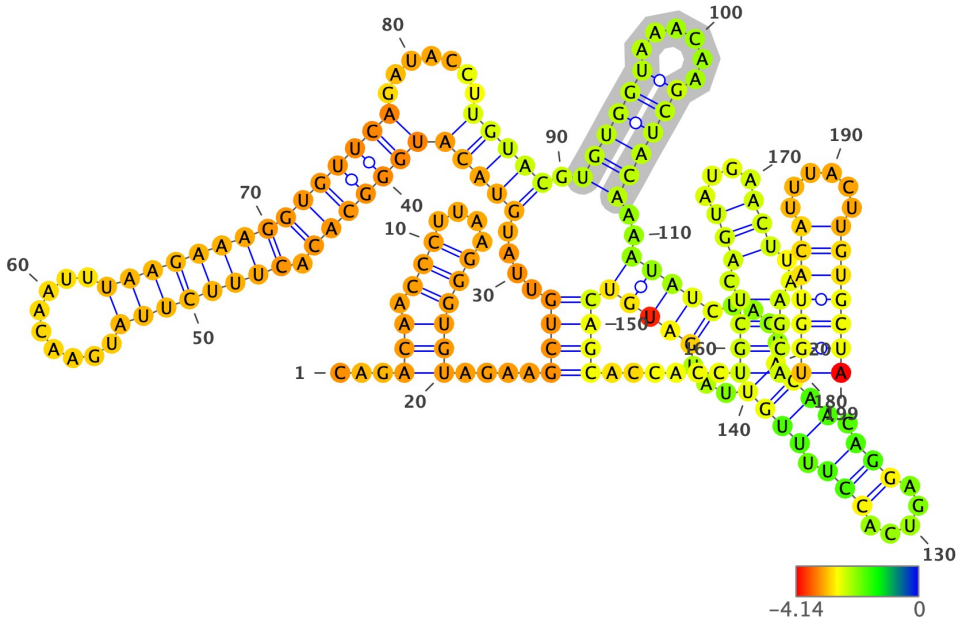
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-UGUGGUAAACAAGCUACA-3'
5'-(((((........)))))-3'
Motif MFE = -4.5; z-score = -4.33; ED = 0.6
```



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

Extracted structure model with flanking nucleotides 5540 to 5738 (motif highlighted in silver):

```
5'-CAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAA
UAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUA-3
5'-...(((.(((....))))))....((((....((((((((((((.((((((((.........)))))))))))))).......))))).((((((......))))))..(
((((....((((.(((.....)).))))...)))))))))......((((.(((....)))..))))(((((((......)))))))-3'
MFE = -52.1; z-score = -3.42; ED = 34.29
```

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

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

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

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

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

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

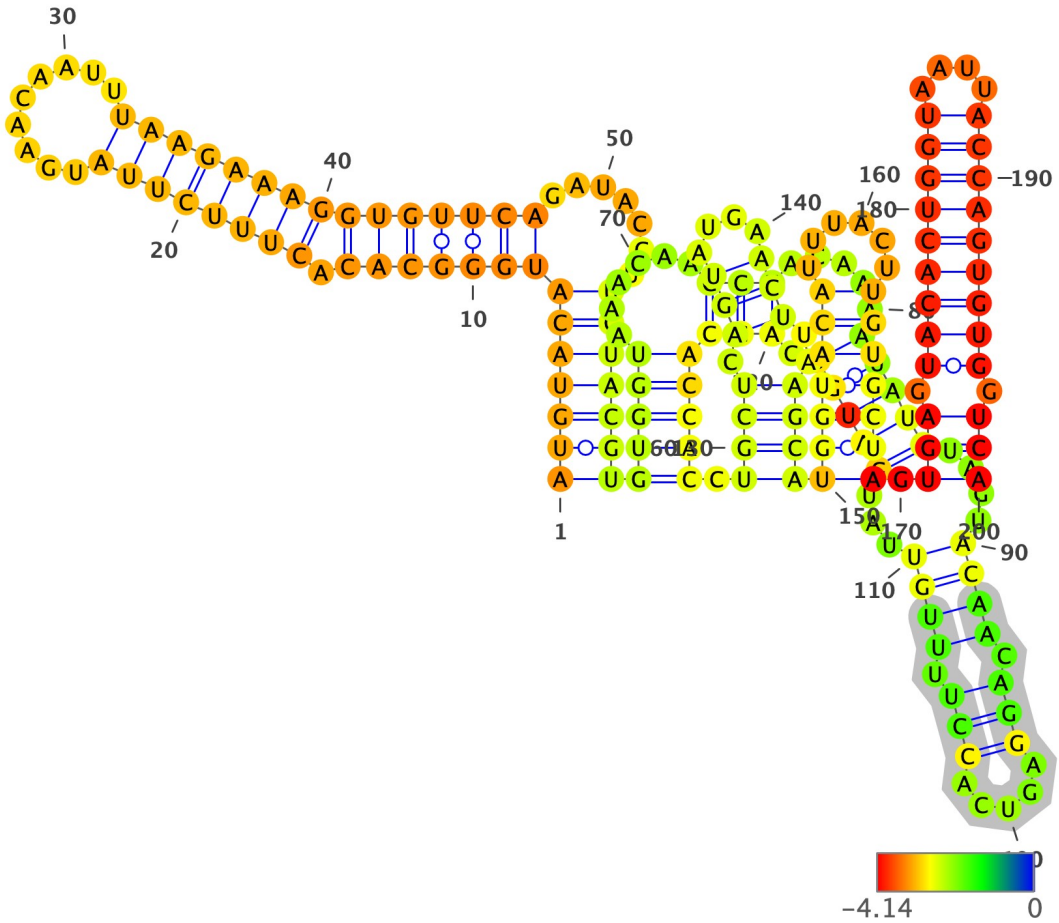
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 116 from nt 5661 to 5677 (nt 92 to 108)

```
5'-AACAGGAGUCACCUUUU-3'
5'-((.((.......)).))-3'
Motif MFE = -0.9; z-score = -0.37; 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 5570 to 5769 (motif highlighted in silver):

```
5'-AUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAAUAUCUAGUACAACAGGAGUCACCUUUUGUU
AUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCA-3
5'-(((((((((((((.((((((((.........))))))))))))))).......)))))))(((((......(((.....(((((....((((.(((.....))).)))).
..))))).)))))))).((((.(((....)))..))))(((((((......)))))))).(((.((((((((....)))))))))).)))-3'
MFE = -61.4; z-score = -4.66; ED = 32.15
```

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(+)

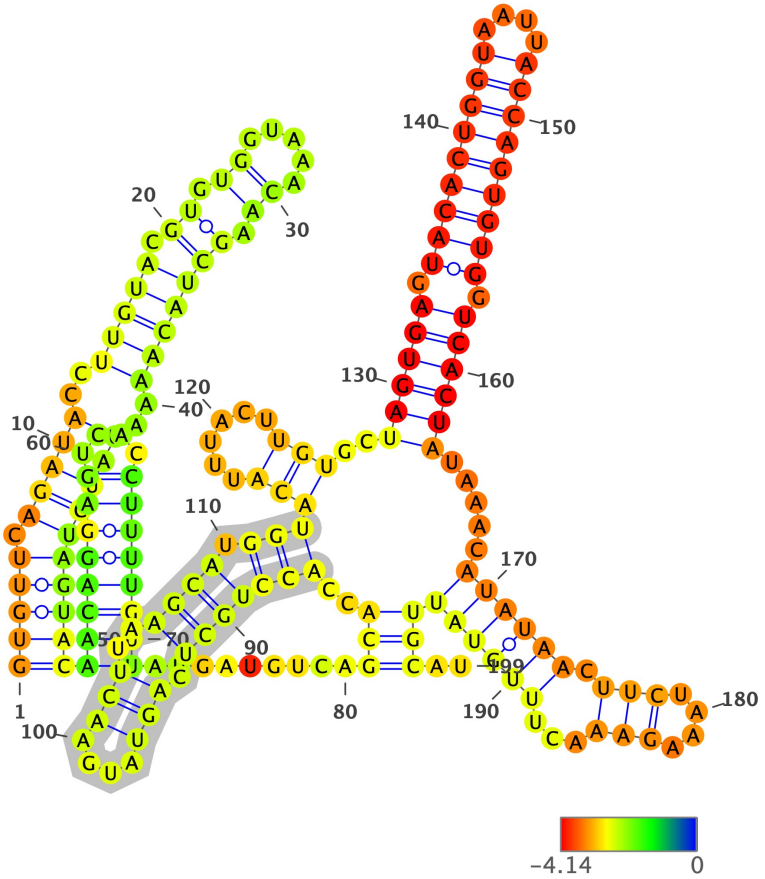
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 117 from nt 5695 to 5722 (nt 86 to 113)

```
5'-ACCUGCUCAGUAUGAACUUAAGCAUGGU-3'
5'-(((((((.(((....)))..)))).)))-3'
Motif MFE = -6.4; z-score = -2.0; 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 = -3.0; ED = 48.19
```

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

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

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

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

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

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

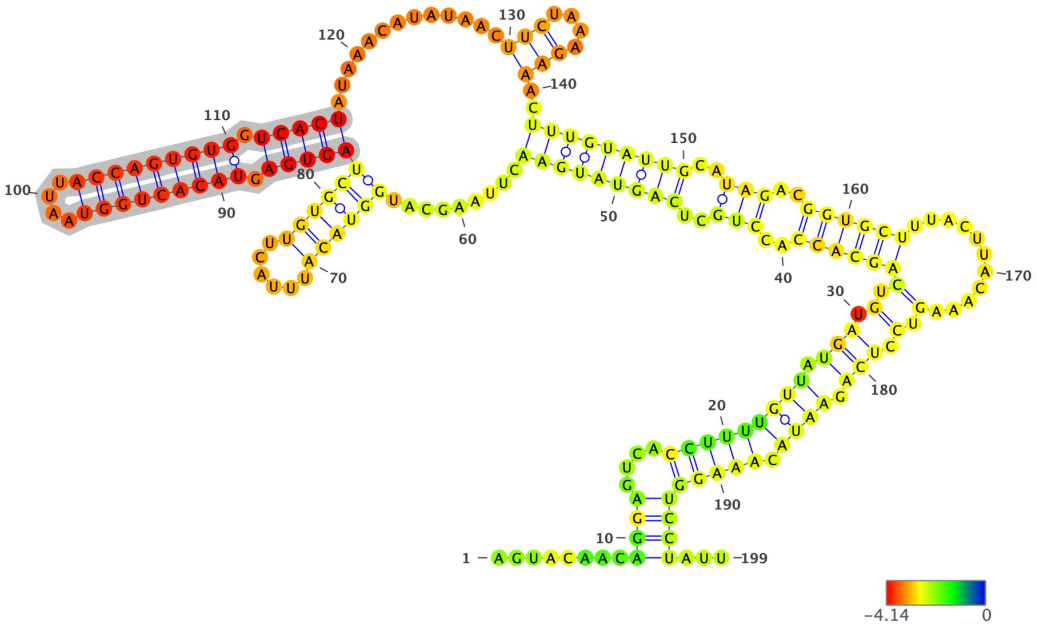
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 118 from nt 5738 to 5771 (nt 83 to 116)

```
5'-AGUGAGUACACUGGUAAUUACCAGUGUGGUCACU-3'
5'-(((((.((((((((((....)))))))))).)))))-3'
Motif MFE = -20.9; z-score = -5.87; 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 = -3.34; 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(+)

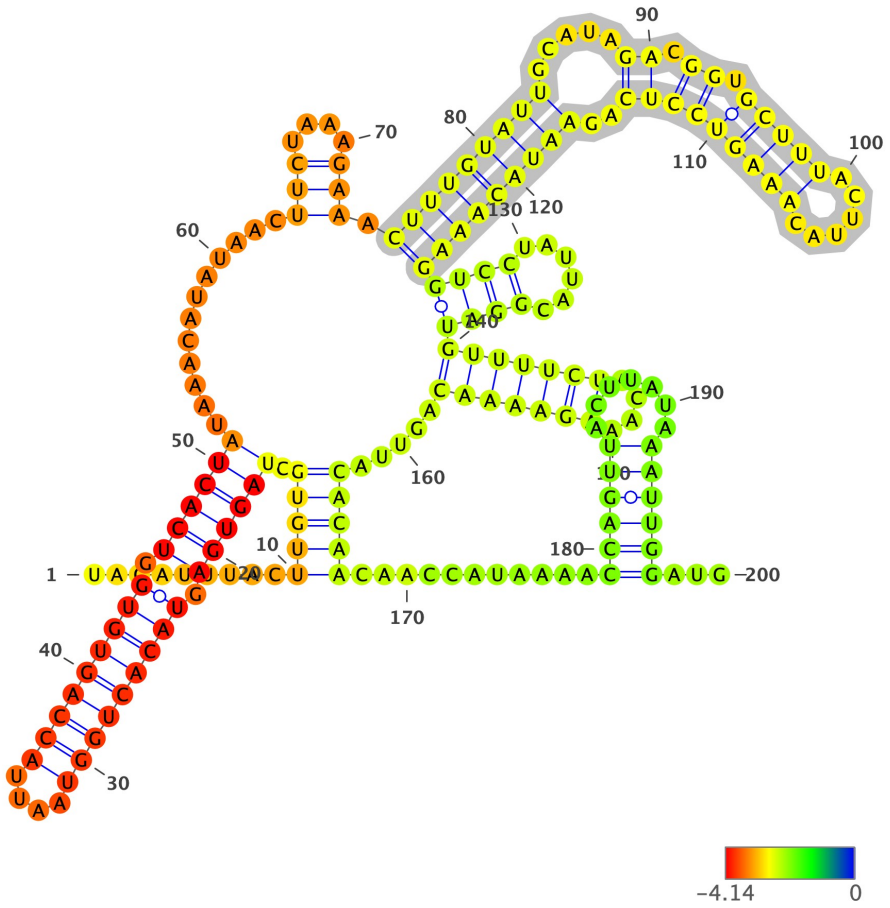
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-CUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAG-3'
5'-(((((((((.....((.((.(((((.....)))))))))..)))))))))-3'
Motif MFE = -10.9; z-score = -1.68; 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 = -4.83; ED = 15.13
```

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

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

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

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

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

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

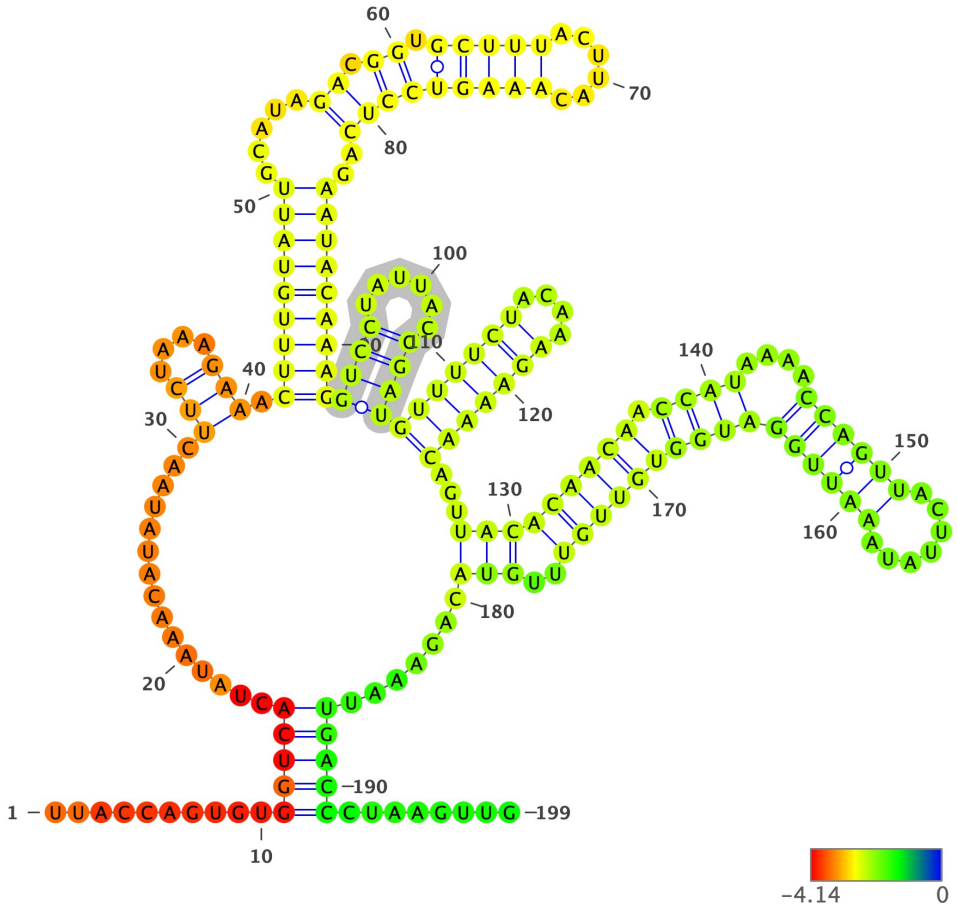
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 120 from nt 5847 to 5860 (nt 93 to 106)

```
5'-GUCCUAUUACGGAU-3'
5'-((((......))))-3'
Motif MFE = -2.6; z-score = -3.48; 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 = -2.36; ED = 22.72
```

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

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

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

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

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

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

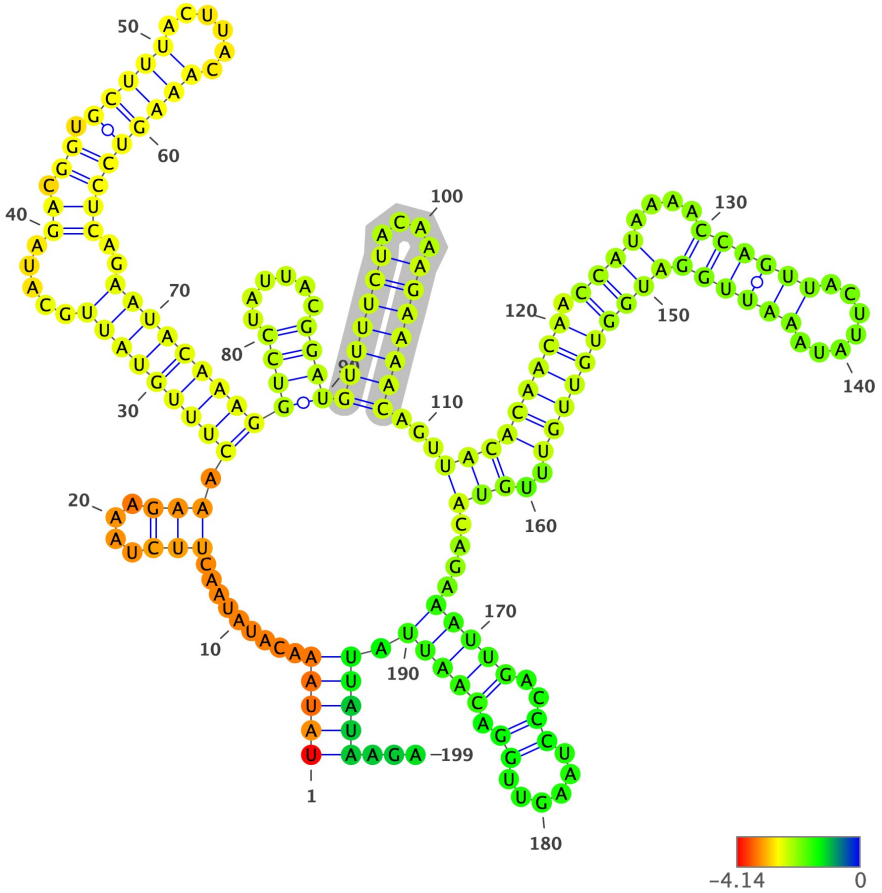
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 121 from nt 5861 to 5878 (nt 91 to 108)

```
5'-GUUUUCUACAAAGAAAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -5.32; 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 = -2.69; ED = 30.2
```

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

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

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

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

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

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

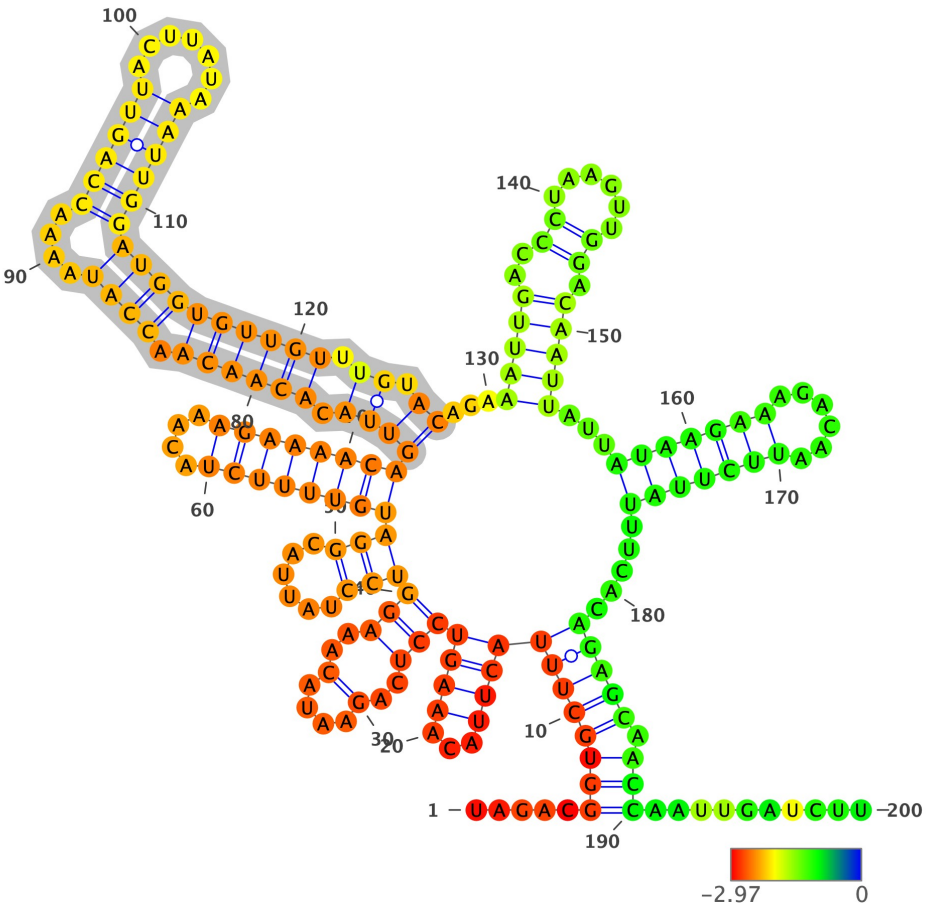
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 122 from nt 5880 to 5934 (nt 73 to 127)

```
5'-GUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUAC-3'
5'-((...((((((.((((....((((((.......)))))))))))))))....))-3'
Motif MFE = -13.5; z-score = -3.18; ED = 5.14
```



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

Extracted structure model with flanking nucleotides 5808 to 6007 (motif highlighted in silver):

```
5'-UAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGG
AUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUU-3
5'-.....(((((((((((...))))(((..(....)..)))(((......)))((((((((....))))))))((((.((((((.((((....((((((.......))))))
))))))))))).)).))...(((((..((......)).)))))...(((((((......)))))))).....))))).)))..........-3'
MFE = -39.0; z-score = -2.11; ED = 17.84
```

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(+)

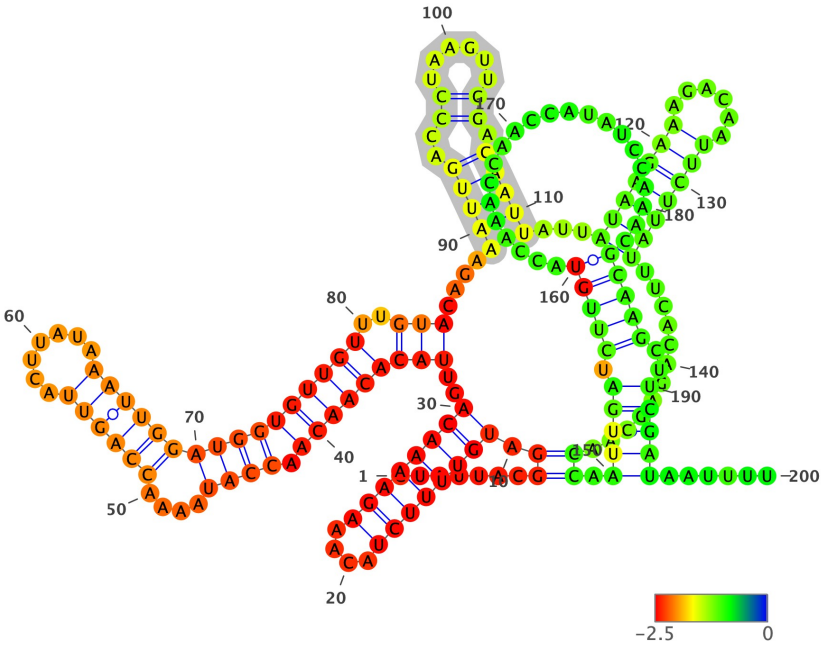
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 123 from nt 5938 to 5960 (nt 89 to 111)

```
5'-AAUUGACCCUAAGUUGGACAAUU-3'
5'-(((((..((......)).)))))-3'
Motif MFE = -2.2; z-score = -0.57; ED = 3.34
```



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

Extracted structure model with flanking nucleotides 5850 to 6049 (motif highlighted in silver):

```
5'-CUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUU
AUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUU-3
5'-.......((.(((((((((....)))))))))..(((((((((.((((....((((((.......)))))))))))))))))))..)))....(((((..((......)).)))))
...((((((.....)))))).............)).(((((.(((((.....................)))))..)))))......-3'
MFE = -33.2; z-score = -1.79; ED = 34.57
```

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

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

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

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

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

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

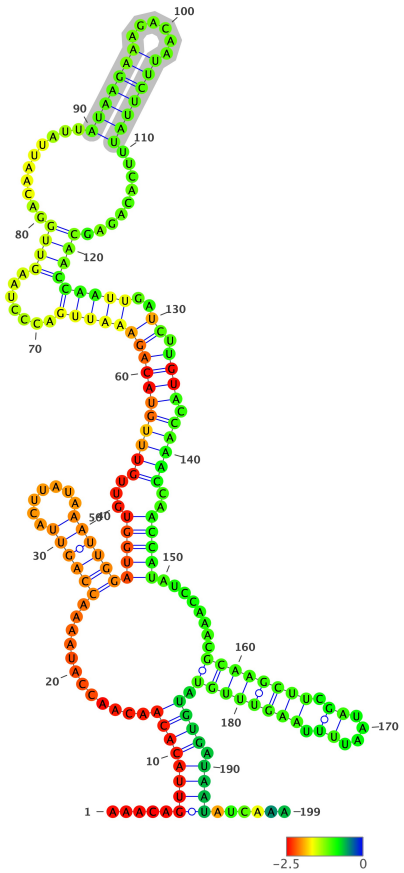
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 124 from nt 5964 to 5983 (nt 90 to 109)

```
5'-AUAAGAAAGACAAUUCUUAU-3'
5'-(((((..........)))))-3'
Motif MFE = -3.1; z-score = -4.96; 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 = -1.99; 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(+)

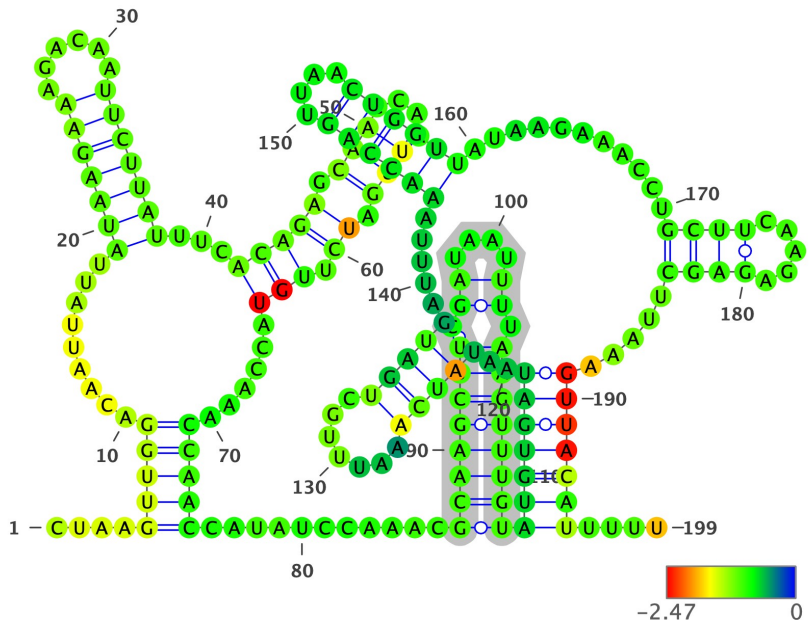
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 125 from nt 6032 to 6057 (nt 87 to 112)

```
5'-GCAAGCUUCGAUAAUUUUAAGUUUGU-3'
5'-(((((((((..(....)..)))))))))-3'
Motif MFE = -6.1; z-score = -2.68; ED = 1.79
```



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

Extracted structure model with flanking nucleotides 5946 to 6144 (motif highlighted in silver):

```
5'-CUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUG
UAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUU-3
5'-....(((((.........(((((((......)))))))...(((((.(((....)))).)).)))......)))))...........(((((((.((....)).)))))))
)(((((((..(((((.......)))))).....((((((....))))))...........((((.....)))).....)))))))....-3'
MFE = -30.0; z-score = -0.35; ED = 44.64
```

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(+)

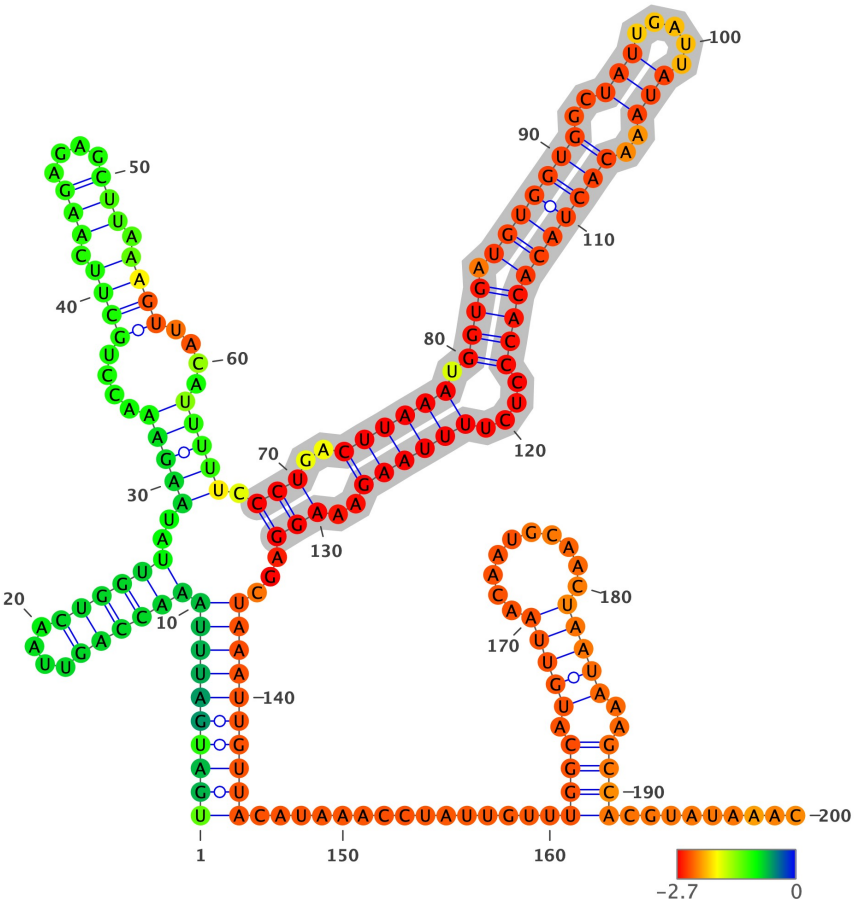
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-CCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGG-3'
5'-(((..(((((((.(((((.(((((((..(((.....)))..)))))))))))....))))))..)))-3'
Motif MFE = -21.2; z-score = -3.83; 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 = -1.89; ED = 39.58
```

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

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

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

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

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

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

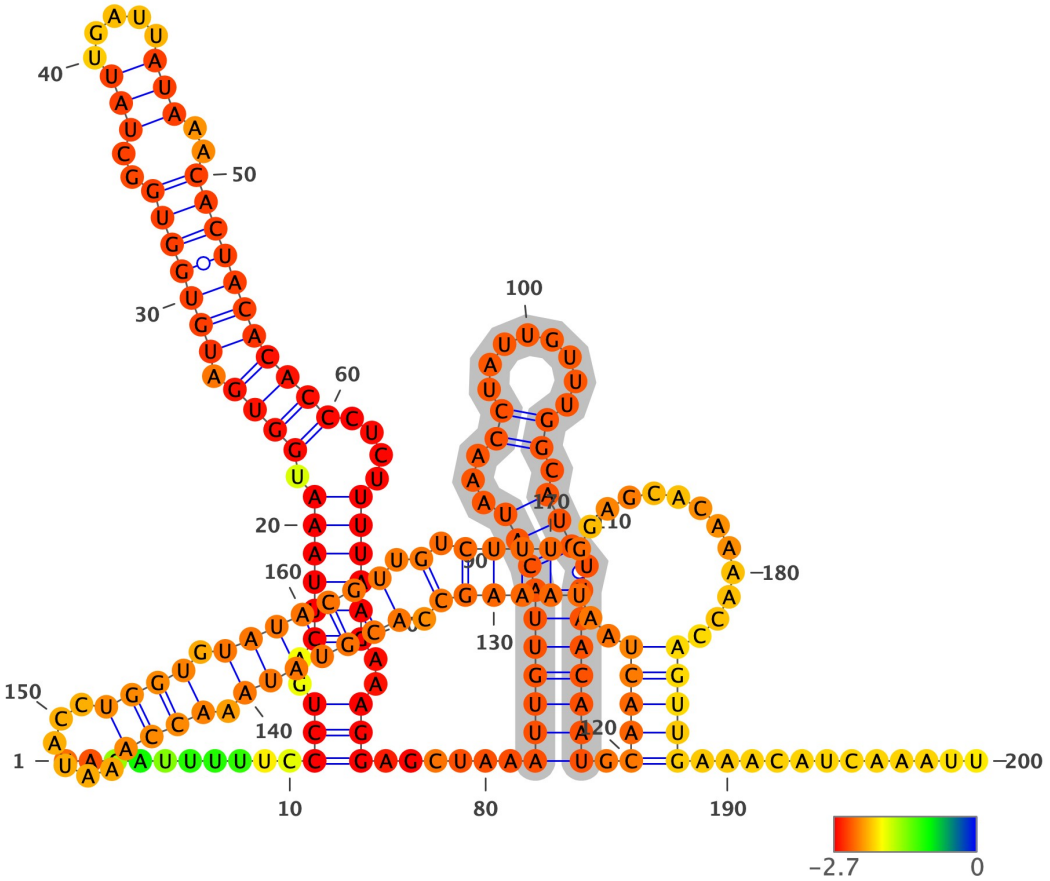
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 127 from nt 6217 to 6253 (nt 82 to 118)

```
5'-AUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAU-3'
5'-((((((((((...((........)).))).)))))))-3'
Motif MFE = -6.5; z-score = -2.2; 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 = -3.75; 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(+)

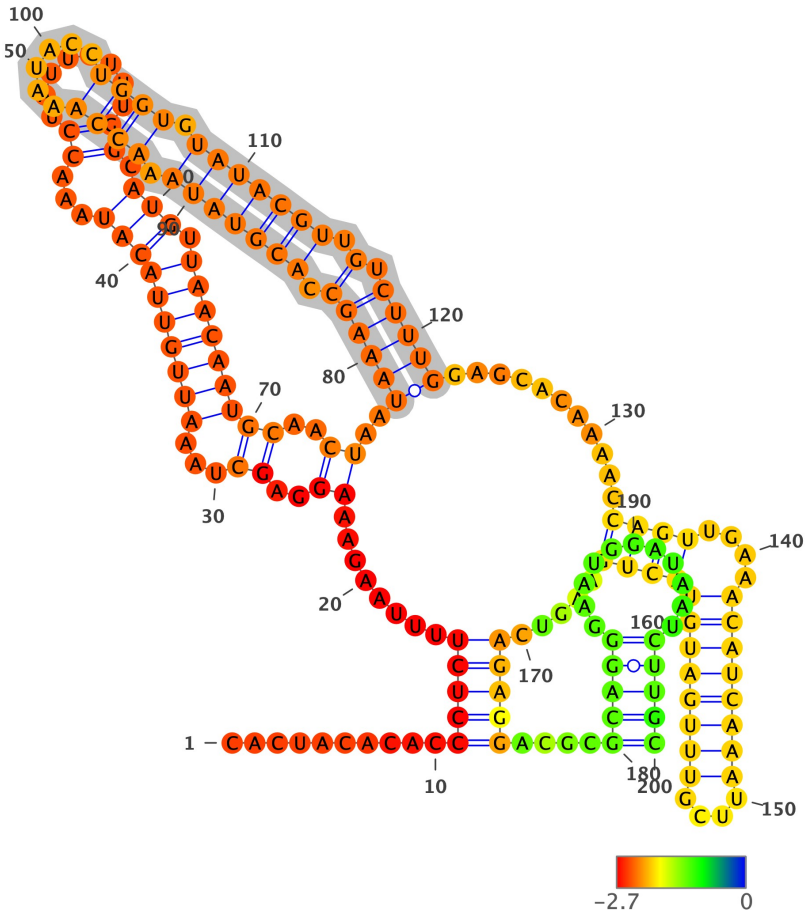
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-UAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUG-3'
5'-((((((.(((((((.((((......)))).)))))))).).)))))-3'
Motif MFE = -14.1; z-score = -4.02; 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 = -1.39; ED = 29.12
```

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

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

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

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

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

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

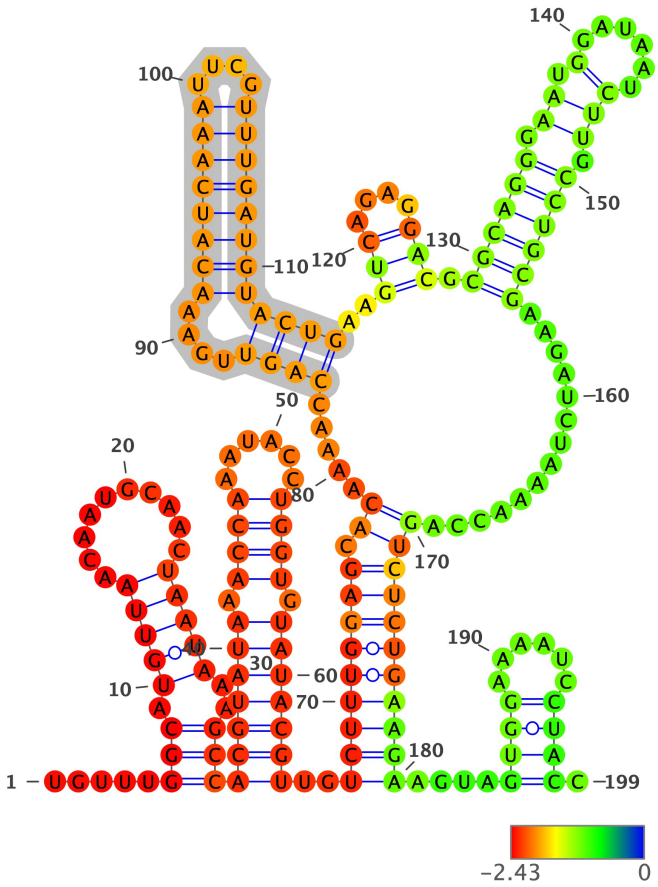
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 129 from nt 6318 to 6349 (nt 84 to 115)

```
5'-CAGUUGAAACAUCAAAUUCGUUUGAUGUACUG-3'
5'-((((....(((((((((....)))))))))))))-3'
Motif MFE = -8.0; z-score = -2.59; 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 = -2.21; 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(+)

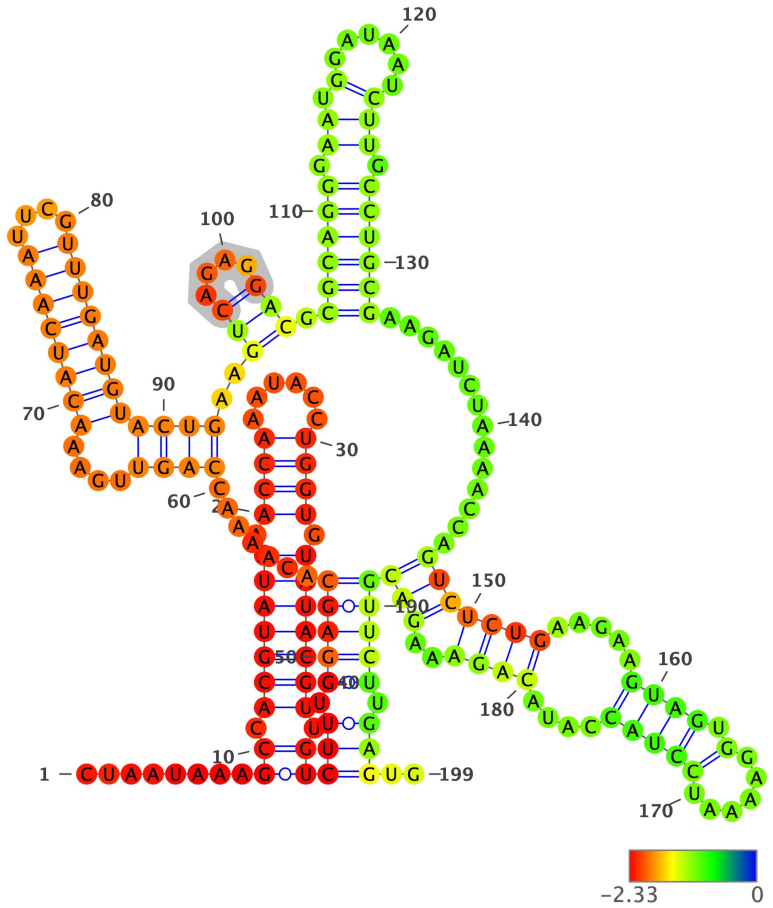
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 130 from nt 6354 to 6359 (nt 97 to 102)

```
5'-CAGAGG-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 6258 to 6456 (motif highlighted in silver):

```
5'-CUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGG
GAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUG-3
5'-........((.(((((((.((((......)))).)))))))).))(((.(((((.......((((....((((((((....)))))))))))))..(((....))).((((((
.((.(......))).))))))..............(((((((.....((((.(......)))))....))))..)))))))).)))..-3'
MFE = -49.4; z-score = -2.53; ED = 28.48
```

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(+)

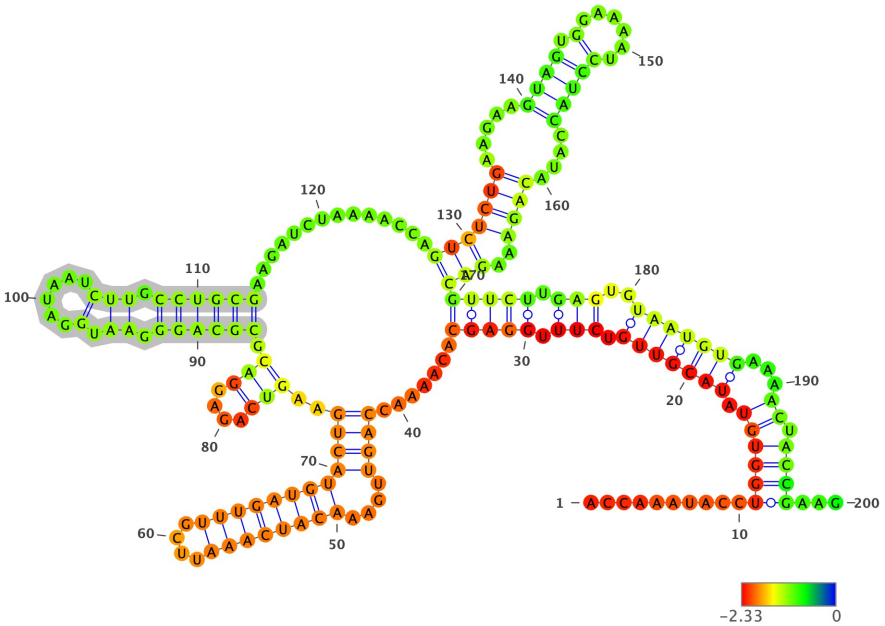
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 131 from nt 6363 to 6389 (nt 87 to 113)

```
5'-CGCAGGGAAUGGAUAAUCUUGCCUGCG-3'
5'-((((((.((.(.....)).)))))))-3'
Motif MFE = -10.0; z-score = -2.18; 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 = -1.18; 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(+)

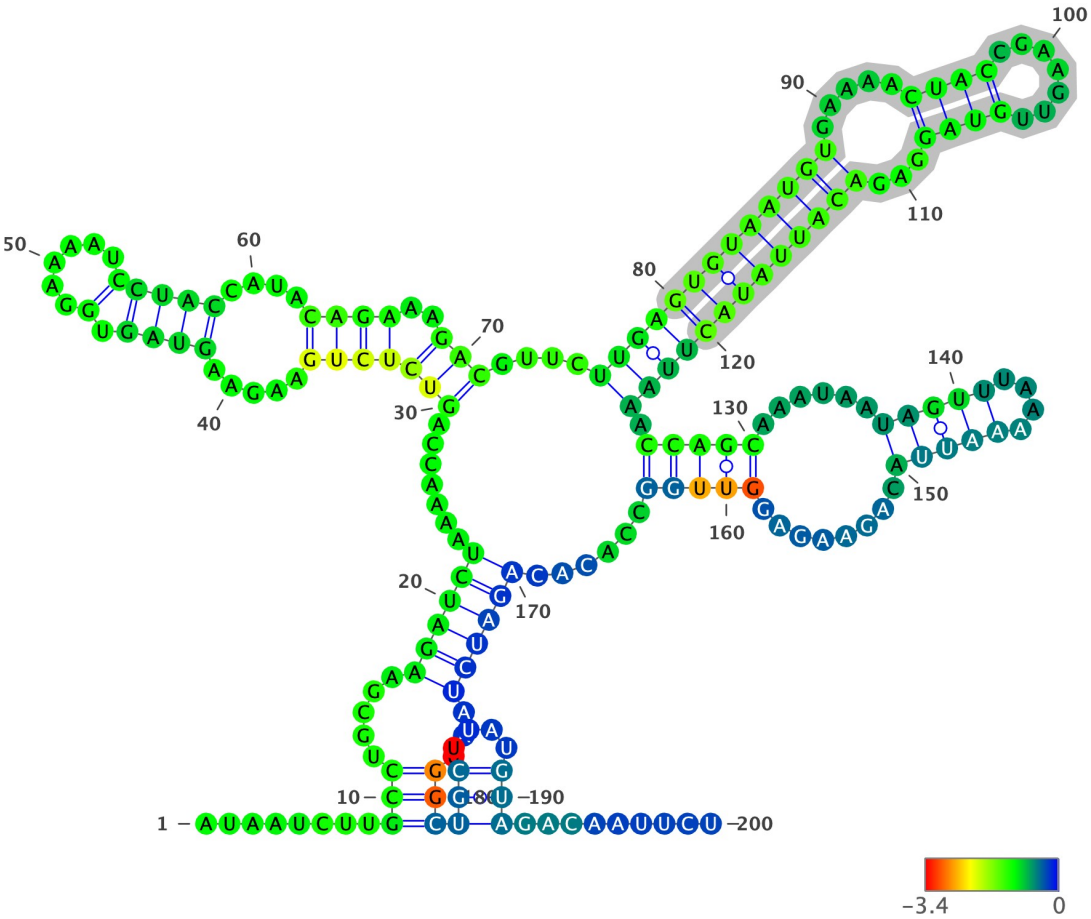
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 132 from nt 6454 to 6494 (nt 80 to 120)

```
5'-GUGUAAUGUGAAAACUACCGAAGUUGUAGGAGACAUUAUAC-3'
5'-(((((((((.....((((.......))))...)))))))))-3'
Motif MFE = -10.4; z-score = -2.75; ED = 1.07
```



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

Extracted structure model with flanking nucleotides 6375 to 6574 (motif highlighted in silver):

```
5'-AUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAG
ACAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCU-3
5'-........(((.....((((((.......(((((((.....((((.(......)))))....))))..)))....((((((((((((.....((((.......))))...
))))))))))))).(((((......(((((....)))))........)))))......))))))...)))(((....)))........-3'
MFE = -37.6; z-score = -0.61; ED = 42.55
```

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

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

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

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

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

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

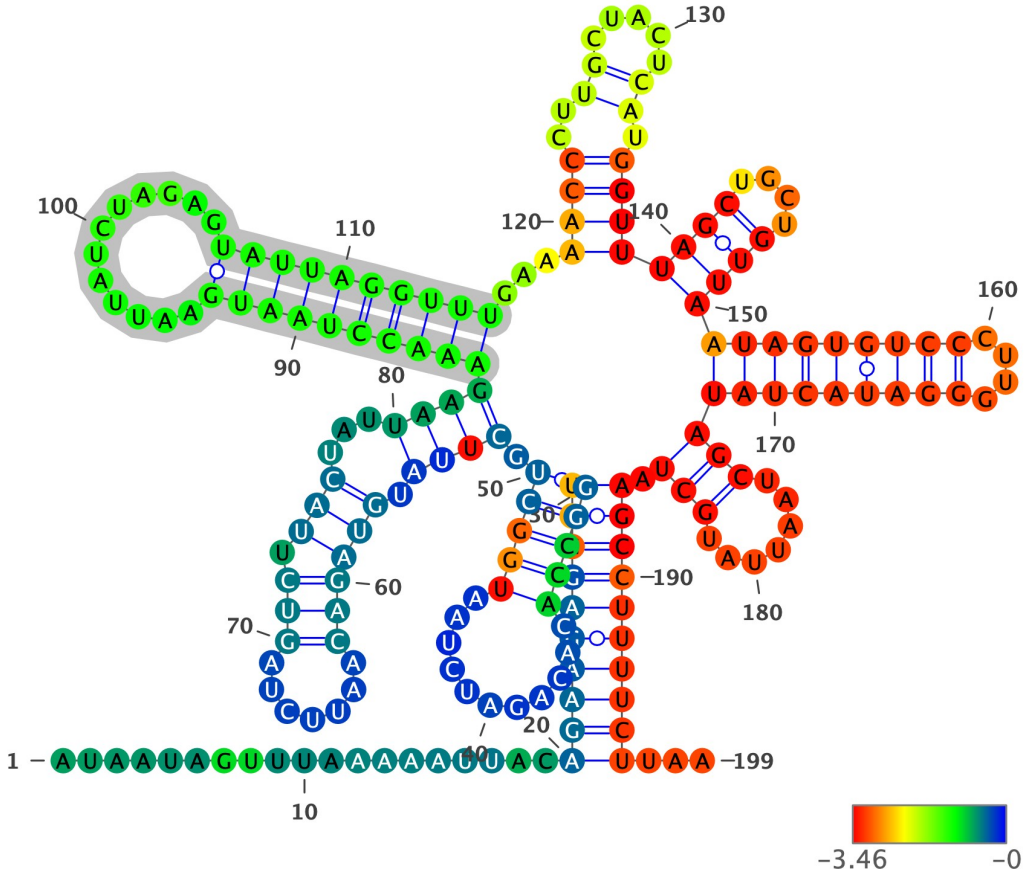
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 133 from nt 6590 to 6621 (nt 84 to 115)

```
5'-AAACCUAAUGAAUUAUCUAGAGUAUUAGGUUU-3'
5'-((((((((((.........))))))))))-3'
Motif MFE = -6.8; z-score = -2.53; ED = 2.83
```



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

Extracted structure model with flanking nucleotides 6507 to 6705 (motif highlighted in silver):

```
5'-AUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAG
GUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAA-3
5'-...................((((((((((((((((.........)))))).((((.((((((.......))).))).))))((((((((((.........))))))
))))).....((((..(.....)).)))))((....))))((((((((((....)))))))))((.......))).))))))))))...-3'
MFE = -46.9; z-score = -2.63; ED = 33.32
```

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

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

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

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

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

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

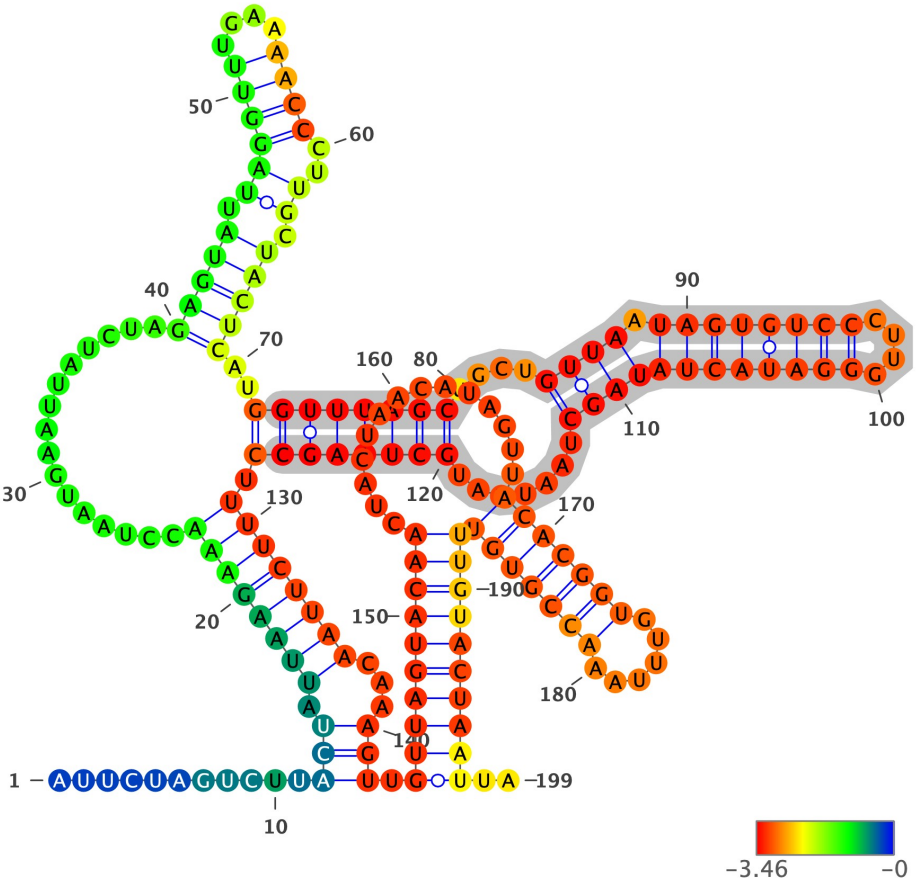
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 134 from nt 6642 to 6695 (nt 73 to 126)

```
5'-GUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGC-3'
5'-(((((((....((((.((((((((....)))))))))))).......)))))))-3'
Motif MFE = -18.4; z-score = -3.66; ED = 4.92
```



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

Extracted structure model with flanking nucleotides 6570 to 6768 (motif highlighted in silver):

```
5'-AUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAGGUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAG
CUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUA-3
5'-...........(((.((((((((.................(((((.((((((....))))..)).)))))..((((((((....((((.((((((((....)))))))))))
).......))))))))).))))))))...))).((((((((((.............(((((((......)))))))))))))))))..-3'
MFE = -51.4; z-score = -4.39; ED = 38.37
```

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(+)

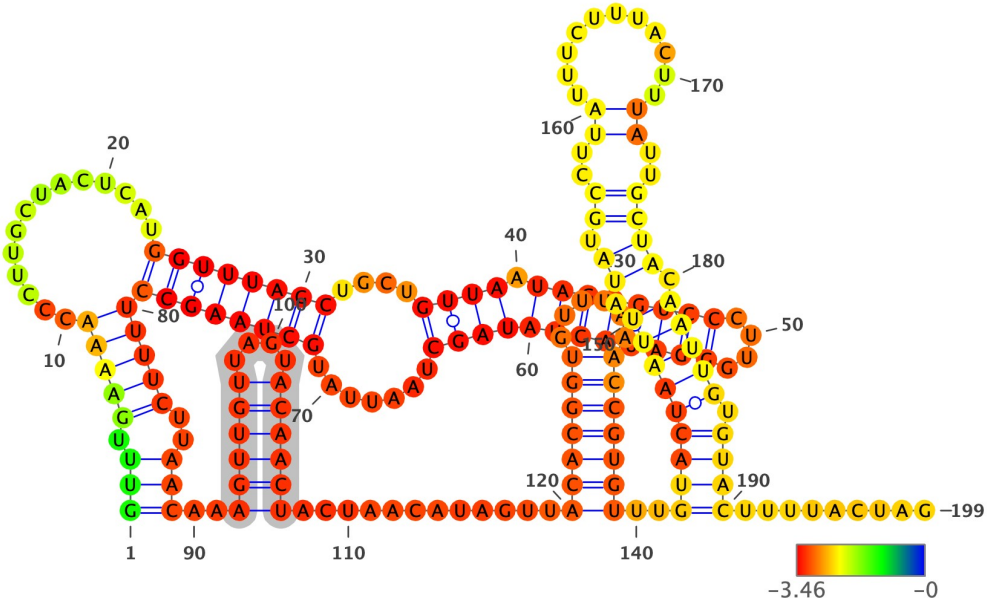
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 135 from nt 6709 to 6724 (nt 92 to 107)

```
5'-AGUUGUUAGUACAACU-3'
5'-((((((....)))))))-3'
Motif MFE = -4.3; z-score = -5.27; ED = 0.52
```



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

Extracted structure model with flanking nucleotides 6618 to 6816 (motif highlighted in silver):

```
5'-GUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUA
ACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAG-3
5'-(((.(((((.............(((((((....((((.(((((((((....)))))))))))).......)))))))))))))..)))..((((((....)))))))....
........(((((((.....)))))))..(((((((((.((.((..((...........)).)))).)))))).)))).........-3'
MFE = -44.5; z-score = -3.48; ED = 26.97
```

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

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

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

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

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

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

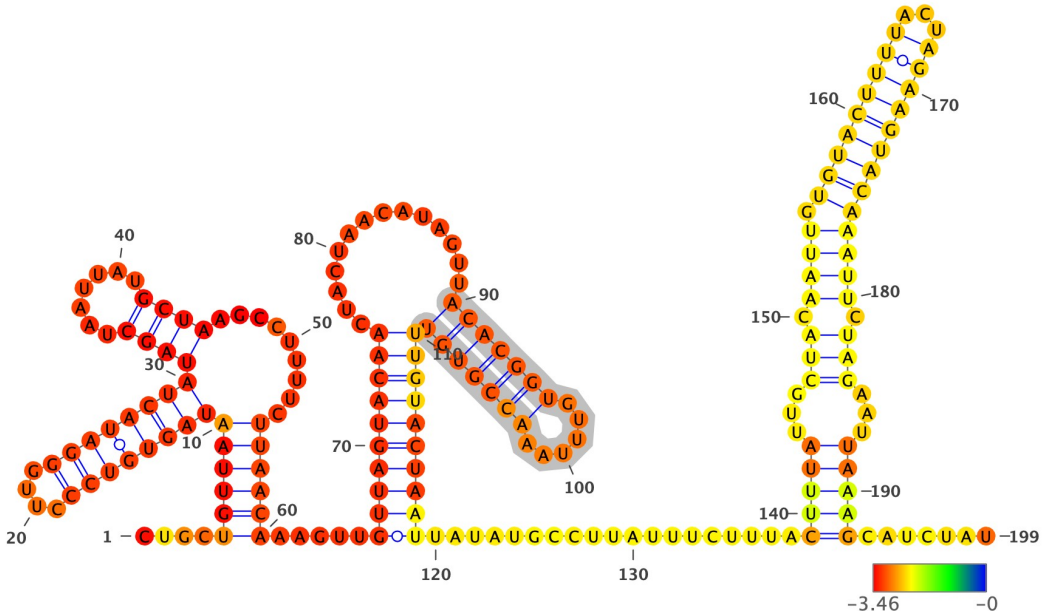
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 136 from nt 6737 to 6756 (nt 90 to 109)

```
5'-ACACGGUGUUUAAACCGUGU-3'
5'-(((((..........)))))-3'
Motif MFE = -10.0; z-score = -3.99; ED = 0.44
```



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

Extracted structure model with flanking nucleotides 6648 to 6846 (motif highlighted in silver):

```
5'-CUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUU
GUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAU-3
5'-....(((((((((((((....)))))))))((((.......)))).........)))))).....((((((((((.............((((((.....))))))))))
)))))))).................(((((...((((.((((.((((((((...)))))))))))))).)))...)))))).......-3'
MFE = -45.9; z-score = -3.94; 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(+)

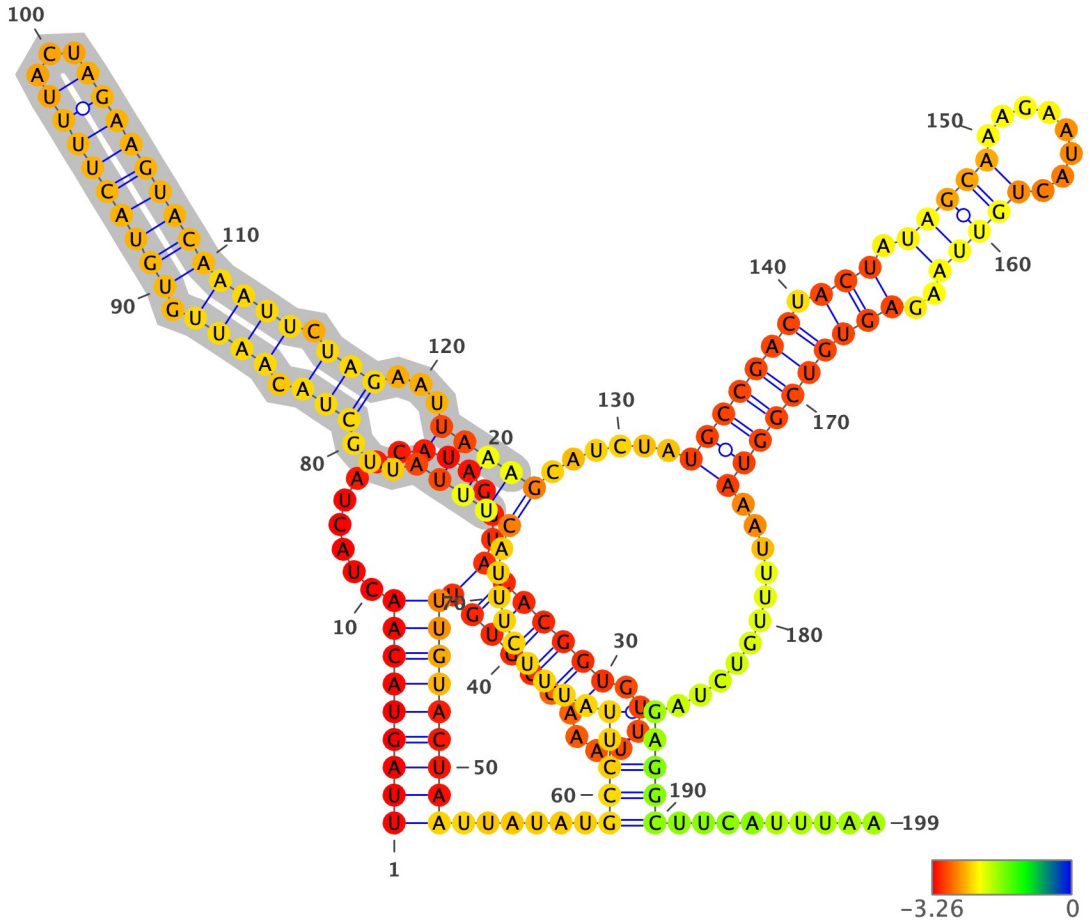
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 137 from nt 6787 to 6838 (nt 74 to 125)

```
5'-UUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAA-3'
5'-((.....(((.((((.((((((((.....)))))))))))).)))).....))-3'
Motif MFE = -9.7; z-score = -2.18; ED = 4.82
```



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 6714 to 6912 (motif highlighted in silver):

```
5'-UUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAA
AUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAA-3
5'-(((((((((.............(((((((......)))))))))))))))).....(((((.........(((((...(((.((((.(((((((((...)))))))))))
))).)))...)))))......(((((((.(((.(((((........)))))..)))))))))).....)))))..........-3'
MFE = -51.4; z-score = -4.47; ED = 11.25
```

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(+)

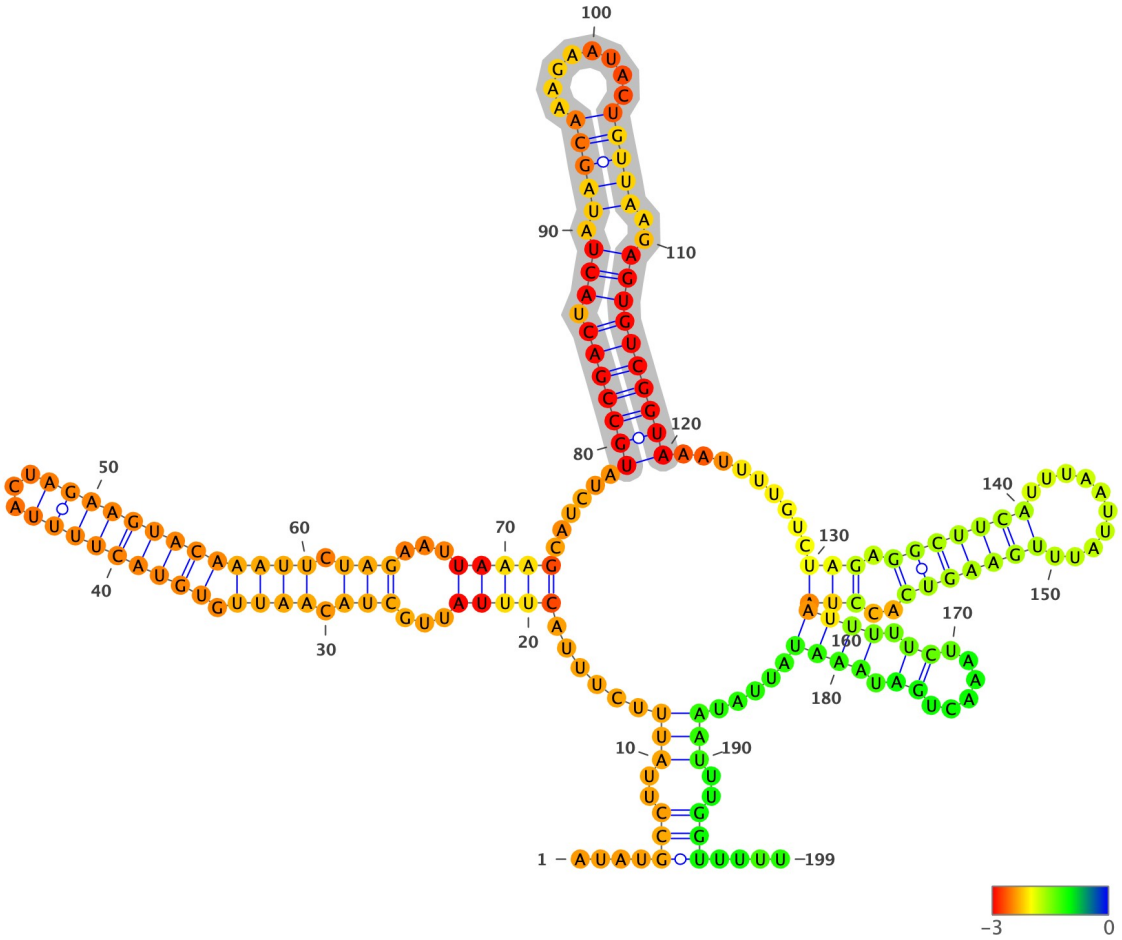
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 138 from nt 6846 to 6887 (nt 79 to 120)

```
5'-UGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUA-3'
5'-(((((((.(((.....................))))))))))-3'
Motif MFE = -14.8; z-score = -4.68; 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 = -2.99; ED = 21.8
```

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(+)

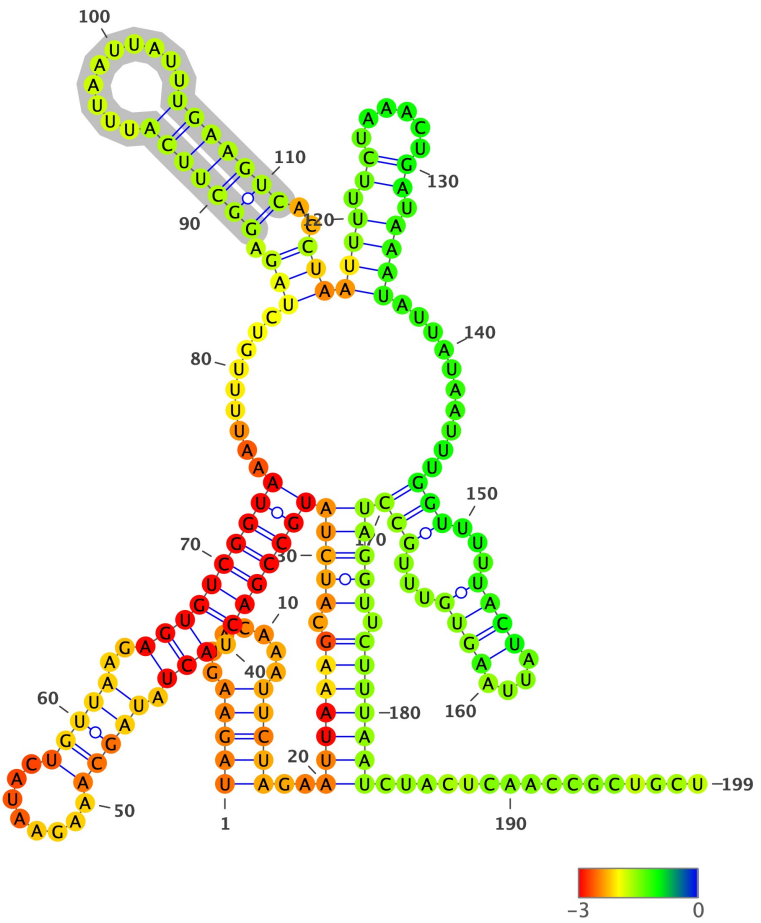
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 139 from nt 6901 to 6924 (nt 88 to 111)

```
5'-GGCUUCAUUUAAUUAUUUGAAGUC-3'
5'-(((((((..........)))))))-3'
Motif MFE = -6.2; z-score = -3.36; 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 = -1.86; 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(+)

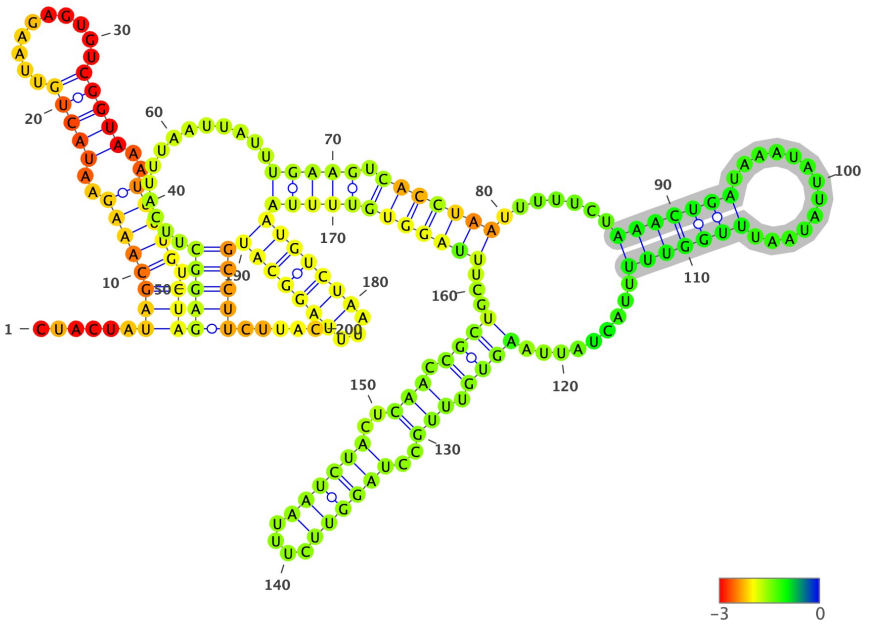
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 140 from nt 6938 to 6964 (nt 87 to 113)

```
5'-AAACUGAUAAAUAUUAUAAUUUGGUUU-3'
5'-(((((((.............)))))))-3'
Motif MFE = -1.0; z-score = -0.04; ED = 3.92
```



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 6852 to 7051 (motif highlighted in silver):

```
5'-CUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGU
UUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUAC-3
5'-......((((((((..(((((..........)))))..)))))).)))(((((..............(((((.(((((((.......(((((((.............)))))
)).........((((.(((..((((((....))))))..))).))))...))))))))))))(((((((...)))))))))))).....-3'
MFE = -35.1; z-score = -0.85; ED = 35.83
```

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

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

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

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

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

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

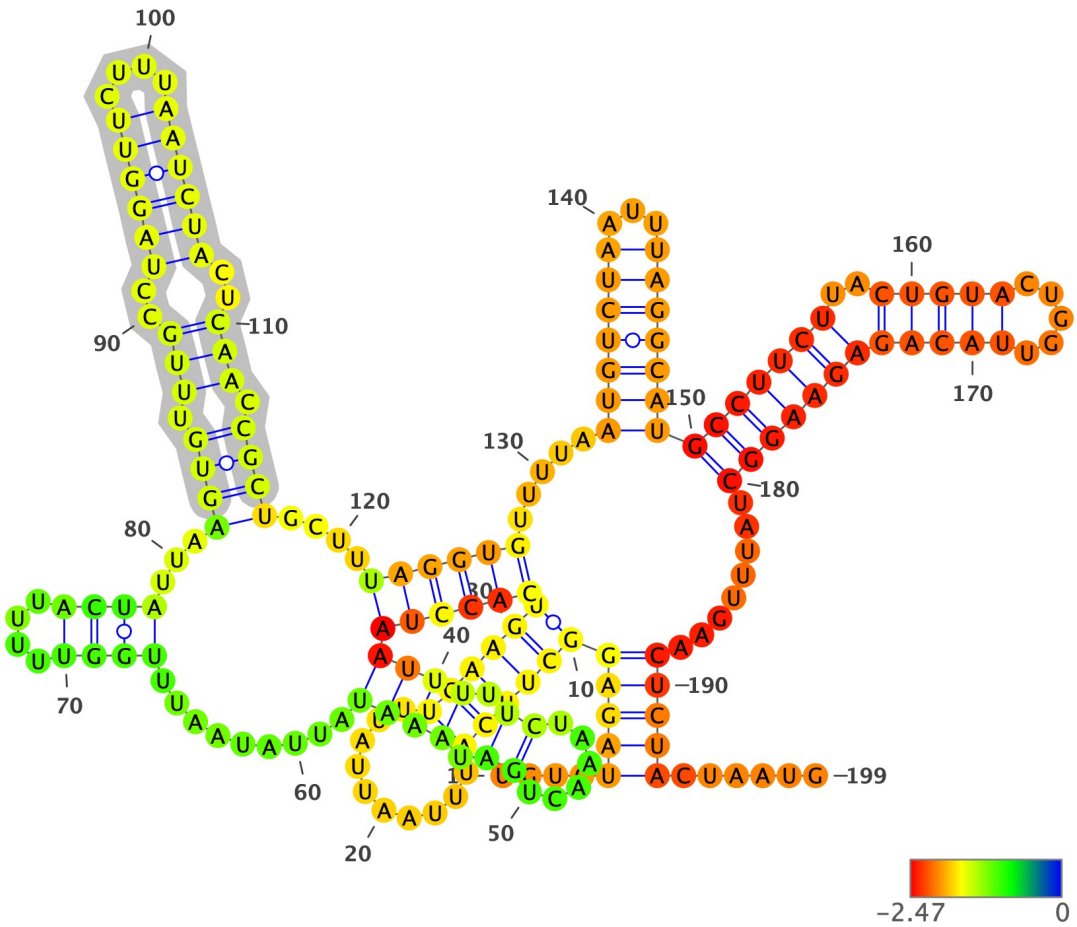
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 6975 to 7008 (nt 83 to 116)

```
5'-GUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGC-3'
5'-(((.(((..((((((....))))))..))).)))-3'
Motif MFE = -5.6; z-score = -1.3; ED = 1.5
```



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

Extracted structure model with flanking nucleotides 6893 to 7091 (motif highlighted in silver):

```
5'-UGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCA
ACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUG-3
5'-....(((((((((((.........))))))((((((((((.((......)).))))).........((((....))))...((((.(((..((((((....))))))..))
).))))....))))))).....(((((((...)))))))(((((((..(((((.....)))))))))))).........)))))......-3'
MFE = -46.1; z-score = -3.53; ED = 19.36
```

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

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

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

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

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

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

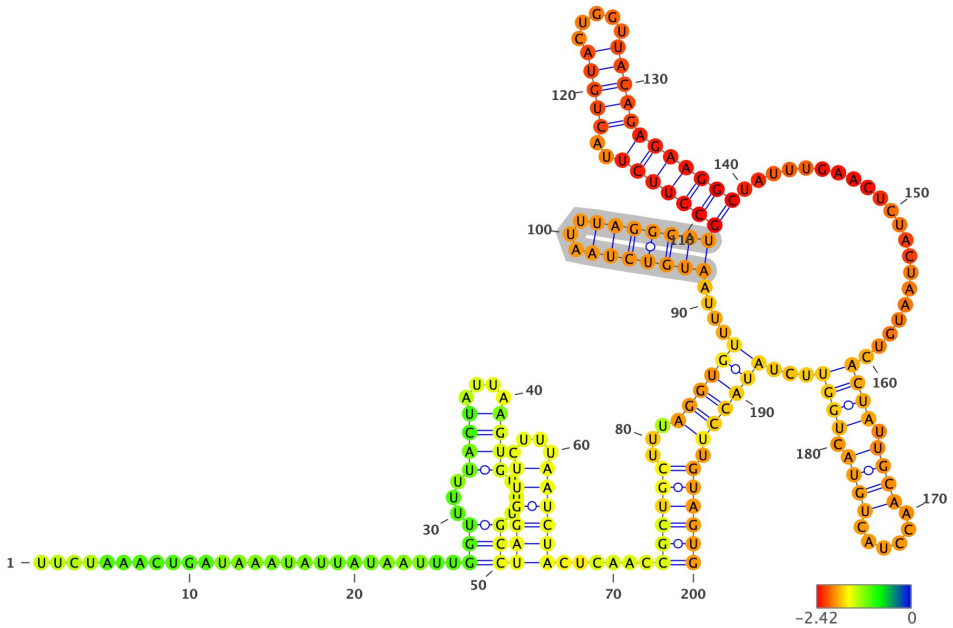
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 142 from nt 7025 to 7041 (nt 92 to 108)

```
5'-AUGUCUAAUUUAGGCAU-3'
5'-((((((.....))))))-3'
Motif MFE = -4.2; z-score = -5.31; ED = 1.02
```



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

Extracted structure model with flanking nucleotides 6934 to 7133 (motif highlighted in silver):

```
5'-UUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCC
UUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUG-3
5'-.........................(((...((((....))))...)))((((((....))))))......((((((...((((((....(((((((...)))))))(((
((((..(((((.....)))))))))))).....................((((.((((......)))).))))...)))))).))))))-3'
MFE = -41.7; z-score = -1.92; 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(+)

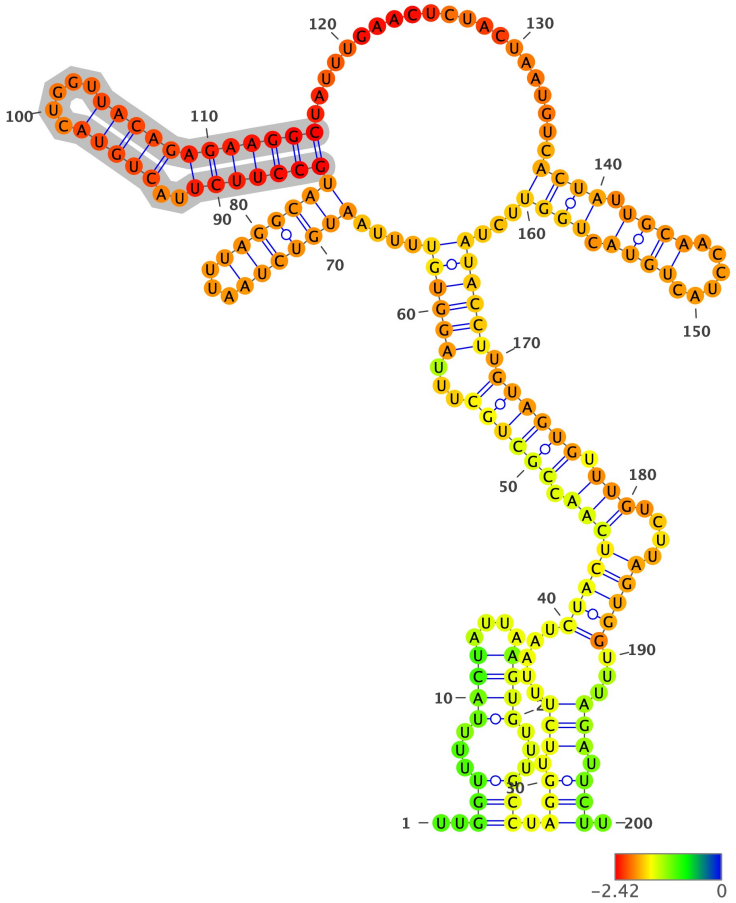
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 143 from nt 7042 to 7072 (nt 85 to 115)

```
5'-GCCUUCUUACUGUACUGGUUACAGAGAAGGC-3'
5'-(((((((..(((((.....)))))))))))-3'
Motif MFE = -13.1; z-score = -3.83; ED = 1.16
```



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

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

```
5'-UUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGA
AGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUU-3
5'-..(((...((((....))))...))).(((.(((.....((((((((.((((((...((((((....(((((((...)))))))(((((((..(((((.....))))))))
))))....................((((.((((......)))).))))...)))))).)))))).)))....)))))...))).))).-3'
MFE = -48.6; z-score = -3.11; 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(+)

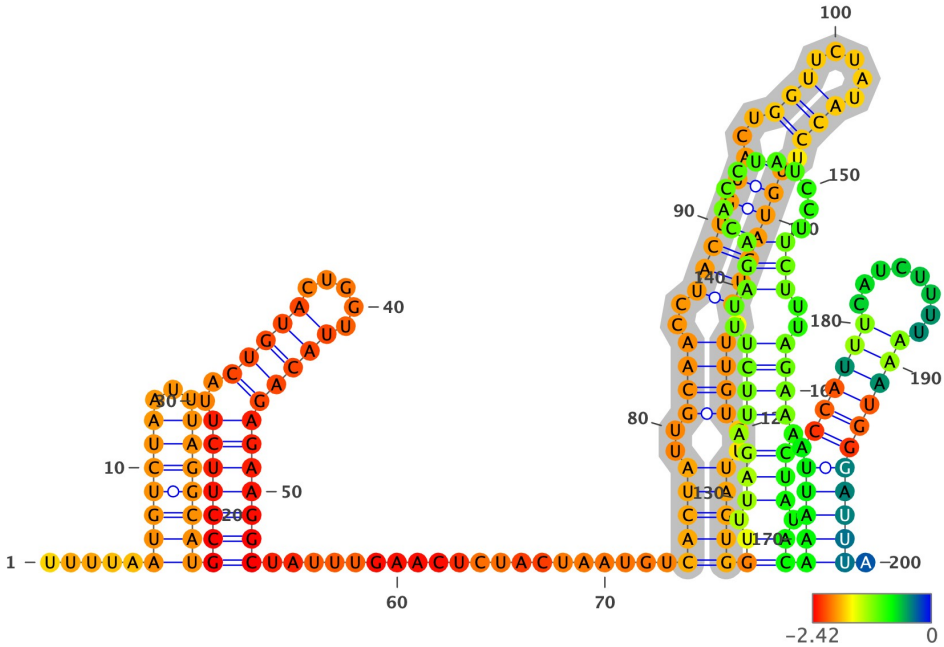
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 144 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 = -2.96; 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(+)

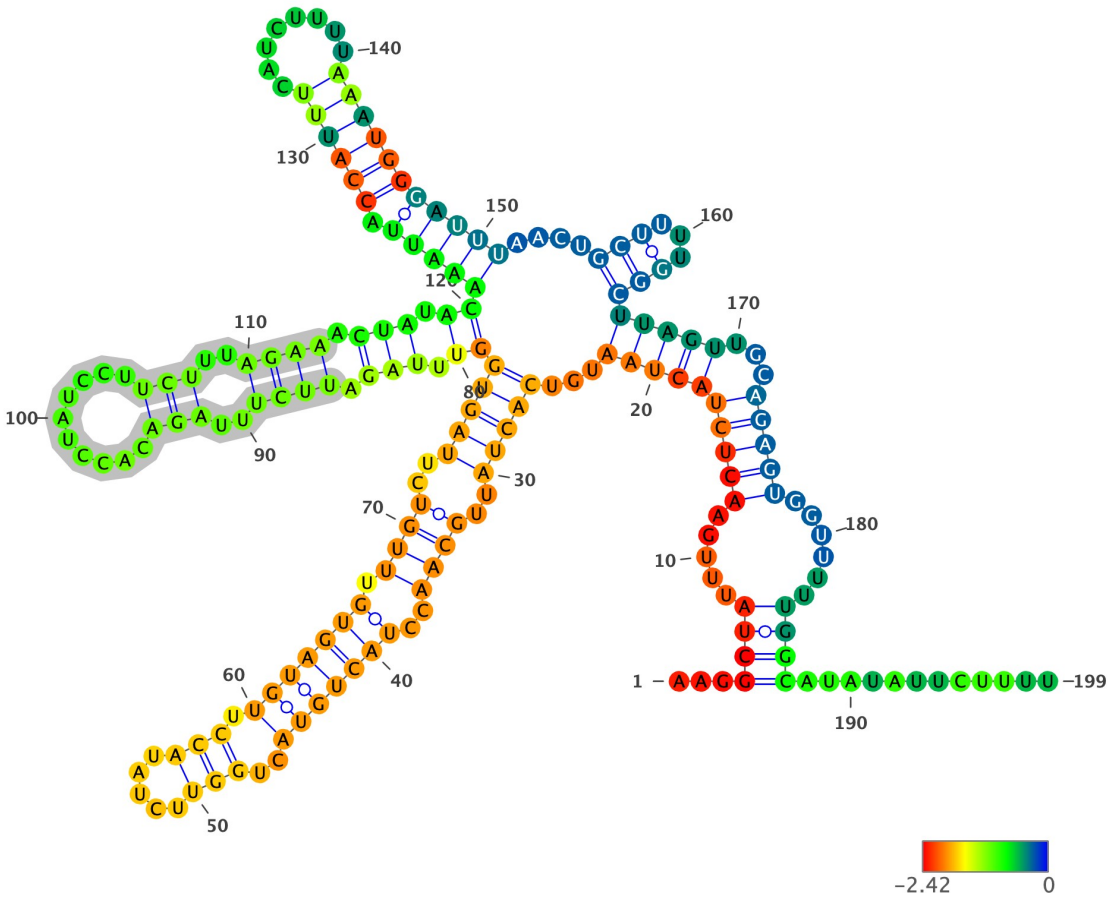
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 145 from nt 7153 to 7180 (nt 86 to 113)

```
5'-UUCUUUAGACACCUAUCCUUCUUUAGAA-3'
5'-((((..(((..........)))..))))-3'
Motif MFE = -2.1; z-score = -2.52; ED = 2.06
```



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

Extracted structure model with flanking nucleotides 7068 to 7266 (motif highlighted in silver):

```
5'-AAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAG
AAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUU-3
5'-...((((.....((((((((((...(((((..((((..(((((((..(((.....))).)))))))).))))..)))))((.(((.((((..(((..........)))..))
)).))).))(((((.((((((........)))))))))))....(((...)))))))))...)))))......))))............-3'
MFE = -37.9; z-score = -1.27; ED = 34.02
```

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(+)

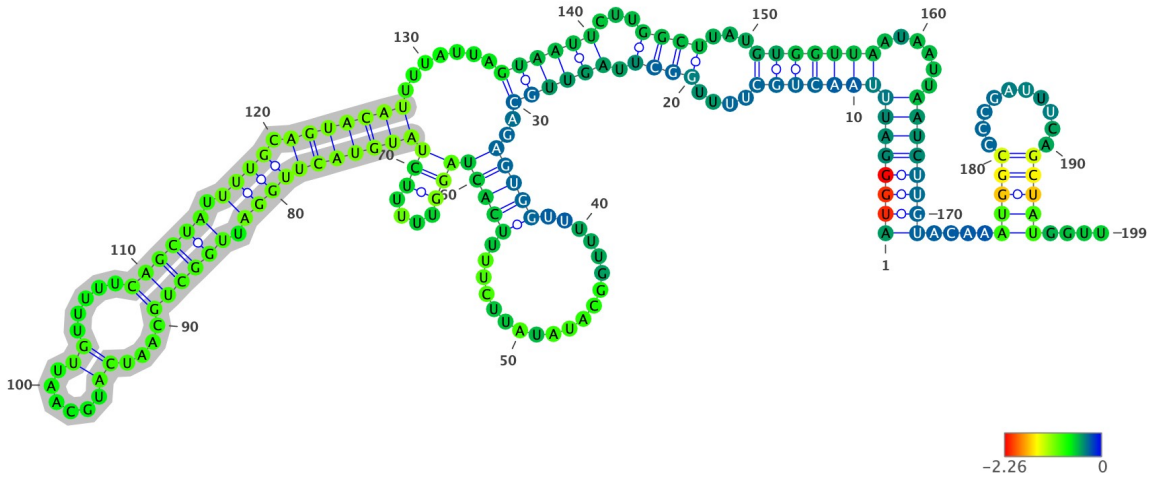
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 146 from nt 7281 to 7336 (nt 72 to 127)

```
5'-AUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAGCUAUUUUGCAGUACAU-3'
5'-(((((((((((.................................)))).)))))))-3'
Motif MFE = -14.5; z-score = -2.52; 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 = 0.13; 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(+)

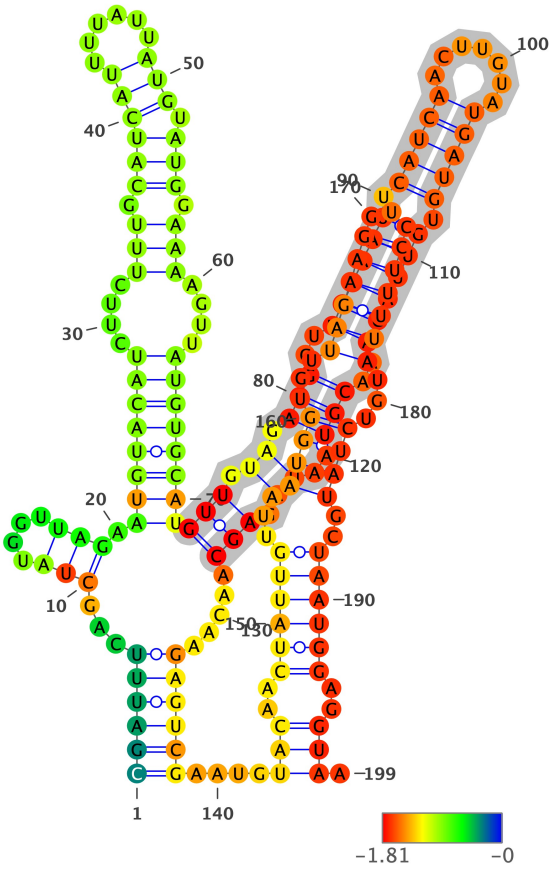
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 147 from nt 7463 to 7518 (nt 72 to 127)

```
5'-GUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGC-3'
5'-(((....(((..((((((.(((((.......))))).))))))..)))).....)))-3'
Motif MFE = -16.3; z-score = -2.92; 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 = -1.38; ED = 52.79
```

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(+)

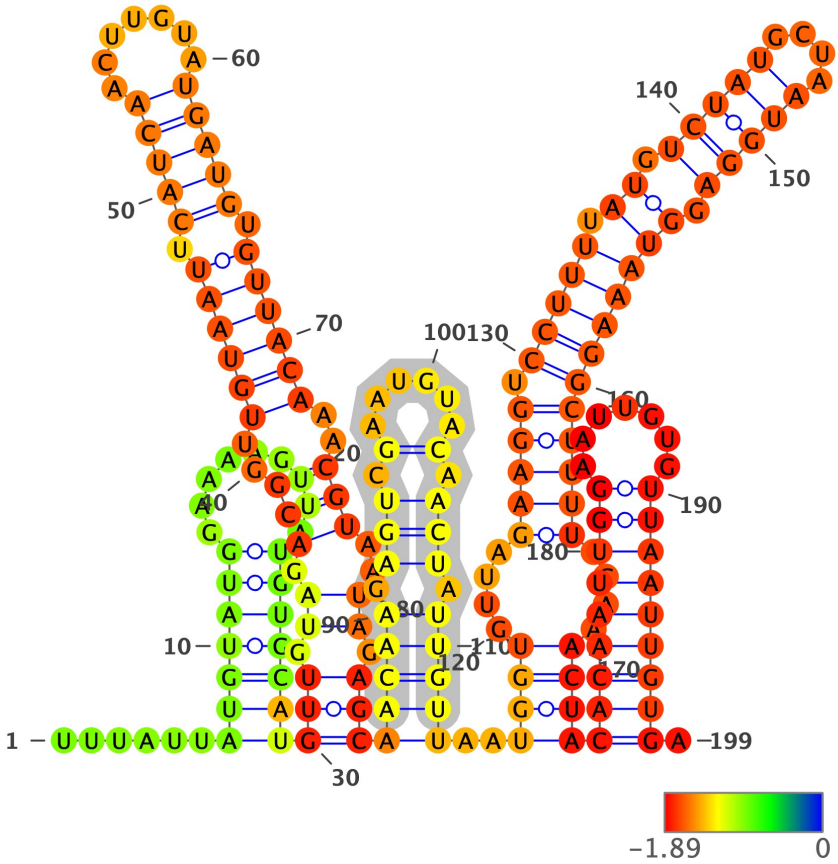
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 148 from nt 7520 to 7545 (nt 87 to 112)

```
5'-ACAAGAGUCGAAUGUACAACUAUUGU-3'
5'-((((.(((.(......).))).))))-3'
Motif MFE = -1.6; z-score = 0.04; ED = 2.36
```



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 7434 to 7632 (motif highlighted in silver):

```
5'-UUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUG
UUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGA-3
5'-......(((((((.........)))))))(((.((.(((..((((((.(((((.......))))).))))))..)))..)).)))(((((.(((.(......).))).)))
))..((((....(((((.(((((.((.(((((....))))).))))))))))))....))))((((((((.......)))))))).-3'
MFE = -47.5; z-score = -2.02; ED = 24.34
```

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(+)

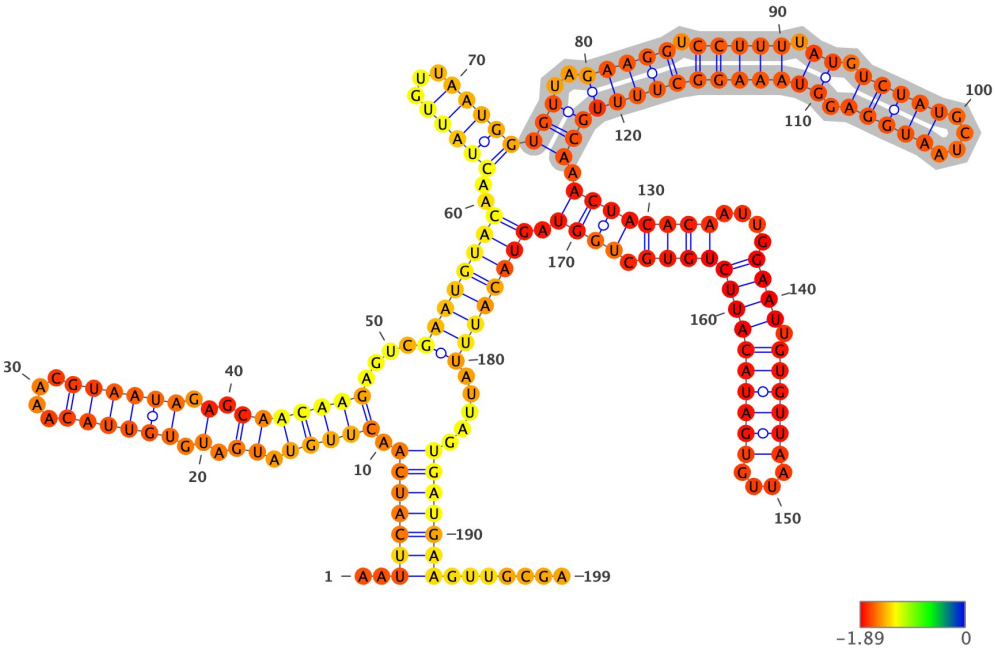
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 149 from nt 7552 to 7601 (nt 75 to 124)

```
5'-UGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCA-3'
5'-(((...((((.(((((.((.(((((....)))))).)))))))))))).)))-3'
Motif MFE = -14.1; z-score = -3.32; 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 7478 to 7676 (motif highlighted in silver):

```
5'-AAUUCAUCAACUUGUAUGAUGUGUUACAAACGUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGU
AAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGA-3
5'-..(((((((.(((((.((.(.((((((....)))))).).)))))))....(((((((..(((((...)))))))((..(((((.(((((.((.(((((....)))))).))
)))))))))))).((((((((....((((.((((((....)))))))))))))).)))).)))))))).....)))))))).......-3'
MFE = -48.0; z-score = -2.19; ED = 37.99
```

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

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

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

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

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

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

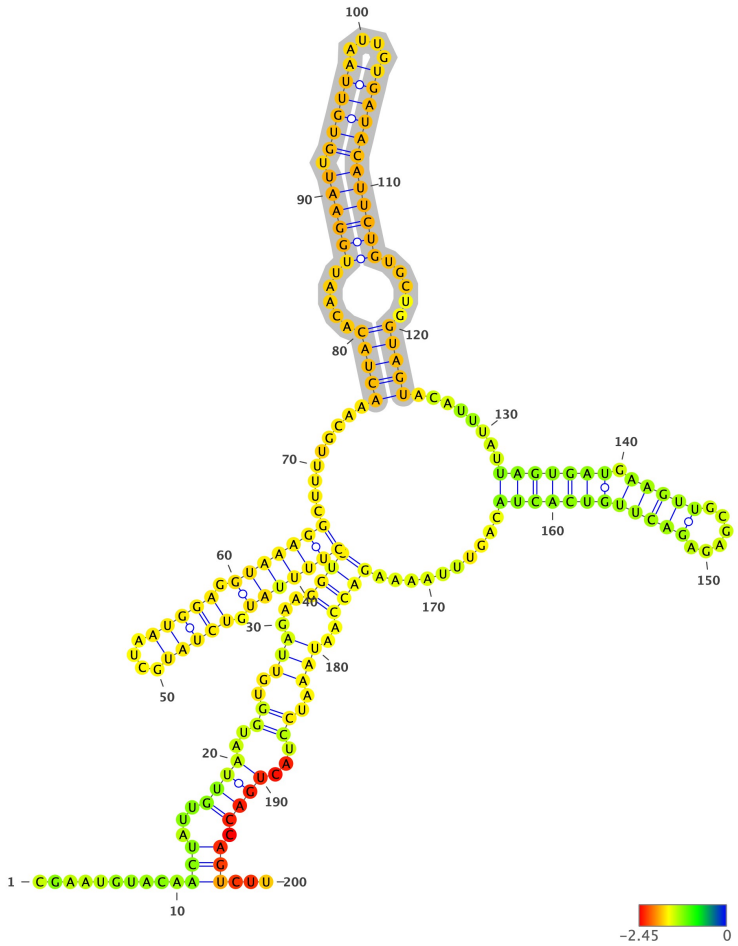
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 150 from nt 7603 to 7651 (nt 76 to 124)

```
5'-ACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUUCUGUGCUGGUAGU-3'
5'-(((((......(((((.(((((......)))))))))).....)))))-3'
Motif MFE = -11.6; z-score = -2.03; ED = 5.96
```



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

Extracted structure model with flanking nucleotides 7528 to 7727 (motif highlighted in silver):

```
5'-CGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUU
CUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUU-3
5'-..........(((...((((..((..(((...(((((((((((.(((((....))))).)))))))).........(((((.....((((((.((((((....)))))))))
)))).....)))))........(((((((.(((((......))))))))))))..........))))..)))..))...)))).)))...-3'
MFE = -43.5; z-score = -2.84; ED = 50.46
```

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

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

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

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

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

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

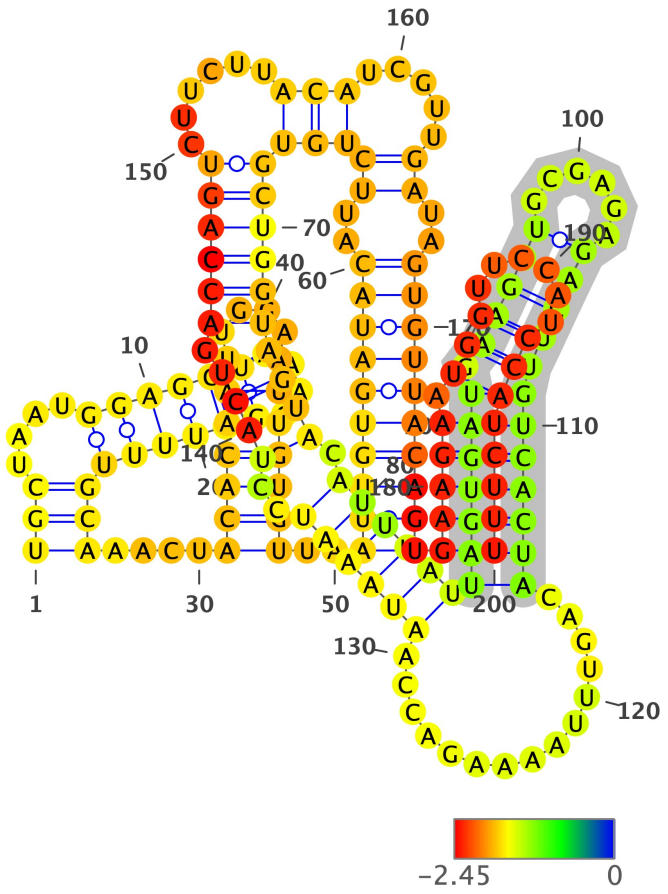
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 151 from nt 7660 to 7690 (nt 85 to 115)

```
5'-UAGUGAUGAAGUUGCGAGAGACUUGUCACUA-3'
5'-(((((((.(((((.....))))))))))))-3'
Motif MFE = -10.2; z-score = -3.26; 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 = -1.18; 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(+)

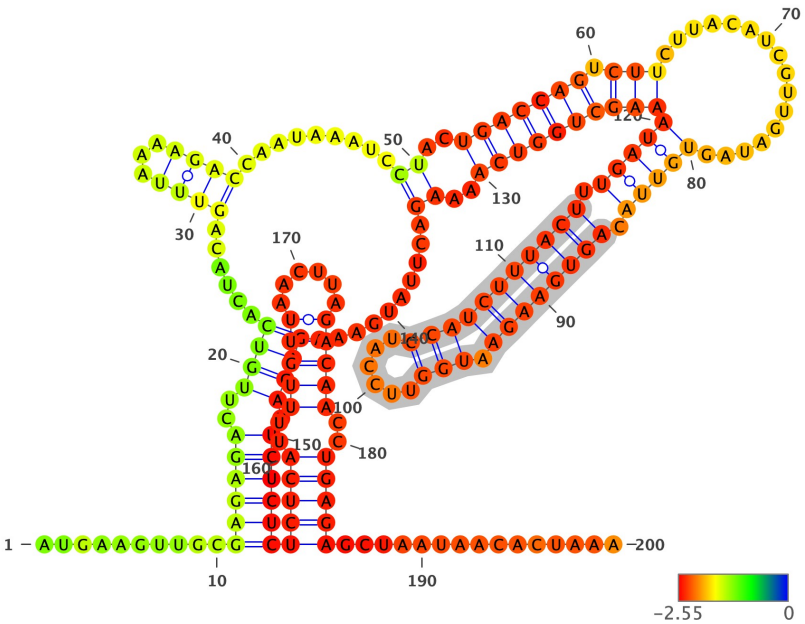
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 152 from nt 7750 to 7778 (nt 86 to 114)

```
5'-AGUGAAGAAUGGUUCCAUCCAUCUUUACU-3'
5'-((((((((.(((......)))))))))))-3'
Motif MFE = -10.4; z-score = -3.76; ED = 1.47
```



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

Extracted structure model with flanking nucleotides 7665 to 7864 (motif highlighted in silver):

```
5'-AUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUU
ACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAA-3
5'-..........((((((..((((......((((...))))..........((..(((((((.(((................(((((.((((((((.(((......))))))))
))).))))))))))))))..)).........))))).))))))(((((..(((((......)))))..)))))................-3'
MFE = -44.4; z-score = -2.76; ED = 44.86
```

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

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

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

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

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

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

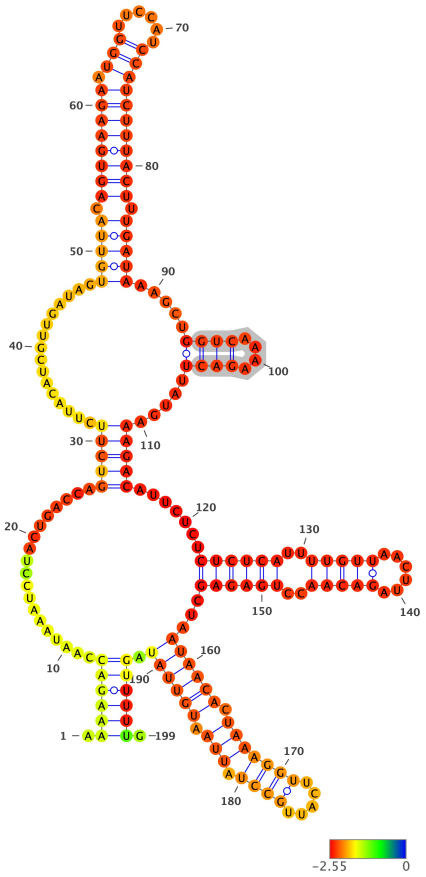
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 153 from nt 7791 to 7800 (nt 95 to 104)

```
5'-GUCAAAAGAC-3'
5'-(((....)))-3'
Motif MFE = -0.5; z-score = -10.1; 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 7697 to 7895 (motif highlighted in silver):

```
5'-AAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAA
AGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUG-3
5'-.((((((.....................(((((.................(((((.((((((((.(((......)))))))))))).)))))).....((((....)))).....)
))))).......((((((..(((((......)))))..))))))...((((((.(((((((.....)))).))).)))))).)))))).-3'
MFE = -40.5; z-score = -3.34; ED = 26.73
```

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(+)

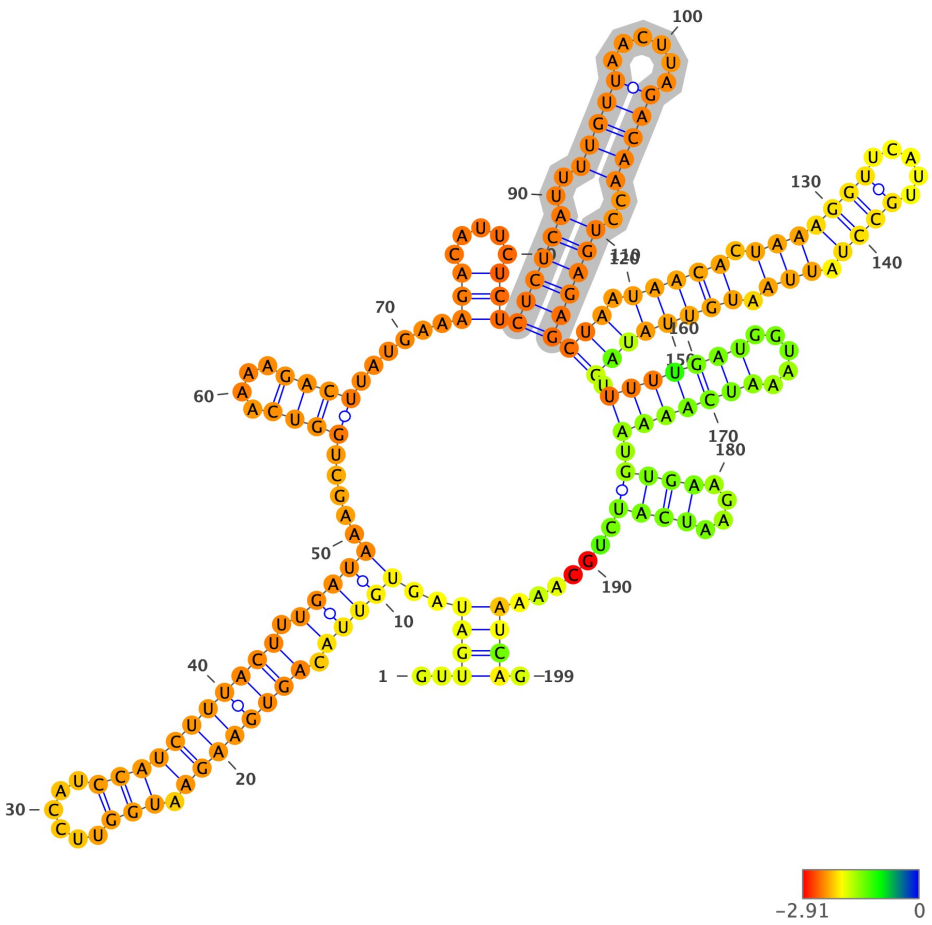
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 154 from nt 7819 to 7850 (nt 84 to 115)

```
5'-CUCUCAUUUUGUUAACUUAGACAACCUGAGAG-3'
5'-((((((..(((((......)))))..))))))-3'
Motif MFE = -10.3; z-score = -4.91; 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 = -2.68; 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(+)

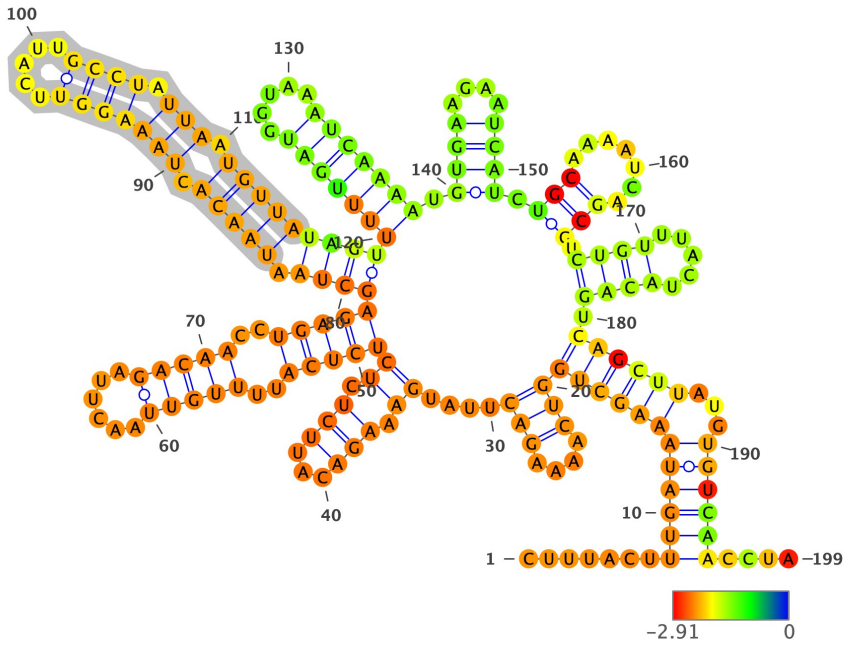
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 155 from nt 7855 to 7886 (nt 84 to 115)

```
5'-UAACACUAAAGGUUCAUUGCCUAUUAAUGUUA-3'
5'-(((((.(((((((.....)))).))).)))))-3'
Motif MFE = -6.5; z-score = -2.78; 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 = -2.72; 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(+)

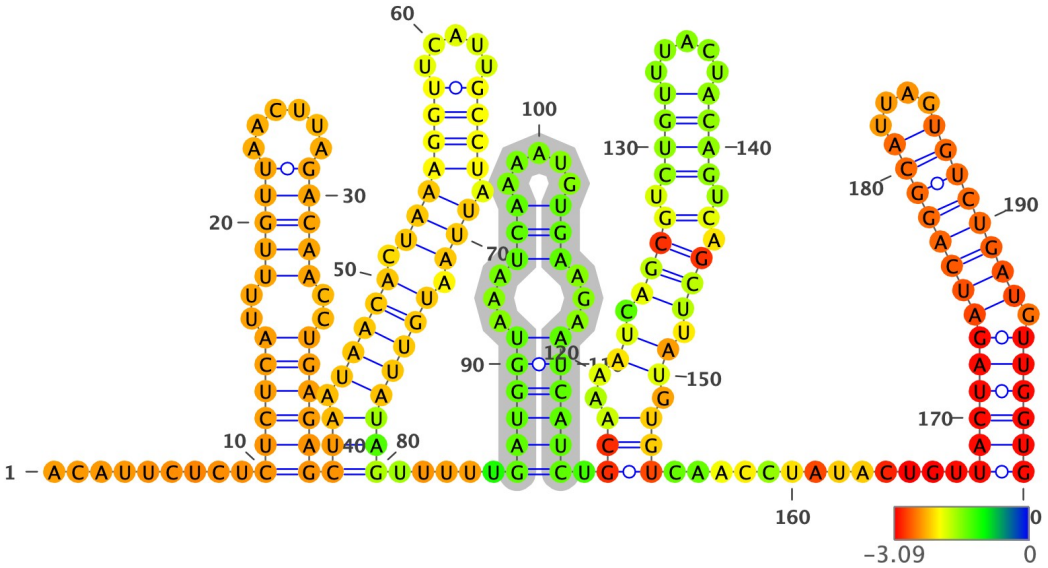
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 156 from nt 7895 to 7923 (nt 86 to 114)

```
5'-GAUGGUAAAUCAAAAUGUGAAGAAUCAUC-3'
5'-((((((...(((.....)))...))))))-3'
Motif MFE = -4.2; z-score = -2.17; ED = 1.56
```



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

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

```
5'-ACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUC
AUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUG-3
5'-.........((((((..(((((......)))))..))))))(((.(((((.(((((((.....)))).))).))))))))).....((((((...(((.....)))...)))
))).(((..((.((((.((((.....)))).).))).)).))).............((((((((((((((....)))))))).))))))-3'
MFE = -44.9; z-score = -2.16; 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(+)

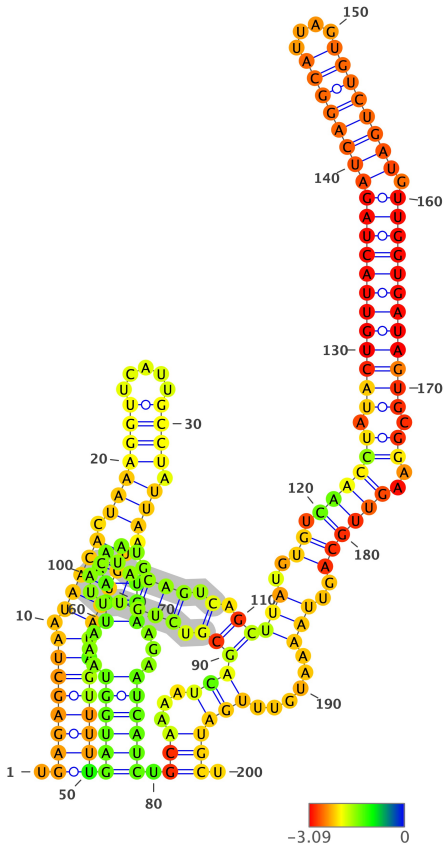
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 157 from nt 7936 to 7952 (nt 92 to 108)

```
5'-GUCUGUUUACUACAGUC-3'
5'-(.((((.....)))).)-3'
Motif MFE = -2.3; z-score = -1.98; ED = 0.71
```



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

Extracted structure model with flanking nucleotides 7845 to 8044 (motif highlighted in silver):

```
5'-UGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGC
UUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCU-3
5'-.((((((((.(((((.(((((((.....)))).))).))))))))))))((((((...(((.....)))...)))))).(((...((((((.((((.....)))).).))
(((..((.((((((.((((((((((((((((((((....)))))))).))))))))))))).))..)))))).))).....)))))).-3'
MFE = -53.3; z-score = -3.06; ED = 32.58
```

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(+)

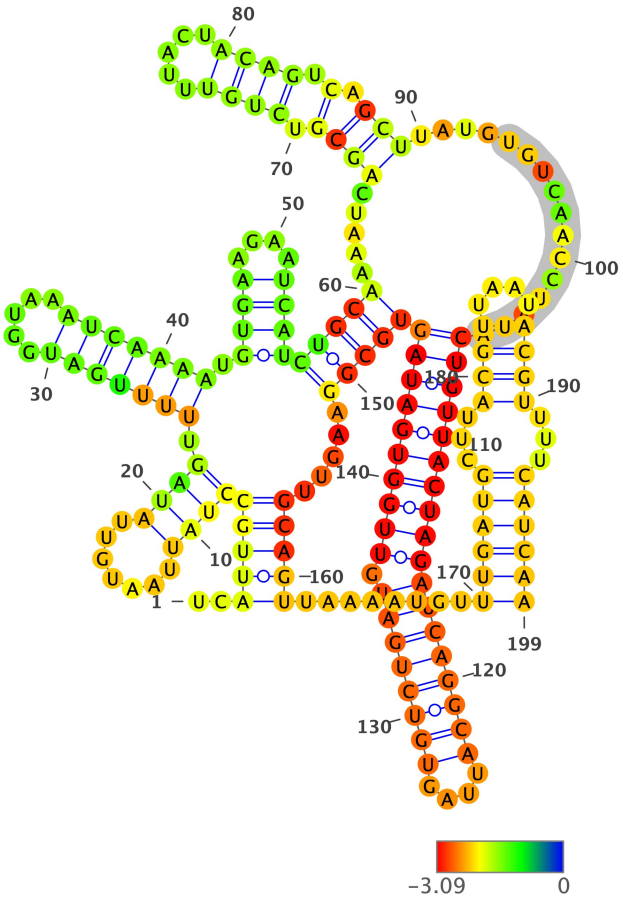
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 158 from nt 7961 to 7972 (nt 94 to 105)

```
5'-UGUCAACCUAUA-3'
5'-((........))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.06
```



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 7868 to 8066 (motif highlighted in silver):

```
5'-UCAUUGCCUAUUAAUGUUAUAGUUUUUGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUA
CUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAA-3
5'-..(((((((((.......)))).(((((((.....))))))).((((....))))(((((.....((((.((((.....)))).).))).................((((((
((((((((((((....)))))))).))))))))))))))).....)))))........((((((...((((....))))...))))))-3'
MFE = -47.5; z-score = -2.57; ED = 30.51
```

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(+)

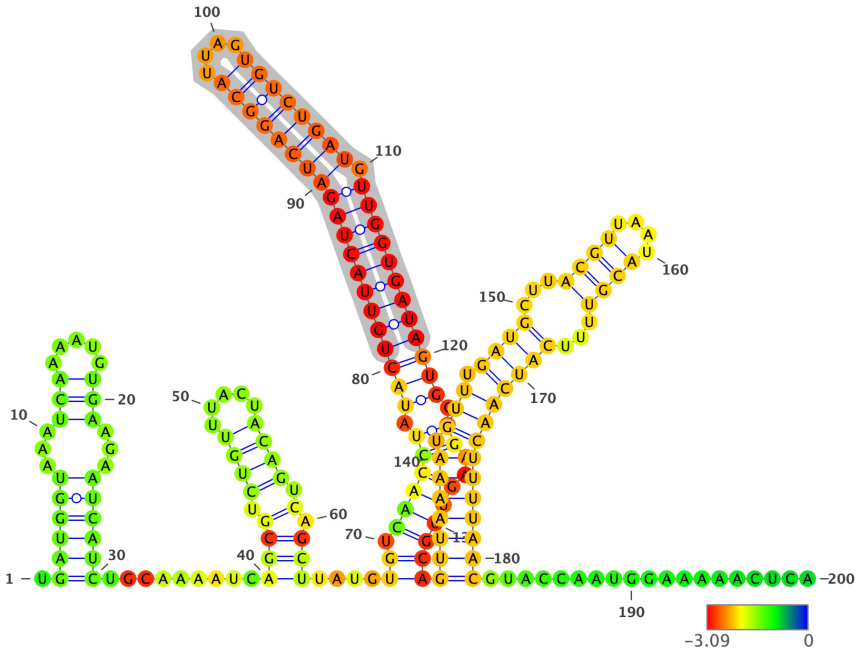
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 159 from nt 7974 to 8012 (nt 81 to 119)

```
5'-UGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUA-3'
5'-(((((((((((((((((....))))))))).)))))))))-3'
Motif MFE = -15.9; z-score = -4.98; 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 7894 to 8093 (motif highlighted in silver):

```
5'-UGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGU
UGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCA-3
5'-.((((((...(((.....)))...))))))........((((.((((.....)))).).)))....((.((((((.((((((((((((((((((((....))))))))).)
))))))))))).))..))))))(((((((.(((.((((...((((....))))...)))))))))))))).....................-3'
MFE = -51.9; z-score = -2.74; ED = 28.48
```

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

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

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

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

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

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

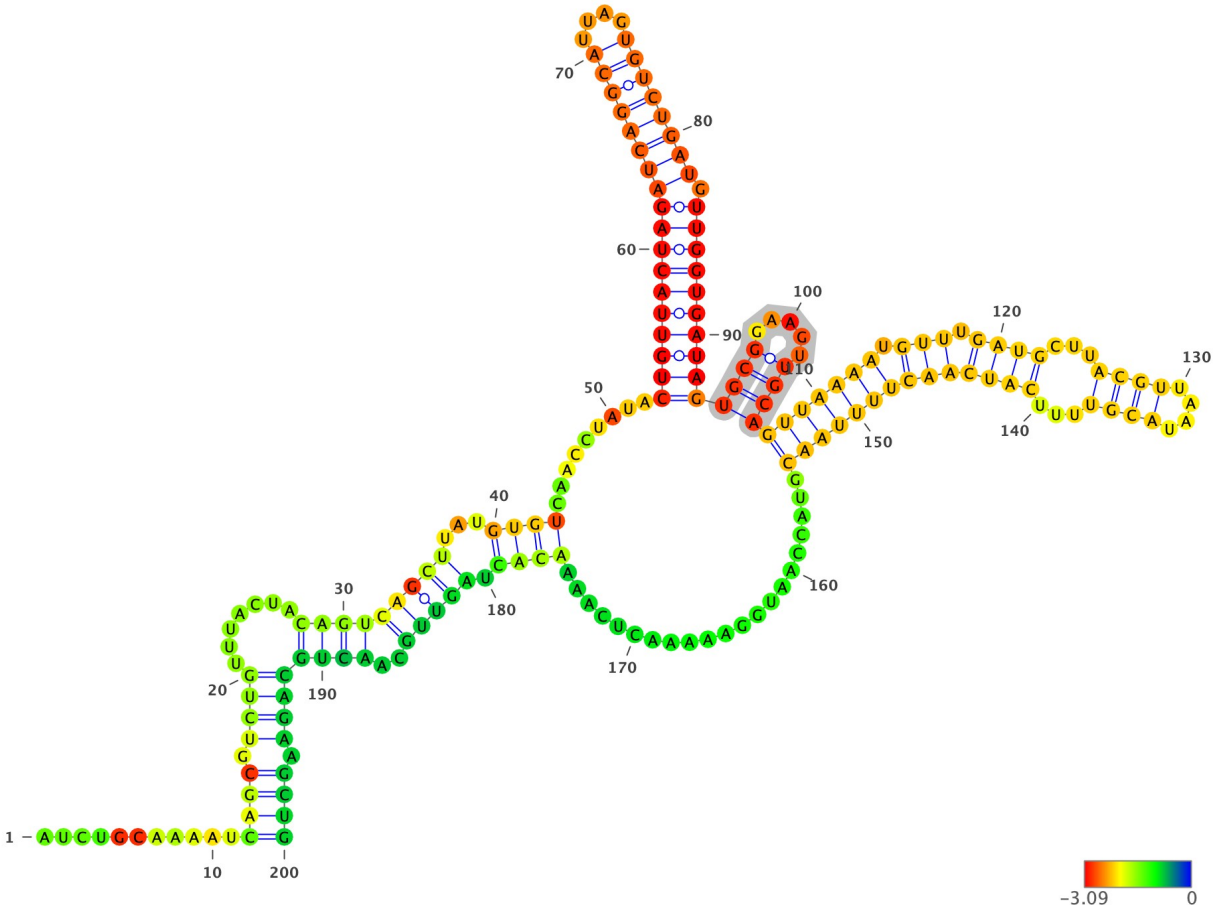
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 160 from nt 8014 to 8026 (nt 94 to 106)

```
5'-UGCGGAAGUUGCA-3'
5'-((((.....))))-3'
Motif MFE = -1.2; z-score = -1.17; 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 7921 to 8120 (motif highlighted in silver):

```
5'-AUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGUUGGUGAUAGUGCGGAAGUUGCAGUUAA
AAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUG-3
5'-...........((((.((((.......(((((((((...((((.........((((((((((((((((((....))))))))).))))))))))((((.....))))(((((
((.(((.((((...((((....))))...))))))))))))))).....................)))).)))))..)))))))).))))-3'
MFE = -52.3; z-score = -3.51; ED = 33.09
```

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, 266-13468(+)

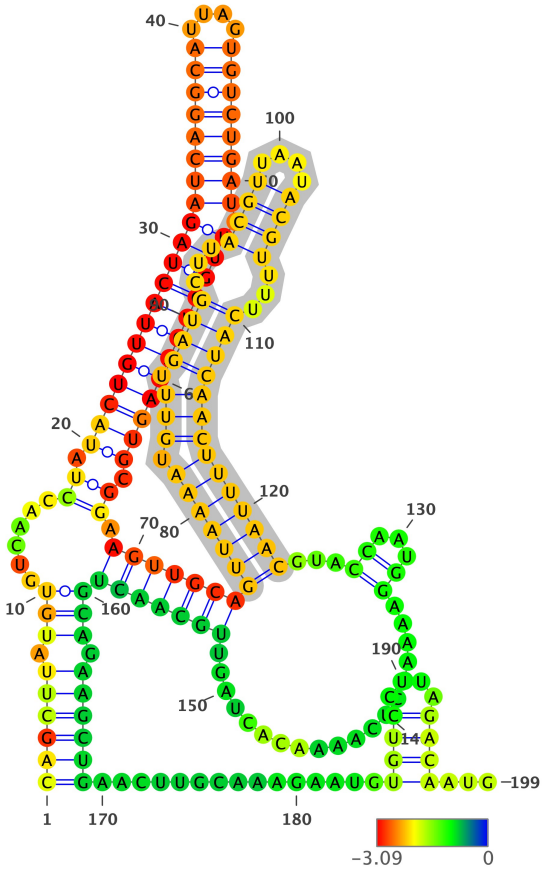
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 8027 to 8074 (nt 76 to 123)

```
5'-GUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAAC-3'
5'-(((((((.(((.((((...((((....))))...)))))))))))))-3'
Motif MFE = -12.4; z-score = -3.95; 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 = -3.3; 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(+)

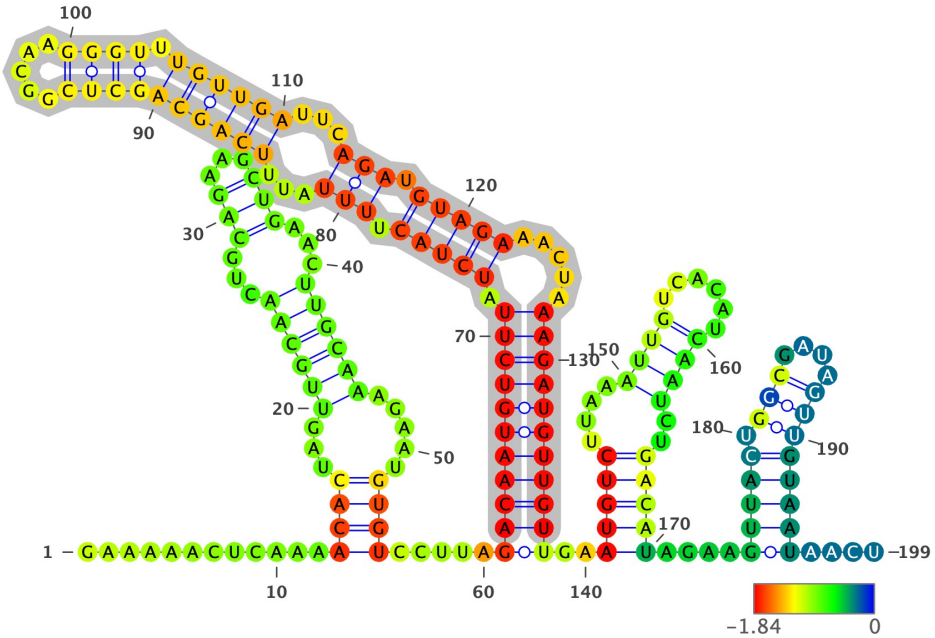
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 162 from nt 8145 to 8220 (nt 62 to 137)

```
5'-ACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAUUCAGAUGUAGAAACUAAAGAUGUUGU-3'
5'-((((((((((.(((((.(((...((((((((((.....)))).))))))...))).)))))).....))))))))))-3'
Motif MFE = -22.3; z-score = -3.4; ED = 5.97
```



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

Extracted structure model with flanking nucleotides 8084 to 8282 (motif highlighted in silver):

```
5'-GAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAU
UCAGAUGUAGAAACUAAAGAUGUUGUUGAAUGUCUUAAAUUGUCACAUCAAUCUGACAUAGAAGUUACUGGCGAUAGUUGUAAUAACU-3
5'-............((((...((((((...(((...)))...))))))).....)))).....((((((((((.(((((.(((...((((((((((.....)))).))))))).
..))).)))))).....))))))))))..(((((....((((......)))).))))).....(((((.(((....))))))))....-3'
MFE = -43.2; z-score = -1.91; ED = 38.47
```

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(+)

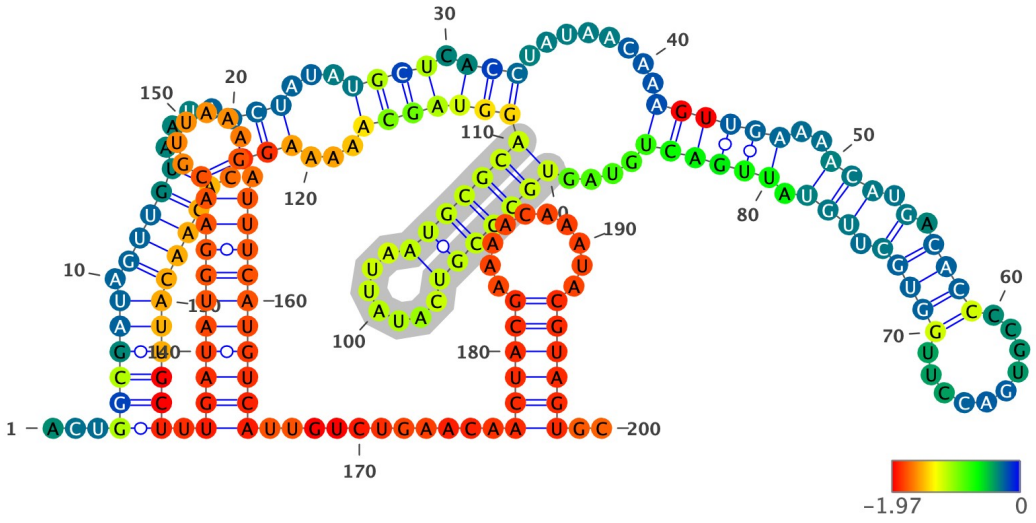
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 163 from nt 8350 to 8370 (nt 90 to 110)

```
5'-UGCGCGUCAUAUUAAUGCGCA-3'
5'-(((((((.......)))))))-3'
Motif MFE = -7.8; z-score = -4.28; ED = 0.93
```



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

Extracted structure model with flanking nucleotides 8261 to 8460 (motif highlighted in silver):

```
5'-ACUGGCGAUAGUUGUAAUAACUAUAUGCUCACCUAUAACAAAGUUGAAAACAUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAG
GUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGC-3
5'-...((((((.(((((....(((...((((.(((........((((((..(((.(.((((..........))))).))).))))))....(((((((.......))))))))
))))))...))).))))))))))).((((((((((.......).))))))))))...........((((((..........))))))..-3'
MFE = -47.6; z-score = -2.19; ED = 11.92
```

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

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

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

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

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

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

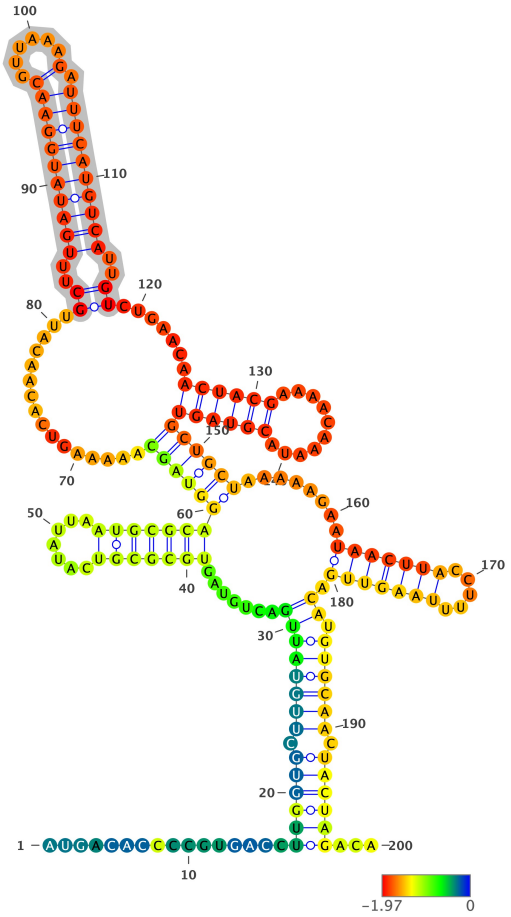
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 164 from nt 8393 to 8429 (nt 82 to 118)

```
5'-GCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGU-3'
5'-((..((((((((((((......).))))))))))..))-3'
Motif MFE = -11.0; z-score = -3.28; ED = 1.03
```



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

Extracted structure model with flanking nucleotides 8312 to 8511 (motif highlighted in silver):

```
5'-AUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUG
UCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACA-3
5'-................((((((.((((((((.......(((((((.......)))))))((((((.................((..((((((((((((......).)))))))
)))..))).......((((((..........)))))))))))).........(((((((.....)))))))).)).)))))).))))))...-3'
MFE = -42.4; z-score = -1.04; ED = 43.97
```

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

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

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

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

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

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

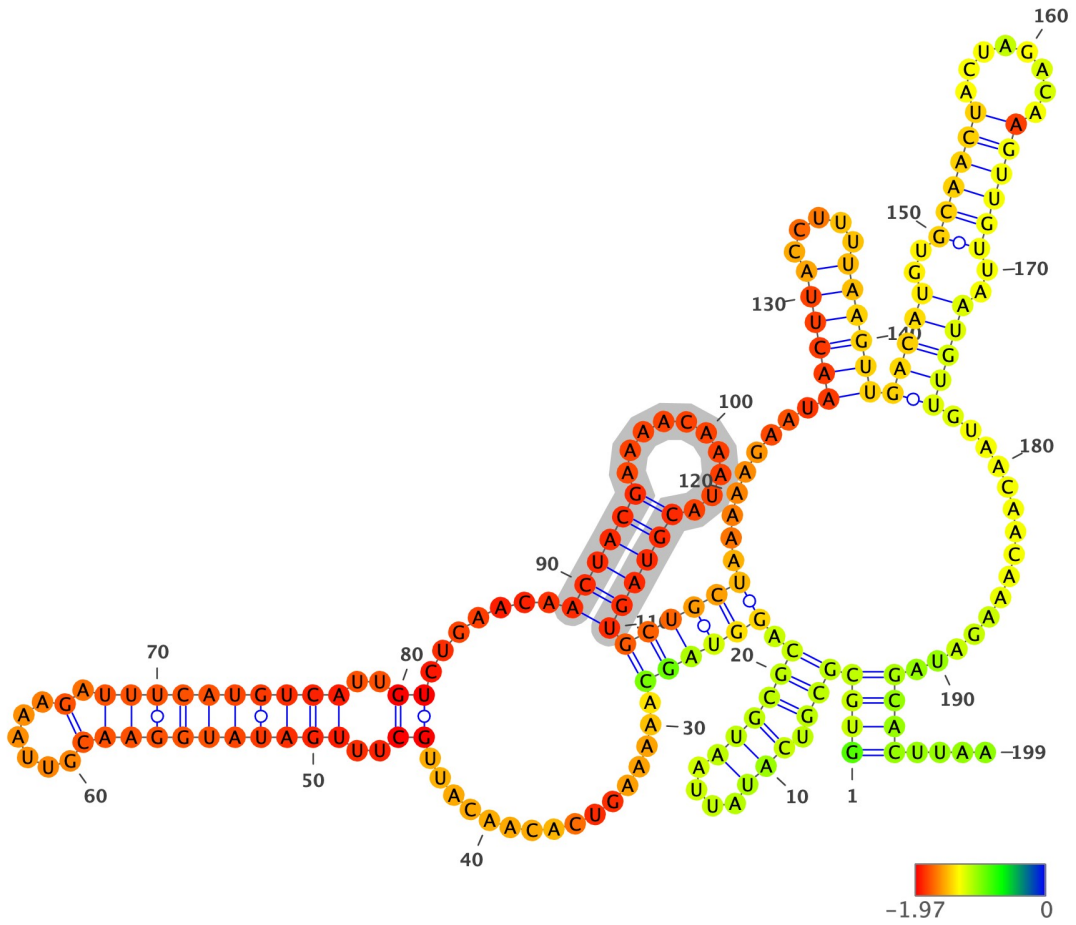
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 165 from nt 8437 to 8458 (nt 89 to 110)

```
5'-ACUACGAAAACAAAUACGUAGU-3'
5'-((((((..........))))))-3'
Motif MFE = -4.3; z-score = -5.02; ED = 0.86
```



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

Extracted structure model with flanking nucleotides 8349 to 8547 (motif highlighted in silver):

```
5'-GUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUG
CUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAA-3
5'-(((((((.(((....)))))).((((((................((..((((((((((.......).))))))))))..)).......((((((..........)))))))
)))))).........((((((.....))))))(((((..((((((........))))))..)))))...............))))....-3'
MFE = -46.2; z-score = -3.24; ED = 37.99
```

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

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

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

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

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

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

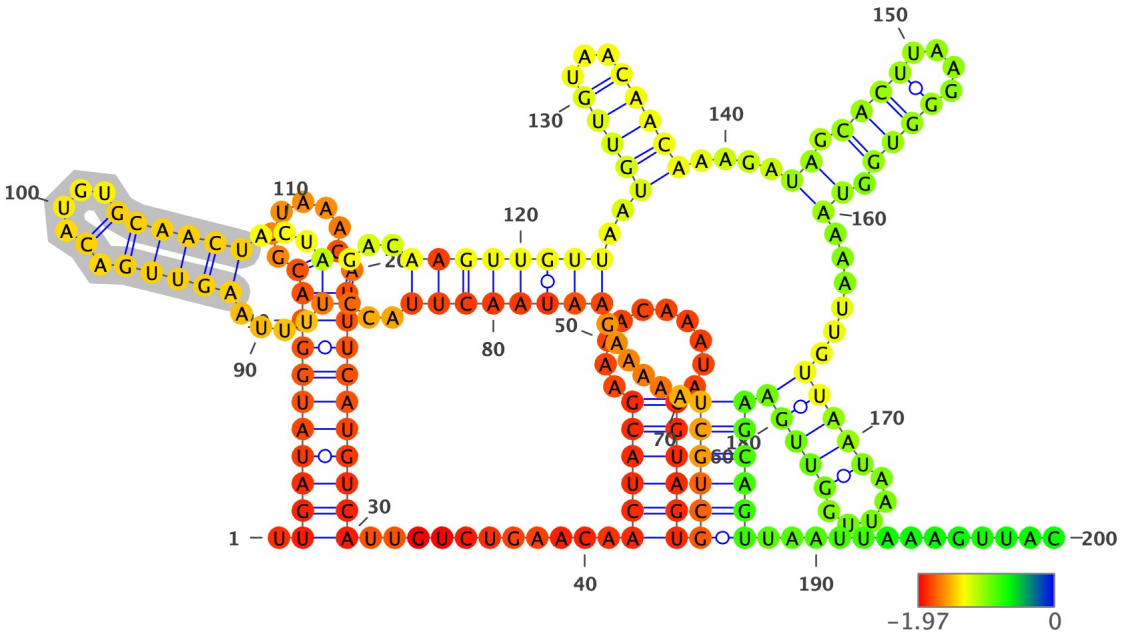
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 166 from nt 8487 to 8503 (nt 92 to 108)

```
5'-AGUUGACAUGUGCAACU-3'
5'-(((((.(....))))))-3'
Motif MFE = -2.3; z-score = -1.52; ED = 1.07
```



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

Extracted structure model with flanking nucleotides 8396 to 8595 (motif highlighted in silver):

```
5'-UUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACU
AGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAAUUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUAC-3
5'-.(((((((((((......).))))))))))...........((((((..........))))))((((((......((((((((..((....(((((.(....))))))...
))..))))))))..(((((...)))))....((.((((....)))).))......(((((.....)))))))))))).............-3'
MFE = -38.3; z-score = -2.02; ED = 44.77
```

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

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

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

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

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

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

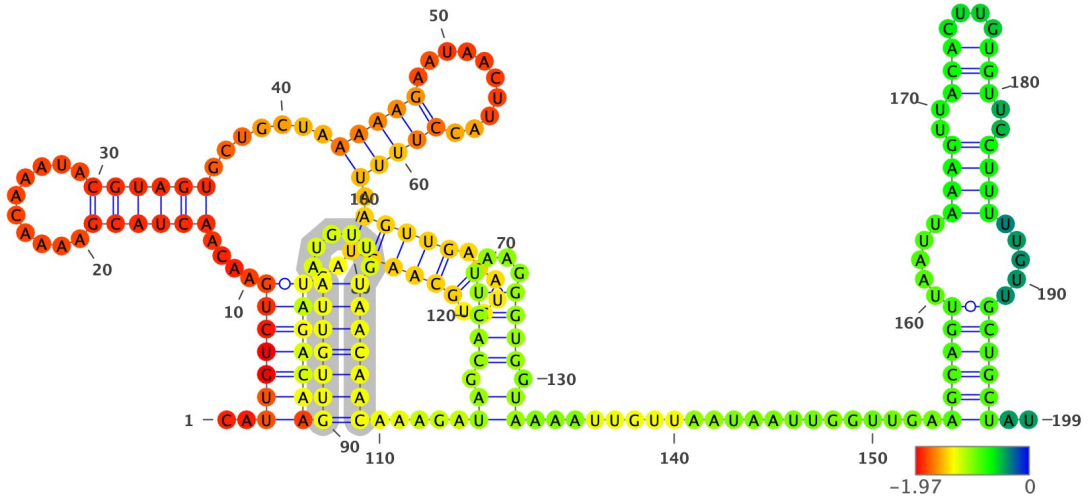
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 167 from nt 8513 to 8532 (nt 90 to 109)

```
5'-GUUGUUAAUGUUGUAACAAC-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.5; z-score = -3.46; 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 8424 to 8622 (motif highlighted in silver):

```
5'-CAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAA
AGAUAGCACUUAAGGGUGGUAAAAUUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUACACUUGUGUUCCUUUUUGUUGCUGCUAU-3
5'-..(((((((....((((((..........))))))......(((((..........))))).(((((.(....))))))..)))))))(((((((......)))))))..
...((.((((....)))).))....................((((((.....((((..(((....)))..))))).....))))))..-3'
MFE = -36.5; z-score = -0.9; ED = 57.25
```

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(+)

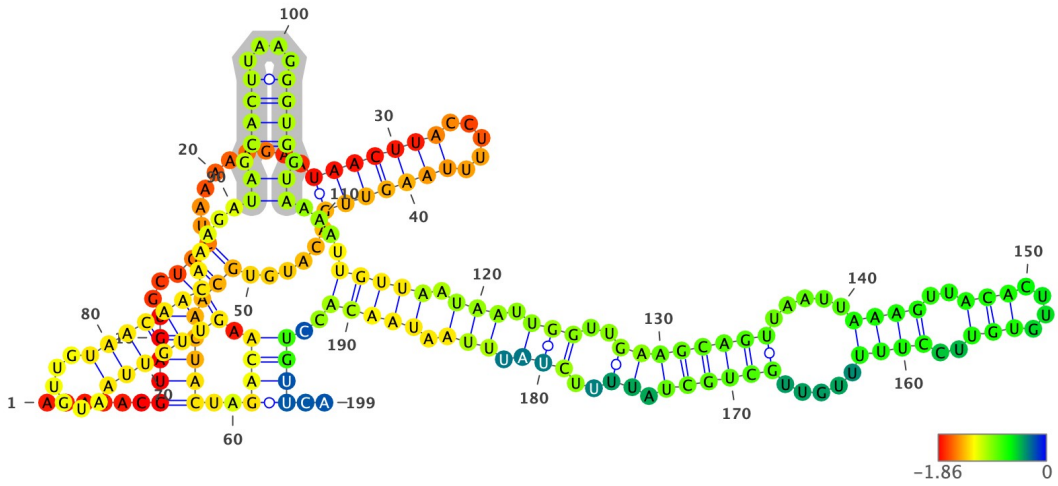
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 168 from nt 8538 to 8555 (nt 91 to 108)

```
5'-UAGCACUUAAGGGUGGUA-3'
5'-((.((((....)))).))-3'
Motif MFE = -3.2; z-score = -2.73; ED = 1.14
```



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

Extracted structure model with flanking nucleotides 8448 to 8646 (motif highlighted in silver):

```
5'-AAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAA
UUGUUAAUAAUUGGUUGAAGCAGUUAAUUAAAGUUACACUUGUGUUCCUUUUUGUUGCUGCUAUUUUCUAUUUAAUAACACCUGUUCA-3
5'-......(((((..(((.........(((((((.....)))))))).....)))))))..((((.(((((((.....)))))))).....((.((((....)))).)).....(((((.(((.((..((((((((.....((((..(((....)))).)).)))).....)))))))..)).)).)))).)))))..-3'
MFE = -37.0; z-score = -0.86; 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(+)

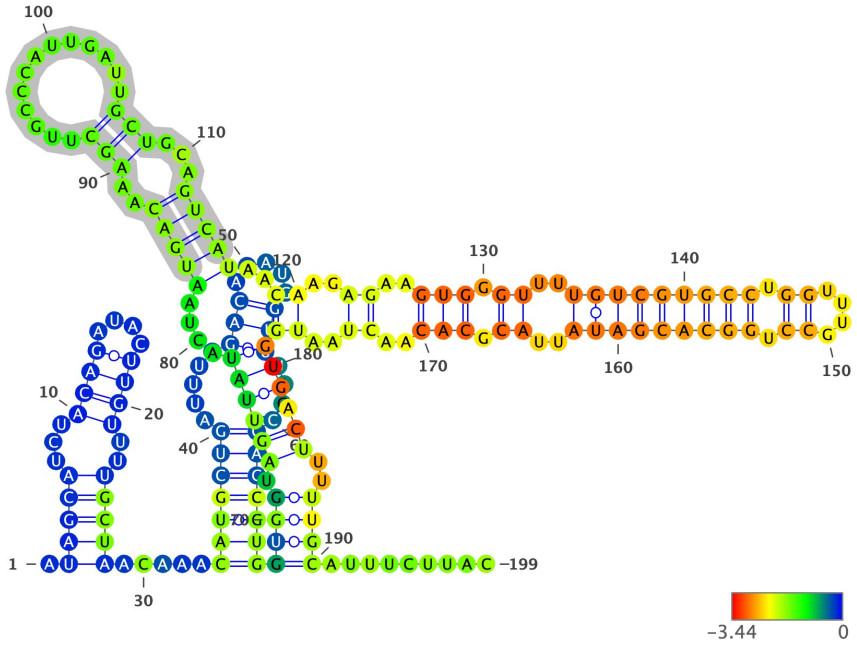
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 169 from nt 8806 to 8837 (nt 84 to 115)

```
5'-UGACAAAGCUUGCCCAUUGAUUGCUGCAGUCA-3'
5'-((((..(((.............)))...))))-3'
Motif MFE = -4.8; z-score = -0.38; 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 8723 to 8921 (motif highlighted in silver):

```
5'-AUAGCAUCUACAGAUACUUGUUUUGCUAACAAACAUGCUGAUUUUGACACAUGGUUUAGCCAGCGUGGUGGUAGUUAUACUAAUGACAAAGCUUGCCCAUUGAUUGCUGCA
GUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUAC-3
5'-.(((((...((((....))))..)))))).....(((((((.....(((.....))).....)))))))((((.((((((....(((((..(((.............)))...
)))))..((..((..(((.((..((((((((((.((....)).))))))))))..)).)))..))..))))))))..))))..........-3'
MFE = -53.0; z-score = -2.17; ED = 27.1
```

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(+)

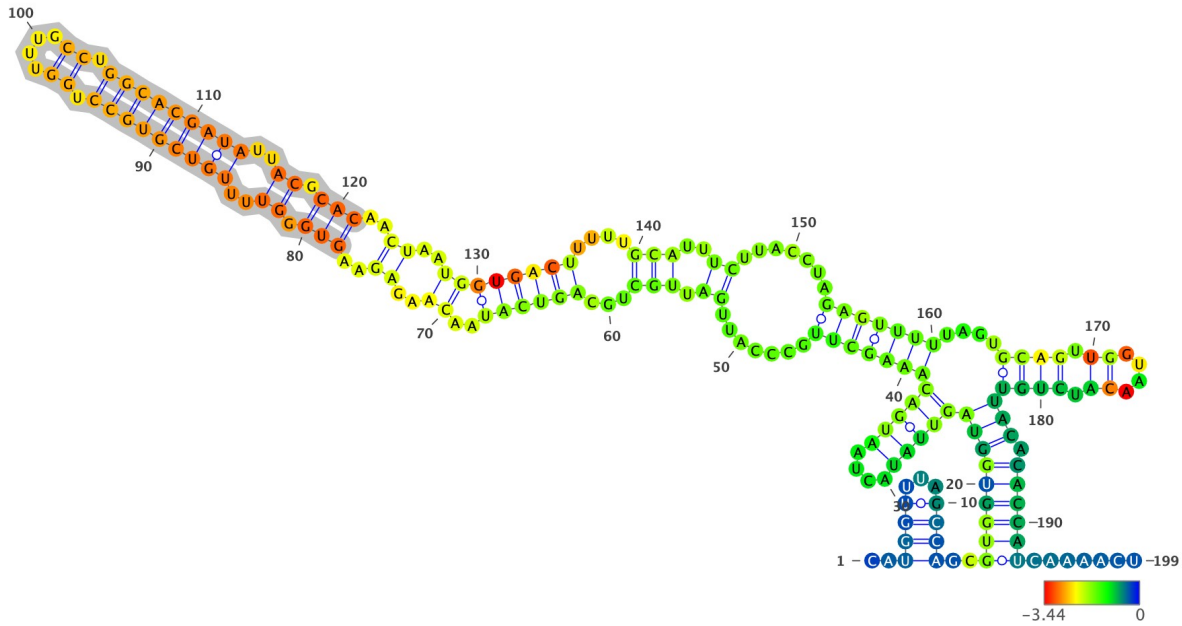
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 170 from nt 8849 to 8892 (nt 78 to 121)

```
5'-GUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCAC-3'
5'-(((.((..(((((((((.((....)).)))))))))..)).)))-3'
Motif MFE = -24.5; z-score = -4.95; 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 8772 to 8970 (motif highlighted in silver):

```
5'-CAUGGUUUAGCCAGCGUGGUGGUAGUUAUACUAAUGACAAAGCUUGCCCAUUGAUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGA
UAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGUGCAGUUGGUAACAUCUGUUACACACCAUCAAAACU-3
5'-..((((...)))).(((((((((((((((....)))))))))))))).....((.((((...((((((..((..((..((((.((..((((((((((.((....)).)))))))
))..))..)))..))..))))))))....)))..))).....))))))....((((.((....)).)))))))..))))))).....-3'
MFE = -59.2; z-score = -2.46; ED = 38.89
```

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

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

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

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

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

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

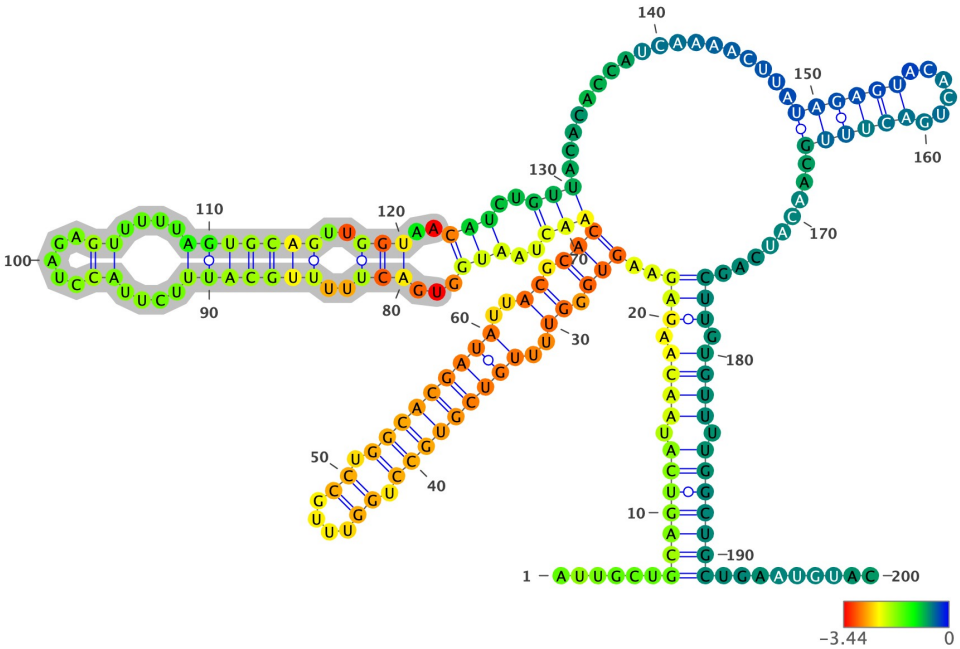
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 8902 to 8946 (nt 78 to 122)

```
5'-UGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGUGCAGUUGGUAA-3'
5'-(..(.....(((.......(.....).......)))).....)..)-3'
Motif MFE = -7.0; z-score = -1.0; ED = 4.94
```



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 8825 to 9024 (motif highlighted in silver):

```
5'-AUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGU
GCAGUUGGUAACAUCUGUUACACACCAUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUAC-3
5'-......(((((((.((((.(((..(((.((..(((((((((.((....)).)))))))))..)).)))(((..(((...(((..(((((((....((.....)).....)))
))))..)))..)))..))).................((((((.....)))))).........))).)))).)))))))).........-3'
MFE = -54.8; z-score = -3.44; ED = 20.53
```

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

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

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

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

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

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

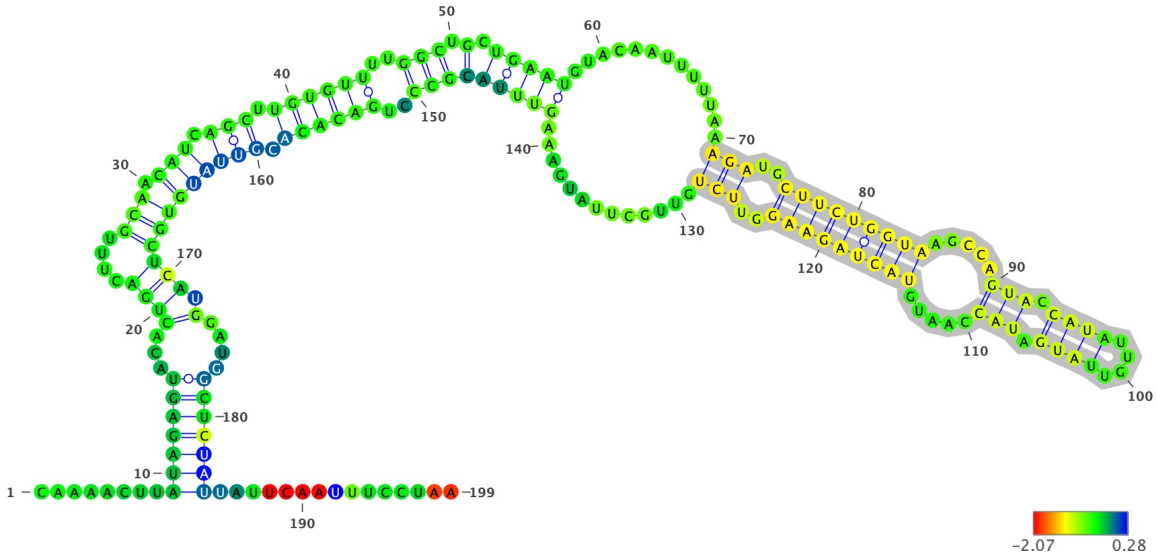
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 172 from nt 9034 to 9091 (nt 71 to 128)

```
5'-AGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCAAUGUACUAGAAGGUUCU-3'
5'-(((..(((((((((.....(((.(((......))).)))).....))))))))).)))-3'
Motif MFE = -17.4; z-score = -2.91; ED = 1.27
```



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

Extracted structure model with flanking nucleotides 8964 to 9162 (motif highlighted in silver):

```
5'-CAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCA
AUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGCCCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAA-3
5'-........(((((((...((((....(((.(((.(((((((..(((.(.(((((.............(((..(((((((((.....(((.((((....)))).)))..
...)))))))))..)))............)))))))))..)))))).))))))))))))).)....)))))))................-3'
MFE = -46.2; z-score = -1.77; ED = 17.58
```

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

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

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

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

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

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

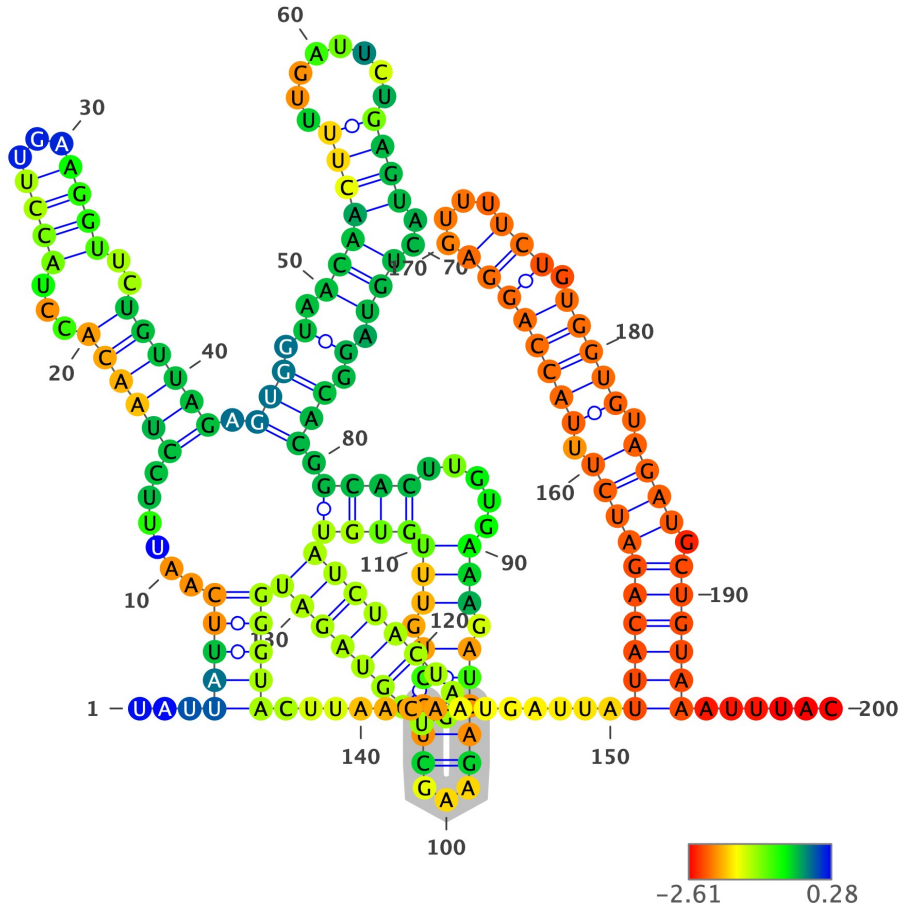
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 173 from nt 9240 to 9248 (nt 96 to 104)

```
5'-CAGAAGCUG-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.12; 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 9145 to 9344 (motif highlighted in silver):

```
5'-UAUUAUUCAAUUUCCUAACACCUACCUUGAAGGUUCUGUUAGAGUGGUAACAACUUUUGAUUCUGAGUACUGUAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUG
UGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUAC-3
5'-...(((((......((((((...((((...))))..)))))).(((.(.(((((((.........))))..))).).))).((((.....(((.(((((...))))).))))
)))(((((((...))))))))))))..............((((((((((.((((((((....))).))))).)))).))))))......-3'
MFE = -45.4; z-score = -1.15; ED = 43.4
```

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(+)

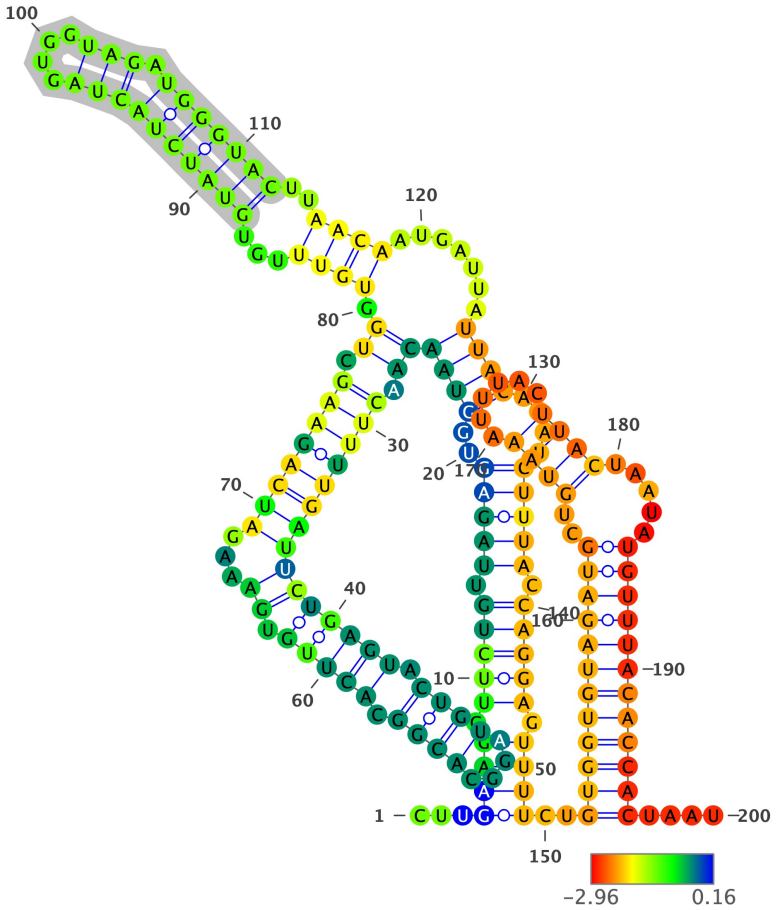
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 174 from nt 9257 to 9281 (nt 88 to 112)

```
5'-GUAUCUACUAGUGGUAGAUGGGUAC-3'
5'-((((((((((....))).)))))))-3'
Motif MFE = -6.8; z-score = -2.72; 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 = -1.59; 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(+)

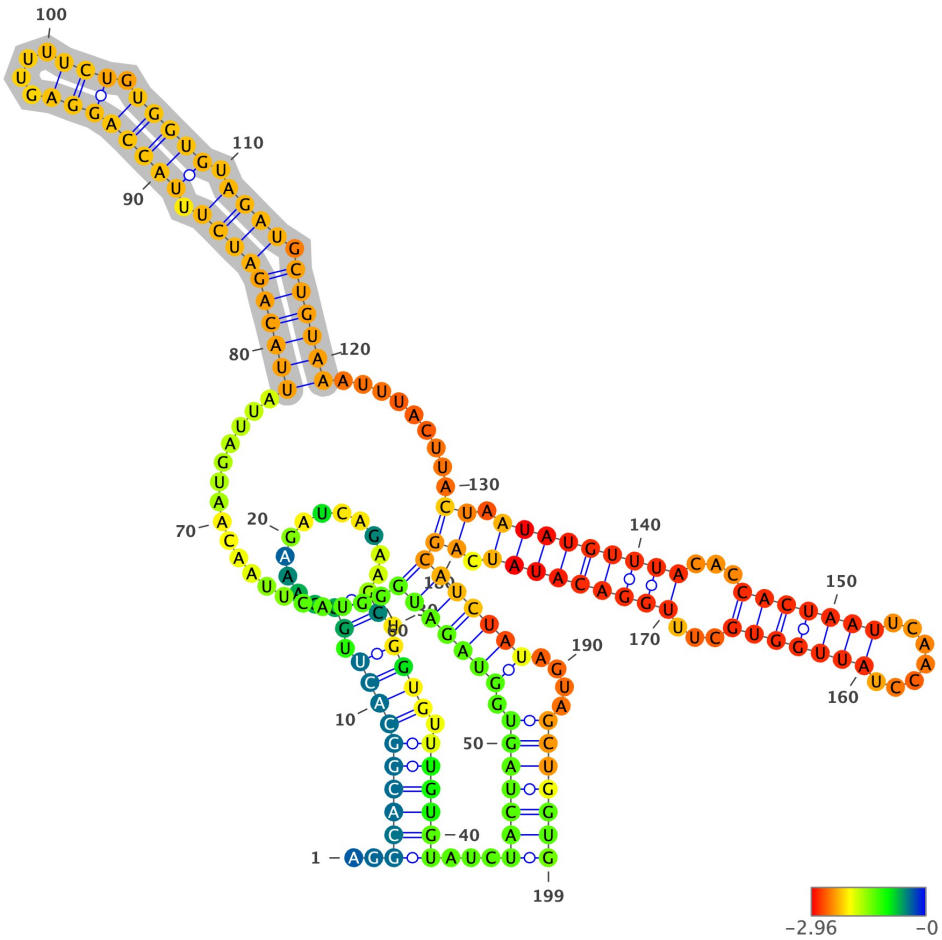
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 175 from nt 9295 to 9338 (nt 78 to 121)

```
5'-UUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAA-3'
5'-(((((((((.(((((.((....)).)))))).)))).)))))-3'
Motif MFE = -15.6; z-score = -3.91; 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 9218 to 9416 (motif highlighted in silver):

```
5'-AGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUA
GAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG-3
5'-..((((((((((.((............)).)))).)))))).....(((((((.(((((((.................((((((((((.(((((((((....)))).)))))).)
))).)))))).........((.((((((((...(((((((.......)))))))...)))))))).)))))))))....)))))))-3'
MFE = -50.3; z-score = -1.97; ED = 51.45
```

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(+)

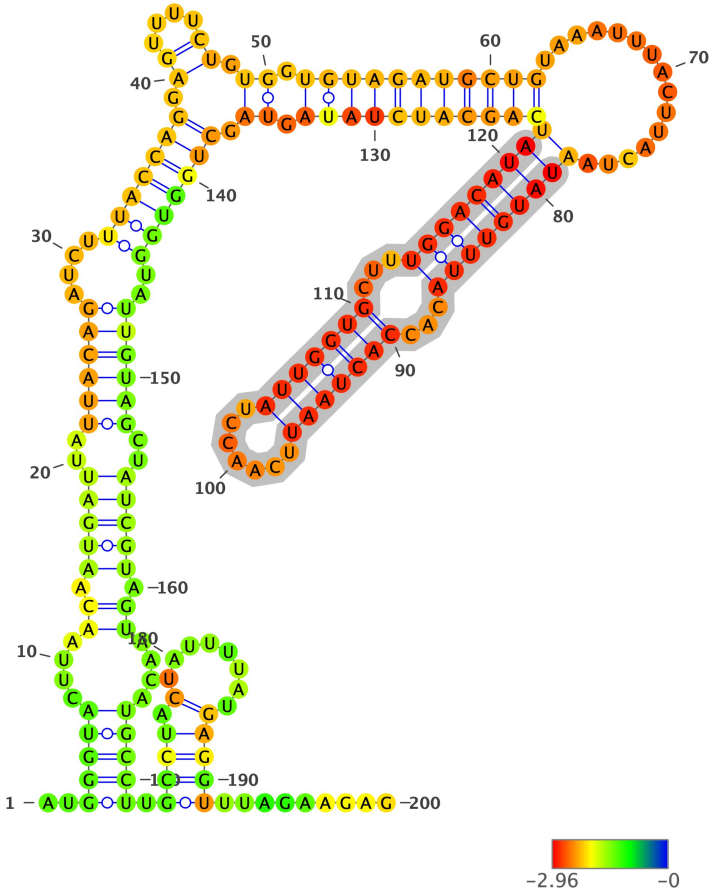
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 176 from nt 9352 to 9394 (nt 79 to 121)

```
5'-UAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUA-3'
5'-(((((((((...(((((((.......)))))))...)))))))))-3'
Motif MFE = -10.6; z-score = -3.88; ED = 3.88
```



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 9274 to 9473 (motif highlighted in silver):

```
5'-AUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGC
UUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAG-3
5'-..((((((....((.((((((..(((((((....(((((((.((....)).((.(((((((((((.............(((((((((...(((((((.......)))))))).
..))))))))))))))))))))).)).)))))))..)))))).)))))..)).....)))))).((((.(........)))))).........-3'
MFE = -48.3; z-score = -2.03; ED = 57.15
```

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(+)

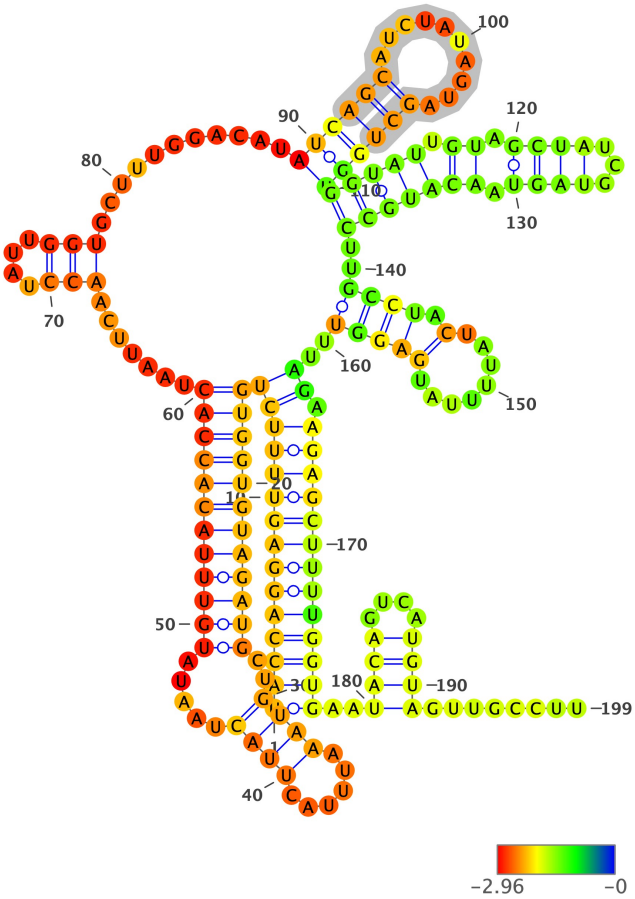
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 177 from nt 9397 to 9412 (nt 92 to 107)

```
5'-AGCAUCUAUAGUAGCU-3'
5'-(((..........)))-3'
Motif MFE = 0.0; z-score = 0.36; 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 9306 to 9504 (motif highlighted in silver):

```
5'-UACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUG
GUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUU-3
5'-(((((((((((((((((((((((((((..((((......))))).....)))))))))))).......(((....))).........((((((..........))))))(
((((.((.((((...)))).)))))))..((((.(........)))))..)).)))))))))))))..((((....))))........-3'
MFE = -51.3; z-score = -2.87; ED = 21.44
```

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(+)

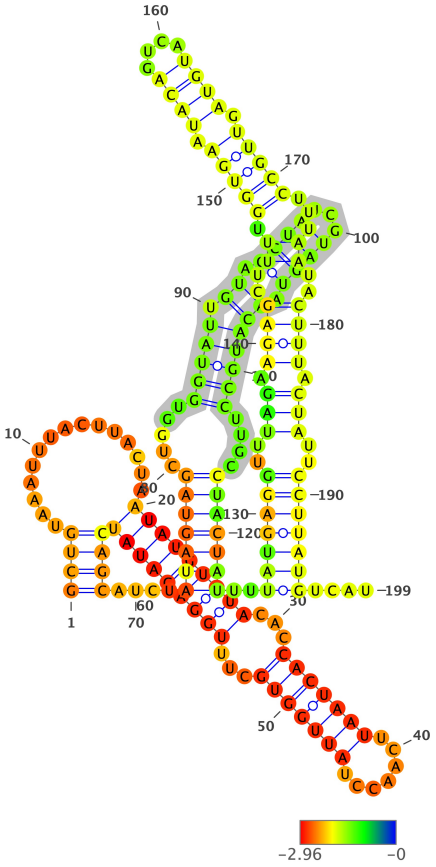
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 178 from nt 9414 to 9447 (nt 83 to 116)

```
5'-GUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGC-3'
5'-(((((((.((.(((.....))).)))))))..))-3'
Motif MFE = -7.7; z-score = -1.12; ED = 1.91
```



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

Extracted structure model with flanking nucleotides 9332 to 9530 (motif highlighted in silver):

```
5'-GCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGC
CUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAU-3
5'-((((...............(((((((((...(((((((.......)))))))...))))))))))))....(((((((.....(((((.((.((((...)))).))))))
)....)))))))..(((((((..(((.((((..((.(((((.((((....)))).)))))...))..)))).)))..)))))))....-3'
MFE = -49.1; z-score = -3.21; ED = 16.89
```

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

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

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

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

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

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

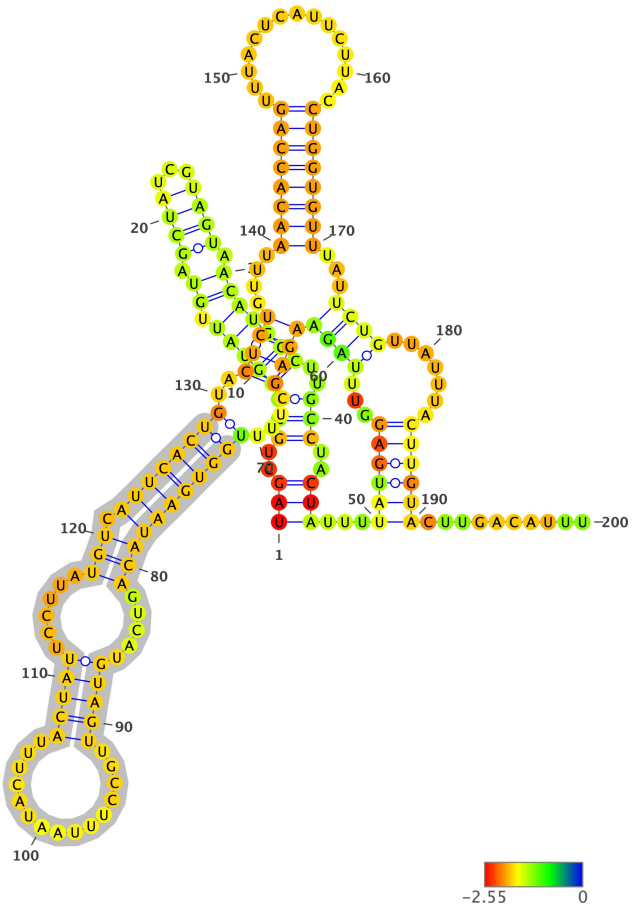
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 9479 to 9535 (nt 72 to 128)

```
5'-GGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAUUCACU-3'
5'-((((((((((.....(((((...............)))))......))).)))))))-3'
Motif MFE = -10.1; z-score = -2.73; ED = 1.85
```



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

Extracted structure model with flanking nucleotides 9408 to 9607 (motif highlighted in silver):

```
5'-UAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAU
UCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUU-3
5'-(((..((((((((.((.((((...)))).)))))))..)))..)))...((((((...((((((((....((((((((((.....(((((.................)))))
......))).))))))))..)))))....((((((((.................))))))))...))))).......))))))..........-3'
MFE = -36.8; z-score = -2.1; ED = 36.83
```

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

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

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

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

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

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

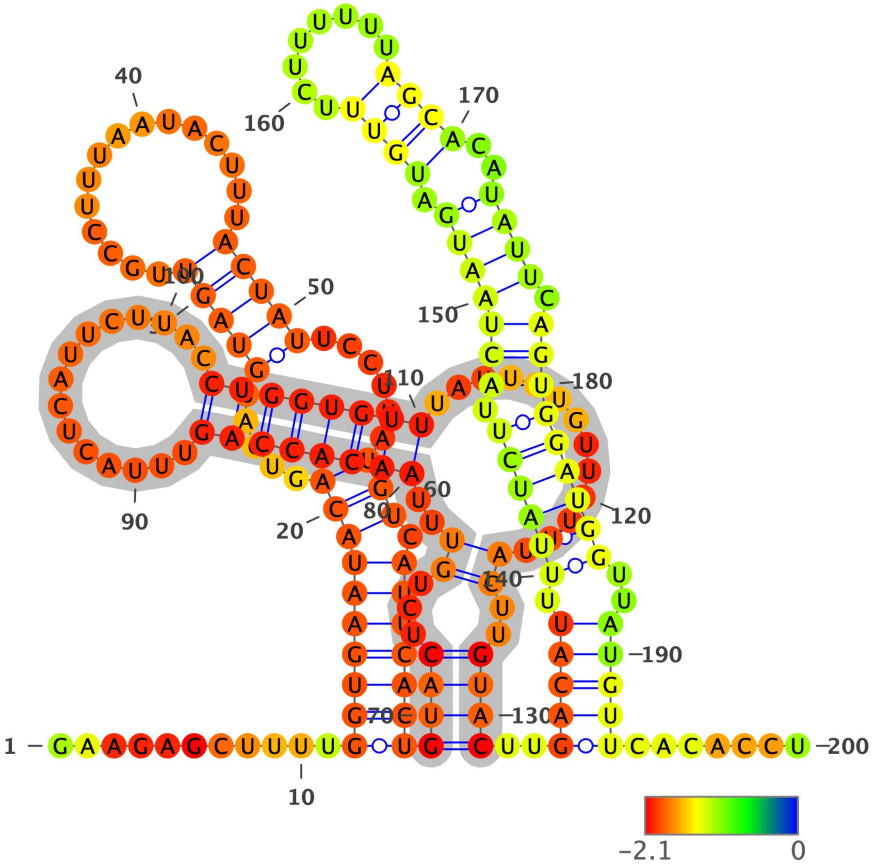
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 9536 to 9598 (nt 69 to 131)

```
5'-GUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUAC-3'
5'-(..(.......((((((((...............))))))))..................)..)-3'
Motif MFE = -9.0; z-score = -2.22; ED = 7.52
```



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 9468 to 9667 (motif highlighted in silver):

```
5'-GAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUU
AUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCU-3
5'-...........((((((((((.....(((((...............)))))......))).)))))))((((...((..((((((((...............))))))))).
............))..))))..(((((.((((((.(((((((.((((........))))..)))).))))))))))..)))))........-3'
MFE = -30.6; z-score = -1.52; ED = 40.17
```

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(+)

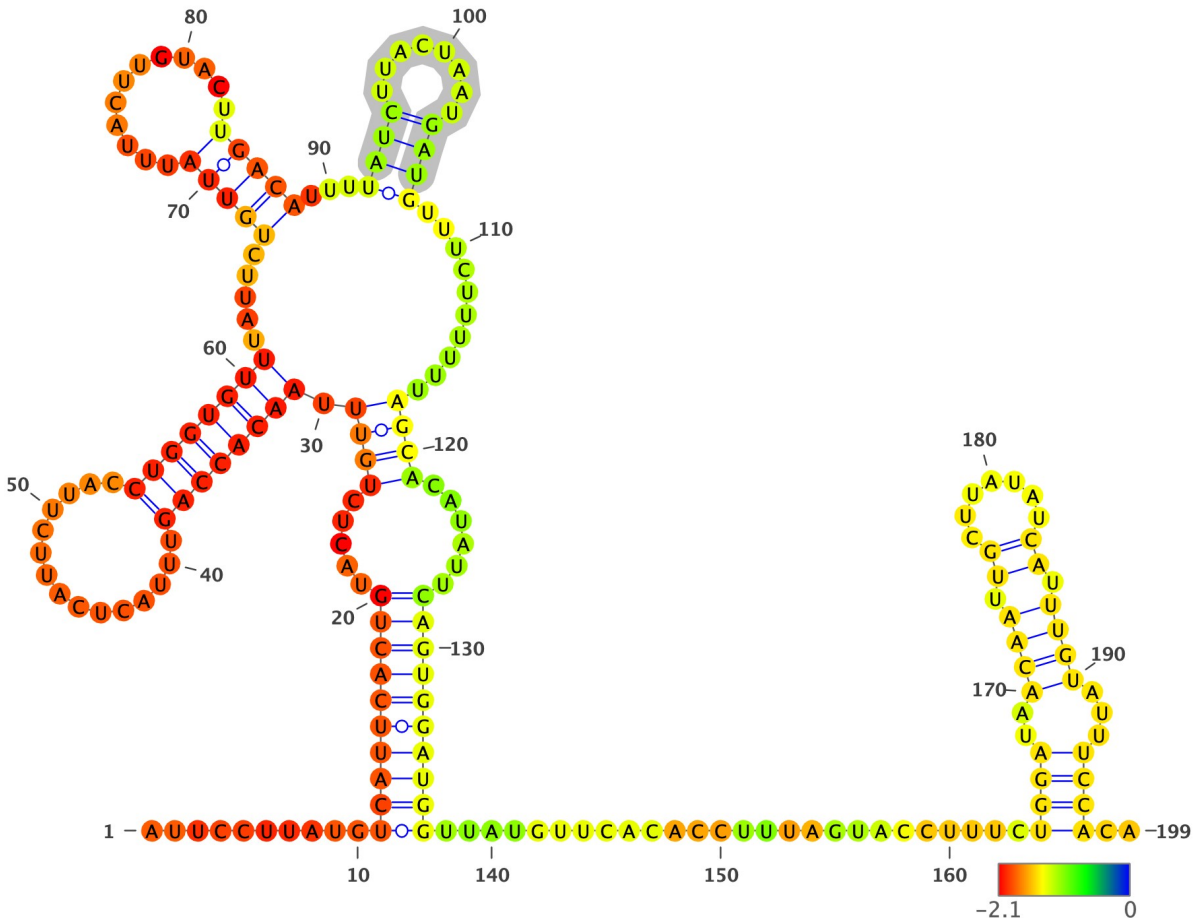
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 181 from nt 9609 to 9622 (nt 93 to 106)

```
5'-AUCUUACUAAUGAU-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.1; 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 9517 to 9715 (motif highlighted in silver):

```
5'-AUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUC
UUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACA-3
5'-..........(((((((((.....((((.((((((((...............))))))))).....(((((.............)))))...((((........))))....
......))))......))))))))))..........................((((..((((.((.......)).))))...))))..-3'
MFE = -28.8; z-score = -1.75; ED = 18.67
```

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(+)

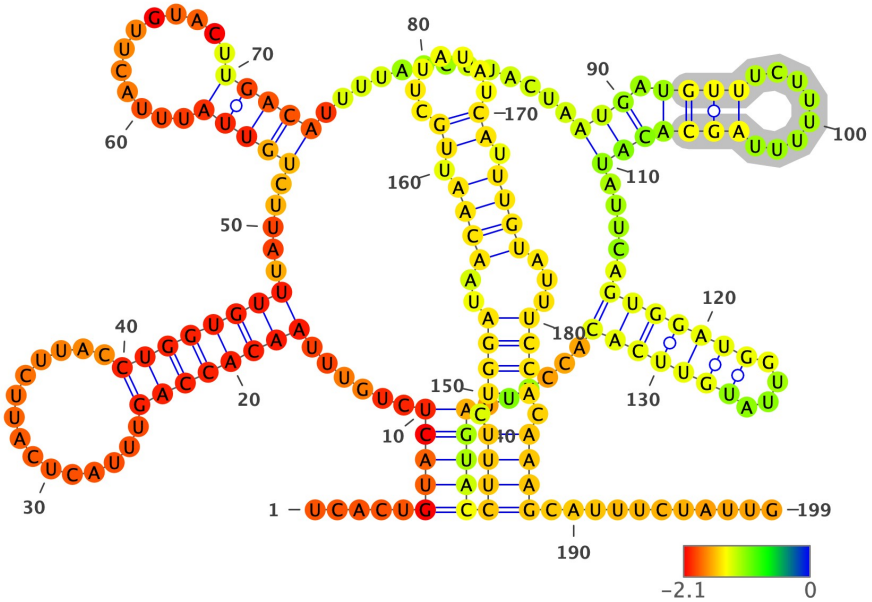
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 182 from nt 9623 to 9636 (nt 93 to 106)

```
5'-GUUUCUUUUUUAGC-3'
5'-(((........)))-3'
Motif MFE = 0.0; z-score = 0.14; 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 9531 to 9729 (motif highlighted in silver):

```
5'-UCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUA
UUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUG-3
5'-.....(((((......((((((((...............))))))))).....(((((............)))))..............(((.((((........)))))))).
....(((((((....)))))))......)))))((((.((((..((((.((.......)).))))...)))).)))).............-3'
MFE = -29.4; z-score = -1.25; 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(+)

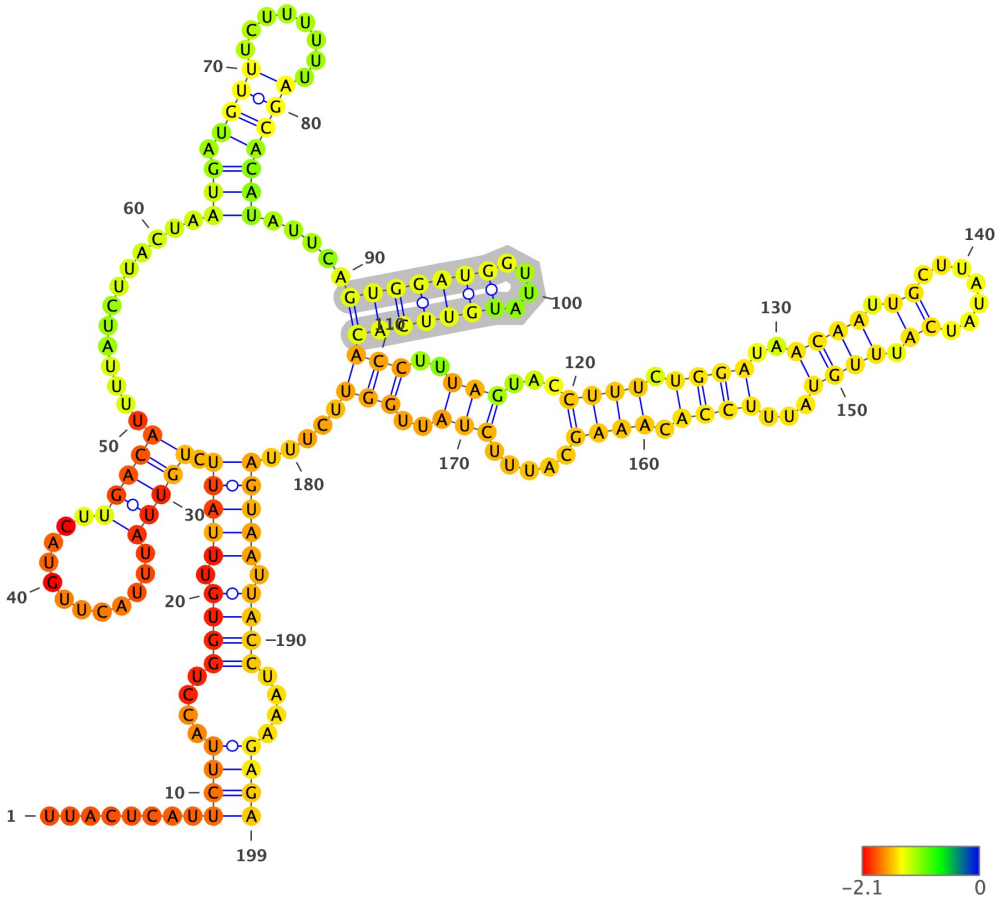
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 183 from nt 9646 to 9663 (nt 91 to 108)

```
5'-GUGGAUGGUUAUGUUCAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.6; z-score = -2.41; 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 9556 to 9754 (motif highlighted in silver):

```
5'-UUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACC
UUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGA-3
5'-........((((....((((.(((((.(((((............)))))).............(((.(((((........)))))))).....(((((((....)))))))(((
..((((...((((.((((..((((.((.......)).)))))...)))))).)))).....)))..)))).....)))))).)))).....))))-3'
MFE = -29.7; z-score = -1.02; ED = 29.39
```

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(+)

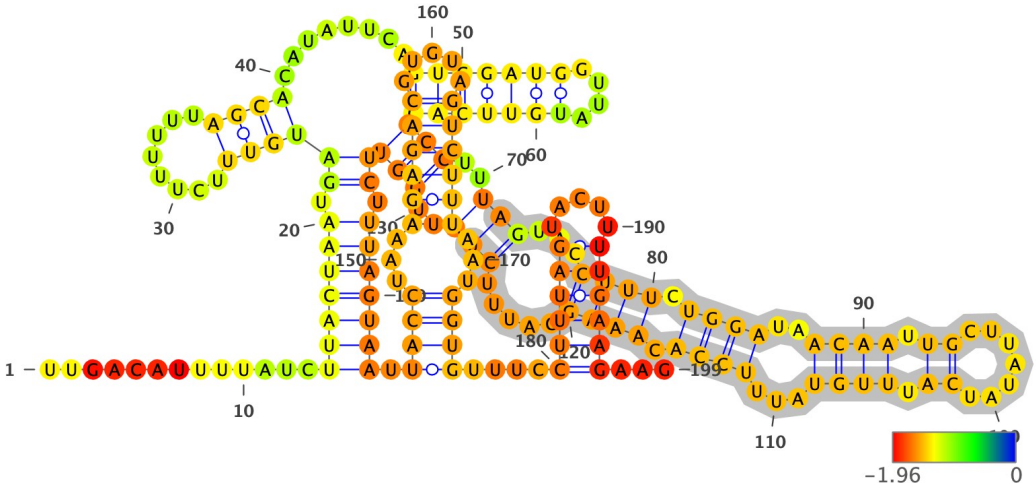
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 184 from nt 9670 to 9725 (nt 72 to 127)

```
5'-AGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCU-3'
5'-(....((((.((((..((((.((.......)).))))...)))).))))......)-3'
Motif MFE = -7.4; z-score = -2.01; ED = 3.24
```



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

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

```
5'-UUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUU
UCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAG-3
5'-.............(((((((.((((((........))))........(((((((....)))))))(((..(((...((((.((((..((((.((.......)).))))...
)))).))))).....)))..))))).))))))).((((...((((((.....))))))...)))).....((((((.....))))))...-3'
MFE = -36.1; z-score = -1.38; ED = 52.63
```

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(+)

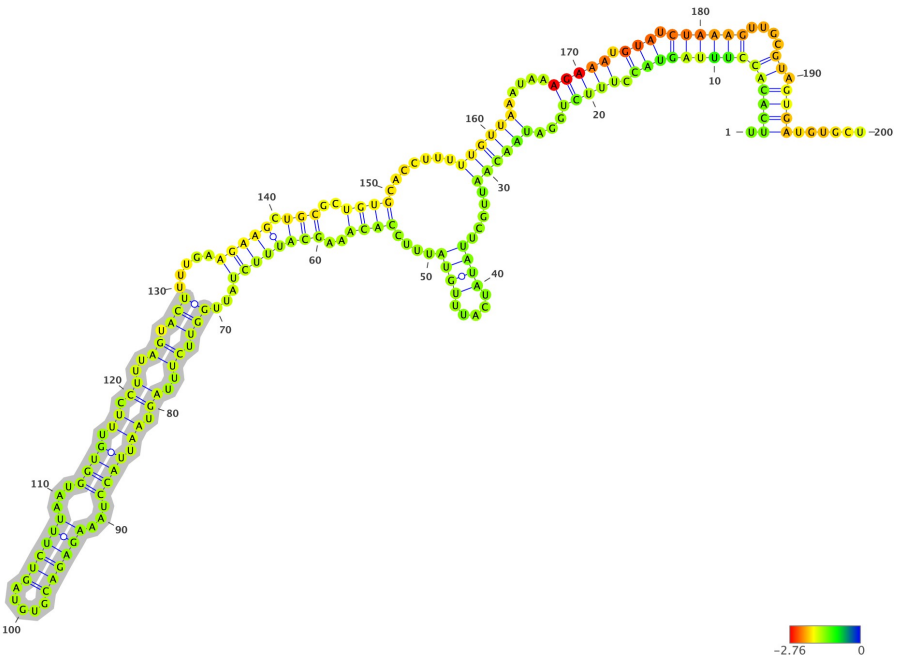
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 185 from nt 9729 to 9787 (nt 71 to 129)

```
5'-GGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACU-3'
5'-(((.((..((.((..(((...((((((.....))))))...)))..)).))..)).)))-3'
Motif MFE = -13.8; z-score = -2.31; ED = 2.72
```



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

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

```
5'-UUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAU
GGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCU-3
5'-.(((((((((((((((.(((((...((((((.....((((.....))))....((((..((((((((...(((.((..((.((.((((...((((((.....))))))...
)))).)).))..)).))).....))))).)))..))))).......))))))).....))))).))).))))))....)).))))......-3'
MFE = -40.2; z-score = -1.24; ED = 41.8
```

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

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

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

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

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

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

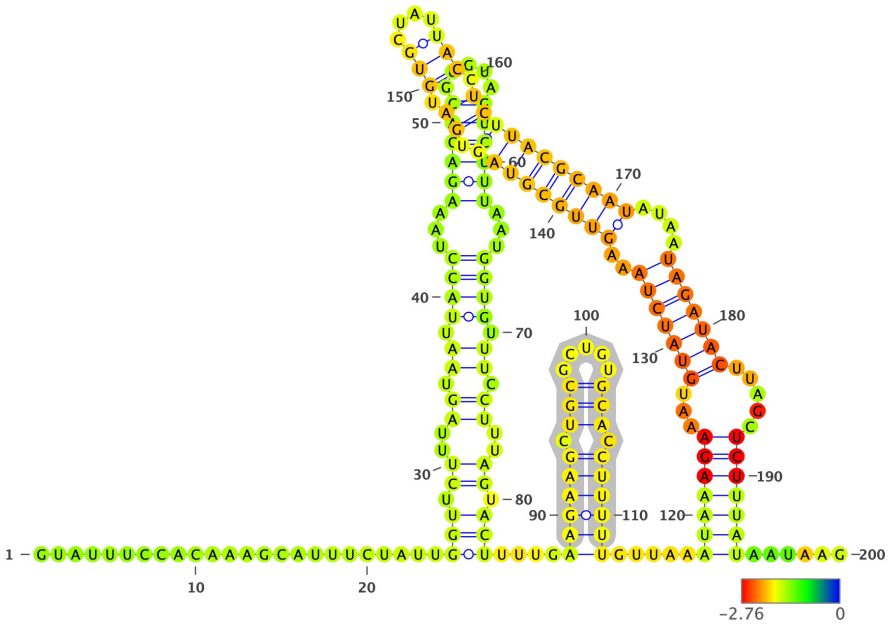
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 186 from nt 9793 to 9815 (nt 89 to 111)

```
5'-AGAAGCUGCGCUGUGCACCUUUU-3'
5'-(((((.(((.....))).)))))-3'
Motif MFE = -4.6; z-score = -0.8; 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 9705 to 9904 (motif highlighted in silver):

```
5'-GUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUU
UGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAG-3
5'-.......................(((.((..((.((.((((...((((((.....))))))...)))).)).))..)).))).....((((((.(((.....))).)))))
).....(((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....)))))))......-3'
MFE = -43.9; z-score = -2.91; ED = 23.94
```

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(+)

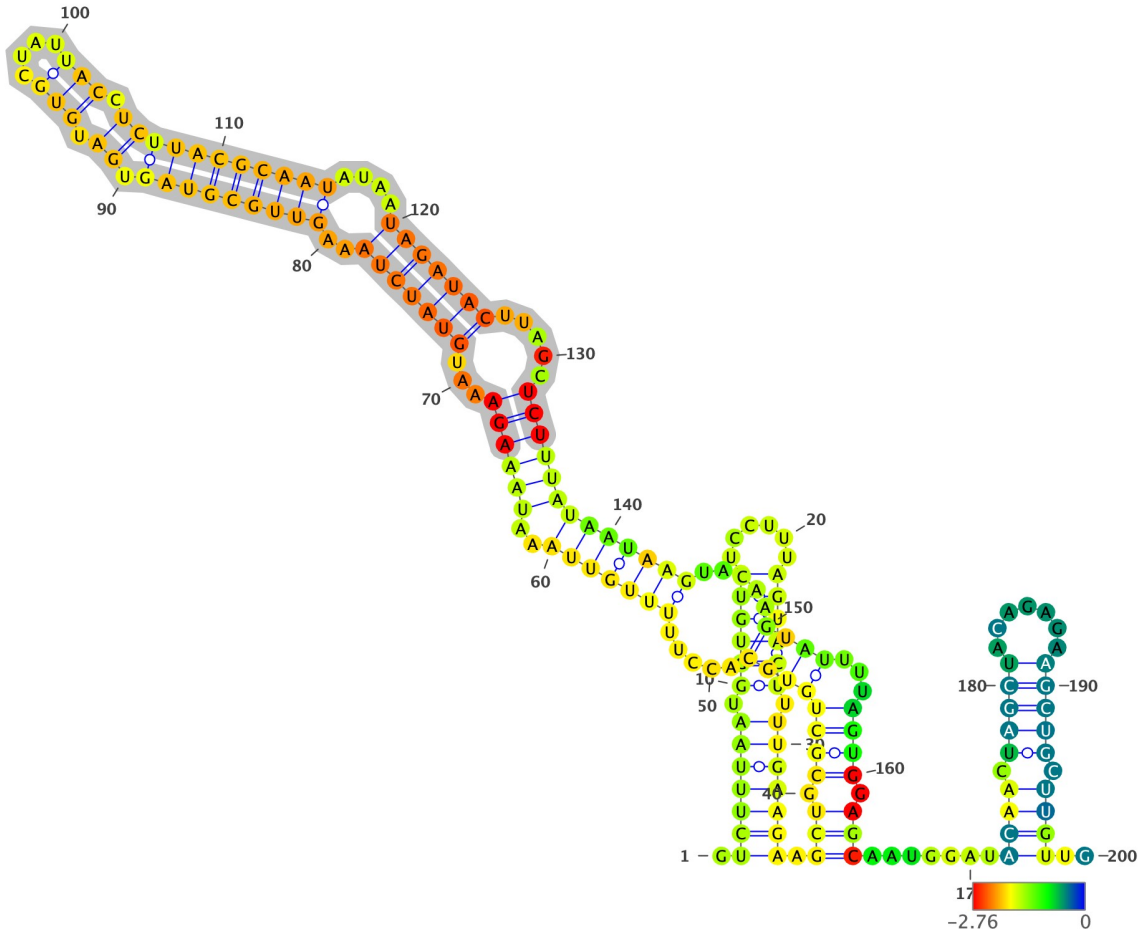
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 187 from nt 9826 to 9894 (nt 66 to 134)

```
5'-AGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCU-3'
5'-(((...(((((((..(((((((((..((.((......)).)).)))))))).....)))))))).....)))-3'
Motif MFE = -18.6; z-score = -3.38; ED = 6.01
```



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 9761 to 9960 (motif highlighted in silver):

```
5'-GUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACG
CAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAGUGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUUG-3
5'-.(((((((.((((((......))))))).)))))))).(((.(((((((((.....(((((((..((((((...(((((((..(((((((((.((.(((....))).)))))))
))))....)))))))).....))))))))))))).....))))...)))).))).......((((.(((((.......))))).))))..-3'
MFE = -50.0; z-score = -2.75; ED = 19.38
```

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(+)

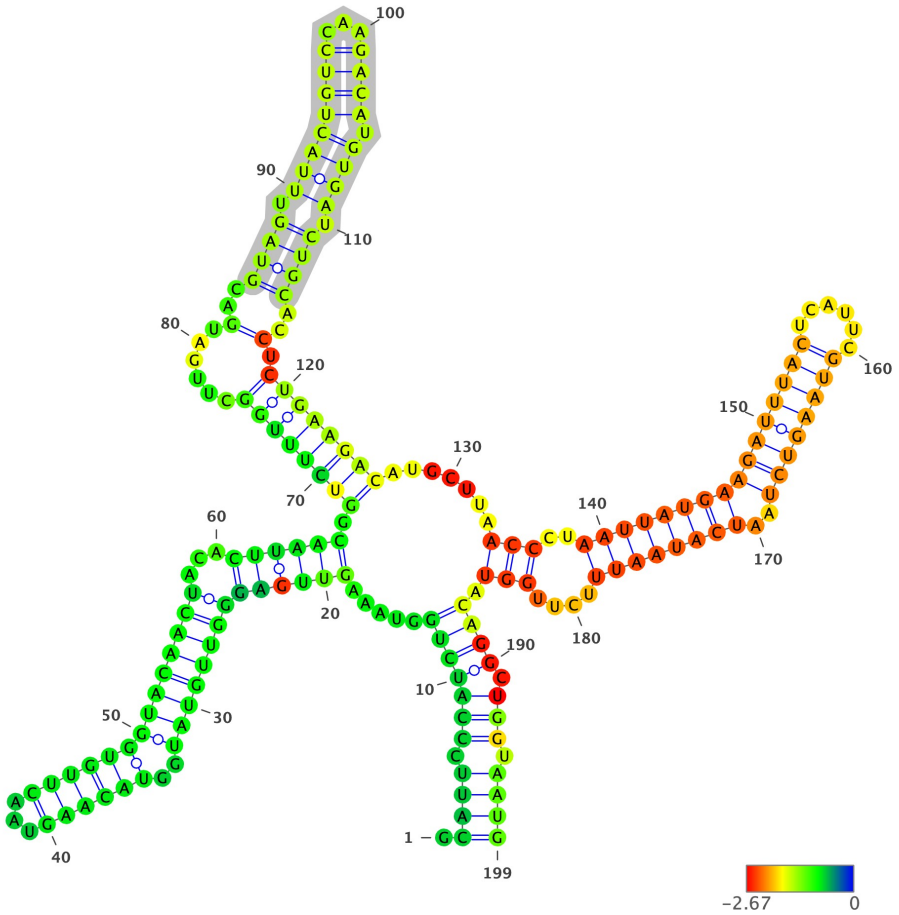
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 188 from nt 10157 to 10186 (nt 85 to 114)

```
5'-GUAGUUUACUGUCCAAGACAUGUGAUCUGC-3'
5'-((((.((((((((...)))).)))).))))-3'
Motif MFE = -8.9; z-score = -2.52; ED = 0.34
```



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

Extracted structure model with flanking nucleotides 10073 to 10271 (motif highlighted in silver):

```
5'-GCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUC
UGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUG-3
5'-.((((.(((((((.....(((((((((((((..((((((...)))))))))))))...)))))).((((((((......(..((((.((((((((...)))).)))).)
)))..).))))))))).......(((..((((((((((((((((.....))))))))..))))))))....))).)))).))).))))-3'
MFE = -55.2; z-score = -2.82; ED = 15.79
```

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(+)

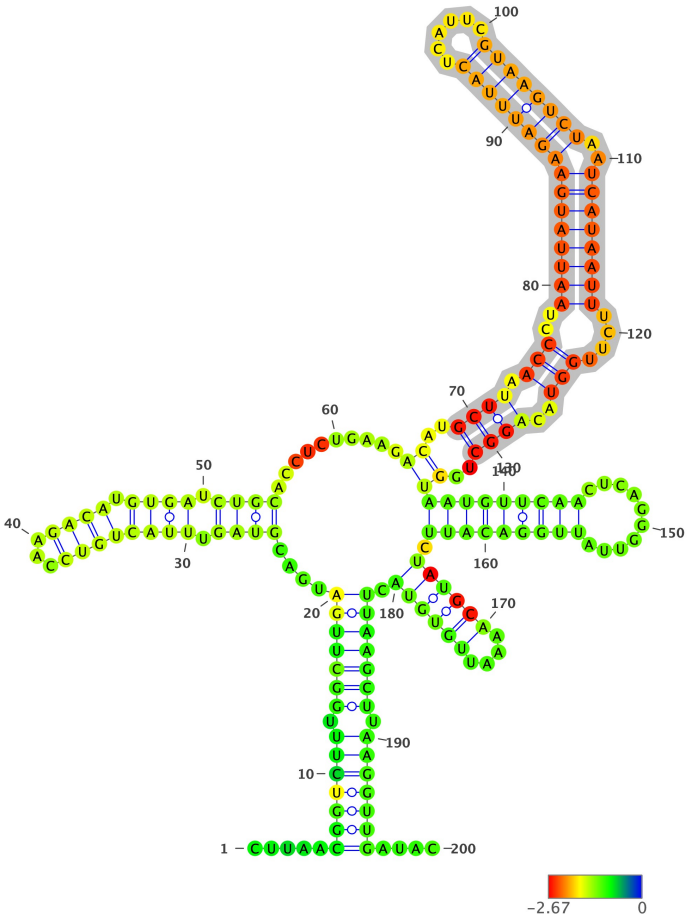
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 189 from nt 10201 to 10263 (nt 69 to 131)

```
5'-GCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGC-3'
5'-(((..(((..(((((((((((((((((.....))))))))..))))))))....)))...)))-3'
Motif MFE = -17.5; z-score = -3.48; 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 = -3.0; ED = 25.6
```

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(+)

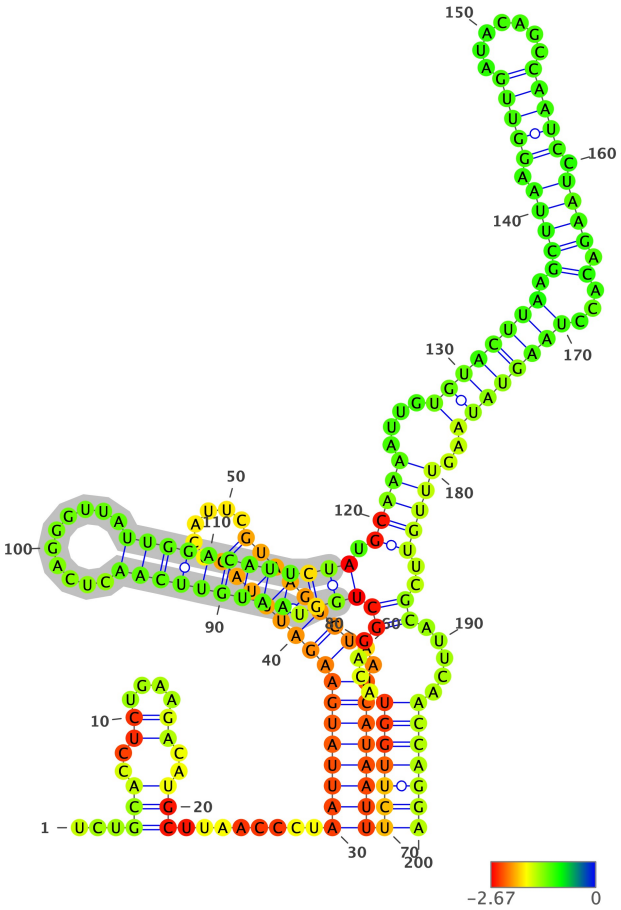
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 190 from nt 10265 to 10297 (nt 84 to 116)

```
5'-GGUAAUGUUCAACUCAGGGUUAUUGGACAUUCU-3'
5'-(..((((((((((.........))))))))).)-3'
Motif MFE = -5.9; z-score = -0.79; ED = 3.88
```



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 10182 to 10381 (motif highlighted in silver):

```
5'-UCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGAC
AUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGA-3
5'-...(((..((....))..)))........(((((((((((((((.....))))))))..))))))))(((((((....(((((.((((((((.........))))))
)))))).(((((....((((((((.(((((.(((((.......))))).)))).)...))))))))..)))))..))).....)))))))-3'
MFE = -45.2; z-score = -2.09; ED = 37.12
```

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(+)

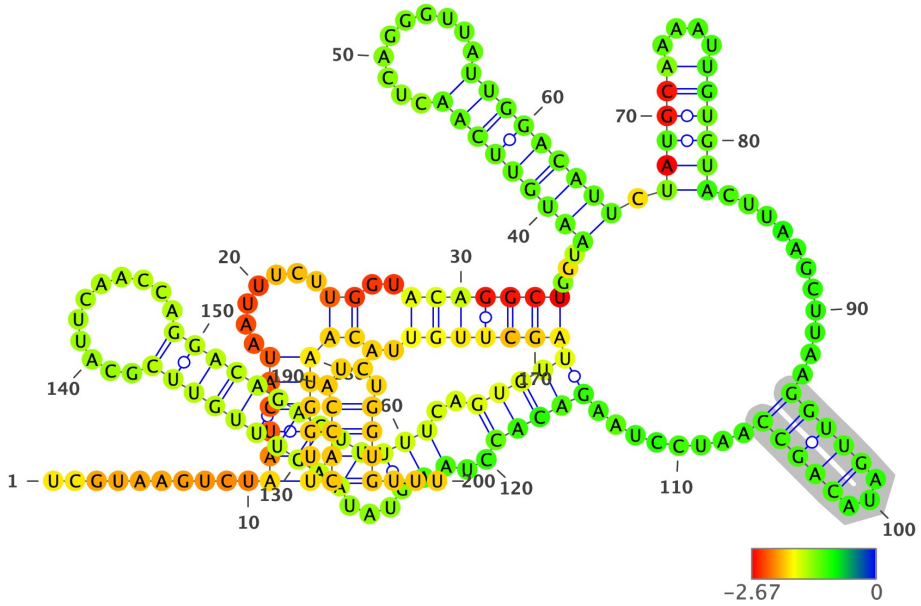
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 191 from nt 10324 to 10336 (nt 94 to 106)

```
5'-GGUUGAUACAGCC-3'
5'-(((((...)))))-3'
Motif MFE = -3.1; z-score = -3.2; 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 = -0.63; 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(+)

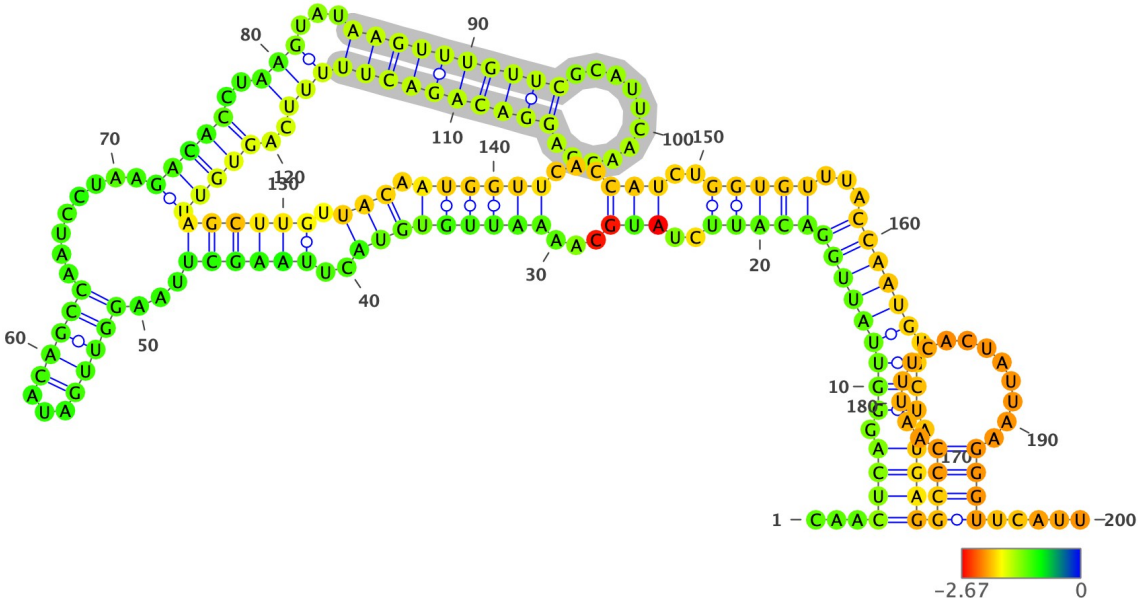
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 192 from nt 10358 to 10388 (nt 85 to 115)

```
5'-AAGUUUGUUCGCAUUCAACCAGGACAGACUU-3'
5'-((((((((((...........))))))))))-3'
Motif MFE = -9.4; z-score = -3.56; ED = 0.74
```



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

Extracted structure model with flanking nucleotides 10274 to 10473 (motif highlighted in silver):

```
5'-CAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAG
ACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUU-3
5'-...((((.(((((((((((((..(((...((((((((((..((((((...(((((...)))))........(((((..(((...((((((((((...........))))))
)))))))..))))))))))).))).))))))...)))..)))))...))))))).))).))))((((..............))))).....-3'
MFE = -44.5; z-score = -1.05; ED = 60.64
```

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

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

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

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

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

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

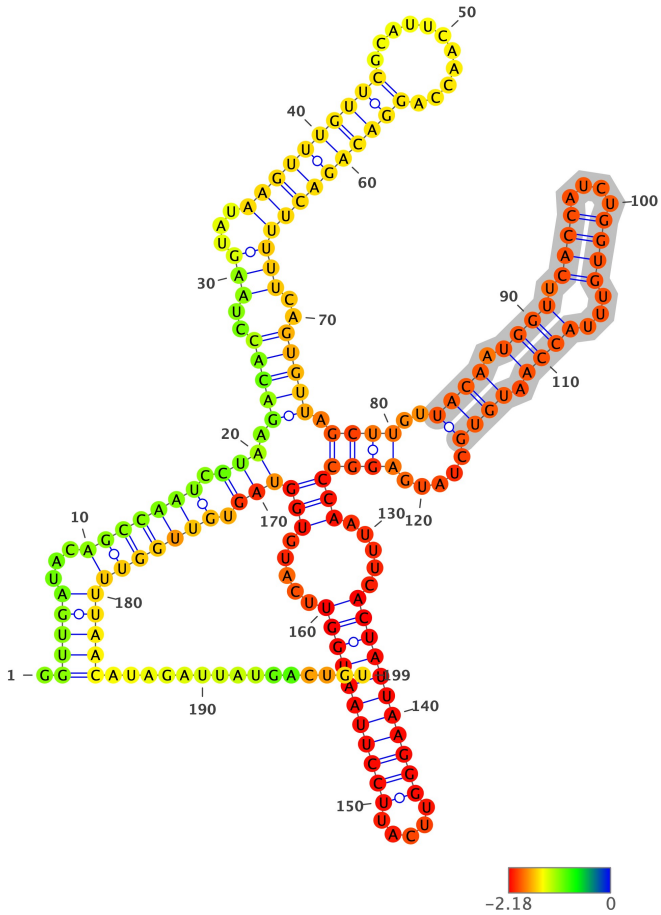
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 193 from nt 10406 to 10439 (nt 83 to 116)

```
5'-UACAAUGGUUCACCAUCUGGUGUUUACCAAUGUG-3'
5'-((((.((((.((((....))))...)))).))))-3'
Motif MFE = -11.0; z-score = -3.42; 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 10324 to 10522 (motif highlighted in silver):

```
5'-GGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCA
AUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGU-3
5'-.(((((...(((((((.(((.(((((..(((...((((((((((.....))))))))))))..))))).((((..((((.((((.((((....))))...))))
.))))).....))))(((.....((((((((((.....))))))))))).....)))))).))))))))))))...............-3'
MFE = -53.4; z-score = -2.71; ED = 24.05
```

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(+)

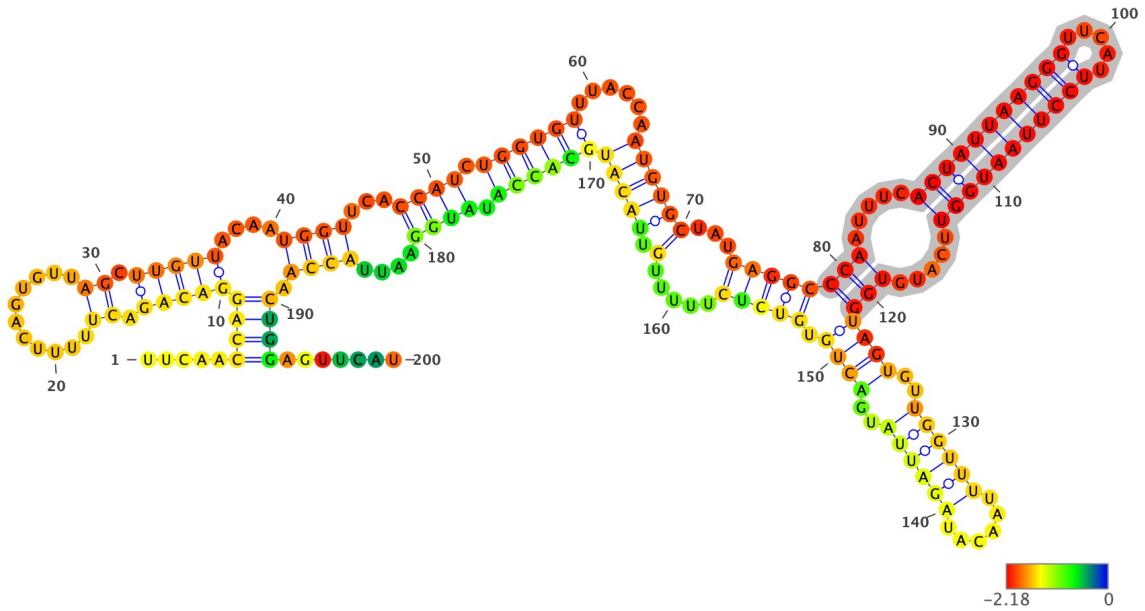
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 194 from nt 10449 to 10491 (nt 79 to 121)

```
5'-CCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGG-3'
5'-(((.....(((((((((((.....)))))))))))).....)))-3'
Motif MFE = -14.0; 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 10371 to 10570 (motif highlighted in silver):

```
5'-UUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUG
GUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAU-3
5'-.....(((((((((.((...........)).)))))....((((...((((.((((((......((((((...((((((((.....((((((((((.....))))))))))
))).....)))((((..((((((......))))))..)))).)))))).....).))))))))))).))))....)))).)))).......-3'
MFE = -46.9; z-score = -1.69; ED = 59.64
```

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(+)

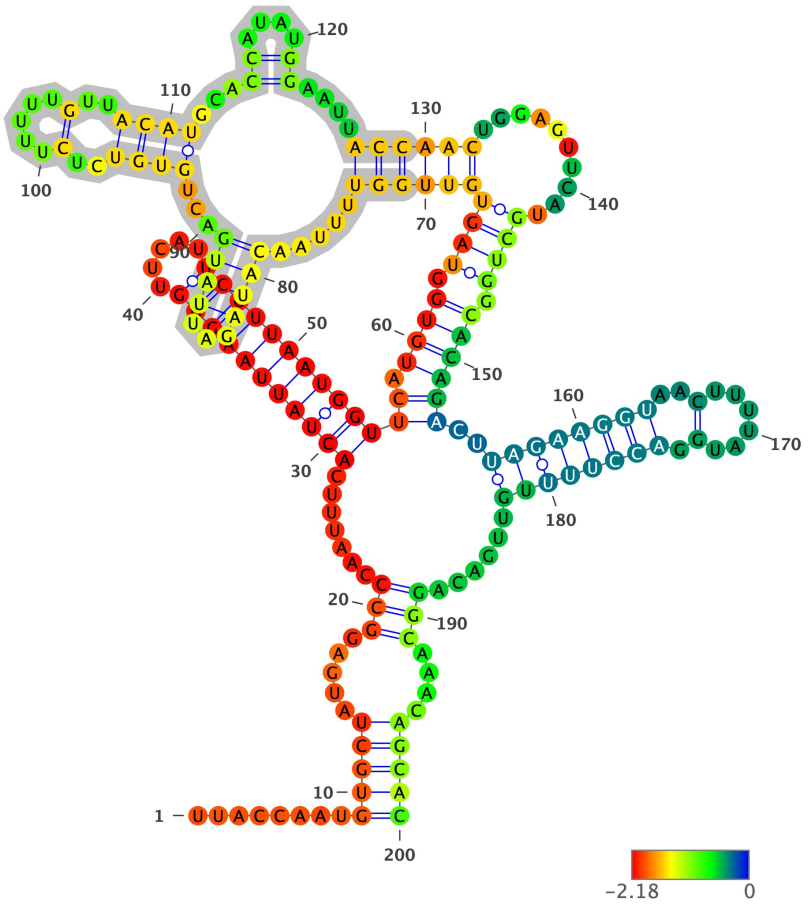
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 195 from nt 10499 to 10557 (nt 71 to 129)

```
5'-GGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACC-3'
5'-(((...................((((..(.....)..))))...((....))....)))-3'
Motif MFE = -6.1; z-score = 0.57; ED = 15.42
```



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 10429 to 10628 (motif highlighted in silver):

```
5'-UUACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAU
GCACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCAC-3
5'-.........(((((.....(((.......((((((((((.....)))))))))))((.((((.((((((((((.....((((...))))...((((..(.....)..))))
...((....))....))))))..........)))).))))))..((((((((..(......).)))))))).....)))....)))))-3'
MFE = -42.5; z-score = -1.56; ED = 27.98
```

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

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

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

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

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

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

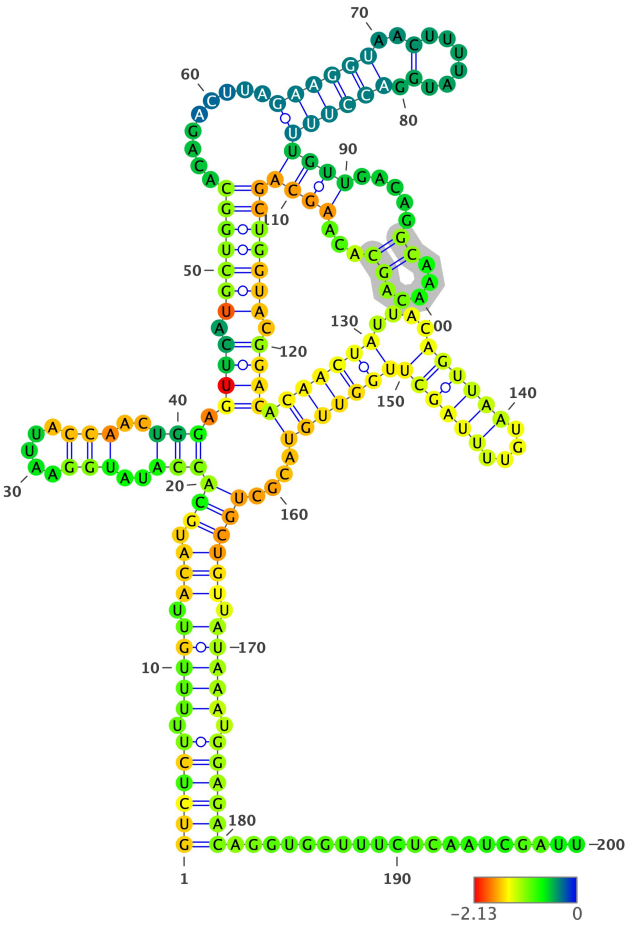
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 196 from nt 10618 to 10626 (nt 96 to 104)

```
5'-GCAAACAGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.1; 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 10523 to 10722 (motif highlighted in silver):

```
5'-GUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCA
GCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUU-3
5'-((((((.(((((.(((.((((((..(((.....)))..))).((((.(((((((.........((((((..(......).))))))((((.....((.....))...))))
))))))).))))(((((((....((((((....))))))))))))....)))))).))))).))))))....................-3'
MFE = -48.6; z-score = -1.53; ED = 41.8
```

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

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

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

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

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

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

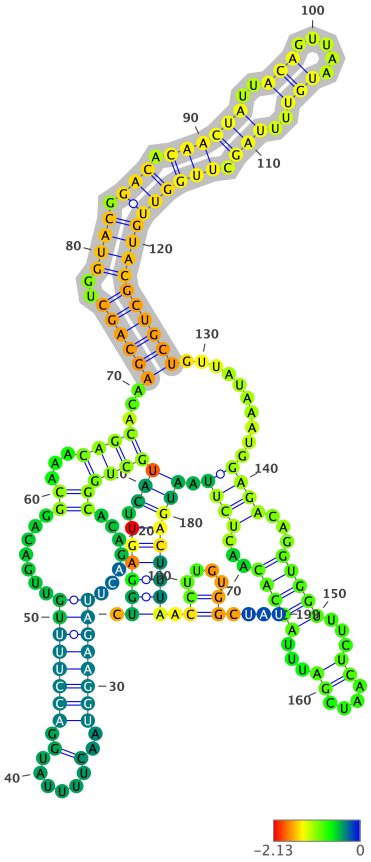
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 197 from nt 10630 to 10687 (nt 71 to 128)

```
5'-AGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCU-3'
5'-((((((..((((.(((.((((((..(((.....)))..))).))))))))))))))))-3'
Motif MFE = -19.9; z-score = -4.18; ED = 2.99
```



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

Extracted structure model with flanking nucleotides 10560 to 10758 (motif highlighted in silver):

```
5'-CUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAG
CUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCACAACUCUUAAUGACUUUAACCUUGUGGCUAU-3
5'-.((((((.(((((((((.......((((((((..(......).))))))))).......))...))))...((((((..((((.(((.((((((..(((.....)))..)))
.))))))))))))))))..........((((...(((((...((....))...)))))...)))).))))))))).((....)).....-3'
MFE = -49.3; z-score = -0.83; 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_gp01, 266-21555(+)

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

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

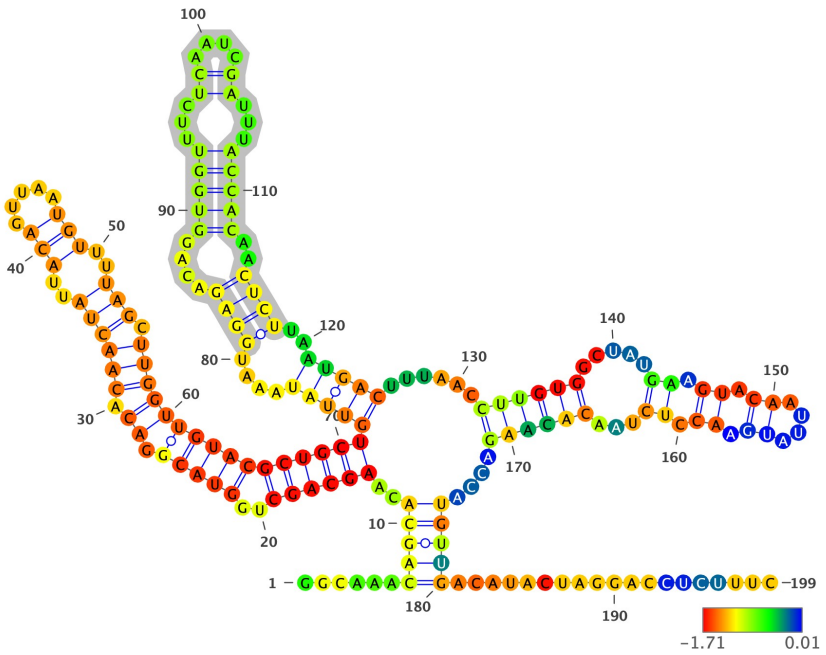
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 10697 to 10734 (nt 81 to 118)

```
5'-GGAGACAGGUGGUUUCUCAAUCGAUUUACCACAACUCU-3'
5'-((((.............................))))-3'
Motif MFE = -9.0; z-score = -1.71; ED = 3.4
```



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

Extracted structure model with flanking nucleotides 10617 to 10815 (motif highlighted in silver):

```
5'-GGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCA
CAACUCUUAAUGACUUUAACCUUGUGGCUAUGAAGUACAAUUAUGAACCUCUAACACAAGACCAUGUUGACAUACUAGGACCUCUUUC-3
5'-......(((((..((((((..(((((.((.((((((..(((.....)))..))).))))))))))))))))(((((....((((....(((((...((....))...))))
)..))))..)))))......((((((.....((.((.((....)).)).))...))))))....)))))...................-3'
MFE = -44.1; z-score = -1.09; ED = 16.53
```

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

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

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

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

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

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

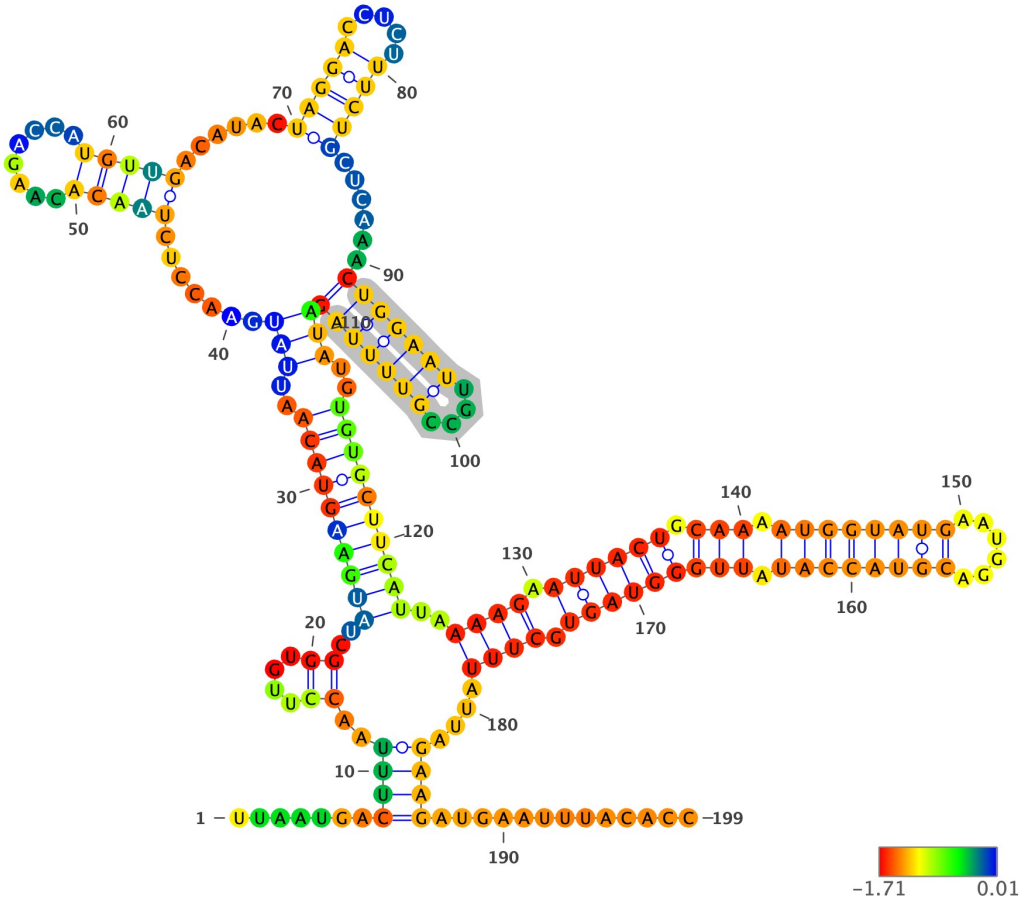
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 199 from nt 10825 to 10840 (nt 92 to 107)

```
5'-UGGAAUUGCCGUUUUA-3'
5'-((((((....))))))-3'
Motif MFE = -0.4; z-score = 0.03; 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 10734 to 10932 (motif highlighted in silver):

```
5'-UUAAUGACUUUAACCUUGUGGCUAUGAAGUACAAUUAUGAACCUCUAACACAAGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUA
UGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACC-3
5'-.......((((..((....))..(((((((((((..(((.......(((((........)))))......(((((.....)))))......(((((((....)))))))))))
..)))))))))))..((((.((((((.((((.(((((((((.....))))))))).))))))))).))))....))))..............-3'
MFE = -36.6; z-score = -0.59; ED = 38.59
```

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

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

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

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

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

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

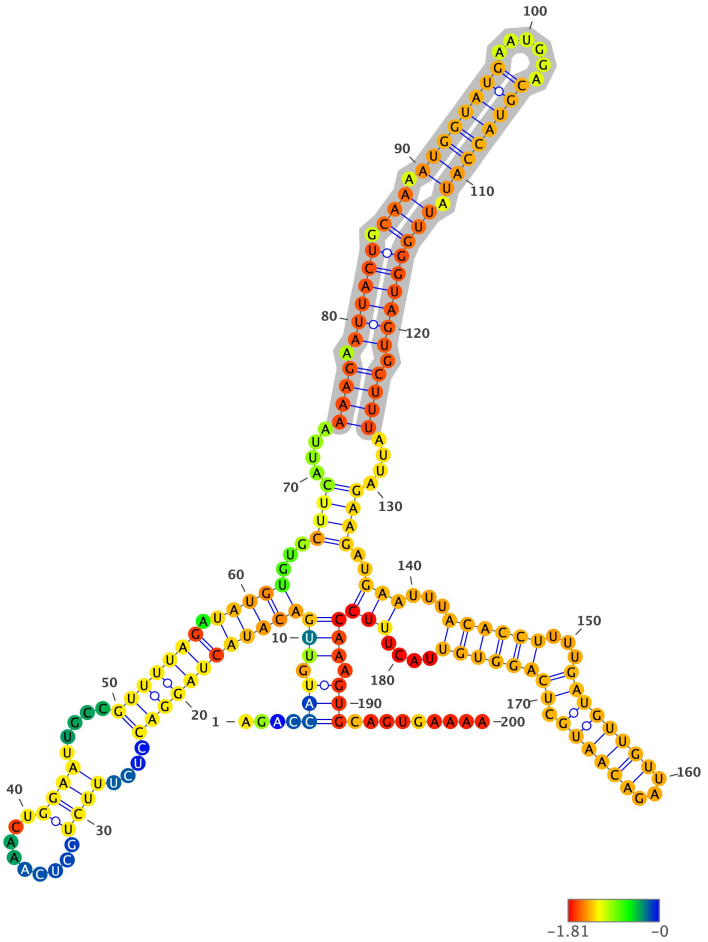
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 = -4.34; 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 = -0.29; 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(+)

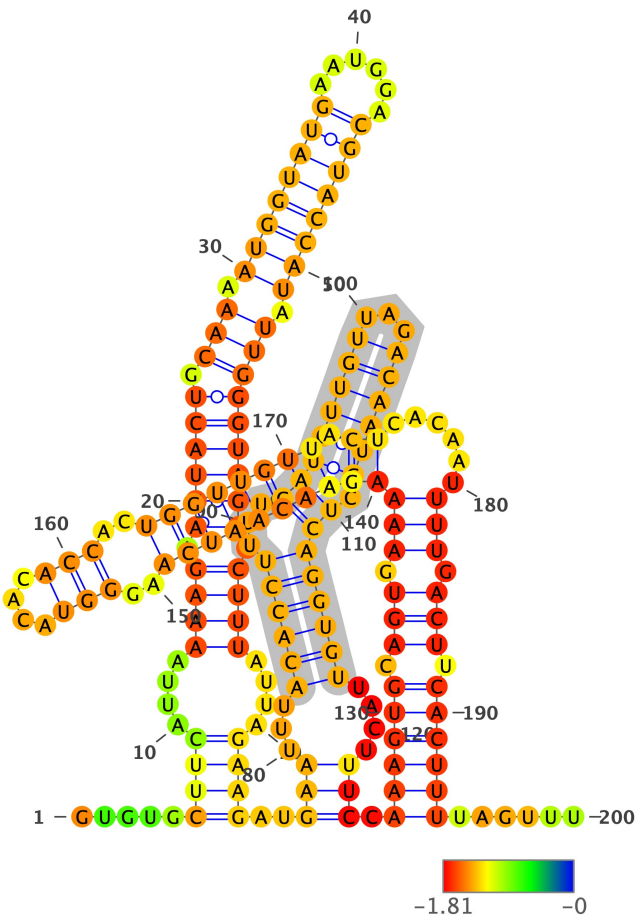
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 = -2.33; 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(+)

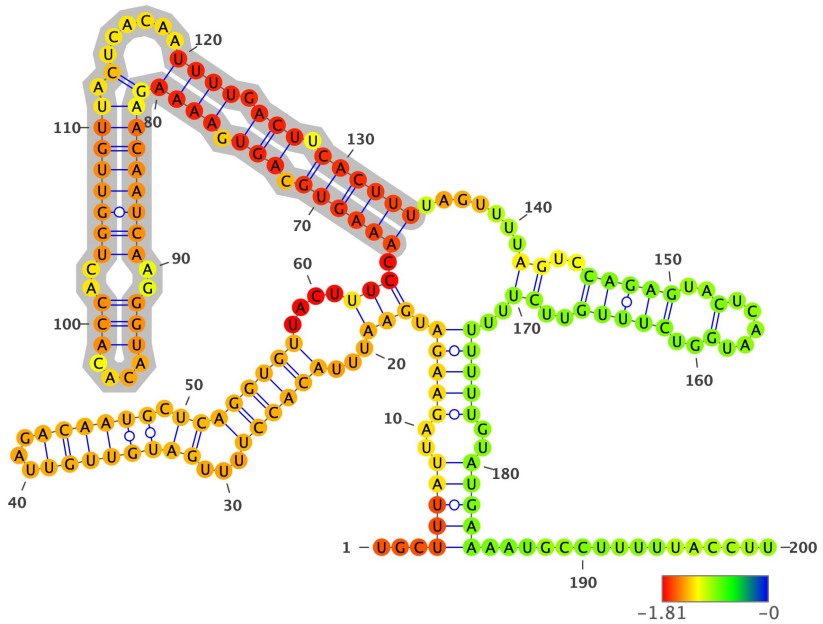
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 = -3.17; ED = 4.8
```



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

Extracted structure model with flanking nucleotides 10906 to 11105 (motif highlighted in silver):

```
5'-UGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUU
ACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUU-3
5'-...(((((..(((((.(((...((((((...((((((((...)))))).))))))))....))).((((((.(((.((((((((((((..(((....)))..))))))))
.).....)))).))).))))))).......((..(((((..(.....)..)))))..))..)))))..)))))................-3'
MFE = -37.5; z-score = -0.86; ED = 37.99
```

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

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

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

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

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

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

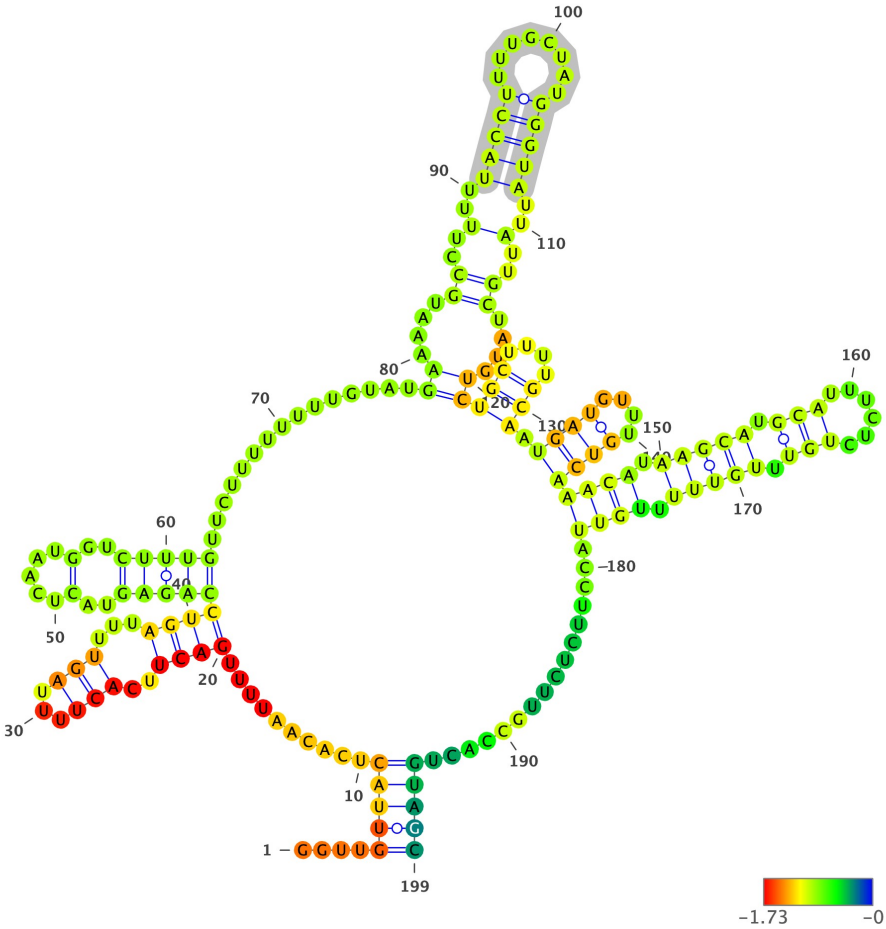
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 203 from nt 11100 to 11117 (nt 91 to 108)

```
5'-UACCUUUUGCUAUGGGUA-3'
5'-(((((........)))))-3'
Motif MFE = -3.8; z-score = -3.27; ED = 0.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11010 to 11208 (motif highlighted in silver):

```
5'-GGUUGUUACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUA
UUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGC-3
5'-....(((((..........((((..(((...)))...))))(((((..(.....)..)))))...............((....((..(..(((((........)))))..)
..))....))(((....))).((((....))))((((.(((((.(((......))).)))))).))))................)))))-3'
MFE = -31.5; z-score = -0.51; ED = 44.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

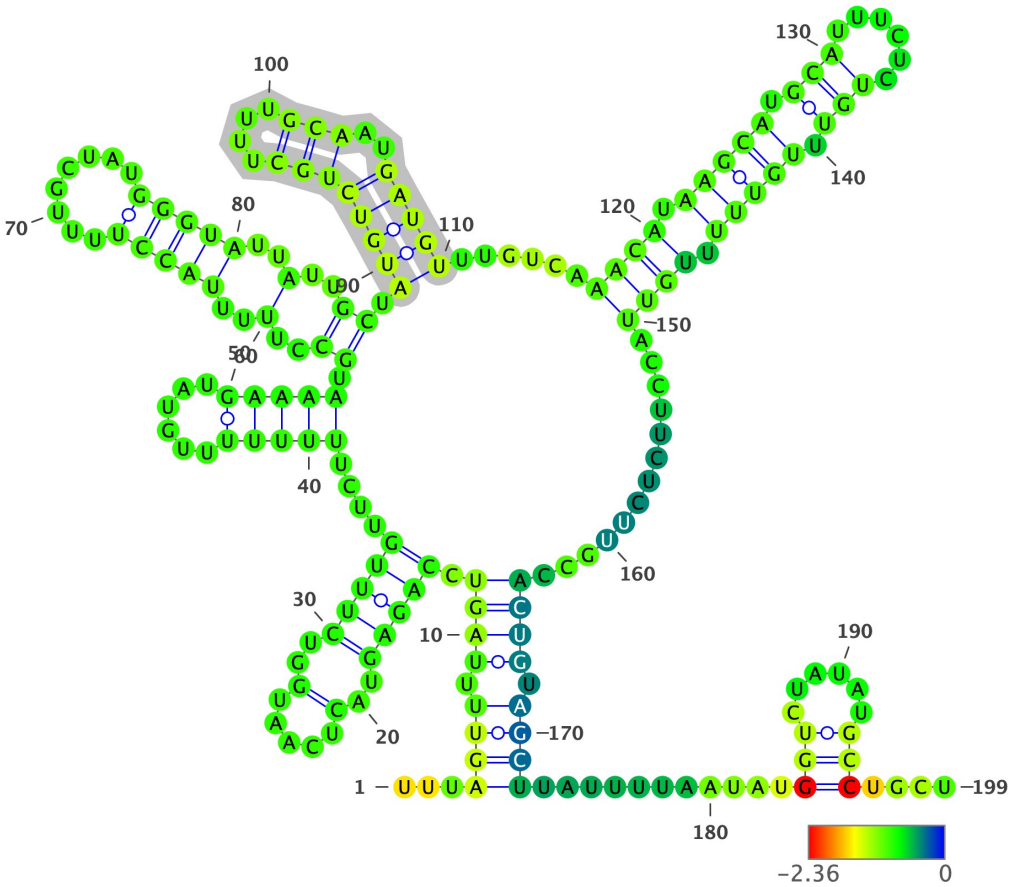
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 204 from nt 11126 to 11147 (nt 89 to 110)

```
5'-AUGUCUGCUUUUGCAAUGAUGU-3'
5'-((((((((....)))..)))))-3'
Motif MFE = -3.1; z-score = -1.0; ED = 2.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11038 to 11236 (motif highlighted in silver):

```
5'-UUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUU
UGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCU-3
5'-...((((.((((.(((((..(.....)..)))))....(((((......))))).((..(..(((((........)))))..)..)).((((((((....)))..))))).
.....((((.(((((.(((......))).))))).))))............)))).))))...........(((......)))....-3'
MFE = -30.4; z-score = -1.01; ED = 41.43
```

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(+)

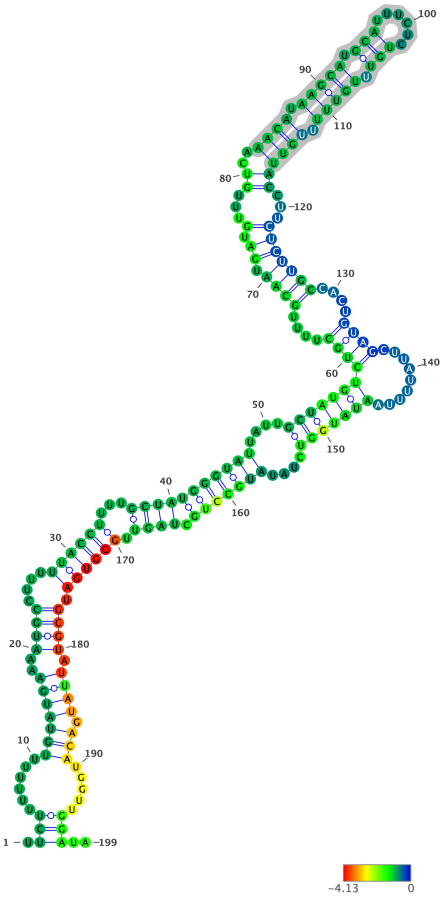
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 205 from nt 11154 to 11187 (nt 83 to 116)

```
5'-AACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUU-3'
5'-(((..((.....................))..)))-3'
Motif MFE = -7.2; z-score = -2.81; 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 = -0.96; 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(+)

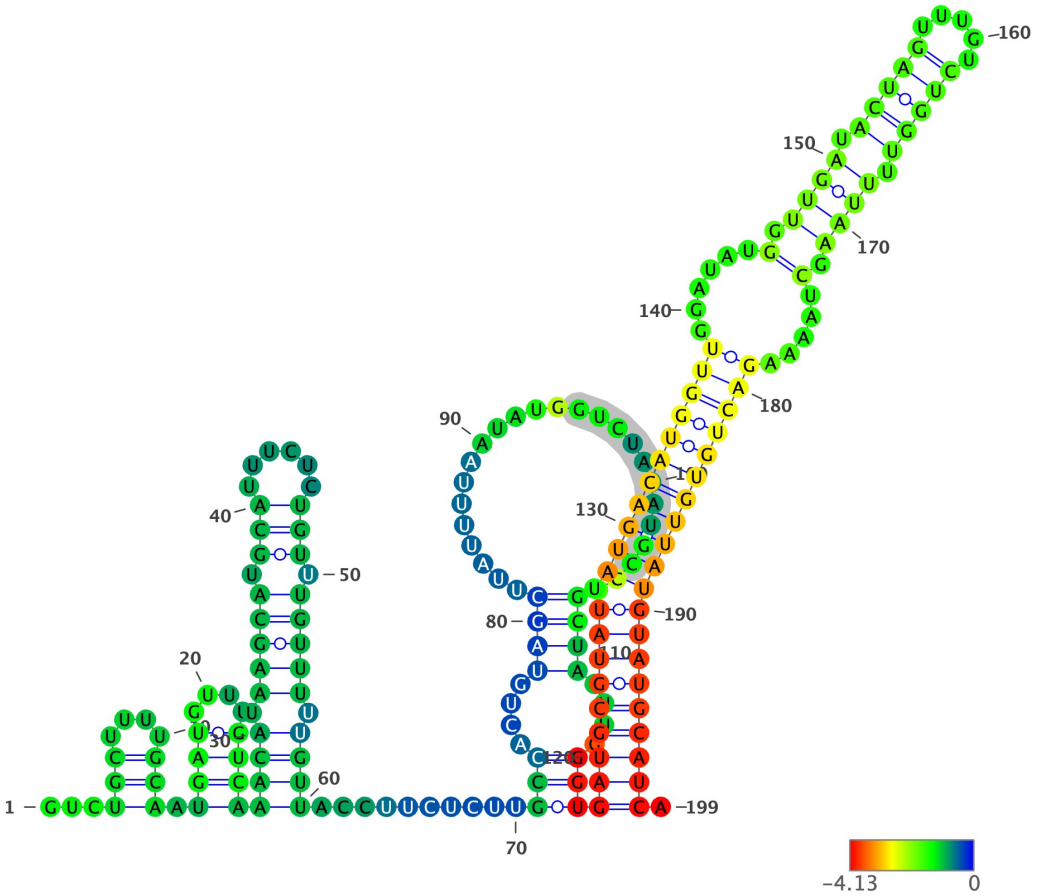
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 11222 to 11231 (nt 95 to 104)

```
5'-GUCUAUAUGC-3'
5'-((......))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 0.06
```



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 11128 to 11326 (motif highlighted in silver):

```
5'-GUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAG
UUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCA-3
5'-...(((....))).((((....))))((((.(((((.(((......))).))))).))))..........(((....((((.........................)))).
...)))(((((((((.(((((((((((......(.((((.(((((.....))))).)))).).....))))))))))))))))))).-3'
MFE = -49.6; z-score = -3.33; ED = 30.27
```

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(+)

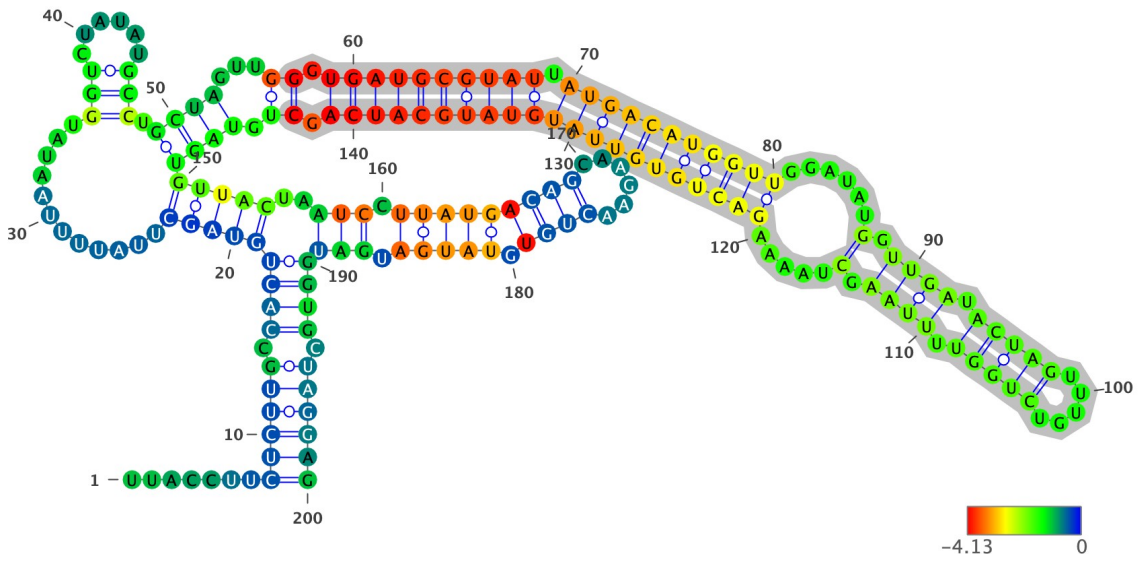
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 207 from nt 11242 to 11328 (nt 57 to 143)

```
5'-GGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCAGC-3'
5'-(.(((((((((((.(((((((((((.....(.((((.(((((.....))))).)))).).....))))))))))))))))))))).)-3'
Motif MFE = -33.7; z-score = -6.1; ED = 5.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11186 to 11385 (motif highlighted in silver):

```
5'-UUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUU
AAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAG-3
5'-.......((((((.(((((((((.............(((......))).((((...((.(((((((((((.(((((((((((.......(.((((.(((((.....))))).))
)).).....))))))))))))))))))))).)).))))))))..(((.(((((((((.......)))).))))).)))))))).))))))-3'
MFE = -56.4; z-score = -2.41; ED = 28.66
```

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(+)

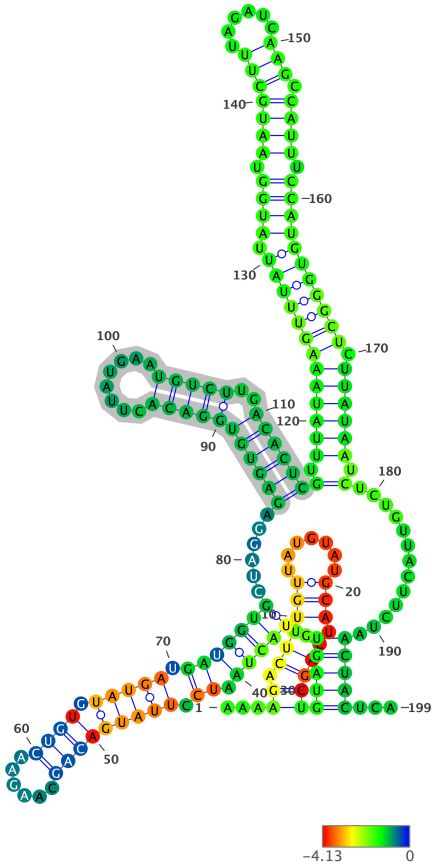
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 208 from nt 11385 to 11416 (nt 84 to 115)

```
5'-GAGUGUGGACACUUAUGAAUGUCUUGACACUC-3'
5'-((((((....................))))))-3'
Motif MFE = -10.6; z-score = -2.73; 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 = -0.61; ED = 22.83
```

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(+)

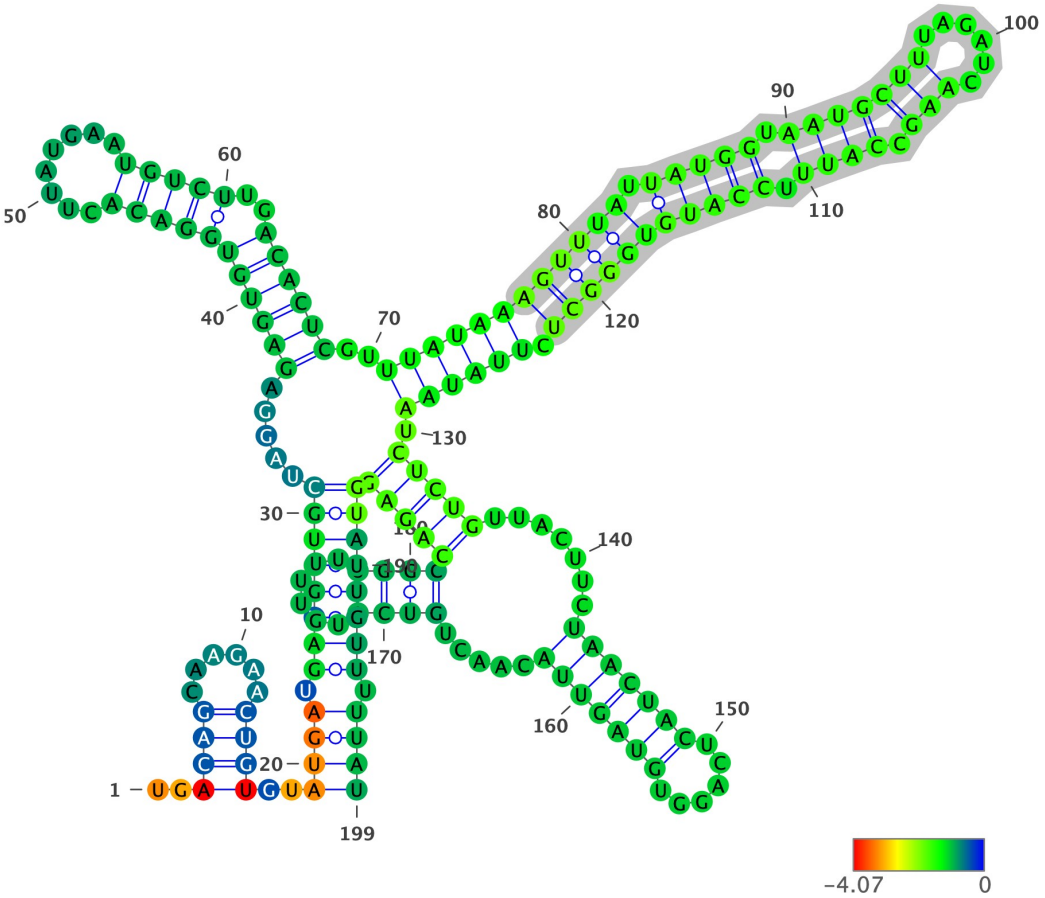
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 209 from nt 11425 to 11470 (nt 77 to 122)

```
5'-AGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUUCCAUGUGGGCU-3'
5'-((((...(((((.(((((((.....))).)))).)))))..))))-3'
Motif MFE = -11.4; z-score = -2.38; ED = 3.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11349 to 11547 (motif highlighted in silver):

```
5'-UGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGAGAGUGUGGACACUUAUGAAUGUCUUGACACUCGUUUAUAAAGUUUAUUAUGGUAAUGCUUUAGAUCAAGCCAUUU
CCAUGUGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAU-3
5'-..((((......))))..((((.((((((((.....((((((((((.........)))))..))))))..((((((((((((.(((((.(((((((......))).)))).
)))))))))))).)))))).(((((.......(((((((......)))))))).....((((......)))))))))))))))))).))))-3'
MFE = -48.4; z-score = -1.31; ED = 33.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

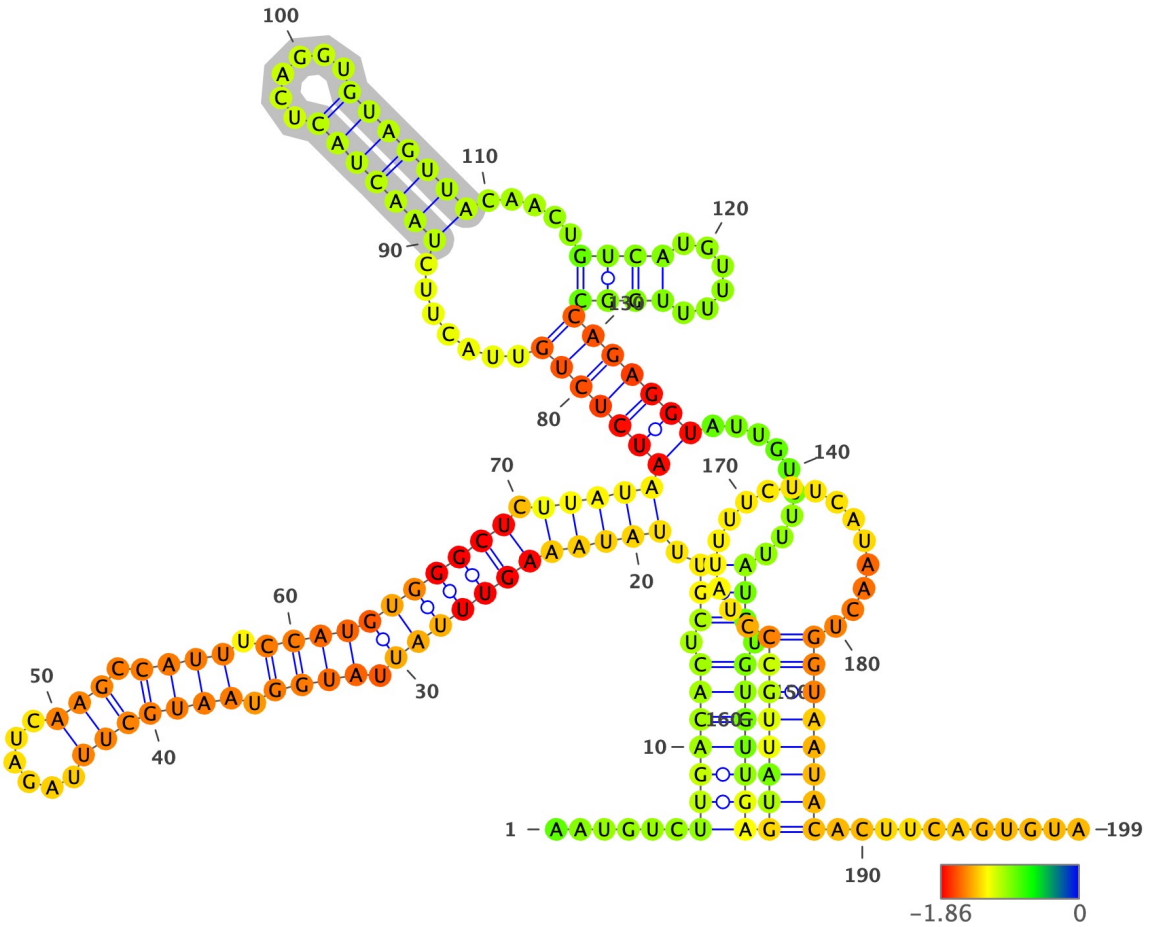
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 210 from nt 11491 to 11510 (nt 90 to 109)

```
5'-UAACUACUCAGGUGUAGUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.2; z-score = -4.19; 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 = -1.87; 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(+)

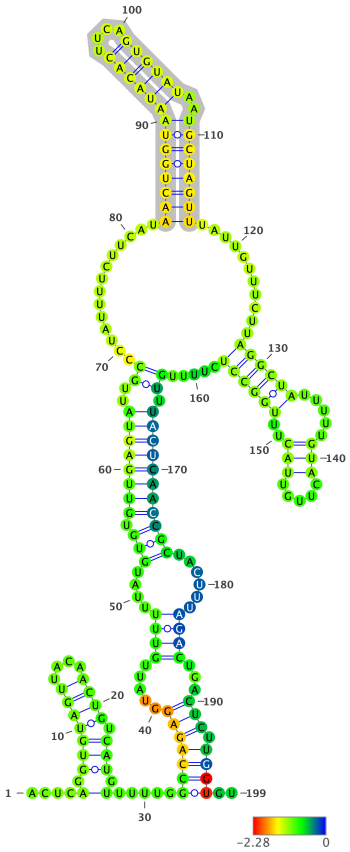
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 211 from nt 11578 to 11611 (nt 83 to 116)

```
5'-AACUGGUAAUACACUUCAGUGUAUAAUGCUAGUU-3'
5'-(((((((.((((((....))))))...)))))))-3'
Motif MFE = -11.8; z-score = -4.41; 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 = -1.81; 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(+)

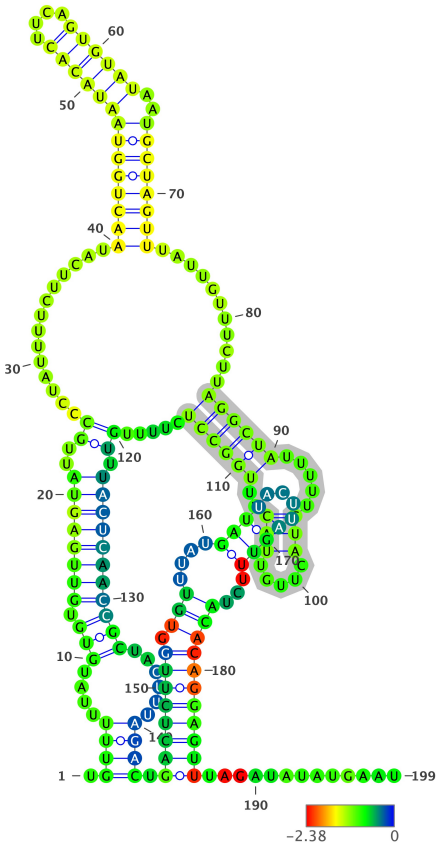
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 212 from nt 11623 to 11652 (nt 85 to 114)

```
5'-AGGCUAUUUUUGUACUUGUUACUUUGGCCU-3'
5'-((((((.....(((.....)))..))))))-3'
Motif MFE = -6.0; z-score = -2.89; 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 = -2.52; 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(+)

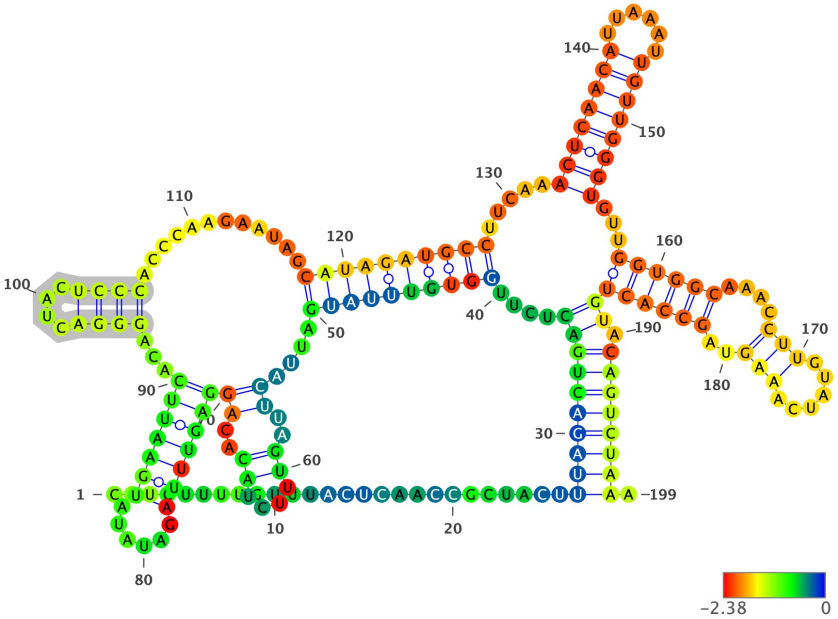
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 213 from nt 11743 to 11754 (nt 94 to 105)

```
5'-GGGACUACUCCC-3'
5'-((((....))))-3'
Motif MFE = -3.6; z-score = -3.73; 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 11650 to 11848 (motif highlighted in silver):

```
5'-CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAA
GAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAA-3
5'-.........................((((((((((....((((((((((....((..((....))..))(((((((......)))))))...((((....))))......
......))))))))))).....((((((((......))))))))...((((((....(((......)))..)))))))).)))))))).-3'
MFE = -47.9; z-score = -2.46; ED = 38.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

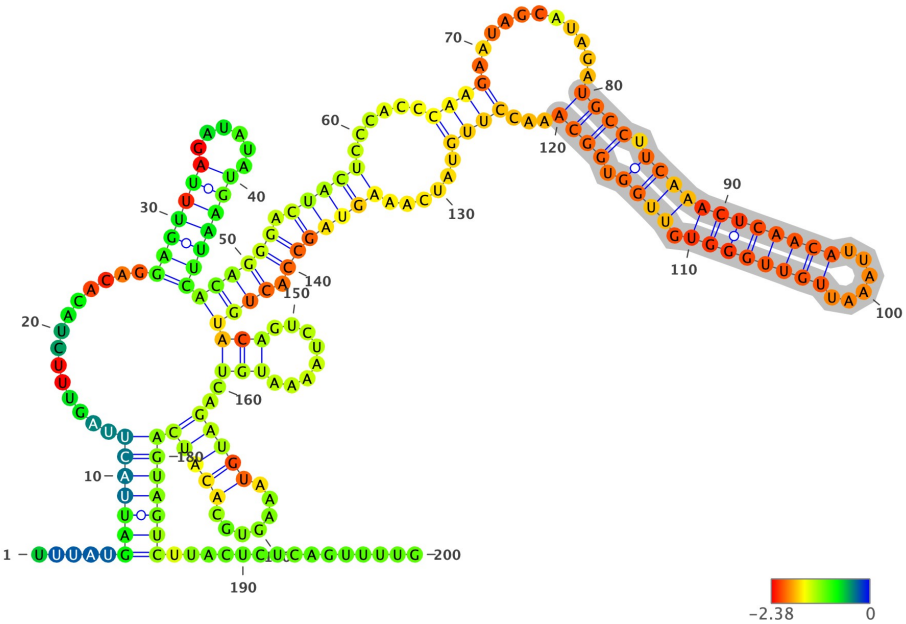
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 214 from nt 11773 to 11813 (nt 80 to 120)

```
5'-UGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCA-3'
5'-((((.((..((((((((.....))))))))...)).))))-3'
Motif MFE = -17.7; z-score = -4.41; ED = 1.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11694 to 11893 (motif highlighted in silver):

```
5'-UUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUG
UUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUG-3
5'-.....(((((((..............(((((((......)))))))((((((.(((((......((((...........((((.(((((((((((.....))))))))).
)))).))))...))))......))))))).))))(((........)))..(((((.......)))))))))))).................-3'
MFE = -45.0; z-score = -1.65; ED = 28.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

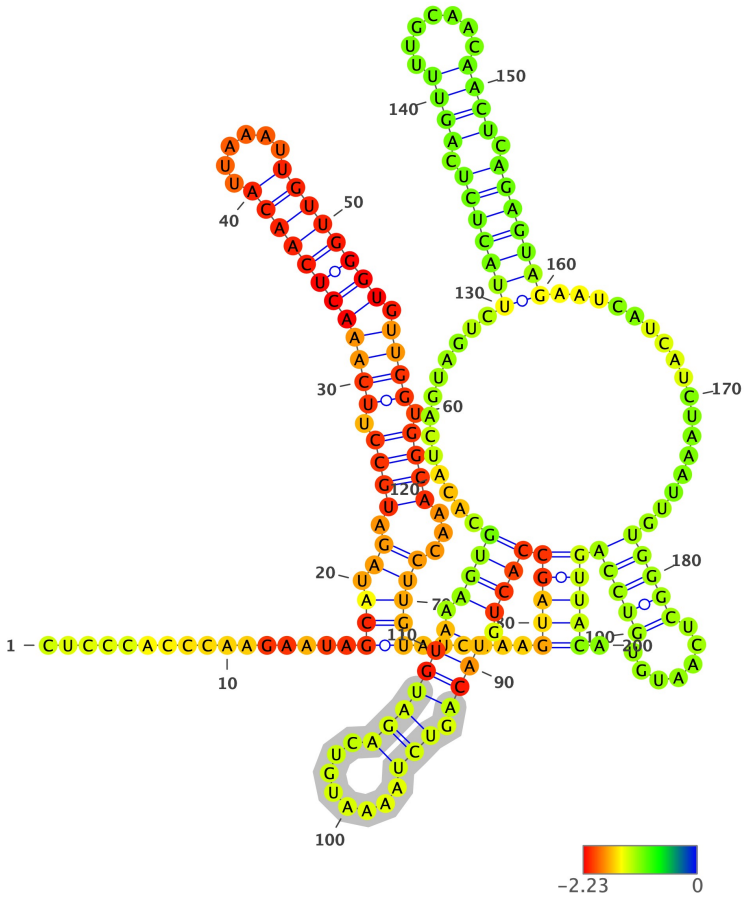
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 215 from nt 11841 to 11857 (nt 92 to 108)

```
5'-AGUCUAAAAUGUCAGAU-3'
5'-(.(((........))))-3'
Motif MFE = -0.5; z-score = -0.28; 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 11750 to 11949 (motif highlighted in silver):

```
5'-CUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUA
AAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACA-3
5'-................(((.((.((((.(((((((((((.....))))))))).)))).))))...)))))......(((((((((.((((.(((........)))))))
.))))............(((((((.((((.......)))).)))))))................(((((.......)))))))))).-3'
MFE = -44.7; z-score = -1.73; ED = 30.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

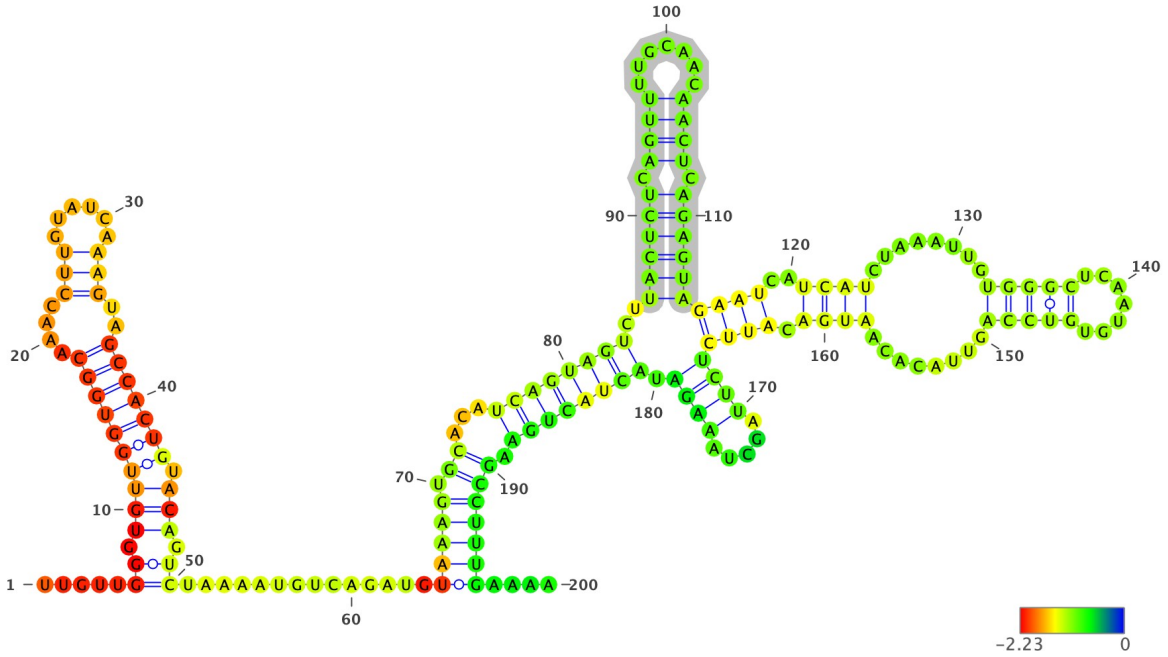
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 216 from nt 11880 to 11908 (nt 86 to 114)

```
5'-UACUCUCAGUUUUGCAACAACUCAGAGUA-3'
5'-((((((.((((.......)))).))))))-3'
Motif MFE = -7.0; z-score = -3.46; 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 = -1.23; 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(+)

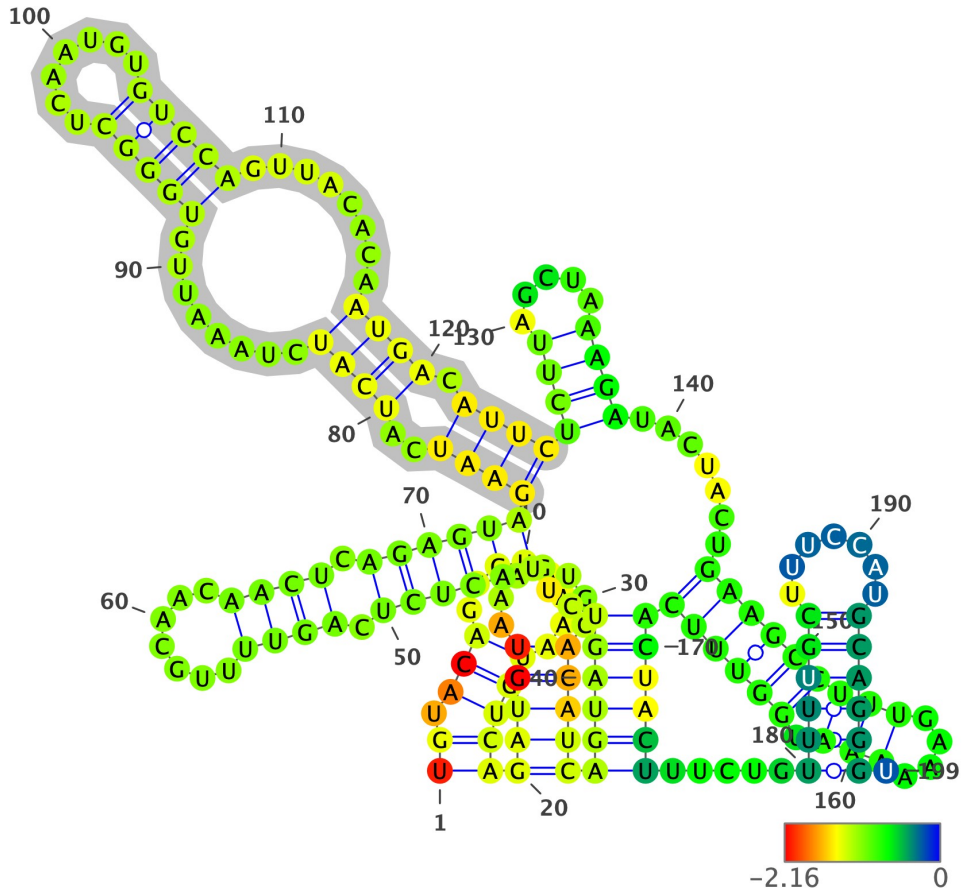
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 217 from nt 11909 to 11960 (nt 74 to 125)

```
5'-GAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUC-3'
5'-((((..((((........(((((.......)))))........)))).))))-3'
Motif MFE = -8.4; z-score = -1.0; ED = 7.56
```



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 11836 to 12034 (motif highlighted in silver):

```
5'-UGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUU
ACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAAAAUGGUUUCACUACUUUCUGUUUUGCUUUCCAUGCAGGGU-3
5'-((.(((........)))))(((((.......)))))((((((..((((((.((((.......)))).))))))((((..((((........(((((.......)))))...
.....)))).))))((((.....)))).......(((((((((....))).))))))))))).....((((((.......)))))).-3'
MFE = -38.3; z-score = -0.99; ED = 38.05
```

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(+)

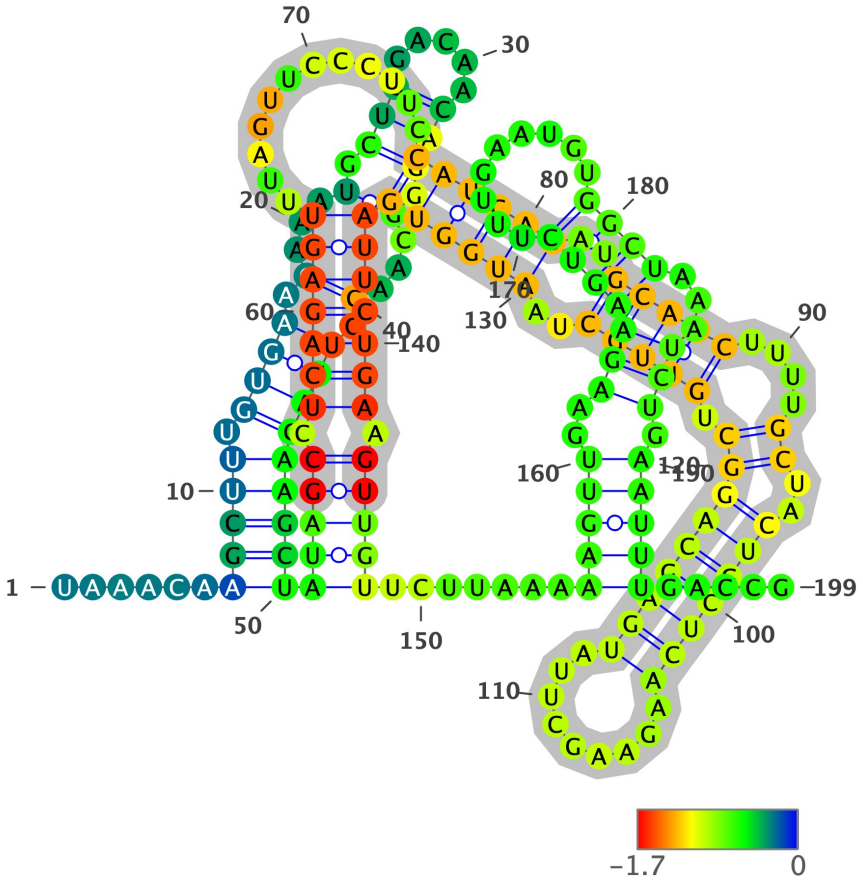
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 218 from nt 12098 to 12189 (nt 54 to 145)

```
5'-GCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUUAUGAGCAGGCUGUUGCUAAUGGUGAUUCUGAAGU-3'
5'-((.(((((((.............((((((..(((((....((..(.....................))).)))))..))))))))))))).))-3'
Motif MFE = -26.1; z-score = -2.42; ED = 8.95
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12045 to 12243 (motif highlighted in silver):

```
5'-UAAACAAGCUUUGUGAAGAAAUGCUGGACAACAGGGCAACCUUACAAGCUAUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUU
AUGAGCAGGCUGUUGCUAAUGGUGAUUCUGAAGUUGUUCUUAAAAAGUUGAAGAAGUCUUUGAAUGUGGCUAAAUCUGAAUUUGACCG-3
5'-......(((((.((((.(...(.(((.....))).)...).)))))))))(((((.(((((((.............((((((..(((((....((..(((((((........
.)))))))))).)))))..))))))))))))).)))))).......(((((..(((((((.........))))...))).)))))).....-3'
MFE = -43.8; z-score = -0.29; ED = 28.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

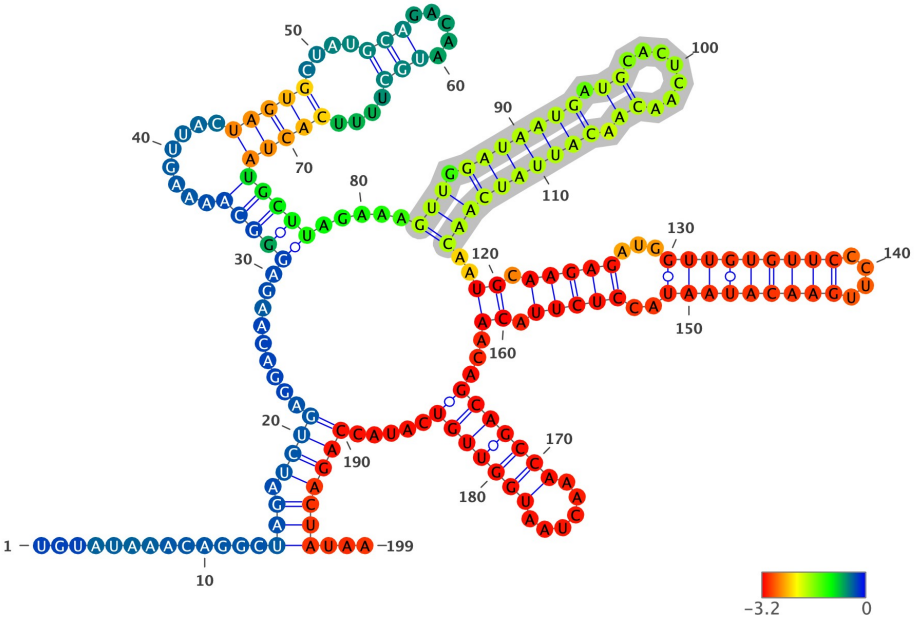
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 219 from nt 12382 to 12415 (nt 83 to 116)

```
5'-GUUGGAUAAUGAUGCACUCAACAACAUUAUCAAC-3'
5'-(((.(((((((.((.......)).))))))))))-3'
Motif MFE = -6.3; z-score = -2.16; 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 = -2.52; ED = 27.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

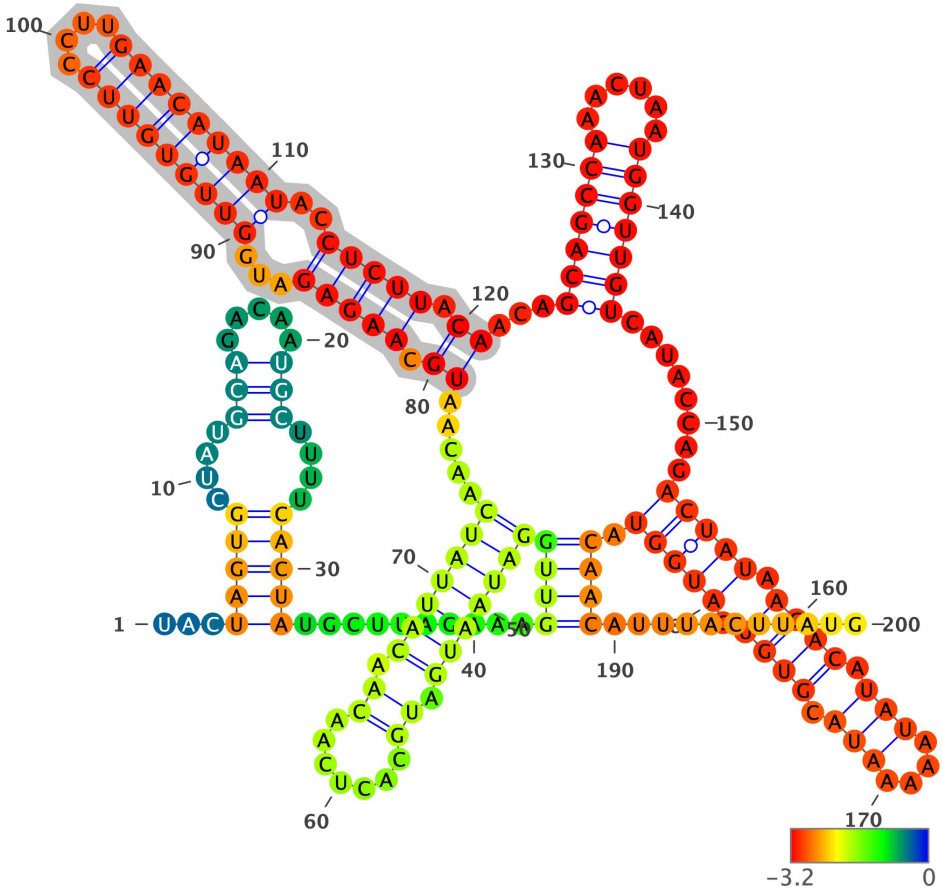
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 220 from nt 12418 to 12460 (nt 79 to 121)

```
5'-UGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACA-3'
5'-((.(((((...(((((((((....)))))))))..)))))).))-3'
Motif MFE = -12.6; z-score = -2.33; 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 = -3.79; 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(+)

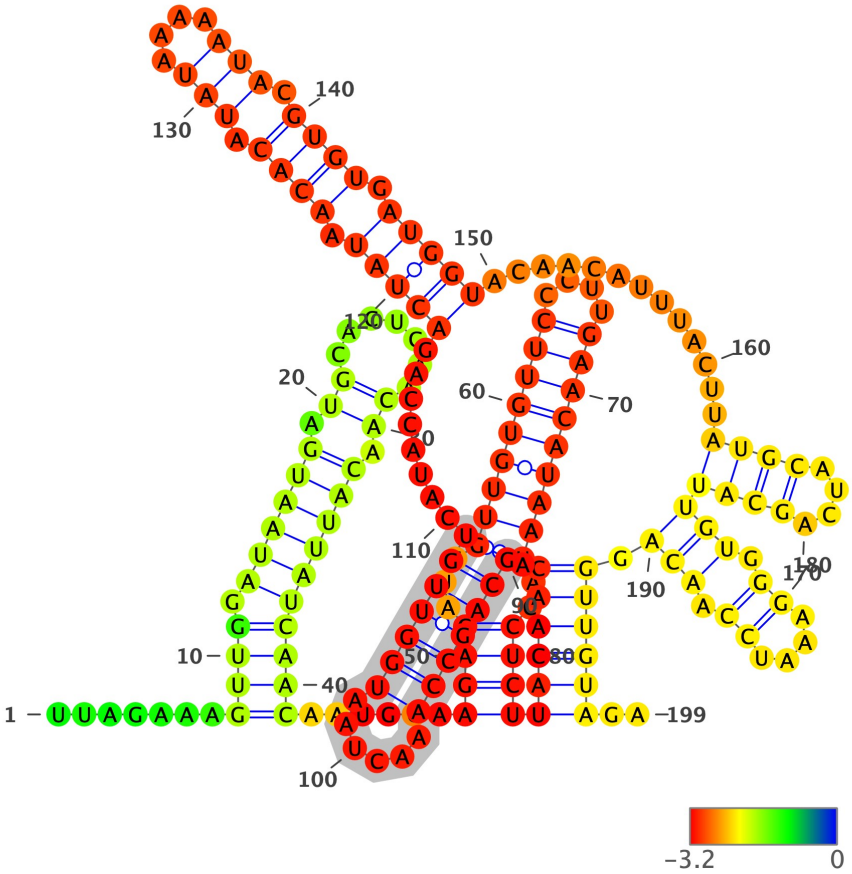
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 221 from nt 12464 to 12483 (nt 90 to 109)

```
5'-GCAGCCAAACUAAUGGUUGU-3'
5'-(((((((......)))))))-3'
Motif MFE = -7.5; z-score = -3.95; ED = 0.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12375 to 12573 (motif highlighted in silver):

```
5'-UUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAUACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCA
UACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGA-3
5'-.......((((.((((((.((.......)).))))))))))......((((...((((((((((....)))))))))..))))((((((.(((((((......)))))))..
......(((((.((((.(((....))).)))).)))))..............((((....))))(((.((....)).))).))))))..-3'
MFE = -46.3; z-score = -3.29; 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(+)

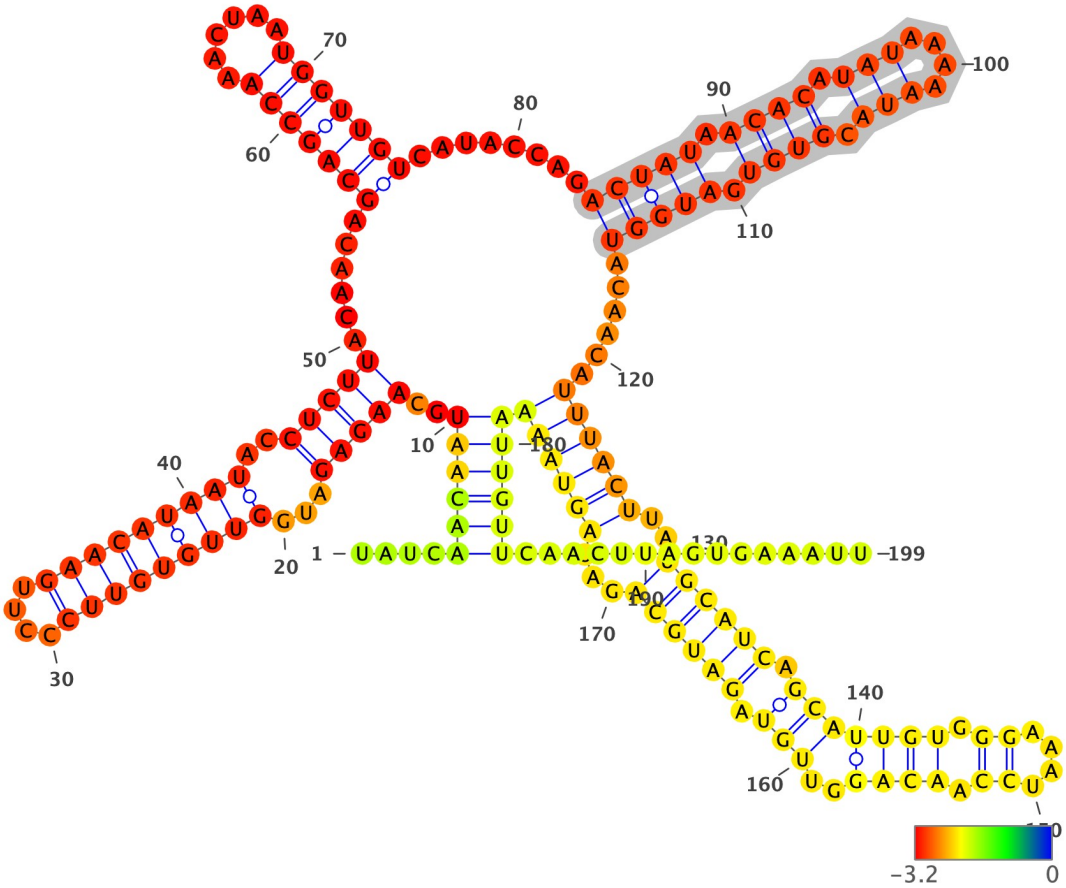
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 222 from nt 12492 to 12523 (nt 84 to 115)

```
5'-ACUAUAACACAUAUAAAAAUACGUGUGAUGGU-3'
5'-(((((.((((............)))).)))))-3'
Motif MFE = -6.6; z-score = -2.57; 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 = -3.49; ED = 23.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 223 from nt 12538 to 12577 (nt 80 to 119)

```
5'-UGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCA-3'
5'-((((((.(((((((.((....)).)))))..)))).)))))-3'
Motif MFE = -12.1; z-score = -2.1; ED = 7.45
```

Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12459 to 12657 (motif highlighted in silver):

```
5'-CAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUG
UAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUU-3
5'-....((..(((((..(((((((((.....))))).(((((.(((((.(((....)))).)))))..))))).....(((((..((((((.(((((((.((....)).)))))..))
).)))))).)))))(((((((((((.........))).)))))))))........)))))..))))..)).....................-3'
MFE = -44.0; z-score = -2.27; ED = 25.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

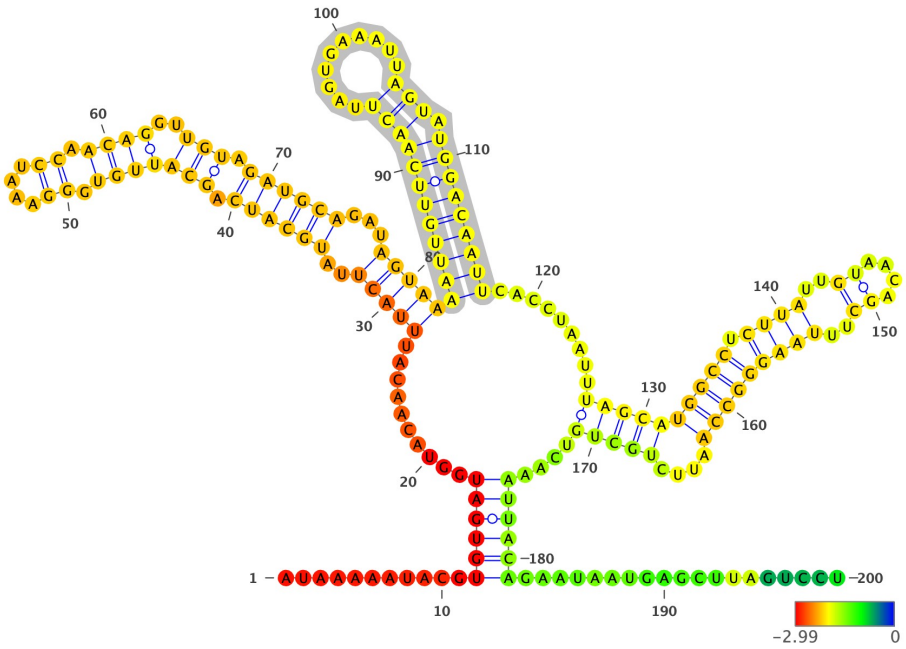
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 224 from nt 12586 to 12620 (nt 83 to 117)

```
5'-AAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUU-3'
5'-((((((((((((.........)))).)))))))))-3'
Motif MFE = -7.4; z-score = -2.59; ED = 4.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12504 to 12703 (motif highlighted in silver):

```
5'-AUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGG
ACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGCCAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCU-3
5'-...........((((((..........(((((..((((((.(((((((.((....)).)))))..)))).)))))))...)))))((((((((((((.........)))).)))
))))))........((((((((((.((((..((....))..)))))))))....)))))....)))))).................-3'
MFE = -45.3; z-score = -2.17; 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(+)

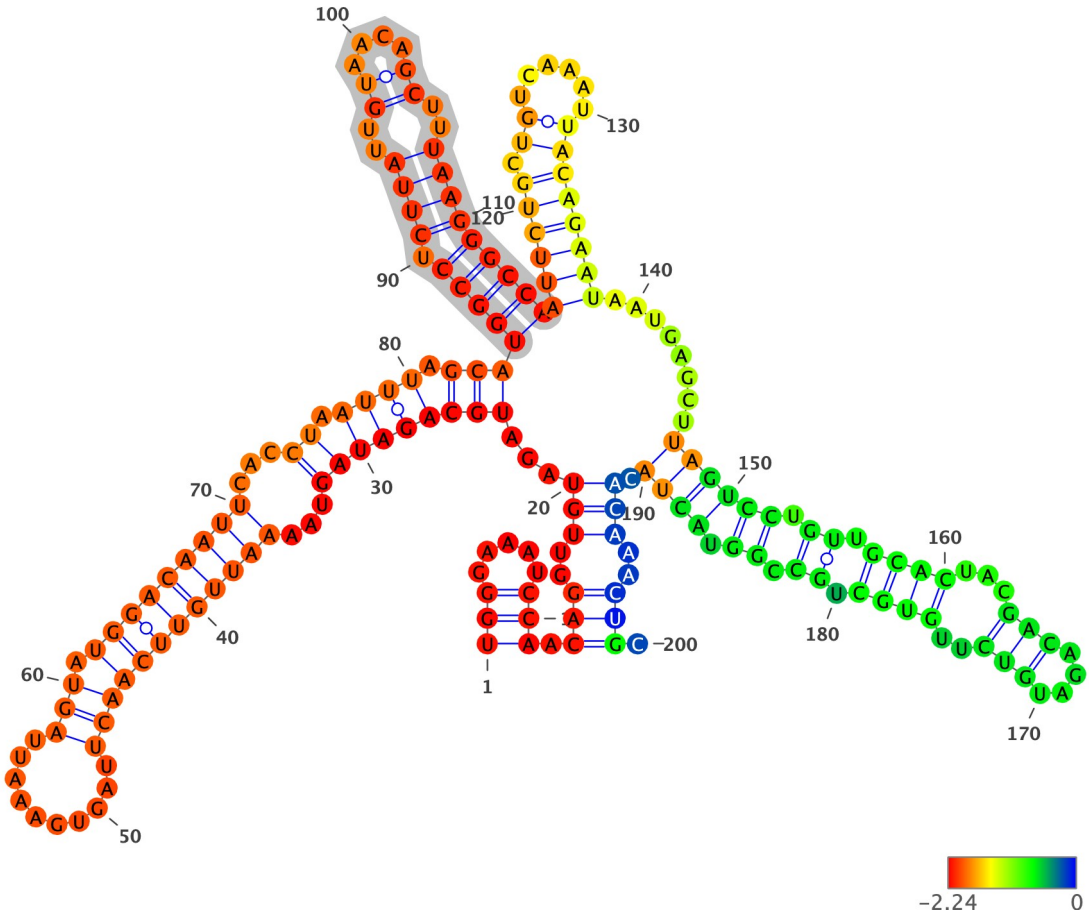
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 225 from nt 12635 to 12665 (nt 85 to 115)

```
5'-UGGCCUCUUAUUGUAACAGCUUUAAGGGCCA-3'
5'-(((((.((((..(......)..)))))))))-3'
Motif MFE = -12.7; z-score = -4.27; 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 = -2.22; 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(+)

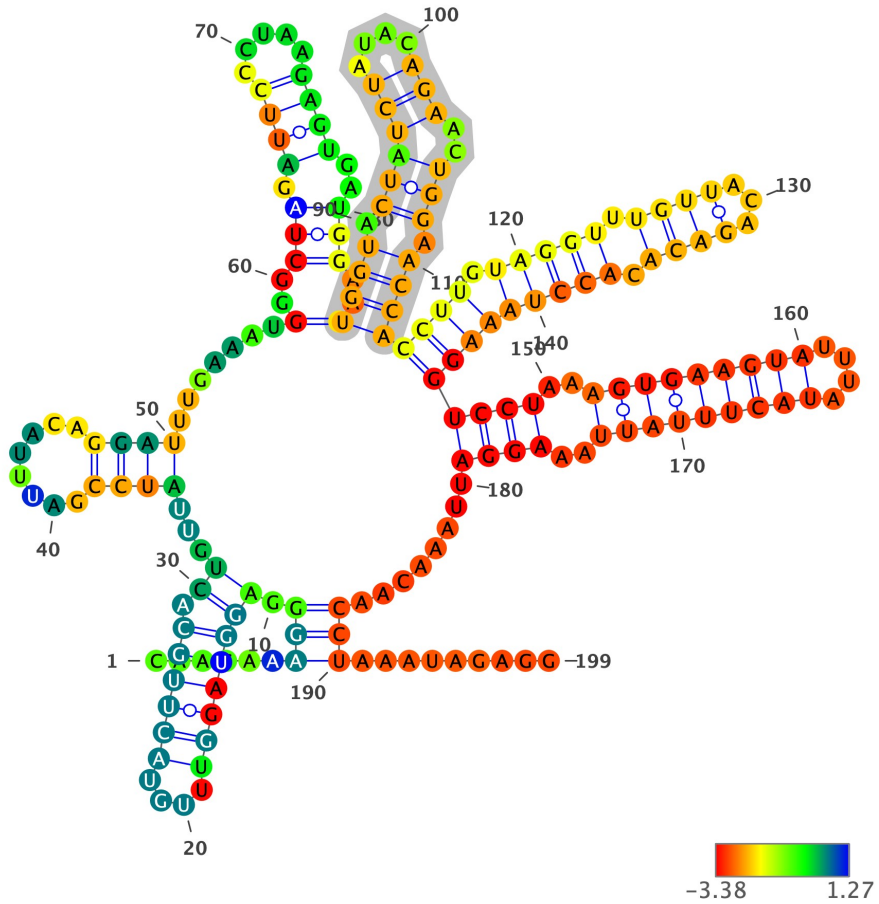
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 226 from nt 12871 to 12898 (nt 86 to 113)

```
5'-UGGUACUAUCUAUACAGAACUGGAACCA-3'
5'-((((.((.(((....)))...)).))))-3'
Motif MFE = -4.4; z-score = -1.28; ED = 2.36
```



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 12786 to 12984 (motif highlighted in silver):

```
5'-CAACAAAGGGAGGUAGGUUUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAAC
CACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGG-3
5'-......(((.(((((((((....)))))).))...((((.........))))........(..(((.((((.....))))..)))..)((((.((((((....)))..))).))
))((((.(((((.((((...)))).)))))))))((((..(((((((((....)))))))))..))))........)))..........-3'
MFE = -44.1; z-score = -1.53; ED = 39.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

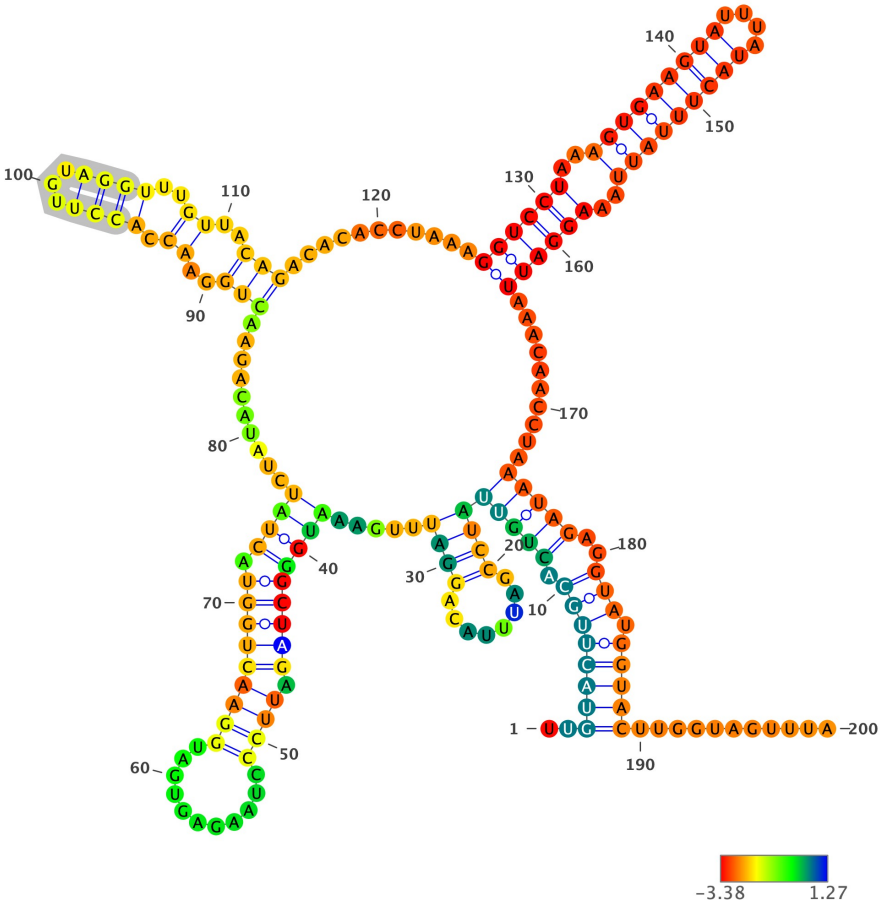
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 227 from nt 12899 to 12907 (nt 96 to 104)

```
5'-CCUUGUAGG-3'
5'-(((...)))-3'
Motif MFE = 0.0; z-score = 0.11; ED = 1.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12804 to 13003 (motif highlighted in silver):

```
5'-UUGUACUUGCACUGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUA
CAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUA-3
5'-..((((((((.(((((((((.........))))).....((((((((.((((...........))))))))).))))..........(((..((.((((...))))..))..
)))...........((((((..((((((((((....)))))))))..))))))..........)))))..))).)))))...........-3'
MFE = -41.1; z-score = -1.35; ED = 39.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

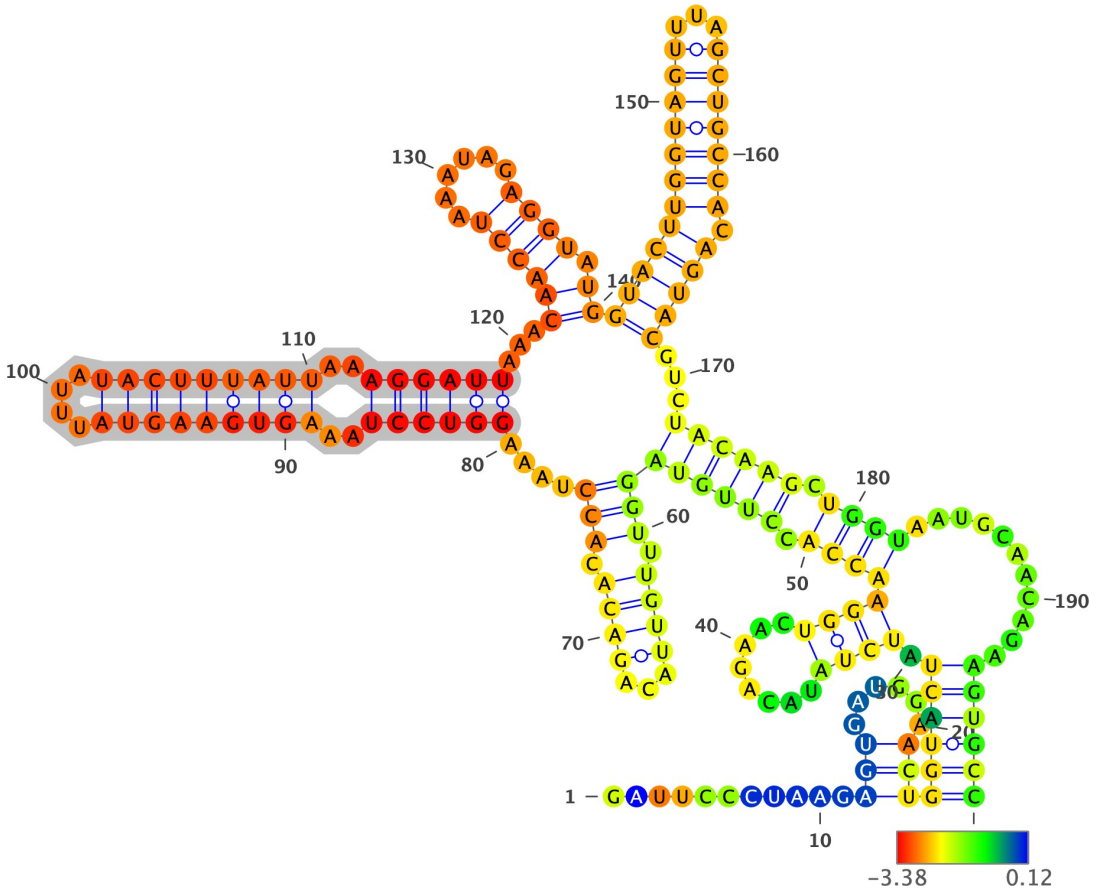
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 228 from nt 12929 to 12966 (nt 81 to 118)

```
5'-GGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUU-3'
5'-((((((......(((((....)))))......))))))-3'
Motif MFE = -11.9; z-score = -4.02; ED = 1.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12849 to 13047 (motif highlighted in silver):

```
5'-GAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUA
AAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCC-3
5'-...........(((......)))((((((.((((........))))((((.(((((((((.((((...)))).)))....((((((..(((((((((....))))))))).
.))))))...((((((......)))).))((((((((((((...)))))))).)))))...))))))).))))...........))))))-3'
MFE = -52.5; z-score = -2.51; ED = 24.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

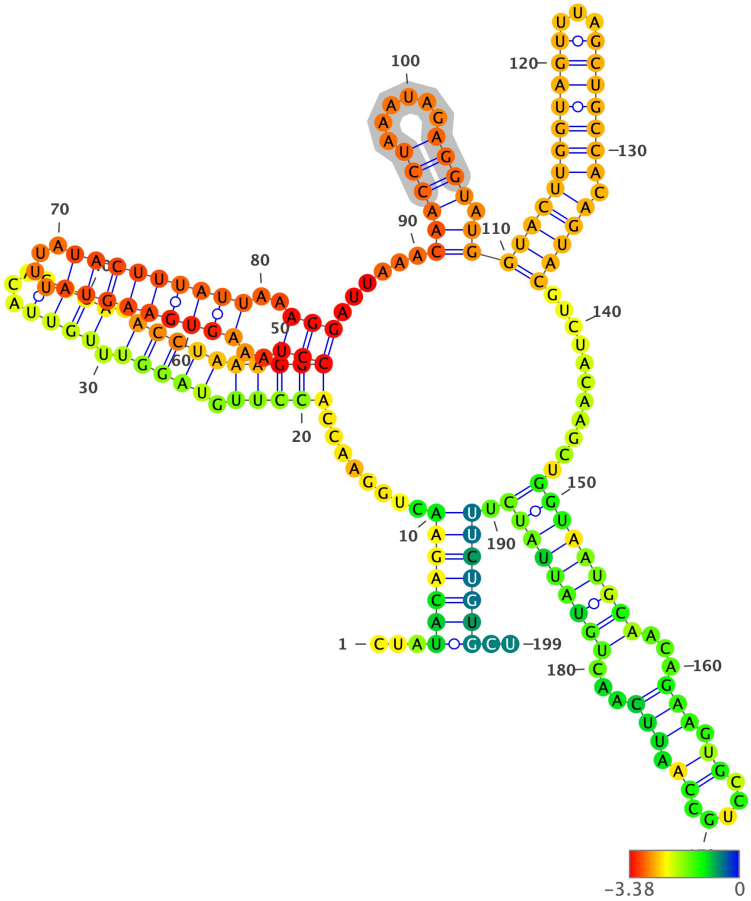
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 229 from nt 12973 to 12984 (nt 94 to 105)

```
5'-CCUAAAUAGAGG-3'
5'-(((......)))-3'
Motif MFE = -0.5; z-score = -2.61; ED = 1.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12880 to 13078 (motif highlighted in silver):

```
5'-CUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGU
ACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCU-3
5'-...(((((((.........(((((.(((((.((((...)))).))))))))))(((..((((((((((....)))))))))..)))......((((((......)))).))((
((((((((((...)))))))).)))))...........((((((((...(((.((.....)).)))...))))))))).)))))))..-3'
MFE = -55.3; z-score = -3.43; ED = 29.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

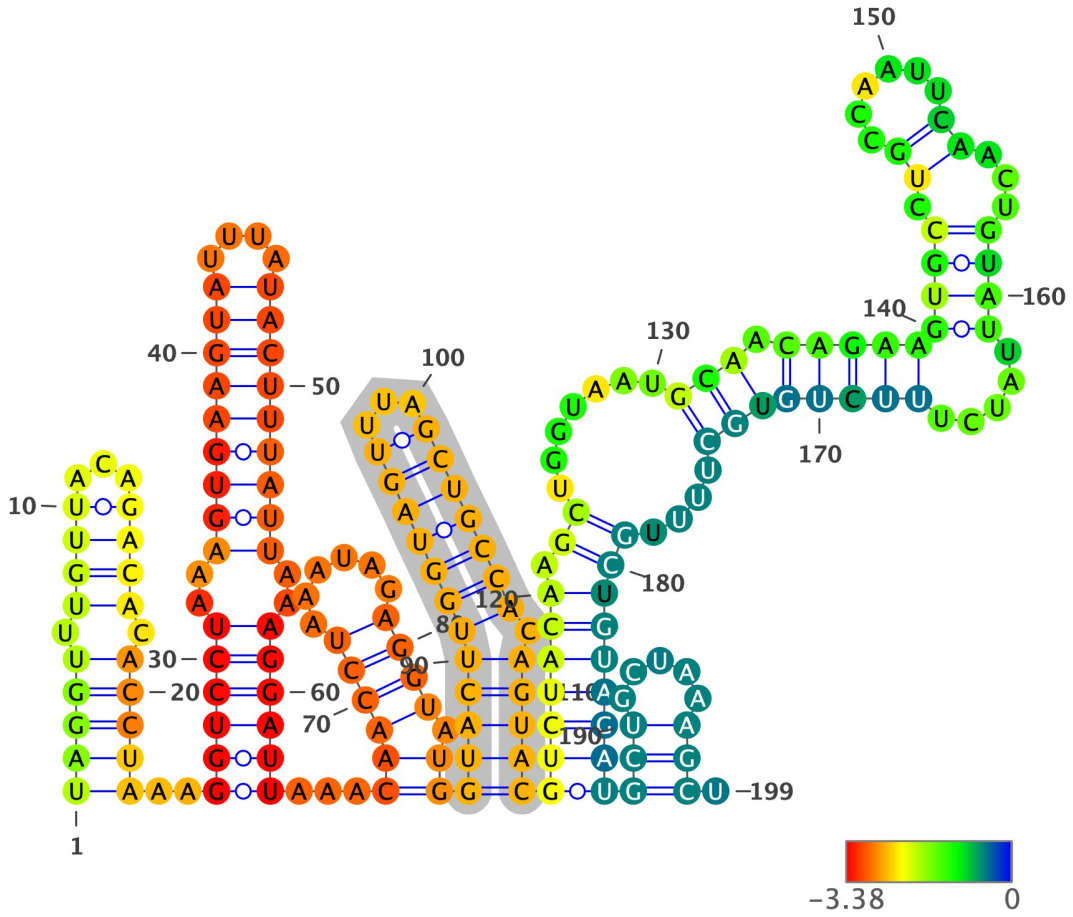
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 230 from nt 12989 to 13016 (nt 86 to 113)

```
5'-GUACUUGGUAGUUUAGCUGCCACAGUAC-3'
5'-(((((((((((...)))))))).)))))-3'
Motif MFE = -12.5; z-score = -4.39; 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 = -3.95; 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(+)

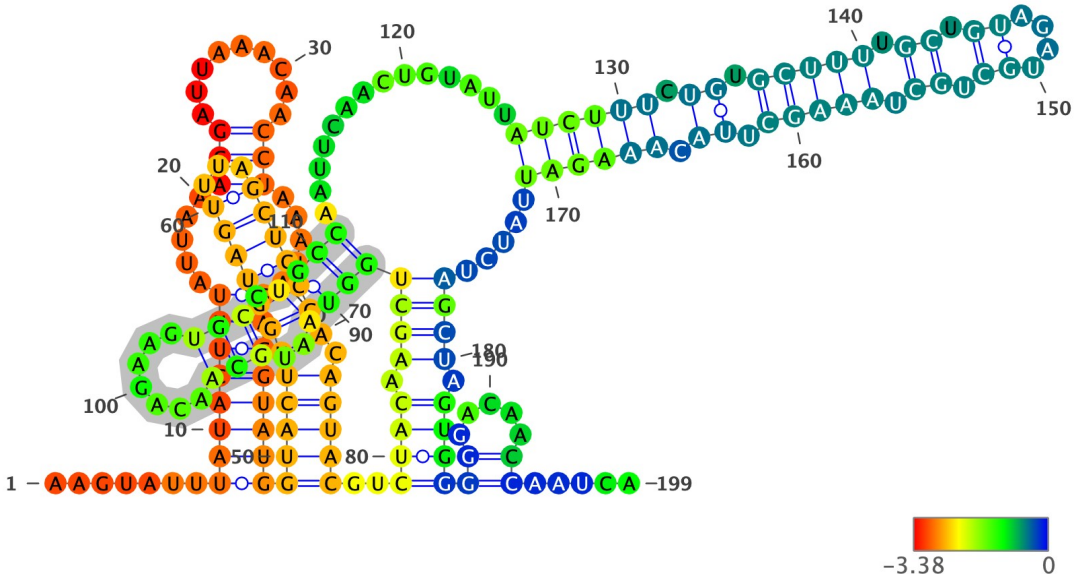
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 231 from nt 13028 to 13051 (nt 88 to 111)

```
5'-GGUAAUGCAACAGAAGUGCCUGCC-3'
5'-(((....(.........)...)))-3'
Motif MFE = -3.6; z-score = -0.51; 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 12941 to 13139 (motif highlighted in silver):

```
5'-AAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCC
AAUUCAACUGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCA-3
5'-.......(((((((((.....((((.........)))).....)))))))))((((((((((((...)))))))).))))))..((((.(((((((((..(((.......))).))))
.............((((((.((.((((((.((.((....)).)).)).)))))).)).)))))).....)))).)))))((.....)).....-3'
MFE = -45.6; z-score = -1.72; ED = 31.67
```

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(+)

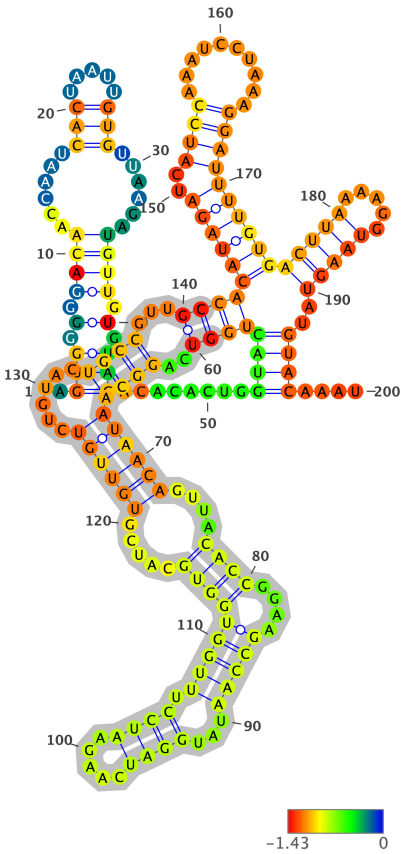
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 232 from nt 13179 to 13261 (nt 59 to 141)

```
5'-GUCAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGC-3'
5'-((......((.(((.............................................))).)).............))-3'
Motif MFE = -22.4; z-score = -0.95; ED = 19.19
```



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 13121 to 13320 (motif highlighted in silver):

```
5'-AGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAUGUUGUGUACACACACUGGUACUGGUCAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGU
GGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAU-3
5'-.(((.(.((((......(((.....)))......)))).).))).........((((((((..((((((((((....((((....(((((...((((.....)))).)))))
))))).....))))))......))))...))))((((((..((((..........))))))))))(((((.....)))))..))))....-3'
MFE = -44.2; z-score = -0.89; ED = 39.37
```

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(+)

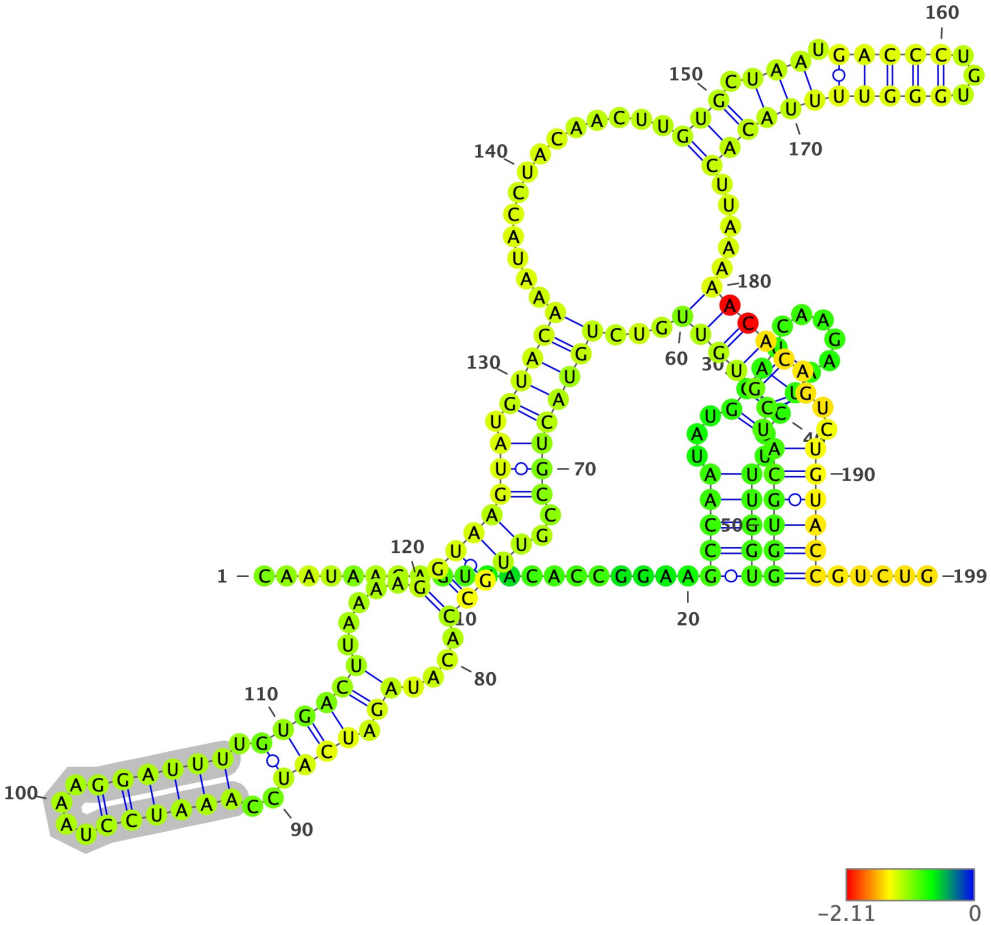
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 233 from nt 13276 to 13291 (nt 92 to 107)

```
5'-AAAUCCUAAAGGAUUU-3'
5'-((((((....))))))-3'
Motif MFE = -3.5; z-score = -6.84; 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 13185 to 13383 (motif highlighted in silver):

```
5'-CAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUG
ACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUG-3
5'-....................(((((...((((.....)))).)))))((((((.((((((...((((((((..(((((....((.((((..((((((....)))))).)))
)))).....)))))))).)))))..............(((.(((.(((((...)))))))))))).....)))))).)..))))))).....-3'
MFE = -43.2; z-score = -0.56; ED = 40.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

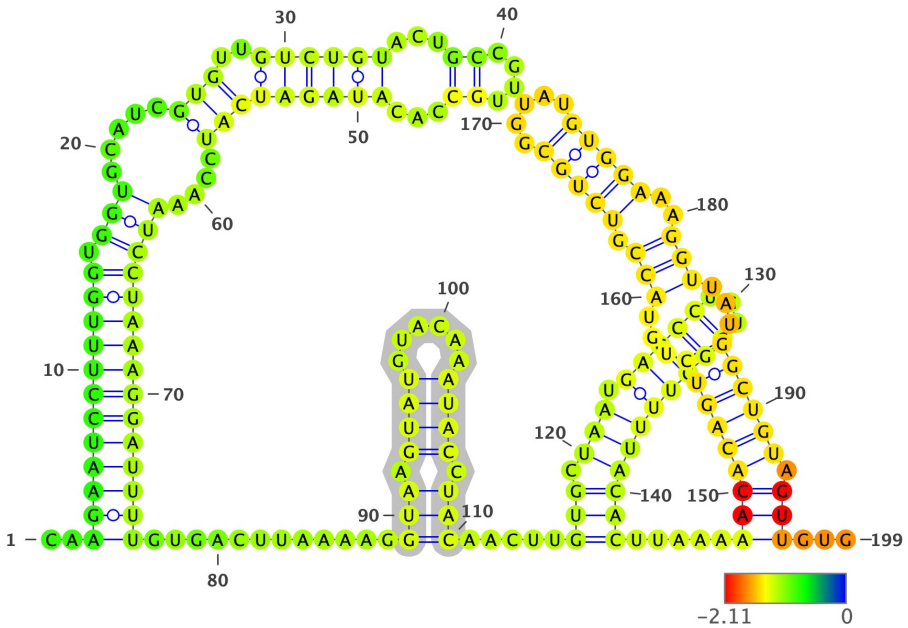
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 234 from nt 13305 to 13326 (nt 89 to 110)

```
5'-GUAAGUAUGUACAAAUACCUAC-3'
5'-(((.((((......)))).)))-3'
Motif MFE = -3.0; z-score = -2.6; ED = 1.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13217 to 13415 (motif highlighted in silver):

```
5'-CAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACA
ACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUG-3
5'-..(((((((((((.(((.....(((..((((((...((....))...)))))))))....))))))))))))))).............(((.((((......)))).))).
....(((.(((.(((((...)))))))))))).....(((((((((...(((.(((((.....)))))..)))...)))))).)))...-3'
MFE = -49.6; z-score = -1.38; ED = 57.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

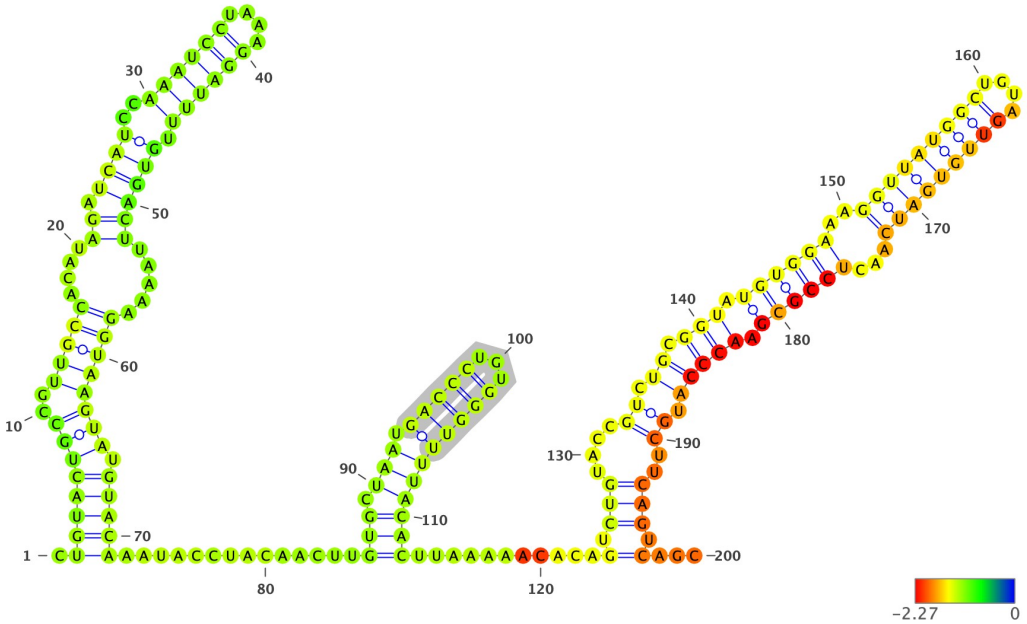
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 235 from nt 13340 to 13352 (nt 94 to 106)

```
5'-GACCCUGUGGGUU-3'
5'-(((((...)))))-3'
Motif MFE = -4.2; z-score = -3.94; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13247 to 13446 (motif highlighted in silver):

```
5'-CUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACA
CUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGC-3
5'-.((((((((..(((((....((.((((..((((((....)))))).))))))).....)))))))).))))).............(((.(((.(((((...)))))))))
)...........(.(((....((.((.(((.((((((..(((((((((....)))))))))...)))))).))))).))..))).)...-3'
MFE = -47.6; z-score = -0.96; ED = 55.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

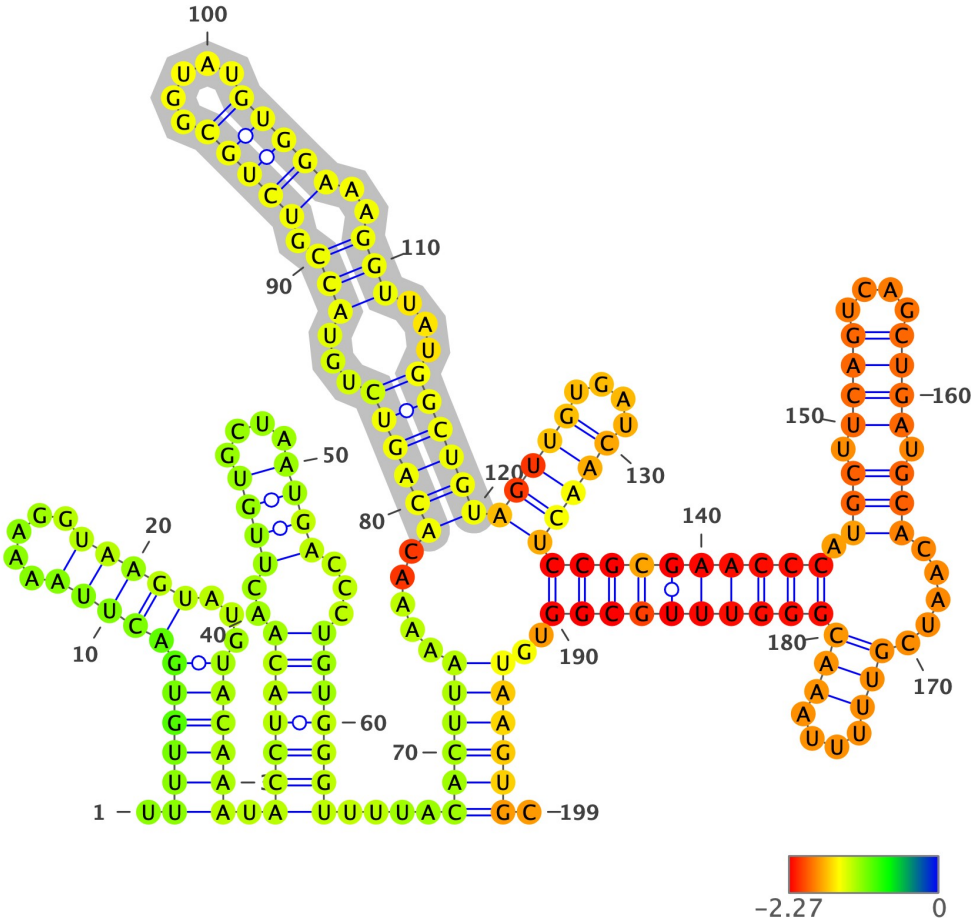
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 236 from nt 13367 to 13408 (nt 79 to 120)

```
5'-ACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGU-3'
5'-(((((....(((.(((((.....)))))..)))....)))))-3'
Motif MFE = -14.5; z-score = -2.41; ED = 2.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13289 to 13487 (motif highlighted in silver):

```
5'-UUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGU
UAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGC-3
5'-.((((((((((.....)))))...)))))).(((((((..((((....))))...))))))).....((((((.....((((((...(((.(((((.....)))))..)))
...))))))(((((....)))))((((((((((.(((.((((....)))).)))).....(((....)))))))))))))..)))))).-3'
MFE = -57.6; z-score = -2.51; ED = 40.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 180--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 180 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

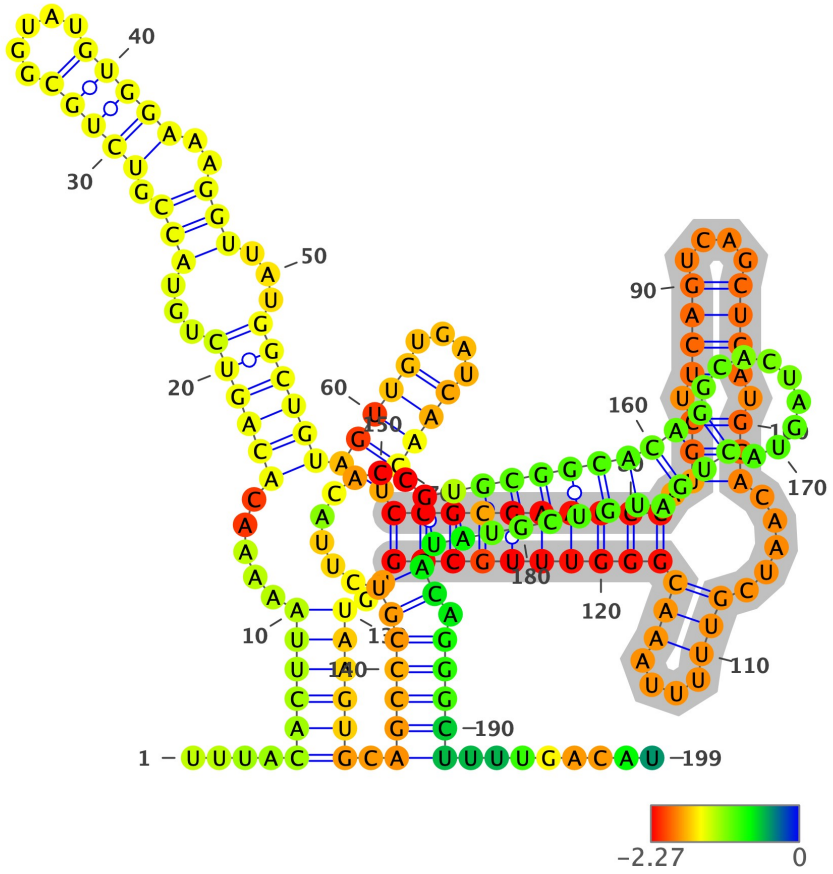
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 195--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 237 from nt 13423 to 13478 (nt 72 to 127)

```
5'-CCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGG-3'
5'-(((.((((((..((.((((....)))).)).................)))))).)))-3'
Motif MFE = -22.5; z-score = -3.28; ED = 2.5
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13352 to 13550 (motif highlighted in silver):

```
5'-UUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUU
UUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAU-3
5'-....((((((.....((((((...(((.(((((.....)))))..)))...))))))(((((....)))))((((((((((.(((.((((....)))).))).....(((.
...))))))))))))..)))))).(((((((........((((((((((.........))).))))))))))).)))))........-3'
MFE = -65.5; z-score = -3.08; ED = 15.86
```

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 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(+)

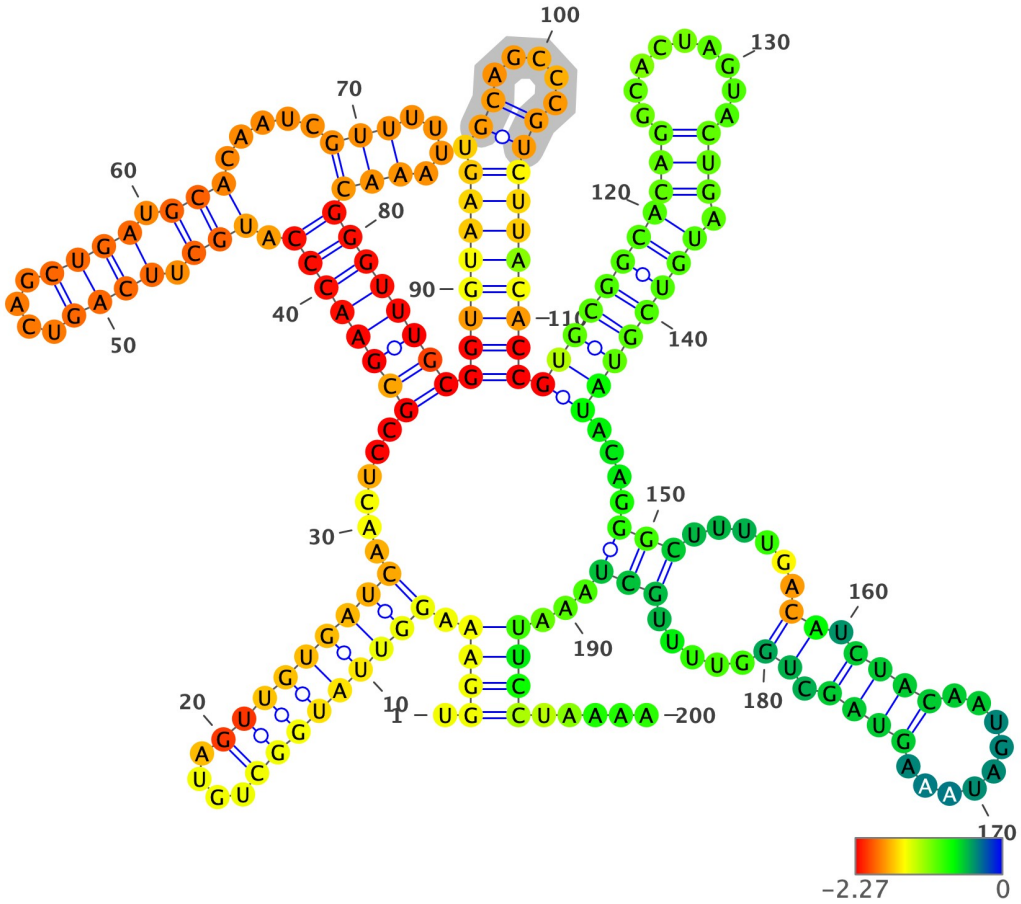
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 238 from nt 13486 to 13494 (nt 96 to 104)

```
5'-GCAGCCCGU-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.19; 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 13391 to 13590 (motif highlighted in silver):

```
5'-UGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACAC
CGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAA-3
5'-.((((.(((((((((....)))))))))......((((((((.(((.((((....)))).)))).....(((....)))))))))))((((((((.((.....)))))))))
)((((((((((.........))).)))))))).....(((......((.((((.........)))).)).....)))...))))).....-3'
MFE = -58.8; z-score = -1.92; ED = 38.79
```

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 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 200--CDS, cds-YP_009724389.1, 13468-21555(+)

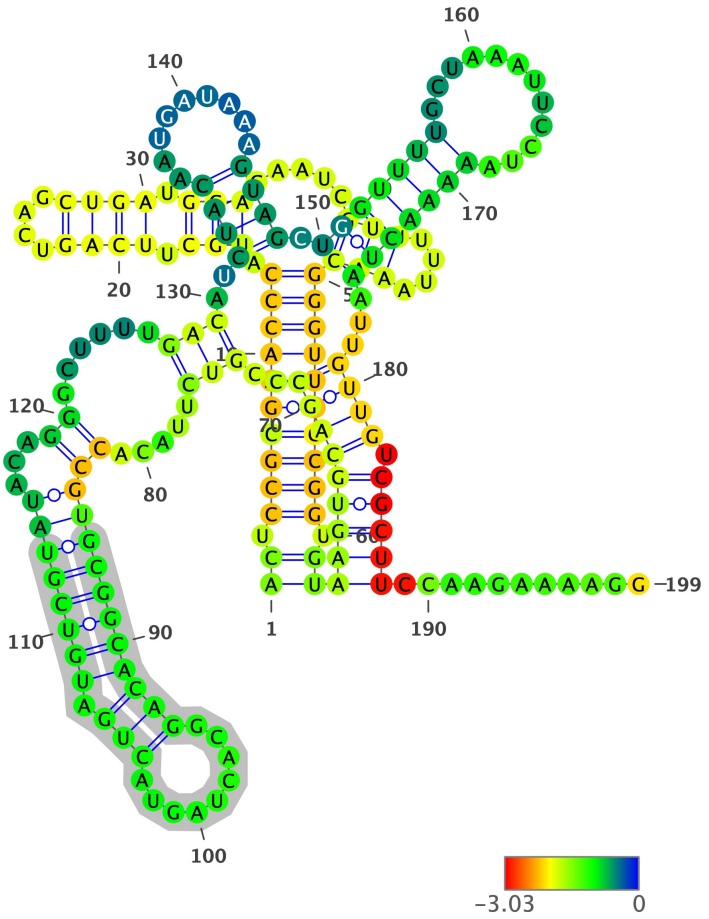
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

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 239 from nt 13505 to 13532 (nt 86 to 113)

```
5'-GCGGCACAGGCACUAGUACUGAUGUCGU-3'
5'-((....(((.........)))).....))-3'
Motif MFE = -9.2; z-score = -1.78; ED = 1.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13420 to 13618 (motif highlighted in silver):

```
5'-ACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUC
GUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGG-3
5'-((.(((((((((((.(((.((((....)))).))).....(((....)))))))))))))).))(((((((((..(((.....(((((((((((((.........))).))))
))))...))......)))..((((.........)))).(((((((.............)))))))...)))).)))))...........-3'
MFE = -52.5; z-score = -1.33; ED = 45.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 49--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 49 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

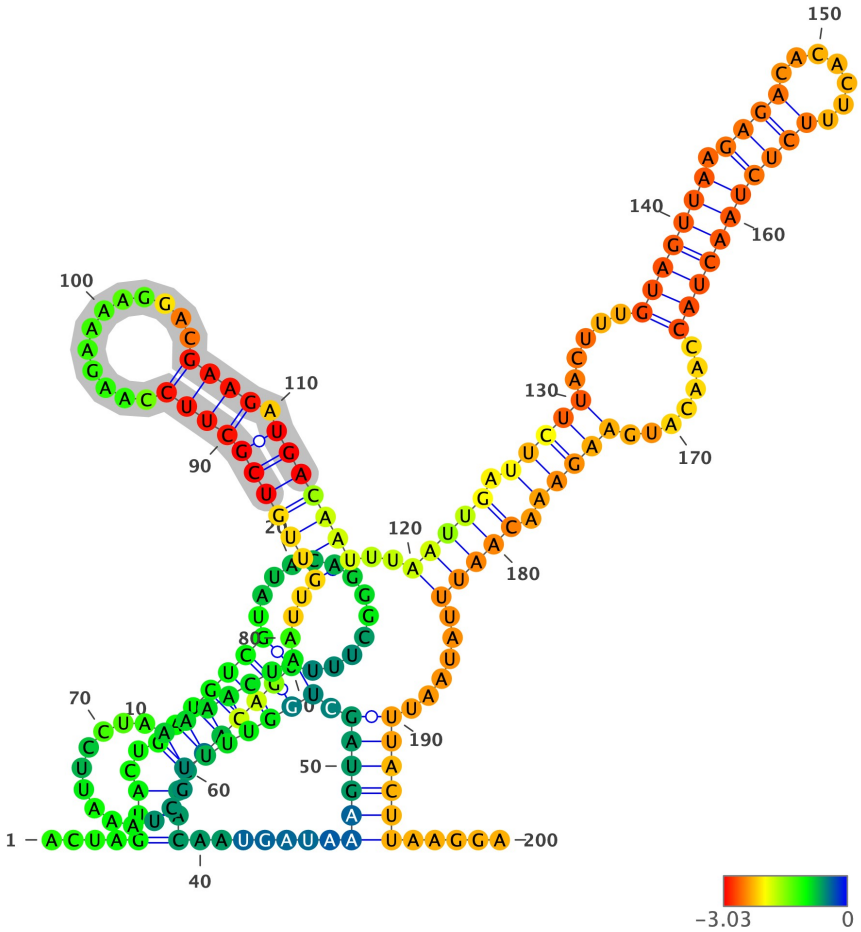
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 64--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 240 from nt 13602 to 13628 (nt 87 to 113)

```
5'-UCGCUUCCAAGAAAAGGACGAAGAUGA-3'
5'-(((((((............)))).)))-3'
Motif MFE = -3.0; z-score = -0.75; ED = 5.64
```



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 13516 to 13715 (motif highlighted in silver):

```
5'-ACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAU
GACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGA-3
5'-....(((..(((((((.............))))))))).......((((((.(((((((.............)))))))...((((((((((((.............)))).)
))))))..(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))......))))))).....-3'
MFE = -37.5; z-score = -1.75; ED = 32.0
```

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(+)

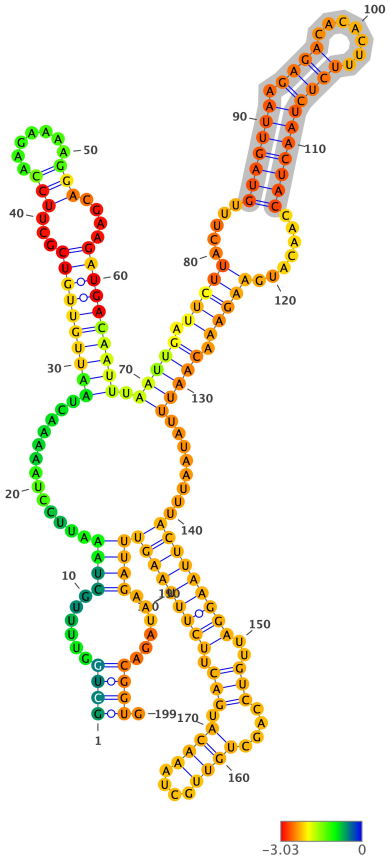
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 241 from nt 13651 to 13680 (nt 85 to 114)

```
5'-GUAGUUAAGAGACACACUUUCUCUAACUAC-3'
5'-(((((((.((((.......)))))))))))-3'
Motif MFE = -9.4; z-score = -3.6; 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 13567 to 13765 (motif highlighted in silver):

```
5'-GCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAUGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAAC
UACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUG-3
5'-((((......((((.............((((((((((...(((.......)))....)))))))))).(((((.(((((.....(((((((.((((.......))))))))
)))).......))))).)))))........(((((((((..(((....((((....)))).))).))))))))))))).....)))).-3'
MFE = -42.4; z-score = -2.67; 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_gp01, 266-21555(+)

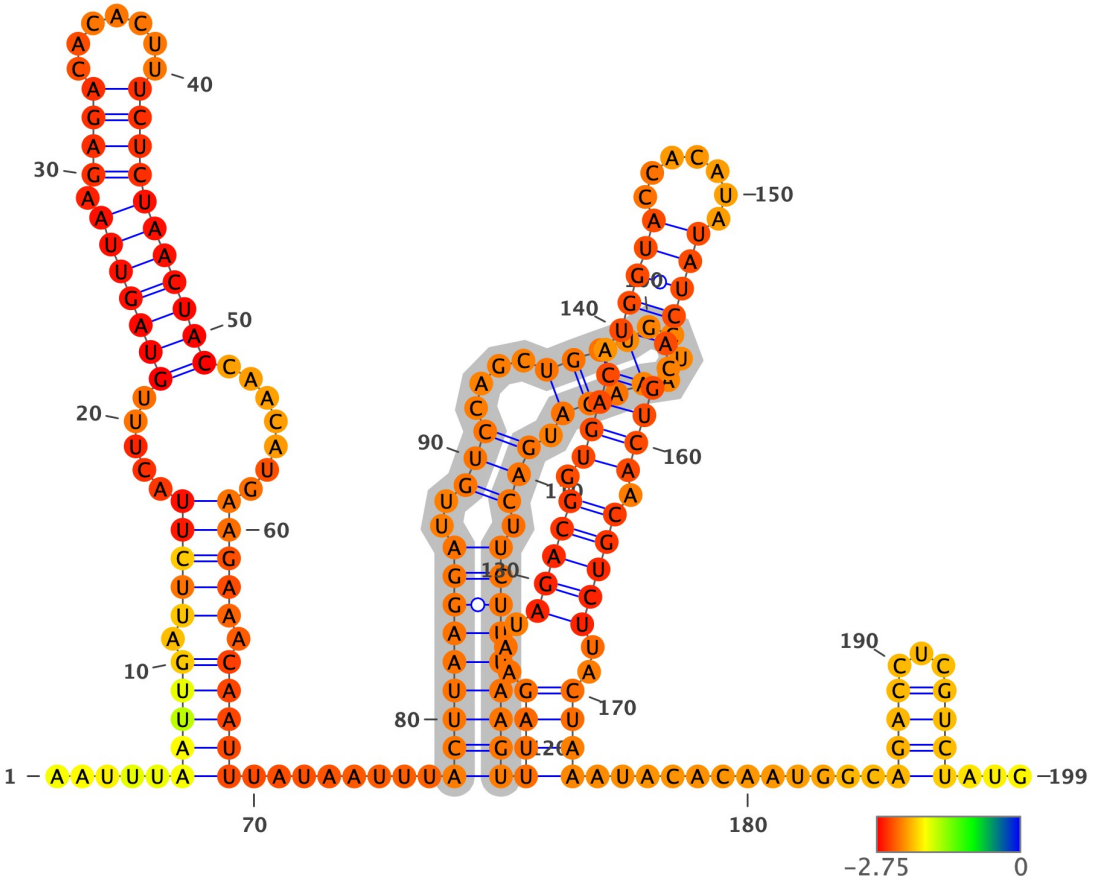
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 242 from nt 13707 to 13750 (nt 78 to 121)

```
5'-ACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGU-3'
5'-(((((((((..(((....(((......))).))).)))))))))-3'
Motif MFE = -11.0; z-score = -2.58; 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 = -3.8; 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(+)

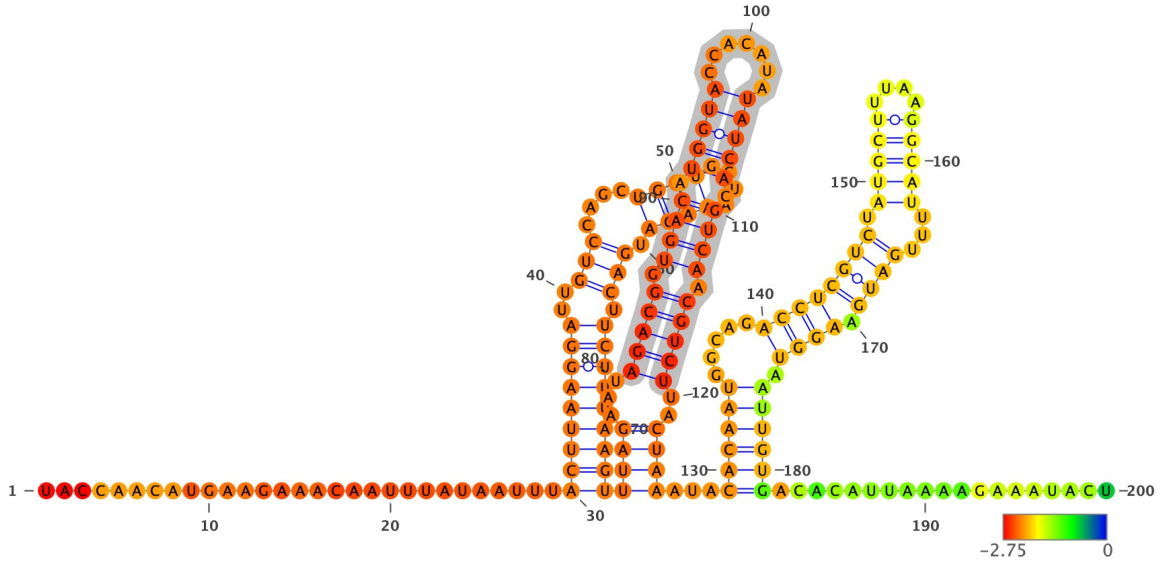
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 243 from nt 13758 to 13796 (nt 81 to 119)

```
5'-AGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCU-3'
5'-(((((.((((.(((((.......))))).)))).)))))-3'
Motif MFE = -13.3; z-score = -3.39; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13678 to 13877 (motif highlighted in silver):

```
5'-UACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGU
CAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUGAAGGUAAUUGUGACACAUUAAAAGAAAUACU-3
5'-...............................(((((((((..(((....((((....)))).))).)))))))))((((...(((((.((((.(((((.......)))))).))
)).)))))..)))))...((((((.....((((((((.(((((....)))))...)))))).)))).)))))).....................-3'
MFE = -42.5; z-score = -2.32; ED = 32.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

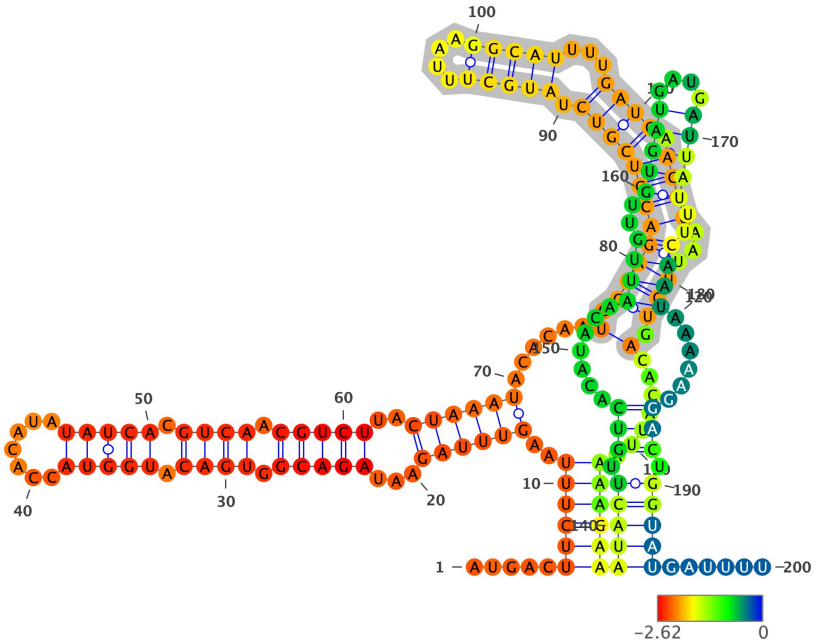
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 244 from nt 13811 to 13859 (nt 76 to 124)

```
5'-UGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUGAAGGUAAUUGUGA-3'
5'-(.(((.((((((((.((((......))))...)))).))))...))).)-3'
Motif MFE = -13.4; z-score = -2.27; ED = 3.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13736 to 13935 (motif highlighted in silver):

```
5'-AUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUG
AAGGUAAUUGUGACACAUUAAAAGAAAUACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAUUUU-3
5'-.....((((((..((((((...(((((.((((.(((((.......)))))).)))).)))))..))))))......(.(((((((((((.(((((....)))))...))))
.))))..)))).).......))))))(((((.(((.......((((..(((((....)))))..)))).....))).)))))......-3'
MFE = -44.6; z-score = -3.0; ED = 34.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

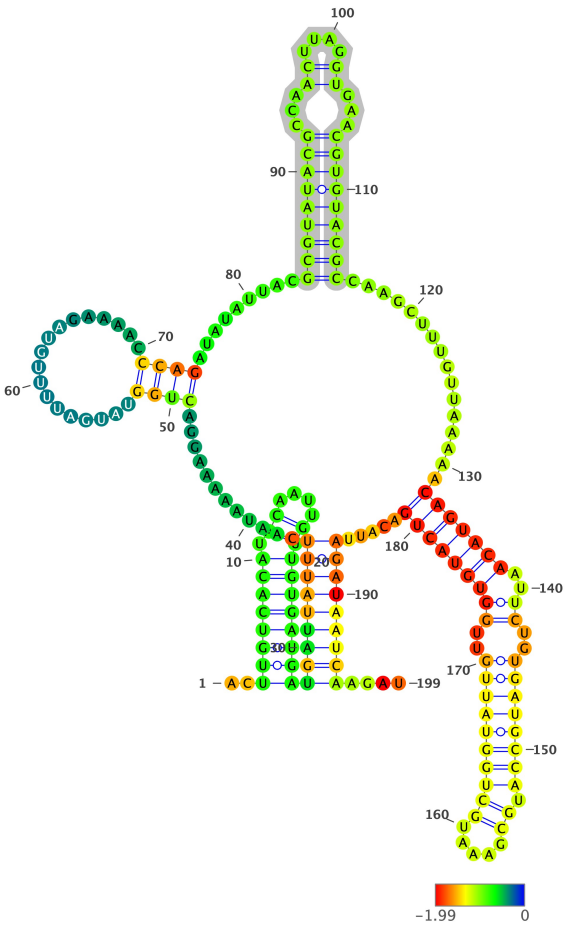
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 245 from nt 13958 to 13989 (nt 84 to 115)

```
5'-GCGUAUACGCCAACUUAGGUGAACGUGUACGC-3'
5'-((((((((((...((....))...)))))))))-3'
Motif MFE = -13.3; z-score = -3.08; 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 = -1.79; 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(+)

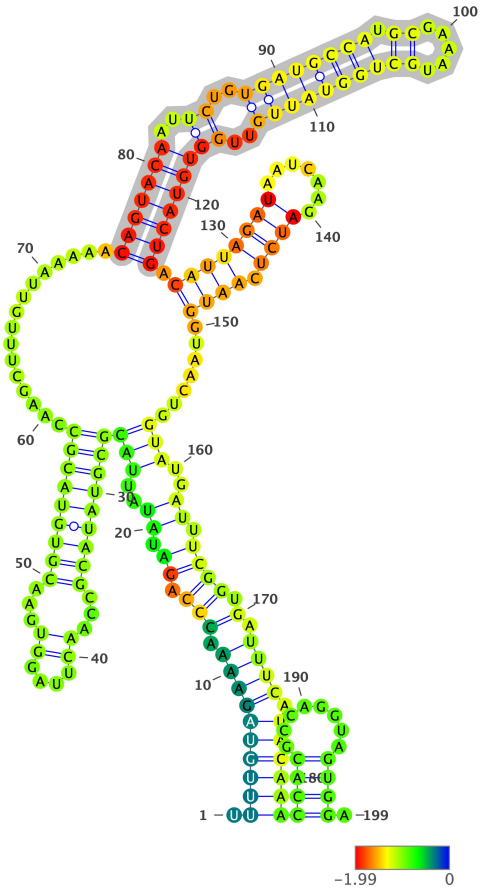
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 246 from nt 14006 to 14055 (nt 75 to 124)

```
5'-CAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUG-3'
5'-(((((((.......(((((((.((.....)))))))))).....)))))))-3'
Motif MFE = -16.7; z-score = -3.38; 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 = -2.05; ED = 24.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

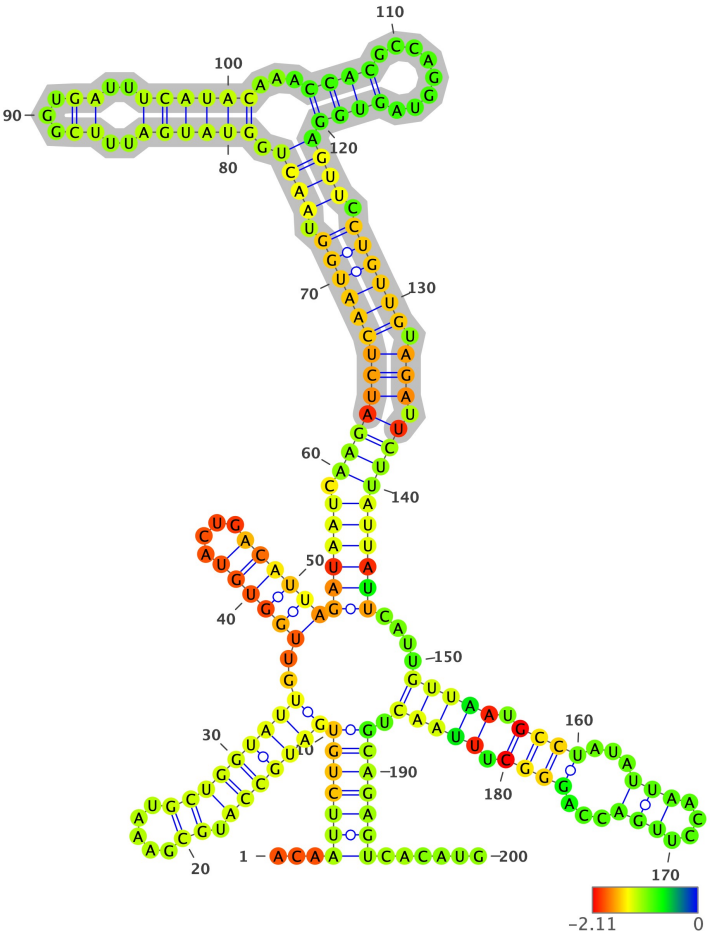
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 247 from nt 14072 to 14146 (nt 63 to 137)

```
5'-AUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUU-3'
5'-((((((((((.(((..(((((((..((...))..))))))...................))).)))))).))).)-3'
Motif MFE = -20.5; z-score = -2.47; 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 = -1.98; ED = 36.9
```

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(+)

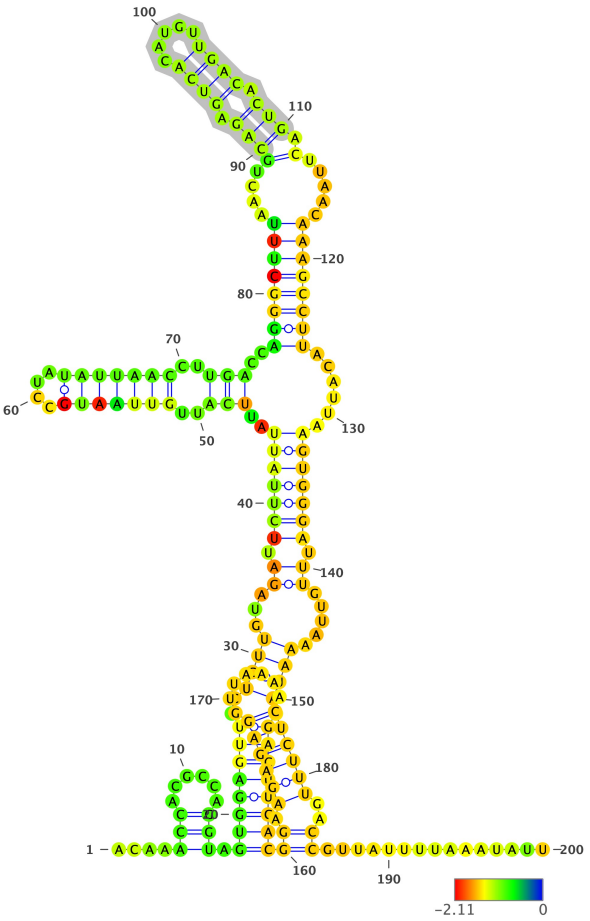
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14198 to 14218 (nt 90 to 110)

```
5'-CAGAGUCACAUGUUGACACUG-3'
5'-(((.((((.....)))).)))-3'
Motif MFE = -4.5; z-score = -2.19; ED = 0.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14109 to 14308 (motif highlighted in silver):

```
5'-ACAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGA
CUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUU-3
5'-....(((......))).((((((((..((((...((.(((((((..(((..(((((((....)))))))..)))..((((((((....((((.((((.....)))).))).
).....))))))))......)))))))).))).....)))).))))))))((.((((((.......))))))..)).................-3'
MFE = -43.0; z-score = -1.24; 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(+)

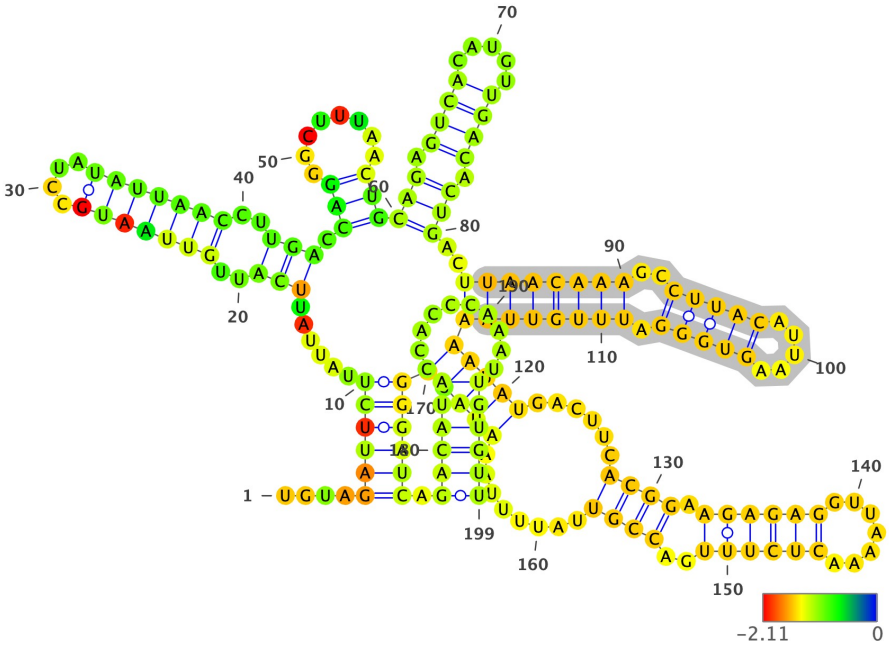
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 249 from nt 14222 to 14253 (nt 84 to 115)

```
5'-UAACAAAGCCUUACAUUAAGUGGGAUUUGUUA-3'
5'-(((((((..(((((.....)))))).)))))))-3'
Motif MFE = -7.5; z-score = -2.73; ED = 4.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14139 to 14337 (motif highlighted in silver):

```
5'-UGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUU
GUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUU-3
5'-....((((((.....(((..(((((((....)))))))..))).(((........)))((((.((((.....)))).))).))..((((((((..(((((.....)))))).)))
)))))((((.....((((.((((((.......))))))..)))).......)))))))))).((((((..........))))))-3'
MFE = -41.7; z-score = -1.56; ED = 31.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

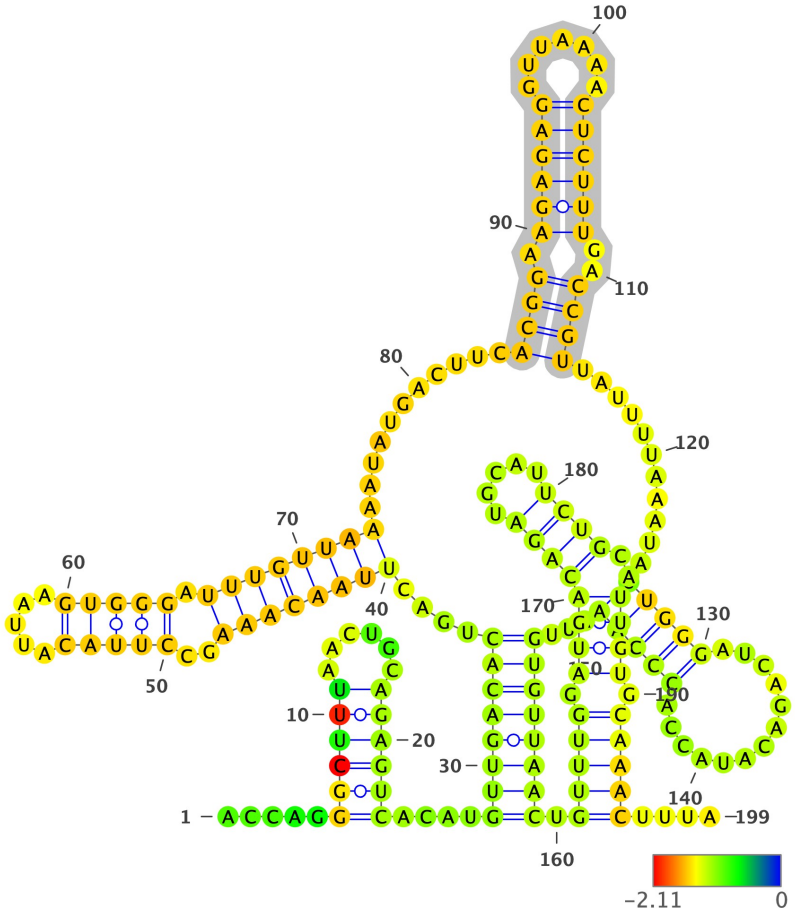
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 250 from nt 14266 to 14295 (nt 85 to 114)

```
5'-ACGGAAGAGAGGUUAAAACUCUUUGACCGU-3'
5'-((((.((((((.......))))))..))))-3'
Motif MFE = -10.5; z-score = -3.97; ED = 0.72
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14182 to 14380 (motif highlighted in silver):

```
5'-ACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGAC
CGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUA-3
5'-.....((((((......))))))....((((((((....((((((((..(((((.....))))).))))))))...........((((.((((((.......))))))..)
)))...........(((((.............)))))...)))))))).(((((.((((((((.....))))..)))).)))))....-3'
MFE = -47.5; z-score = -1.95; 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(+)

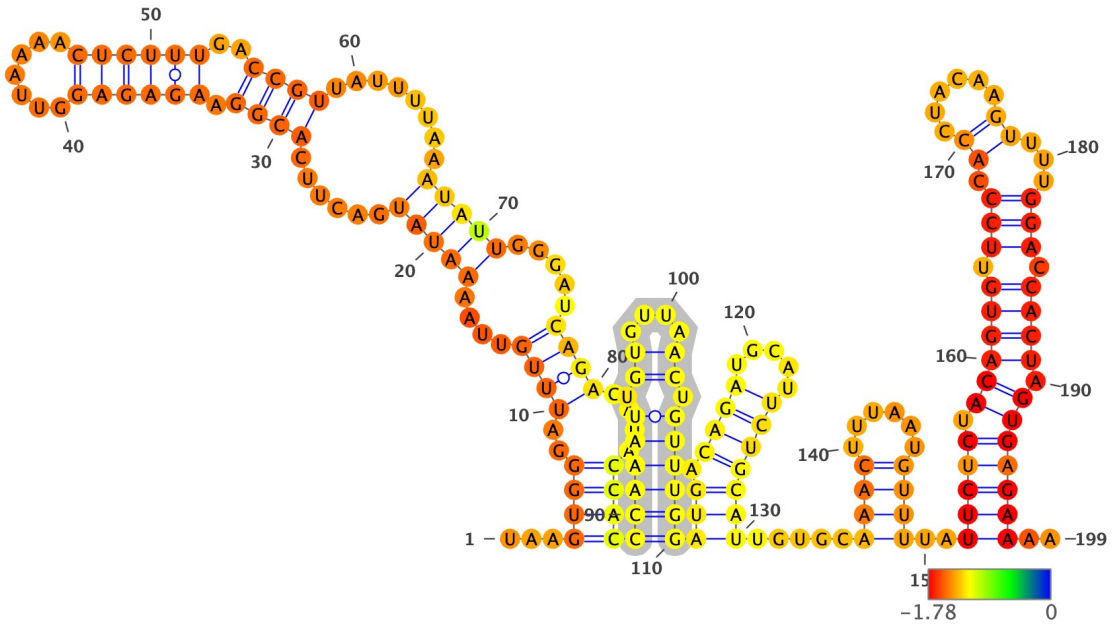
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 251 from nt 14326 to 14347 (nt 89 to 110)

```
5'-CCAAAUUGUGUUAACUGUUUGG-3'
5'-((((((.((....)).)))))))-3'
Motif MFE = -5.6; z-score = -3.09; 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 = -1.18; 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(+)

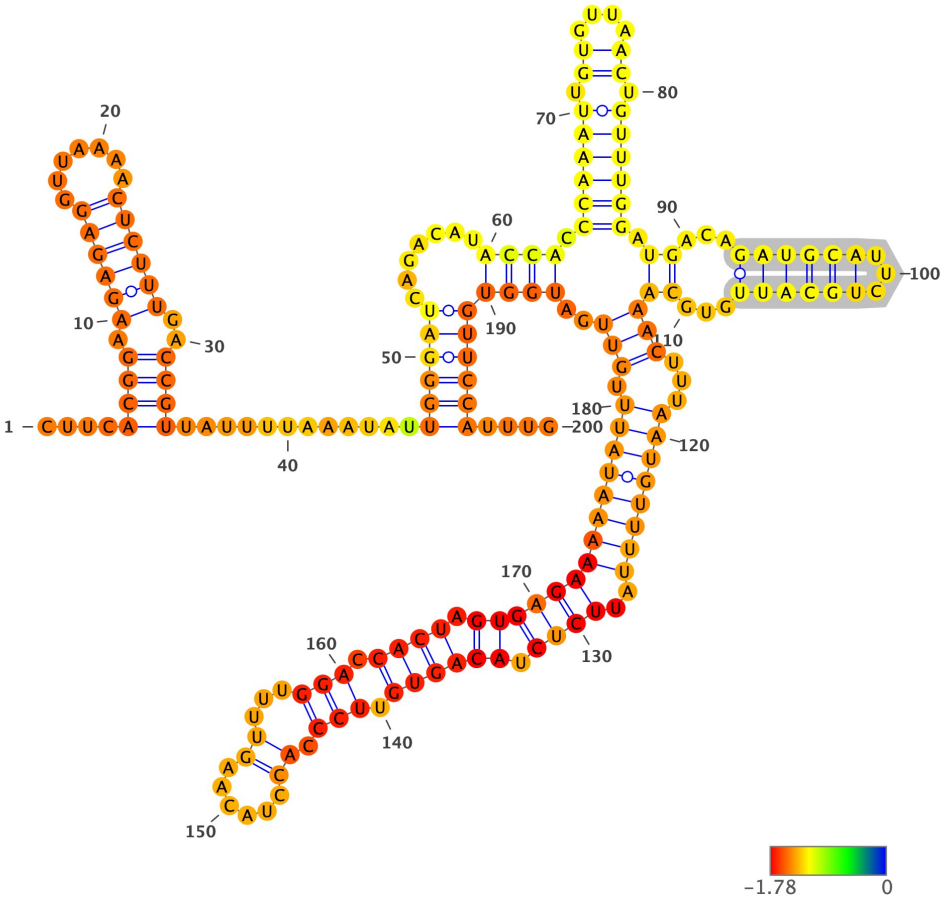
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 252 from nt 14354 to 14368 (nt 93 to 107)

```
5'-GAUGCAUUCUGCAUU-3'
5'-(((((.....)))))-3'
Motif MFE = -3.6; z-score = -5.02; ED = 1.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14262 to 14461 (motif highlighted in silver):

```
5'-CUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGC
AAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUG-3
5'-....((((.((((((.......))))))..))))............((((((.......((((.((((((.((....)).)))))).((...((((((...))))))...)
)(((...((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))).)))..)))))))))....-3'
MFE = -45.5; z-score = -1.5; 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(+)

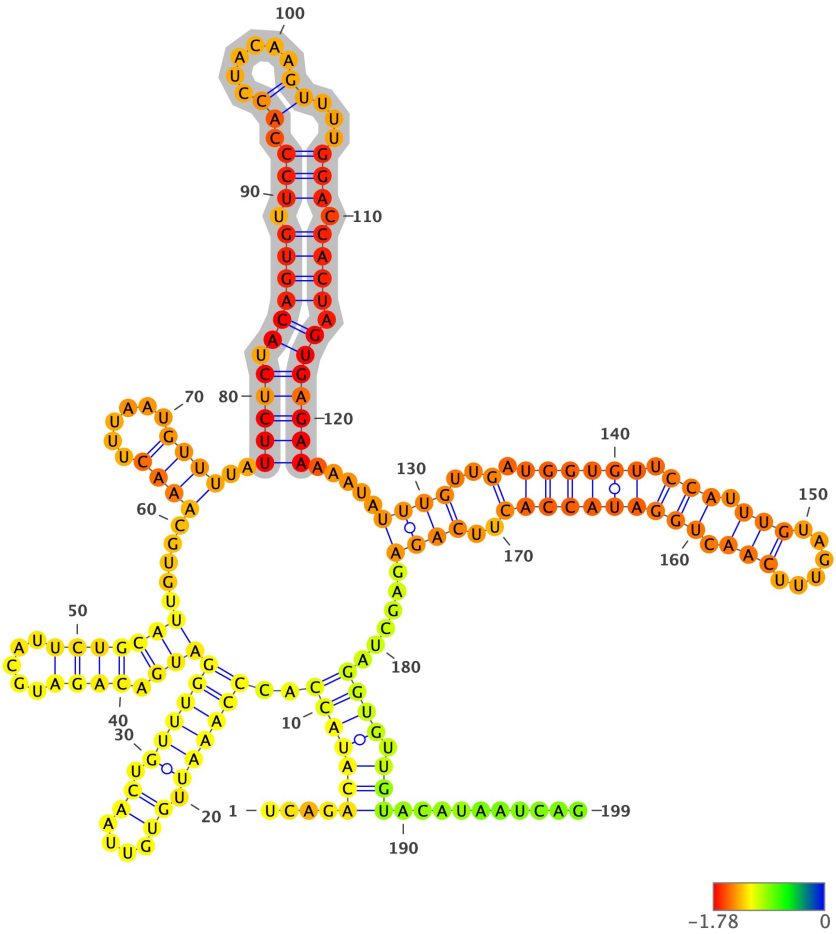
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 253 from nt 14389 to 14434 (nt 77 to 122)

```
5'-UUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAA-3'
5'-(((.(.(((((((.(((..............))).)))).))).)))-3'
Motif MFE = -11.9; z-score = -3.29; 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 14313 to 14511 (motif highlighted in silver):

```
5'-UCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACC
ACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAG-3
5'-....(((((((..(((((((.((....)).))))))(((.((((.....)))))))).....((((......))))..(((((.(((((((.(((.((......))...))).)
))).)))))))).....((((..(.(((((((.(((.(((......))).))))))))))..))))......)))).))).........-3'
MFE = -46.8; z-score = -1.8; ED = 35.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

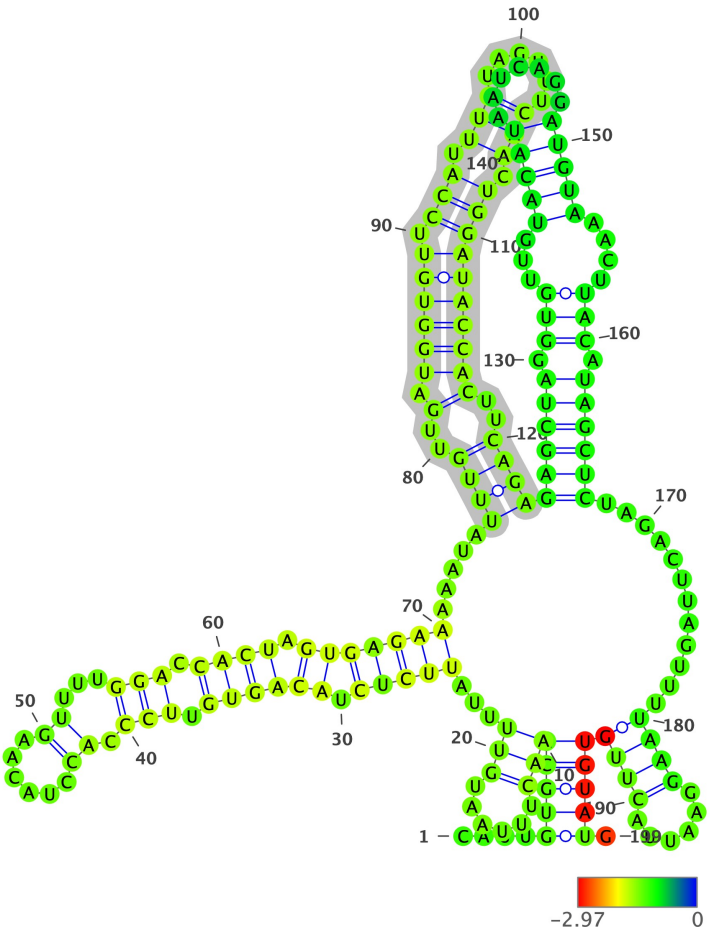
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14440 to 14487 (nt 76 to 123)

```
5'-UUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGA-3'
5'-((((..(.(((((((.(((.(((......))).))))))))))..))))-3'
Motif MFE = -13.8; z-score = -3.2; ED = 4.67
```



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 14365 to 14563 (motif highlighted in silver):

```
5'-CAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGA
UACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUG-3
5'-....((((((((......)))...(((((.((((((.(((.((......))...))).)))).)))))))).....((((..(.((((((.(((.(((......))).))))
))))))..))))((((((.(((...(((((.......)))))....))).))))))............((((......)))))))))).-3'
MFE = -44.9; z-score = -1.8; ED = 22.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

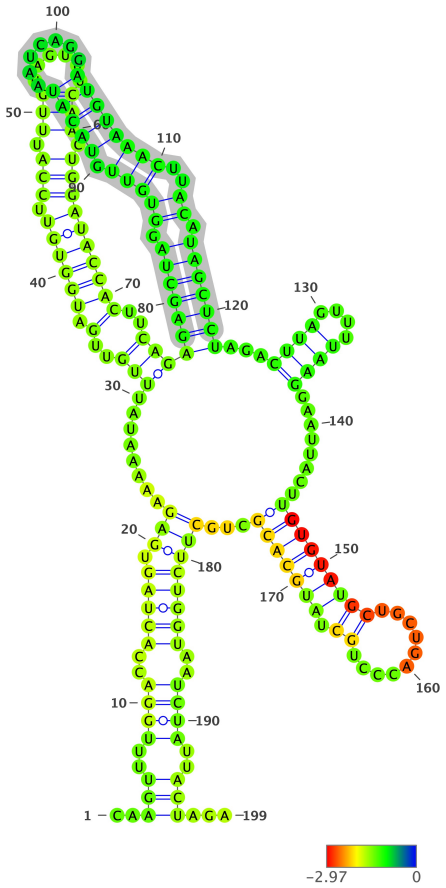
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 255 from nt 14488 to 14531 (nt 78 to 121)

```
5'-GAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUC-3'
5'-((((((.(((((.................)))..)).))))))-3'
Motif MFE = -11.8; z-score = -2.74; ED = 2.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14411 to 14609 (motif highlighted in silver):

```
5'-CAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACU
UACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGA-3
5'-..(((..((((..(((((.(((.........(((..(.((((((.(((.(((......))).))))))))))..)))(((((((.(((((.(((((.......))))))))).
.)).)))))))...((((....))))........(((((((((..........)).)))))))...))))))))..))))..)))...-3'
MFE = -47.2; z-score = -1.36; ED = 47.05
```

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(+)

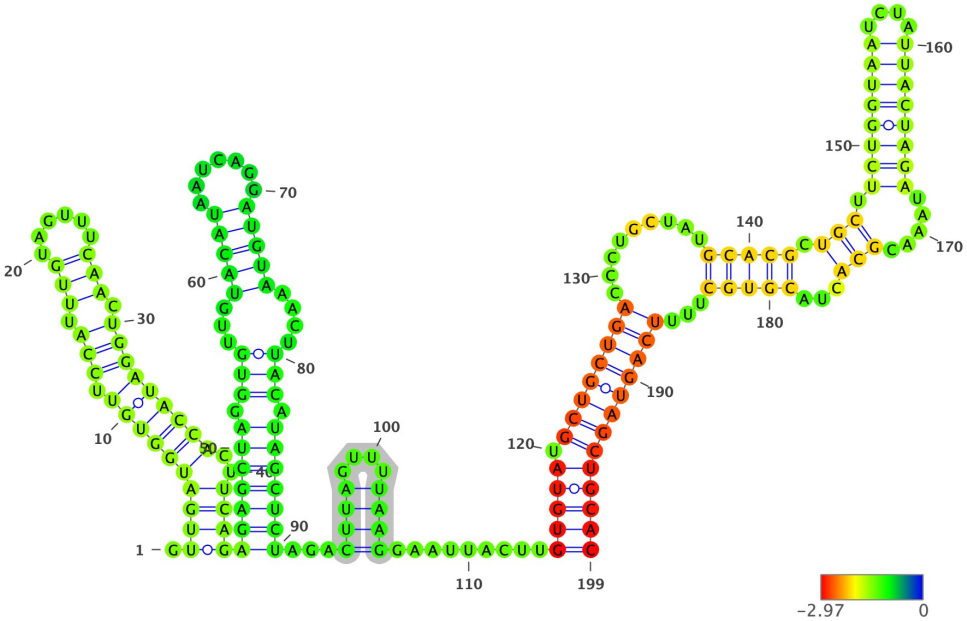
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14536 to 14547 (nt 94 to 105)

```
5'-CUUAGUUUUAAG-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = 0.1; 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 = -3.59; 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(+)

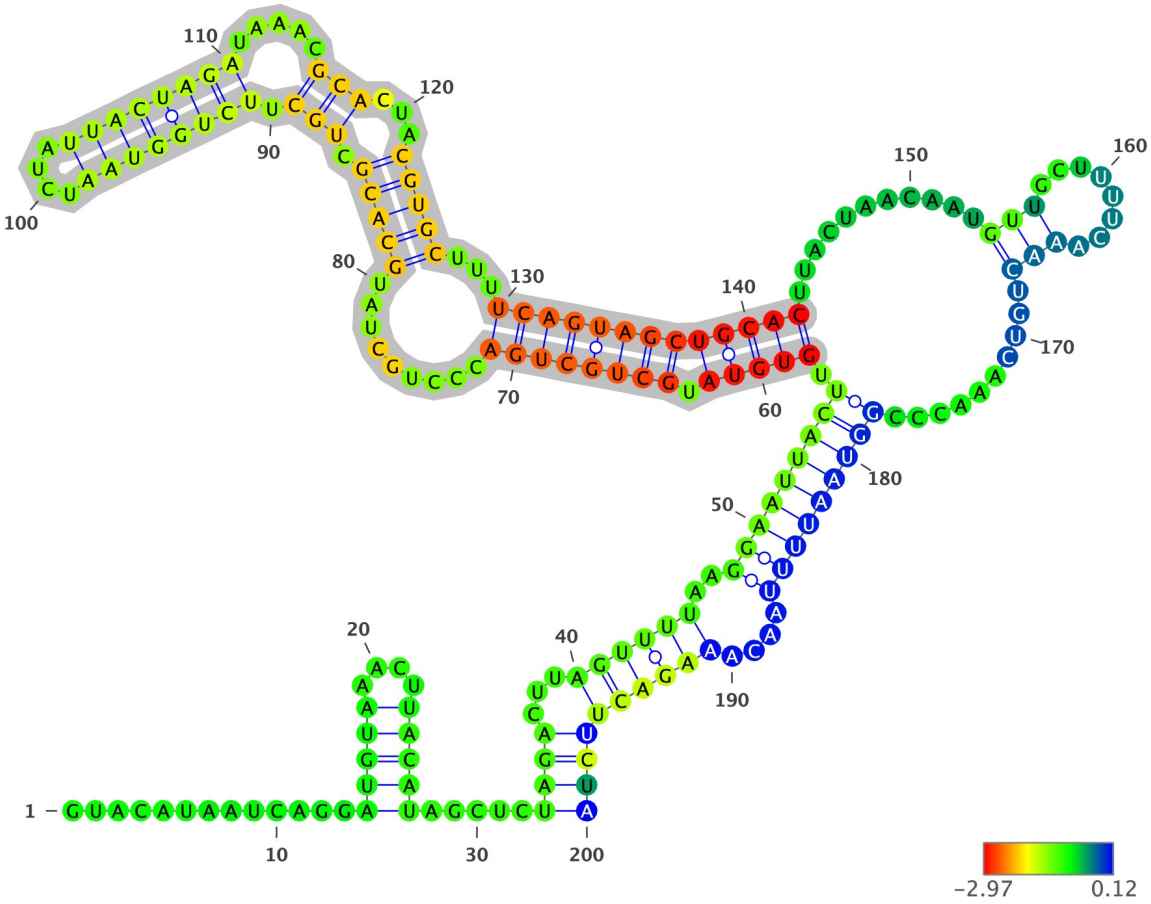
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 257 from nt 14557 to 14641 (nt 58 to 142)

```
5'-GUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAGAUAAACGCACUACGUGCUUUUCAGUAGCUGCAC-3'
5'-(((((.(((((((((.........(((((.(((.((((((((....))))))))).....)))...)))))...))))))))))))-3'
Motif MFE = -29.9; z-score = -4.33; 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 = -1.3; 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(+)

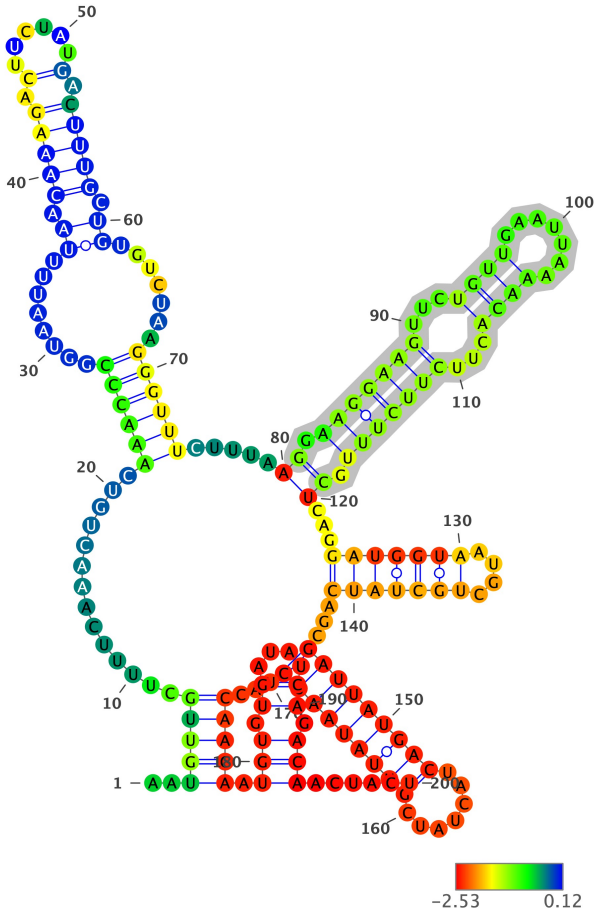
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 258 from nt 14730 to 14768 (nt 81 to 119)

```
5'-GGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGC-3'
5'-(..(((((((...((((.......))))...)))))))..)-3'
Motif MFE = -9.0; z-score = -2.03; ED = 2.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14650 to 14849 (motif highlighted in silver):

```
5'-AAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUC
UUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACU-3
5'-..(((((.............((((((........((.((((((.(......).)))))).)).......)))))).....((.(((((((...((((.......)))))...)
))))))).))...(((((((....)))))))...(((((((((.......)))))))))...)))))).(((.((....)).))).......-3'
MFE = -42.4; z-score = -1.39; ED = 33.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

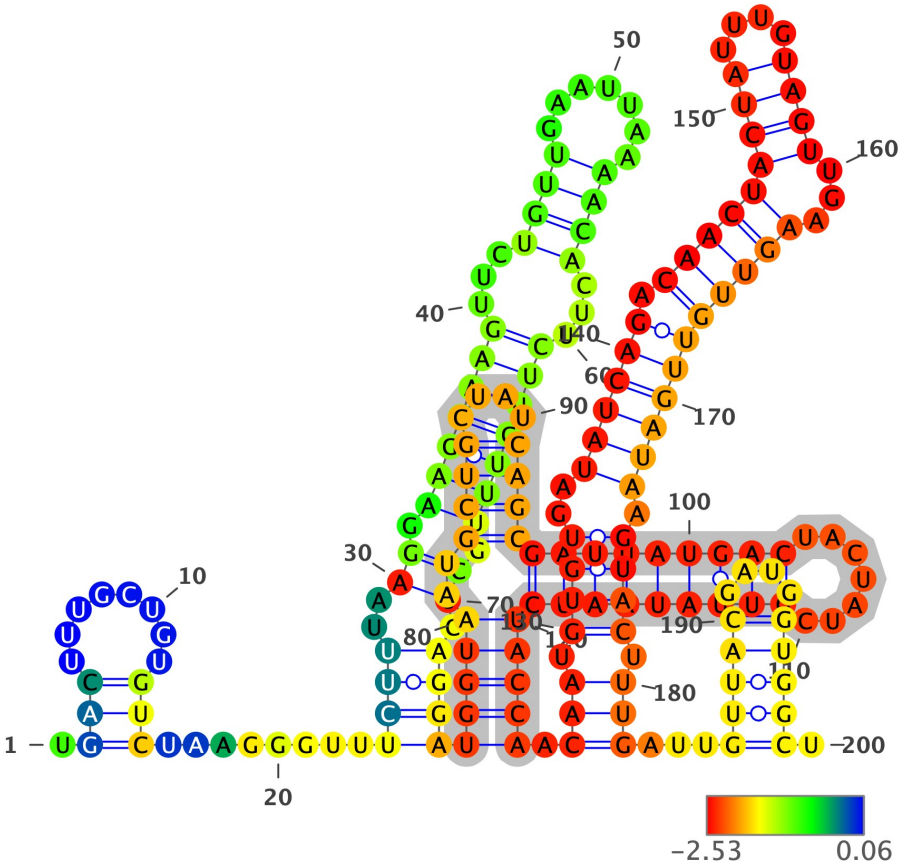
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 259 from nt 14775 to 14823 (nt 76 to 124)

```
5'-UGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCA-3'
5'-((((...((((....))))((((((((.......)))))))).))))-3'
Motif MFE = -14.4; z-score = -3.81; ED = 1.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14700 to 14899 (motif highlighted in silver):

```
5'-UGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCG
UUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCU-3
5'-.(((........)))........((((..((.(((((((...((((.......))))...)))))))).)).))))(((((..((((....))))((((((((.......)
))))))))))))).(((.((((..((((((.((((((((....))))...)))))))))))).)))).)))...(((((....))))).-3'
MFE = -46.6; z-score = -2.41; ED = 53.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

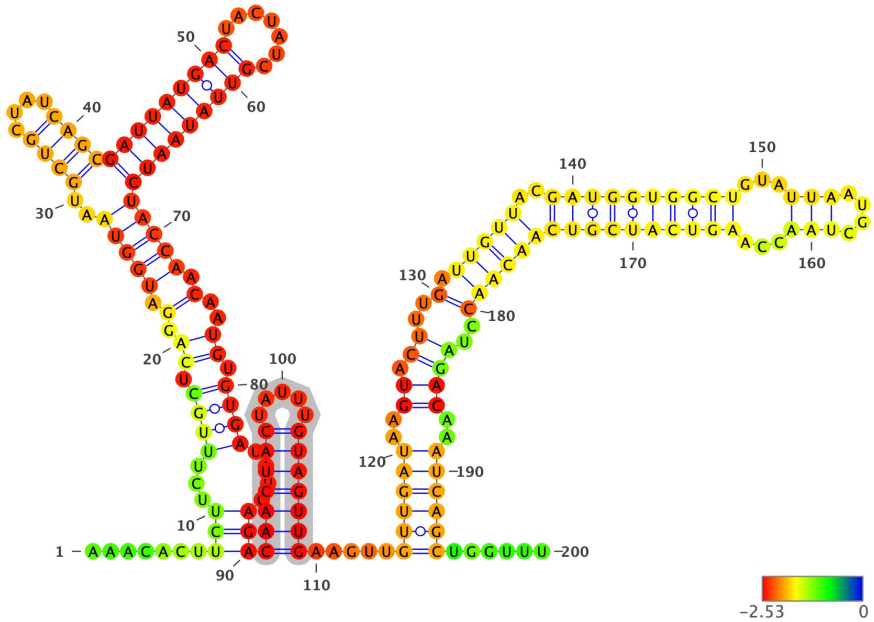
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 260 from nt 14842 to 14860 (nt 91 to 109)

```
5'-CAACUACUAUUUGUAGUUG-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.2; z-score = -6.67; ED = 0.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14752 to 14951 (motif highlighted in silver):

```
5'-AAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAA
GUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGCUGGUUU-3
5'-.......(((...((((.((.(.(((((..((((....))))((((((((.......)))))))))))))).)..)).))))....)))(((((((.....)))))))..
...((((((..((.((..(.(((((..((((((((((...(((....)))...)))))))))))))))..))))..))))))......-3'
MFE = -48.8; z-score = -2.21; ED = 41.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

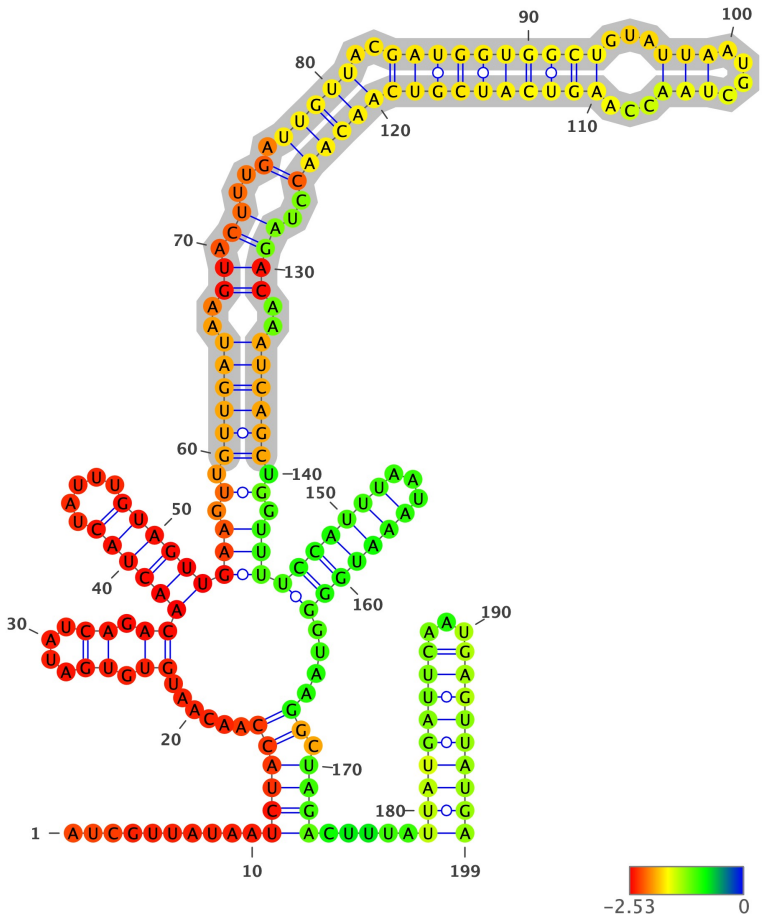
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 261 from nt 14866 to 14945 (nt 60 to 139)

```
5'-GUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGC-3'
5'-((((((...........(((((..((((((((((.................)))))))))))))))).........))))))-3'
Motif MFE = -20.6; z-score = -2.44; ED = 10.5
```



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 14807 to 15005 (motif highlighted in silver):

```
5'-AUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAG
UCAUCGUCAACAACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGA-3
5'-..........((((((......((.((....)).))((((((.....))))))(((.(.((((((..((.((..(.(((((..((((((((((...(((....)))...))
))))))))))))))..))))..)))))).).)))(((((((...)))))))....)).)))).....(((((((((...)))))))))-3'
MFE = -43.4; z-score = -1.94; ED = 32.24
```

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(+)

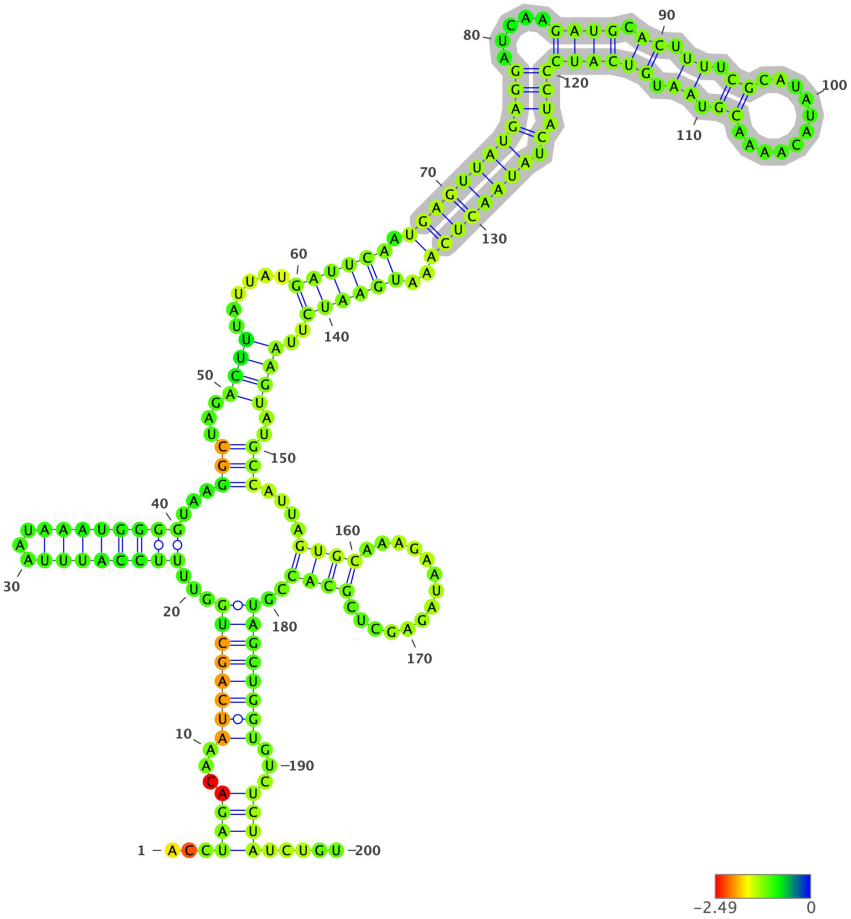
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 262 from nt 14997 to 15061 (nt 68 to 132)

```
5'-GAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUC-3'
5'-((..(((((((.....((((.((.((.((...........)).)).)))))))))).).)))..))-3'
Motif MFE = -11.1; z-score = -1.66; ED = 11.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14930 to 15129 (motif highlighted in silver):

```
5'-ACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUA
AUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGU-3
5'-...((((...((((((((...((((((((...))))))))...(((...((((......((((((.(((((((((((((.....((((.((.((.((...........)).)
).)))))))))).).))))))))..))))))..))))..)))....((((..............))))..))))))))...))))).....-3'
MFE = -44.2; z-score = -1.69; ED = 36.97
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

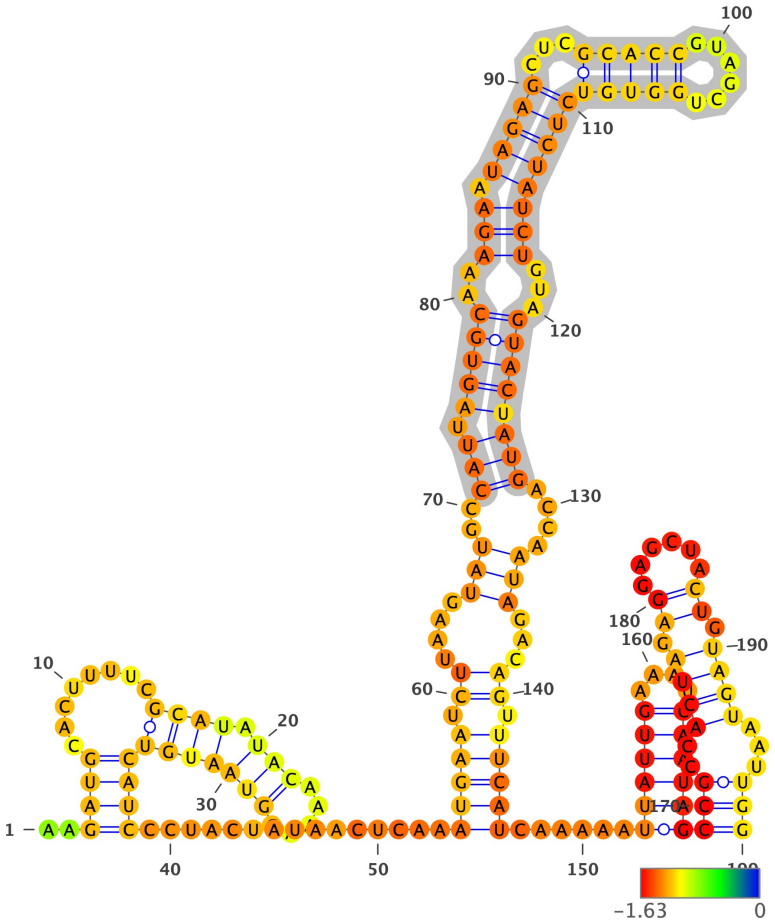
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 263 from nt 15081 to 15138 (nt 71 to 128)

```
5'-CAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUG-3'
5'-(((..((((..(((.(((((...(((((......))))))))))))...)))).)))-3'
Motif MFE = -19.4; z-score = -3.08; ED = 3.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15011 to 15209 (motif highlighted in silver):

```
5'-AAGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCU
CUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGG-3
5'-..((((........((((.(((.....)))))))))).................(((((.((....(((..(((.(((((..(((.(((((...(((((......)))))))
))))))...))))))))....)))...)).)))))......((((((....))))))(((..((((.((......)).))))...)))-3'
MFE = -34.8; z-score = -0.38; ED = 42.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

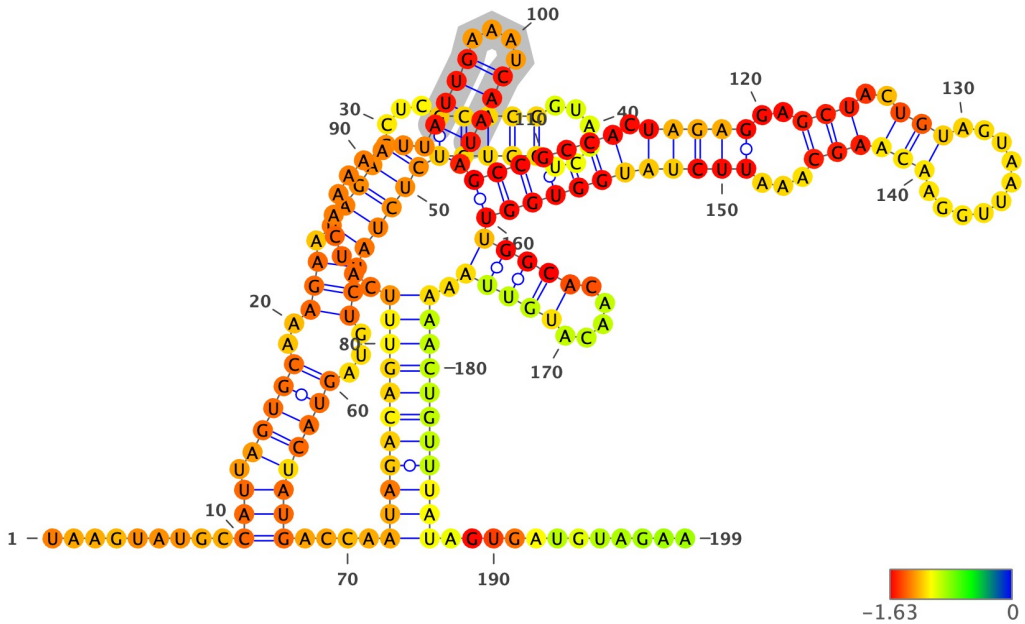
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 264 from nt 15165 to 15176 (nt 94 to 105)

```
5'-AUUGAAAUCAAU-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = 0.1; 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 = -2.86; 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(+)

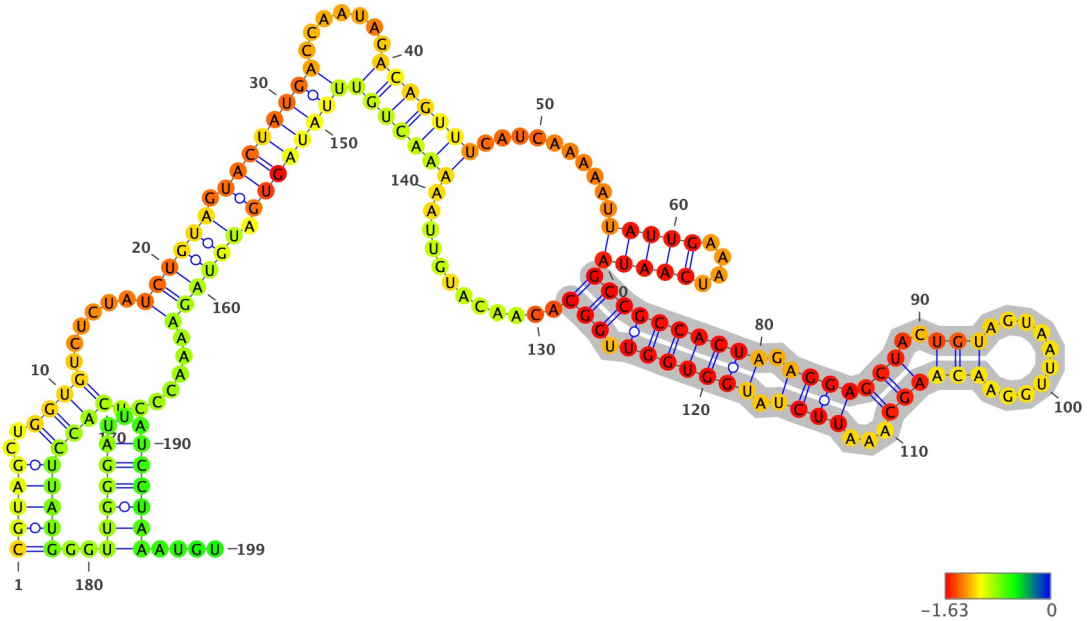
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 265 from nt 15178 to 15235 (nt 71 to 128)

```
5'-GCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGC-3'
5'-(((((((((...((((((.................)))...)))...)))))).)))-3'
Motif MFE = -16.8; z-score = -1.78; ED = 13.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15108 to 15306 (motif highlighted in silver):

```
5'-CGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAA
AUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAUGU-3
5'-(((((..((((......((((((.((((((((.......((((((.........(((((....)))))((((((((((.(((((((..(((.........))))))..
.)))).)))))))).)))............))))))))))))))).))))))).......)))))))))..((((((...))))))....-3'
MFE = -42.7; z-score = -0.68; ED = 37.05
```

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(+)

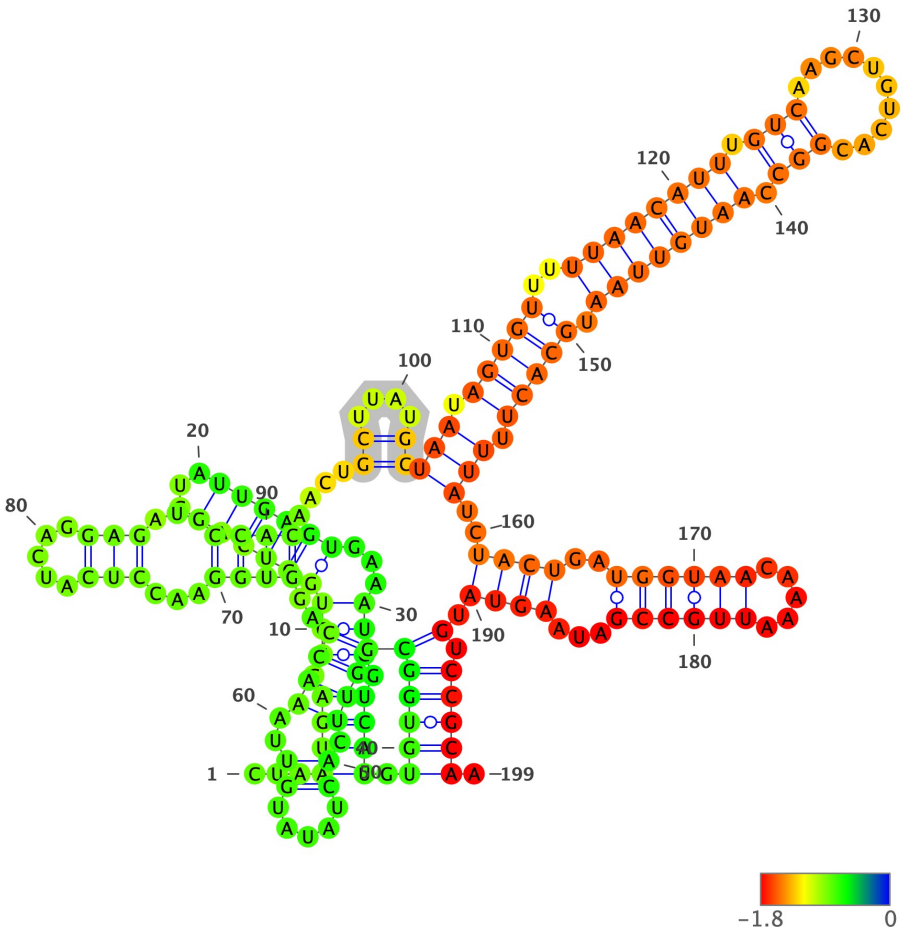
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 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 = -0.79; 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(+)

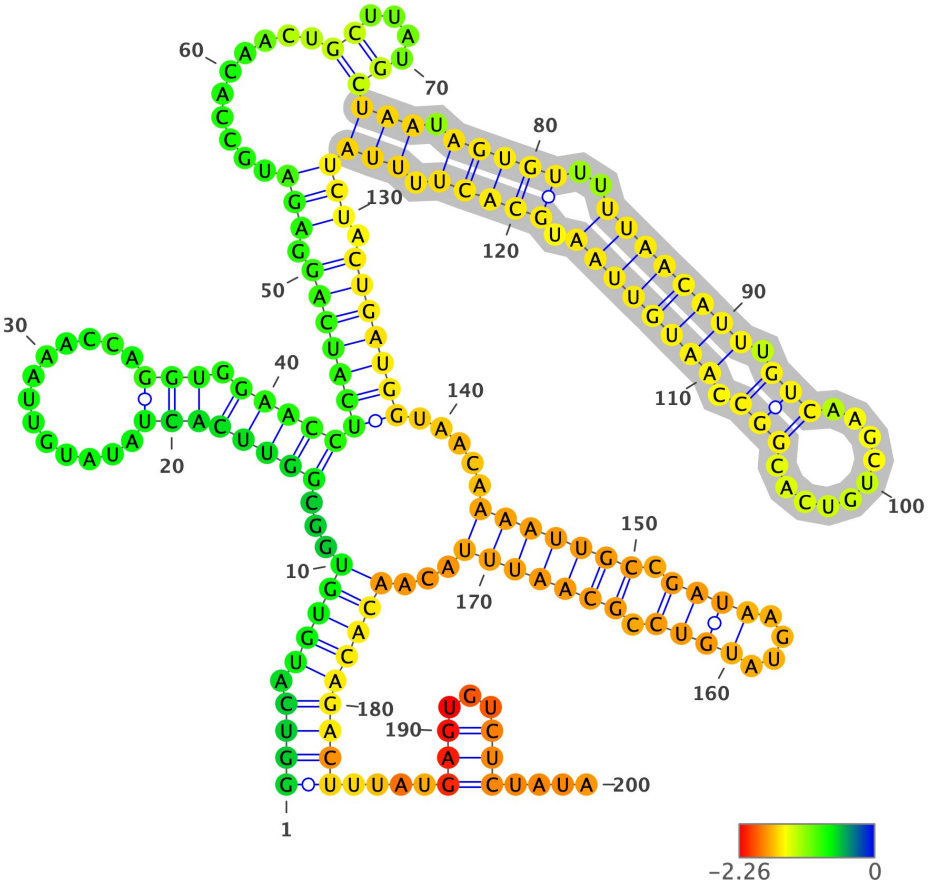
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 267 from nt 15510 to 15564 (nt 73 to 127)

```
5'-UAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUA-3'
5'-(((.(((((..(((((((((.(((..........))).)))))))).))))).)))-3'
Motif MFE = -13.3; z-score = -2.59; 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 = -1.87; 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(+)

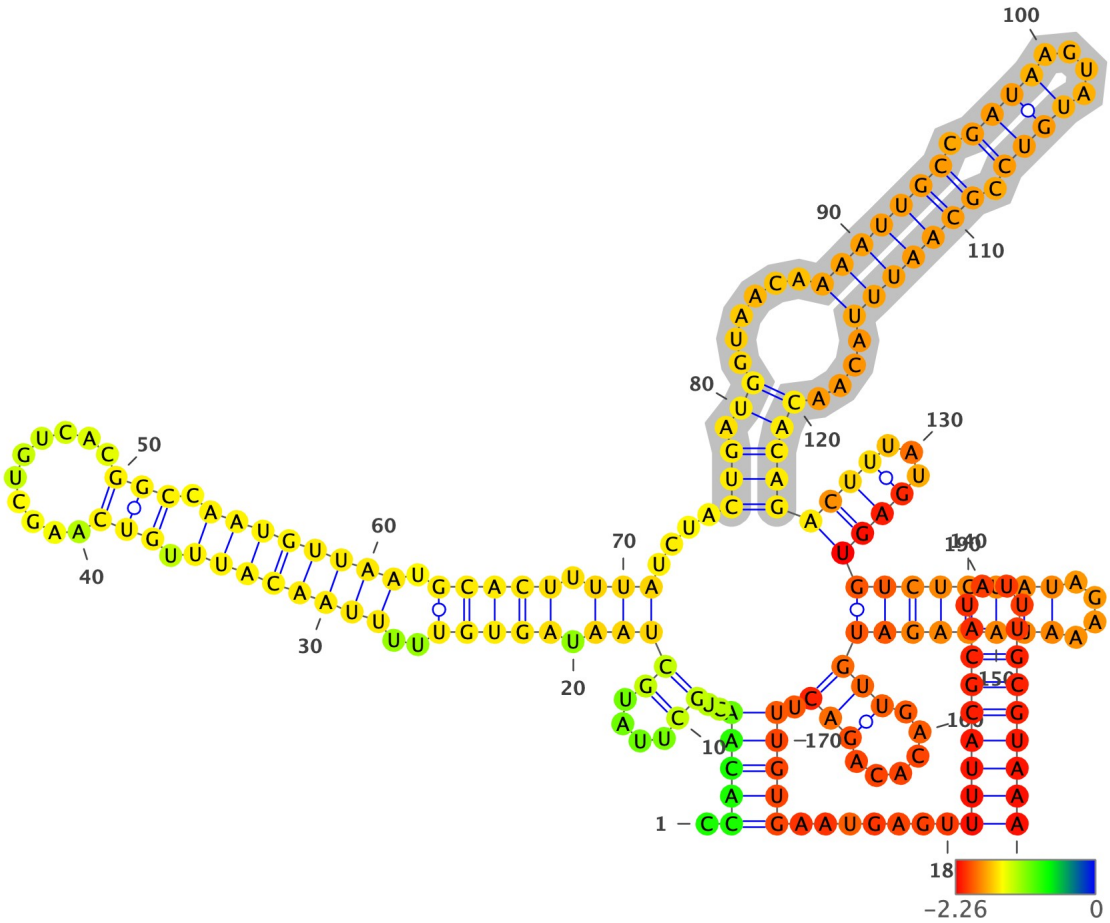
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 268 from nt 15569 to 15617 (nt 76 to 124)

```
5'-CUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAG-3'
5'-(((.((......(((((((.(((......))).)))))))....)))))-3'
Motif MFE = -9.6; z-score = -1.98; ED = 6.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15494 to 15693 (motif highlighted in silver):

```
5'-CCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCA
AUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAA-3
5'-.(((((..((....))(((.(((((..((((((((.(((..........))).)))))))).))))).)))....(((.((......(((((((.((((....)))).)))
))))....)))))((((...))))((((((((....))))))))(((......))).)))))........((((((((....))))))))-3'
MFE = -49.0; z-score = -2.92; 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(+)

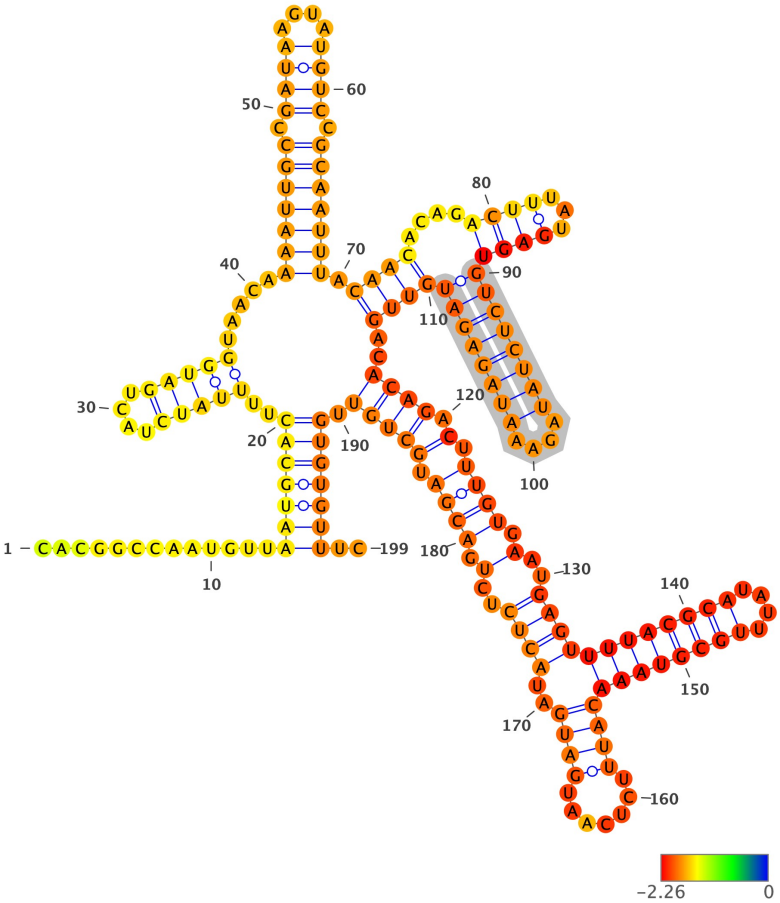
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 269 from nt 15629 to 15648 (nt 90 to 109)

```
5'-GUCUCUAUAGAAAUAGAGAU-3'
5'-((((((((....))))))))-3'
Motif MFE = -7.2; z-score = -6.4; 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 = -1.26; 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(+)

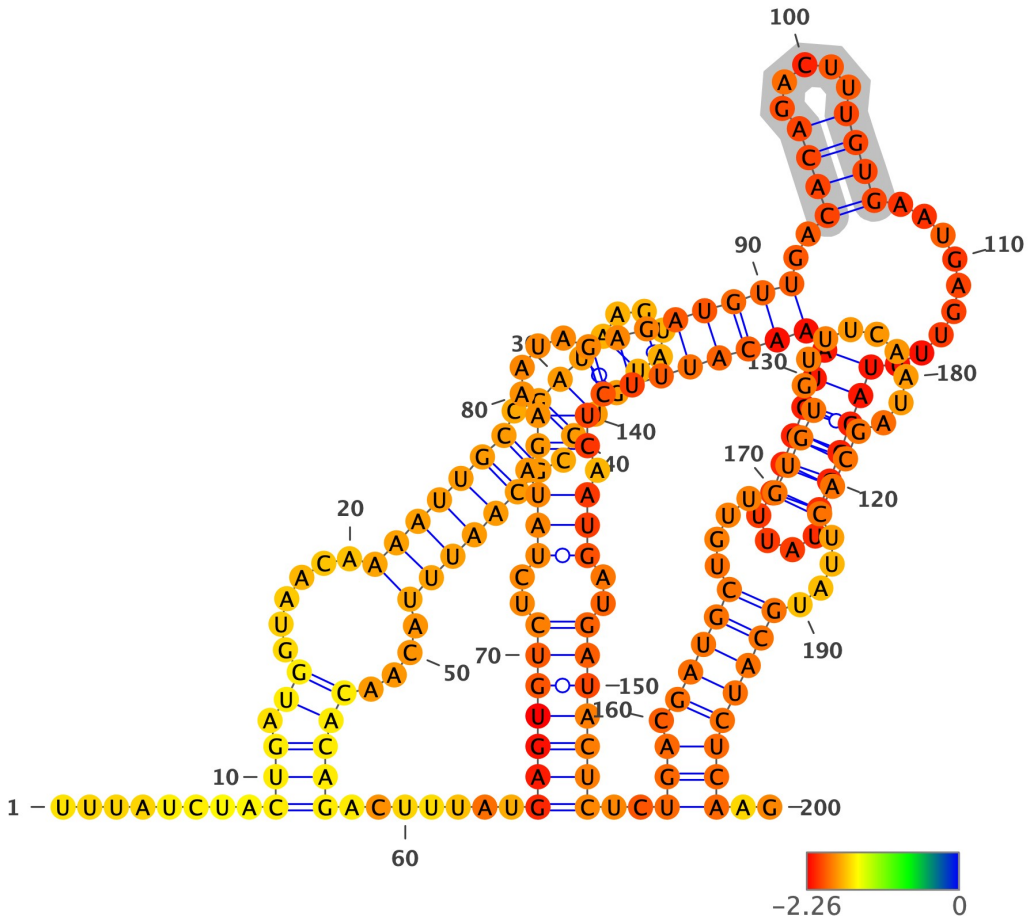
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 270 from nt 15654 to 15666 (nt 94 to 106)

```
5'-CACAGACUUUGUG-3'
5'-((((.....))))-3'
Motif MFE = -1.2; z-score = -1.67; 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 15561 to 15760 (motif highlighted in silver):

```
5'-UUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGA
GUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAG-3
5'-........(((.((......(((((((.((((....)))).)))))))....)))))).......(((((((..(((.((....((((((((..((((.....)))).....
....((((((....))))))))))))))))).)))..)))))))..(((.(((((....((((.........))))....))))))))..-3'
MFE = -48.0; z-score = -2.59; ED = 47.94
```

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(+)

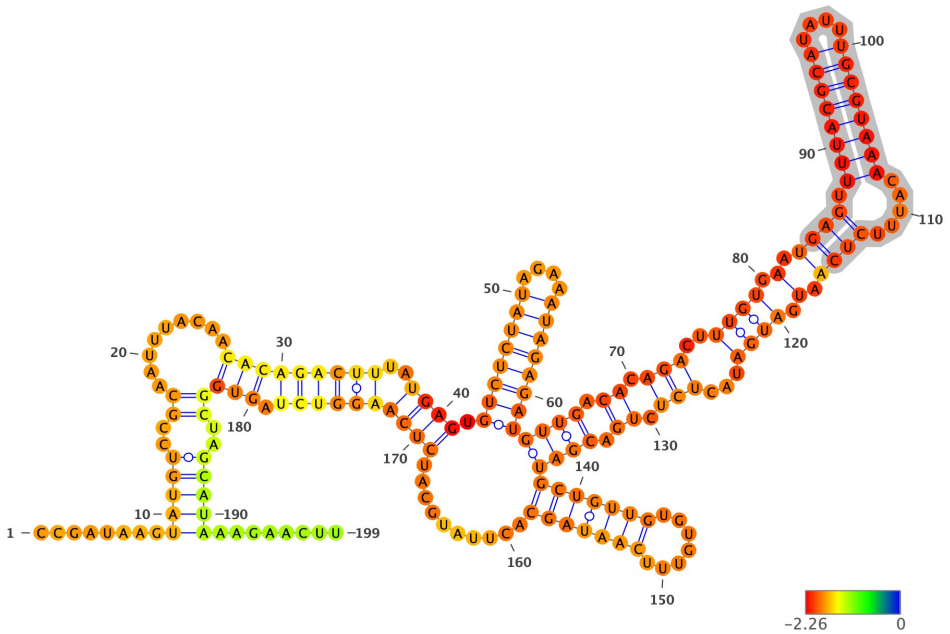
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 15670 to 15701 (nt 84 to 115)

```
5'-GAGUUUUACGCAUAUUUGCGUAAACAUUUCUC-3'
5'-(...(((((((......)))))))).......)-3'
Motif MFE = -9.3; z-score = -3.59; ED = 4.96
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15587 to 15785 (motif highlighted in silver):

```
5'-CCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUU
UCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUU-3
5'-........(((((..((.........(((((((((..((((.((((((((....))))))))((((.((.(((..((((.(.((((.((((((((....))))))))....
.)))).).))))...))).)).))))(((((((.......)))))))..........))))))))))).)))))..)))))........-3'
MFE = -45.7; z-score = -2.03; ED = 55.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

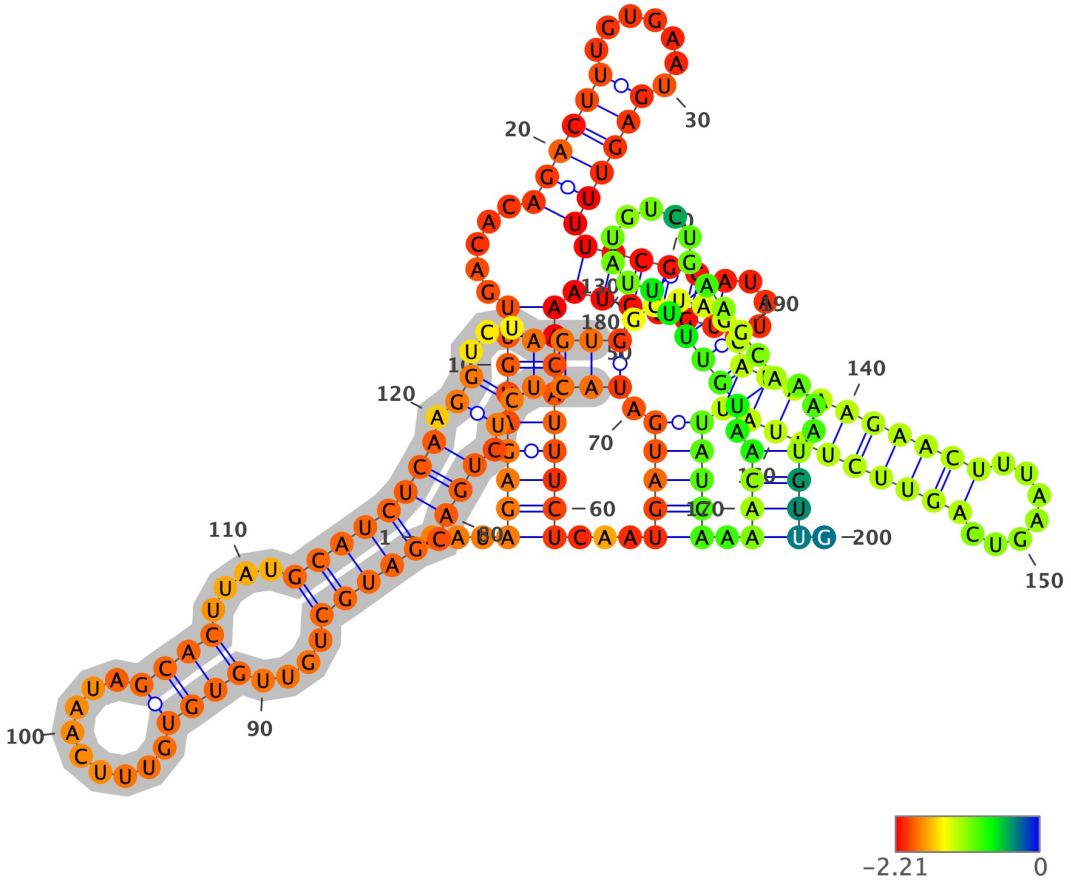
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 272 from nt 15711 to 15767 (nt 72 to 128)

```
5'-ACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGU-3'
5'-(((((.(((.(((((....((((.........))))....)))))))).))...)))-3'
Motif MFE = -13.0; z-score = -1.32; ED = 11.33
```



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 15640 to 15839 (motif highlighted in silver):

```
5'-AAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAU
GCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGUUG-3
5'-...(((((((((.....((((((.......))))))((((((....)))))))))))))))...(((((.((((((.(((.(((((....((((.........))))....
))))))))).))...))))......((((((((((.......)))))))))))))).((((.((((((.......))))))...)))).-3'
MFE = -43.9; z-score = -3.14; ED = 44.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

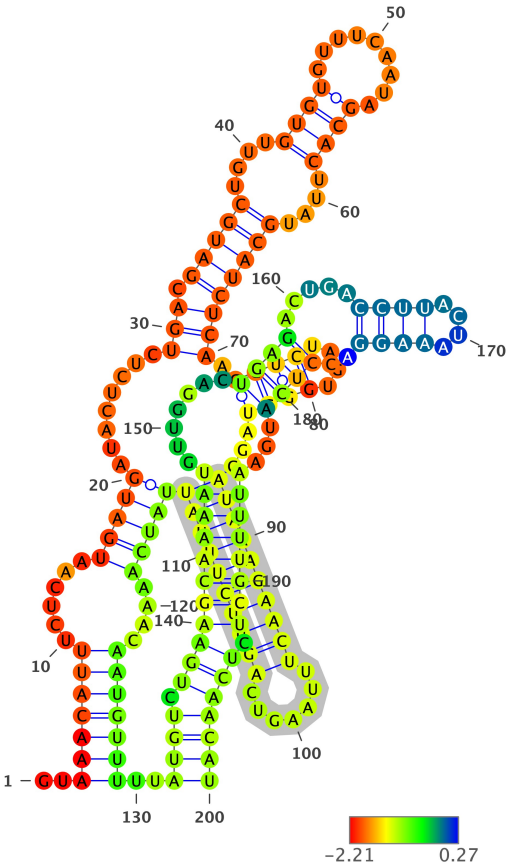
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 273 from nt 15775 to 15801 (nt 87 to 113)

```
5'-AUAAAGAACUUUAAGUCAGUUCUUUAU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -7.5; z-score = -4.5; 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 = -1.31; 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(+)

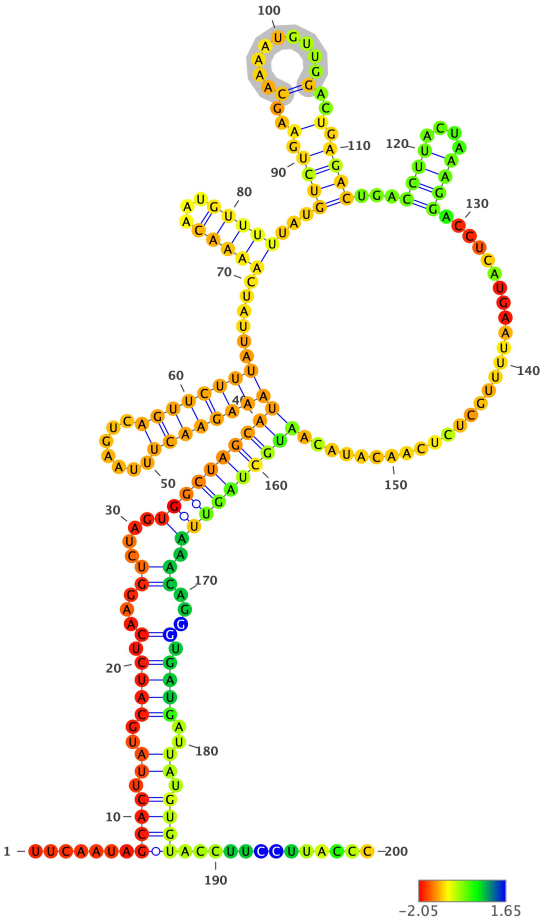
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 274 from nt 15830 to 15840 (nt 95 to 105)

```
5'-CAAAAUGUUGG-3'
5'-(.........)-3'
Motif MFE = 0.0; z-score = #DIV/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 15736 to 15935 (motif highlighted in silver):

```
5'-UUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGUUGGACUGAG
ACUGACCUUACUAAAGGACCUCAUGAAUUUUGCUCUCAACAUACAAUGCUAGUUAAACAGGGUGAUGAUUAUGUGUACCUUCCUUACCC-3
5'-.......((((.((..((((.(...((....(((((((((((((((((((.......))))))))).....(((((...)))))...((((.(..(.........)..).))
))...((((....))))..........................))))))))))).))...).))))..)).))))............-3'
MFE = -33.0; z-score = -1.71; ED = 32.43
```

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(+)

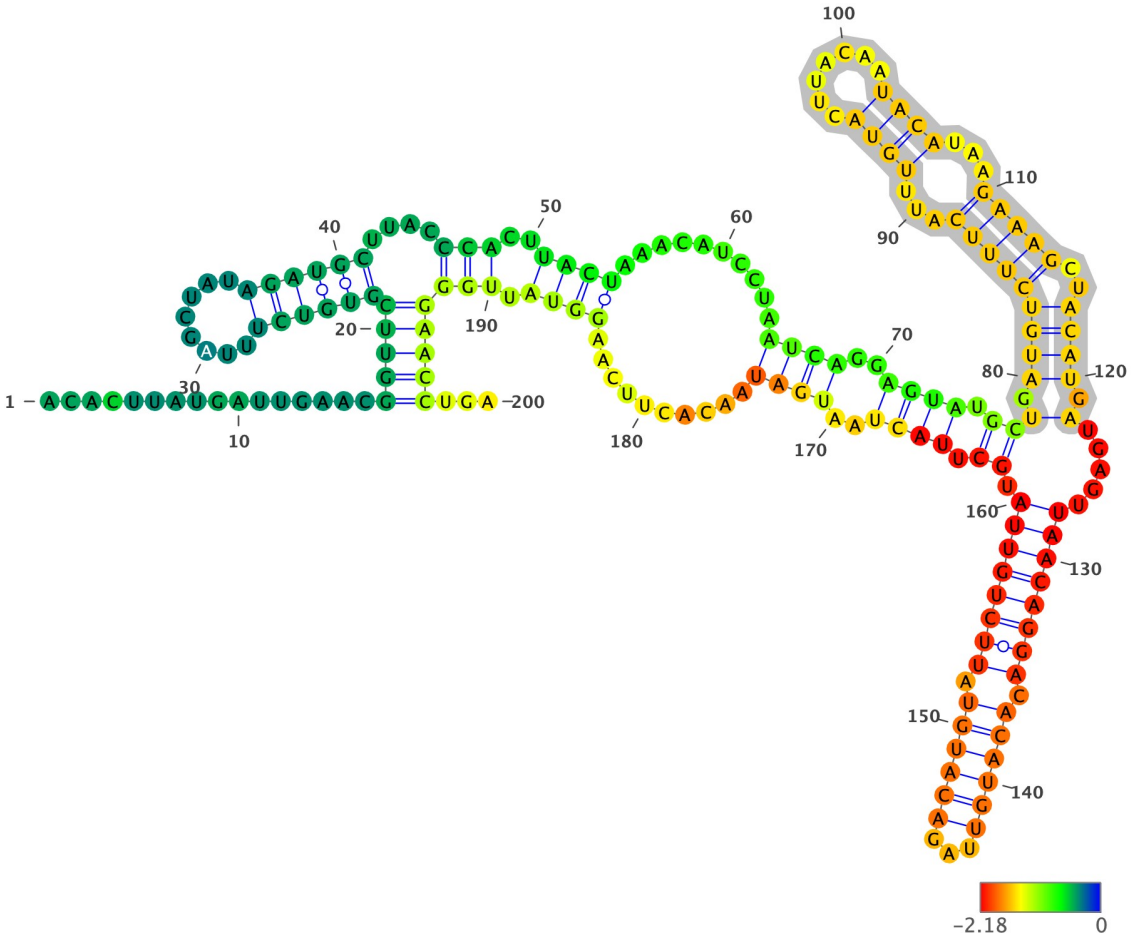
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 275 from nt 16074 to 16118 (nt 78 to 122)

```
5'-UGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGA-3'
5'-(.(((((((((...((((.......))))...)))))..)))).)-3'
Motif MFE = -6.7; z-score = -1.31; 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 = -1.84; ED = 29.21
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

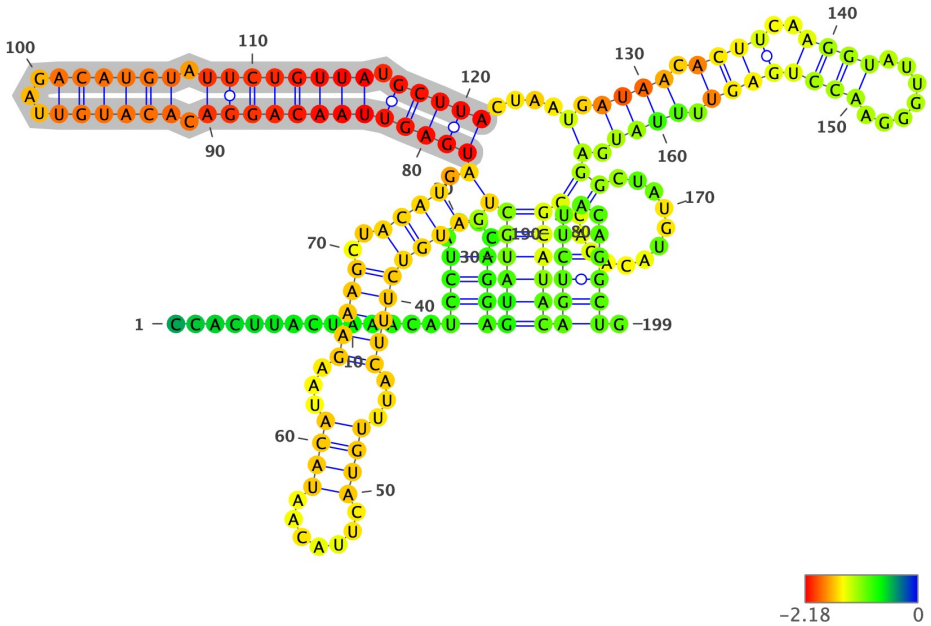
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 276 from nt 16119 to 16162 (nt 78 to 121)

```
5'-UGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUA-3'
5'-(((((((((((((.((((((...)))))).)))))))).)))))-3'
Motif MFE = -16.5; z-score = -4.72; 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 = -1.28; ED = 46.98
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

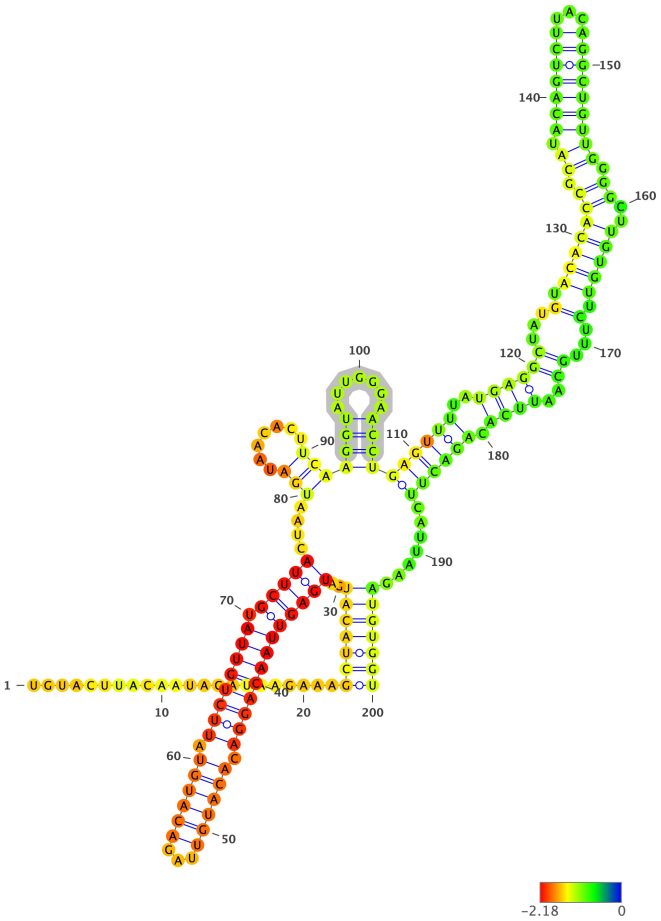
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 277 from nt 16181 to 16193 (nt 94 to 106)

```
5'-GGUAUUGGGAACC-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.43; 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 16088 to 16287 (motif highlighted in silver):

```
5'-UGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGU
UUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUUCACAGACUUCAUUAAGAUGUGGU-3
5'-.......................(((((((..(((((((((((((.((((((...)))))).)))))))).)))))....(((.......)))((((.......))))((((
((..((((((...(.(((((((.((.(((((((...)))))))))).))..)))))).)...))..)))).))))))).......)))))))-3'
MFE = -50.1; z-score = -2.12; ED = 34.85
```

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_gp01, 266-21555(+)

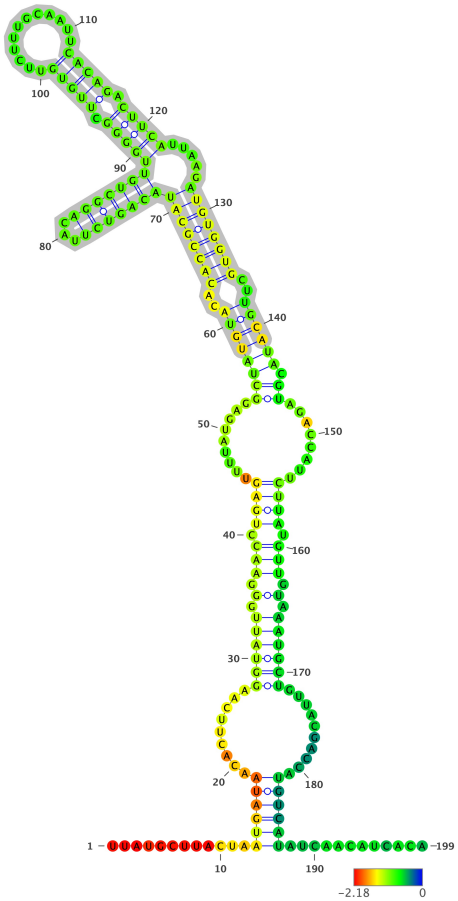
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 16211 to 16294 (nt 58 to 141)

```
5'-UGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUUCACAGACUUCAUUAAGAUGUGGUGCUUGCA-3'
5'-((....(((((((.................((..............................))......)))))))....))-3'
Motif MFE = -25.9; z-score = -2.34; ED = 19.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16154 to 16352 (motif highlighted in silver):

```
5'-UUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUU
CACAGACUUCAUUAAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACA-3
5'-............((((((.........((((((.(.(((.((((.........((((((((..((((((((((((((((...)))))))(((((.(((((............
))))).)))))).....))))))))..)))))).))........)))).))).).))))))..........))))))............-3'
MFE = -43.6; z-score = -0.8; ED = 36.64
```

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(+)

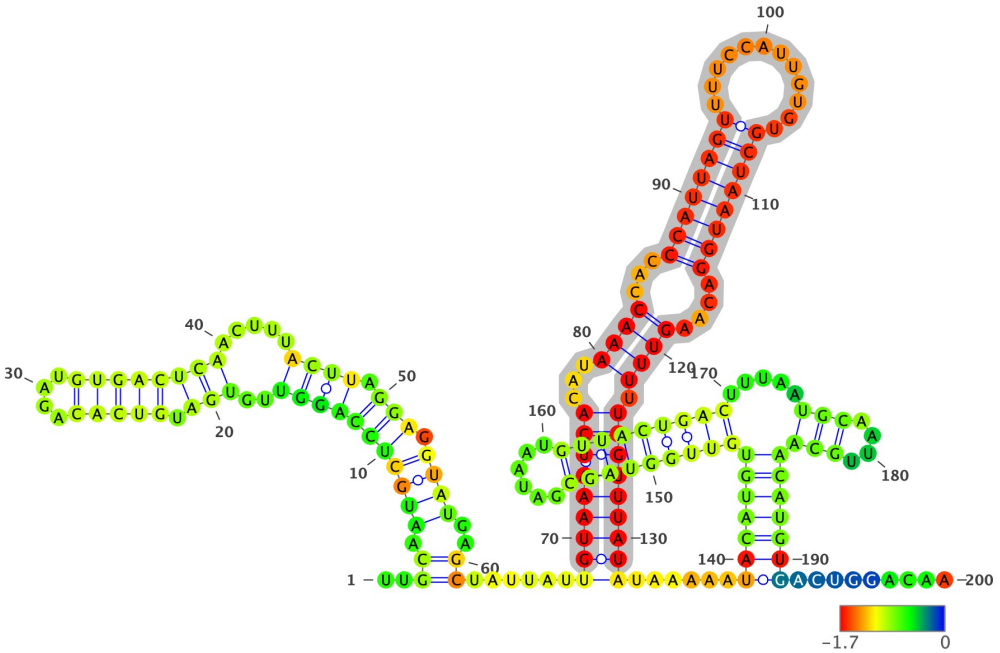
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 279 from nt 16451 to 16513 (nt 69 to 131)

```
5'-GUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAU-3'
5'-((((((((...((((...((((((((.............))))))))....)))).))))))))-3'
Motif MFE = -14.1; z-score = -2.21; 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 = -1.99; 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(+)

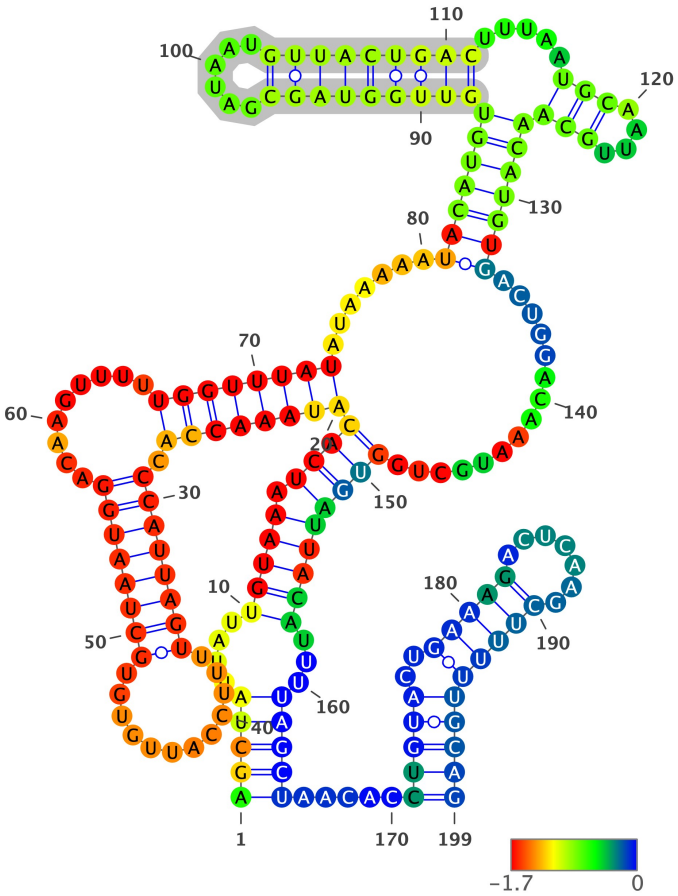
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 280 from nt 16528 to 16551 (nt 88 to 111)

```
5'-GUUGGUAGCGAUAAUGUUACUGAC-3'
5'-(((.................)))-3'
Motif MFE = -8.0; z-score = -3.42; ED = 0.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16441 to 16639 (motif highlighted in silver):

```
5'-AGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGAC
UUUAAUGCAAUUGCAACAUGUGACUGGACAAAUGCUGGUGAUUACAUUUUAGCUAACACCUGUACUGAAAGACUCAAGCUUUUUGCAG-3
5'-(((((....(((((.(((((((((((((.((((((((.............)))))))).........))))))))).......((((((((((((((((......))))))))))
.....(((....))))))))))).............))))))))...)))))).....(((((..(((((.......))))))))))-3'
MFE = -45.0; z-score = -2.38; 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(+)

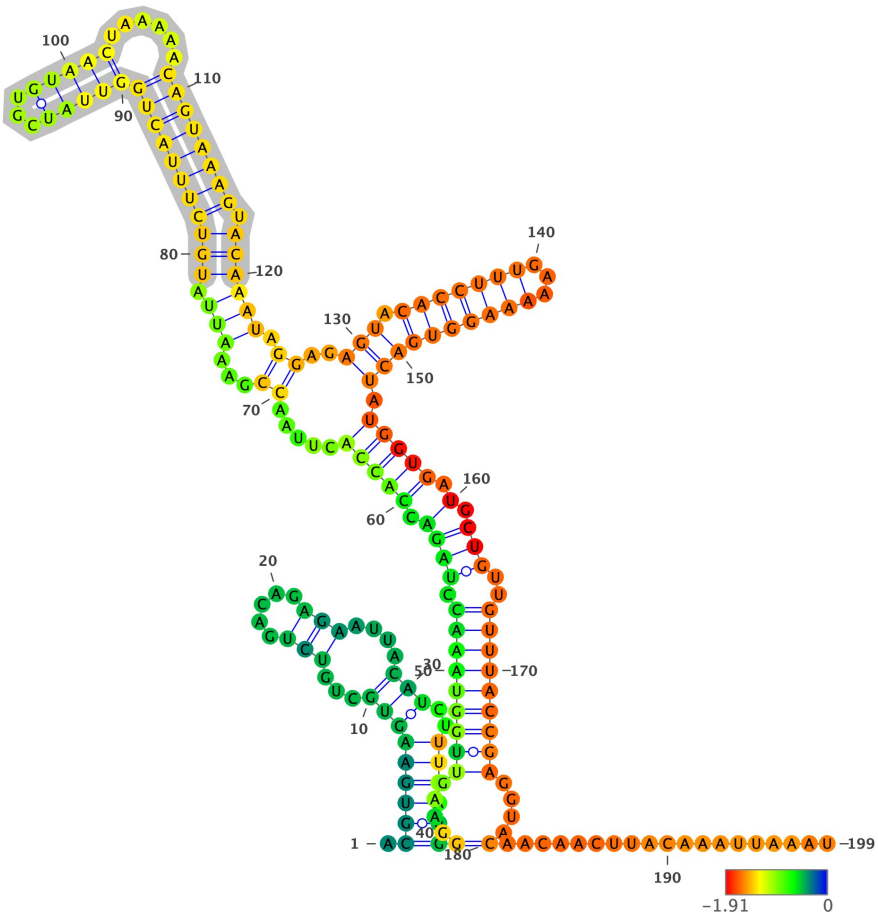
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 281 from nt 16776 to 16817 (nt 79 to 120)

```
5'-UGUCUUUACUGGUUAUCGUGUAACUAAAAACAGUAAAGUACA-3'
5'-(((((((((((.................))))))))).)))-3'
Motif MFE = -9.5; z-score = -2.96; 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 = -1.1; ED = 49.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

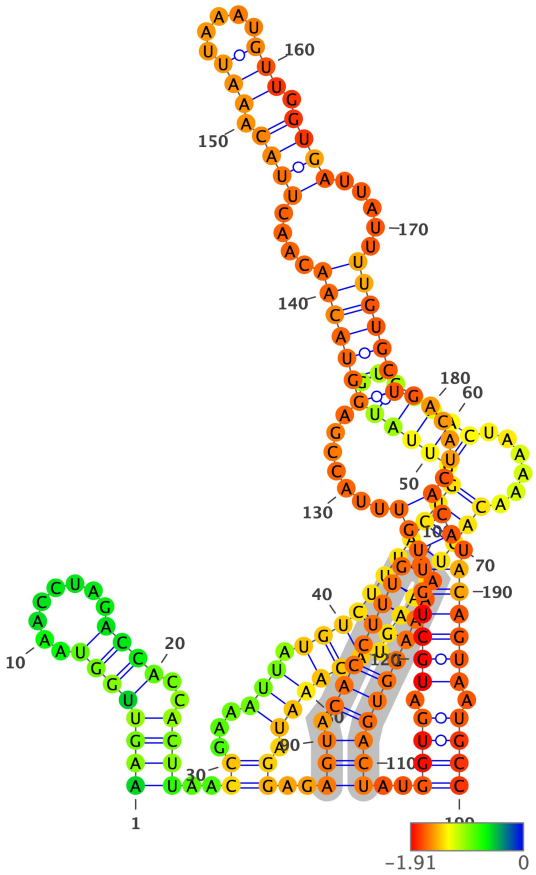
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 282 from nt 16826 to 16849 (nt 88 to 111)

```
5'-AGUACACCUUUGAAAAAGGUGACU-3'
5'-(((.((((((.....)))))))))-3'
Motif MFE = -8.0; z-score = -4.09; 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 = -1.34; 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(+)

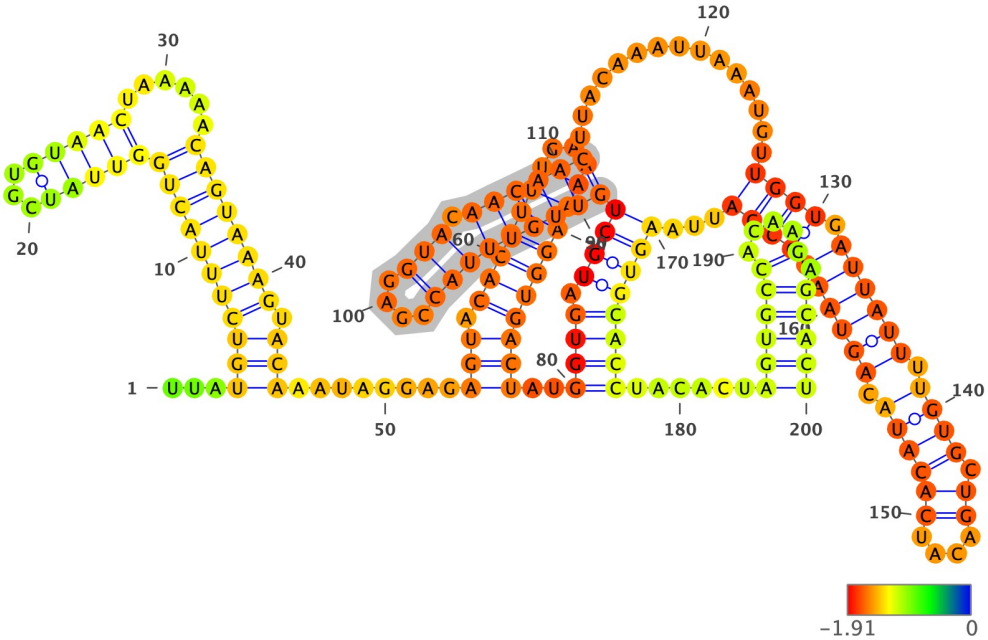
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 283 from nt 16861 to 16883 (nt 89 to 111)

```
5'-GUUGUUUACCGAGGUACAACAAC-3'
5'-(((((((((....))).)))))))-3'
Motif MFE = -5.4; z-score = -2.47; ED = 3.84
```



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 16773 to 16972 (motif highlighted in silver):

```
5'-UUAUGUCUUUACUGGUUAUCGUGUAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAAC
UUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACU-3
5'-...((((((((((((((((...)))))).....))))))))).))).......(((.(((((((...)))))))))))..((((.((((((((((((....)))).))))))
..............((((.((((((.((((.((....)))))).)))))))))...)))))))).....((((((....).)))))-3'
MFE = -46.4; z-score = -2.49; ED = 31.68
```

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(+)

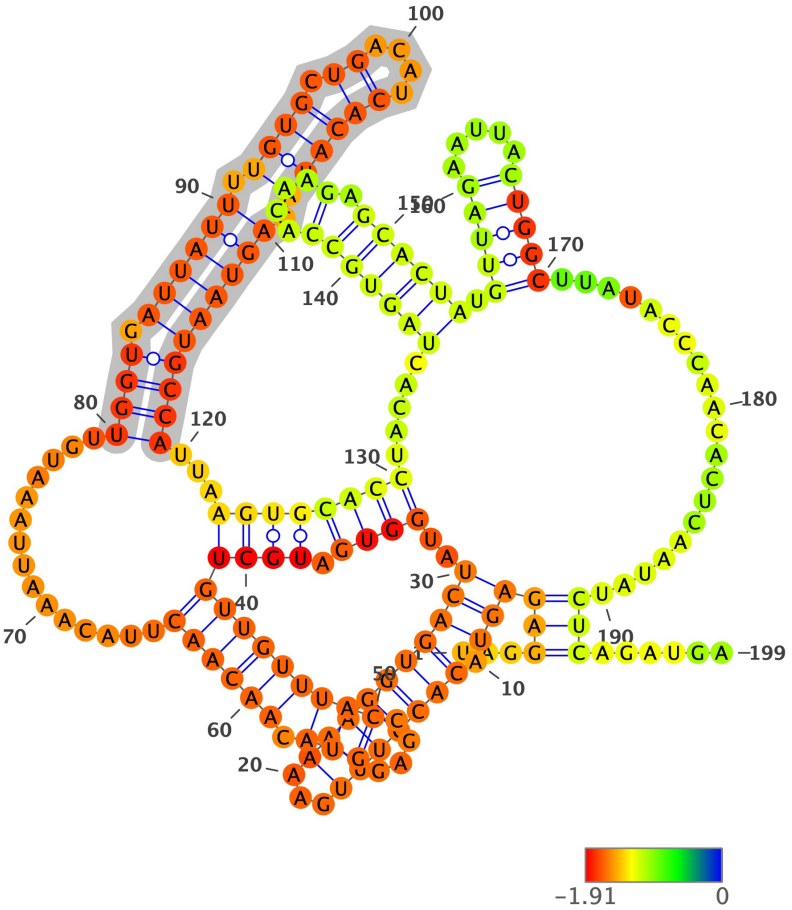
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 16899 to 16938 (nt 80 to 119)

```
5'-UGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCA-3'
5'-((((.(((((((..(((.((....))))).))))))))))-3'
Motif MFE = -8.9; z-score = -1.62; ED = 3.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16820 to 17018 (motif highlighted in silver):

```
5'-UAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAG
UAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGA-3
5'-...((((((.(((((((...)))))))))).((((.((((((((((((....))).)))))).................((((.((((((.((((.((....)))))).))
))))))))...)))))))).....(((((((....).)))))).(((((.....)))))....................))).....-3'
MFE = -43.3; z-score = -1.81; ED = 35.52
```

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(+)

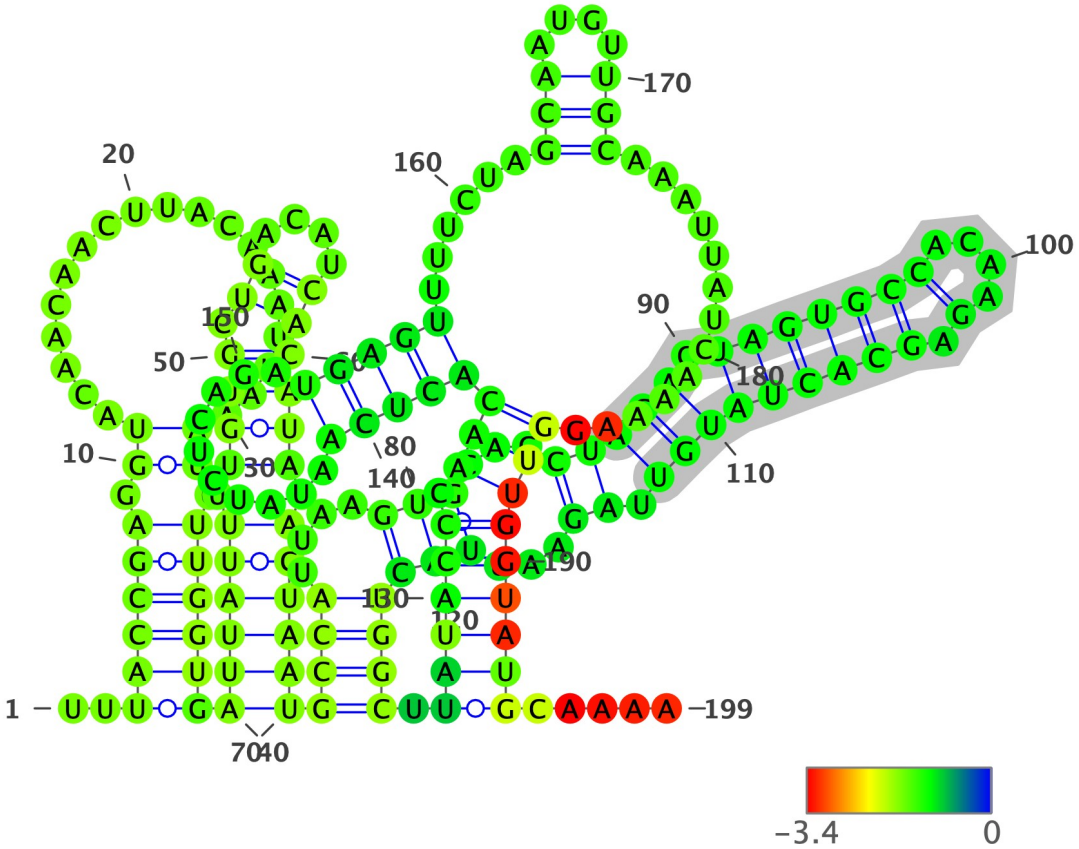
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 285 from nt 16951 to 16976 (nt 87 to 112)

```
5'-ACACUAGUGCCACAAGAGCACUAUGU-3'
5'-(((.((((((.......)))))))))-3'
Motif MFE = -7.6; z-score = -3.55; 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 16865 to 17063 (motif highlighted in silver):

```
5'-UUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUG
UUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAA-3
5'-..((((((.((...................)).))))))((((((.((((.((....)))))).))))))((((....(((...(((((.(((((((....).))))))))
).))...)))))))).((((((.((((((((..........)))))......(((....)))............))))))))).....-3'
MFE = -34.1; z-score = -0.21; ED = 59.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

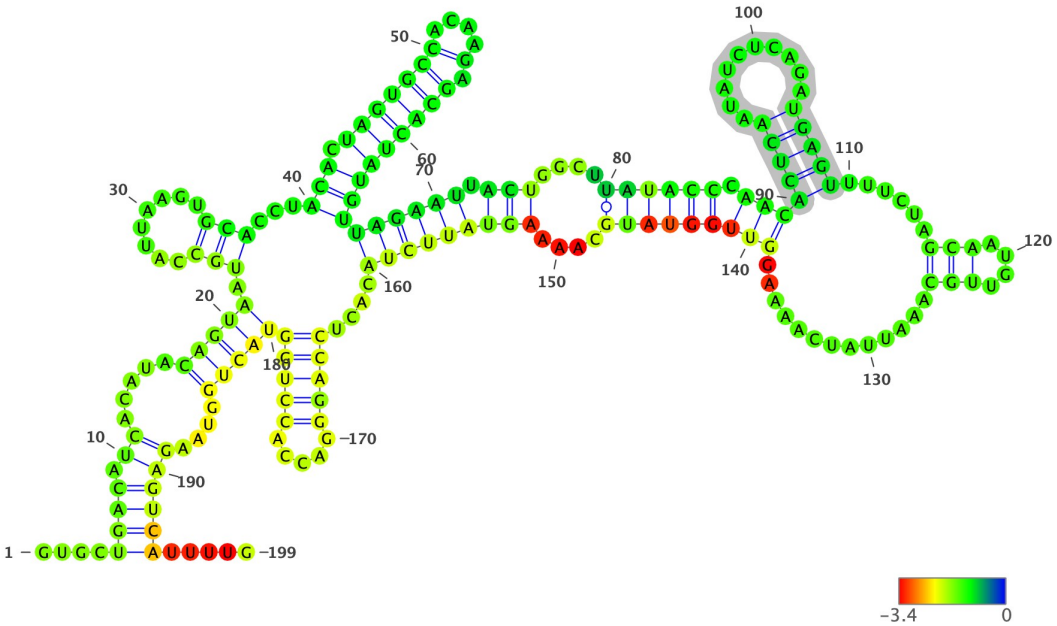
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 286 from nt 17001 to 17020 (nt 90 to 109)

```
5'-ACUCAAUAUCUCAGAUGAGU-3'
5'-(((((.............))))-3'
Motif MFE = -2.1; z-score = -1.56; 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 = -1.19; ED = 45.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

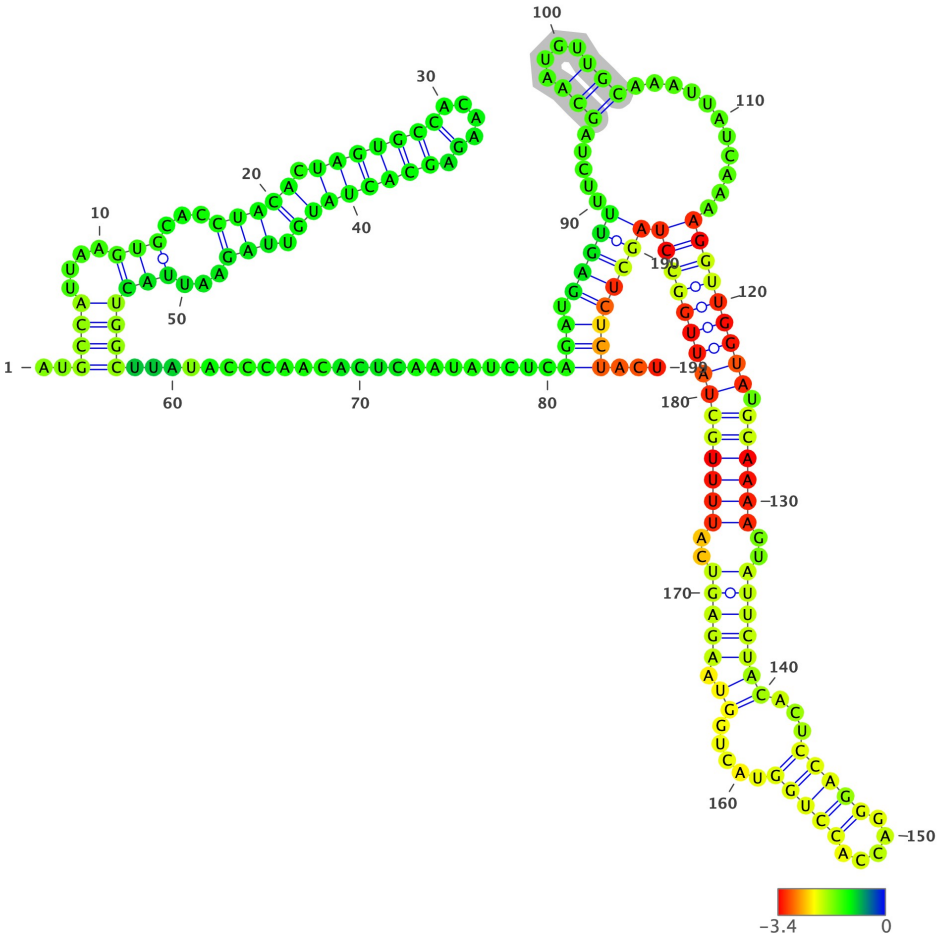
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 287 from nt 17027 to 17036 (nt 95 to 104)

```
5'-GCAAUGUUGC-3'
5'-((......))-3'
Motif MFE = -0.4; z-score = -1.97; 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 = -2.63; ED = 34.48
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

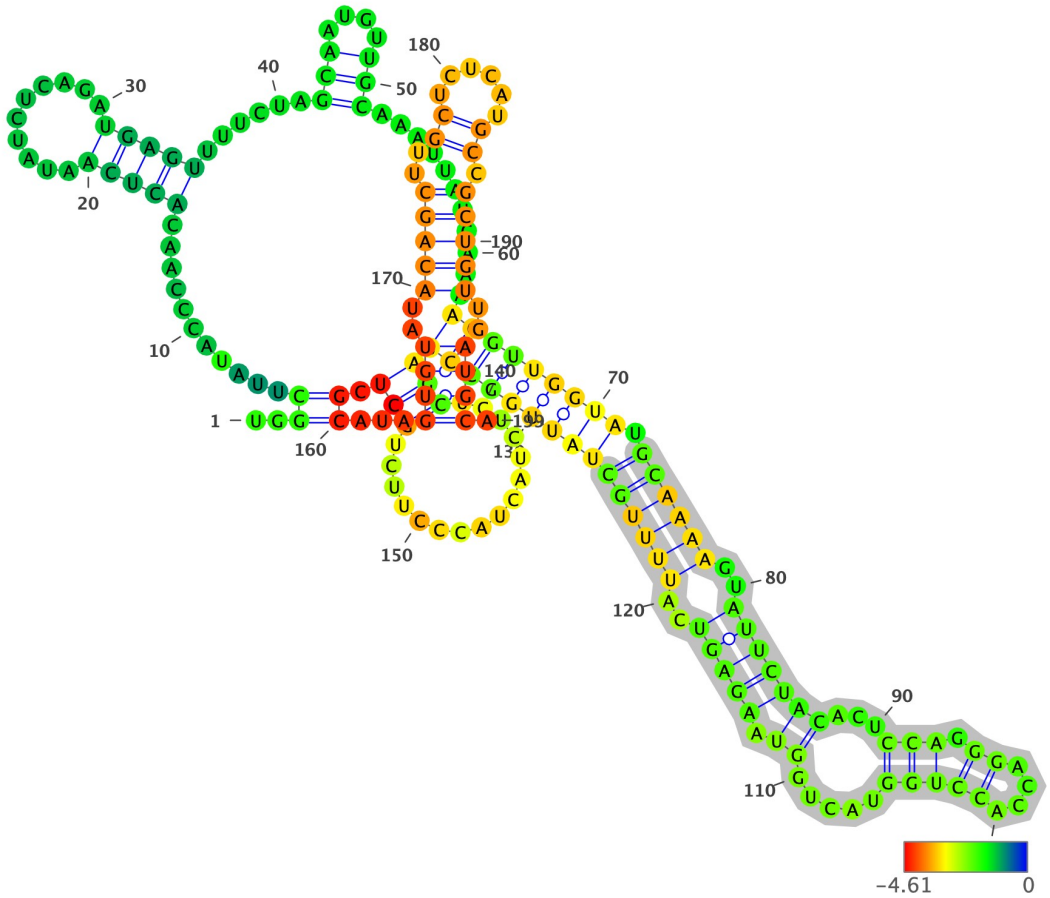
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 288 from nt 17058 to 17111 (nt 73 to 126)

```
5'-GCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUGC-3'
5'-((......(((((.....(((.((....)))))........)))))......))-3'
Motif MFE = -18.1; z-score = -3.44; ED = 3.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16986 to 17184 (motif highlighted in silver):

```
5'-UGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGG
UAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCA-3
5'-..((...........(((((..........)))))......(((....)))...........(((((((((.((((((..(((((((...(((.((....)))))).....)
).)))))..))))))))))))))(((................))).))...((((..(((((..((......)).)))))..)))).-3'
MFE = -41.4; z-score = -1.2; ED = 31.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

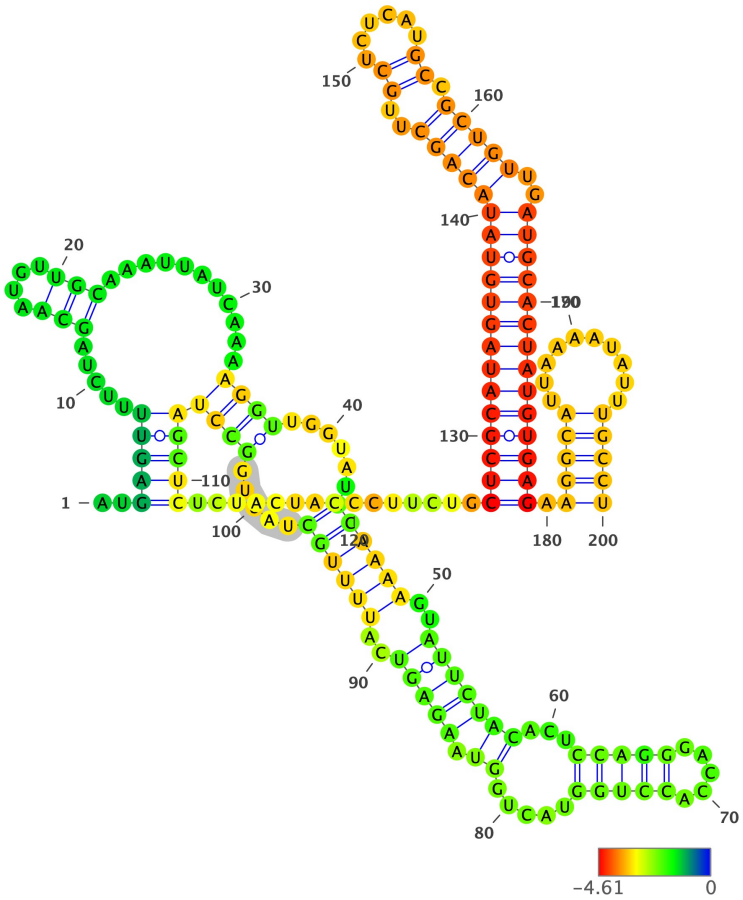
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 289 from nt 17112 to 17116 (nt 98 to 102)

```
5'-UAUUG-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 17015 to 17214 (motif highlighted in silver):

```
5'-AUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUGGUAAGAGUCAUUUUGCUAUUGGCCUAGCUC
UCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCU-3
5'-..(((((.....(((....))).........(((.......((((((..(((((((...(((((.....)))))).....)).)))))..))))))).....))))))))
...............((((((((((((((((((..((.......)).)))))..))))))))))))))).(((((..........)))))-3'
MFE = -61.7; z-score = -4.92; ED = 24.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

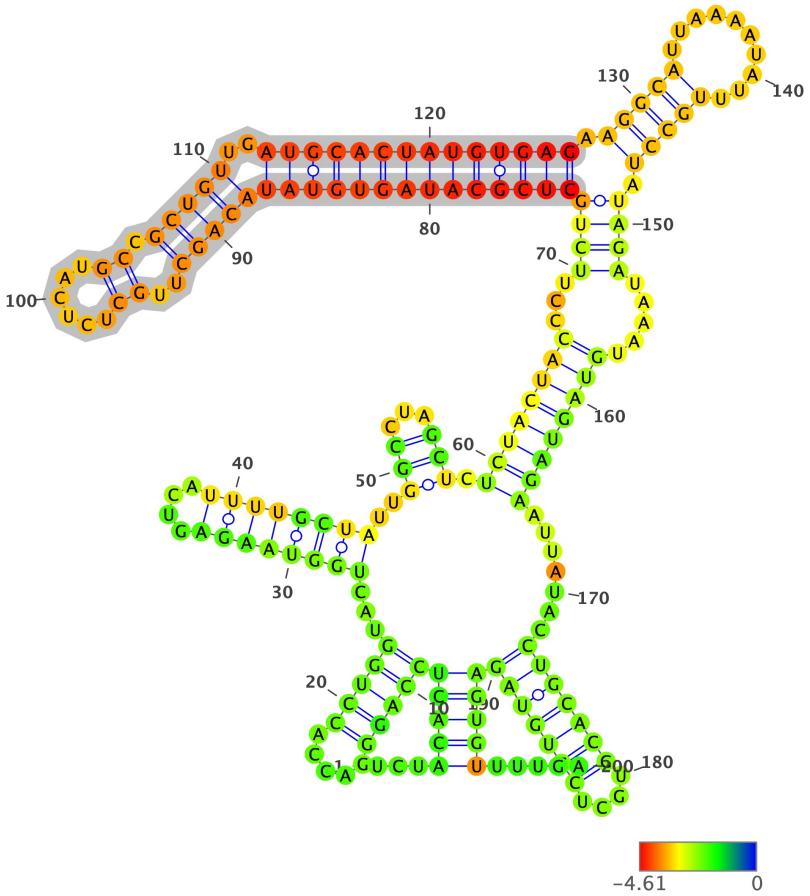
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 290 from nt 17141 to 17193 (nt 74 to 126)

```
5'-CUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAG-3'
5'-(((((((((((((((((((..((......)).)))))..))))))))))))))-3'
Motif MFE = -27.7; z-score = -5.16; 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 = -5.37; ED = 14.79
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

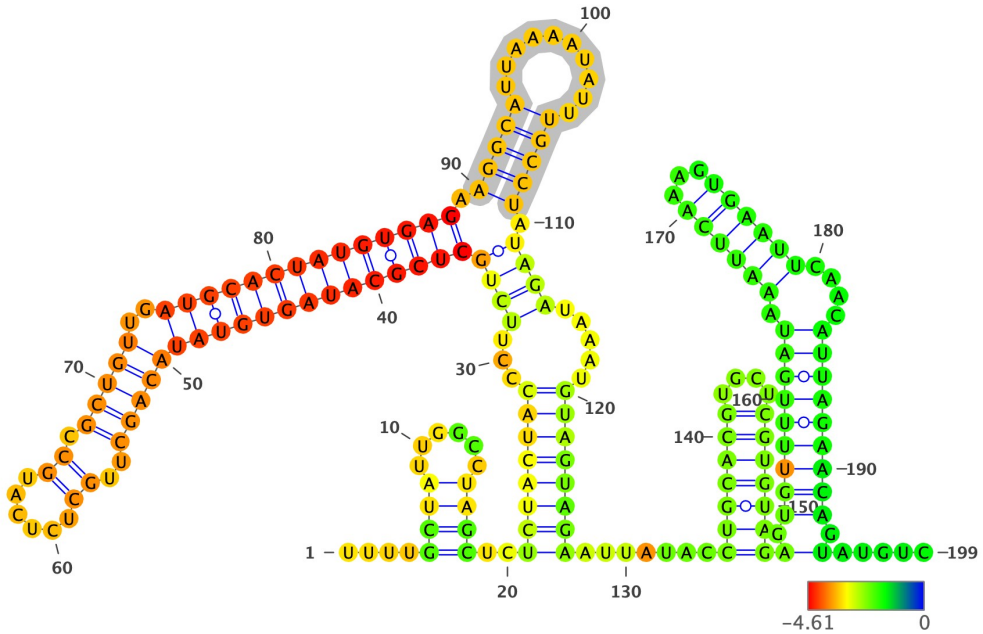
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 291 from nt 17195 to 17214 (nt 90 to 109)

```
5'-AGGCAUUAAAAUAUUUGCCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.1; z-score = -4.53; 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 = -5.26; ED = 24.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

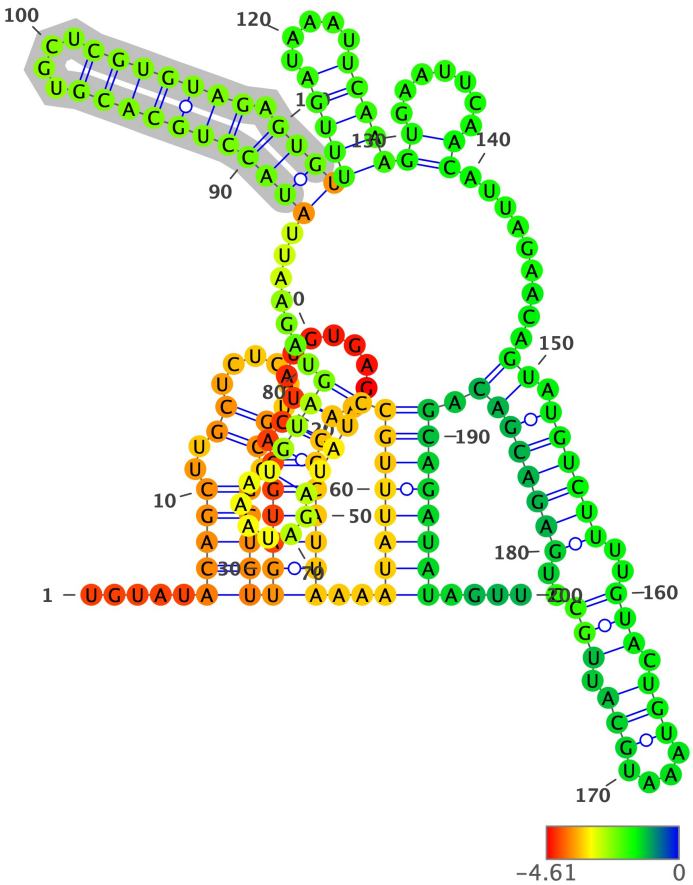
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 292 from nt 17237 to 17261 (nt 88 to 112)

```
5'-UACCUGCACGUGCUCGUGUAGAGUG-3'
5'-((((((((((....)))))))).)))-3'
Motif MFE = -10.5; z-score = -2.88; ED = 1.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17150 to 17349 (motif highlighted in silver):

```
5'-UGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGU
GUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUU-3
5'-.....(((((..((......)).)))))((((((.((........))))))))..((((((((((((.....)))))).......((((((((((....)))))))).))
))(((((.....)))))((.......))........((.((((((..(((.(((....))).))).)))))))).))))))))....-3'
MFE = -48.0; z-score = -1.93; ED = 61.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

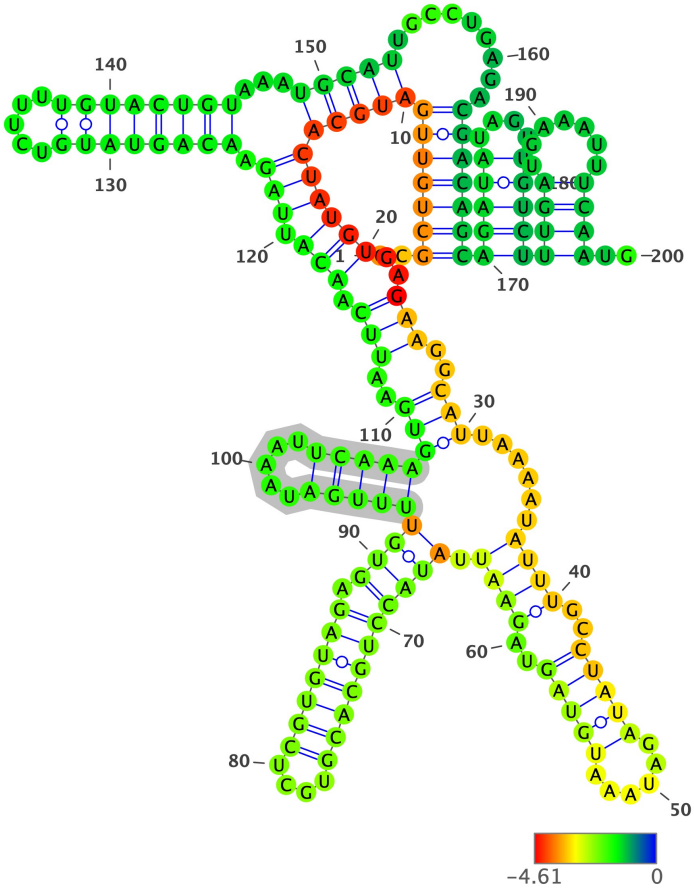
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 293 from nt 17263 to 17277 (nt 93 to 107)

```
5'-UUUGAUAAAUUCAAA-3'
5'-(((((.....)))))-3'
Motif MFE = -1.4; z-score = -9.54; 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 17171 to 17370 (motif highlighted in silver):

```
5'-CCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGA
AUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUG-3
5'-..(((((((((((((((((..(((..(((......((((..(((((......)))))..)))).((((((((((....)))))))).))))(((((.....))))))))).
.))).))).))).((((((((.....))))))))...)))))).........)))))))(((((....)))))((((.......))))..-3'
MFE = -45.7; z-score = -1.7; ED = 55.57
```

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(+)

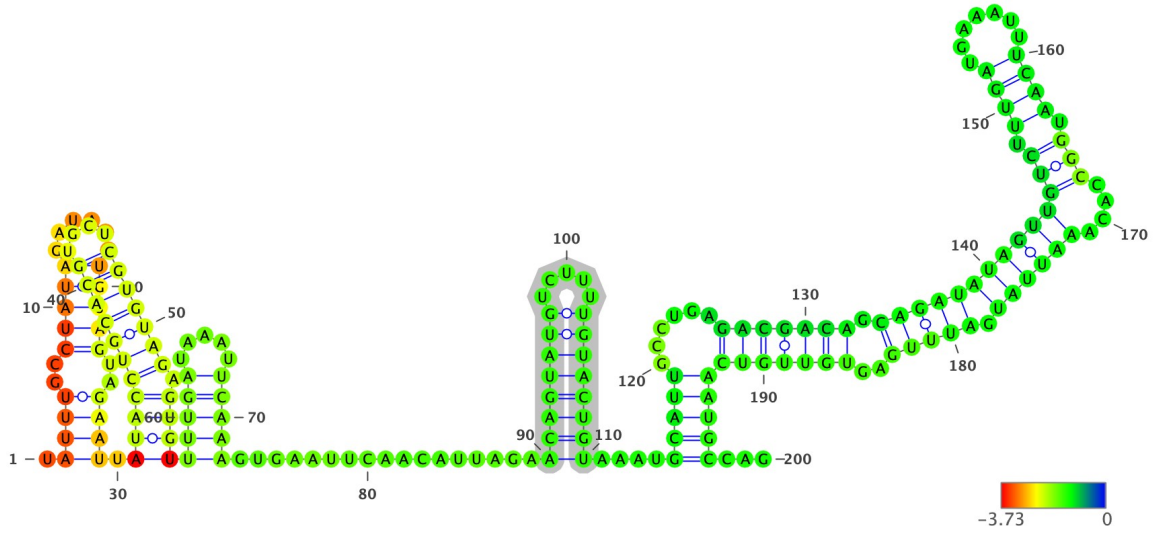
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 294 from nt 17295 to 17315 (nt 90 to 110)

```
5'-ACAGUAUGUCUUUUGUACUGU-3'
5'-(((((((.......)))))))-3'
Motif MFE = -5.8; z-score = -3.96; ED = 0.85
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17206 to 17405 (motif highlighted in silver):

```
5'-UAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUA
AAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAG-3
5'-.((((..(((((......)))))..)))).((((((((((....)))))))).))))(((((.....)))))..................((((((((.....)))))))).
...(((((......(((((((.((((((((((((((.((((.......)))).)))....)))))).)))))..))))))))))))...-3'
MFE = -46.0; z-score = -1.67; ED = 31.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

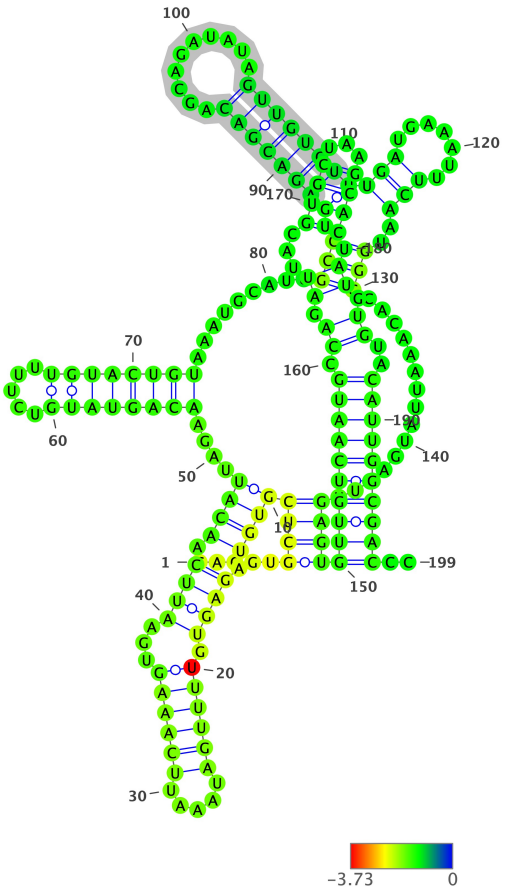
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 295 from nt 17330 to 17353 (nt 88 to 111)

```
5'-AGACGACAGCAGAUAUAGUUGUCU-3'
5'-(((((((..........)))))))-3'
Motif MFE = -6.7; z-score = -2.53; ED = 6.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17243 to 17441 (motif highlighted in silver):

```
5'-CACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCU
UUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCC-3
5'-.....((((((((.((((.((((((.....))))))...)))).)))).....((((((((.....))))))))..........(((.((((((((..........)))))))
)(((.......)))..)))...............))))((((((((((.((.((...((((...)))).)).))..))))))))))..-3'
MFE = -44.6; z-score = -0.59; ED = 40.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

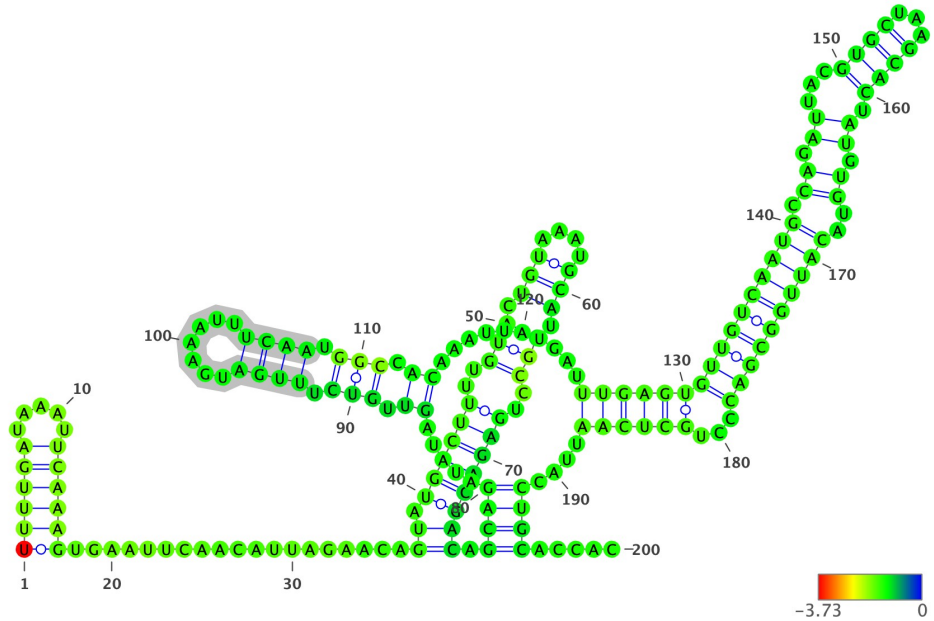
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 296 from nt 17354 to 17368 (nt 93 to 107)

```
5'-UUGAUGAAAUUUCAA-3'
5'-((((.......))))-3'
Motif MFE = -0.2; z-score = -0.83; ED = 2.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17262 to 17461 (motif highlighted in silver):

```
5'-UUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGC
CACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCAC-3
5'-((((((.....))))))...................((.((((((..(((.(((....))).)))..)))))))).((((.....((.(((.((((.......)))).)))
.)).........((((((((((((((((.((.((...((((...)))).)).)).)..))))))))))...))))))....))))).....-3'
MFE = -44.8; z-score = -1.11; ED = 42.21
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

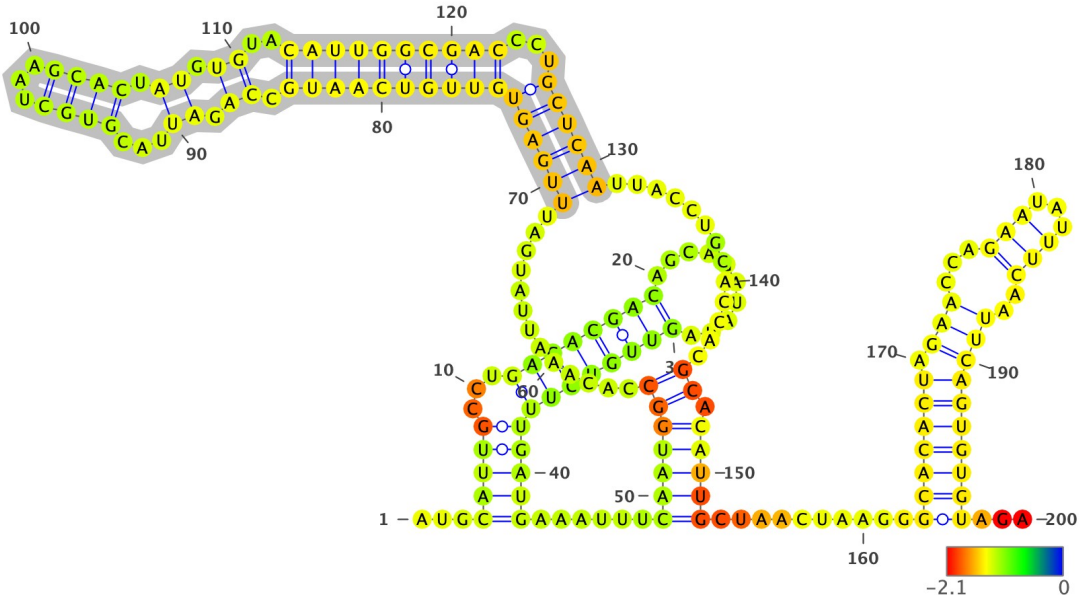
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 297 from nt 17386 to 17448 (nt 69 to 131)

```
5'-UUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAA-3'
5'-(((((((((((((((.((.((...((((...)))).)).)).)).))))))))))...)))))))-3'
Motif MFE = -21.9; z-score = -3.52; 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 = -1.25; 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(+)

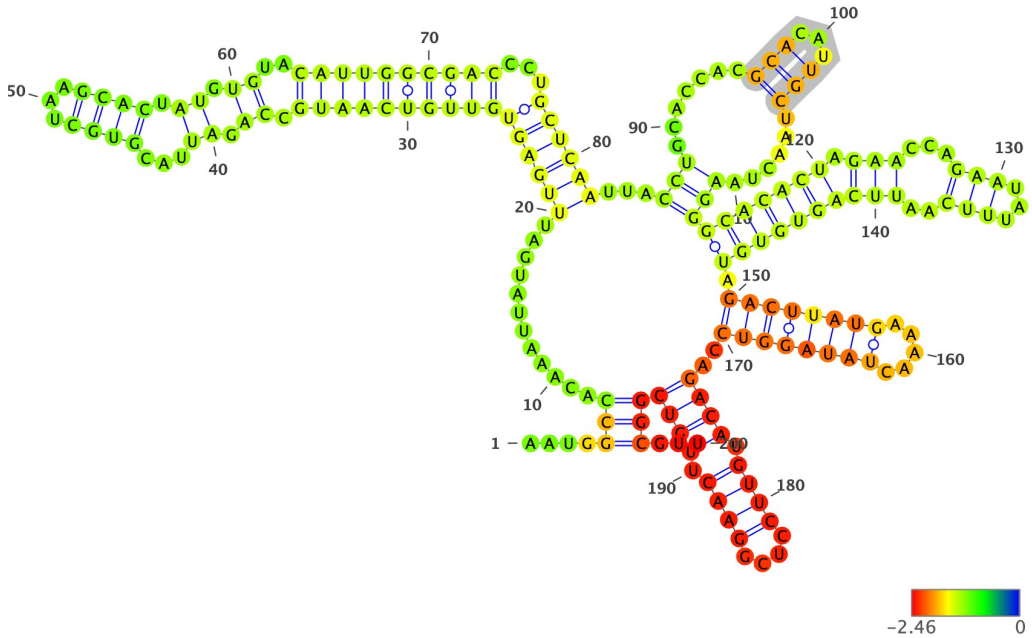
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 298 from nt 17462 to 17470 (nt 96 to 104)

```
5'-GCACAUUGC-3'
5'-(((...)))-3'
Motif MFE = 0.0; z-score = 0.14; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17367 to 17566 (motif highlighted in silver):

```
5'-AAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAA
GGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUU-3
5'-....(((............((((((((((((((((.((.((...((((...)))).)).))..))))))))))...))))))...(((.......(((...)))......)
))(((((((.(((...(((...)))..)))))))))).((((((((.....))))))))..((((.((((....)))).)))))))...-3'
MFE = -58.3; z-score = -2.96; ED = 11.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

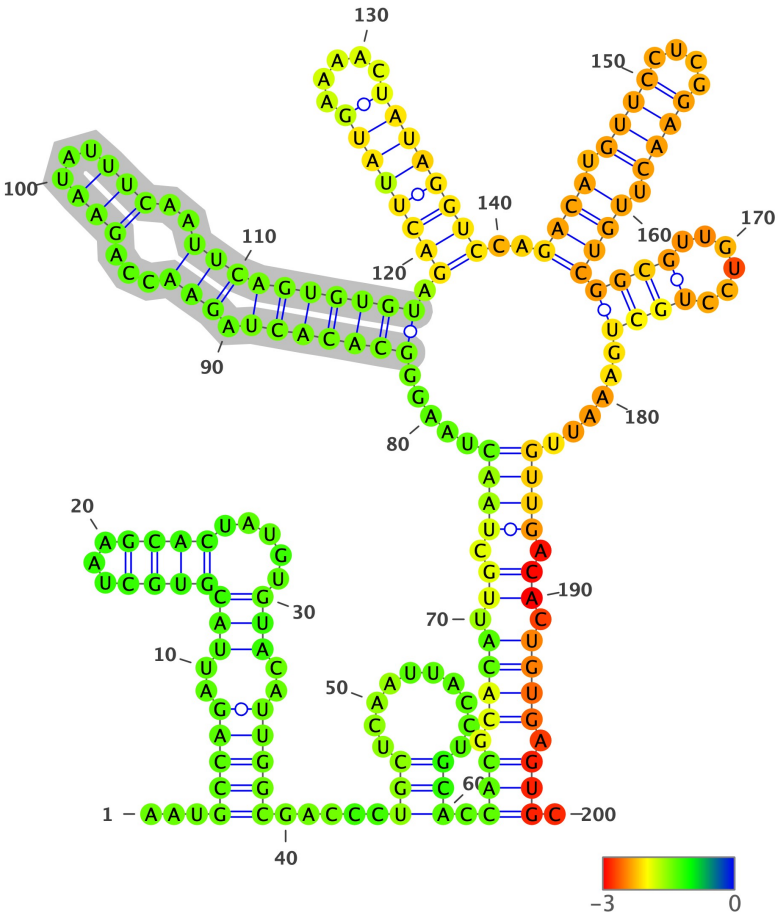
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 299 from nt 17480 to 17514 (nt 83 to 117)

```
5'-GCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGU-3'
5'-(((((((.....................)))))))-3'
Motif MFE = -8.4; z-score = -2.47; ED = 3.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17398 to 17597 (motif highlighted in silver):

```
5'-AAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCA
GUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGC-3
5'-...(((((..(((((((...))))).....)))..)))))).....(((..........))).(((.((((.((.((((.....(((((((.(((...(((...)))..))))
)))))).((((((((.....))))))))..((((.((((....)))).))))((((......))))......)))).)).)))).))).-3'
MFE = -50.2; z-score = -1.16; ED = 42.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

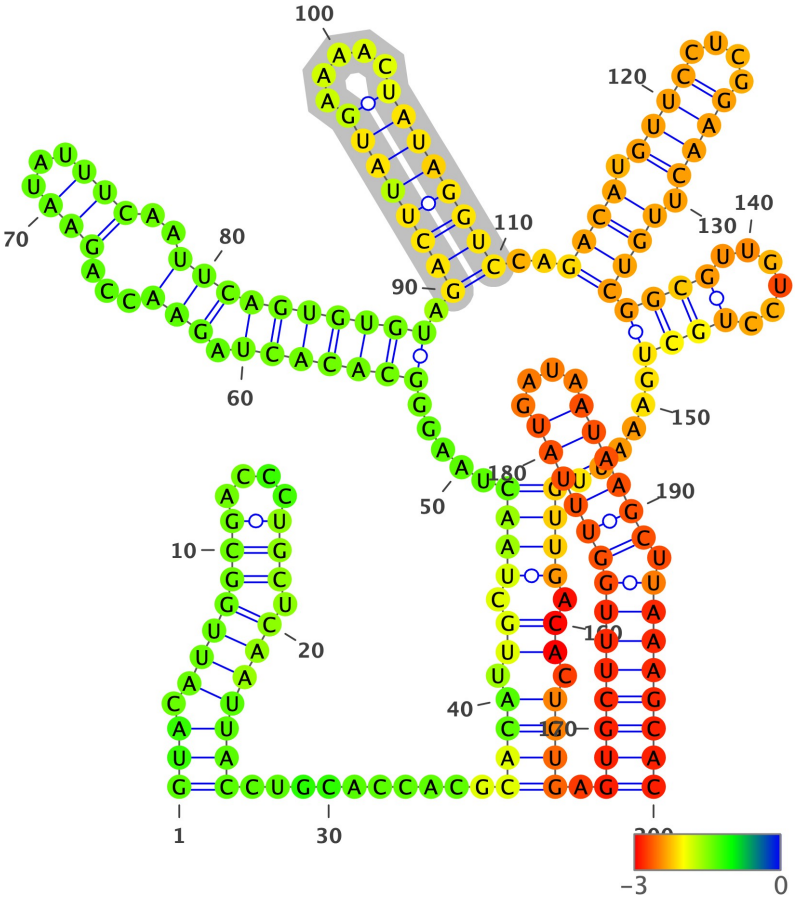
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 300 from nt 17516 to 17536 (nt 90 to 110)

```
5'-GACUUAUGAAAACUAUAGGUC-3'
5'-(((((.((.......)).))))-3'
Motif MFE = -5.5; z-score = -3.98; 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 = -2.58; ED = 34.43
```

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(+)

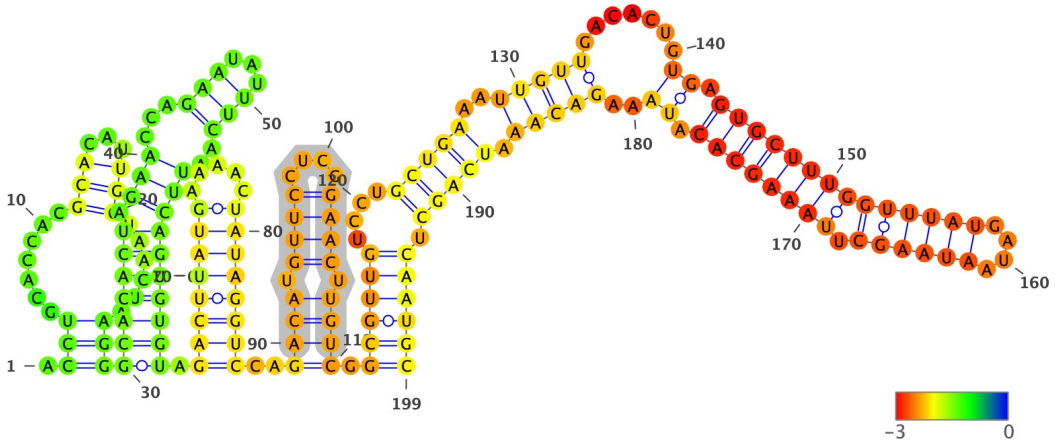
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 301 from nt 17540 to 17559 (nt 90 to 109)

```
5'-ACAUGUUCCUCGGAACUUGU-3'
5'-(((.((((....)))).)))-3'
Motif MFE = -6.0; z-score = -3.58; ED = 0.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17451 to 17649 (motif highlighted in silver):

```
5'-ACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCG
GCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGC-3
5'-.(((.......(((...))).....)))(((((((.(((...(((...)))..)))))))))).((((((((.....)))))))).((((.((((....)))).)))).
((((((....(((((..((((.......((.(((((((((((((....)))))))).))))))))..))..)))))).)))))).))))))-3'
MFE = -56.6; z-score = -3.17; ED = 16.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

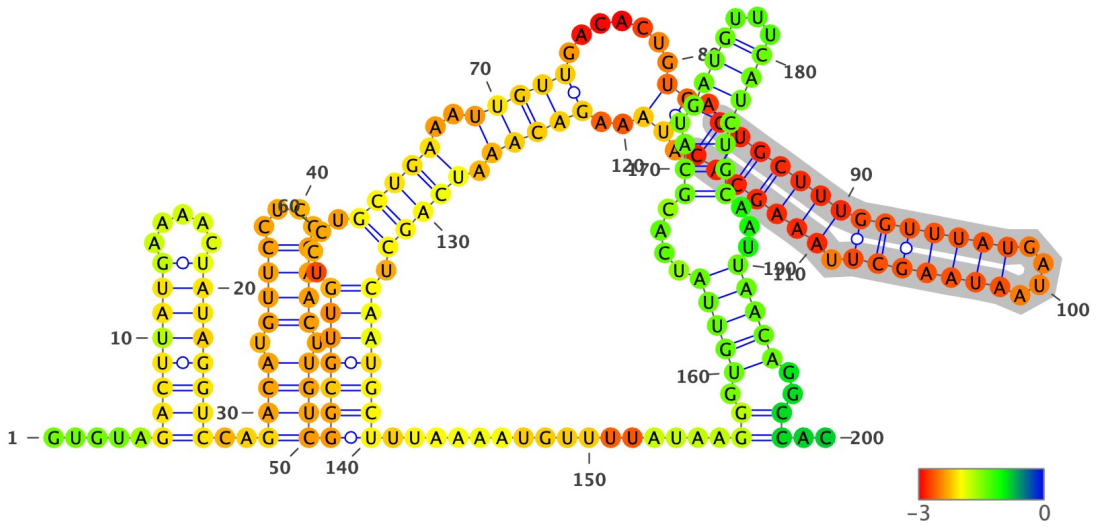
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 302 from nt 17594 to 17626 (nt 84 to 116)

```
5'-GUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCAC-3'
5'-(((((((((((((....)))))))).)))))))-3'
Motif MFE = -13.2; z-score = -4.78; 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 = -3.51; ED = 24.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

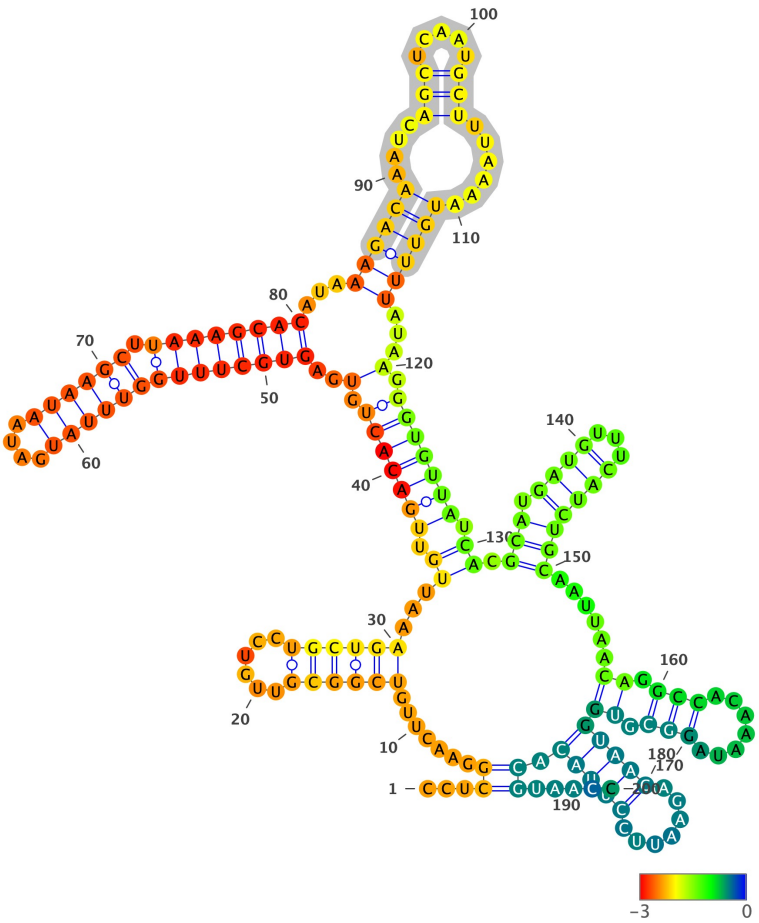
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 303 from nt 17632 to 17660 (nt 86 to 114)

```
5'-GACAAAUCAGCUCAAUGCUUUAAAAUGUU-3'
5'-((((....(((.....)))......))))-3'
Motif MFE = -2.0; z-score = -0.34; ED = 2.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17547 to 17746 (motif highlighted in silver):

```
5'-CCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAU
GUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACC-3
5'-...((.......((((((.....))))))...((.(((((((.(..(((((((((((((((....)))))))).))))))))...((((((....(((.....)))).....)
)))))...).)))))))).)).(((.((((...)))))))).....((.(((.......))).))(((((.......))))).)).....-3'
MFE = -49.1; z-score = -1.7; 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(+)

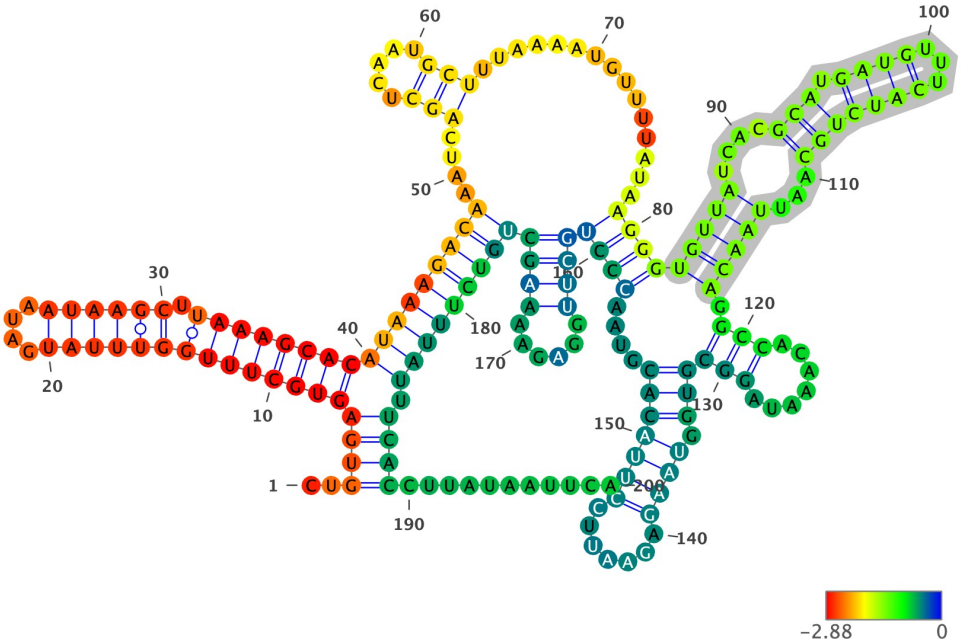
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 304 from nt 17670 to 17704 (nt 83 to 117)

```
5'-UGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACA-3'
5'-(((((....(((.((((...)))))))...)))))-3'
Motif MFE = -7.2; z-score = -2.4; ED = 1.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17588 to 17787 (motif highlighted in silver):

```
5'-CUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAA
UUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCA-3
5'-..((((((((((((((((((....)))))).))))))))((((((((....(((.....)))...............(((((((((....(((.((((...)))))))..
.))))).(((.......)))(((.((((.......)))))))....))))((((......)))))))))))))).))))...........-3'
MFE = -50.2; z-score = -3.88; ED = 17.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

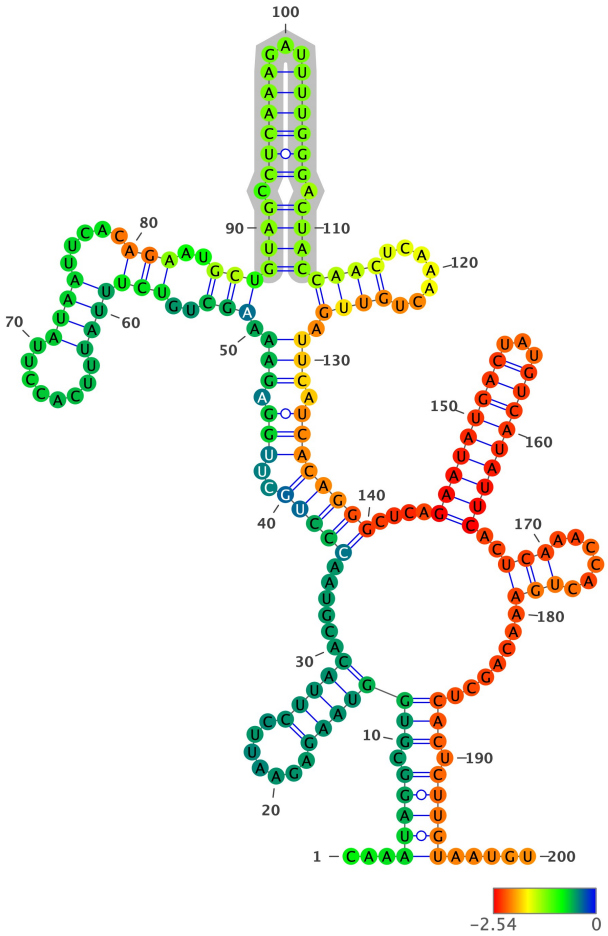
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 305 from nt 17797 to 17821 (nt 88 to 112)

```
5'-GUAGCCUCAAAGAUUUUGGGACUAC-3'
5'-((((.((((((...)))))).))))-3'
Motif MFE = -6.7; z-score = -1.7; ED = 2.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17710 to 17909 (motif highlighted in silver):

```
5'-CAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUA
CCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGU-3
5'-...(((((.((((((((.......)))))......(((((..(((.(((.(((..(((((((.........))))).....))).)))((((.((((((...)))))).)))
)((((.......)))).))).)))))))).....((((((((((...)))))))))..(((......))).......))).)))))).....-3'
MFE = -43.2; z-score = -2.14; ED = 43.68
```

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(+)

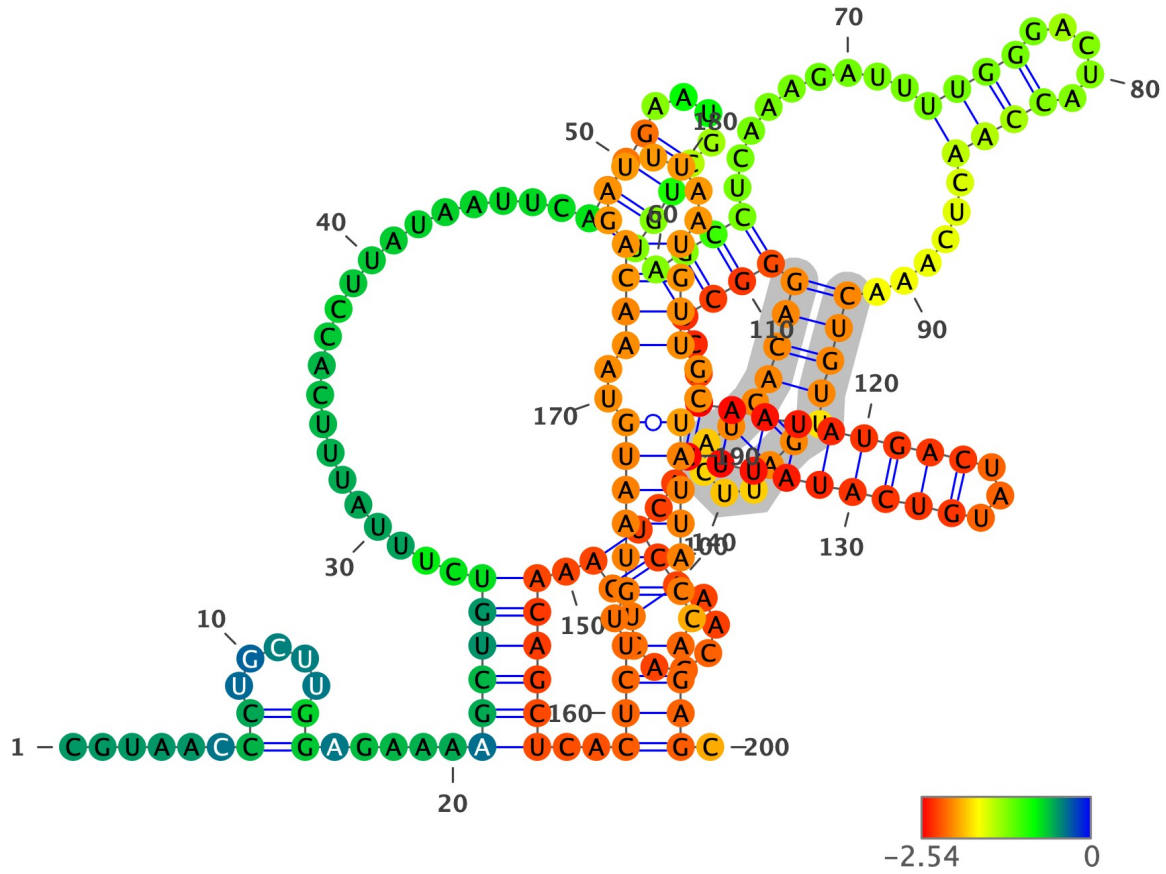
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 17831 to 17847 (nt 92 to 108)

```
5'-CUGUUGAUUCAUCACAG-3'
5'-((((.((....))))))-3'
Motif MFE = -1.6; z-score = -1.69; 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 17740 to 17939 (motif highlighted in silver):

```
5'-CGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGC
UCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGC-3
5'-......((.....)).....((((((.....................((((....))))((((.........((((.....)))).....((((.((....)))))))))
)..(((((((((...)))))))))..(((......))).))))))..((((.((((((..((((.......))))..)))))).)))).-3'
MFE = -41.3; z-score = -2.09; ED = 29.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

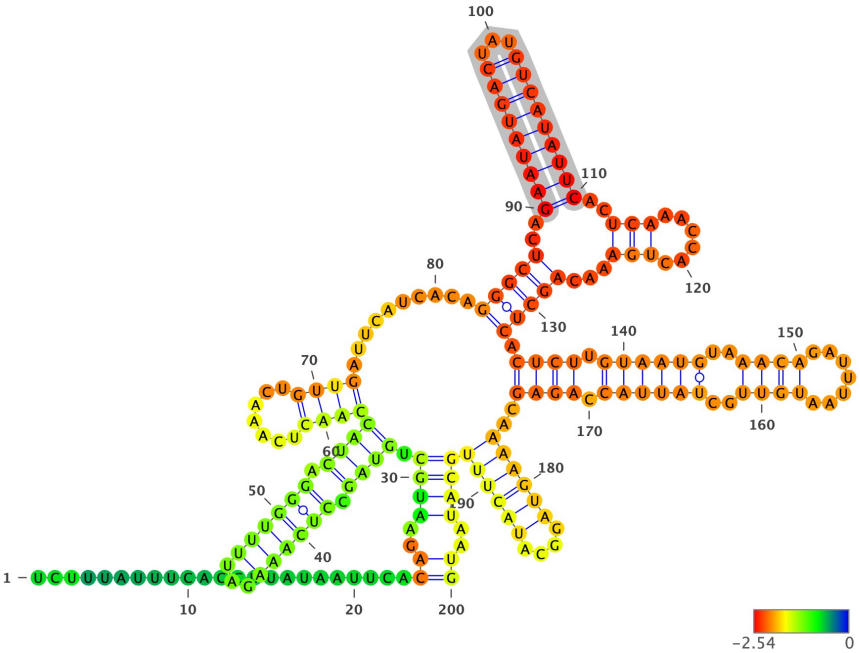
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 307 from nt 17854 to 17874 (nt 90 to 110)

```
5'-GAAUAUGACUAUGUCAUAUUC-3'
5'-((((((((((...)))))))))-3'
Motif MFE = -8.1; z-score = -5.95; 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 17765 to 17964 (motif highlighted in silver):

```
5'-UCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCA
CUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUG-3
5'-.......................((..((((.((((.((((((...)))))).))))((((.......))))..........(((((..(((((((((...))))))))).
.(((......)))...))))).((((.((((((..((((.......))))..)))))).))))..((((((....)))))))))..))-3'
MFE = -43.5; z-score = -2.88; ED = 28.44
```

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(+)

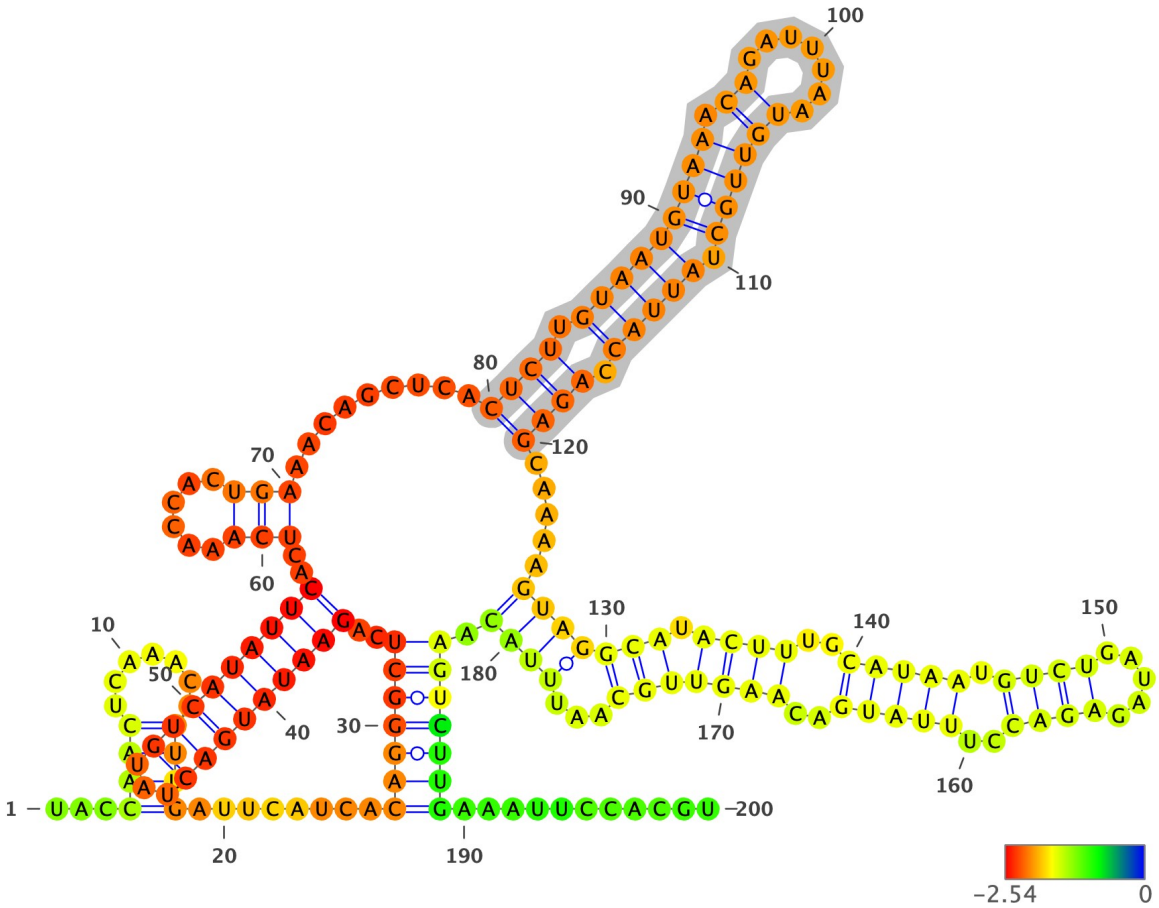
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 308 from nt 17898 to 17938 (nt 80 to 120)

```
5'-CUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAG-3'
5'-((((.(((((((((.((.......)))))).)))))).))))-3'
Motif MFE = -9.7; z-score = -2.55; ED = 3.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17819 to 18018 (motif highlighted in silver):

```
5'-UACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUA
UUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGU-3
5'-...((((.......))))........(((((((..(((((((((...)))))))))..(((......)))..........((((.(((((((((.((.......)))))).)
)))).))))).....(((((((.((((..(((((.((((.....))))..)))))..)))))))...)))).)))))))...........-3'
MFE = -44.4; z-score = -3.38; ED = 19.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

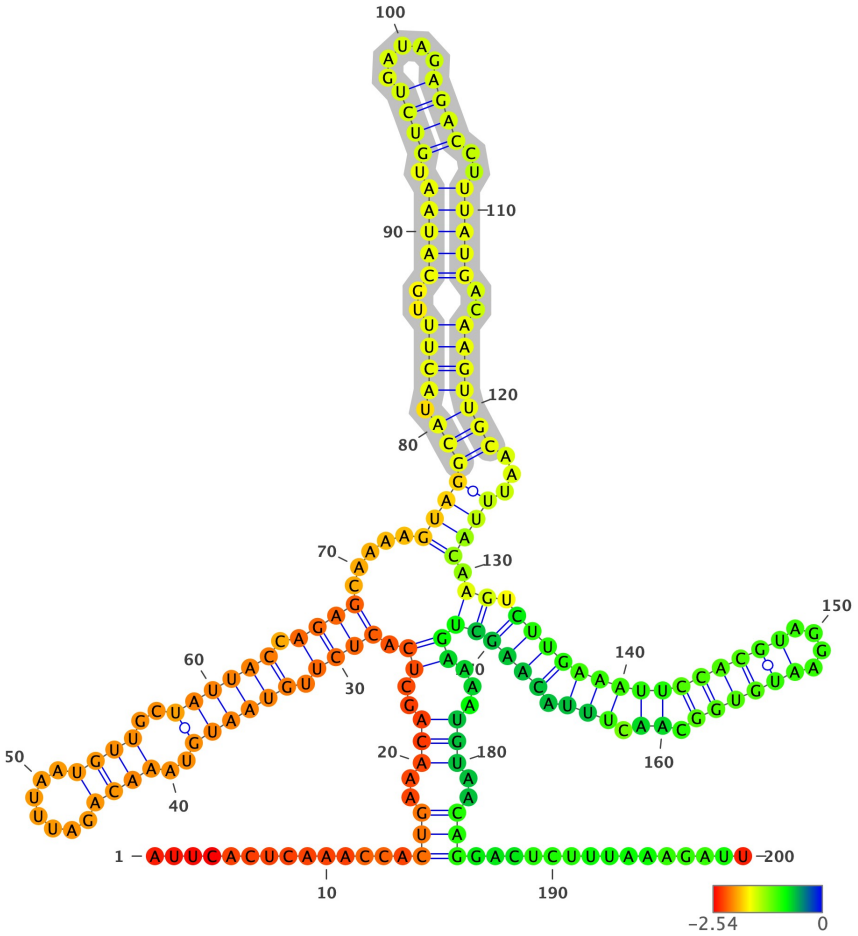
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 309 from nt 17948 to 17992 (nt 78 to 122)

```
5'-GCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGC-3'
5'-(((.(((((..((((((.((((.....)))).)).))))))..)))))))-3'
Motif MFE = -12.2; z-score = -3.29; ED = 3.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17871 to 18070 (motif highlighted in silver):

```
5'-AUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUA
UGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACUUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUU-3
5'-..............(((..((((..((.((((.((((((..((((.......)))).)).)))))).)))).....(((((((.((((..((((((.((((.....)))).)).)))
))..)))))))...)))).((.(((((((((((((((....)))))))).)).)))).)))))))).....))).))).....................-3'
MFE = -38.1; z-score = -1.26; ED = 39.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

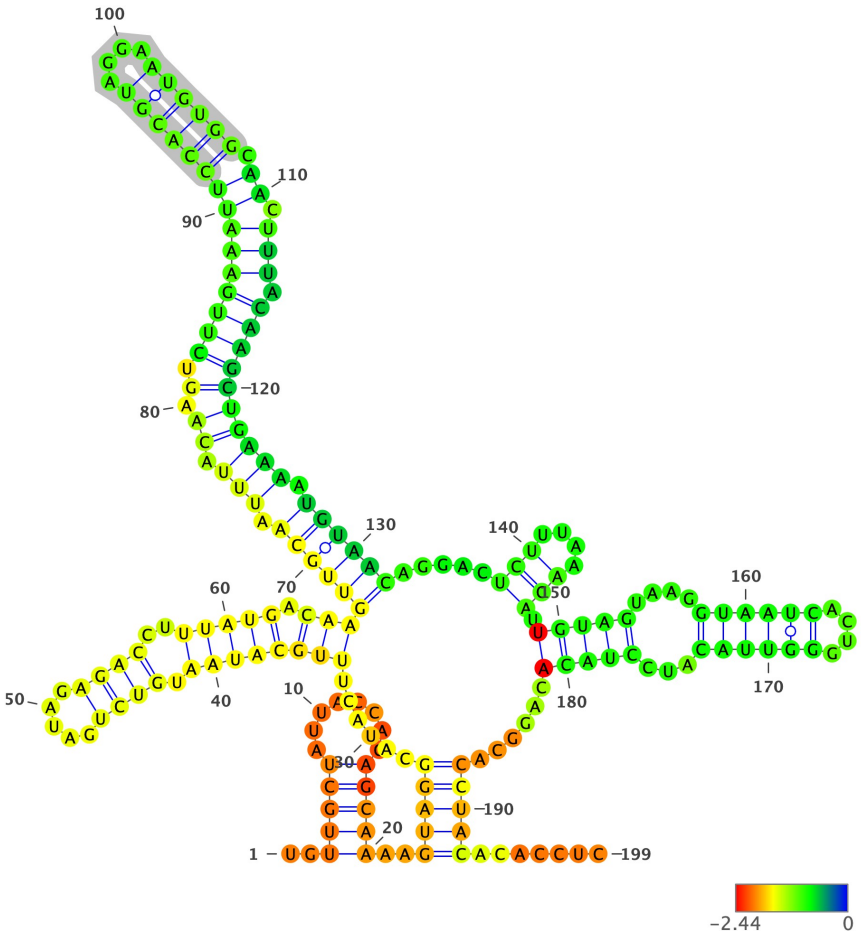
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 310 from nt 18013 to 18028 (nt 92 to 107)

```
5'-CCACGUAGGAAUGUGG-3'
5'-((((........))))-3'
Motif MFE = -5.3; z-score = -2.9; 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 17922 to 18120 (motif highlighted in silver):

```
5'-UGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAAC
UUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUC-3
5'-..(((((........)))))..(((((......((((((((.((((.....))))..))))).)))((((((.(((.((.(.((((((((((((((....))))))).)).
))).))))))))))).))))))).....(((....))).(((((....((((((....))))))...)))))......)))))........-3'
MFE = -44.1; z-score = -2.0; ED = 44.52
```

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(+)

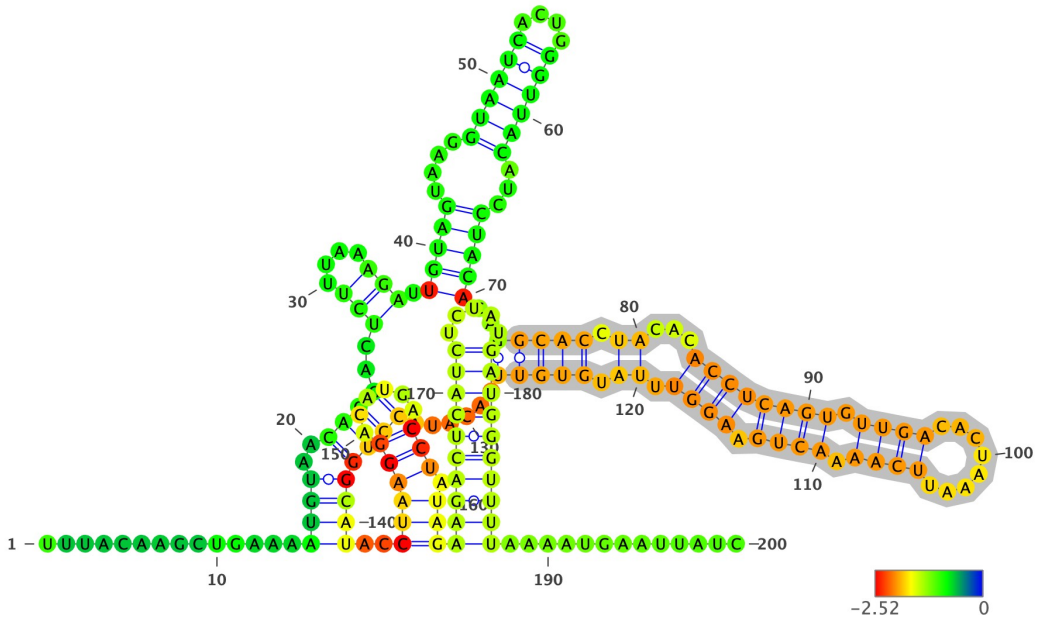
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 311 from nt 18106 to 18158 (nt 74 to 126)

```
5'-GCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGU-3'
5'-((((......((((((((.((((........)))).)))).)))).....))))-3'
Motif MFE = -13.5; z-score = -3.11; ED = 7.76
```



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 18033 to 18232 (motif highlighted in silver):

```
5'-UUUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAAC
UGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUC-3
5'-..............((((..((((..(((....))).(((((....((((((....))))))...)))))..(((((.((...((((((((.((((........)))).))
)).)))).)).)))))......))))))))..((((((......))).)))((((((((((.....))))))))))..............-3'
MFE = -43.1; z-score = -1.83; ED = 25.58
```

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(+)

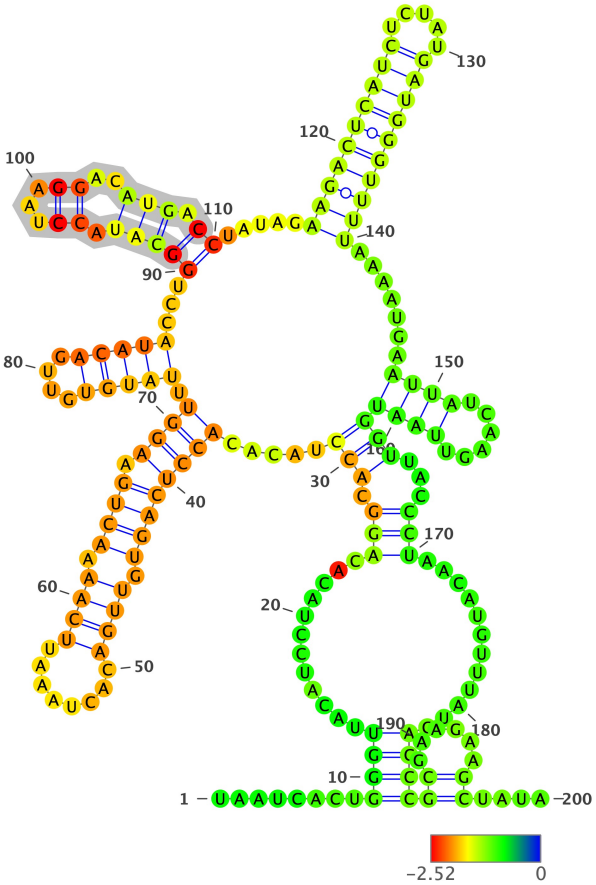
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 18170 to 18188 (nt 91 to 109)

```
5'-GCAUACCUAAGGACAUGAC-3'
5'-(.....(...).......)-3'
Motif MFE = 0.0; z-score = 0.84; ED = 2.63
```



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 18080 to 18279 (motif highlighted in silver):

```
5'-UAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCU
AUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUA-3
5'-........((((............(((.(((.....((((((((.((((........)))).)))).)))).(((((....)))))...(((((.((...)).)))).)).
....((((((((((.....))))))))))).......((((......)))))))...)))............))))((......))....-3'
MFE = -39.1; z-score = -2.18; ED = 38.57
```

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(+)

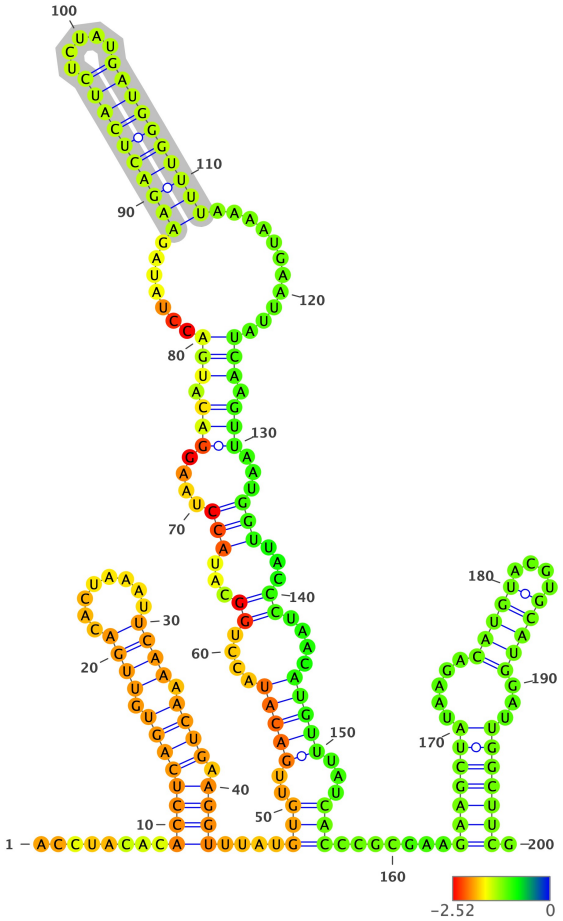
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 313 from nt 18195 to 18219 (nt 88 to 112)

```
5'-AAGACUCAUCUCUAUGAUGGGUUUU-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -10.1; z-score = -4.38; ED = 0.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18108 to 18307 (motif highlighted in silver):

```
5'-ACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUU
UAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCG-3
5'-........((((((((.((((........)))).)))).))))....(((..(((((....((...(((....(((.(((.......((((((((((.....)))))))))
)...........))).)))...)))...))....)))))...)))).......(((((((.....(((((....)))))...)))))))).-3'
MFE = -46.8; z-score = -1.75; 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(+)

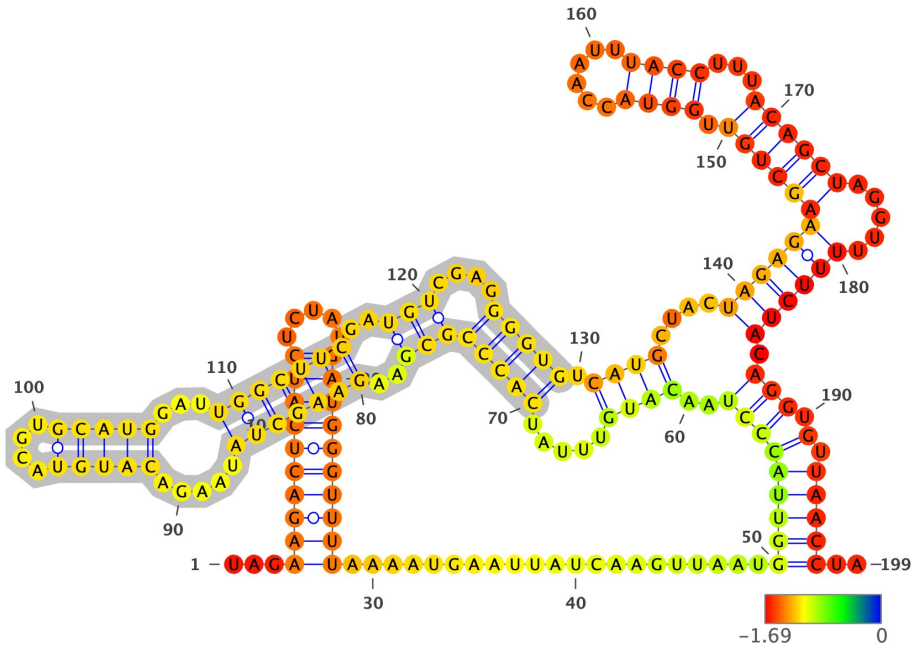
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 314 from nt 18261 to 18320 (nt 70 to 129)

```
5'-CACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUG-3'
5'-(((((((...(((((((.....(((((....)))))...)))))))...)).....)))))-3'
Motif MFE = -22.2; z-score = -2.82; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18192 to 18390 (motif highlighted in silver):

```
5'-UAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGG
CUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUA-3
5'-...((((((((((.....))))))))))....................(((((((((..((((.....((((((((..(((((((.....(((((....)))))...)))
))))..)))....))))).))))....((((((((((((.((((......))))...))))))).....)))))).))).).)))))..-3'
MFE = -53.3; z-score = -2.37; ED = 26.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

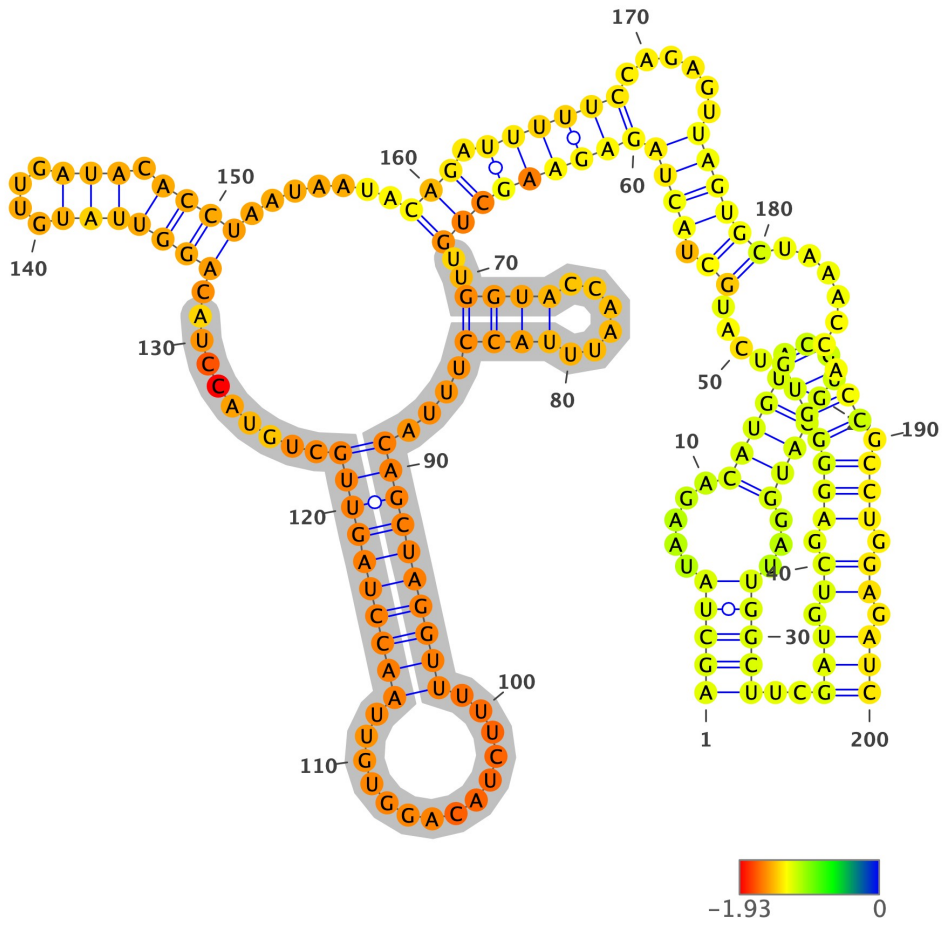
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 315 from nt 18341 to 18403 (nt 69 to 131)

```
5'-UUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUA-3'
5'-(...................((((((((((..............))))))))))........)-3'
Motif MFE = -15.4; z-score = -2.73; 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 18273 to 18472 (motif highlighted in silver):

```
5'-AGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGU
UAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUC-3
5'-(((((.....(((((....)))))...)))))..(((.((.(((((((....((.(((((((((((((..((((......))))....(((((((((.............
.))))))))))..........(((((((....))).))))).......))).))))))......))))))).....)))).))).)).)))-3'
MFE = -51.3; z-score = -1.58; ED = 46.42
```

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(+)

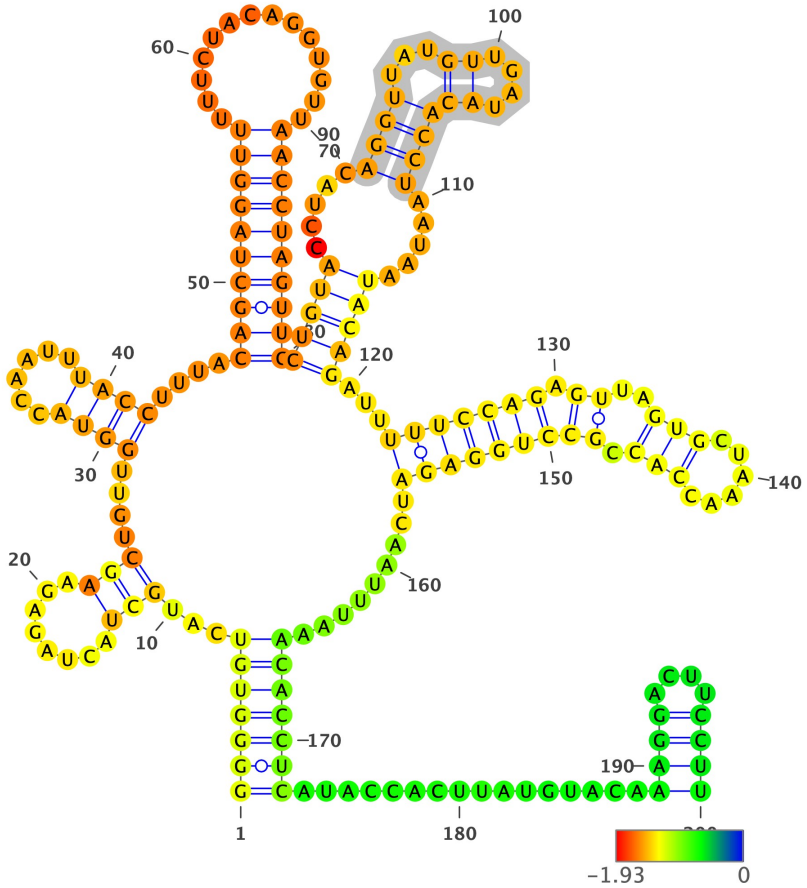
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 316 from nt 18405 to 18423 (nt 91 to 109)

```
5'-AGGUUAUGUUGAUACACCU-3'
5'-(((((...((....)))))))-3'
Motif MFE = -2.5; z-score = -1.74; ED = 2.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18315 to 18514 (motif highlighted in silver):

```
5'-GGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAA
UAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUU-3
5'-(((((((...(((........)))....((((......))))....((((((((((.............)))))))))))(((((.....((((...((....)))))))..
...)))))...(((((((.((..((((......)).)))))))))........)))))))................((((....))))-3'
MFE = -47.3; z-score = -2.36; ED = 21.93
```

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(+)

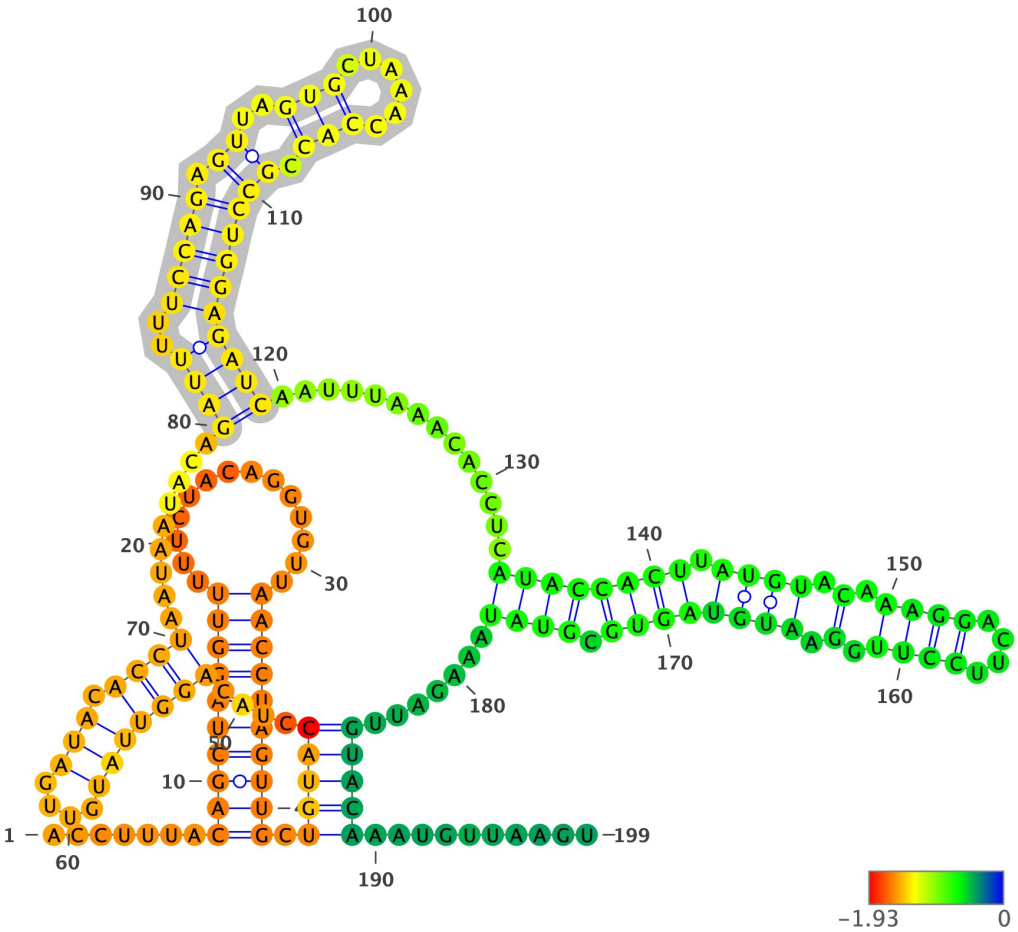
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 317 from nt 18433 to 18472 (nt 80 to 119)

```
5'-GAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUC-3'
5'-(((((..((((((.((..(((.....))).))))))))))-3'
Motif MFE = -10.7; z-score = -2.15; ED = 2.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18354 to 18552 (motif highlighted in silver):

```
5'-ACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCC
UGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUUGGAAUGUAGUGCGUAUAAAGAUUGUACAAAUGUUAAGU-3
5'-.......((((((((((.............)))))))))).(((((....(((((((....)))).))))).........((((..((((((.((..(((.....))).)))
)))))))).............((((((((.((((.(.((((....)))).).)))))))).)))).......)))))..........-3'
MFE = -40.5; z-score = -1.43; ED = 31.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

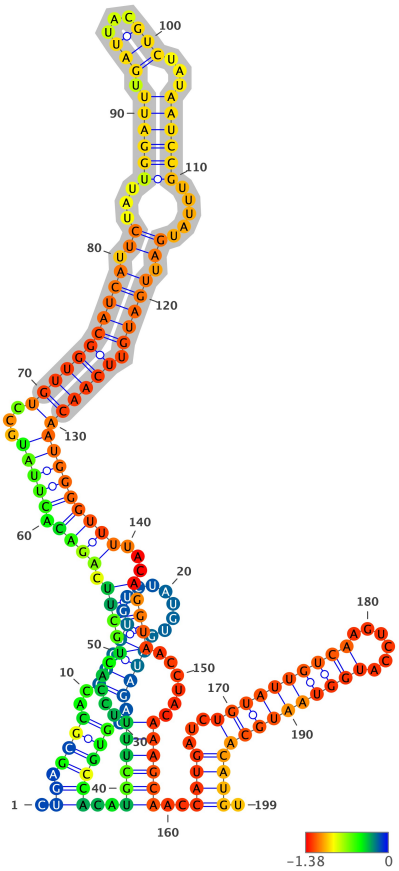
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 318 from nt 18716 to 18775 (nt 70 to 129)

```
5'-GUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAAC-3'
5'-((((((((((.((.................................)).)))))).)))))-3'
Motif MFE = -15.3; z-score = -3.0; ED = 5.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18647 to 18845 (motif highlighted in silver):

```
5'-CUGAGCGCACCUGUUGUCUAUGUGAUAGACGUGCCACAUGCUUUUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGU
UUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGU-3
5'-.((.((((..(((((........)))))..))))))..((((((.....(((((.((((.(((((...((((((((((.((...((((((.(((...)))...)))))).
....)).)))))).))))))))))))))...)))))......))))))..((((...((((((((((......)))))))))))))).-3'
MFE = -46.7; z-score = -1.03; ED = 52.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

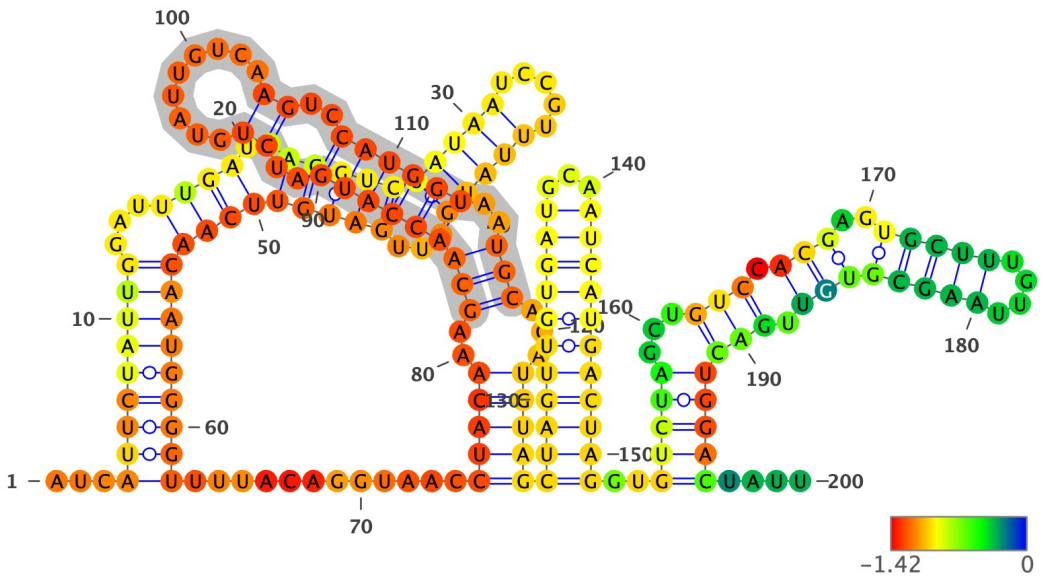
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 319 from nt 18803 to 18839 (nt 82 to 118)

```
5'-GCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGC-3'
5'-(((((((((..((.........))..)))))))..)))-3'
Motif MFE = -9.5; z-score = -2.28; ED = 4.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18722 to 18921 (motif highlighted in silver):

```
5'-AUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUG
GUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUU-3
5'-...(((((((((...((((..((((((((((.....)))))...)))))))))))))))))).............(((((..(((((((((..((.........)).)))))
)).)))...)))))((((((((((...))))))))))..(((((...(((.(((..(((((....)))))))).)))))))).....-3'
MFE = -49.4; z-score = -1.35; ED = 44.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

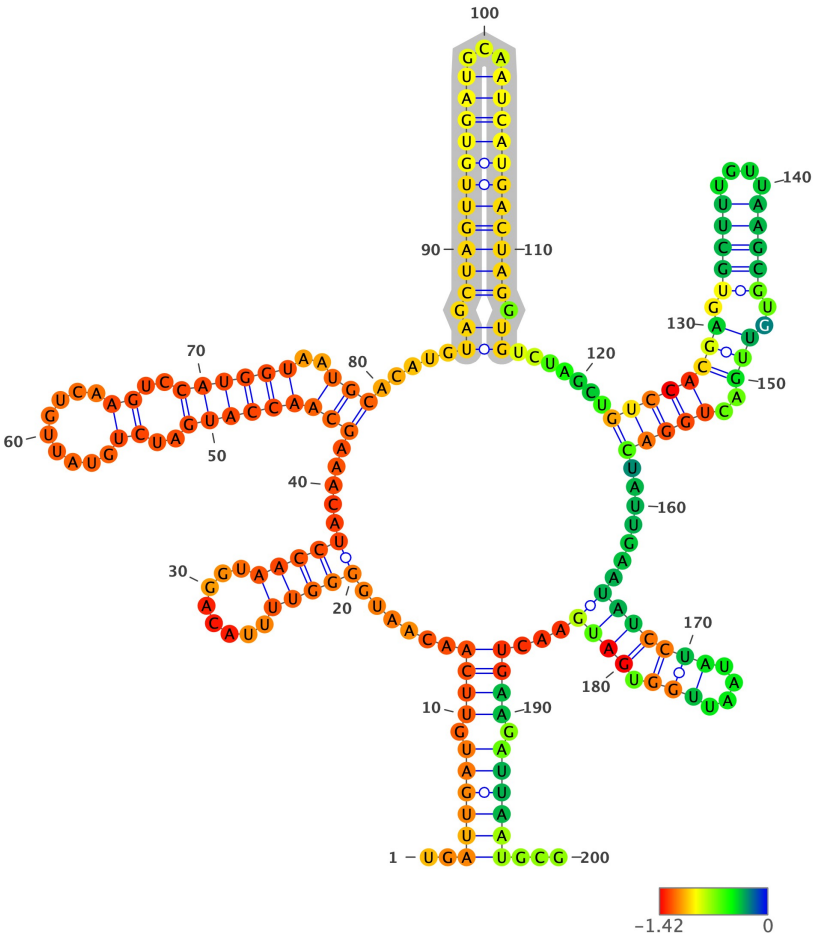
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 320 from nt 18845 to 18875 (nt 85 to 115)

```
5'-UAGCUAGUUGUGAUGCAAUCAUGACUAGGUG-3'
5'-((.((((((.............)))))).))-3'
Motif MFE = -11.7; z-score = -3.53; 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 18761 to 18960 (motif highlighted in silver):

```
5'-UGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUA
GGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGAACUGAAGAUUAAUGCG-3
5'-..((((((.((((......(((((........)))))).....(((((((((..((.........))..))))))..)))).....((.(((((((((((...)))))))))))
).)).......((((((((.(((((....)))))..)))..)))))).......(((((((....))).))))...)))).))))))...-3'
MFE = -50.2; z-score = -0.93; ED = 29.01
```

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(+)

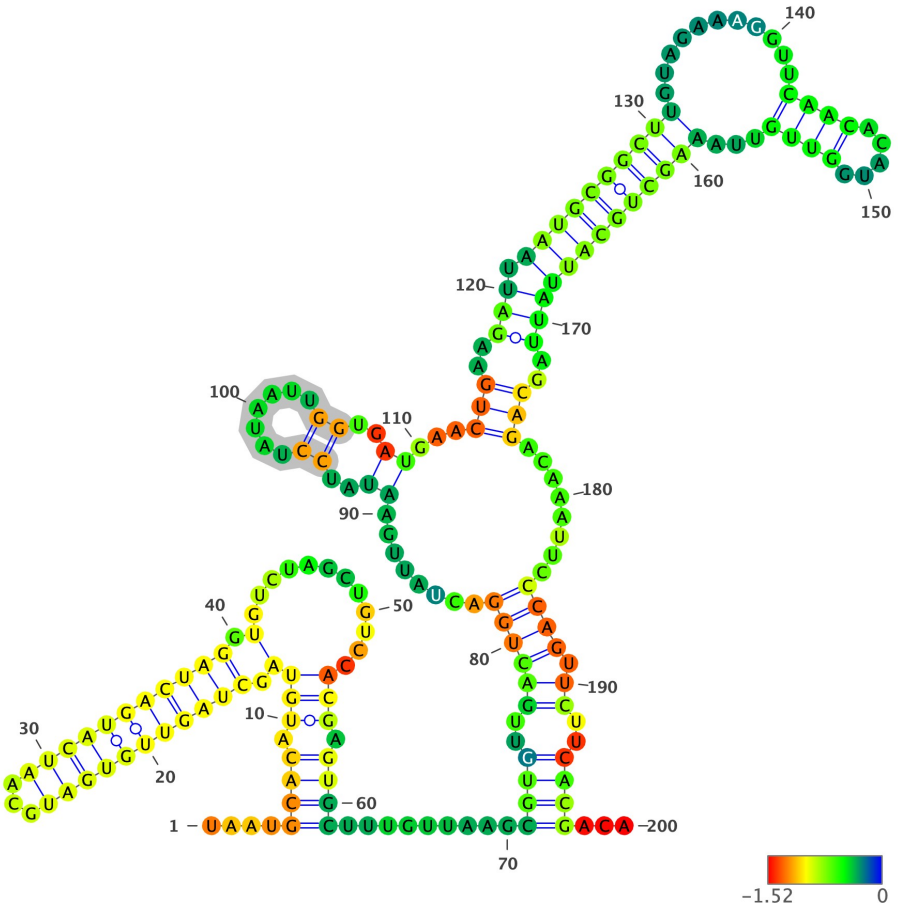
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 18928 to 18938 (nt 95 to 105)

```
5'-CCUAUAAUUGG-3'
5'-((.......))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 1.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18834 to 19033 (motif highlighted in silver):

```
5'-UAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGA
ACUGAAGAUUAAUGCGGCUUGUAGAAAGGUUCAACACAUGGUUGUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACA-3
5'-....((((.((((.(((((((((((...)))))))))))).)............))).))))).........((((..((((((.........((..((.......)).)).)).
.((((..((((.((((((((((.........((((.....)))))...)))))))))))))..)))........)))))..)))..))))...-3'
MFE = -47.8; z-score = -1.43; ED = 35.67
```

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(+)

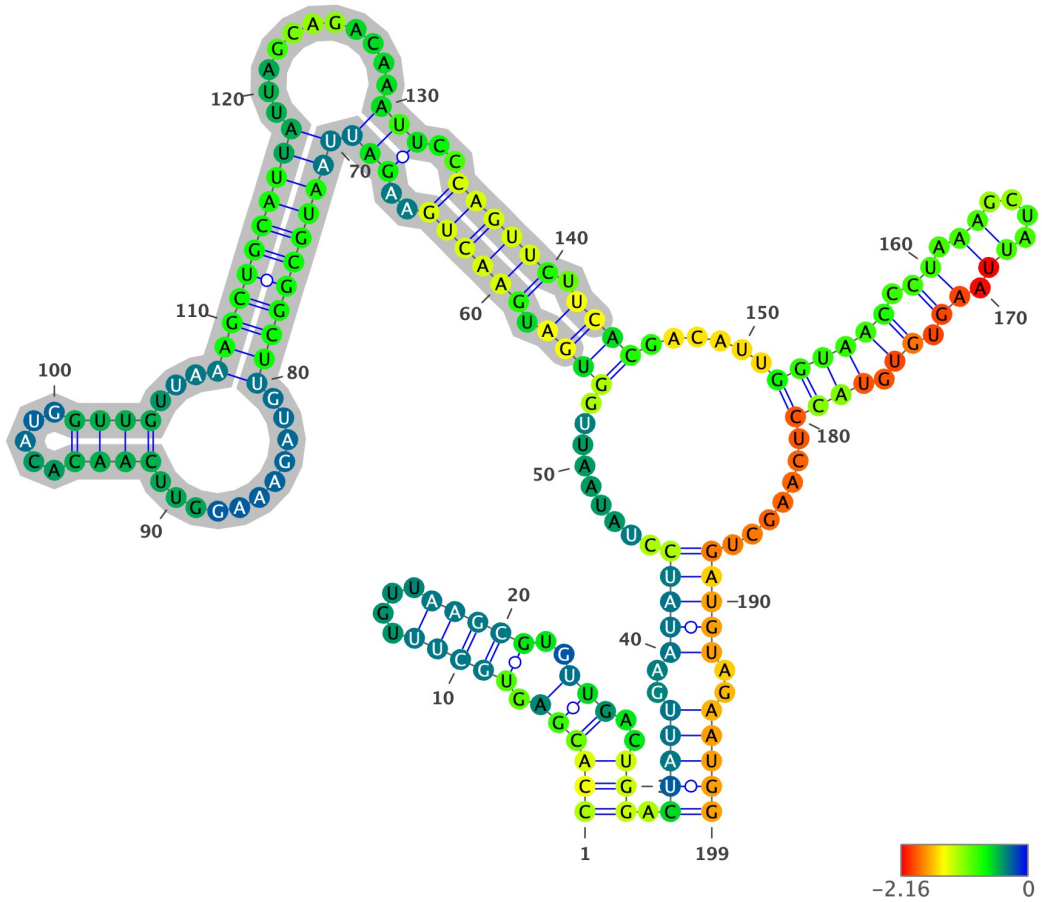
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 18940 to 19027 (nt 56 to 143)

```
5'-GAUGAACUGAAGAUUAAUGCGGCUUGUAGAAAGGUUCAACACAUGGUUGUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUC-3'
5'-((..(((((.....................................................................)))))..))-3'
Motif MFE = -20.5; z-score = -1.9; ED = 12.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18885 to 19083 (motif highlighted in silver):

```
5'-CCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGAACUGAAGAUUAAUGCGGCUUGUAGAAAGGUUCAACACAUGGUUGUUAAAGC
UGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGG-3
5'-((((((.(((((....)))))..)))..))).(((((..(((((.........((((.((((((..(((((((((((((((.........((((.....))))...))))
)))))))..........)))..))))))).))))......((((((.((.((....)).)).)).))))).......)))))..)))))-3'
MFE = -40.7; z-score = 0.64; ED = 35.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

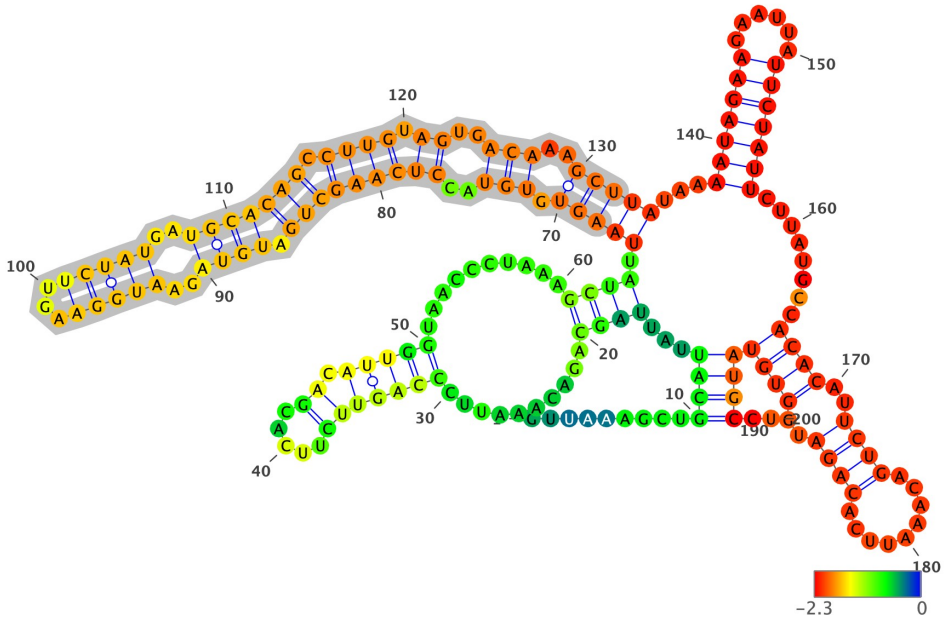
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 323 from nt 19055 to 19119 (nt 68 to 132)

```
5'-AGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCU-3'
5'-(((.(((..(((((((((.(((...((((.....))))...)))))).)))).))..)))..)))-3'
Motif MFE = -18.8; z-score = -2.56; ED = 6.8
```



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 18988 to 19187 (motif highlighted in silver):

```
5'-GUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCA
CAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCU-3
5'-.........((((...((((..........(((((((.....)).)))))..........)))).(((((.(((..(((((((((.((((..(((((...)))))..))))
))).)))).))..)))..)))))...(((((((......)))))))........((((..((((.........))))..))))))))..-3'
MFE = -42.9; z-score = -1.73; ED = 25.27
```

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(+)

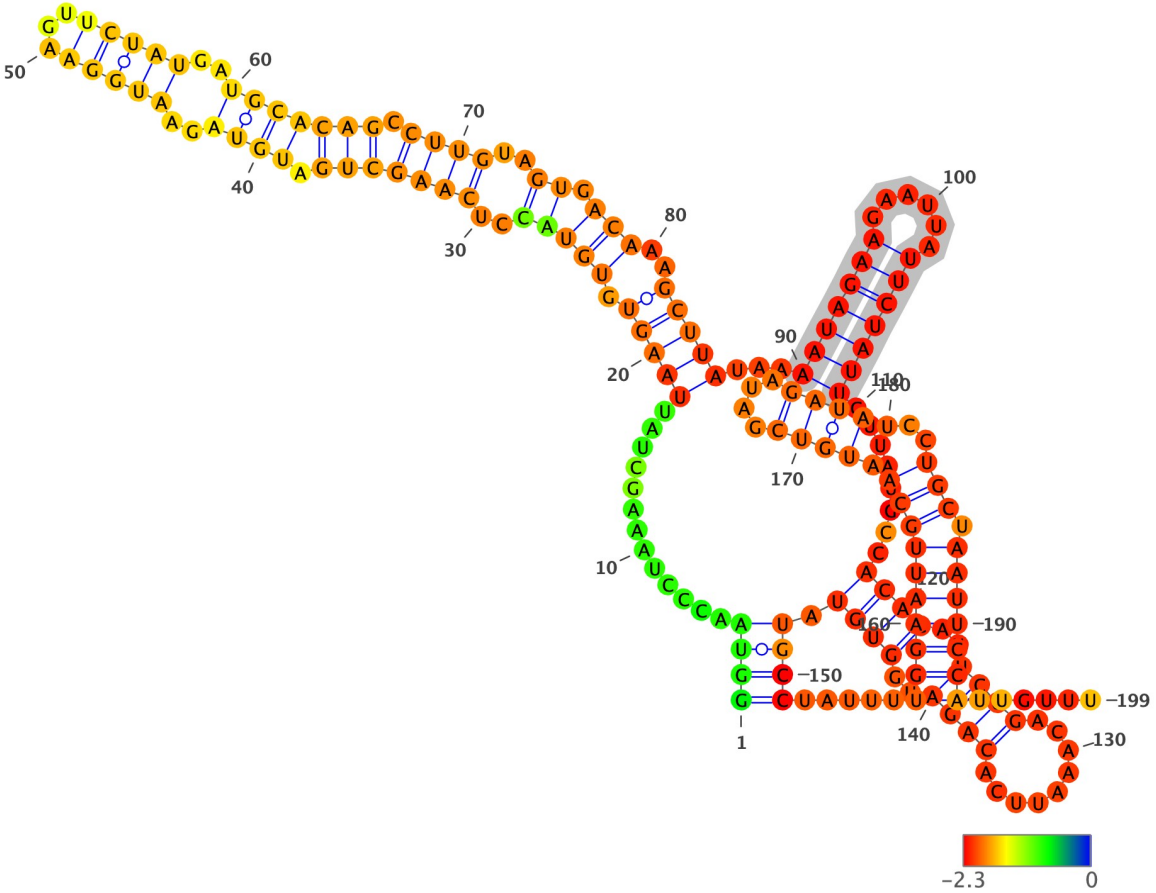
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 324 from nt 19125 to 19144 (nt 90 to 109)

```
5'-AAUAGAAGAAUUAUUCUAUU-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.0; z-score = -5.41; ED = 0.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19036 to 19234 (motif highlighted in silver):

```
5'-GGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCU
UAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUU-3
5'-((((.............(((((.(((((..(((((((.((((..(((((...)))))..)))))))).))))..)).)))..)))))...(((((((......)))))))..
......((((..((((.........))))..)))).))))).....((((((((((((((....)))))..))).)))))))......-3'
MFE = -50.8; z-score = -2.87; ED = 21.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

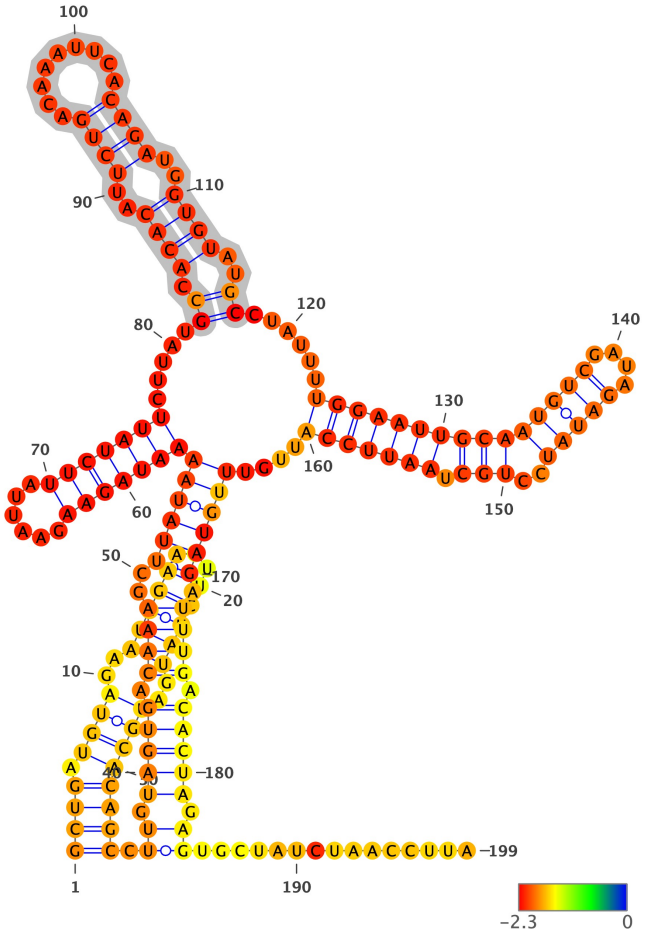
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 325 from nt 19150 to 19185 (nt 82 to 117)

```
5'-GCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGC-3'
5'-(..((((..((((.........))))..))))...)-3'
Motif MFE = -8.2; z-score = -1.87; ED = 1.84
```



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 19069 to 19267 (motif highlighted in silver):

```
5'-GCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGU
GUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUA-3
5'-((((.((((..(((((...)))))..)))))))).((.(((((.((((..((((((((((((((.....)))))))).....((.((((..((((.........))))..))
))..)).....((((((((((((((....)))))..))).)))))))....)))))).)))).)))))).)).................-3'
MFE = -49.7; z-score = -2.8; ED = 24.26
```

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(+)

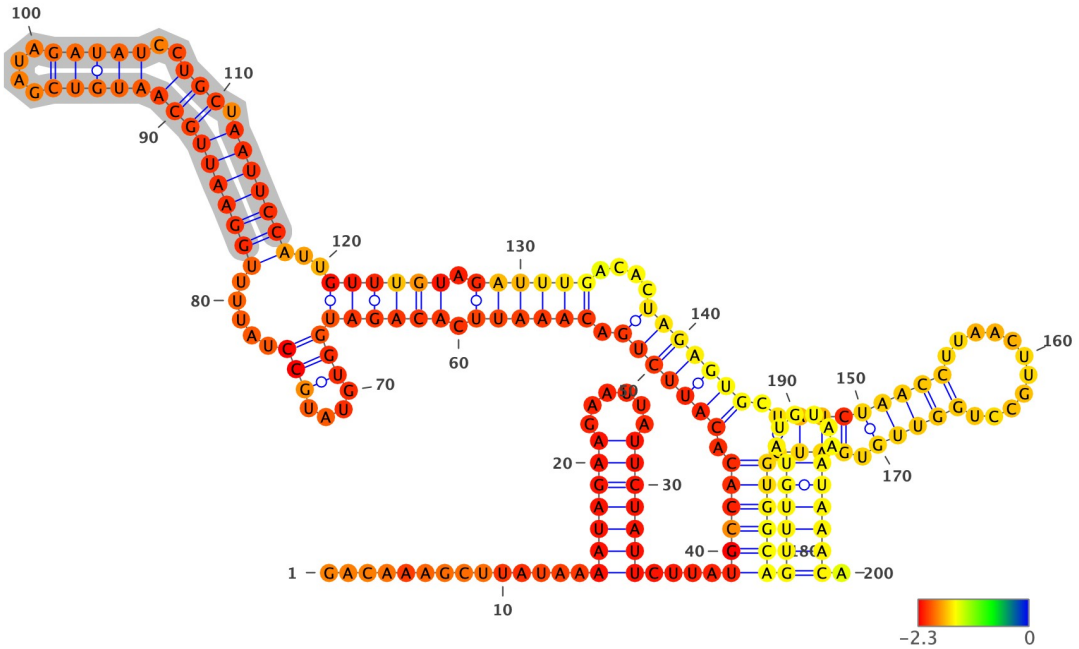
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 326 from nt 19193 to 19227 (nt 83 to 117)

```
5'-GGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCC-3'
5'-(((((((((((((((....)))))..))).))))))-3'
Motif MFE = -11.2; z-score = -3.53; ED = 0.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19111 to 19310 (motif highlighted in silver):

```
5'-GACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCU
AAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACA-3
5'-..............(((((((......)))))))....((((((.(((((((.((((((.((((((((((....)))).....((((((((((((((((....)))))..))).
)))))))..)))))).)))))).....))))))).((((((((((...........)))))).))))))))))((((((......)))))).-3'
MFE = -49.3; z-score = -3.07; ED = 27.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

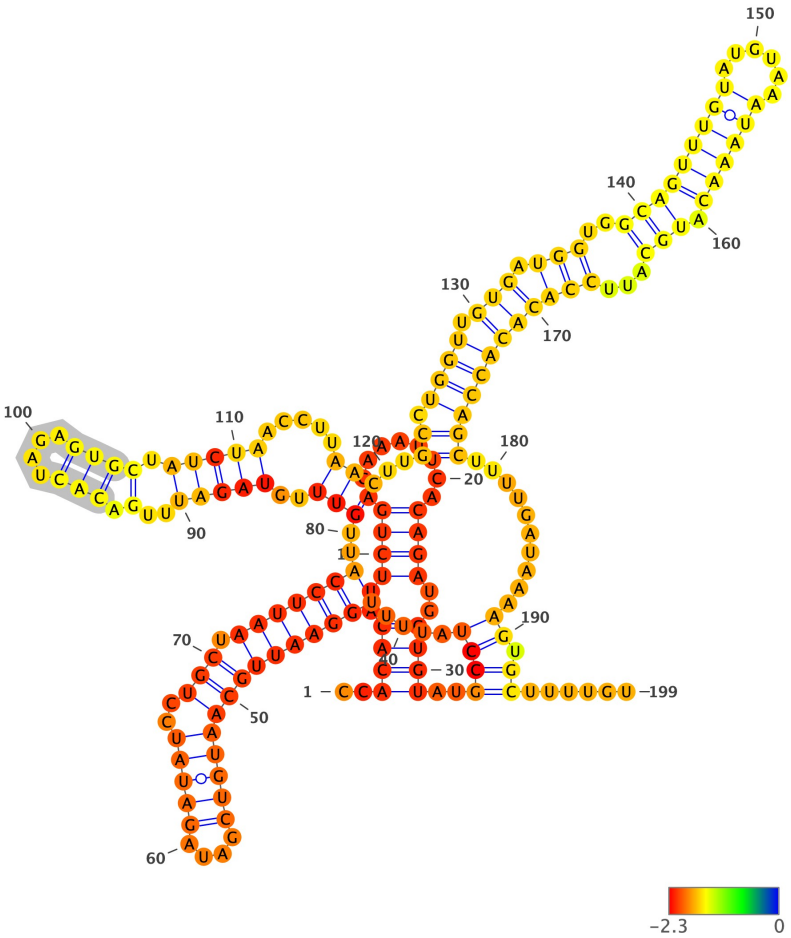
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 327 from nt 19245 to 19254 (nt 95 to 104)

```
5'-CACUAGAGUG-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = 0.21; ED = 1.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19151 to 19349 (motif highlighted in silver):

```
5'-CCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUA
ACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGU-3
5'-..((((..((((.........))))..))))..((((....(((((((((((((((....)))))..))).)))))))..(((..(((((..(.(((....)))).)))))
.....)))..((.((((.(((.(((..(((((((((.....))))))).)))...))))))))))))..........)).)).....-3'
MFE = -47.5; z-score = -1.99; ED = 28.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

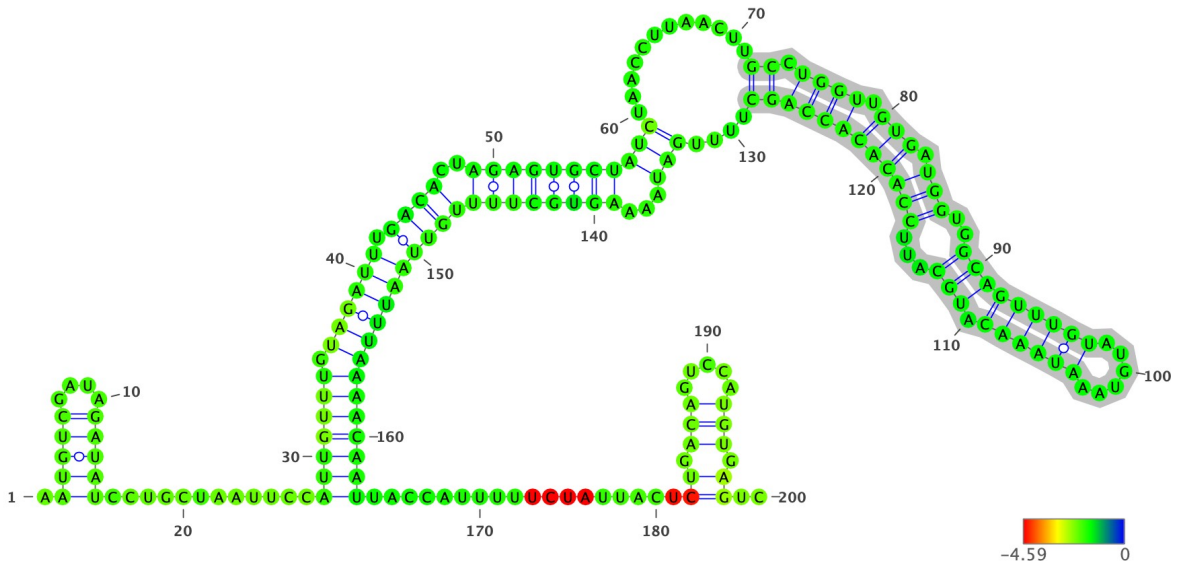
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 328 from nt 19272 to 19328 (nt 72 to 128)

```
5'-GCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGC-3'
5'-((.((((.(((.(((..((((((((((......))))))).)))...)))))))))))))-3'
Motif MFE = -20.3; z-score = -3.09; ED = 3.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19201 to 19400 (motif highlighted in silver):

```
5'-AAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAU
GCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUC-3
5'-.(((((....)))))............(((((((.((((((.((((..(((((((((((.............((.((((.(((.(((..(((((((((......))))))).)
))...))))))))))))....)))...))))))))))))))))))))))))))).................((.(((.....))).))..-3'
MFE = -40.1; z-score = -1.2; 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(+)

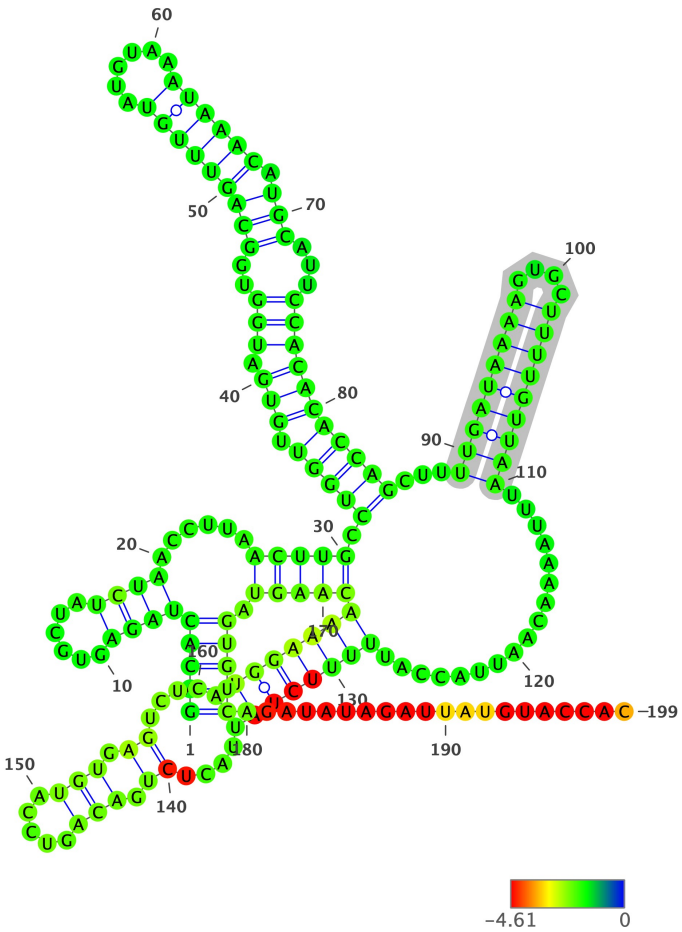
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 329 from nt 19331 to 19352 (nt 89 to 110)

```
5'-UUGAUAAAAGUGCUUUUGUUAA-3'
5'-((((((((((....)))))))))-3'
Motif MFE = -2.8; z-score = -2.04; ED = 1.29
```



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 19243 to 19441 (motif highlighted in silver):

```
5'-GACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAU
UUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCAC-3
5'-((((((((((......))))......(((((.(((((.(((.(((..((((((((((......))))))).)))...))))))))))))...((((((((((....))))))))).
................((((((((....((.(((.....))).)).....)))))))))))))).)))))....................-3'
MFE = -43.8; z-score = -1.7; ED = 39.94
```

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(+)

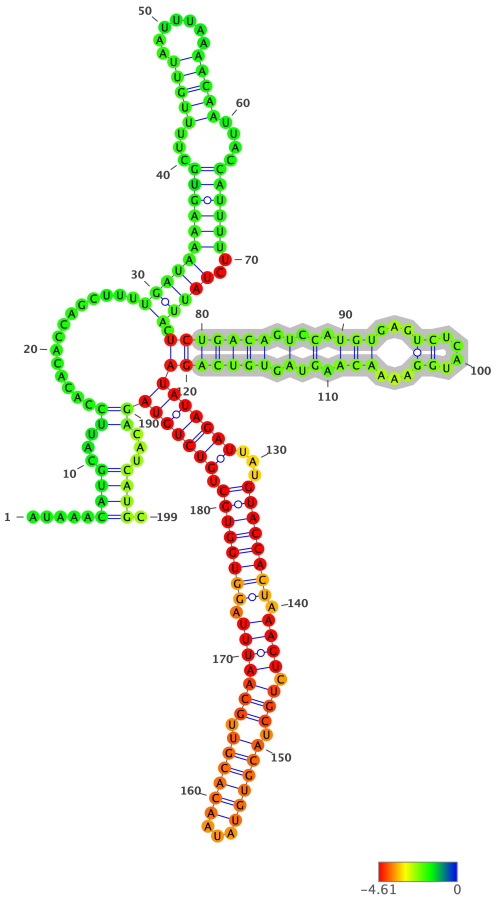
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 19383 to 19422 (nt 80 to 119)

```
5'-UGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCA-3'
5'-(((((.(.(.(((...((....))...))).).).)))))-3'
Motif MFE = -7.9; z-score = -1.14; ED = 6.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19304 to 19502 (motif highlighted in silver):

```
5'-AUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAG
UAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGC-3
5'-.....((((...((..............((((((((((...(((((.......)))))....))))))..))))).(((((((.(.(.(((...((....))...))).)
.).)))))))(((((((...((((((((.((((.(((.((((((...)))))).)))))))).)))))))).))))))))...)))).-3'
MFE = -48.7; z-score = -3.43; ED = 36.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

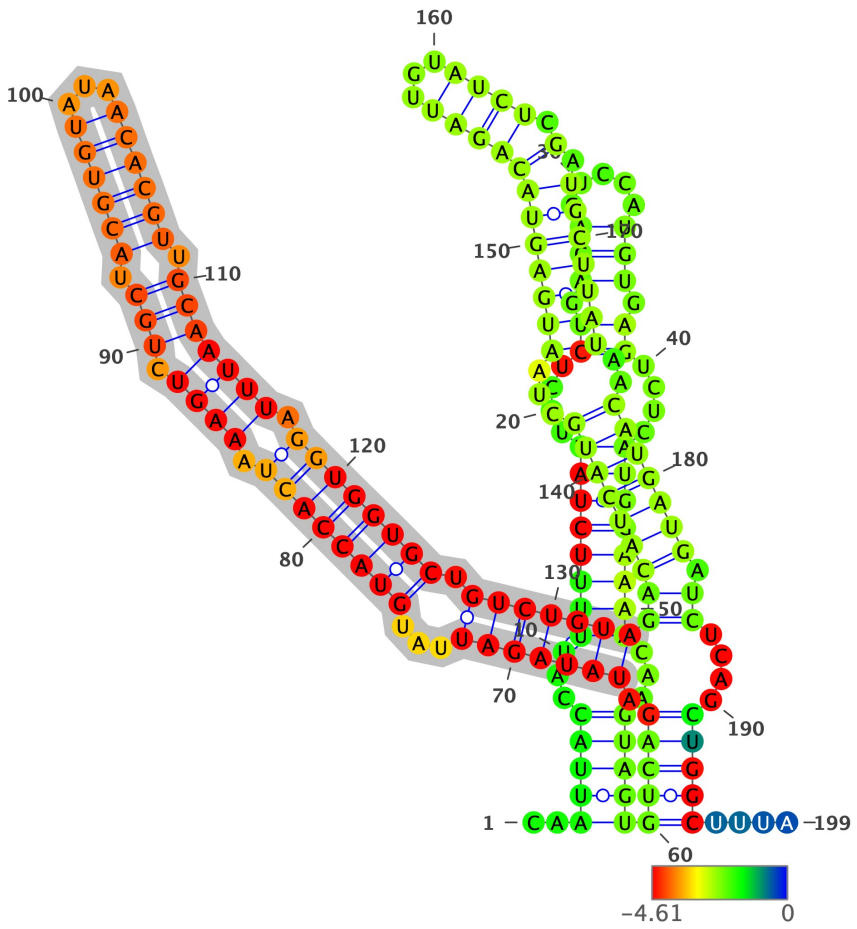
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 331 from nt 19425 to 19492 (nt 66 to 133)

```
5'-UAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUA-3'
5'-(((((((...((((((...((((.(((.((((((...)))))).)))))))...)))))).)))))))-3'
Motif MFE = -29.1; z-score = -6.04; 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 = -4.7; ED = 15.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

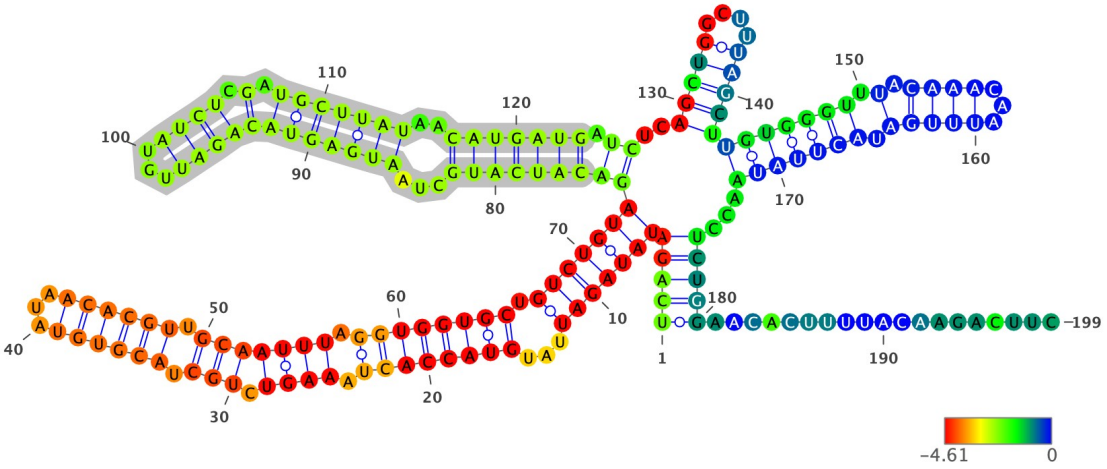
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 332 from nt 19495 to 19542 (nt 76 to 123)

```
5'-CAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUG-3'
5'-(((((((...(((((((((((((...)))).).)))))))..)))))))-3'
Motif MFE = -13.0; z-score = -3.06; ED = 4.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19420 to 19618 (motif highlighted in silver):

```
5'-UCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCU
UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUC-3
5'-(((((((((((...((((((((.((((.((((.((((((...)))))).)))))))).))))))))).)))))))(((((((((...(((((((((((...)))).).))))
)))..)))))))).))..(((((....)))))(((((((.(.((((...)))))).)))))))...)))))).....................-3'
MFE = -56.0; z-score = -4.05; ED = 13.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

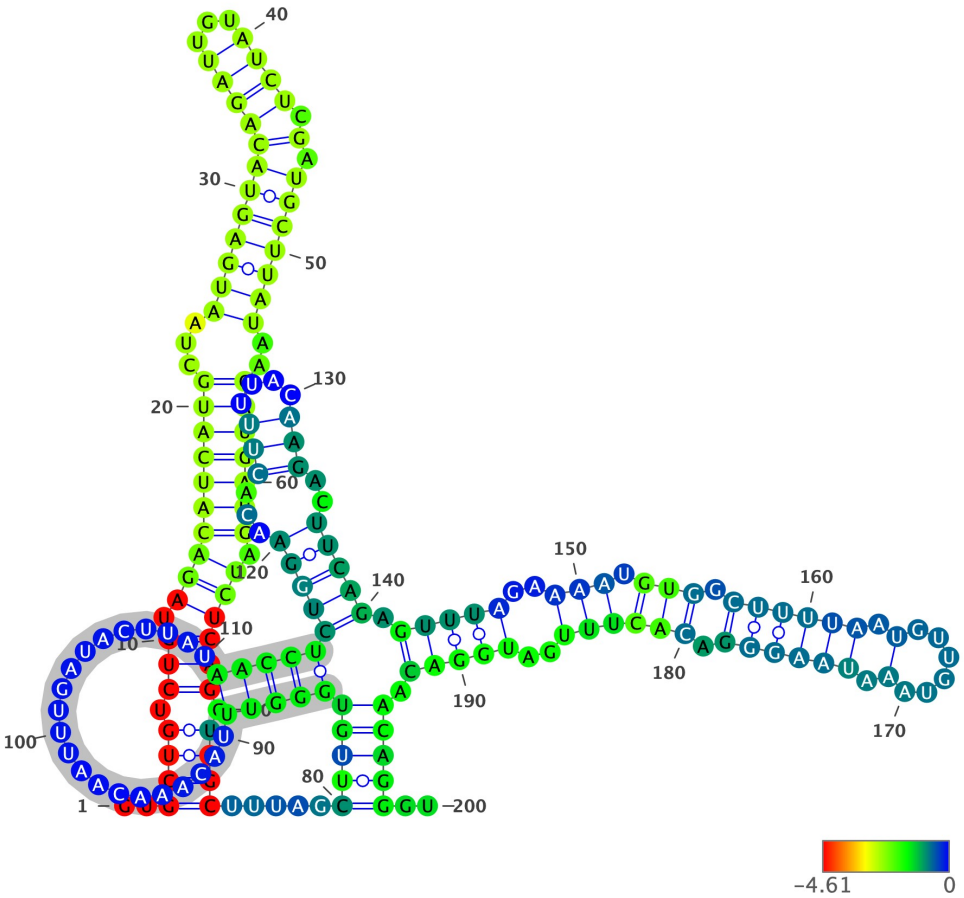
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 333 from nt 19565 to 19595 (nt 85 to 115)

```
5'-GGGUUUACAAACAAUUUGAUACUUAUAACCU-3'
5'-(((((.....................)))))-3'
Motif MFE = -1.6; z-score = 0.15; ED = 6.19
```



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 19481 to 19680 (motif highlighted in silver):

```
5'-GUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUA
ACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGU-3
5'-..(((((.(((.(((((((((((...(((((((((((...)))))).).)))))))..)))))))).)))))).)))).....((((((((((.....................)
))))((((((...(((....))))..)))))).((((((..(((.(((.((((((.(......).)))))).)))))).))))).)))))..-3'
MFE = -41.5; z-score = -0.68; ED = 45.11
```

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(+)

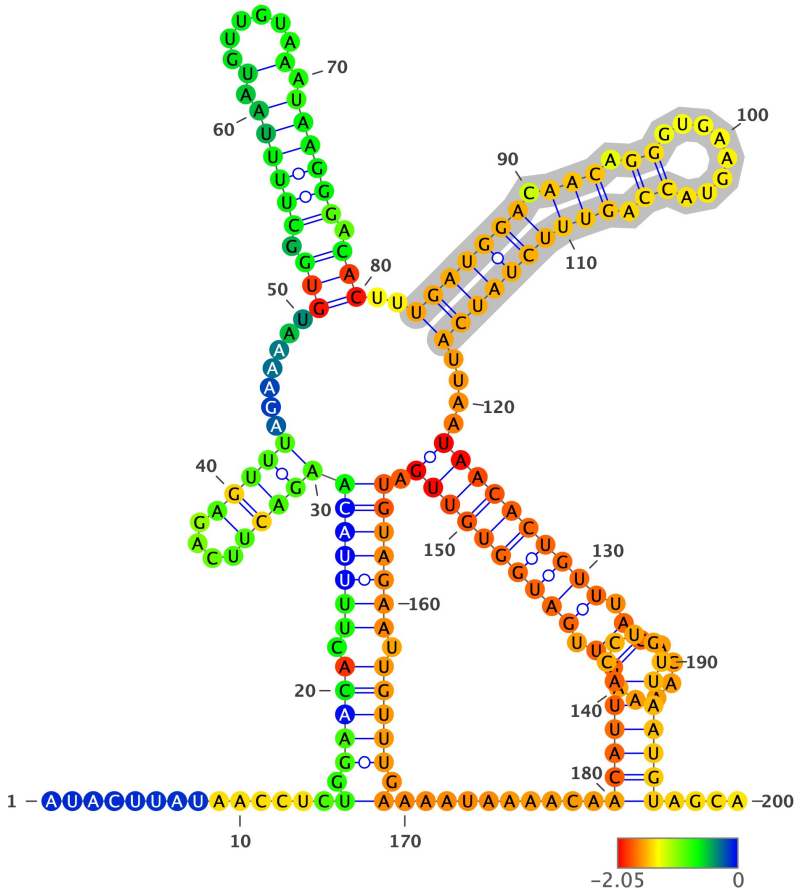
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 334 from nt 19665 to 19699 (nt 83 to 117)

```
5'-UGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCA-3'
5'-(((((((.(((.((........)).))))))))))-3'
Motif MFE = -10.3; z-score = -2.48; ED = 3.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19583 to 19782 (motif highlighted in silver):

```
5'-AUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUU
CUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCA-3
5'-..............(.(((((.(((((((((((((....)))))).......(((.((((((.(......).))))))).)))..(((((((.(((.((........)).))))
))))))....((((((((((.((......)).))))))))))).)))))))).)))))).)..........((((((.....))))))....-3'
MFE = -38.3; z-score = -1.11; ED = 47.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

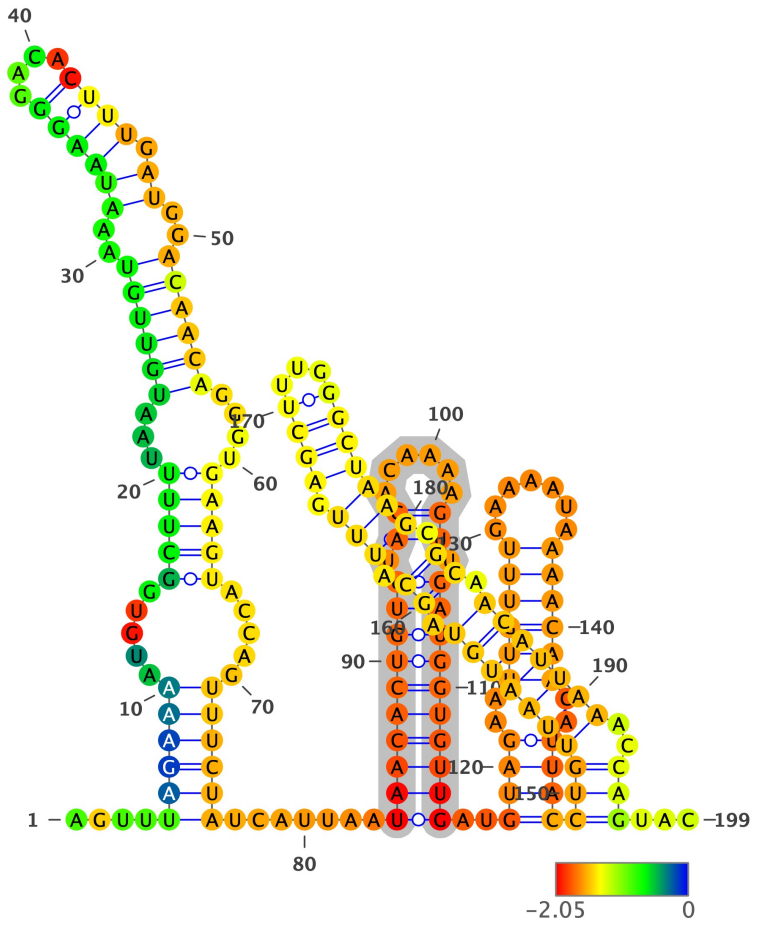
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 335 from nt 19704 to 19735 (nt 84 to 115)

```
5'-UAACACUGUUUACACAAAAGUUGAUGGUGUUG-3'
5'-((((((((((.((......)).))))))))))-3'
Motif MFE = -8.8; z-score = -3.28; ED = 1.48
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19621 to 19819 (motif highlighted in silver):

```
5'-AGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGU
GUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUAC-3
5'-....((((((.....(((((...((((((..((((((....)))).))..))))))....)))))).....)))))).......((((((((((.((......)).))))))
))))..((((..((((((.......))))))..))))((((((((((.((.(((.((((...)))))))).)).)))))))..)))...-3'
MFE = -43.8; z-score = -1.55; ED = 46.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

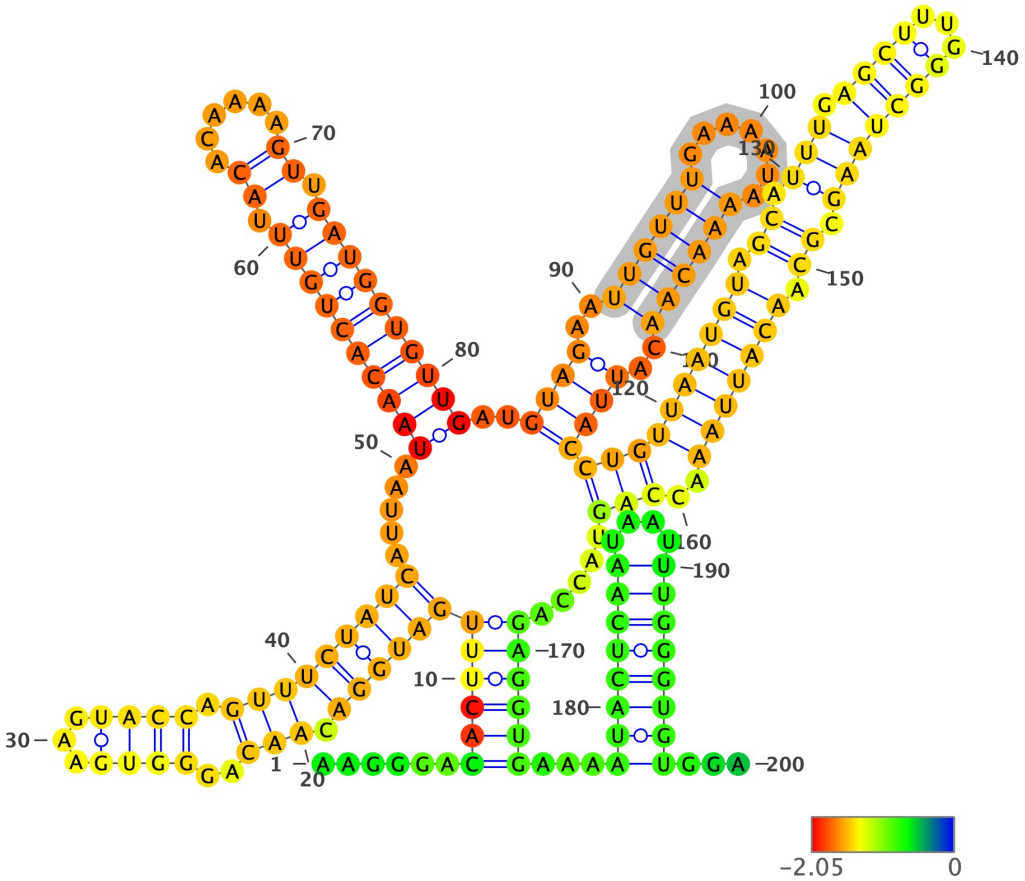
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 336 from nt 19744 to 19762 (nt 91 to 109)

```
5'-UUGUUUGAAAAUAAAACAA-3'
5'-((((((.......))))))-3'
Motif MFE = -2.1; z-score = -3.98; 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 = -2.5; 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(+)

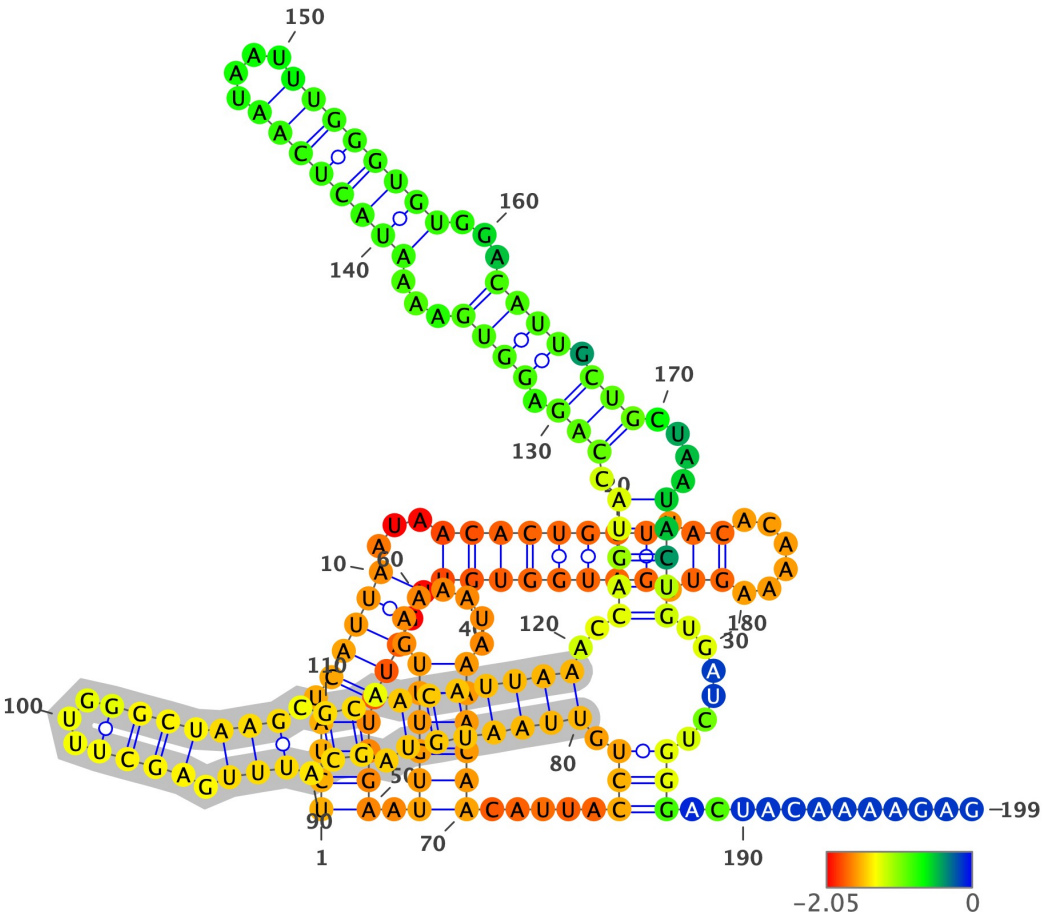
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 337 from nt 19772 to 19811 (nt 80 to 119)

```
5'-UUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAA-3'
5'-(((((((.((.(((.(((.....)))))).)).)))))))-3'
Motif MFE = -10.5; z-score = -2.61; 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 = -1.69; 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(+)

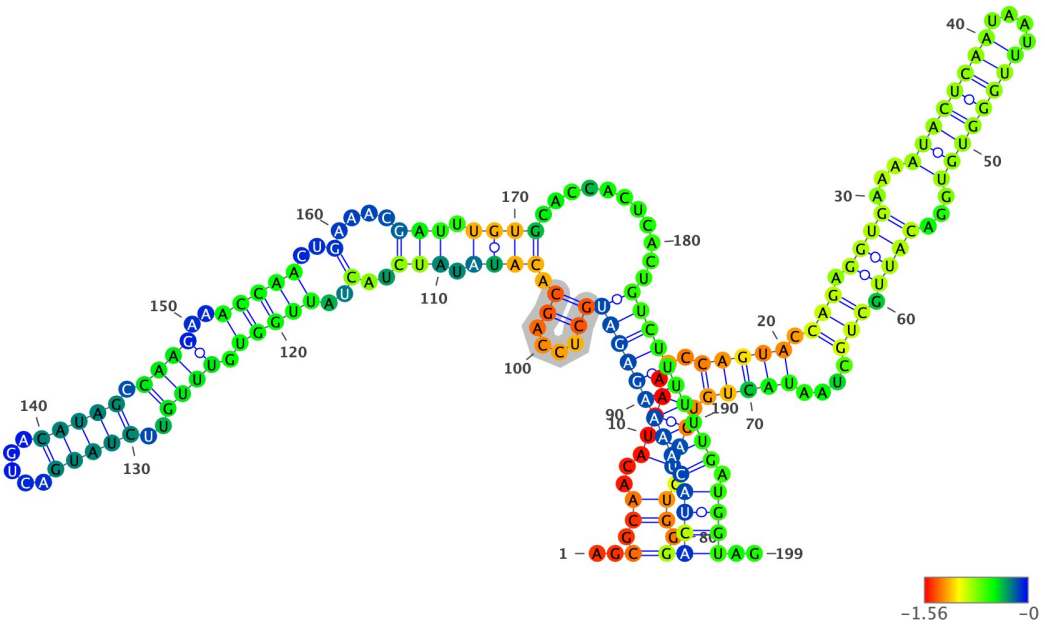
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 338 from nt 19894 to 19901 (nt 96 to 103)

```
5'-GCUCCAGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19799 to 19997 (motif highlighted in silver):

```
5'-AGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAGAUGCUCCAGCACAUAUAU
CUACUAUUGGUGUUUGUUCUAUGACUGACAUAGCCAAGAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAG-3
5'-..(.((..((((...(((((.(((.((((...((((((((....))))))))...)))).)))....)))))))))).)).)((((((((((((((((....)).((((.((
(..(..(((((.((((..(((((.....))))).))))..)))))..)....))).)))).....)))))))))).))))..-3'
MFE = -40.7; z-score = -0.48; ED = 43.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

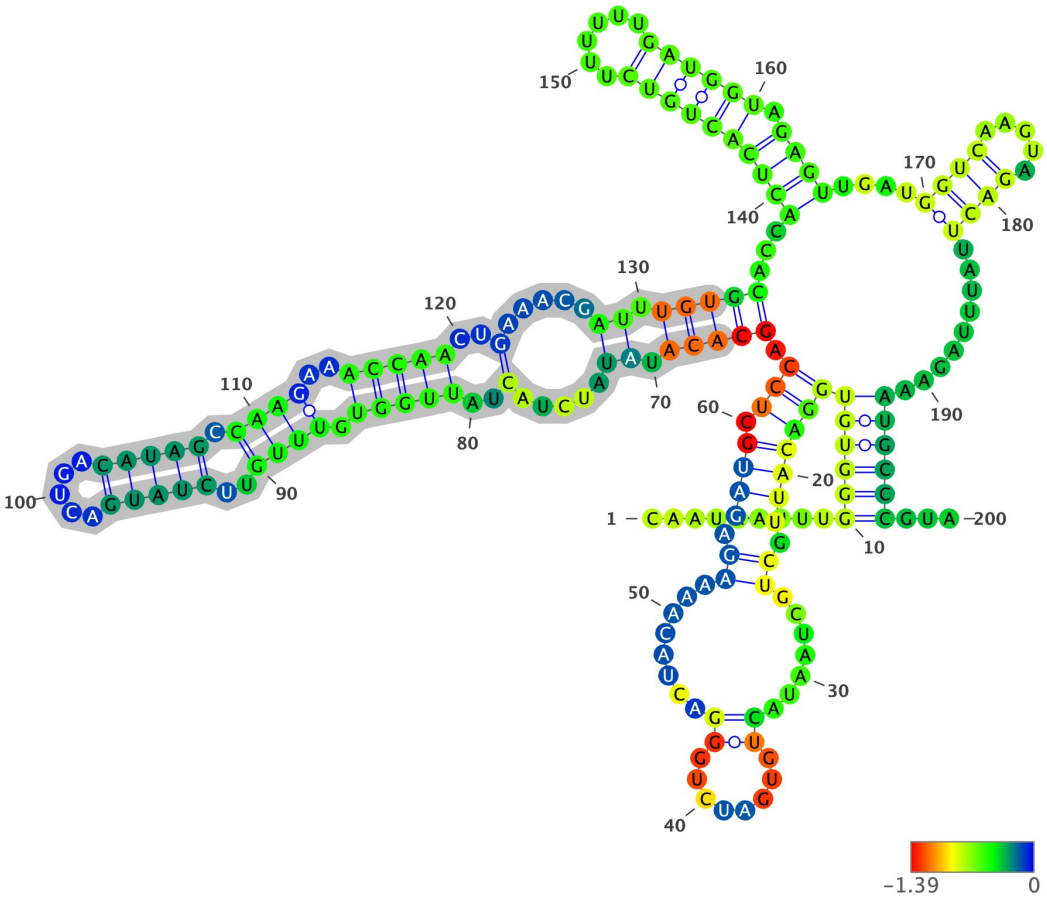
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 339 from nt 19902 to 19968 (nt 67 to 133)

```
5'-ACAUAUAUCUACUAUUGGUGUUUGUUCUAUGACUGACAUAGCCAAGAAACCAACUGAAACGAUUUGU-3'
5'-(((.............................................................)))-3'
Motif MFE = -9.4; z-score = -0.36; ED = 9.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19836 to 20035 (motif highlighted in silver):

```
5'-CAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAGAUGCUCCAGCACAUAUAUCUACUAUUGGUGUUUGUUCUAUGACUGACAUAGCCAA
GAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAGAGUUGAUGGUCAAGUAGACUUAUUUAGAAAUGCCCGUA-3
5'-.........((((((((((((.((.......((........)).......)).)))).))).(((((.((.....(..(((((.((((..(((((.....)))))).)))
)..)))))..).....)).)))))...((((((((((.....)))))).)))).....((((.....)))).........)))))).....-3'
MFE = -42.1; z-score = 0.28; ED = 29.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

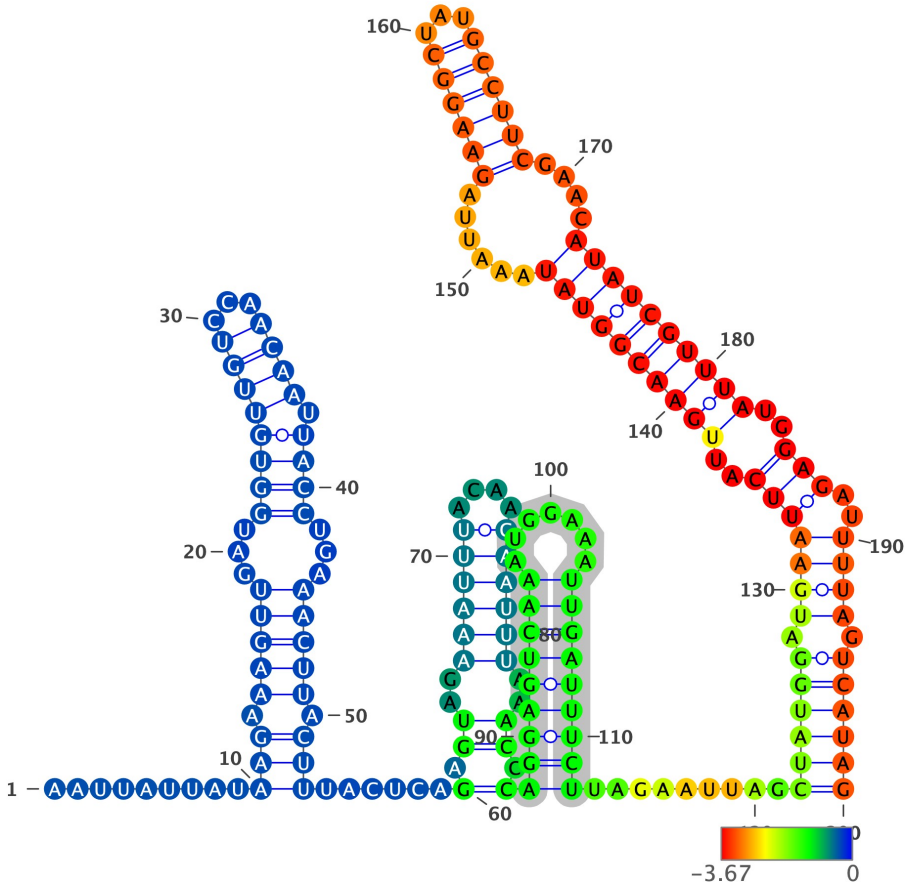
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 340 from nt 20236 to 20260 (nt 88 to 112)

```
5'-AGGAGUCAAAUGGAAAUUGAUUUCU-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.1; z-score = -3.17; 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 = -2.59; 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(+)

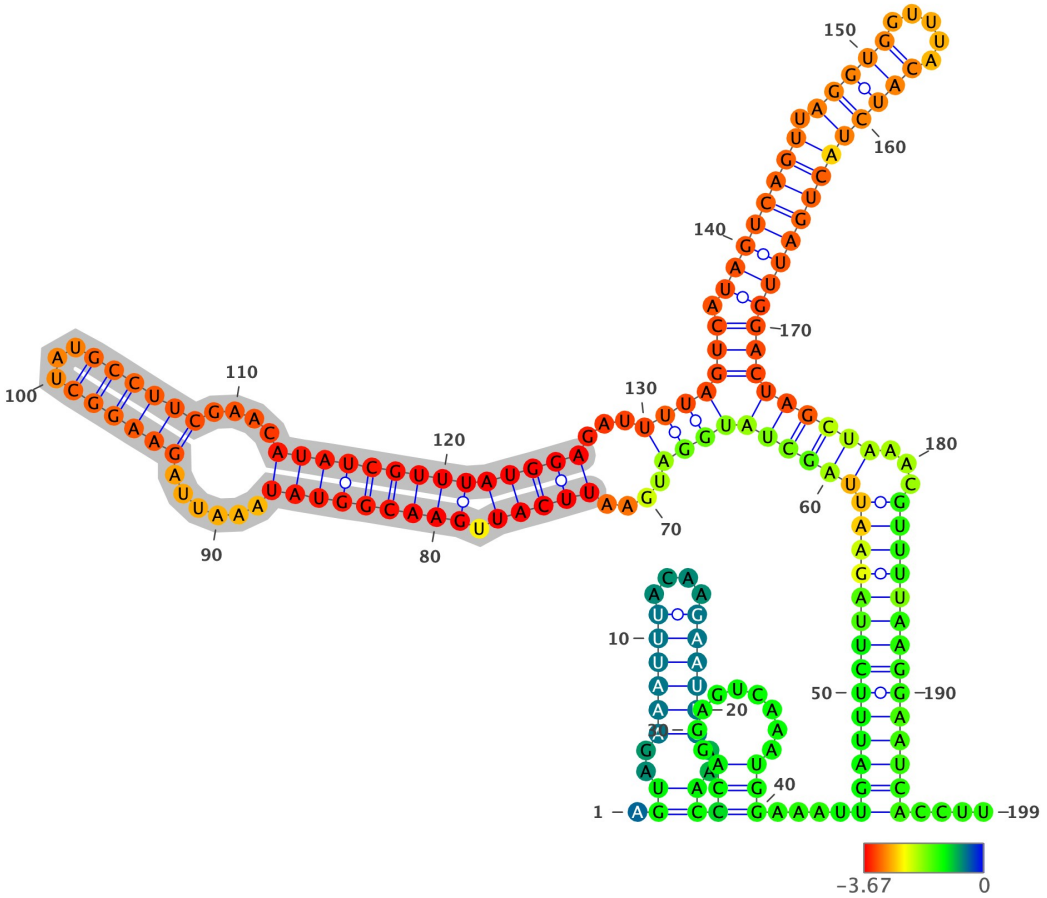
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 341 from nt 20281 to 20334 (nt 73 to 126)

```
5'-UUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGA-3'
5'-(((((.(((((((((.....((((((...))))))....)))))))))))))-3'
Motif MFE = -18.5; z-score = -4.59; ED = 4.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20209 to 20407 (motif highlighted in silver):

```
5'-AGUAGAAAUUUACAAGAAUUUAAACCCAGGAGUCAAAUGGAAAUUGAUUUCUUAGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAA
CAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUU-3
5'-.((..((((((....))))))..))(((.........))).....(((((((((((((((((((((((....(((((.(((((((((.....((((((...))))))...
.)))))))))))))...))))(((.((((((((.(((((.....)))))))))))))))))))))))...)))))))))))))....-3'
MFE = -57.1; z-score = -5.02; ED = 16.16
```

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(+)

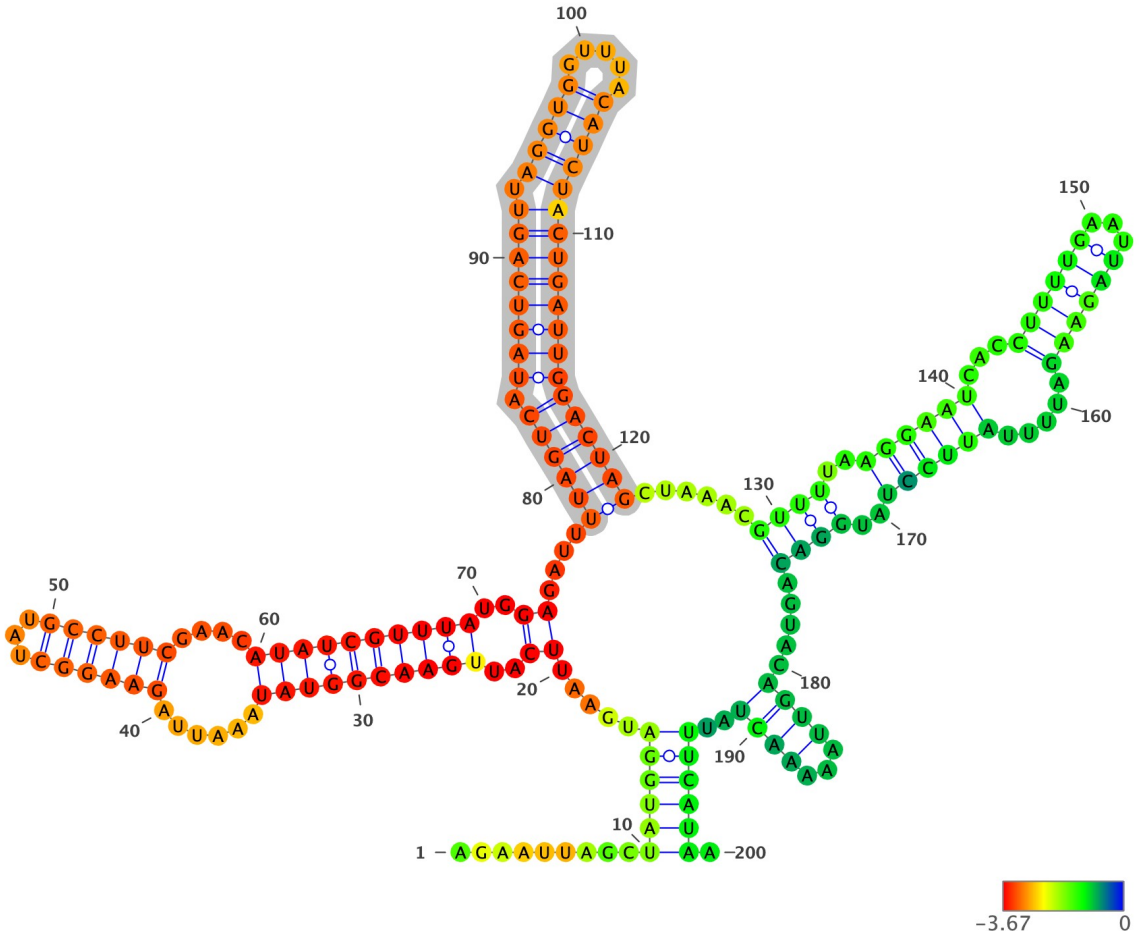
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 20339 to 20383 (nt 78 to 122)

```
5'-UUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAG-3'
5'-((((((..(((((((..((((((.....)))))).)))))))).)))))))-3'
Motif MFE = -20.0; z-score = -5.37; 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 = -3.63; ED = 31.13
```

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(+)

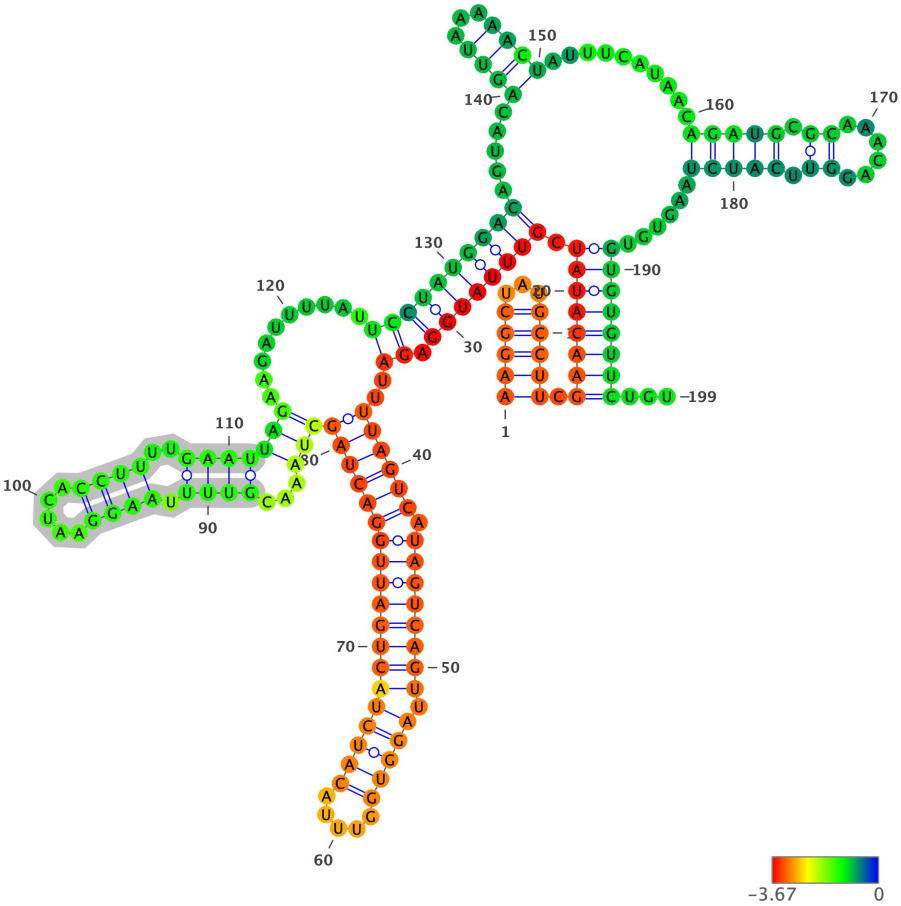
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 20390 to 20413 (nt 88 to 111)

```
5'-GUUUUAAGGAAUCACCUUUUGAAU-3'
5'-((((.((((.....))))..))))-3'
Motif MFE = -1.8; z-score = -0.73; ED = 5.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20303 to 20501 (motif highlighted in silver):

```
5'-AAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAU
UAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGU-3
5'-(((((...))))).(((((((((.(((((((((.((..(((((((.(((((((((.(((((.....)))))))))))))))))))))))((...((((.((((.....)))))..))))
)))).........))))))))))).....((((...)))).........(((((.((......)).)))))......))))))))...-3'
MFE = -45.3; z-score = -1.82; ED = 34.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

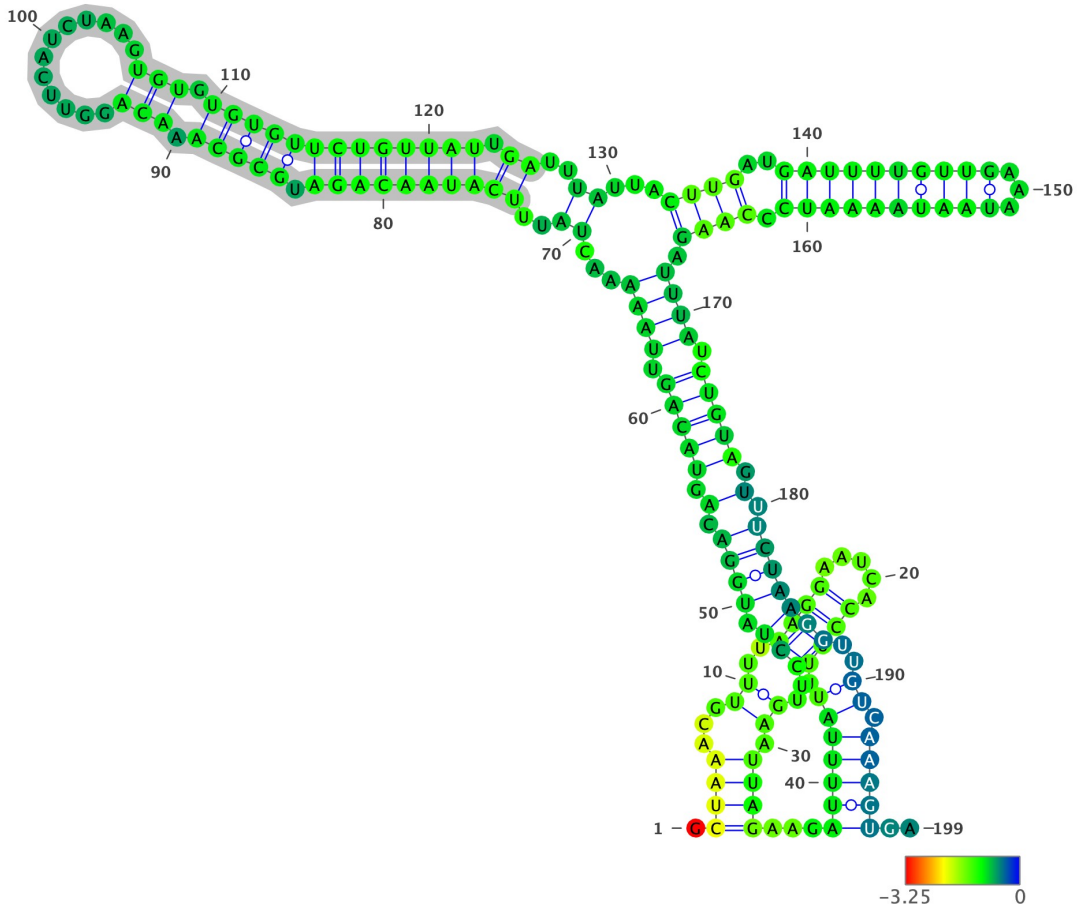
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 344 from nt 20456 to 20507 (nt 74 to 125)

```
5'-UCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGA-3'
5'-((((((((((.(.............................)))))))))).))-3'
Motif MFE = -14.4; z-score = -2.01; 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 = -1.24; ED = 51.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

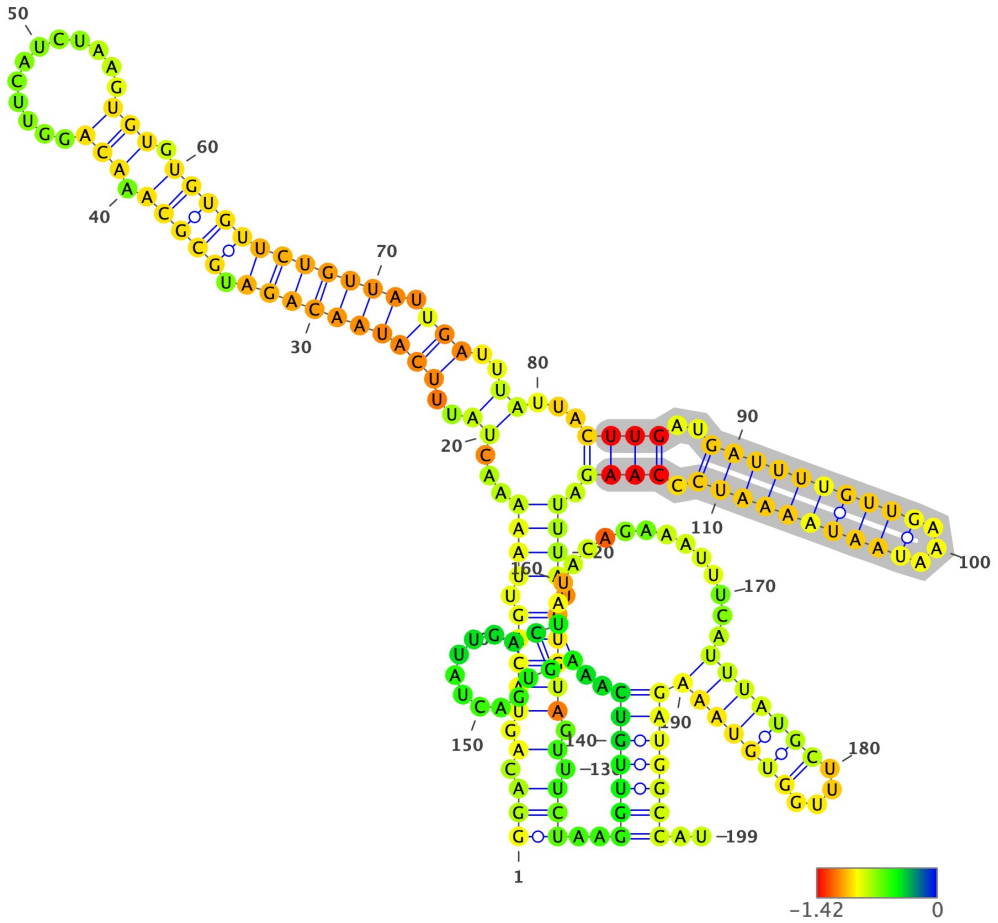
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 345 from nt 20516 to 20547 (nt 84 to 115)

```
5'-UUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAA-3'
5'-(((..(((((.(((.....))).))))).)))-3'
Motif MFE = -5.4; z-score = -2.75; ED = 1.94
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20433 to 20631 (motif highlighted in silver):

```
5'-GGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUC
CCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAU-3
5'-(((.(.(((((.((((...((..((((((((((.(((((.(((............))).))))))))))).)))..))...((((..((((((((((...))))))))))
.)))).)))).)))))).).)))..(((((((..(((........)))..............(((((((....)))))))))))))..-3'
MFE = -41.9; z-score = -1.5; ED = 46.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

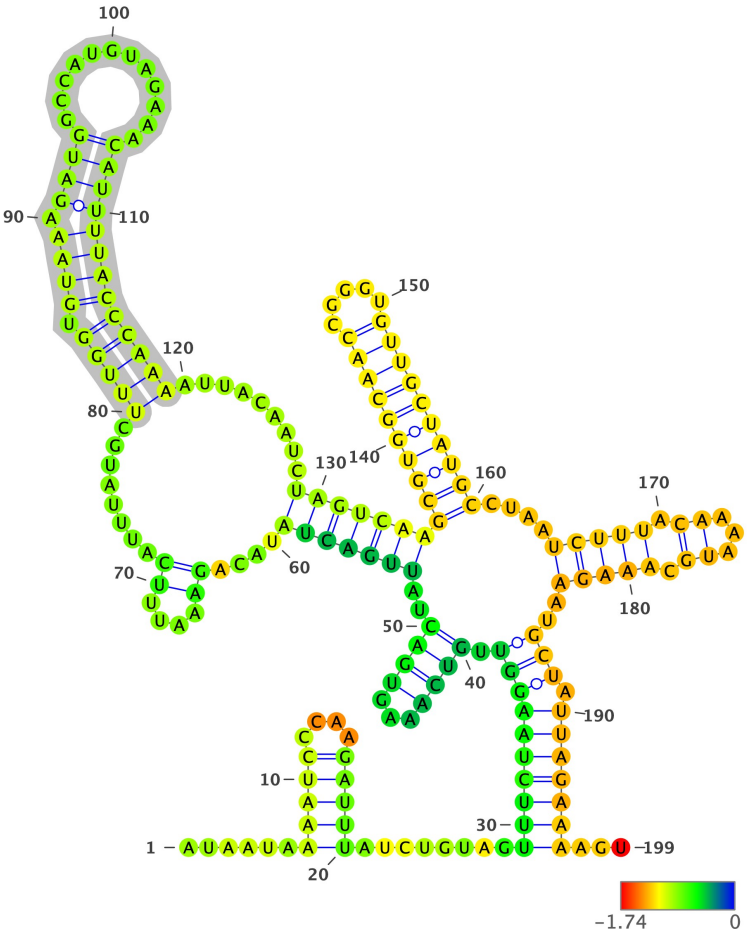
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 346 from nt 20612 to 20651 (nt 80 to 119)

```
5'-UUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAA-3'
5'-((.....................................))-3'
Motif MFE = -7.8; z-score = -2.03; ED = 4.57
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20533 to 20731 (motif highlighted in silver):

```
5'-AUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUU
UACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGU-3
5'-......(((((....)))))........(((((((((.((((...)))).((((((((....((....)).........(((((.((((.((((.............)))))
))))))))).........)))))))((((((((((.....)))))))))....(((((.((...)).)))))..))).)))))))...-3'
MFE = -36.7; z-score = -0.96; ED = 55.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

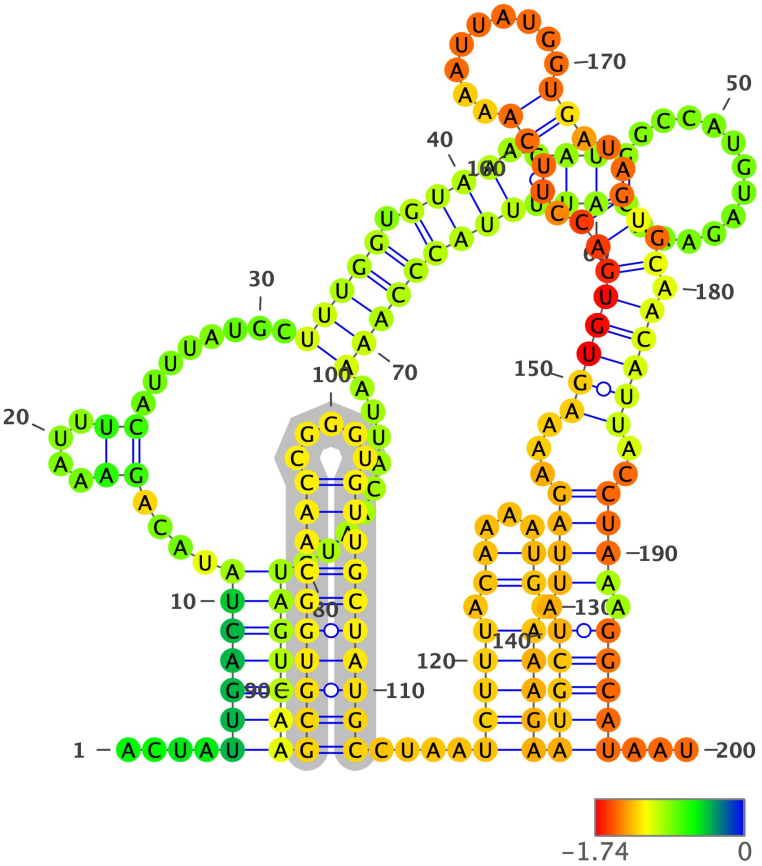
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 347 from nt 20668 to 20692 (nt 88 to 112)

```
5'-GCGUGGCAACCGGGUGUUGCUAUGC-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -13.0; z-score = -3.15; 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 = -1.25; 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(+)

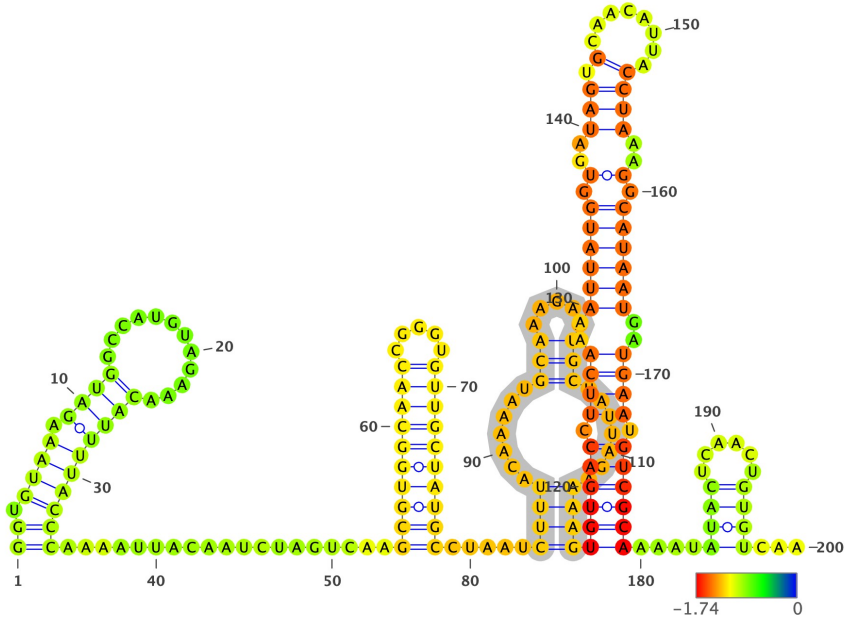
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 348 from nt 20698 to 20730 (nt 84 to 116)

```
5'-CUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAG-3'
5'-((((.......(((.....)))......))))-3'
Motif MFE = -1.3; z-score = -0.11; ED = 5.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20615 to 20814 (motif highlighted in silver):

```
5'-GGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAG
AAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAA-3
5'-((.((((.((((............))))))))).....................((((((((((.....))))))))))).....((((.......(((.....)))......
.))))((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))....((((......))))...-3'
MFE = -41.4; z-score = -2.01; ED = 29.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

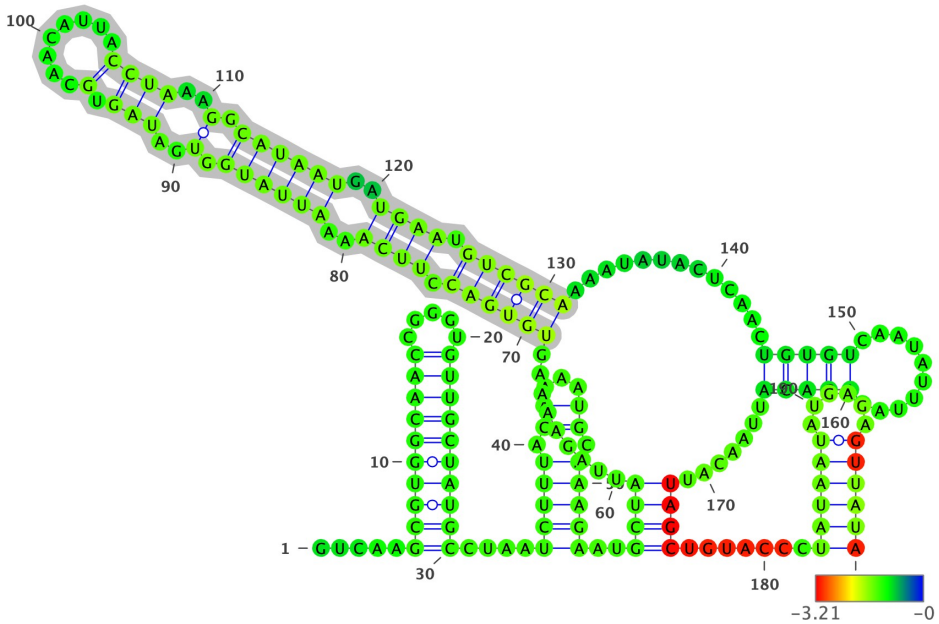
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 349 from nt 20731 to 20793 (nt 69 to 131)

```
5'-UGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCA-3'
5'-((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))-3'
Motif MFE = -17.6; z-score = -2.9; 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 = -1.36; 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(+)

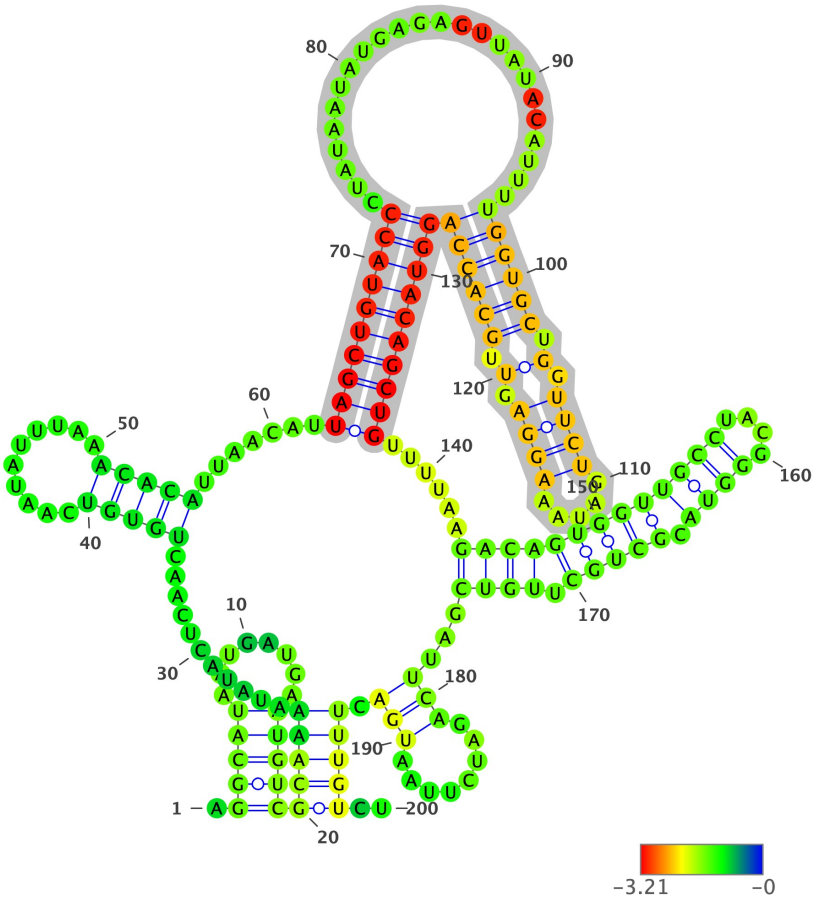
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 350 from nt 20834 to 20908 (nt 63 to 137)

```
5'-UAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUG-3'
5'-((((((((((.............((...)).....(((((.(.((((.....)))).).))))).))))))))))-3'
Motif MFE = -28.8; z-score = -4.67; 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 = -49.7; z-score = -2.34; ED = 39.79
```

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(+)

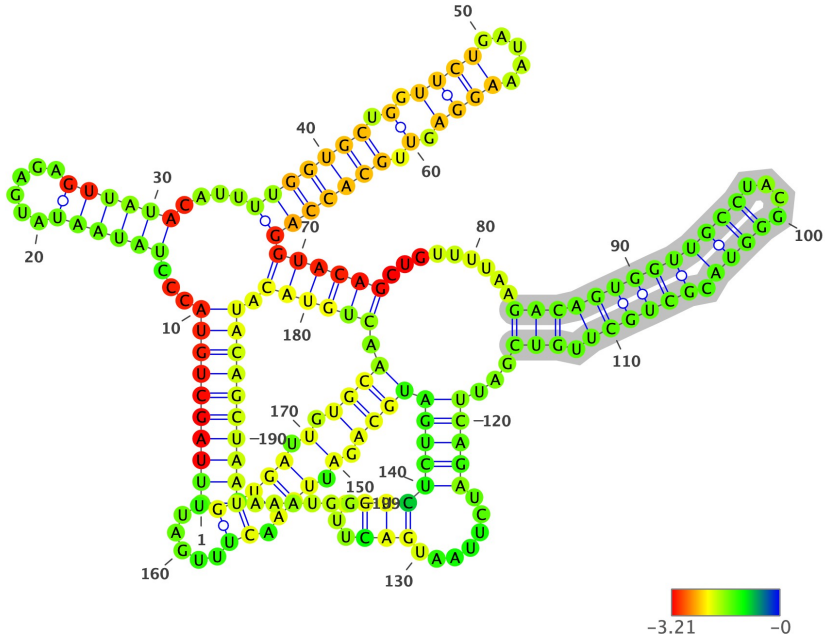
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 351 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 = -2.84; 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(+)

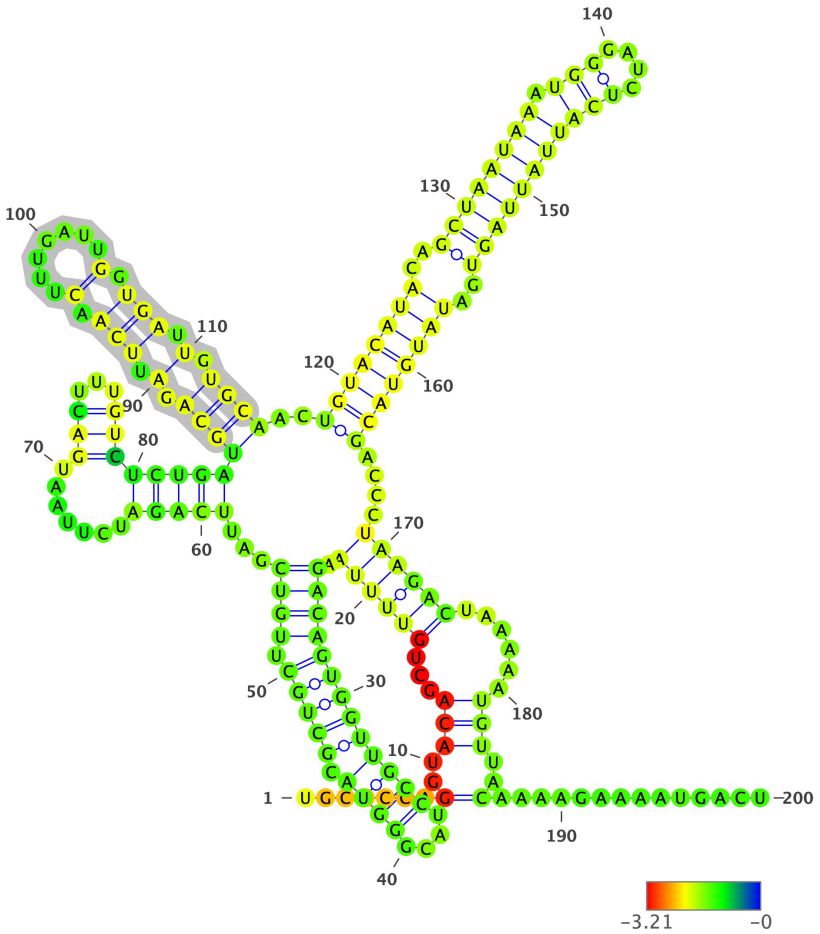
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 352 from nt 20977 to 21005 (nt 86 to 114)

```
5'-GCAGAUUCAACUUUGAUUGGUGAUUGUGC-3'
5'-(((.(.(((.(.......).))).).)))-3'
Motif MFE = -5.5; z-score = -1.0; 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 20892 to 21091 (motif highlighted in silver):

```
5'-UGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUG
UGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACU-3
5'-.......(..(((...((((((.((((((((((((((....)))).))))).))))...(((((.......(((...))))))))((((.(.(((.(.......).))).).
))))..((((((((..((((((((.(((....)))))))))))..))))))))....))))))......)))..)..............-3'
MFE = -46.2; z-score = -1.33; ED = 43.16
```

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(+)

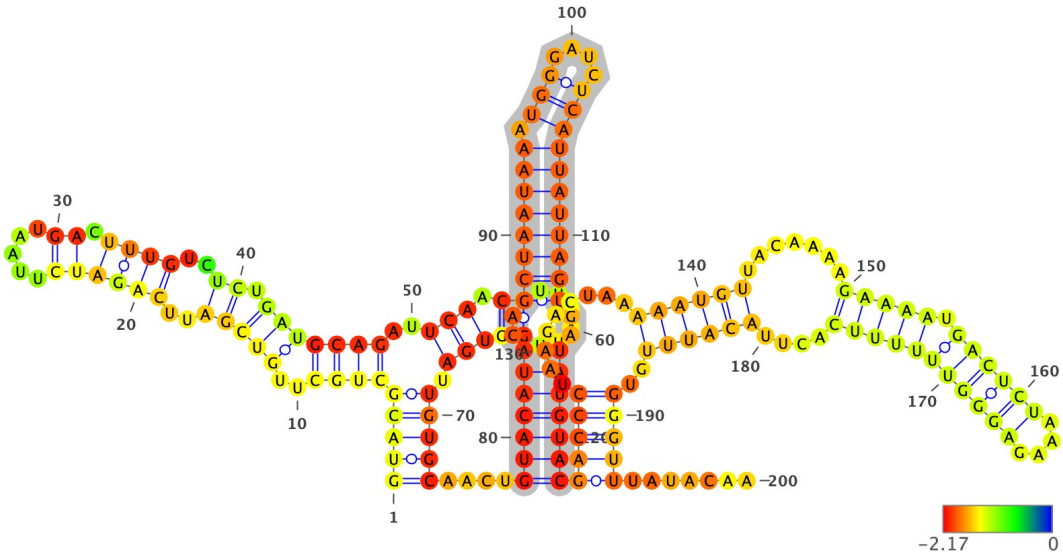
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 353 from nt 21010 to 21054 (nt 78 to 122)

```
5'-GUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUAC-3'
5'-(((((((..((((((((.((......)))))))))..)))))))-3'
Motif MFE = -14.9; z-score = -4.13; ED = 2.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20933 to 21132 (motif highlighted in silver):

```
5'-GUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUA
GUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAA-3
5'-(((((((((..(((((..((((((.....)).))))..)).)))))))..(((.((......))))).)))))....(((((((..((((((((.(((....)))))))))
))..)))))))(((((.........((((((.......(((((.((((((....)))))))))))....))))))..)))))........-3'
MFE = -43.4; z-score = -0.97; ED = 43.59
```

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(+)

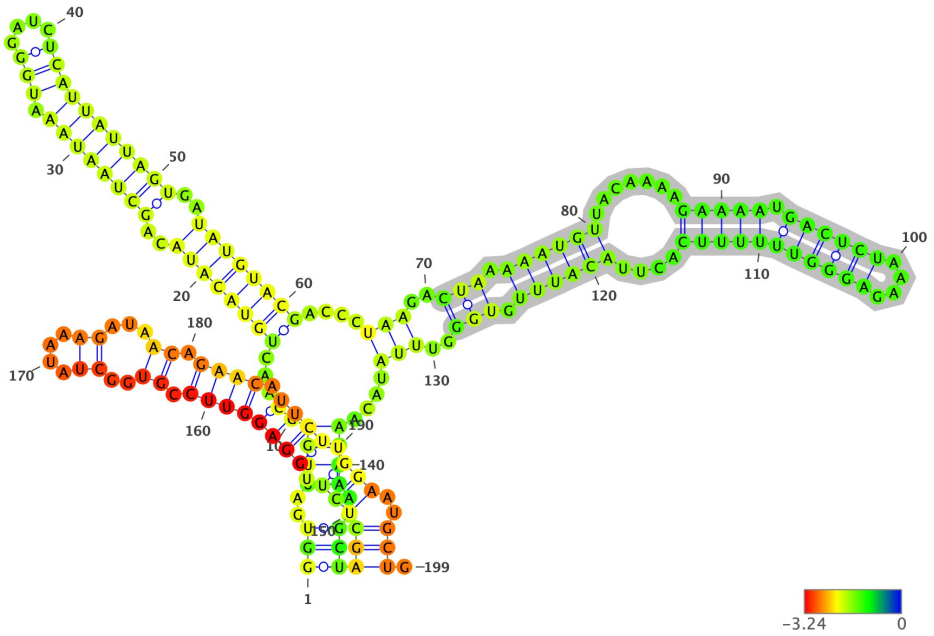
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 354 from nt 21065 to 21122 (nt 71 to 128)

```
5'-CUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGG-3'
5'-(................(((((.(((((((....)))))))))))).............)-3'
Motif MFE = -9.9; z-score = -1.54; ED = 7.85
```



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 20995 to 21193 (motif highlighted in silver):

```
5'-GGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUU
UUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUG-3
5'-(((..((((.....(((((((((..(((((((((.(((....)))))))))))..)))))))))....(((..(((.((((((.......(((((.((((((....)))))))))
)))....)))))).)))..)))....)))))..)))((((((.((((((((.((..((....))...)).)))).)))).)))).)))..))).-3'
MFE = -42.3; z-score = -1.6; 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_gp01, 266-21555(+)

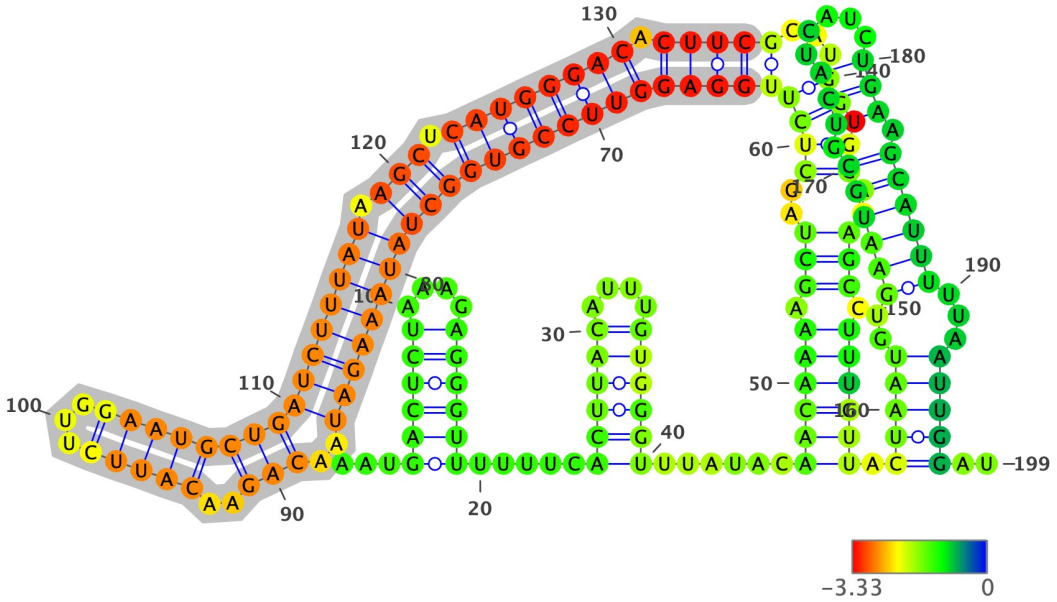
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 21148 to 21219 (nt 64 to 135)

```
5'-GGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAUCUUUAUAAGCUCAUGGGACACUUC-3'
5'-(((((((((((((((((((((((..(((..((((.....))))))))))))))).))).)))))))).))))-3'
Motif MFE = -29.1; z-score = -5.27; ED = 2.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21085 to 21283 (motif highlighted in silver):

```
5'-AAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU
CUUUAUAAGCUCAUGGGACACUUCGCAUGGUGGACAGCCUUUGUUACUAAUGUGAAUGCGUCAUCAUCUGAAGCAUUUUUAAUUGGAU-3
5'-...((((((....))))))).....((((((....))))))......((((((.(((..((((((((((((((((((((((((((((..(((..(((((...)))))))))))
))))))).))).)))))))).)))))...)).))..))).)))))).(((((..((((((.(((.....))).))))))...)))))..-3'
MFE = -57.5; z-score = -3.27; ED = 15.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

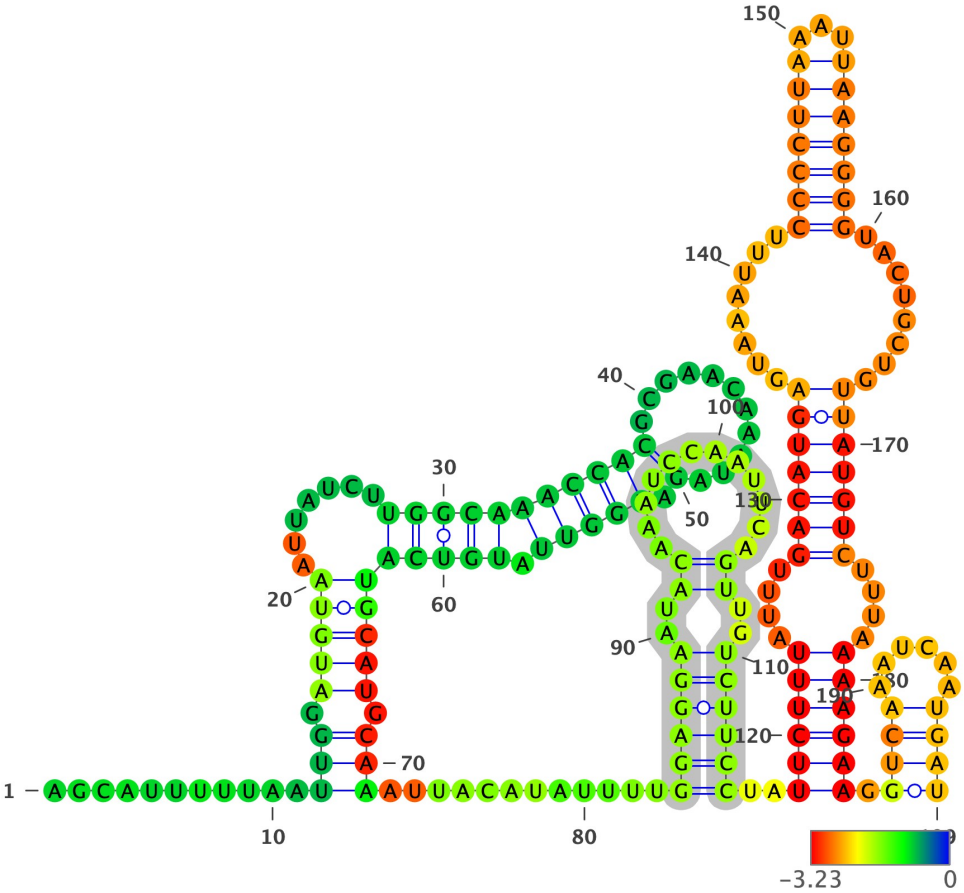
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 356 from nt 21350 to 21381 (nt 84 to 115)

```
5'-GGAGGAAUACAAAUCCAAUUCAGUUGUCUUCC-3'
5'-((((((..((............))..))))))-3'
Motif MFE = -6.4; z-score = -1.77; 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 = -2.24; 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(+)

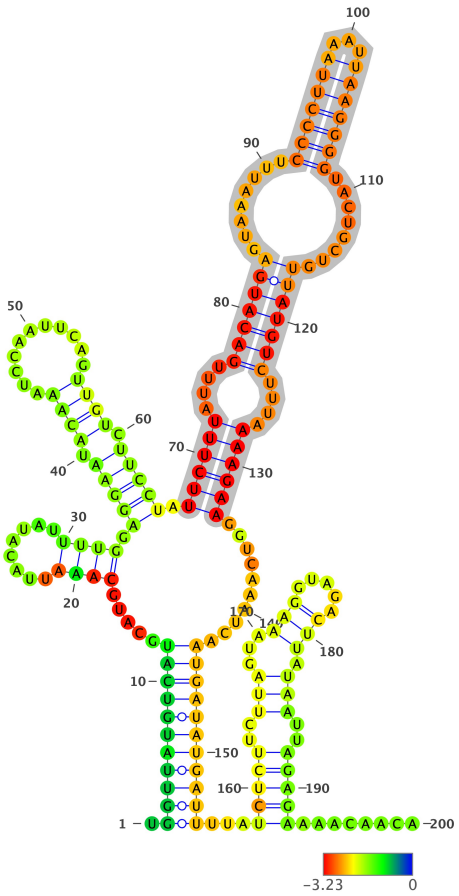
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 357 from nt 21384 to 21450 (nt 67 to 133)

```
5'-UUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAA-3'
5'-((((((.....((((.........((((((.....))))))..........))))).....))))))-3'
Motif MFE = -20.7; z-score = -3.71; 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 21318 to 21517 (motif highlighted in silver):

```
5'-UGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUAC
UGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACA-3
5'-.(((((((((((.....((((........)))).(((((.((((...........)))).))))).((((((....(((((((........(((((((...)))))))...
.....)))))))....))))))..........))))))))))...(((((..(((...(((.....))).)))..)))))........-3'
MFE = -42.8; z-score = -2.19; ED = 37.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

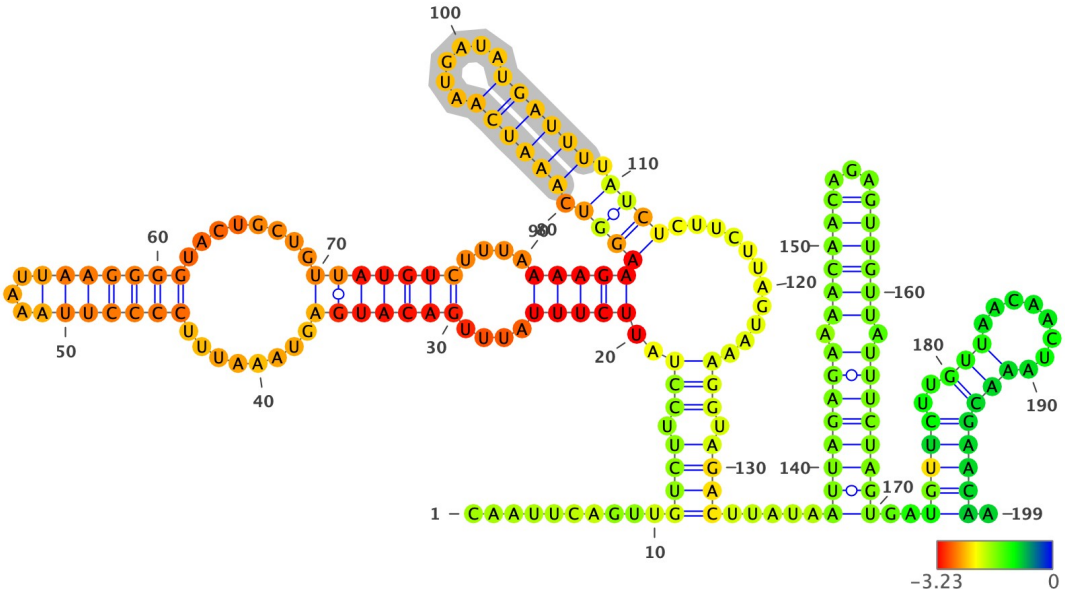
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 358 from nt 21455 to 21472 (nt 91 to 108)

```
5'-AAAUCAAUGAUAUGAUUU-3'
5'-(((((........)))))-3'
Motif MFE = -1.8; z-score = -4.43; ED = 1.28
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21365 to 21563 (motif highlighted in silver):

```
5'-CAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAU
CUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAA-3
5'-..........((((.(((..(((((....(((((((........(((((((...)))))))........)))))))....)))))((((.((((((......))))))..))
))...........))).))))).....((((((((.((((((...)))))).))))))))..(((((..(((........))))))))..-3'
MFE = -46.8; z-score = -3.46; ED = 32.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 191--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 191--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 199 to 199--gene, gene-GU280_gp02, 21563-25384(+)

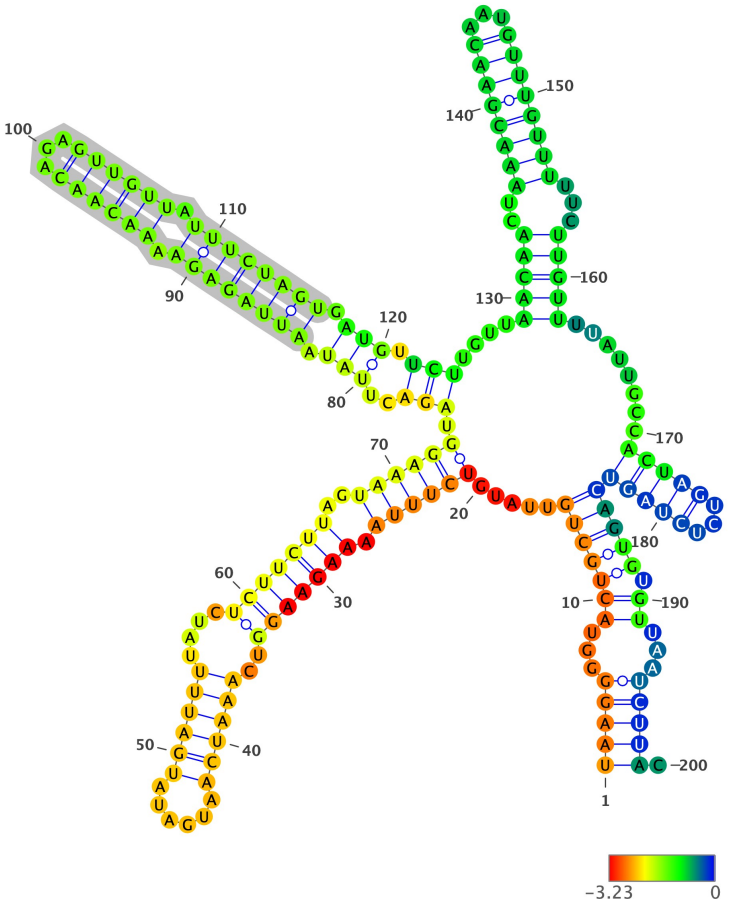
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 199 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 359 from nt 21502 to 21534 (nt 84 to 116)

```
5'-AUUAGAGAAAACAACAGAGUUGUUAUUUCUAGU-3'
5'-((((((((.((((((...)))))).))))))))-3'
Motif MFE = -10.2; z-score = -4.06; 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 = -0.85; 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(+)

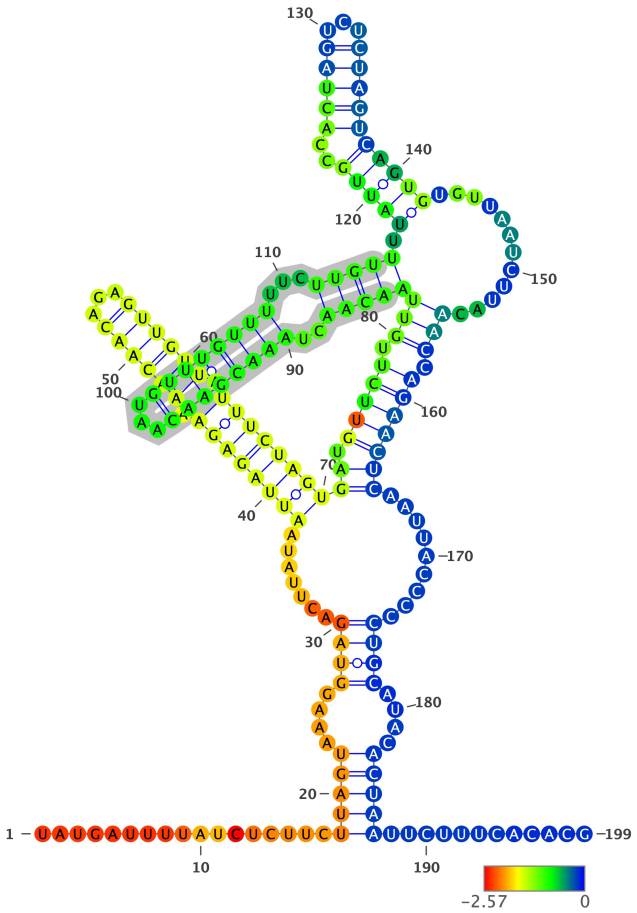
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 360 from nt 21548 to 21579 (nt 84 to 115)

```
5'-ACAACUAAACGAACAAUGUUUGUUUUUCUUGU-3'
5'-((((.......................))))-3'
Motif MFE = -5.4; z-score = -2.42; ED = 2.49
```



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 21465 to 21663 (motif highlighted in silver):

```
5'-UAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUC
UUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACG-3
5'-.................(((((....((((.......((((((((.((((((...)))))).))))))))((.(((((.((((((((..((((((((...))))))))...
))))).(((((..(((((...))))))))))............))).)))))))).........))))....)))))............-3'
MFE = -32.8; z-score = -1.05; ED = 31.57
```

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 91--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 91--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 99 to 199--gene, gene-GU280_gp02, 21563-25384(+)

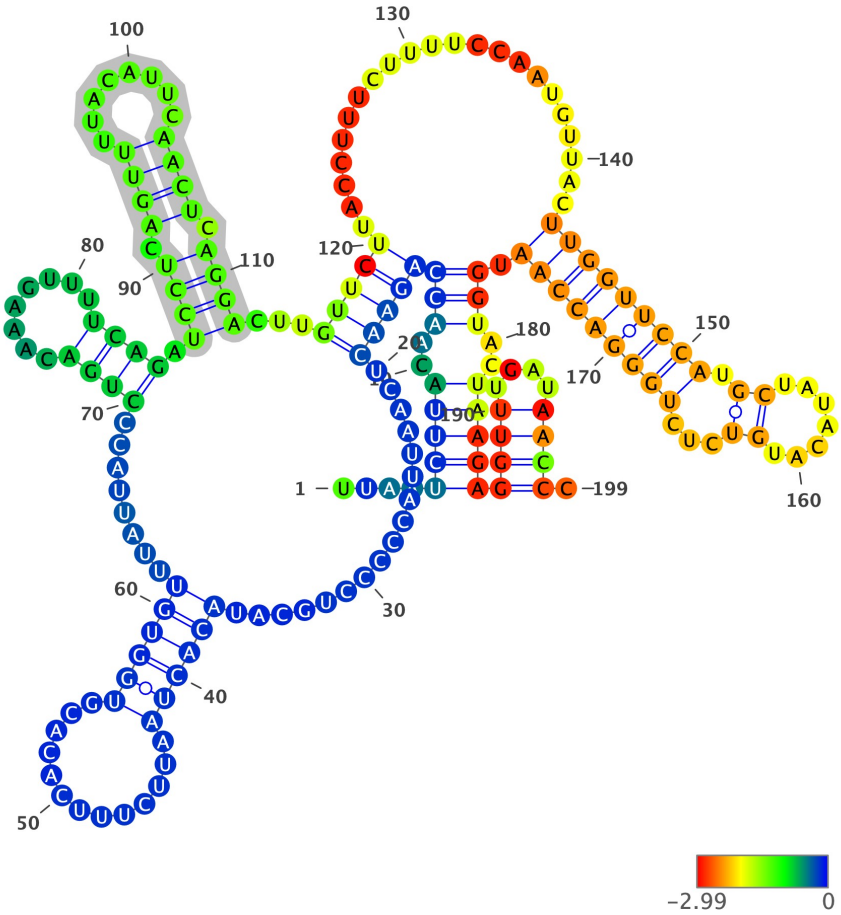
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

5-- nt 99 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 361 from nt 21695 to 21720 (nt 87 to 112)

```
5'-UCCUCAGUUUUACAUUCAACUCAGGA-3'
5'-((((.((((........)))).))))-3'
Motif MFE = -5.2; z-score = -3.41; 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 = -1.8; 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(+)

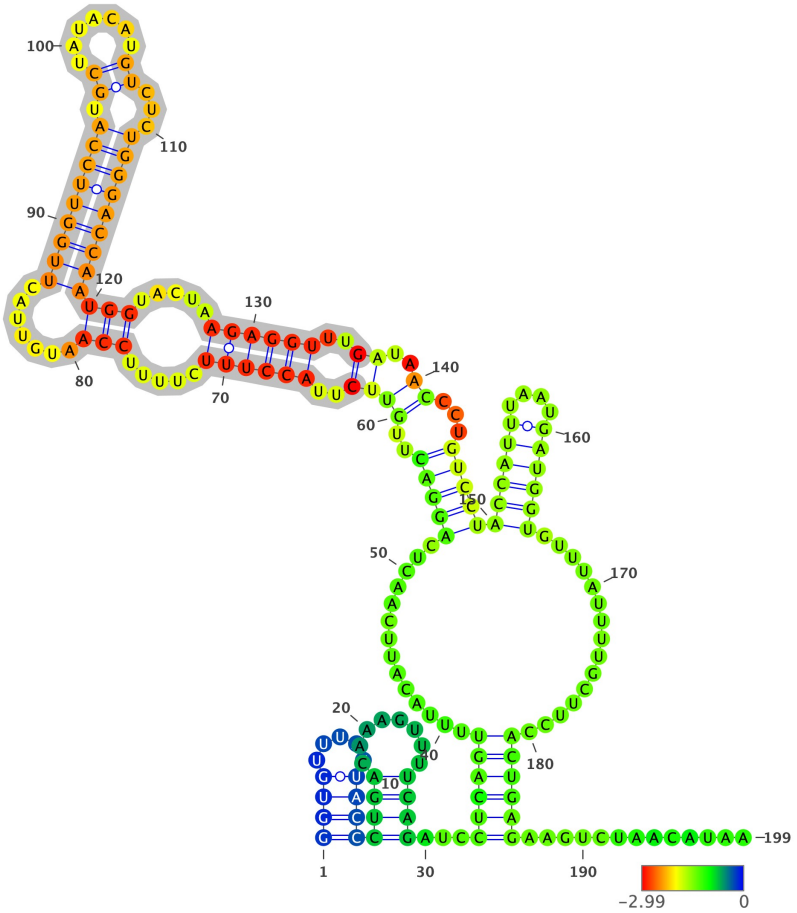
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 362 from nt 21727 to 21800 (nt 63 to 136)

```
5'-CUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUG-3'
5'-(..((((((.....(((.......(((((((((.((.......))...)))))))))))).....))))))..)-3'
Motif MFE = -18.3; z-score = -2.85; 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 21665 to 21863 (motif highlighted in silver):

```
5'-GGUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGGACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCU
GGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAA-3
5'-((((.....))))((((........))))...((((((..............(((((..((((..((((((.....(((.......(((((((((.((.......))...)
))))))))))).....))))))..))..))...)))))((((((....))))))...............))))))..............-3'
MFE = -43.7; z-score = -2.48; ED = 26.76
```

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_gp02, 21563-25384(+)

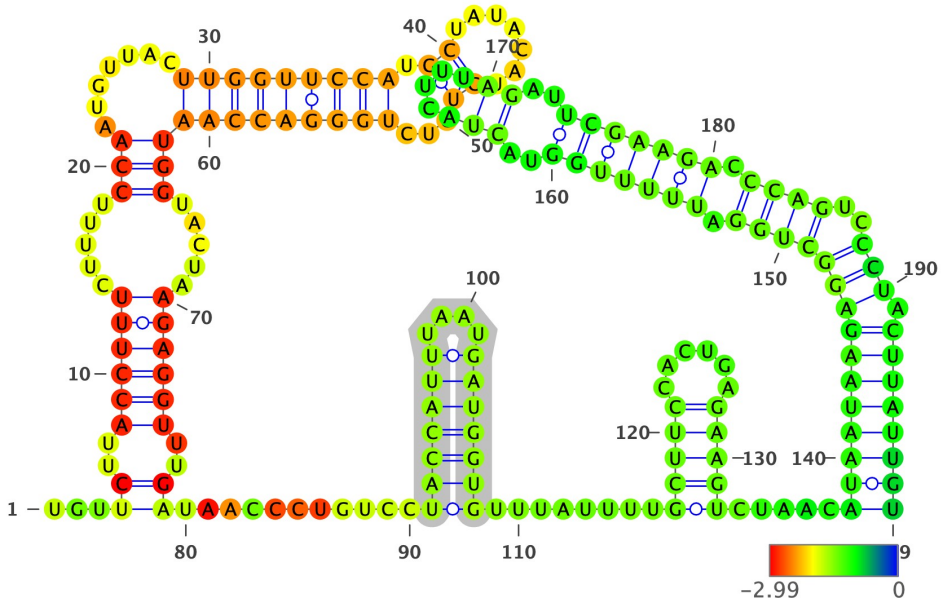
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 363 from nt 21813 to 21830 (nt 91 to 108)

```
5'-UACCAUUUAAUGAUGGUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.8; z-score = -5.85; 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 = -2.99; 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(+)

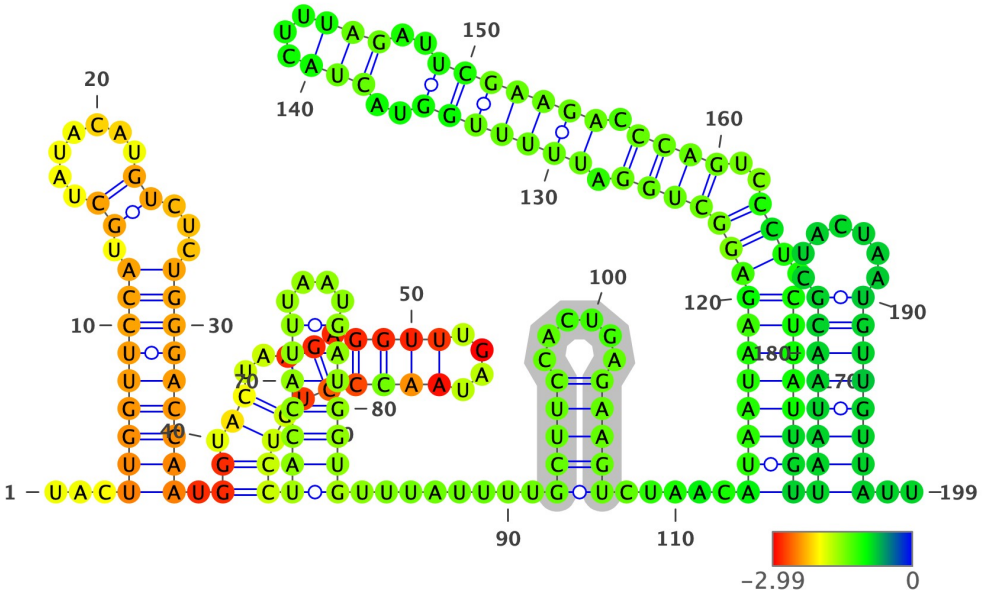
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 364 from nt 21839 to 21854 (nt 92 to 107)

```
5'-GCUUCCACUGAGAAGU-3'
5'-(((((......)))))-3'
Motif MFE = -3.0; z-score = -1.85; 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 = -2.19; 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(+)

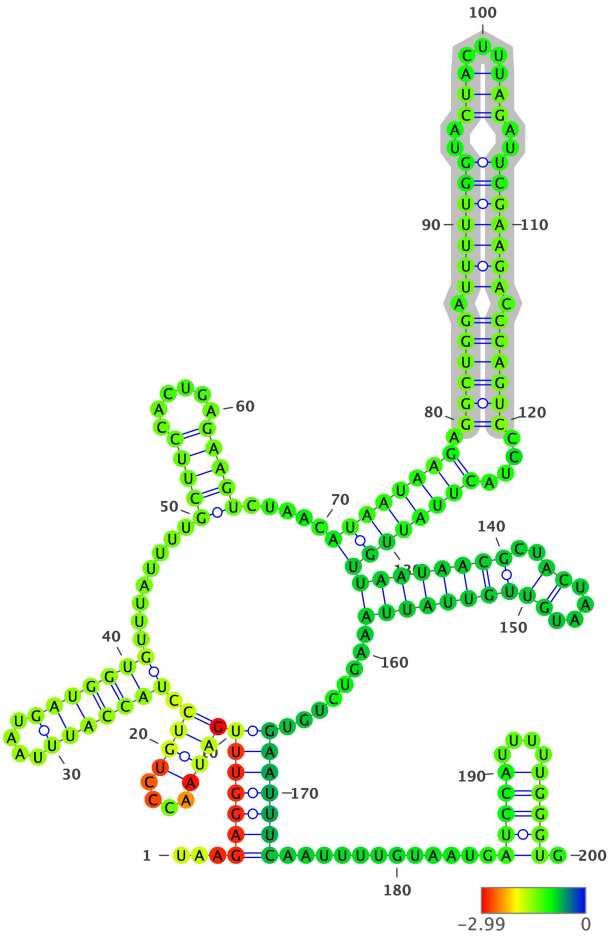
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 365 from nt 21869 to 21909 (nt 80 to 120)

```
5'-GGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGACCCAGUC-3'
5'-((((((.(((((....((.....)).....))))).))))))-3'
Motif MFE = -11.8; z-score = -2.23; ED = 2.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21790 to 21989 (motif highlighted in silver):

```
5'-UAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAA
GACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUG-3
5'-...(((((((((((....)))).(((((((....)))))))........(((((......)))))).....((((((((.((((((.(((((((..(((...)))..)))))
)).))))))....))))))))((((((((..((....)))))))))).........)))))))............(((((....))))).-3'
MFE = -41.5; z-score = -1.08; ED = 38.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

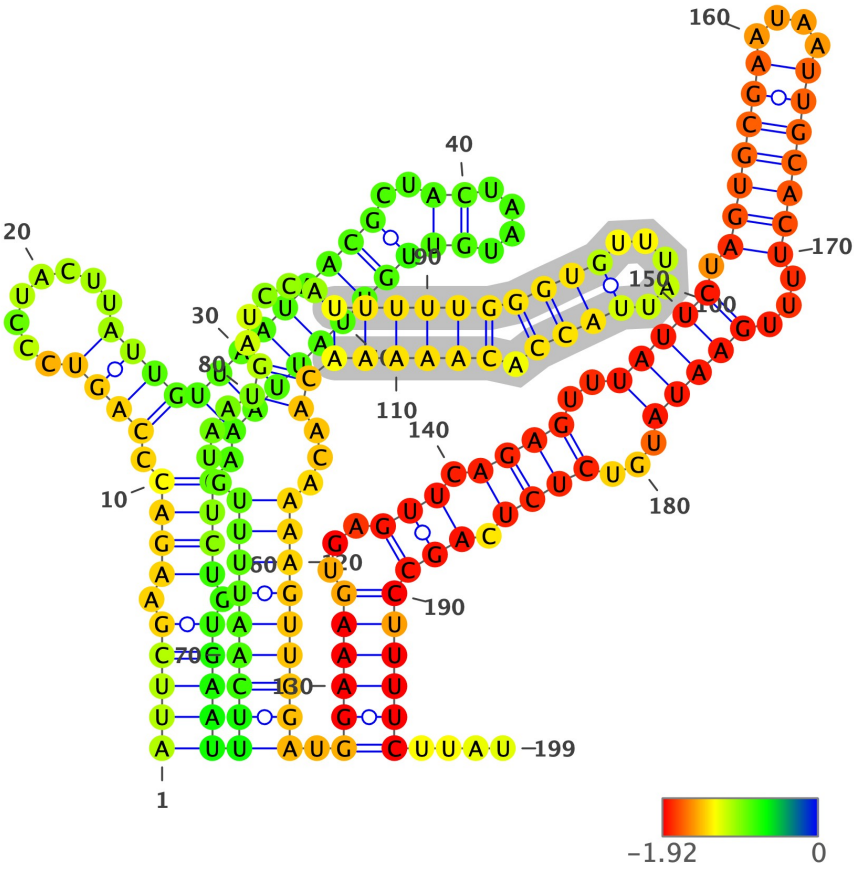
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 366 from nt 21980 to 22005 (nt 87 to 112)

```
5'-UUUUUGGGUGUUUAUUACCACAAAAA-3'
5'-(((((((((.......))).))))))-3'
Motif MFE = -6.6; z-score = -4.14; 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 21894 to 22092 (motif highlighted in silver):

```
5'-AUUCGAAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAA
ACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAU-3
5'-(((((.((((.((((........))))(((((((((..((....)))))))))))).)))).)))))(((((((((....((.....((((((((((.....)))).)))))
)))...))))))))).((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))....-3'
MFE = -40.5; z-score = -1.58; ED = 31.36
```

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(+)

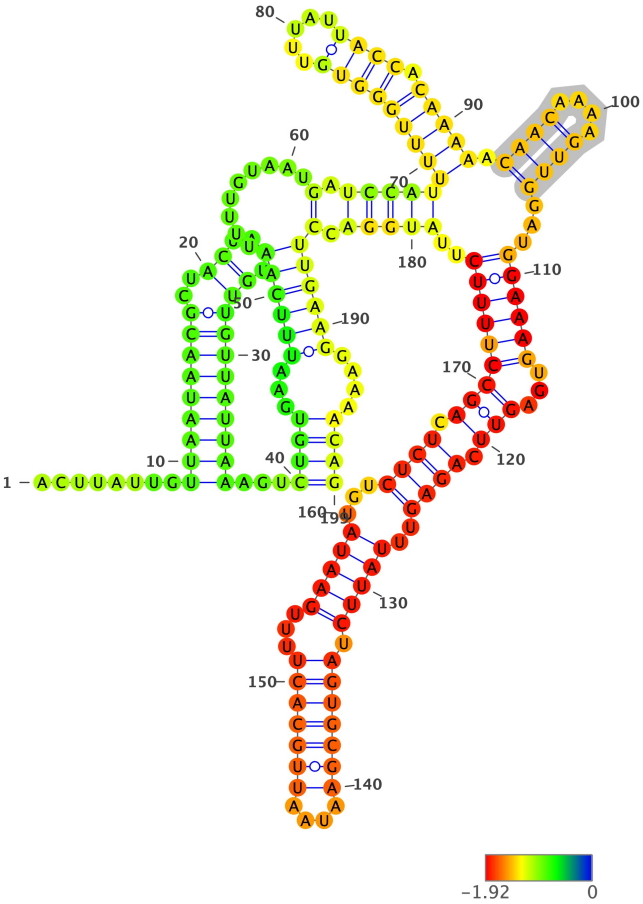
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 367 from nt 22006 to 22017 (nt 94 to 105)

```
5'-CAACAAAAGUUG-3'
5'-((((....))))-3'
Motif MFE = -1.1; z-score = -10.1; 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 = -1.53; 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(+)

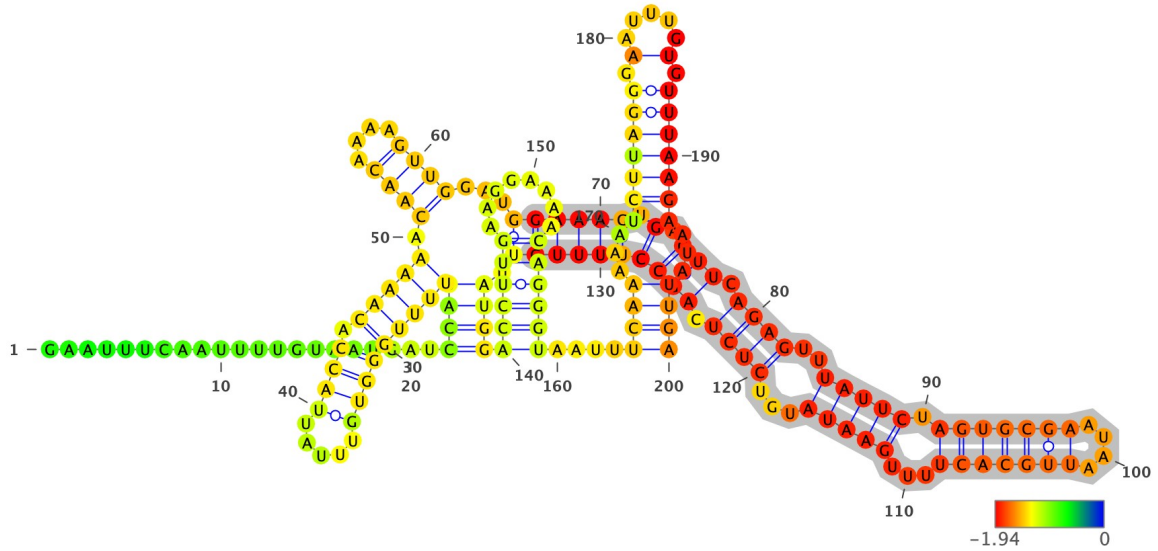
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 368 from nt 22022 to 22088 (nt 67 to 133)

```
5'-GAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUC-3'
5'-((((..(.(((.((((..(((((.(((((((....)))))))...)))))...)))).)))).))))-3'
Motif MFE = -17.6; z-score = -2.79; ED = 7.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21956 to 22155 (motif highlighted in silver):

```
5'-GAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUU
GAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGA-3
5'-.....................(((((((((((((.....)))).))))).((((....))))...((((((.(.(((.((((..(((((.(((((((....)))))))...
)))))...)))).))))))))))).))))((((((........))))))....((((...(((((((.(.....).)))))))...))))-3'
MFE = -42.6; z-score = -1.46; ED = 36.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

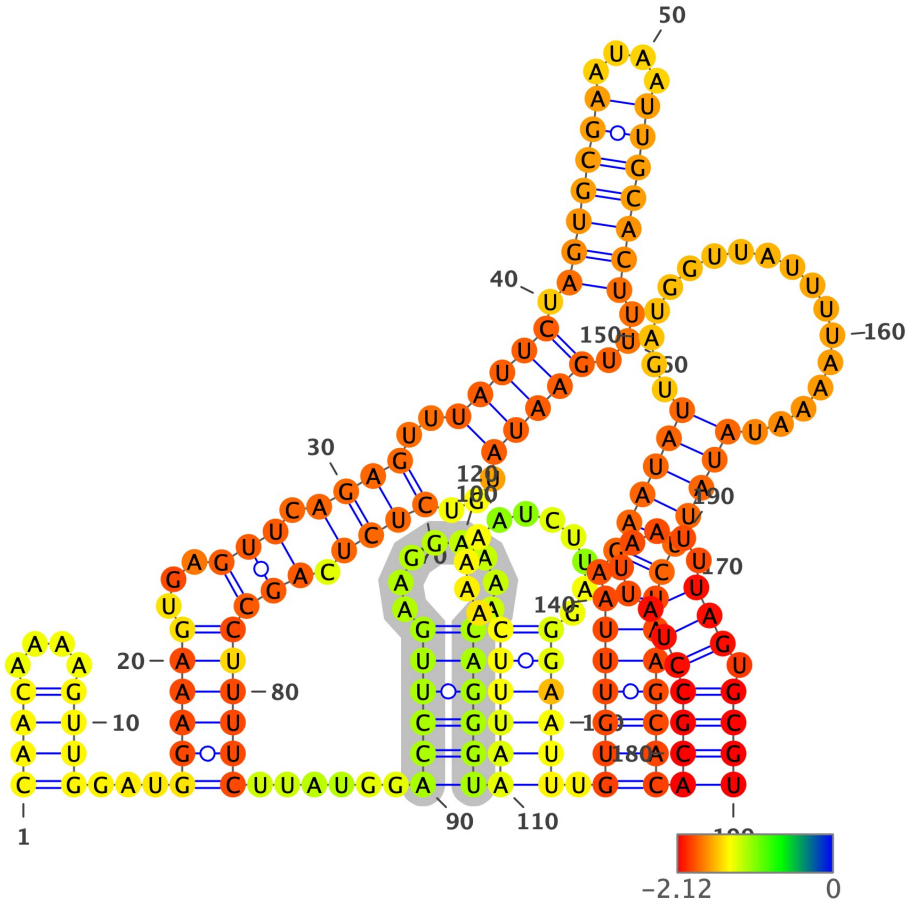
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 369 from nt 22095 to 22114 (nt 90 to 109)

```
5'-ACCUUGAAGGAAAACAGGGU-3'
5'-((((((........))))))-3'
Motif MFE = -5.4; z-score = -3.48; ED = 0.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22006 to 22204 (motif highlighted in silver):

```
5'-CAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAA
UUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGU-3
5'-((((....))))...((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))).....((((((........))))))((
((((...........)))))).(((((((.((((((.................))))))))))))))(((((((......))).))))-3'
MFE = -45.6; z-score = -2.29; 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(+)

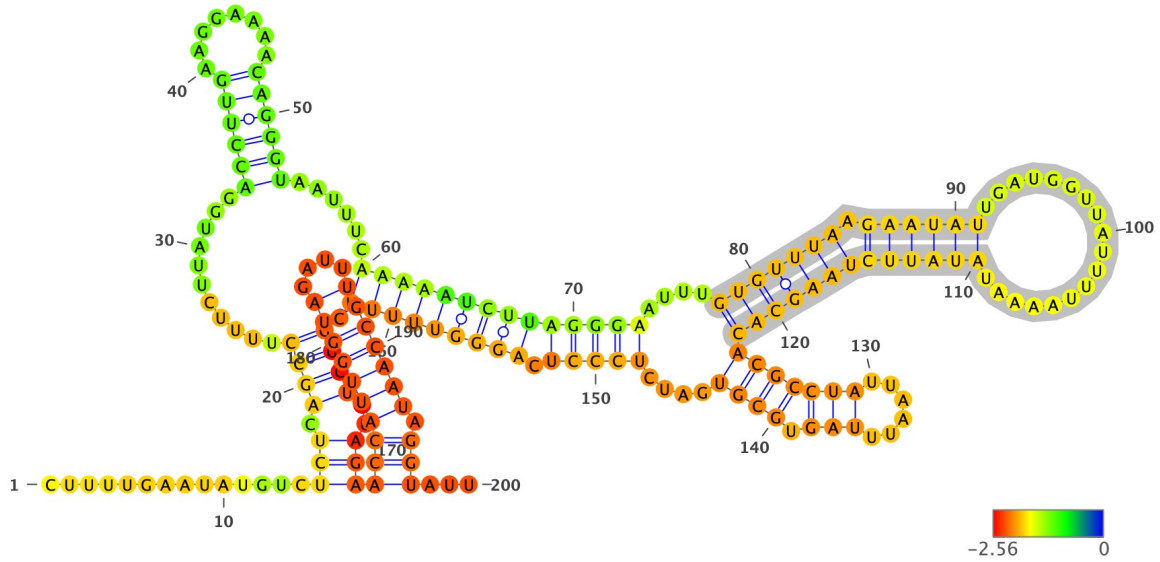
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 370 from nt 22139 to 22183 (nt 78 to 122)

```
5'-GUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCAC-3'
5'-(((((((.((((((.................)))))))))))))-3'
Motif MFE = -8.5; z-score = -2.25; 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 = -2.95; 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(+)

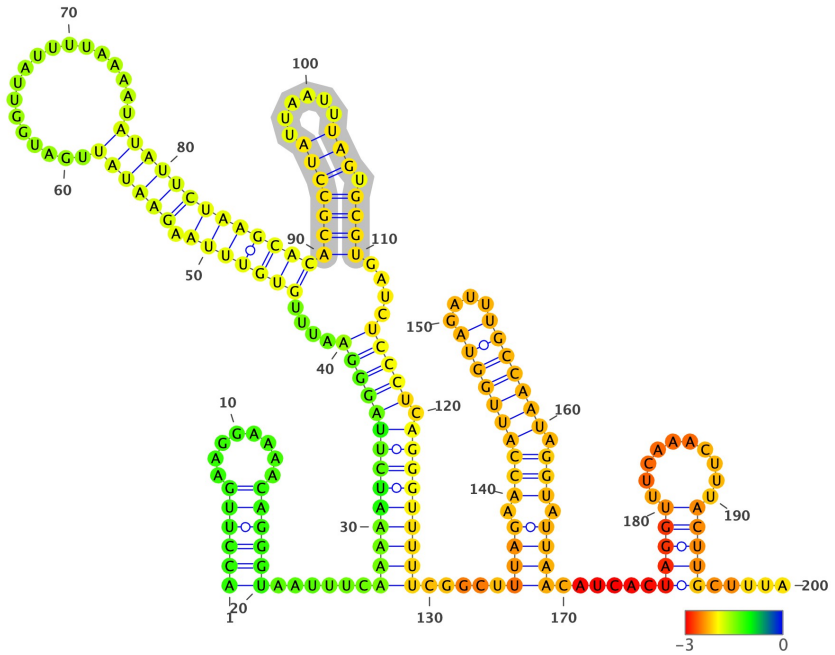
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 371 from nt 22184 to 22204 (nt 90 to 110)

```
5'-ACGCCUAUUAAUUUAGUGCGU-3'
5'-(((((((......))).))))-3'
Motif MFE = -6.2; z-score = -3.99; 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 = -2.82; 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(+)

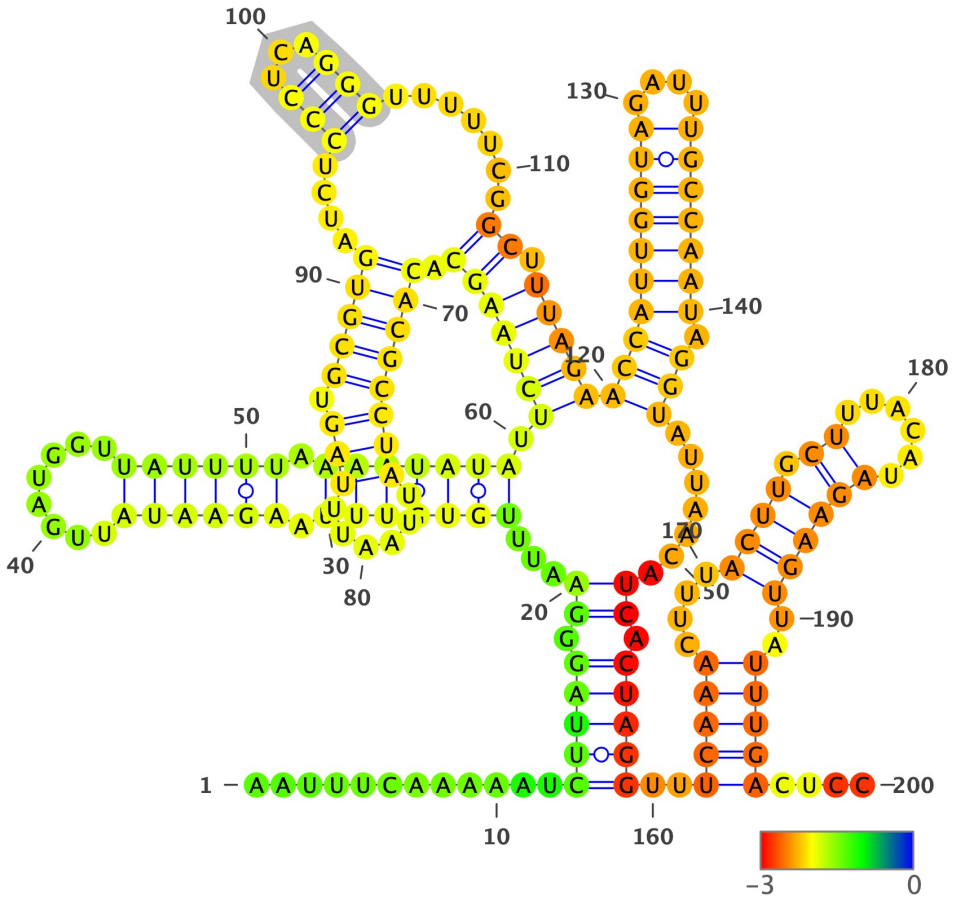
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 372 from nt 22210 to 22218 (nt 96 to 104)

```
5'-CCCUCAGGG-3'
5'-(((...)))-3'
Motif MFE = -1.2; z-score = -7.45; 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 22115 to 22314 (motif highlighted in silver):

```
5'-AAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCG
GCUUUAGAACCAUUGGUAGAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCC-3
5'-............(((((.((...(((((((.((((((........))))))).)))))))).(((((((.((((((((......))).)))))....(((...)))........
)).)))))((((((((((....)))))))).)))........)).)))))..(((((....((((.((......))))))..)))))....-3'
MFE = -38.7; z-score = -2.75; ED = 47.41
```

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(+)

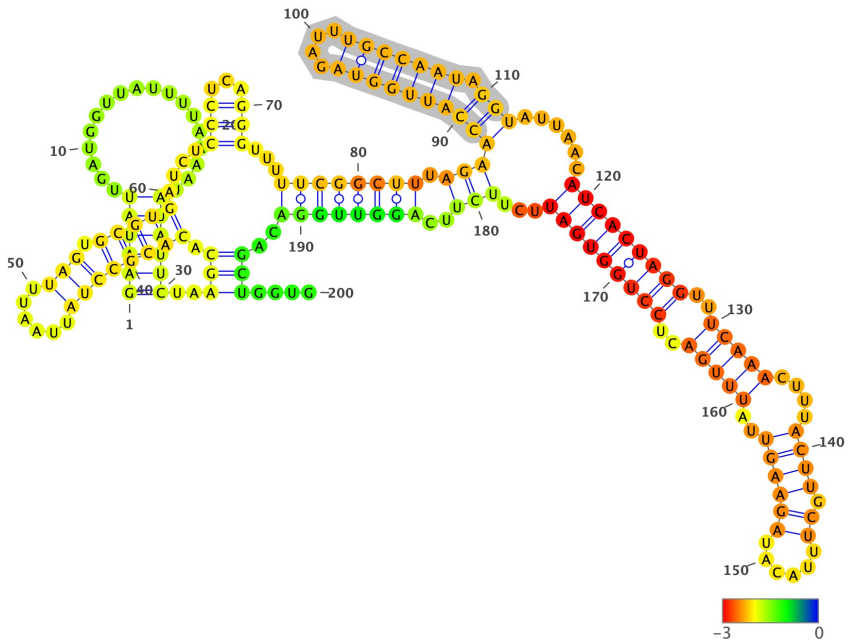
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 373 from nt 22235 to 22257 (nt 89 to 111)

```
5'-CCAUUGGUAGAUUUGCCAAUAGG-3'
5'-((((((((......))))))).))-3'
Motif MFE = -7.4; z-score = -3.25; ED = 1.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22147 to 22346 (motif highlighted in silver):

```
5'-GAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGG
UAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUG-3
5'-((((((.................))))))..(((.((((((((......))).)))))....(((...)))...((((((((.((((((((((((....)))))))).))
).....((((((((..(((((....((((.((......))))))..)))))..)))))))))...)))..)))))))))..)))....-3'
MFE = -50.3; z-score = -2.43; ED = 26.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

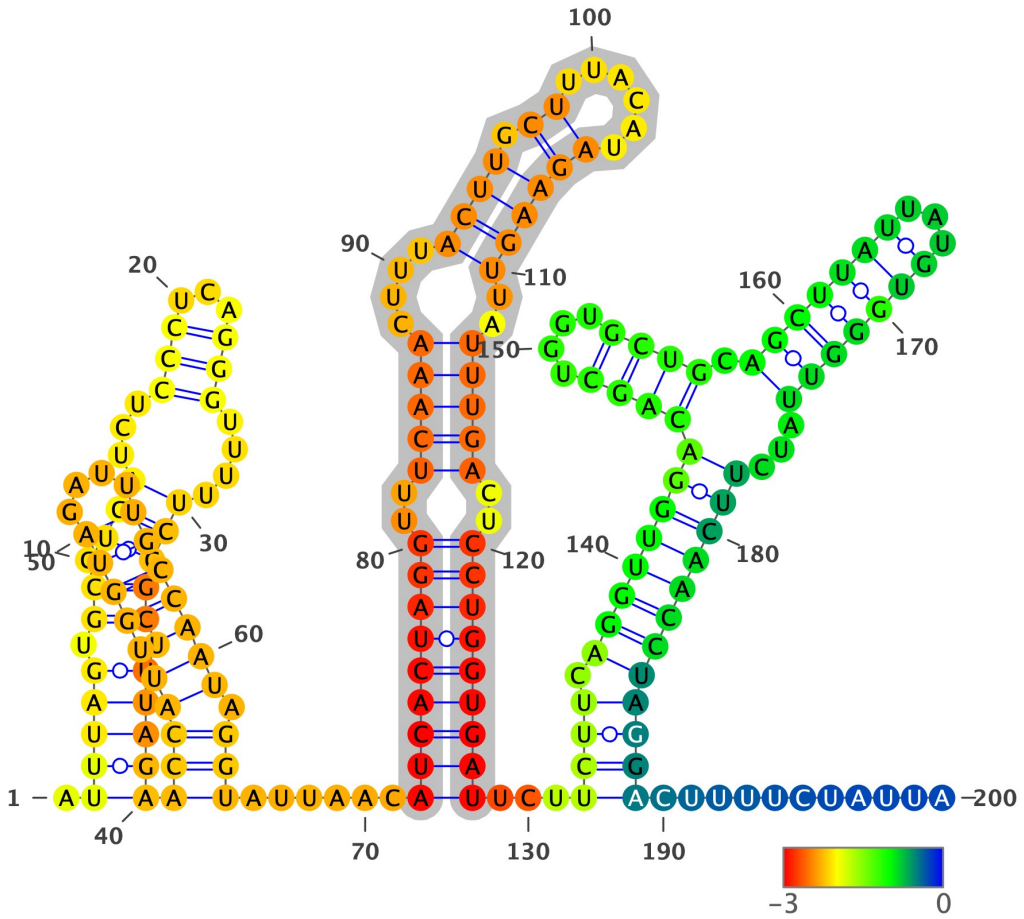
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 374 from nt 22265 to 22321 (nt 72 to 128)

```
5'-AUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAU-3'
5'-(((((((((..(((((....((((.((......)))))))..)))))..)))))))))-3'
Motif MFE = -18.6; z-score = -4.33; 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 = -2.92; 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(+)

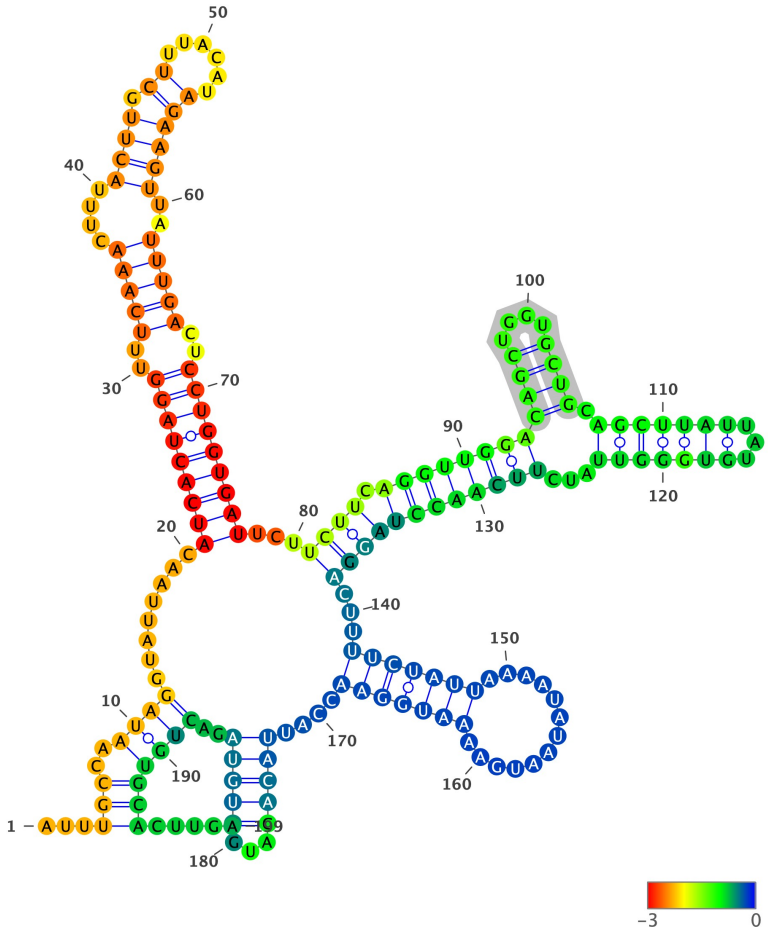
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 375 from nt 22338 to 22349 (nt 94 to 105)

```
5'-CAGCUGGUGCUG-3'
5'-((((....))))-3'
Motif MFE = -4.1; z-score = -3.7; 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 = -1.98; 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(+)

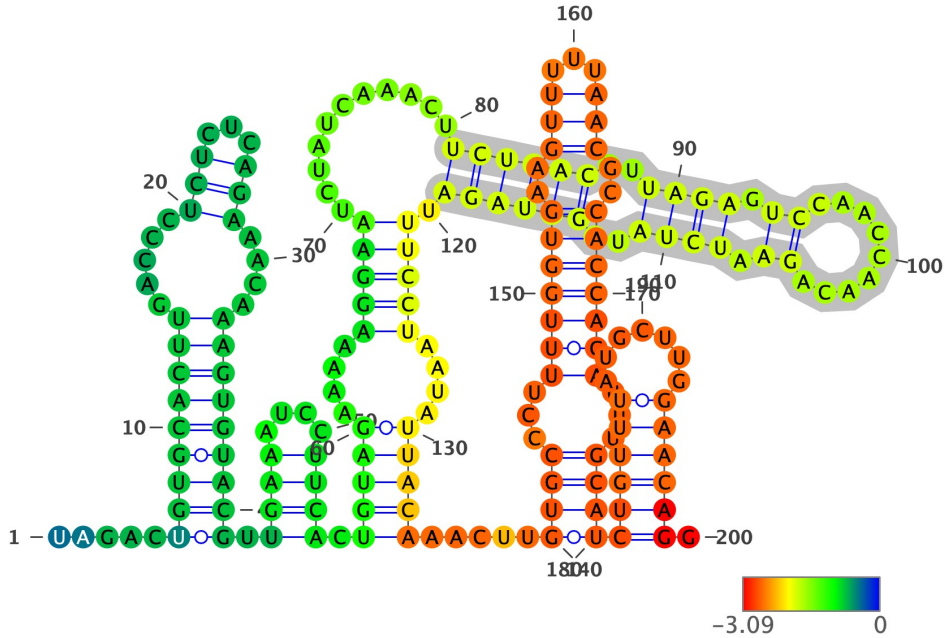
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 376 from nt 22508 to 22546 (nt 81 to 119)

```
5'-UCUAACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGA-3'
5'-((((((..((((.((.........)).))))..))))))-3'
Motif MFE = -9.2; z-score = -3.38; ED = 1.63
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22428 to 22627 (motif highlighted in silver):

```
5'-UAGACUGUGCACUUGACCCUCUCUCAGAAACAAAGUGUACGUUGAAAUCCUUCACUGUAGAAAAAGGAAUCUAUCAAACUUCUAACUUUAGAGUCCAACCAACAGAAUCUA
UUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGG-3
5'-.....((((((((((.....(((...)))....)))))))))).((((....)))).(((((....(((((...........((((((..((((.((.........)).))))
..)))))).)))))....)))))).....((((...(((((((..(((...)))..)))))))...))))((((((.......)))))).-3'
MFE = -42.3; z-score = -1.61; 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(+)

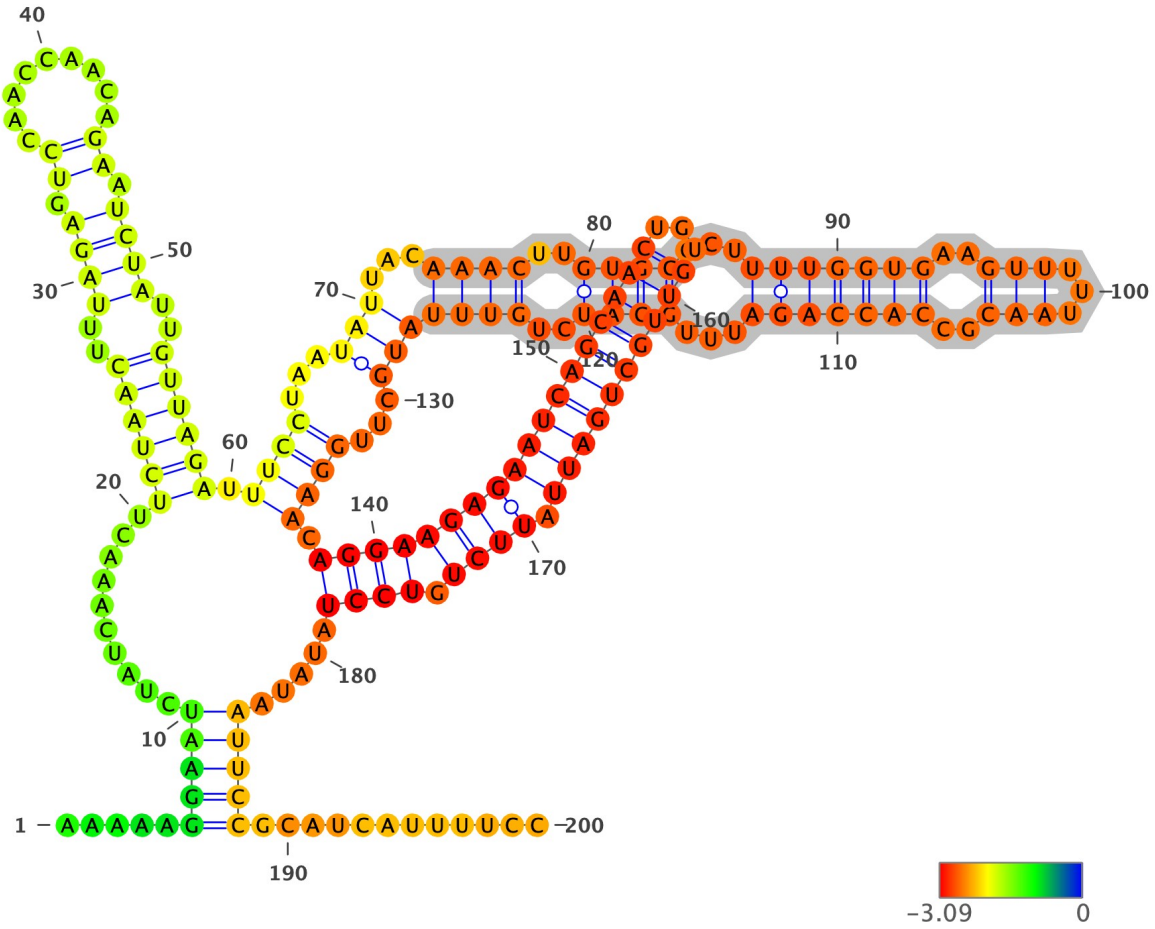
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 377 from nt 22561 to 22613 (nt 74 to 126)

```
5'-AAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUU-3'
5'-(((((..((((...(((((((..(((...)))..)))))))...)))))..))))-3'
Motif MFE = -15.2; z-score = -3.35; 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 = -4.03; 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(+)

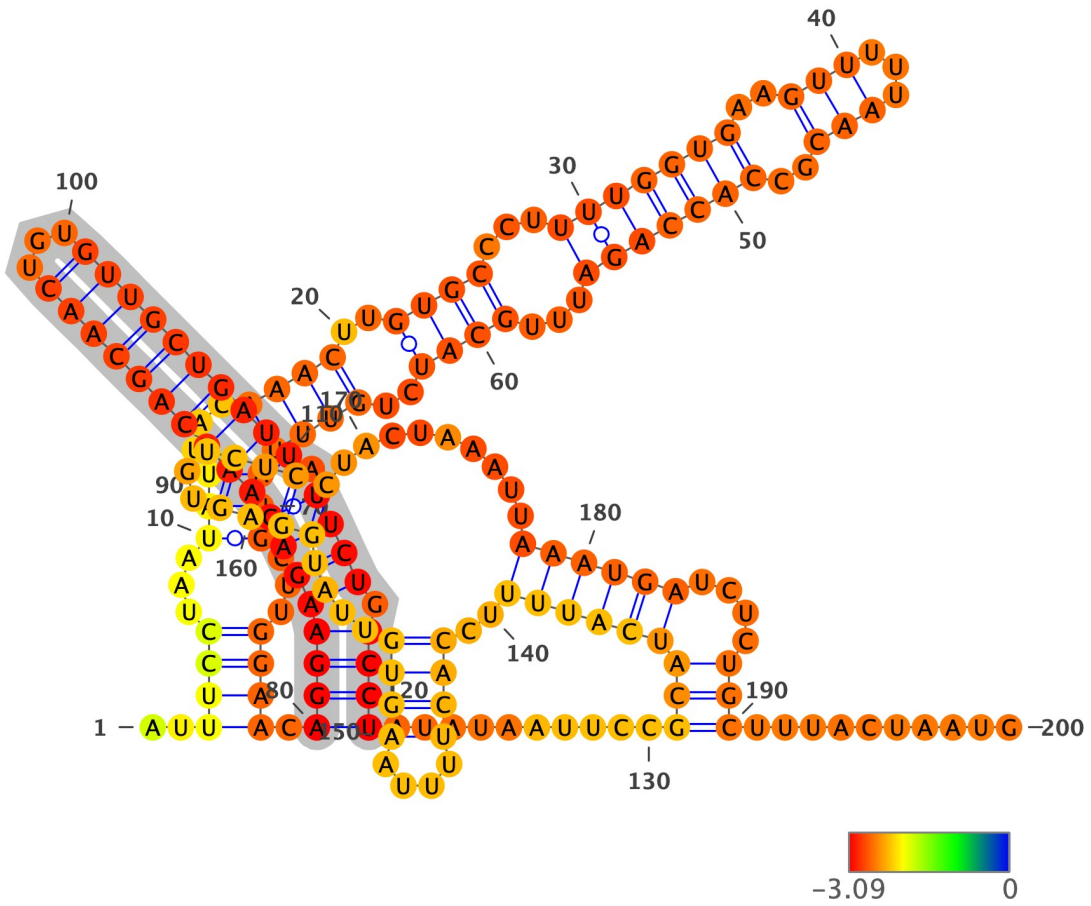
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 378 from nt 22625 to 22665 (nt 80 to 120)

```
5'-AGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCU-3'
5'-(((((((((((((((((...)))))))))).)))).))))-3'
Motif MFE = -18.8; z-score = -4.49; ED = 1.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22546 to 22745 (motif highlighted in silver):

```
5'-AUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUA
UUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUG-3
5'-..((((...(((...((((..((((...(((((((..(((...)))..)))))))...))))..)))))))...)))).((((((((((((((((...)))))))))).
)))).))))..........(((((((((..((((....))))....((((...))))..........))))))....)))..........-3'
MFE = -46.6; z-score = -3.07; ED = 23.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

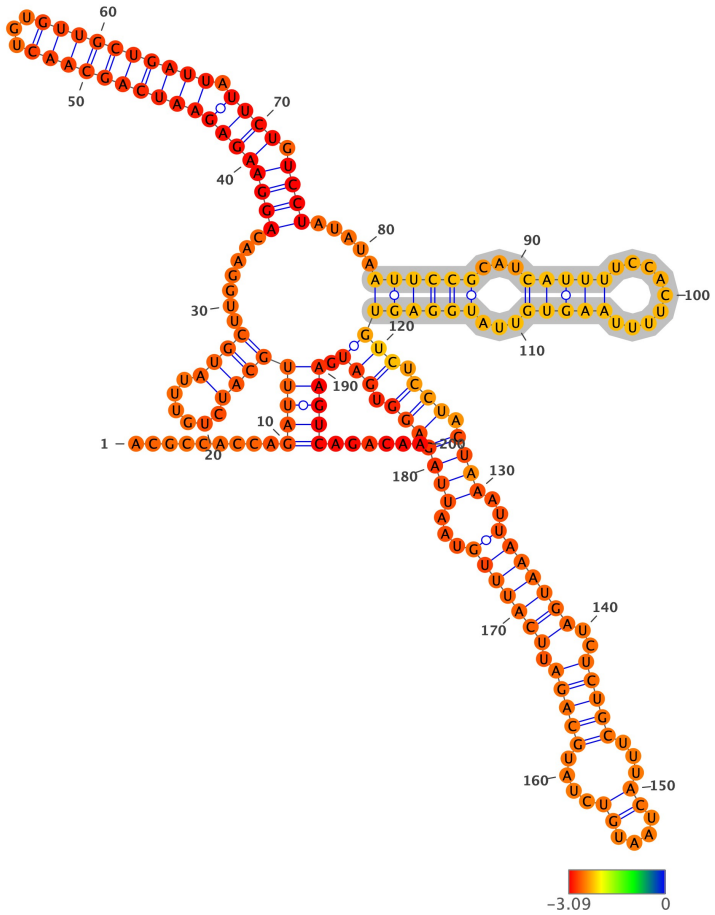
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 379 from nt 22671 to 22707 (nt 82 to 118)

```
5'-AUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGU-3'
5'-((((((...(((((.........)))))...))))))-3'
Motif MFE = -6.0; z-score = -1.56; ED = 3.06
```



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 22590 to 22789 (motif highlighted in silver):

```
5'-ACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUU
AUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAA-3
5'-.........(((((((((......))))........((((((((((((((((((...)))))))))).)))).))))).....((((((...(((((.........)))))..
.))))))(((.(((.((((..(((((((..(((((...((....))....))))).)))))))...)))))))).))).)))))......-3'
MFE = -51.9; z-score = -2.83; ED = 26.76
```

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_gp02, 21563-25384(+)

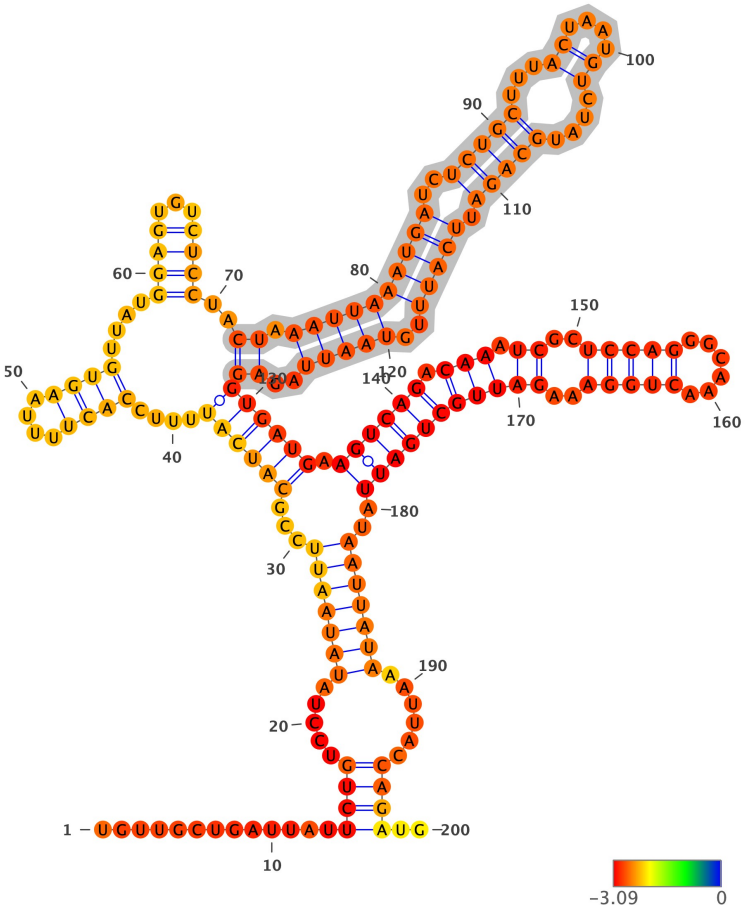
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22716 to 22772 (nt 72 to 128)

```
5'-CUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAG-3'
5'-((.(((((((((((..(((((...((....))....))))).))))))..))))))..))-3'
Motif MFE = -13.0; z-score = -2.55; ED = 3.71
```



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 22645 to 22844 (motif highlighted in silver):

```
5'-UGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGA
UUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUG-3
5'-.............((((.....(((((((...((((((....((((....))))....((((...))))..((.(((((((((((..(((((...((....))....)))))
.)))))..)))))..)))))))).((((((.(((.((..(((((......)))))..))))))))))))..)))))))......))))..-3'
MFE = -41.9; z-score = -2.66; ED = 24.84
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

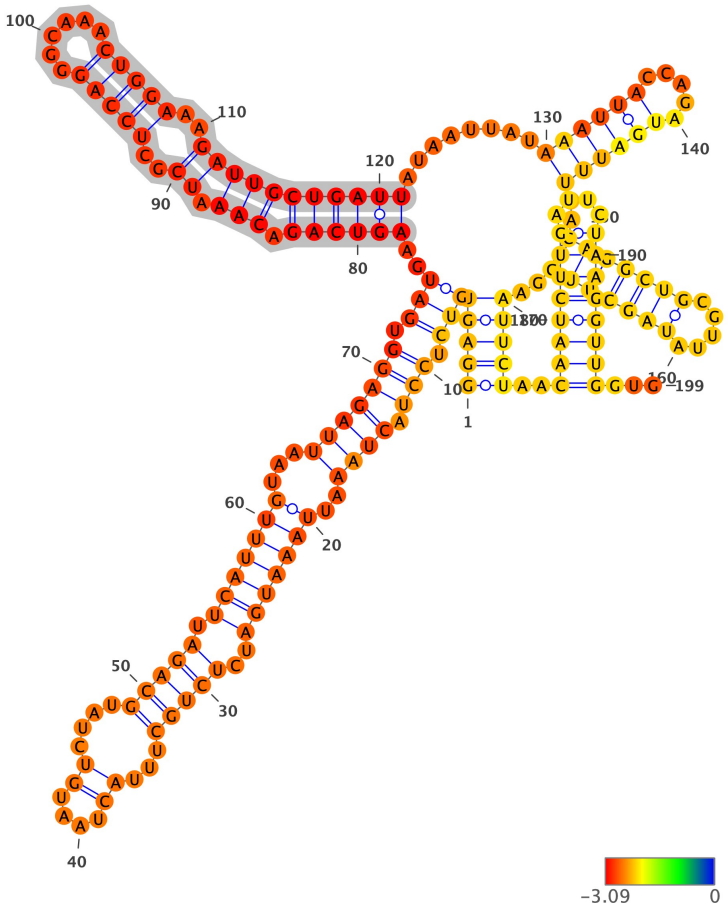
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 381 from nt 22780 to 22823 (nt 78 to 121)

```
5'-AGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUU-3'
5'-((((((.(((.((..(((((.....)))))..)))))))))))-3'
Motif MFE = -16.6; z-score = -3.99; ED = 2.64
```



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 22703 to 22901 (motif highlighted in silver):

```
5'-GGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAG
AUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUG-3
5'-(((((((((.(((.(((((..(((((((..((((((...((....))....)))))).)))))))...)))))))).)))..((((((.(((.((..(((((.....)))))..)
)))))))))).......((((((.....)))))).((((((.....)))))))..)))))..(((((((((....)))))))))...-3'
MFE = -53.4; z-score = -3.39; ED = 19.82
```

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_gp02, 21563-25384(+)

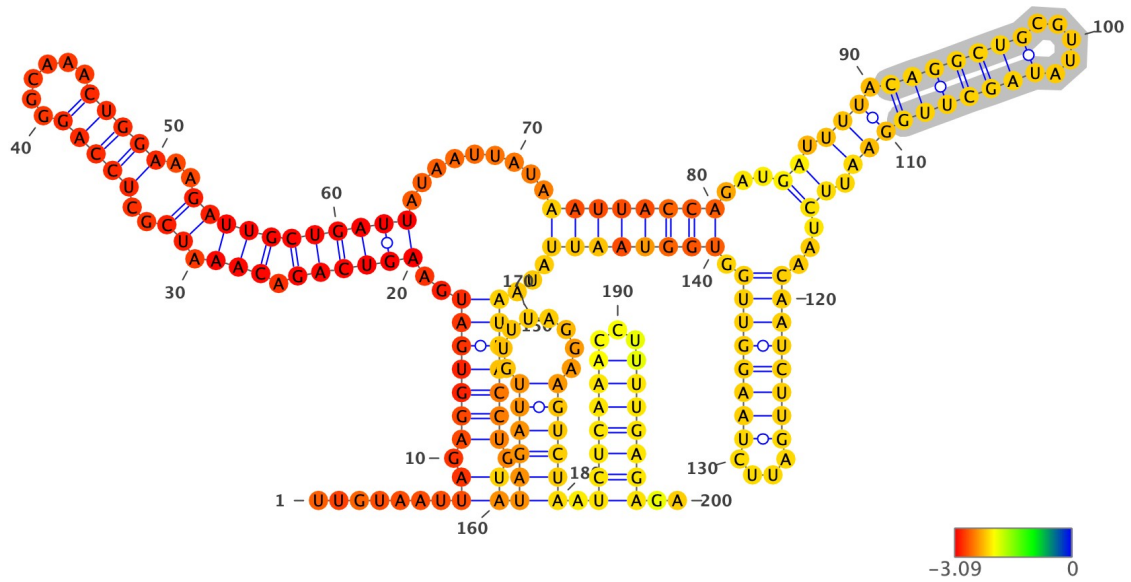
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 382 from nt 22851 to 22869 (nt 91 to 109)

```
5'-CAGGCUGCGUUAUAGCUUG-3'
5'-((((((.......))))))-3'
Motif MFE = -5.7; z-score = -2.75; ED = 0.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22761 to 22960 (motif highlighted in silver):

```
5'-UUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGA
AUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGA-3
5'-.......((.(((((((..((((((.(((.((..(((((.....)))))..))))))))))).........((((((((...((.(((.(((((((.....)))))))))
).))...((((((((....)))))))).))))))))...))))))).))((((((.........)))))).(((((((...)))))))..-3'
MFE = -54.5; z-score = -3.78; ED = 17.04
```

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(+)

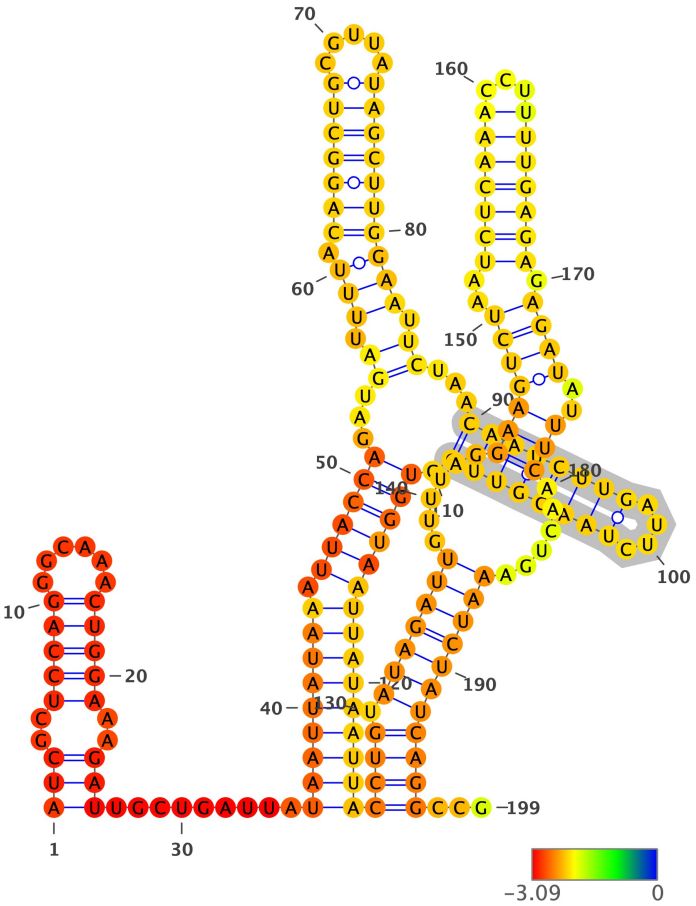
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 383 from nt 22879 to 22898 (nt 90 to 109)

```
5'-CAAUCUUGAUUCUAAGGUUG-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.8; z-score = -2.9; 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 = -3.96; ED = 20.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

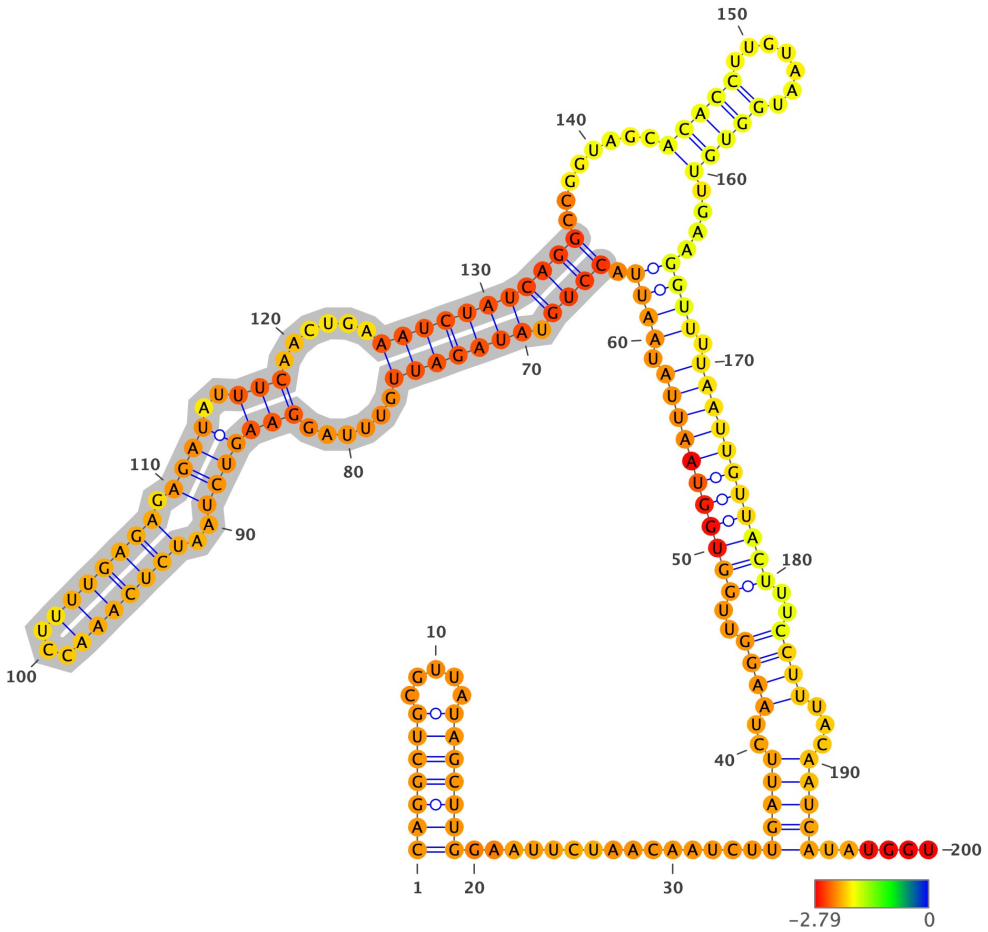
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 384 from nt 22915 to 22985 (nt 65 to 135)

```
5'-CCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGG-3'
5'-((((.(((((((.....(((((((..((((((.....)))))).))))..)))......)))))))))))-3'
Motif MFE = -21.1; z-score = -3.92; ED = 8.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22851 to 23050 (motif highlighted in silver):

```
5'-CAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAG
AUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGU-3
5'-(((((((.....)))))))...............(((((..((((..(((((((((((.((((.((((.(((((((.....(((((((..(((((((...)))))))).))
))..)))......)))))))))))........(((((.......)))))....)))).)))))))))))..))))...)))))......-3'
MFE = -48.4; z-score = -3.23; 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(+)

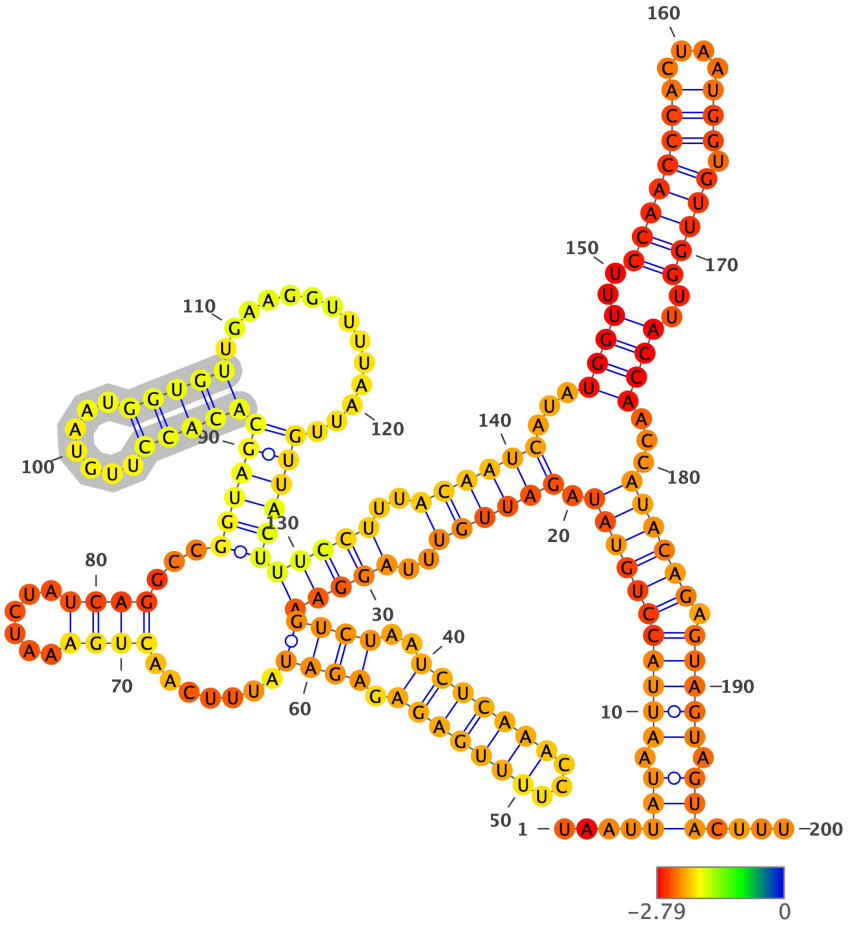
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 385 from nt 22994 to 23010 (nt 92 to 108)

```
5'-ACACCUUGUAAUGGUGU-3'
5'-(((((.......)))))-3'
Motif MFE = -5.4; z-score = -4.13; 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 = -5.36; 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(+)

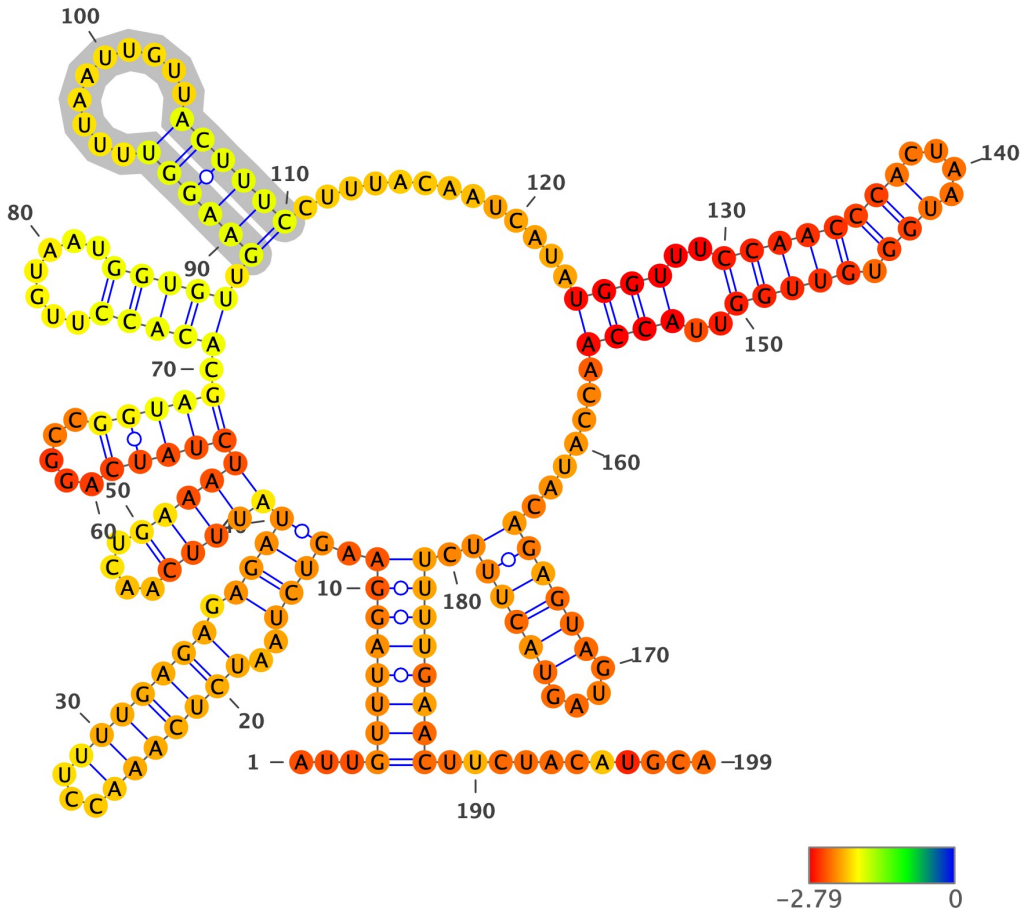
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 386 from nt 23012 to 23033 (nt 89 to 110)

```
5'-GAAGGUUUUAAUUGUUACUUUC-3'
5'-((((((..........))))))-3'
Motif MFE = -2.6; z-score = -1.96; 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 = -2.99; 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(+)

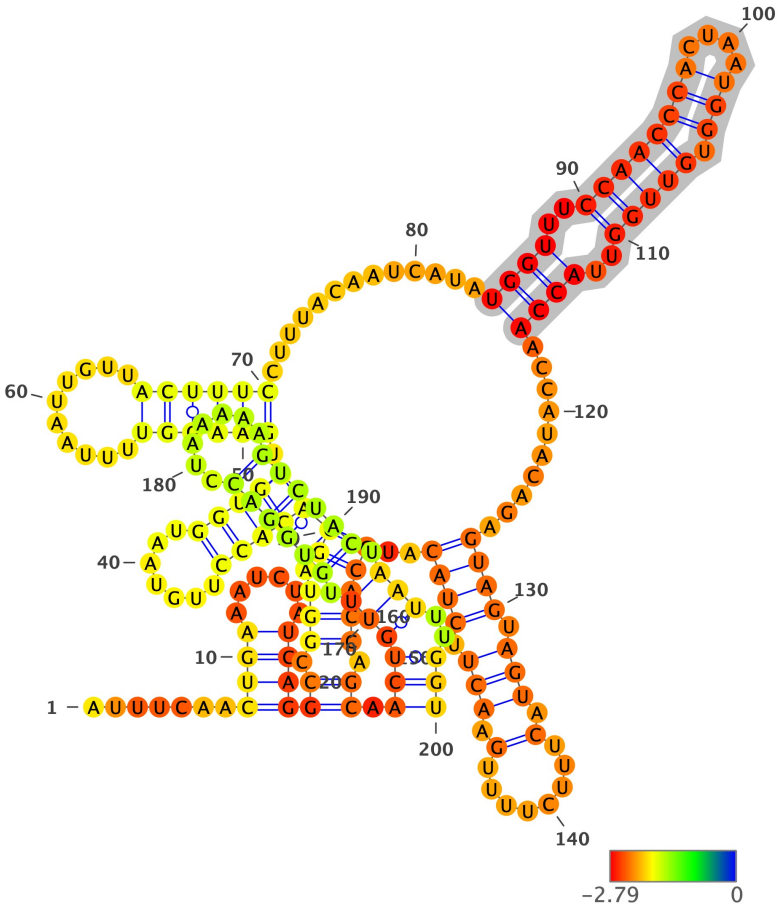
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 387 from nt 23047 to 23079 (nt 84 to 116)

```
5'-UGGUUUCCAACCCACUAAUGGUGUUGGUUACCA-3'
5'-((((..(((((((......)).)))))..))))-3'
Motif MFE = -14.7; z-score = -5.12; 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 = -2.47; 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(+)

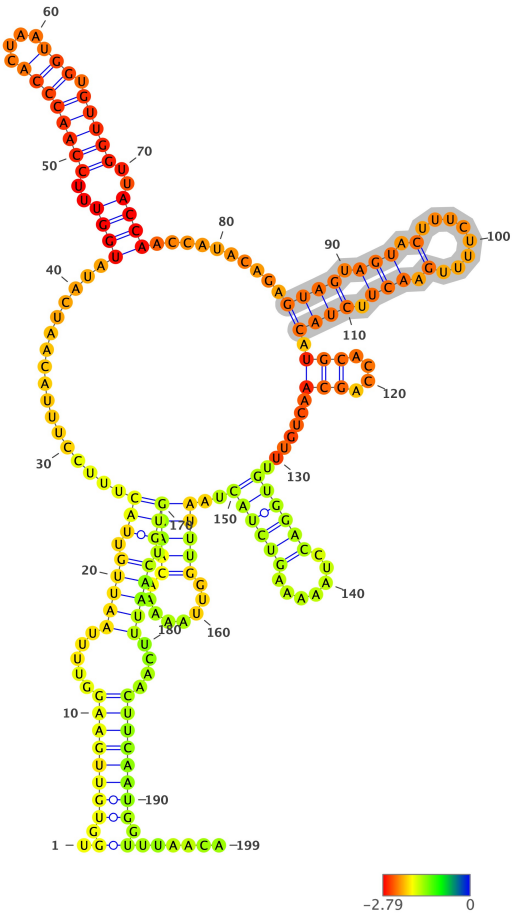
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 388 from nt 23090 to 23117 (nt 86 to 113)

```
5'-GUAGUAGUACUUUCUUUUGAACUUCUAC-3'
5'-((((.(((.(........).))).))))-3'
Motif MFE = -4.1; z-score = -2.05; 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 = -2.3; ED = 29.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

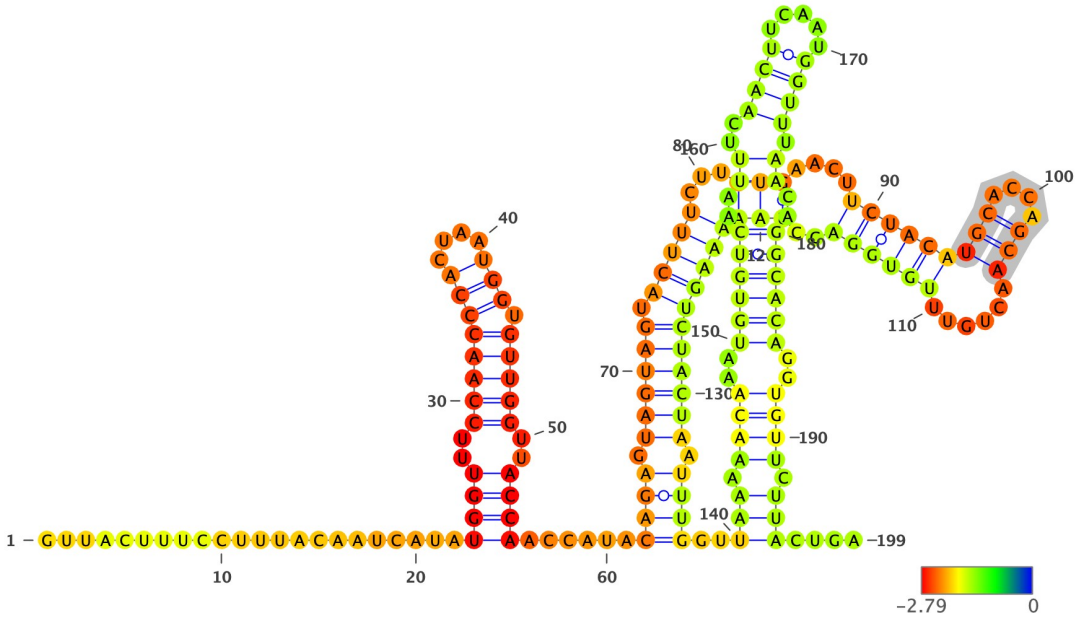
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 389 from nt 23119 to 23128 (nt 95 to 104)

```
5'-UGCACCAGCA-3'
5'-(((....)))-3'
Motif MFE = -0.9; z-score = -7.87; ED = 0.91
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23025 to 23223 (motif highlighted in silver):

```
5'-GUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUU
GUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGA-3
5'-......................((((..(((((((((....)))).)))))..)))).....((((.((((((.(((((...(((....(((((((((....)))).....)
)))))..))))))))))))))..)))).)).((((.((((..((((((..((..((((.....)))).)).)..)))))))..)))).)))....-3'
MFE = -43.5; z-score = -2.66; ED = 35.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

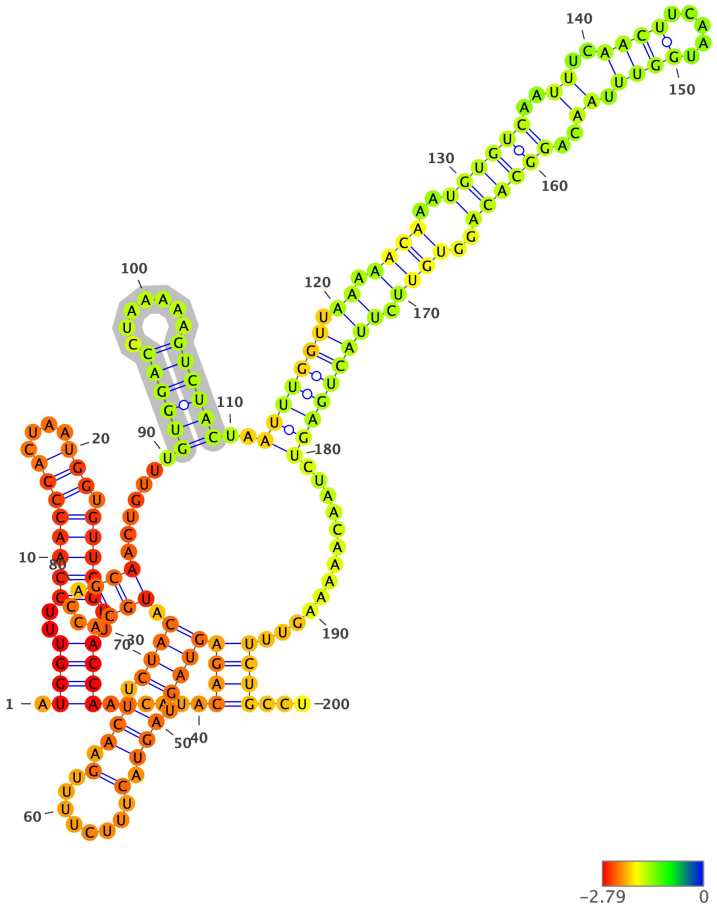
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 390 from nt 23136 to 23154 (nt 91 to 109)

```
5'-GUGGACCUAAAAAGUCUAC-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -3.06; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23046 to 23245 (motif highlighted in silver):

```
5'-AUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUA
AUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCU-3
5'-.((((..((((((((....))).)))))..))))......((((((((.(((.(........).))).)))).(((....)))........((((((.......))))))..
(((((((.((.((((..((((((..((..((((.....)))).))..))))))..)))).))))))))).............))))...-3'
MFE = -47.5; z-score = -2.49; ED = 25.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

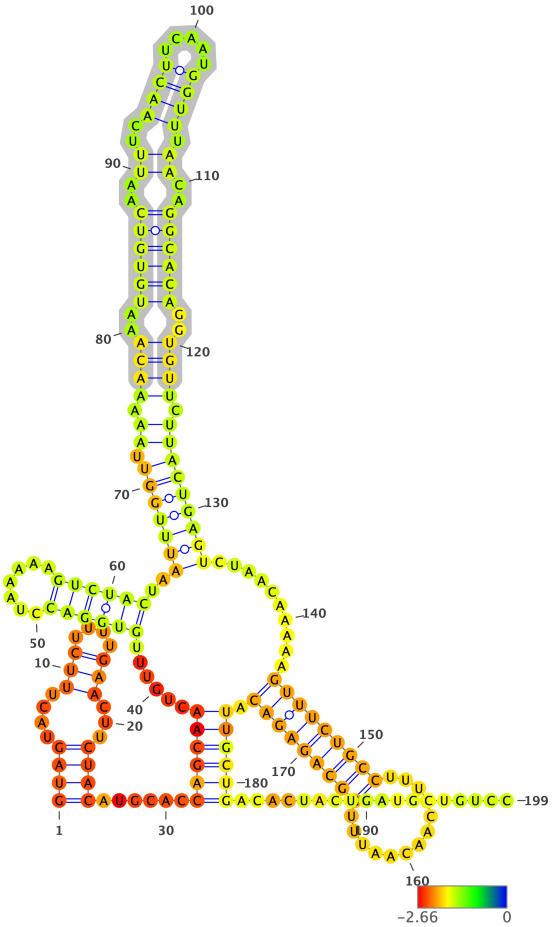
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 391 from nt 23169 to 23214 (nt 77 to 122)

```
5'-ACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGU-3'
5'-(((..(((((((..((..((((.....)))).))..))))))..)))-3'
Motif MFE = -9.8; z-score = -1.55; ED = 2.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23093 to 23291 (motif highlighted in silver):

```
5'-GUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACA
GGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCC-3
5'-((((....(((....)))...)))).....((((((......((((((.......))))))..(((((((.((.((((..((((((..((..((((.....)))).)).. ))))))..)))).))))))))).........(((((((((.............)))))))))).))))))..................-3'
MFE = -46.3; z-score = -2.7; ED = 25.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

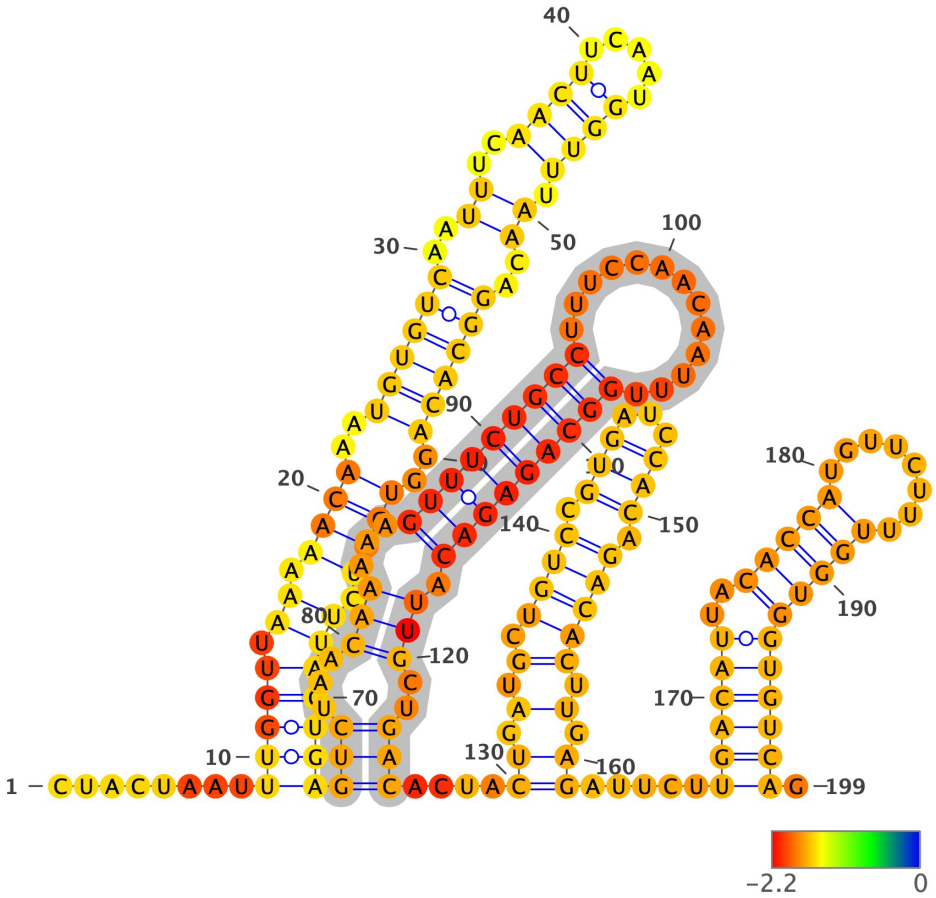
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 392 from nt 23224 to 23275 (nt 74 to 125)

```
5'-GUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGAC-3'
5'-(((.........((((((((((.............)))))))))......)))-3'
Motif MFE = -15.0; z-score = -3.28; ED = 3.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23151 to 23349 (motif highlighted in silver):

```
5'-CUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCA
GAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAG-3
5'-........(((((.((.((((..((((((..((..((((.....)))).))..))))))..)))).)))))))(((...(((...((((((((((.............))))
))))).)))..)))....((.(.(.((((.(((...))).)))))).).)).....((((((..(((((........)))))))))).-3'
MFE = -49.4; z-score = -2.97; ED = 39.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

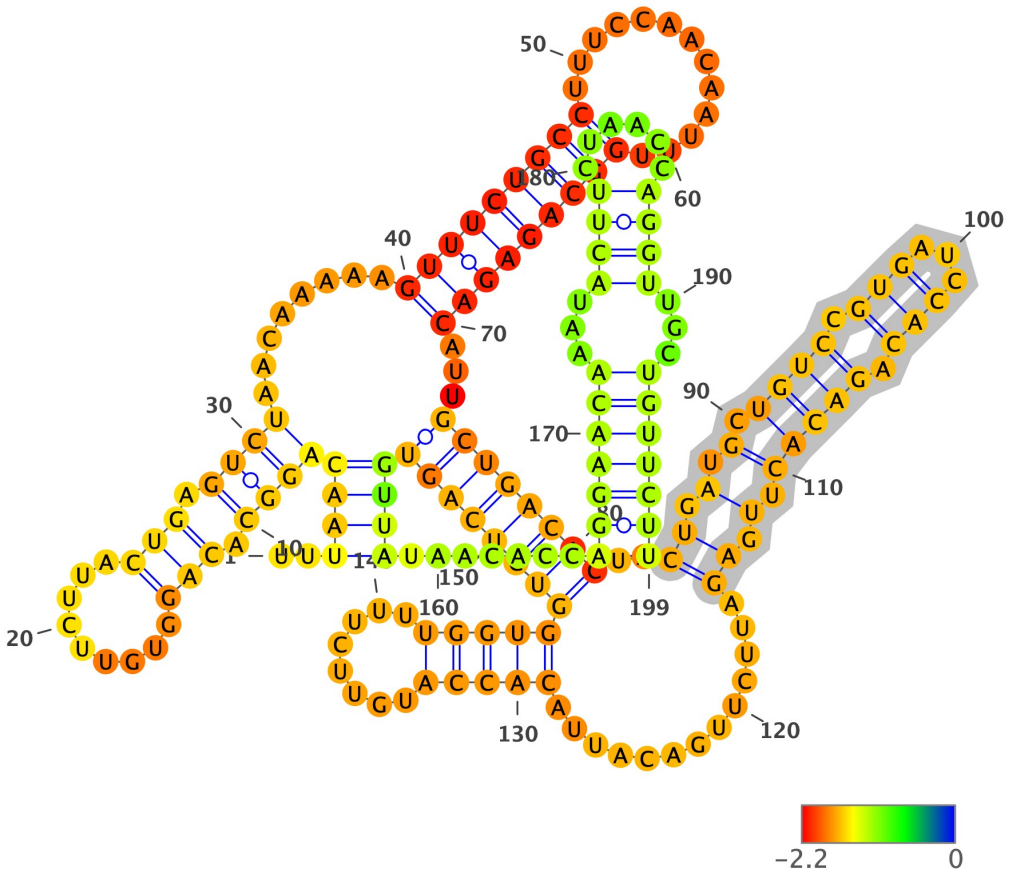
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 393 from nt 23280 to 23311 (nt 84 to 115)

```
5'-CUGAUGCUGUCCGUGAUCCACAGACACUUGAG-3'
5'-((...(.(((((.(((...))).)))))...))-3'
Motif MFE = -5.5; z-score = -0.18; ED = 2.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23197 to 23395 (motif highlighted in silver):

```
5'-UUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACU
UGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUU-3
5'-..(((((((((.(((.........))).)))).......(((((((((.............)))))))))...(((((((((..((.(.(.((((.(((...))).)))))).
).)).............(((((........)))))))))))))))).......(((((((...((((......))))...)))))))-3'
MFE = -51.3; z-score = -2.43; ED = 35.16
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

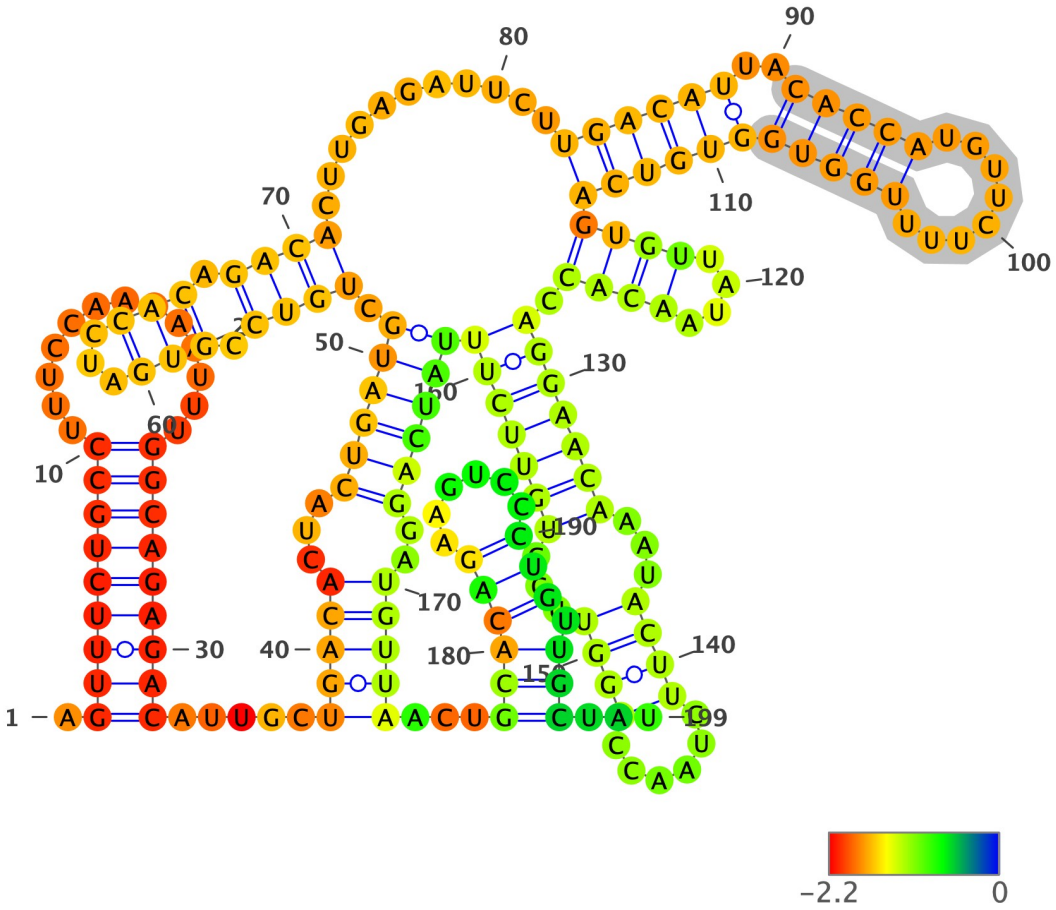
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 394 from nt 23325 to 23342 (nt 91 to 108)

```
5'-CACCAUGUUCUUUUGGUG-3'
5'-(((((........)))))-3'
Motif MFE = -5.4; z-score = -4.58; ED = 0.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23235 to 23433 (motif highlighted in silver):

```
5'-AGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUG
UCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAU-3
5'-.(((((((((.............)))))))))).....(((((...((((((.((((.(((...))).))))...........((((((..(((((........)))))))))
)))((((....)))).(((((((...((((......))))...))))))))))))))..)))))...((((((......))).)))...-3'
MFE = -56.1; z-score = -3.01; ED = 28.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

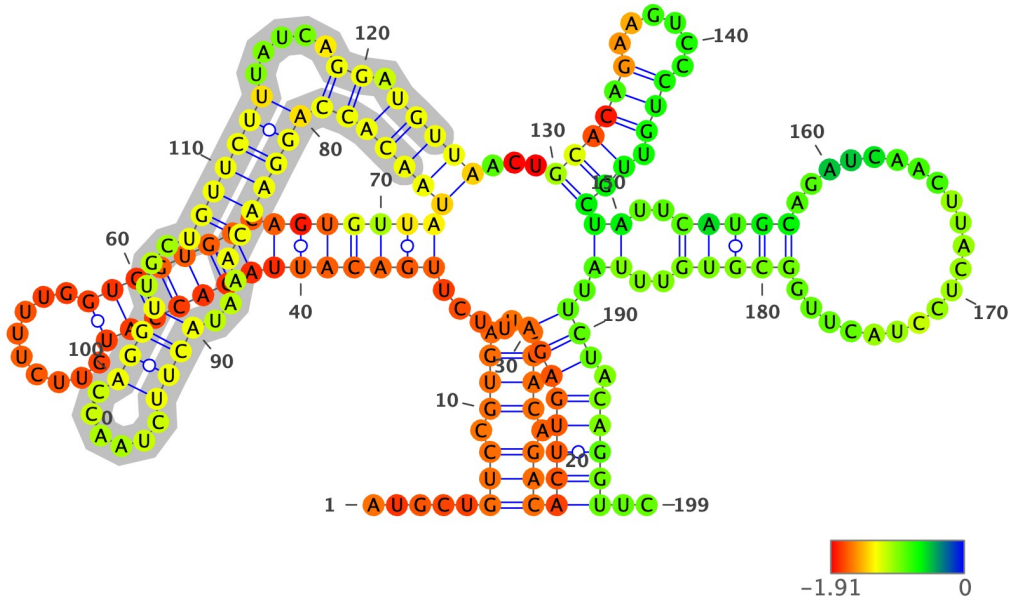
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 395 from nt 23357 to 23406 (nt 75 to 124)

```
5'-ACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGU-3'
5'-(((((((((((...((((......))))...)))))))).....)).)))-3'
Motif MFE = -8.1; z-score = -0.81; 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 23283 to 23481 (motif highlighted in silver):

```
5'-AUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUGUUC
UUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGGUUC-3
5'-.....(((.(((...))).)))((((((((....((((((((((((((.........)))))))).)))))))((((((((((((((...((((......))))...)))))
)).....)).)))))...((((((......))).)))((..(((((.....................)))))..)).))).)))))..-3'
MFE = -45.1; z-score = -0.83; ED = 40.82
```

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_gp02, 21563-25384(+)

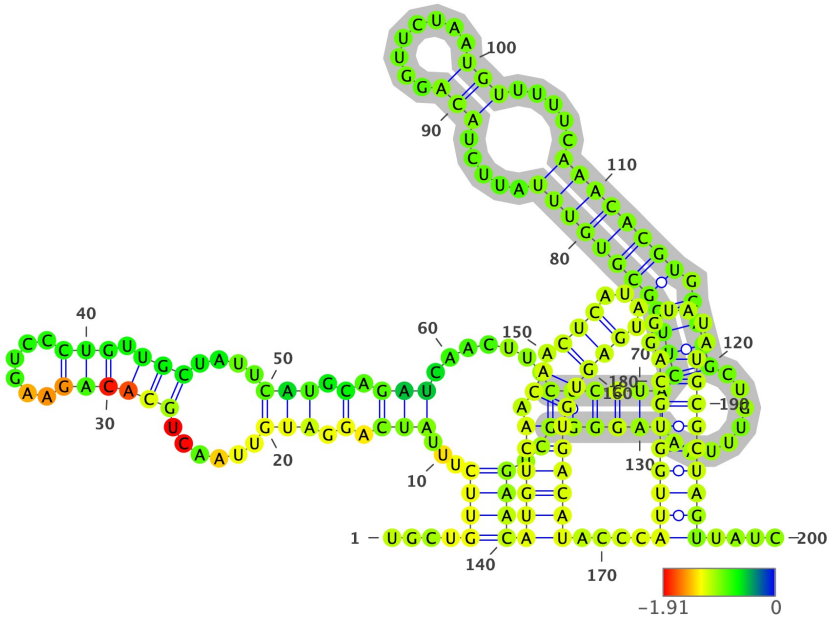
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 396 from nt 23451 to 23519 (nt 66 to 134)

```
5'-CUCCUACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGG-3'
5'-(((.((.............................................................)).)))-3'
Motif MFE = -17.5; z-score = -1.61; 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 23386 to 23585 (motif highlighted in silver):

```
5'-UGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAAC
ACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUC-3
5'-....((((...(((.(.(((......((((((......))).))).....)).).))).......((((((((((((((((.....((........)).....))))
))))).)))).........)))))).)))))((((((.((.(((....)))))))))))....(((((((((.....)))))))))....-3'
MFE = -49.0; z-score = -1.43; ED = 22.31
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

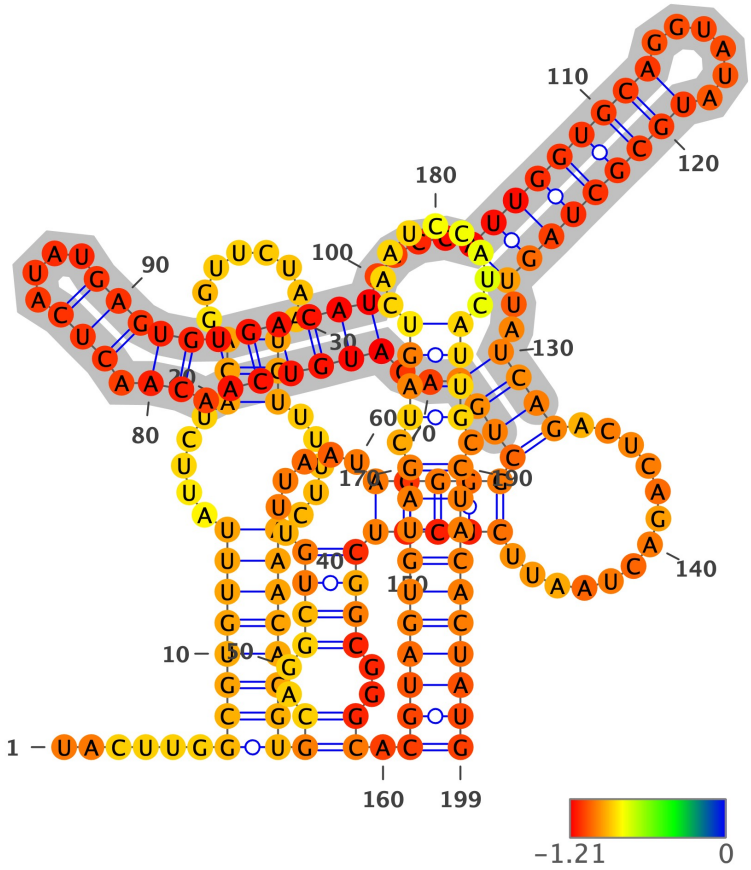
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23521 to 23586 (nt 67 to 132)

```
5'-UGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCA-3'
5'-(.(..(((((((.((.(((....)))))))))))).......((((((......))))))).....).)-3'
Motif MFE = -19.9; z-score = -3.37; 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 23455 to 23653 (motif highlighted in silver):

```
5'-UACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGC
AGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUG-3
5'-......((((((((.....(((.........)))).....))))))))((..((((......((((((((..((((((.((.(((....)))))))))))....((((((((
(......)))))))))..))))............))))))))..)).((((((((((.((((.........)))).))))))))))-3'
MFE = -53.2; z-score = -1.64; ED = 24.58
```

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_gp02, 21563-25384(+)

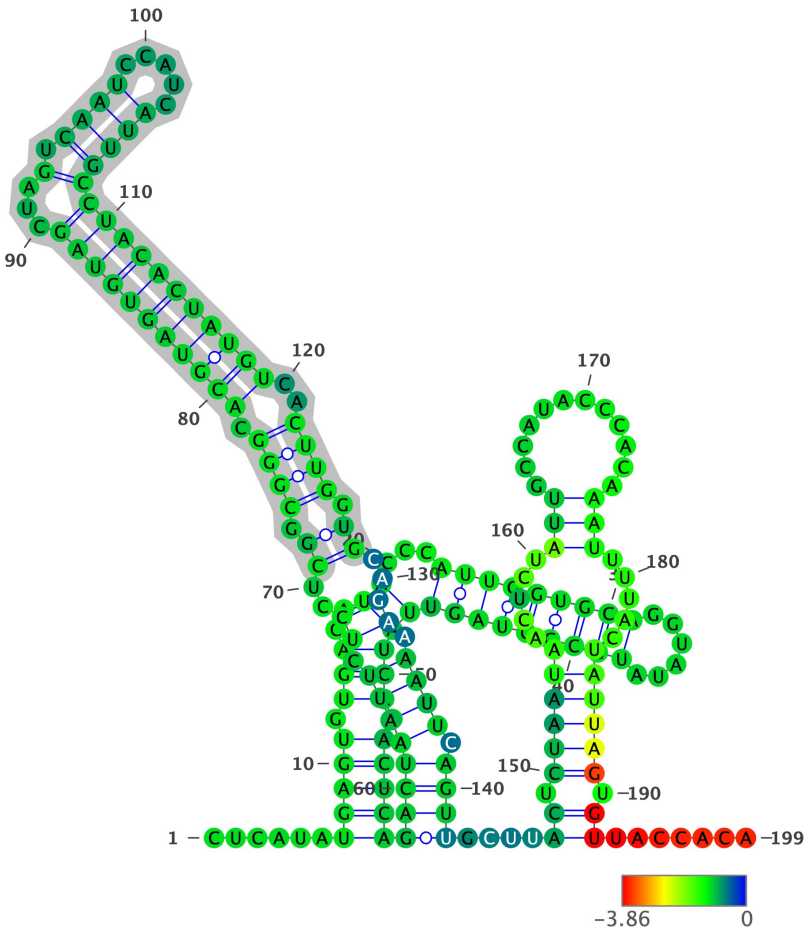
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 398 from nt 23606 to 23663 (nt 71 to 128)

```
5'-CGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACUUGGUG-3'
5'-(..((((.(((((((((((...(..............))))))))))))..))))..)-3'
Motif MFE = -17.6; z-score = -1.74; ED = 6.78
```



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 23536 to 23734 (motif highlighted in silver):

```
5'-CUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUA
CACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACA-3
5'-......(((((.(((..((...(((((((((.....))))))))))))).)))))((((((((.((..((.((((.(((((((((((...(.((((.....))))))))
))))))))..)))).))..)).)))).))))....((.((((((.....(((.............)))).....)))))).)).......-3'
MFE = -42.8; z-score = -1.45; ED = 37.3
```

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_gp02, 21563-25384(+)

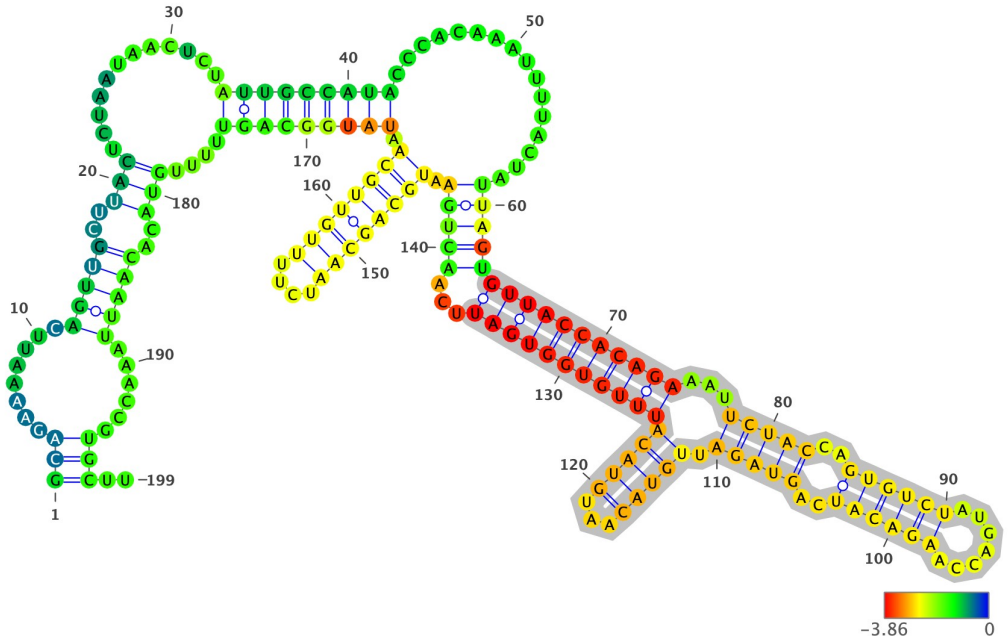
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23726 to 23797 (nt 64 to 135)

```
5'-GUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAU-3'
5'-(((((((((((...(((((..((((((.......))))))..))))))..((((...)))).))))))))))-3'
Motif MFE = -24.5; z-score = -4.69; 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 23663 to 23861 (motif highlighted in silver):

```
5'-GCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAU
UGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUU-3
5'-(((.......(((((..(((............((((((((.................(((((((((((((((...(((((..((((((.......))))))..))))).
(((((...))))))))))))))))...))))).((((((((....)))))))).))))))))....)))..)))))......)))..-3'
MFE = -49.6; z-score = -3.54; ED = 21.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

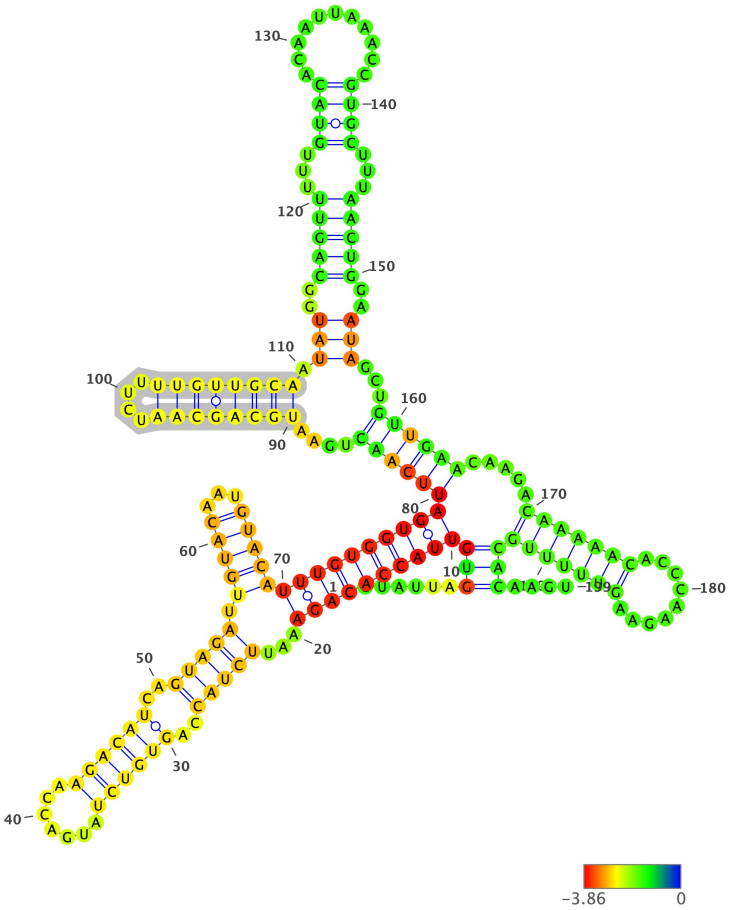
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23807 to 23826 (nt 90 to 109)

```
5'-UGCAGCAAUCUUUUGUUGCA-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.8; z-score = -5.72; ED = 0.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23718 to 23916 (motif highlighted in silver):

```
5'-CUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAU
AUGGCAGUUUUUGUACACAAUUAAACCGUGCUUUAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGU-3
5'-......(((((((((((((...(((((..((((((.......))))))..))))).(((((...))))))))))))))))((((((....((((((((....))))))))).(
((..(((((...((((...........))))...)))))..)))...))))))).....(((((((.........))))))))))....-3'
MFE = -50.2; z-score = -2.89; 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(+)

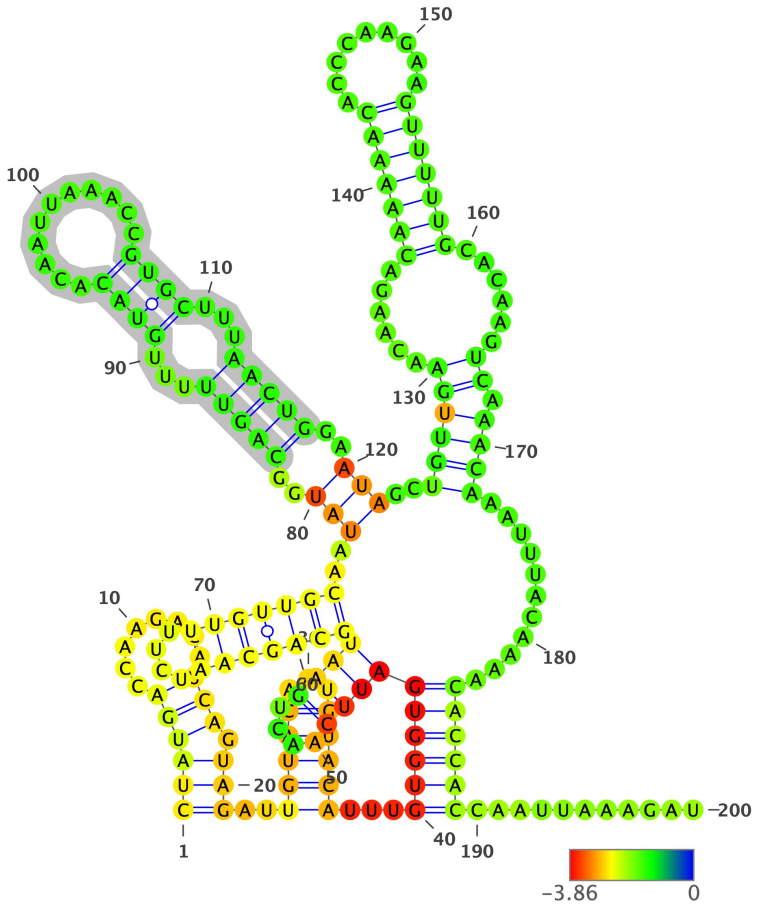
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 401 from nt 23833 to 23867 (nt 83 to 117)

```
5'-CAGUUUUUGUACACAAUUAAACCGUGCUUUAACUG-3'
5'-(((((...((((...........))))...)))))-3'
Motif MFE = -6.4; z-score = -1.99; 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 = -1.55; 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(+)

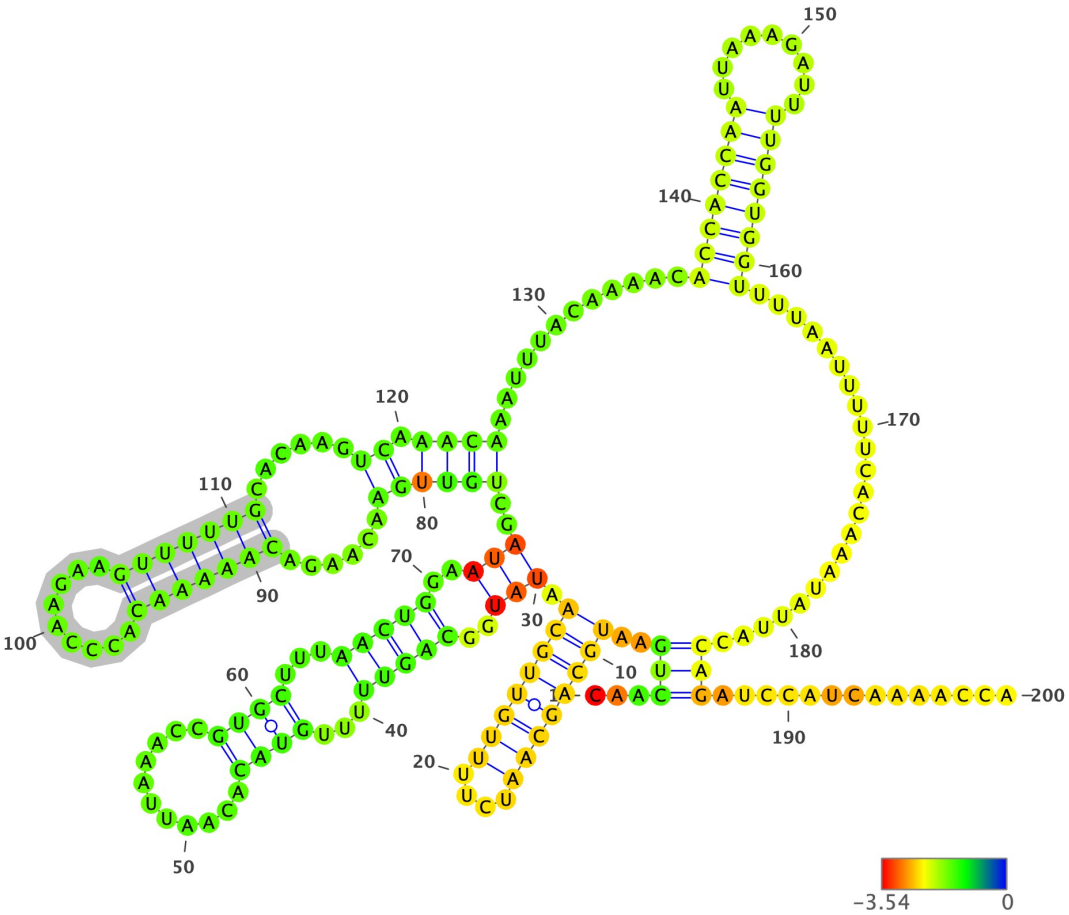
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 402 from nt 23887 to 23909 (nt 89 to 111)

```
5'-CAAAAACACCCAAGAAGUUUUUG-3'
5'-(((((((.........)))))))-3'
Motif MFE = -3.0; z-score = -2.28; 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 = -2.77; 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(+)

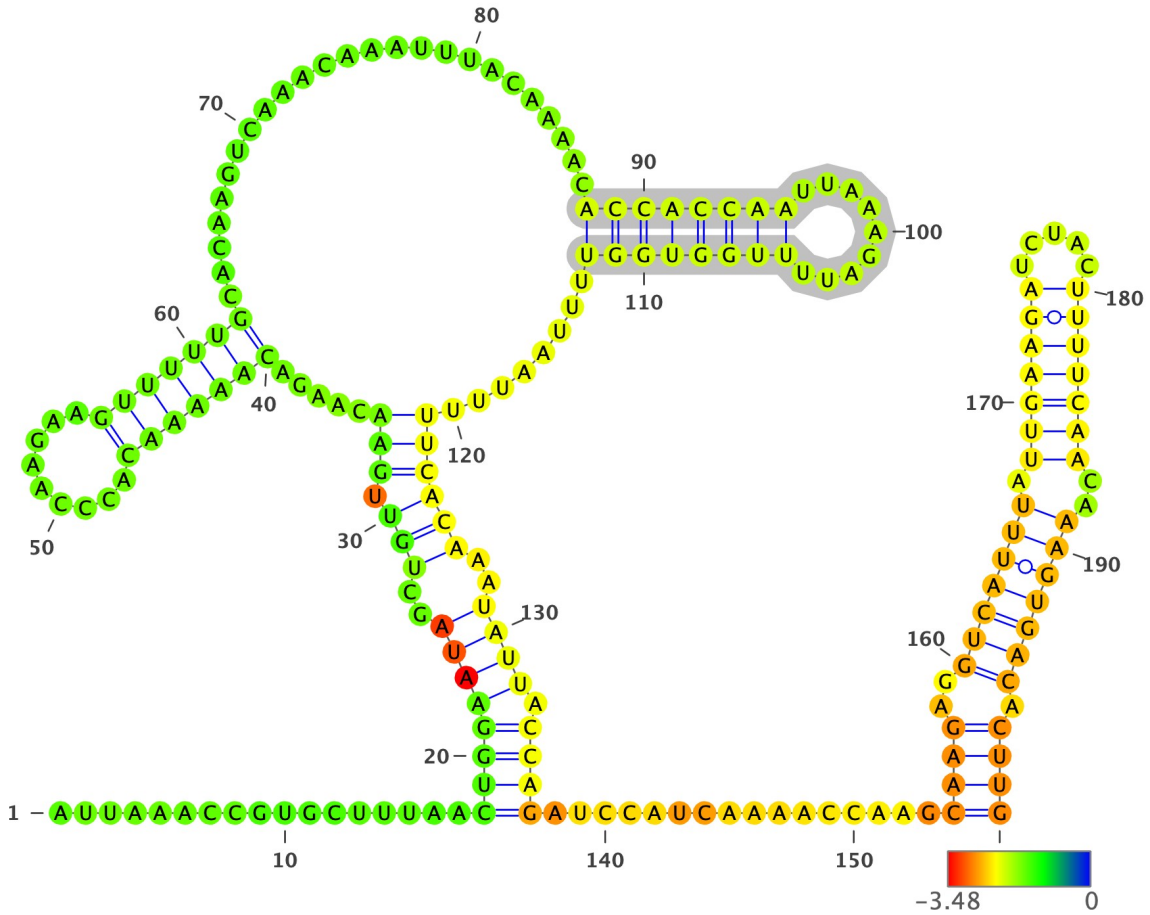
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 403 from nt 23935 to 23959 (nt 88 to 112)

```
5'-ACCACCAAUUAAAGAUUUUGGUGGU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -10.4; z-score = -4.68; 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 = -2.41; 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(+)

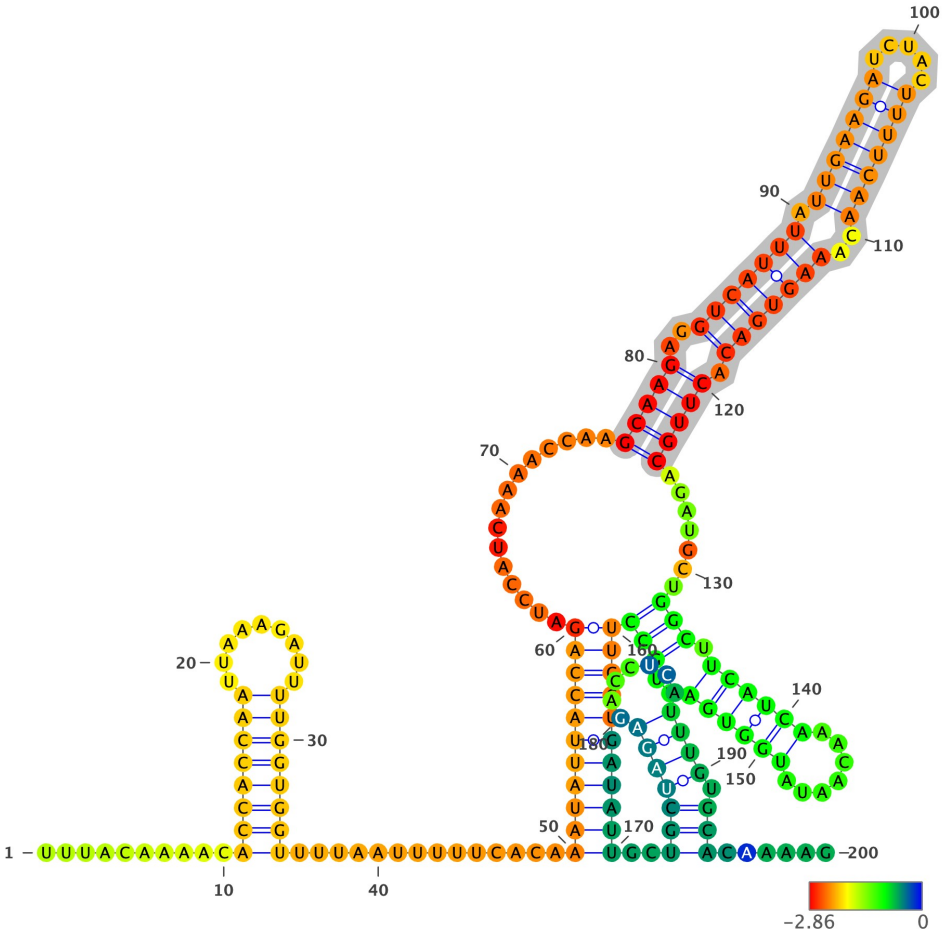
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 404 from nt 24000 to 24048 (nt 76 to 124)

```
5'-GCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUGC-3'
5'-(((((..(((((((.(((((((.....)))))))..)))))))..)))))-3'
Motif MFE = -16.1; z-score = -3.56; 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 = -3.68; 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(+)

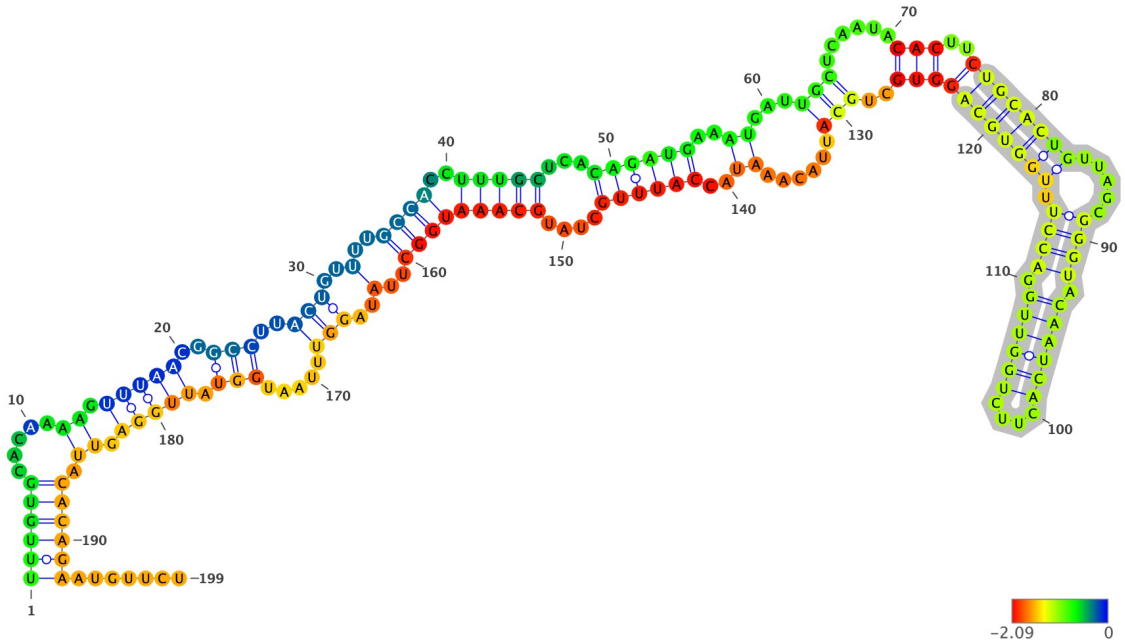
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 405 from nt 24187 to 24232 (nt 77 to 122)

```
5'-UGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCA-3'
5'-(((((.......((((.((((((....)))))).))))...)))))-3'
Motif MFE = -14.3; z-score = -1.7; ED = 3.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24111 to 24309 (motif highlighted in silver):

```
5'-UUUGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGA
CCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCU-3
5'-((((((.....((.(((((..(((..(((..(.((((..(((((...((((((..((...(((......(((..((((((((.....((((.((((((....)))))).)
))).))))))))))..)))......))..))))))....))))))))..)..)))).....))).)))))).)).))))))........-3'
MFE = -44.8; z-score = -1.31; ED = 59.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

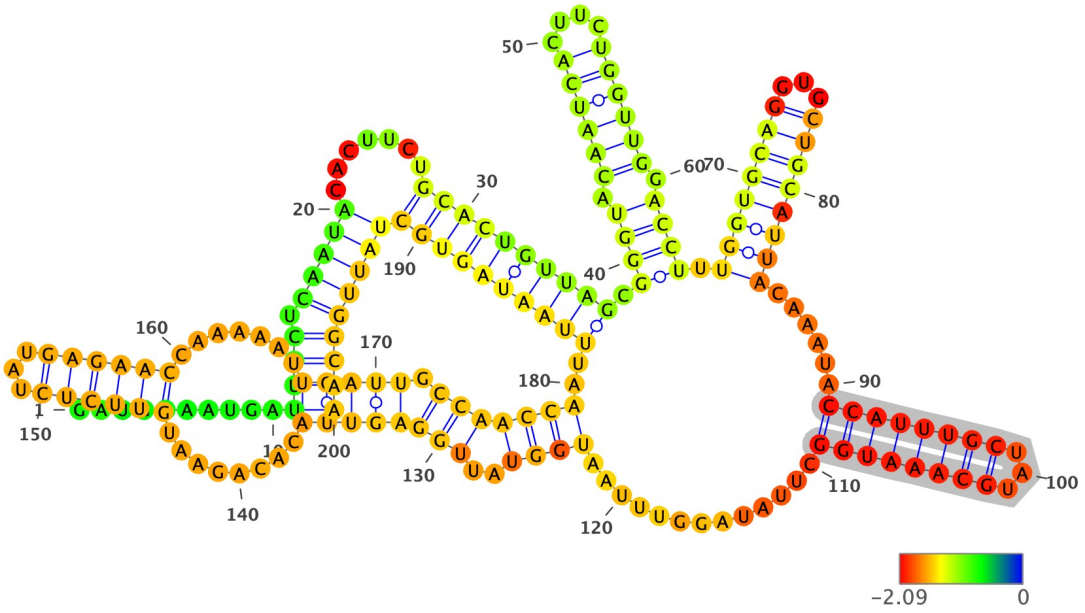
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 406 from nt 24251 to 24269 (nt 91 to 109)

```
5'-CCAUUUGCUAUGCAAAUGG-3'
5'-(((((((...)))))))-3'
Motif MFE = -8.4; z-score = -5.19; ED = 0.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24161 to 24360 (motif highlighted in silver):

```
5'-GAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCU
UAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3
5'-..........((((.(((((.......((((((((((.((((.((((((....)))))).)))).((((((((...)))))))).....(((((((...)))))))).
..........((((..((((((((.......((((((...)))))).......)))))).)))))))..))))))))))))))))))-3'
MFE = -55.2; z-score = -2.94; 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(+)

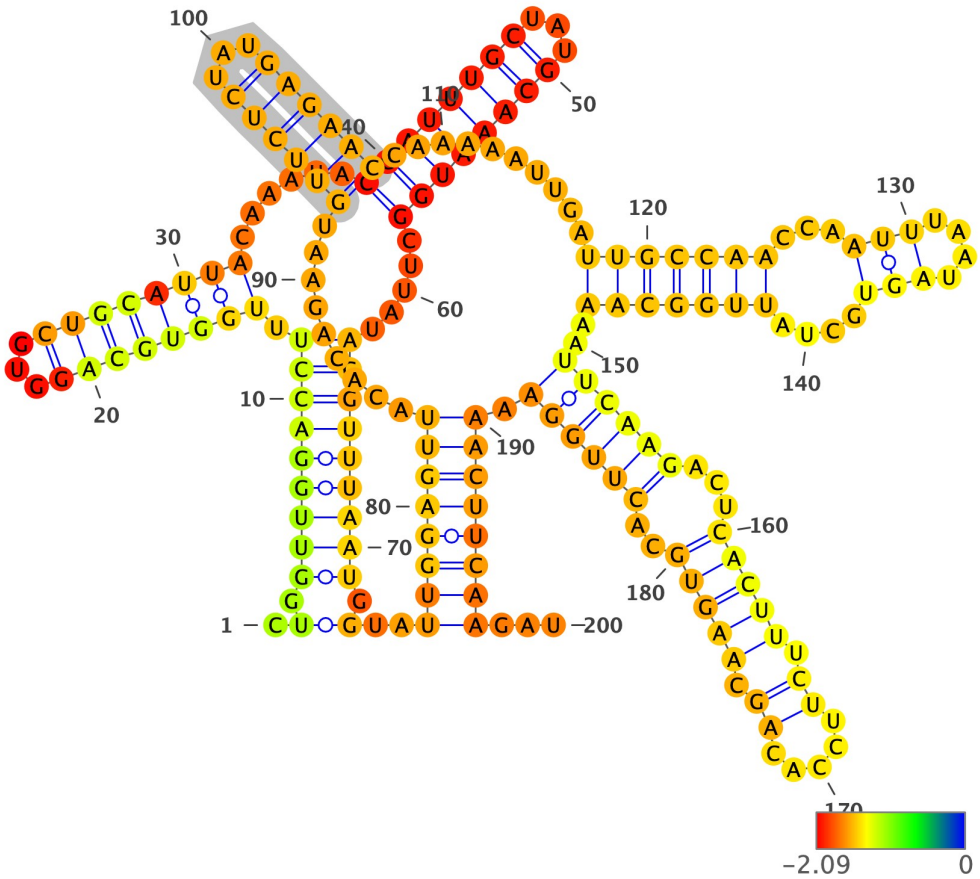
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 407 from nt 24305 to 24319 (nt 93 to 107)

```
5'-GUUCUCUAUGAGAAC-3'
5'-((((((...))))))-3'
Motif MFE = -4.6; z-score = -5.95; ED = 0.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24213 to 24412 (motif highlighted in silver):

```
5'-CUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAA
AAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAU-3
5'-.(.(((((((((.(((((((((...)))))))))......(((((((((...)))))))))).....)))))))))..)..((((((((.........((((((...)))))))....
......(((((((...((((....))))....)))))))..((((((...((((((.((.....)).)))))..)))))).))))))))...-3'
MFE = -50.9; z-score = -2.38; ED = 14.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

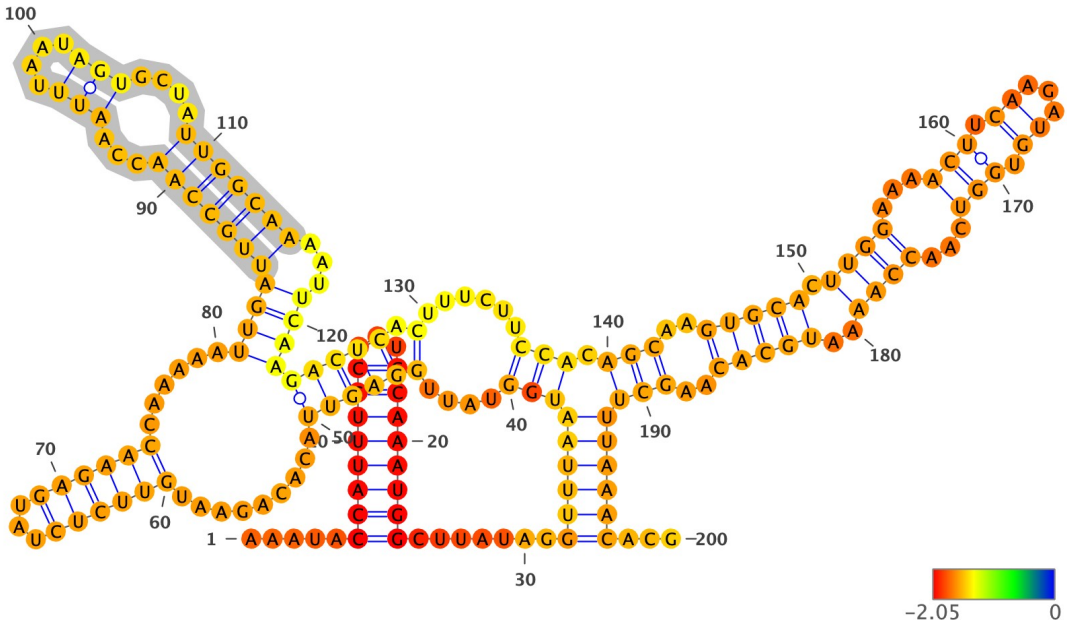
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 408 from nt 24330 to 24360 (nt 85 to 115)

```
5'-UUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3'
5'-(((((((.................)))))))-3'
Motif MFE = -6.5; z-score = -2.5; 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 = -2.41; ED = 41.03
```

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(+)

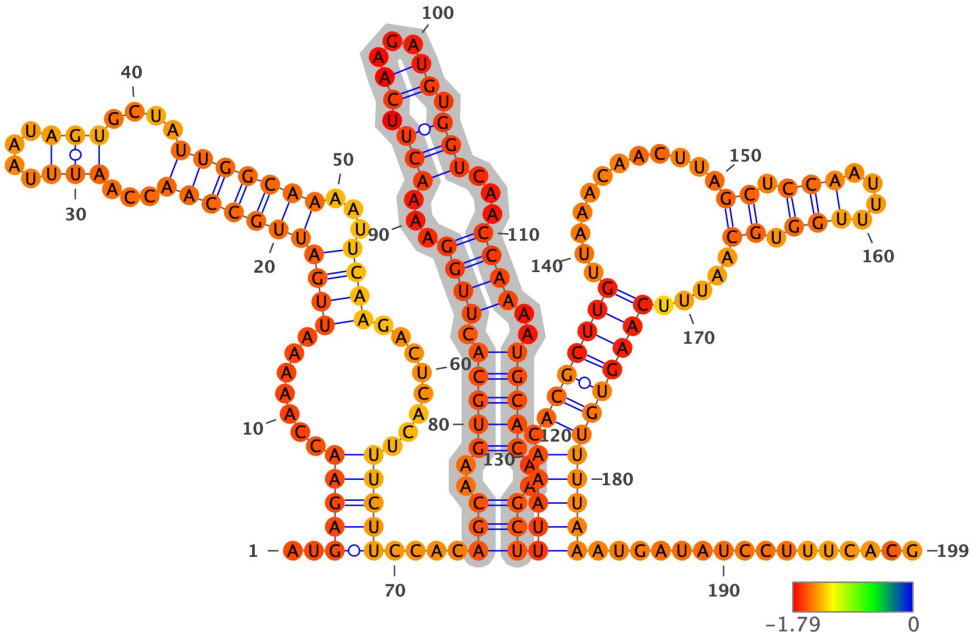
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 409 from nt 24385 to 24436 (nt 74 to 125)

```
5'-AGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCU-3'
5'-(((..(((((.((((...(((.(.....).)))...)))))..)))))..)))-3'
Motif MFE = -13.3; z-score = -2.98; ED = 6.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24312 to 24510 (motif highlighted in silver):

```
5'-AUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACC
AAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACG-3
5'-..(((((.......((((((((((...(((....)))....)))))))...))))........)))))....(((..(((((.((((...(((.((...)).)))...))
))..)))))..)))(((((.(((((((............((.(((....))).)).....))))))))))))).................-3'
MFE = -35.9; z-score = -1.75; ED = 24.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

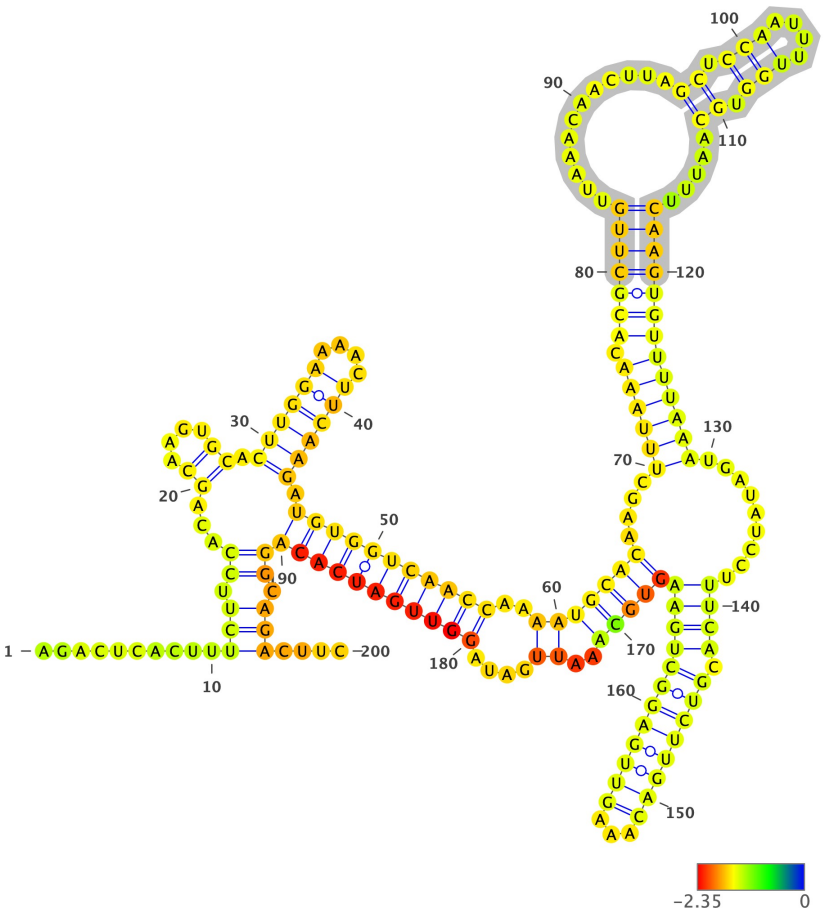
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 410 from nt 24446 to 24486 (nt 80 to 120)

```
5'-CUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAG-3'
5'-((((............((.((......)).)).....))))-3'
Motif MFE = -5.3; z-score = -0.74; 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 24367 to 24566 (motif highlighted in silver):

```
5'-AGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGC
AAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUC-3
5'-..........(((.((...((....)).((((((....)))))).(((((((((((..(((((((....((((((.(((((((.............((.(((....))).))
.....)))))))))))))).........((((.(((((((((...)))))))))))))))))..))....)))))))))))))).)))....-3'
MFE = -47.9; z-score = -2.25; ED = 19.2
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

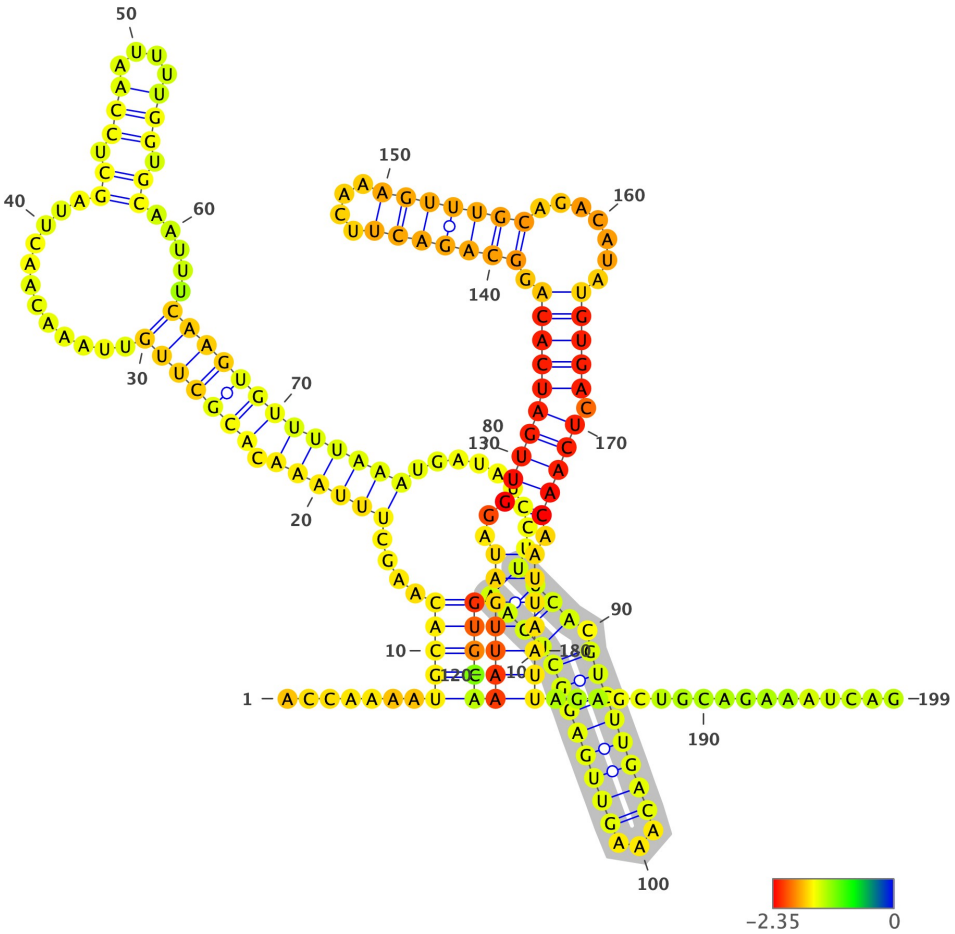
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 411 from nt 24505 to 24532 (nt 86 to 113)

```
5'-UUCACGUCUUGACAAAGUUGAGGCUGAA-3'
5'-((((.((((((((...)))))))))))-3'
Motif MFE = -8.5; z-score = -3.05; 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 = -2.39; 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(+)

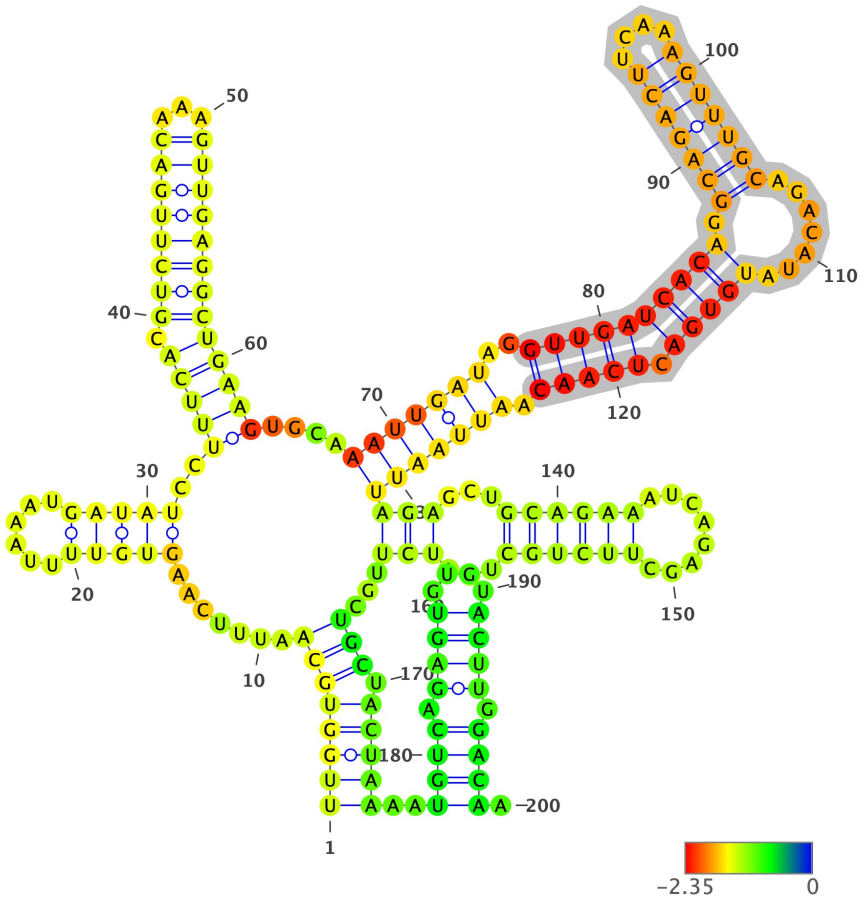
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 412 from nt 24547 to 24593 (nt 77 to 123)

```
5'-GUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAAC-3'
5'-((((((((..(((((((....)))))))........)))).)))))-3'
Motif MFE = -14.0; z-score = -3.04; ED = 1.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24471 to 24670 (motif highlighted in silver):

```
5'-UUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAU
AUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAA-3
5'-((((((((.......(((((......)))))..(((((.((((((((...)))))))))))))....(((((((..((((((((((.(((((((....)))))))......
.))))).))))).)))))))(((...((((((........))))))...)))...))).)))))..((((.((((....)))).)))).-3'
MFE = -50.9; z-score = -2.03; ED = 32.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

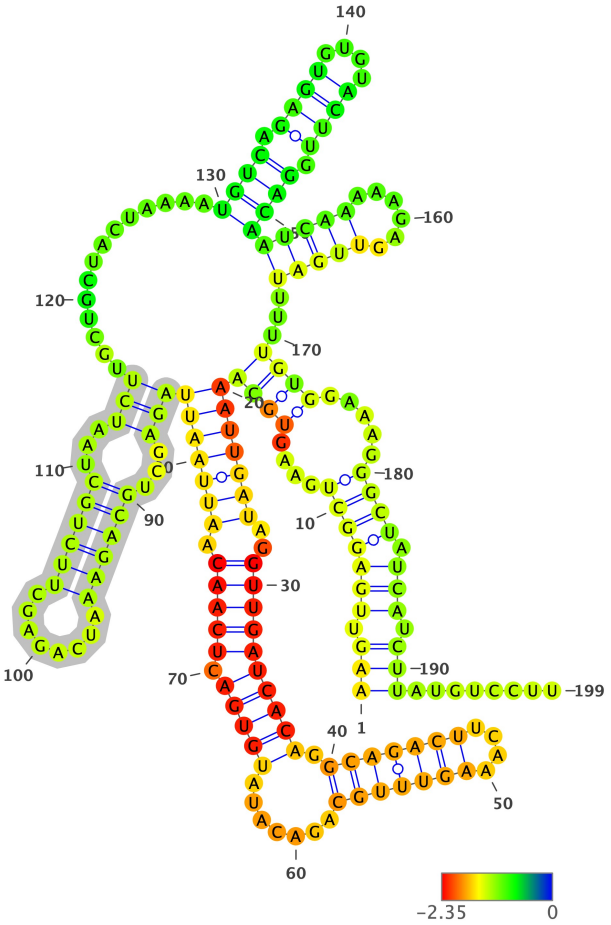
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 413 from nt 24602 to 24633 (nt 84 to 115)

```
5'-AGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCU-3'
5'-(((...((((((........))))))...)))-3'
Motif MFE = -8.8; z-score = -2.18; 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 24519 to 24717 (motif highlighted in silver):

```
5'-AAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUA
AUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU-3
5'-(((.(((((((....(((((((((((..((((((((((.(((((((....)))))))).......))))).))))).)))))))(((...((((((........))))))..
.)))..............((((.((((....)))).))))(((((......)))))...))))).....)))).))).)))........-3'
MFE = -44.8; z-score = -1.08; ED = 37.67
```

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_gp02, 21563-25384(+)

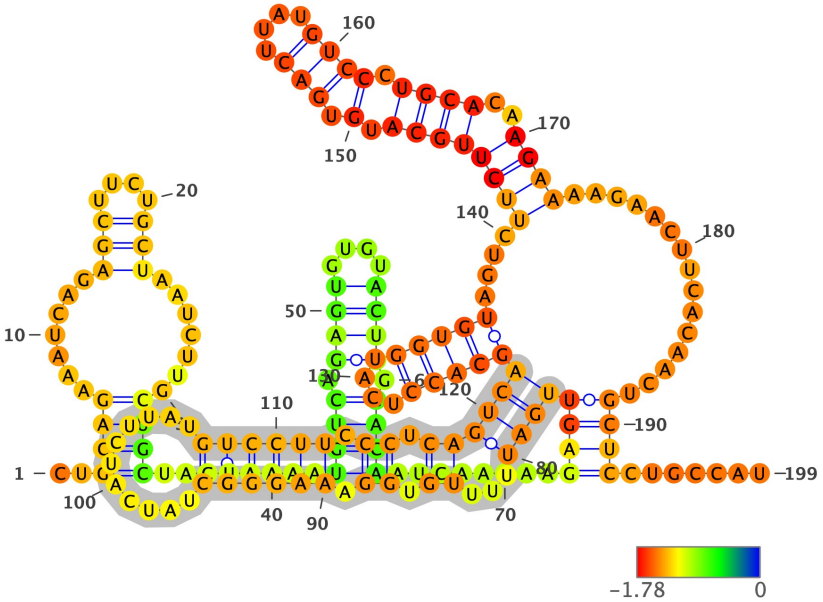
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 414 from nt 24682 to 24727 (nt 77 to 122)

```
5'-UGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCA-3'
5'-((((...((.((.((((((...........))))))).)).))))))-3'
Motif MFE = -11.3; z-score = -2.02; ED = 7.84
```



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 24606 to 24804 (motif highlighted in silver):

```
5'-CUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCU
UCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAU-3
5'-..((((.......(((....)))........))))........((((.((((....)))).))))........((((((((...((.((.((((((...........)))))
).)).))))))(((((....)))))....((((((((.(.(((....)))).)))).)))).................))))........-3'
MFE = -45.7; z-score = -1.21; ED = 41.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

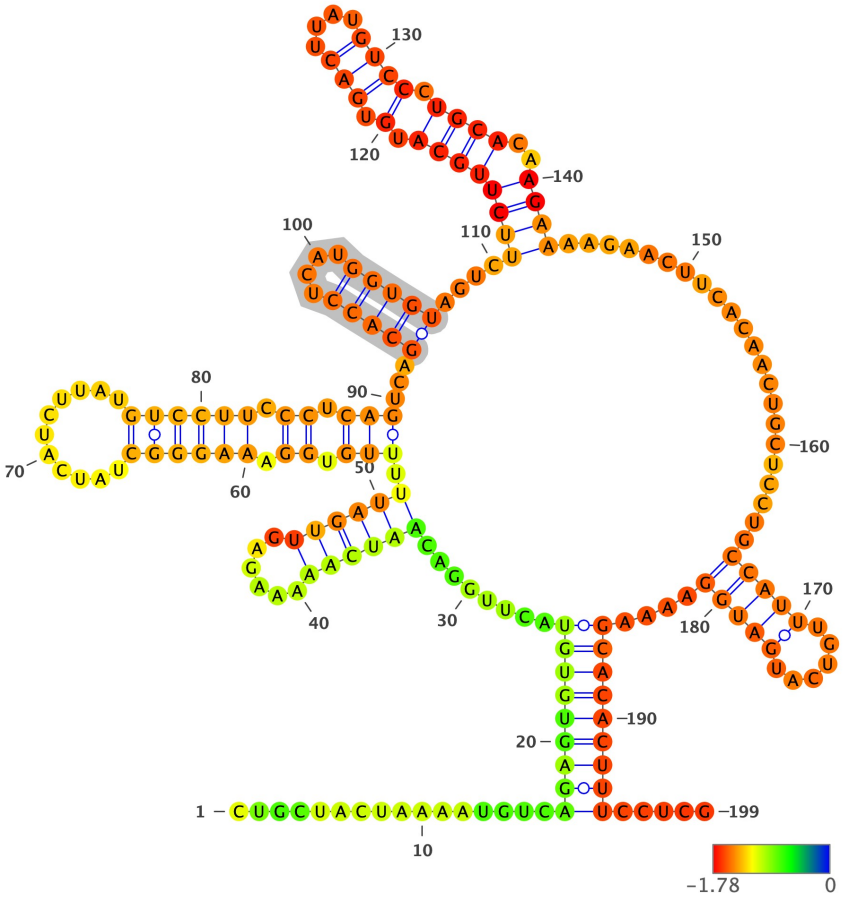
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 415 from nt 24728 to 24741 (nt 93 to 106)

```
5'-GCACCUCAUGGUGU-3'
5'-(((((....)))))-3'
Motif MFE = -6.1; z-score = -4.42; 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 = -1.06; 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(+)

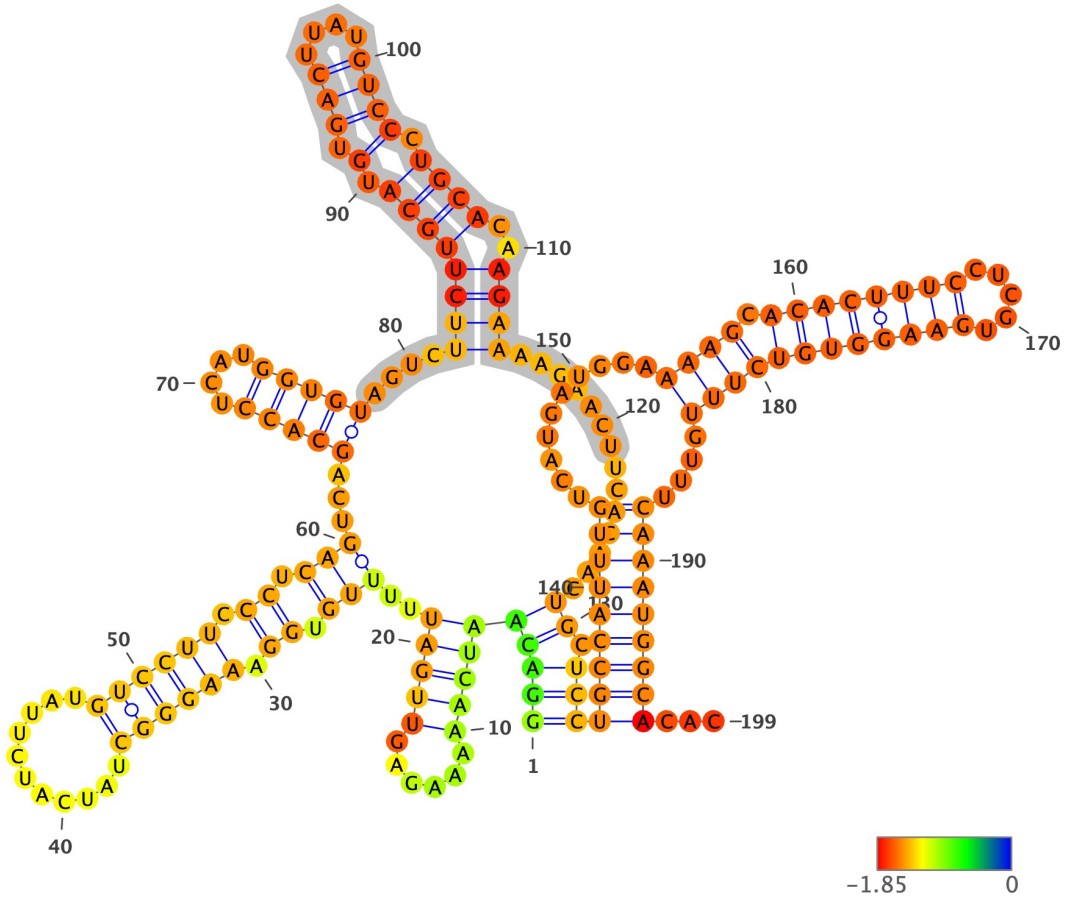
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 416 from nt 24742 to 24785 (nt 78 to 121)

```
5'-AGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACU-3'
5'-(((.....((((.(.(((....)))).)))).........)))-3'
Motif MFE = -9.1; z-score = -1.72; ED = 7.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24665 to 24863 (motif highlighted in silver):

```
5'-GGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAA
GAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACAC-3
5'-((((((((((......)))))..(((.((.((((((...........))))))).)).)))...(((((....)))))....((((((((.(.(((....)))).))))..)
)))..............)).)))((((((((.........((((.((((((((.....))))))))))))....)))))))))...-3'
MFE = -52.9; z-score = -2.48; ED = 33.07
```

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_gp02, 21563-25384(+)

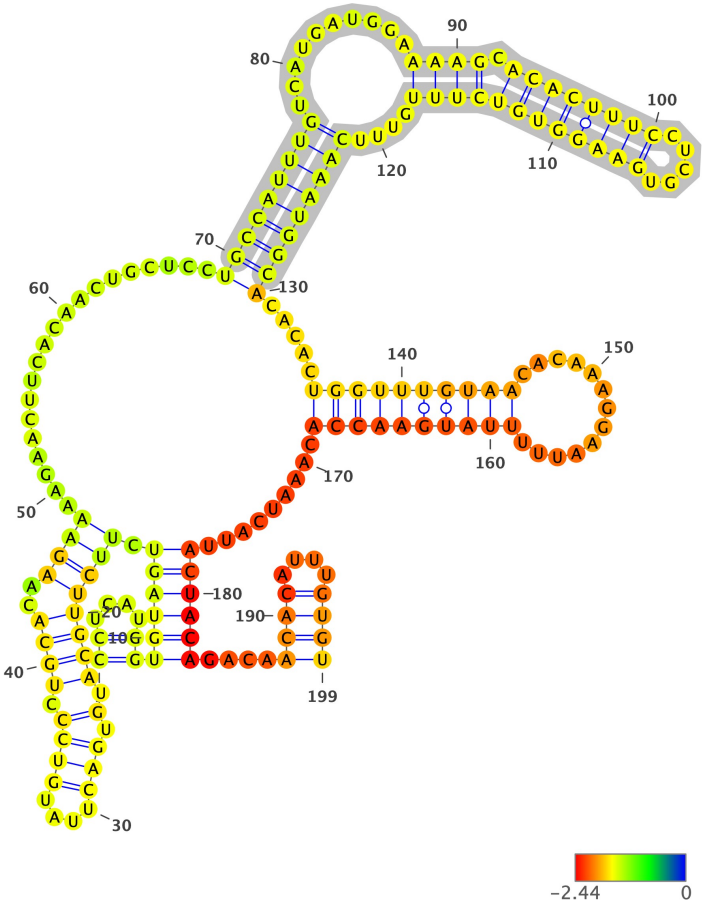
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 417 from nt 24800 to 24859 (nt 70 to 129)

```
5'-GCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGC-3'
5'-(((((((((.........((((.(((((((((.....)))))))))))).....)))))))))-3'
Motif MFE = -18.9; z-score = -2.68; 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 = -1.19; 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(+)

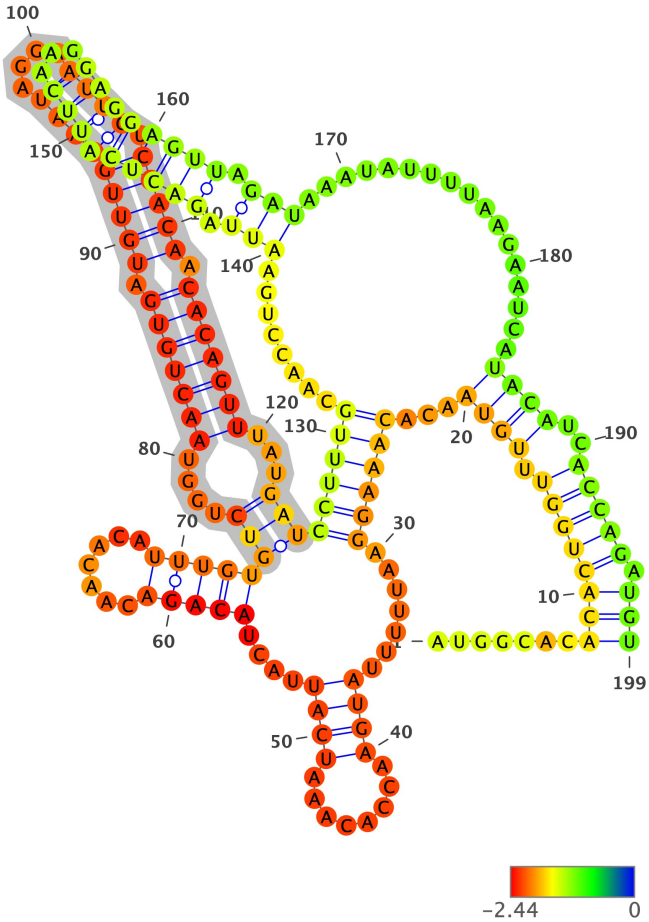
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 418 from nt 24928 to 24979 (nt 74 to 125)

```
5'-GUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAU-3'
5'-(......(((((((.(((((.............))))).)))))))).....)-3'
Motif MFE = -15.4; z-score = -3.63; ED = 5.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24855 to 25053 (motif highlighted in silver):

```
5'-AUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACA
ACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGU-3
5'-.......((((((((.((((...((((((.......((((........)))).....(((((.......)))))(((....(((((((.(((((((((....)))).)))))
.)))))))...)))))))))........(((.(((((.(((...)))))))).)))................))))..)))))).)))-3'
MFE = -36.5; z-score = -2.49; ED = 29.12
```

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(+)

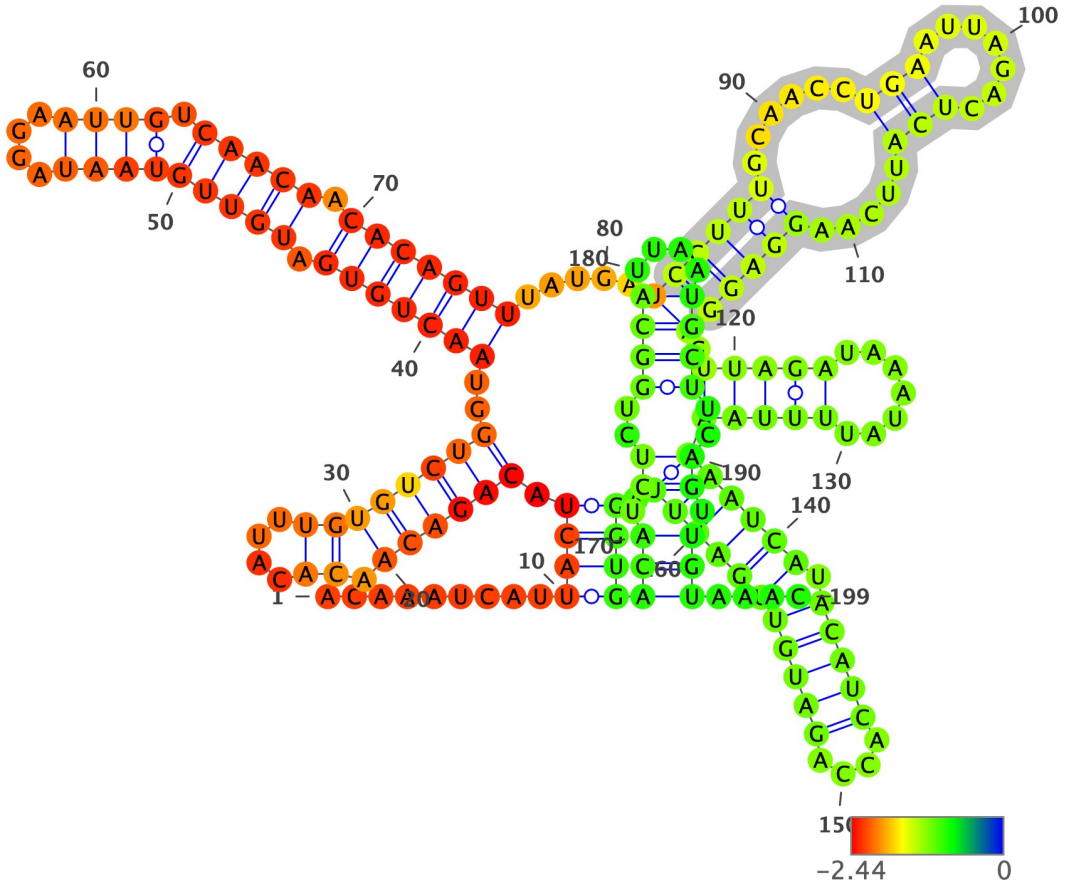
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 419 from nt 24980 to 25013 (nt 83 to 116)

```
5'-CCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGG-3'
5'-((((.........................))))-3'
Motif MFE = -3.3; z-score = 0.41; ED = 7.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24898 to 25096 (motif highlighted in silver):

```
5'-ACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAA
GGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAAC-3
5'-.........((((.((((((.((....))))))))..(((((((.(((((((((....)))).))))).)))))))).....((((((......(((.......)))).....
)))))).(((((.......)))))((((((.(((((....)))))))))))).))))(((.((..((((....))))..)).)))....-3'
MFE = -43.8; z-score = -3.25; ED = 27.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

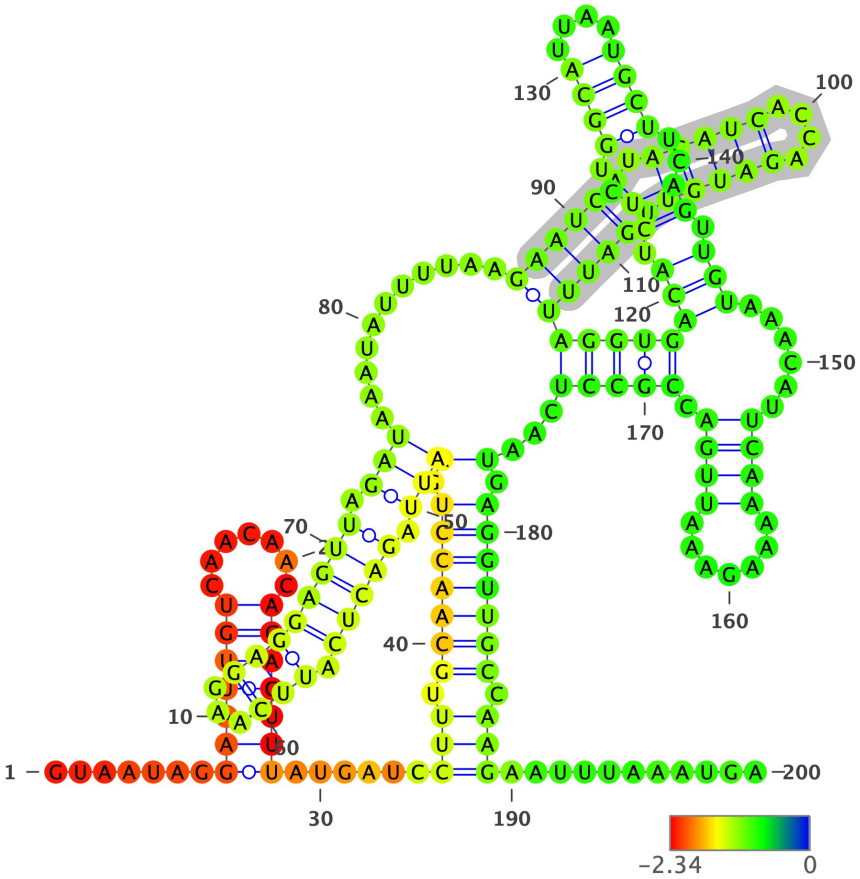
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 420 from nt 25034 to 25058 (nt 88 to 112)

```
5'-AAUCAUACAUCACCAGAUGUUGAUU-3'
5'-(((((.(((((....))))))))))-3'
Motif MFE = -6.8; z-score = -4.32; ED = 0.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24947 to 25146 (motif highlighted in silver):

```
5'-GUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAU
UUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGA-3
5'-.......(((((((.......)))))))......(((.(((((((.((((.(((((.(((...)))))))).))).........((((((.(((((....)))))))))
))((((((((.((..((((....))))..)).)))......((((.......)))).)))))...).)))))))).))).........-3'
MFE = -39.4; z-score = -1.21; ED = 42.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

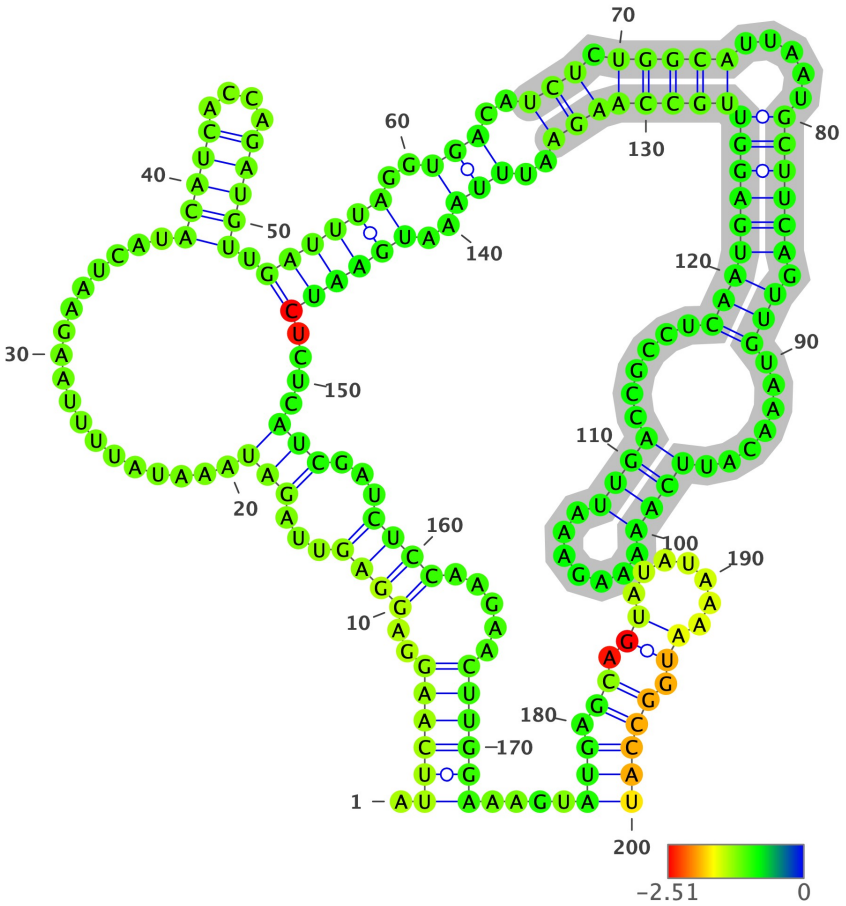
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 421 from nt 25068 to 25136 (nt 66 to 134)

```
5'-UCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGA-3'
5'-(((.(((((.....................................................))))))))-3'
Motif MFE = -13.2; z-score = -1.24; 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 = -0.34; ED = 54.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

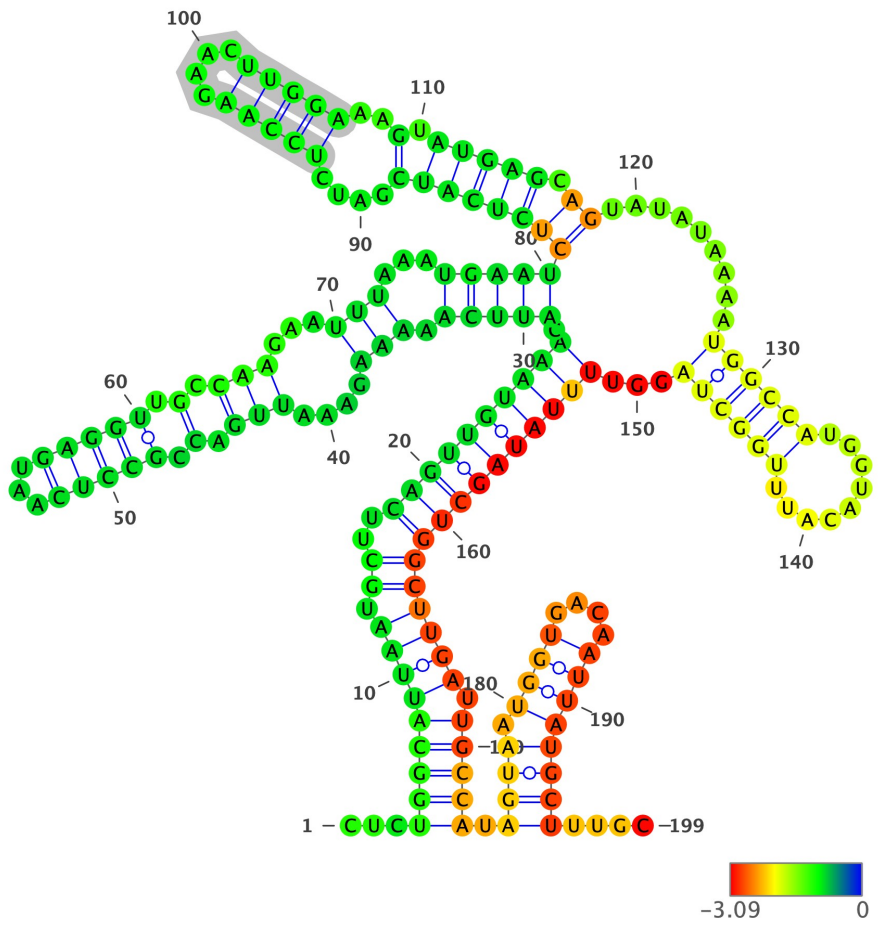
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 422 from nt 25161 to 25174 (nt 93 to 106)

```
5'-UCCAAGAACUUGGA-3'
5'-(((((....)))))-3'
Motif MFE = -3.1; z-score = -3.79; 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 = -1.04; 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(+)

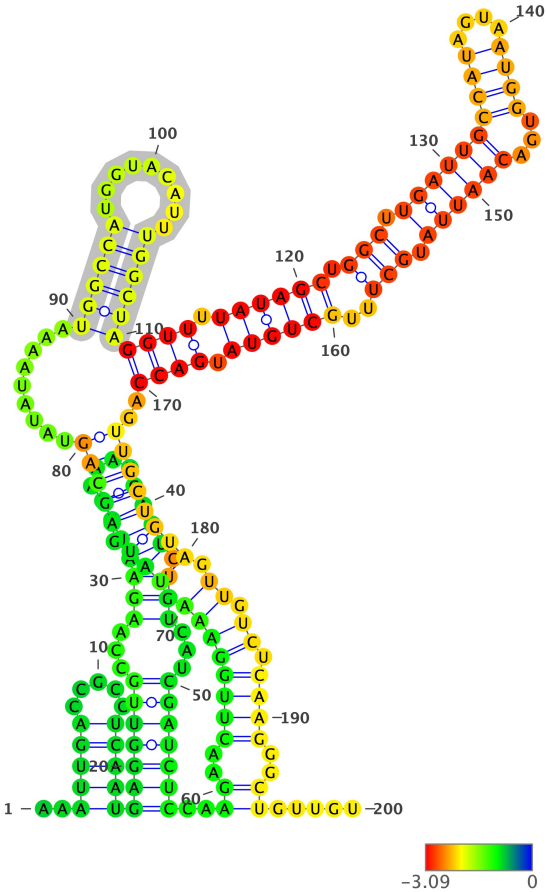
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 423 from nt 25196 to 25216 (nt 90 to 110)

```
5'-UGGCCAUGGUACAUUUGGCUA-3'
5'-((((((.........))))))-3'
Motif MFE = -6.2; z-score = -2.4; 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 25107 to 25306 (motif highlighted in silver):

```
5'-AAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAG
GUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGU-3
5'-..(((((.....)))))(((((((...(((((((....)))).)))...)))))))..((..((((((((.(((.(((((.........((((((.........))))))(
(((.((((((.(((.((((((((((....))))...)))))).)))..)))))).))))..)))))))).)).)).))))..)).....-3'
MFE = -51.3; z-score = -1.58; ED = 58.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

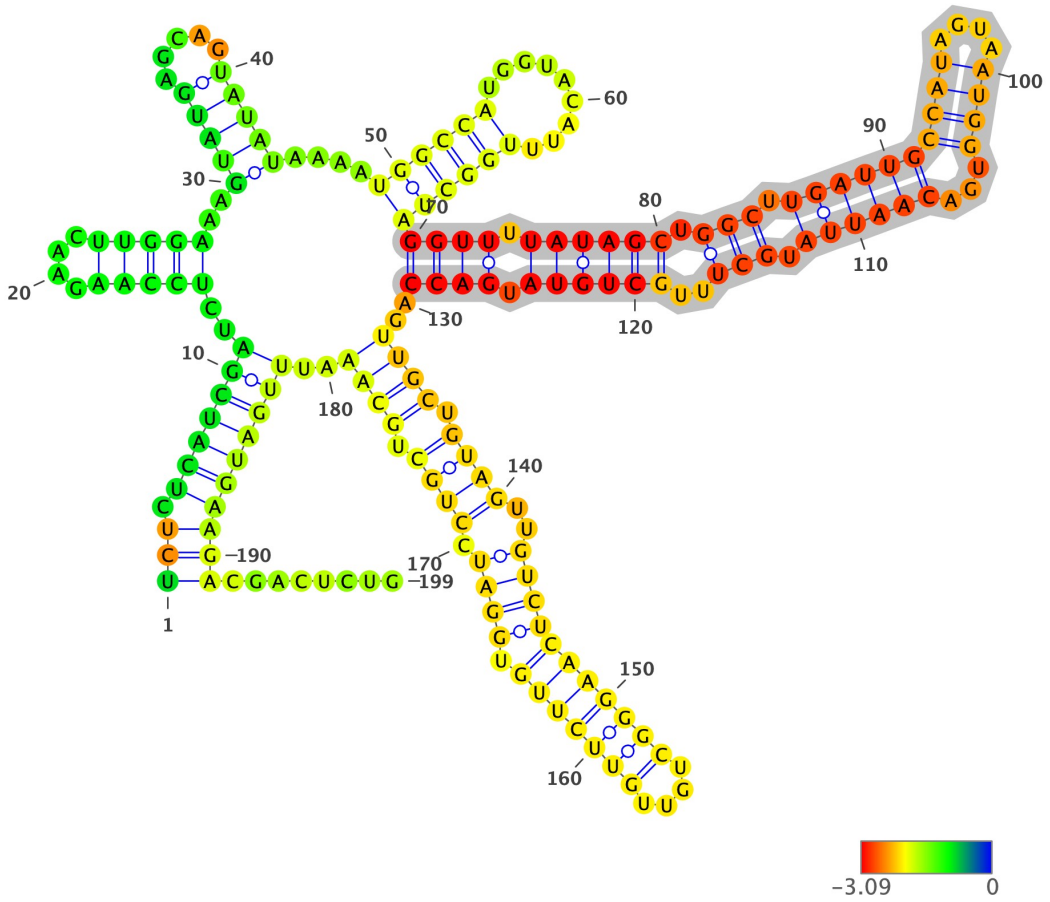
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 424 from nt 25217 to 25276 (nt 70 to 129)

```
5'-GGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACC-3'
5'-((((.(((((..((((.(((((((((((....)))))...)))))))..)))...)))))).))))-3'
Motif MFE = -21.5; z-score = -3.96; 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 = -3.0; 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(+)

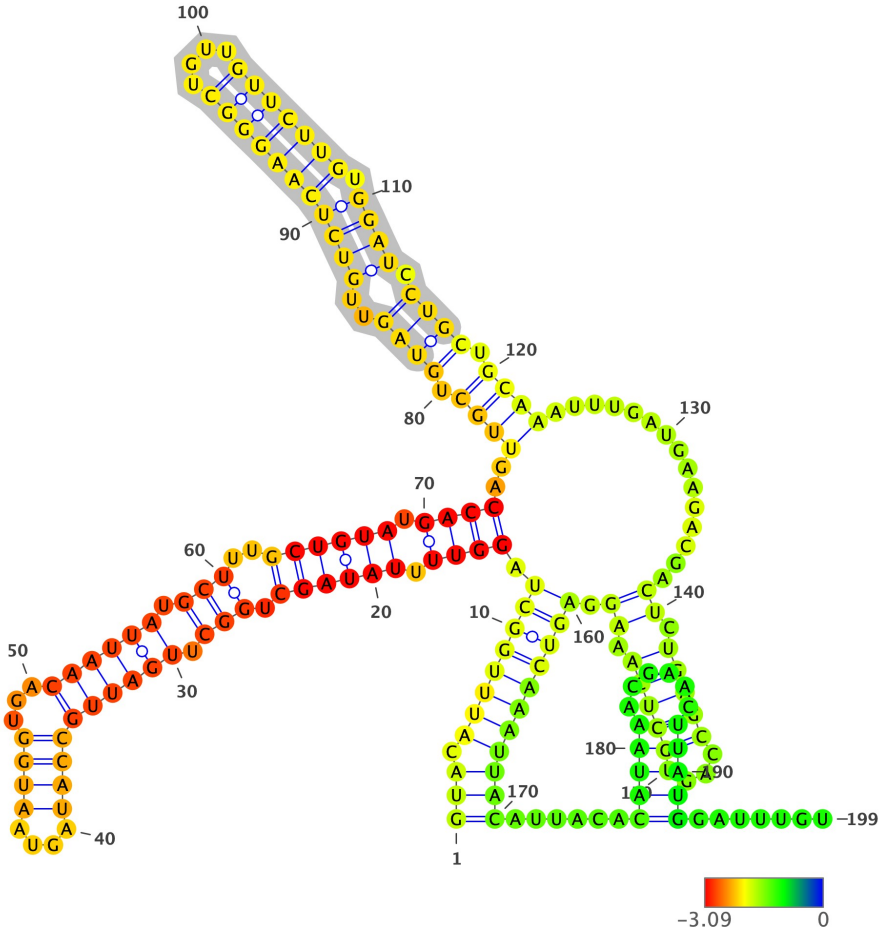
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 425 from nt 25285 to 25320 (nt 82 to 117)

```
5'-UAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUG-3'
5'-(((..((((((((((....)))))))).))))).)))-3'
Motif MFE = -9.7; z-score = -1.86; ED = 3.12
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25204 to 25402 (motif highlighted in silver):

```
5'-GUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGG
AUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGU-3
5'-(((.(((((((((.(((((.((((((.(((.((((((((((....)))).....)))))))).))))..)))))))).)))).)).((((.((((..((((((((((....)))))))).))
)).)))).)))).....................((.((((....)))))).)).)))))))))))).....(((((......)))))........-3'
MFE = -59.0; z-score = -2.56; ED = 28.09
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 181--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 181--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 190 to 199--gene, gene-GU280_gp03, 25393-26220(+)

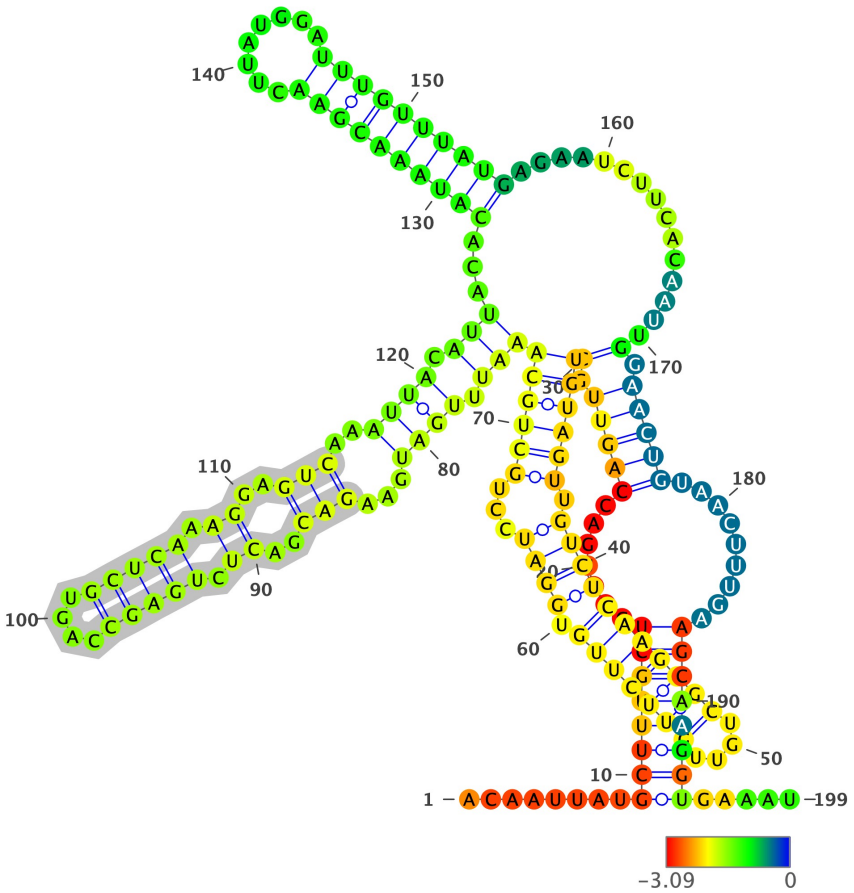
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 190 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 426 from nt 25337 to 25366 (nt 85 to 114)

```
5'-GACGACUCUGAGCCAGUGCUCAAAGGAGUC-3'
5'-(((..((.(((((....))))).))..)))-3'
Motif MFE = -11.7; z-score = -3.16; ED = 5.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25253 to 25451 (motif highlighted in silver):

```
5'-ACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGA
GUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUAUGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAU-3
5'-........((((((((.......(((((.(((((((.((((((((((((....)))))))).))))...))))))(((.((((...(((..((.(((((....))))).))..
)))..)))).)))...((((((((((.........))))))))))...............).)))))........))))))))).....-3'
MFE = -52.3; z-score = -3.0; ED = 32.59
```

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 132--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 132--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 141 to 199--gene, gene-GU280_gp03, 25393-26220(+)

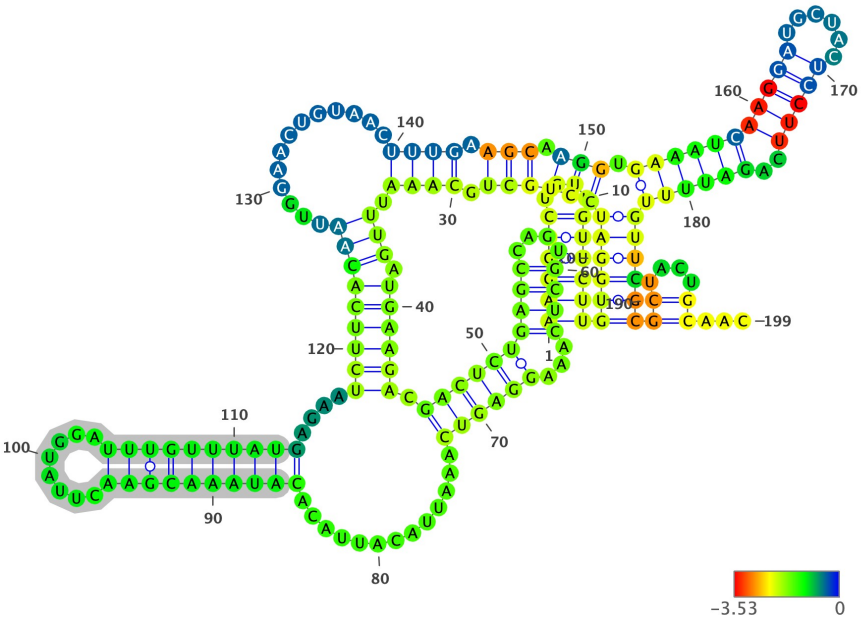
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 141 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 427 from nt 25381 to 25406 (nt 87 to 112)

```
5'-AUAAACGAACUUAUGGAUUUGUUUAU-3'
5'-(((((((((........)))))))))-3'
Motif MFE = -4.1; z-score = -2.07; ED = 2.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25295 to 25493 (motif highlighted in silver):

```
5'-AAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUA
UGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAAC-3
5'-((((((....))))))(((((((((((.((((.(((.((((((.((((((((((....))))...))))))..............((((((((((........))))))))
))....)))))))))..............)))).))).))).((((((((((.......)))))..))))))))))))((....))...-3'
MFE = -45.8; z-score = -0.68; ED = 48.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 90--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 90--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 99 to 199--gene, gene-GU280_gp03, 25393-26220(+)

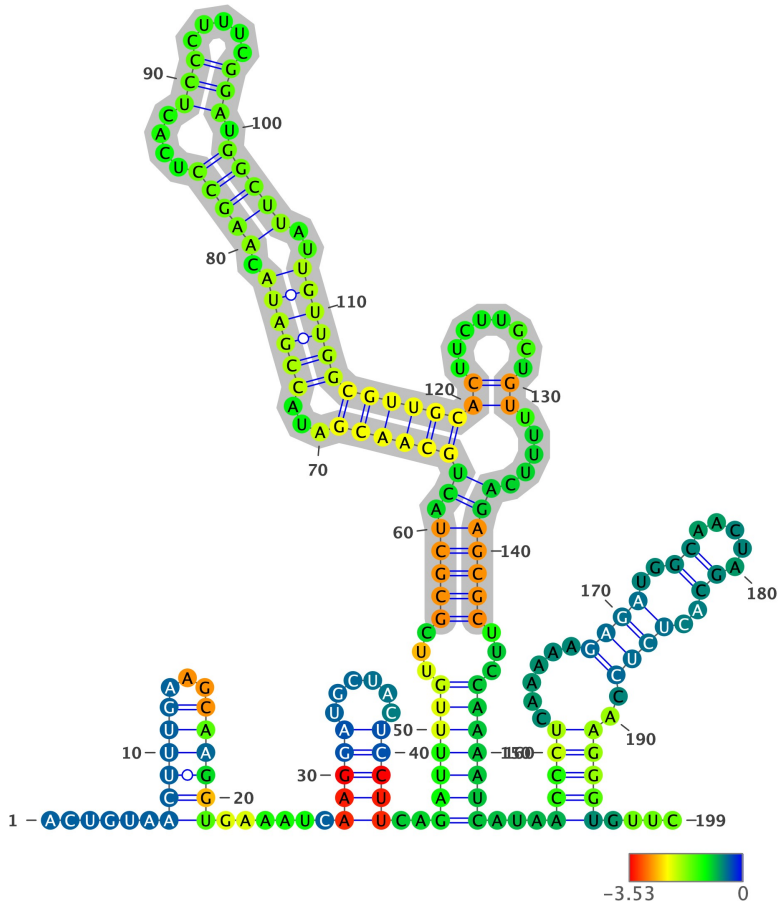
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 99 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 428 from nt 25481 to 25568 (nt 56 to 143)

```
5'-GCGCUACUGCAACGAUACCGAUACAAGCCUCACUCCCUUUCGGAUGGCUUAUUGUUGGCGUUGCACUUCUUGCUGUUUUUCAGAGCGC-3'
5'-(((((...((((((...((((((.(((((....(((.....))).)))))..))))))))))))((........))......)))))-3'
Motif MFE = -27.8; z-score = -2.81; 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 = -50.3; z-score = -2.13; ED = 27.17
```

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_gp03, 25393-26220(+)

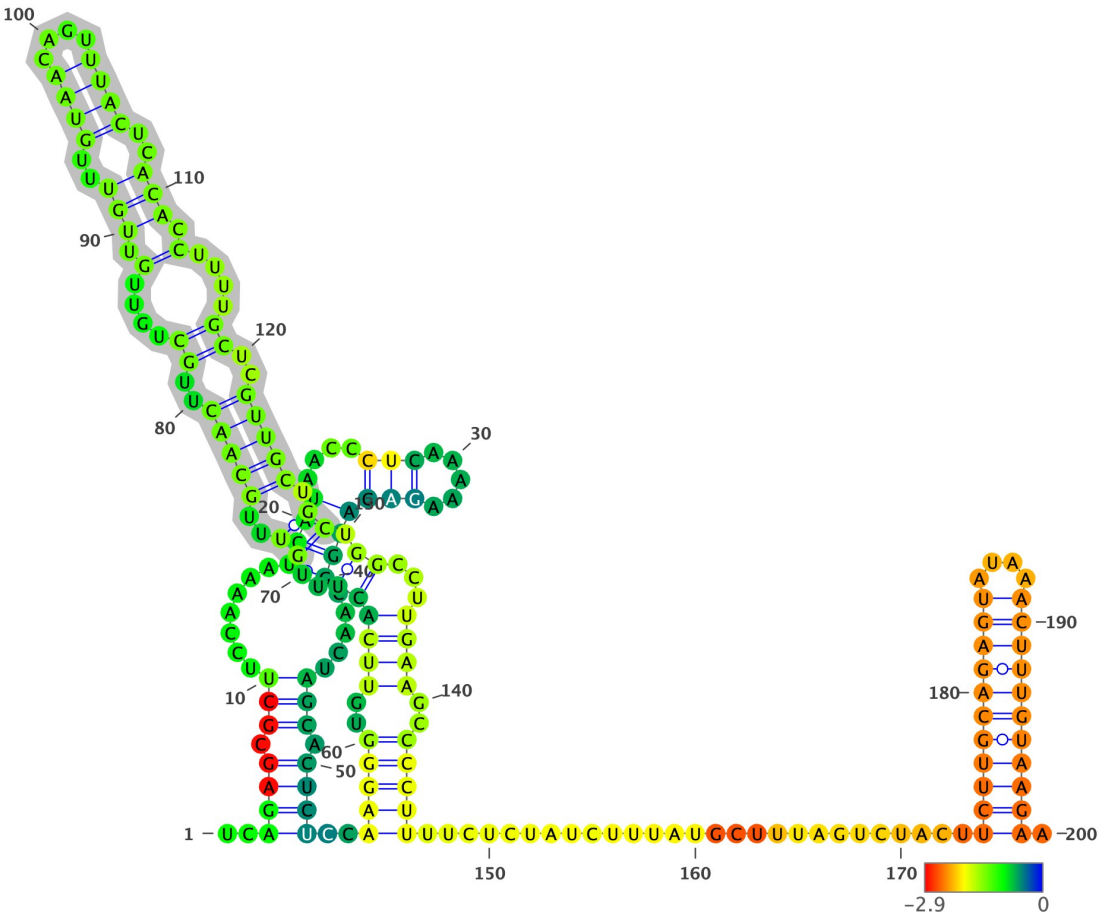
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 429 from nt 25630 to 25688 (nt 71 to 129)

```
5'-GUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGC-3'
5'-((..(((((..((....(.(((..((((....)))).)))).)....))..))))).))-3'
Motif MFE = -12.5; z-score = -2.01; 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 25560 to 25759 (motif highlighted in silver):

```
5'-UCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACA
CCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAA-3
5'-..((((.(((.......((((....(((.....)))))))).....))).))))..(((((..((((((..((..(((((..((....(.(((..((((....)))).)))
.)....))..))))).)).))...)))).)))))..........................(((((((((((....)))))))))))).-3'
MFE = -44.2; z-score = -2.26; ED = 29.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

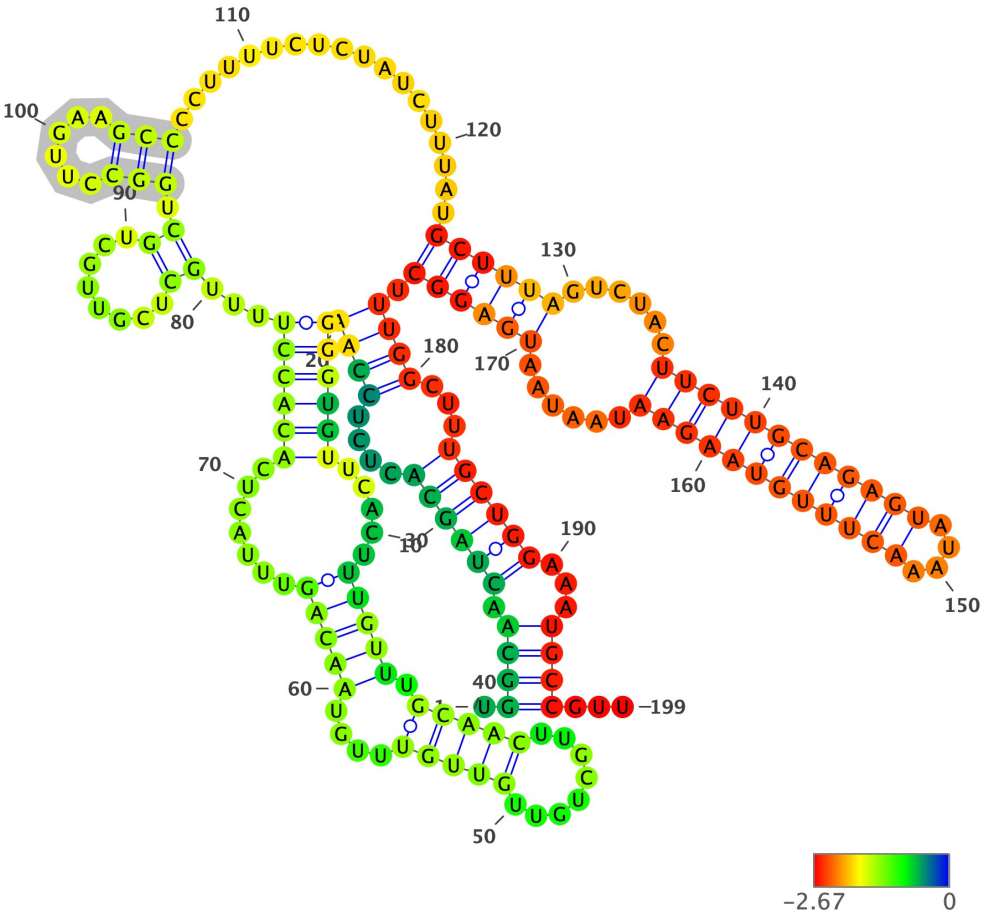
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 430 from nt 25690 to 25701 (nt 94 to 105)

```
5'-GGCCUUGAAGCC-3'
5'-(((......)))-3'
Motif MFE = -2.3; z-score = -1.33; ED = 0.23
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25597 to 25795 (motif highlighted in silver):

```
5'-UGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUUGUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUU
CUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUU-3
5'-.((((.((((((....((((((((((.....(((((.(((((........)))))....)))))).......)))))))...((........)).(((......)))).....
............((((((.....((((((((((((....)))))))))))).....)))))).)))))...)))))))...)))))...-3'
MFE = -52.7; z-score = -3.43; ED = 38.52
```

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_gp03, 25393-26220(+)

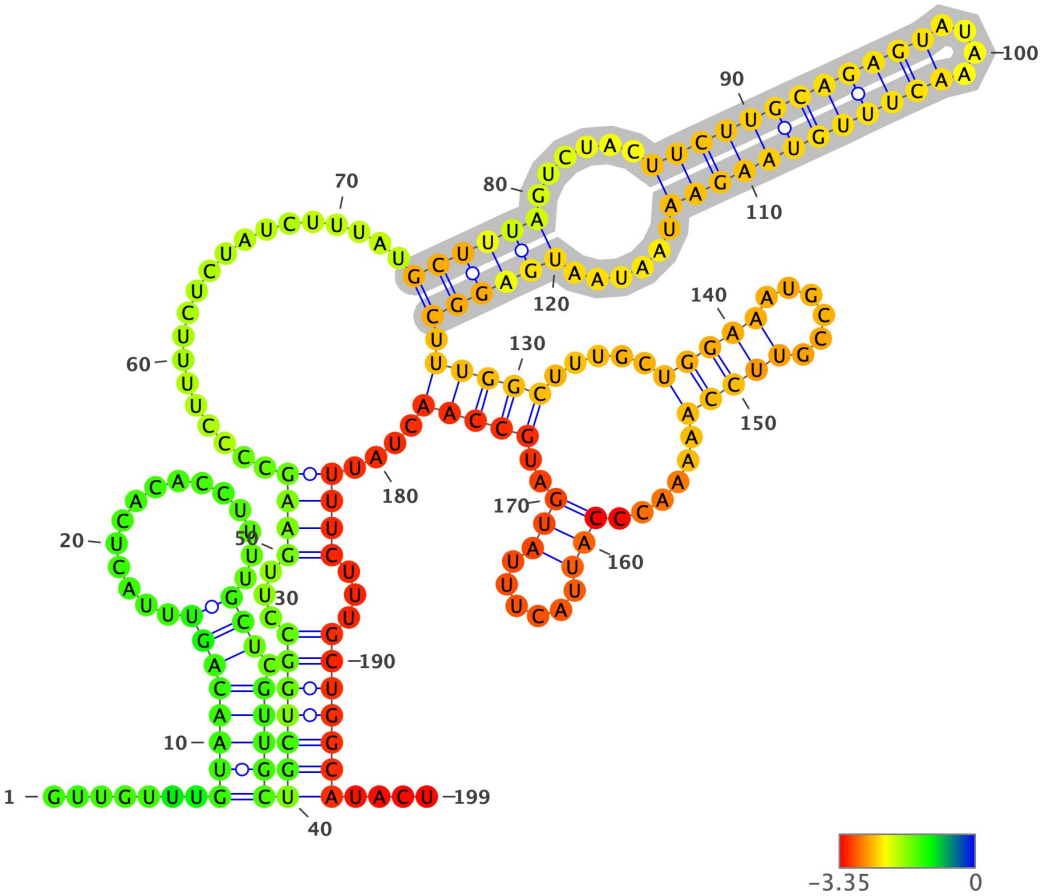
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 431 from nt 25720 to 25771 (nt 74 to 125)

```
5'-GCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGC-3'
5'-(((.........((((((((((((....)))))))))))).........)))-3'
Motif MFE = -18.3; z-score = -4.74; 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 = -1.69; ED = 39.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

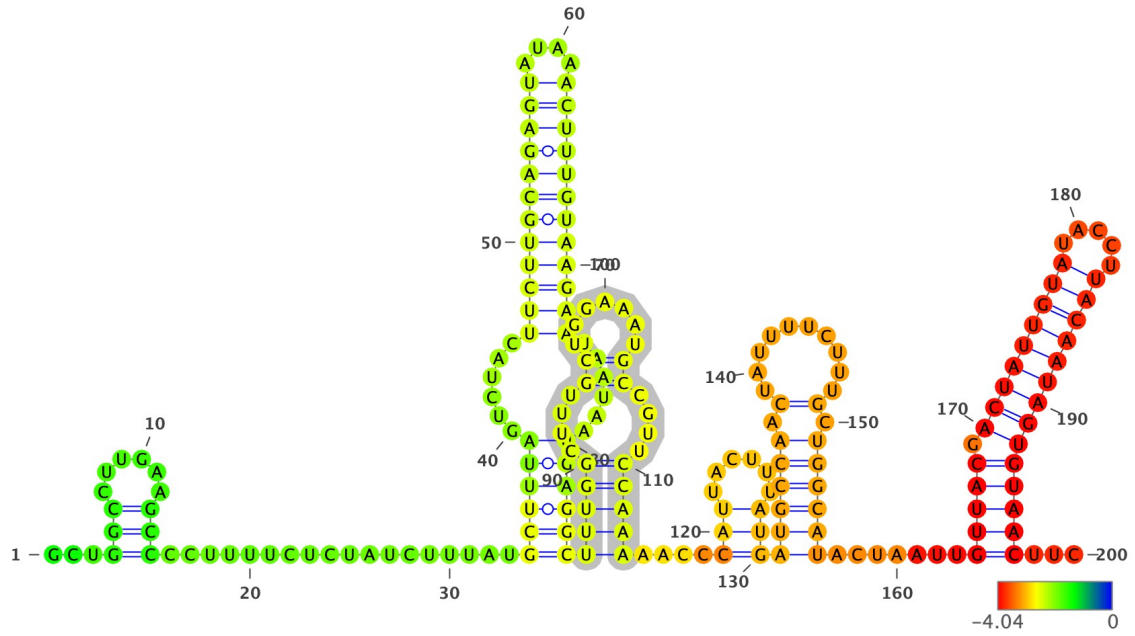
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 432 from nt 25772 to 25800 (nt 86 to 114)

```
5'-UUUGGCUUUGCUGGAAAUGCCGUUCCAAA-3'
5'-(((((....((.......)).....)))))-3'
Motif MFE = -4.4; z-score = -0.46; ED = 7.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25687 to 25886 (motif highlighted in silver):

```
5'-GCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCC
AAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUC-3
5'-...(((......)))..................((((((......((((((((((((....))))))))))))).....))))))(((((....((.......)).....))
)))....(((......)))((((((.(..........).))))))......(((((.(((((((((.....)))))))))))))))...-3'
MFE = -49.5; z-score = -3.97; ED = 25.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

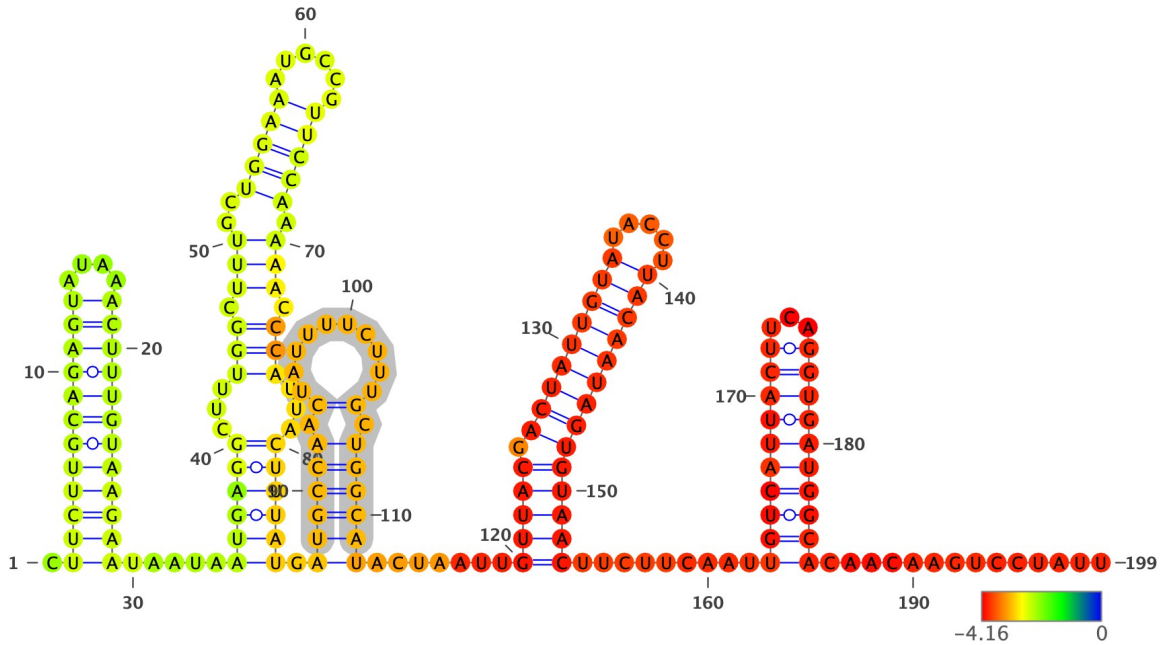
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 433 from nt 25818 to 25841 (nt 88 to 111)

```
5'-UGCCAACUAUUUUCUUUGCUGGCA-3'
5'-(((((.(..........).)))))-3'
Motif MFE = -4.8; z-score = -2.67; ED = 1.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25731 to 25929 (motif highlighted in silver):

```
5'-CUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCA
UACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUU-3
5'-.(((((((((((....))))))))))))).....((((((...(((.(((..(((((......))))).))).)))...)))))).((((((.(..........).)))))
).......(((((.(((((((((.....)))))))))))))).........((((((((((...)))))))))).............-3'
MFE = -56.9; z-score = -5.36; ED = 21.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

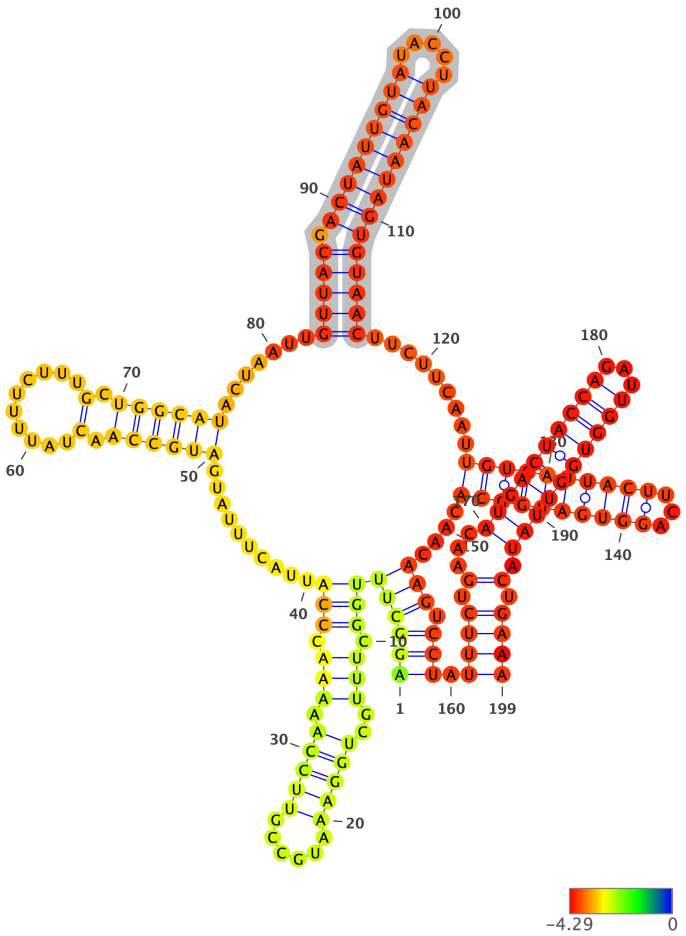
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 434 from nt 25850 to 25883 (nt 83 to 116)

```
5'-GUUACGACUAUUGUAUACCUUACAAUAGUGUAAC-3'
5'-(((((.(((((((((.....)))))))))))))-3'
Motif MFE = -13.6; z-score = -5.63; ED = 1.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25768 to 25966 (motif highlighted in silver):

```
5'-AGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGU
GUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAA-3
5'-(((((((((.(((..(((((.....))))).))).))).........((((((.(..........).))))))).......(((((.(((((((((.....)))))))))
))))).........((((((((((...)))))))))....))).))).((((.(...((((((((((...)))))))))).).))))-3'
MFE = -53.8; z-score = -4.03; 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(+)

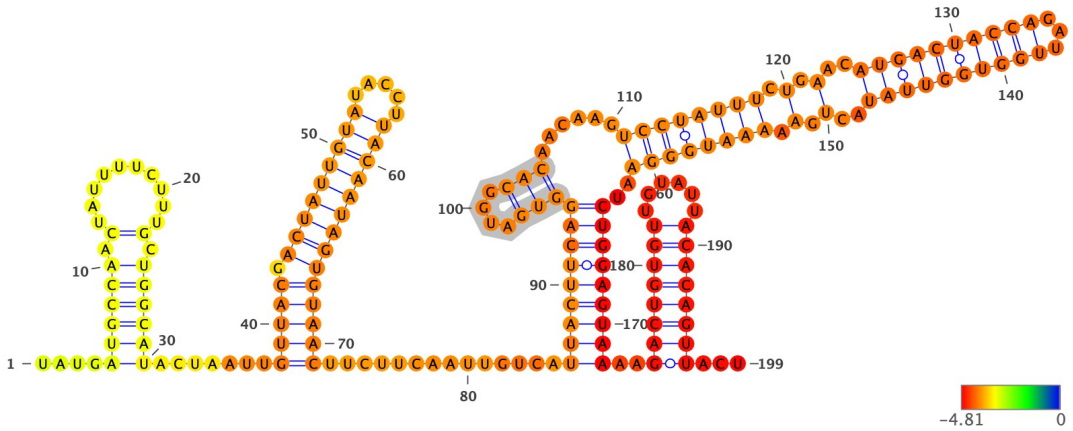
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 435 from nt 25907 to 25916 (nt 95 to 104)

```
5'-GUGAUGGCAC-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = 0.24; 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 25813 to 26011 (motif highlighted in silver):

```
5'-UAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGU
CCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACU-3
5'-....((((((.(..........).))))))......(((((.(((((((((.....)))))))))))))).............(((((((((((....)))......(
(((((((.(.(..(((((((((...)))))))))..).).))))))))..)))))))))..((((((((......))))))))...-3'
MFE = -60.7; z-score = -5.12; ED = 9.18
```

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_gp03, 25393-26220(+)

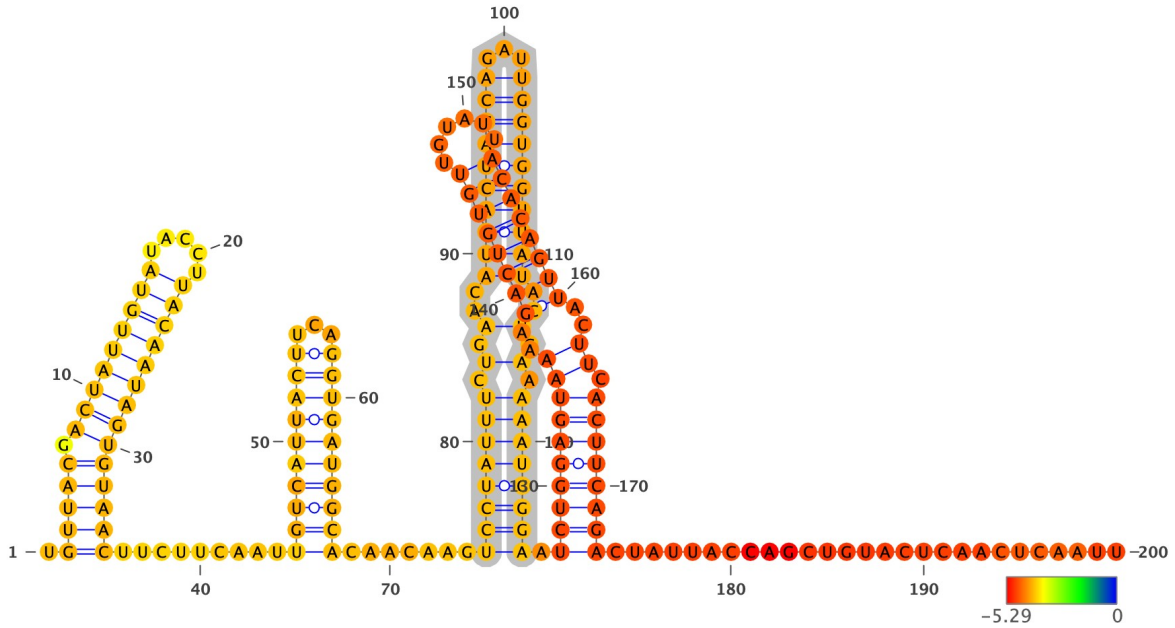
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 436 from nt 25923 to 25973 (nt 75 to 125)

```
5'-UCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGA-3'
5'-(((((((((.(.(..((((((((((.....)))))))))..).).)))))))))-3'
Motif MFE = -17.8; z-score = -4.08; 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 = -5.76; 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(+)

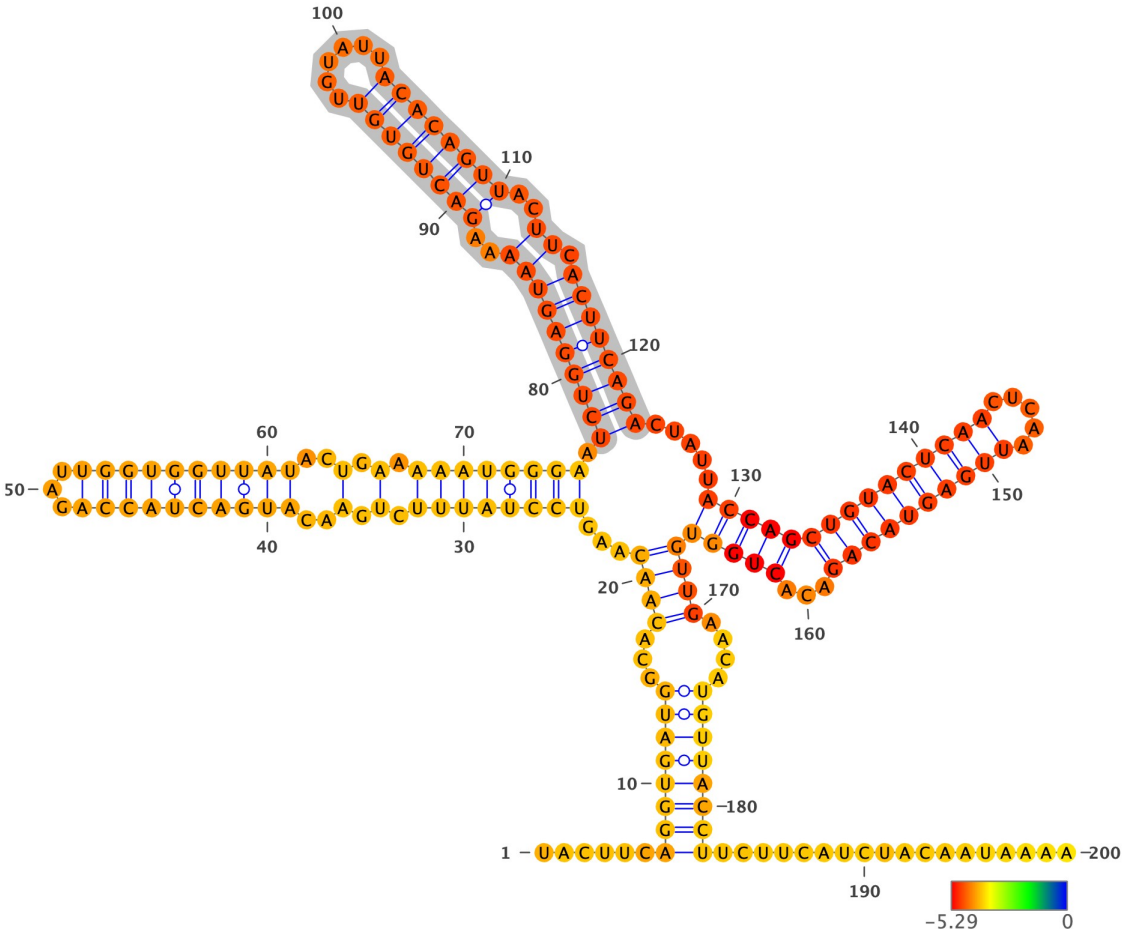
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 437 from nt 25975 to 26021 (nt 77 to 123)

```
5'-UCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGA-3'
5'-((((((((((..((((((((.....))))))))..)).))))))))-3'
Motif MFE = -19.0; z-score = -5.08; 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 = -5.46; 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(+)

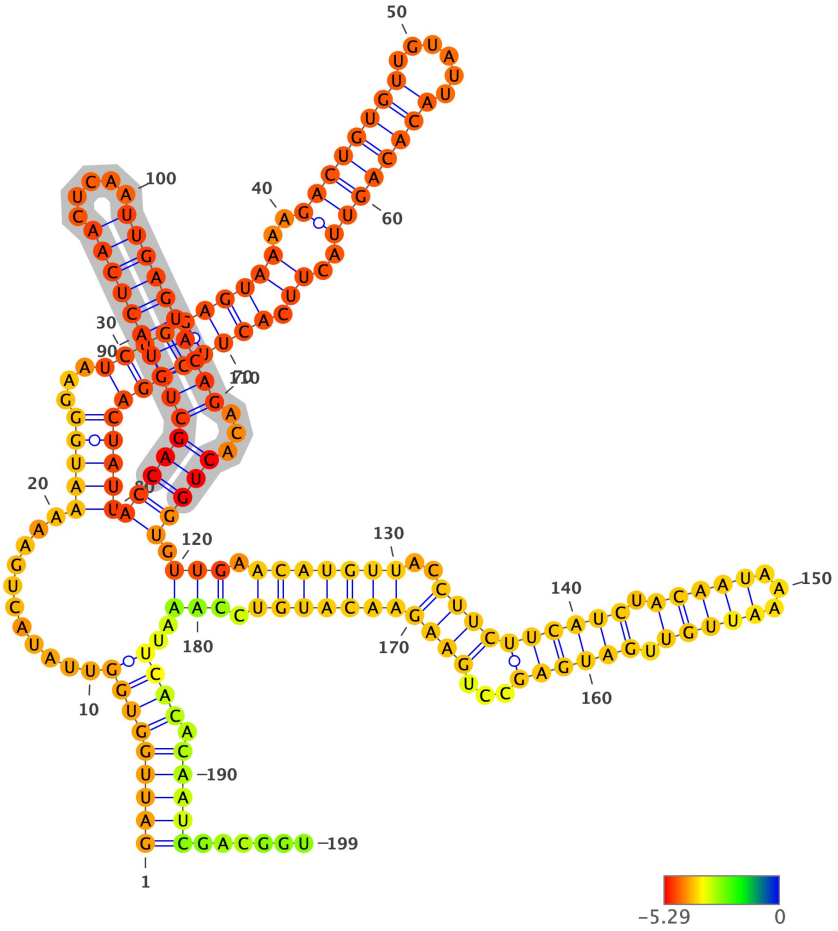
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 438 from nt 26029 to 26062 (nt 83 to 116)

```
5'-CAGCUGUACUCAACUCAAUUGAGUACAGACACUG-3'
5'-(((((((((((((.....)))))))))...)))-3'
Motif MFE = -13.1; z-score = -4.49; ED = 2.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25947 to 26145 (motif highlighted in silver):

```
5'-GAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGA
CACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGU-3
5'-(((((((((...........(((((...(((((((((((..((((((((.....))))))))..)).))))))))))))((((((((((((((.....)))))))))).
..))))).(((.(((((((..((((((((((.(((((...))))).))))))...))))))))))).)))..)))).)))))......-3'
MFE = -66.8; z-score = -6.15; ED = 11.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 439 from nt 26070 to 26123 (nt 73 to 126)

```
5'-ACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGU-3'
5'-(((((((..((((((((((.(((.......))).))))))...)))))))))))-3'
Motif MFE = -16.3; z-score = -3.8; ED = 2.28
```

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 25998 to 26196 (motif highlighted in silver):

```
5'-AUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGACACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGA
GCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACG-3
5'-.............................((((((((((((((((.....))))))))))...))))))(((.(((((((..((((((((((.(((((...))))).)))))
)...)))))))))))).)))...........((.((((((((..((((((....((((....))))..))))))..))))))))).))-3'
MFE = -59.6; z-score = -5.6; ED = 10.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

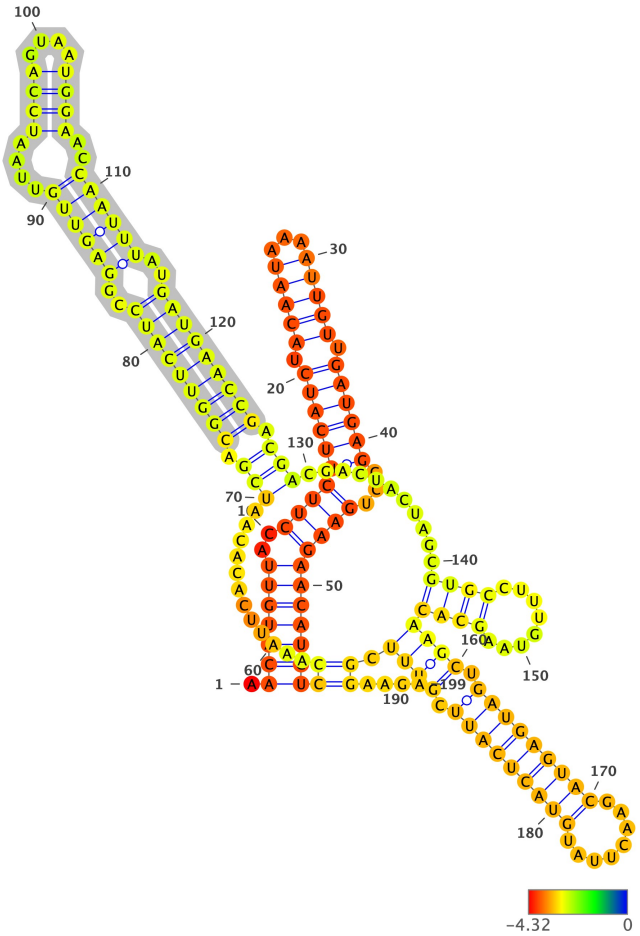
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 440 from nt 26142 to 26193 (nt 74 to 125)

```
5'-CGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCG-3'
5'-(((((((((..((((((....((........))..))))))..)))))))))-3'
Motif MFE = -19.6; z-score = -3.76; ED = 1.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26069 to 26267 (motif highlighted in silver):

```
5'-AACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAA
UUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGA-3
5'-.(((((((..(((((((((((.(((((...))))).))))))...))))))))))))((............(((.(((((((((..((((((....((((....))))..)))
)))..)))))))))).))).........((((........))))((((.(((((((((........))))))))).)))).)).....-3'
MFE = -59.6; z-score = -4.31; ED = 14.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 152--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 152--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 177 to 199--gene, gene-GU280_gp04, 26245-26472(+)

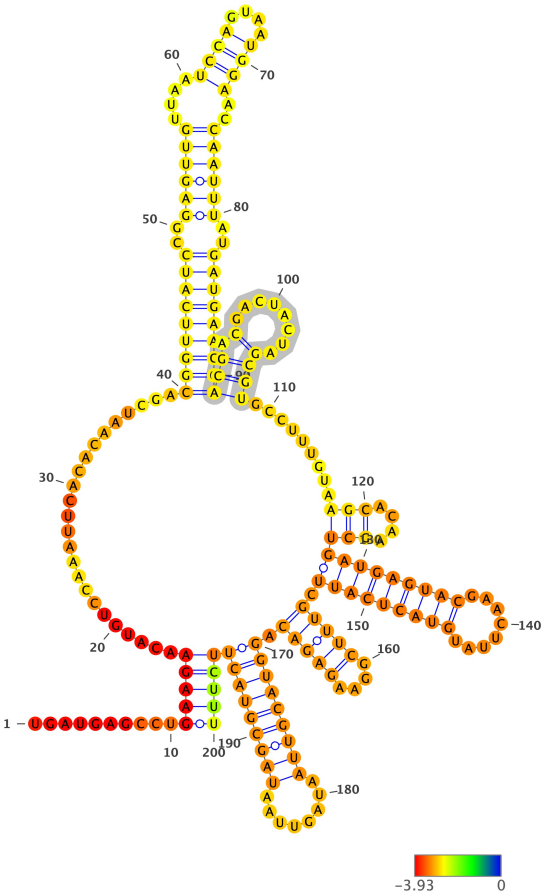
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 177 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 441 from nt 26194 to 26210 (nt 92 to 108)

```
5'-ACGACGACUACUAGCGU-3'
5'-(((.(........))))-3'
Motif MFE = -0.5; z-score = 0.34; 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 26103 to 26302 (motif highlighted in silver):

```
5'-UGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCC
UUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUU-3
5'-..........(((((.........................(((((((((..((((((....((((....))))..))))))..))))))))))(((.(........))))...
......(((....)))((((((((.........))))))))).(((((....))))).(((((((((.........)))))))))))))-3'
MFE = -53.3; z-score = -4.1; ED = 23.17
```

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 118--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 118--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 143 to 200--gene, gene-GU280_gp04, 26245-26472(+)

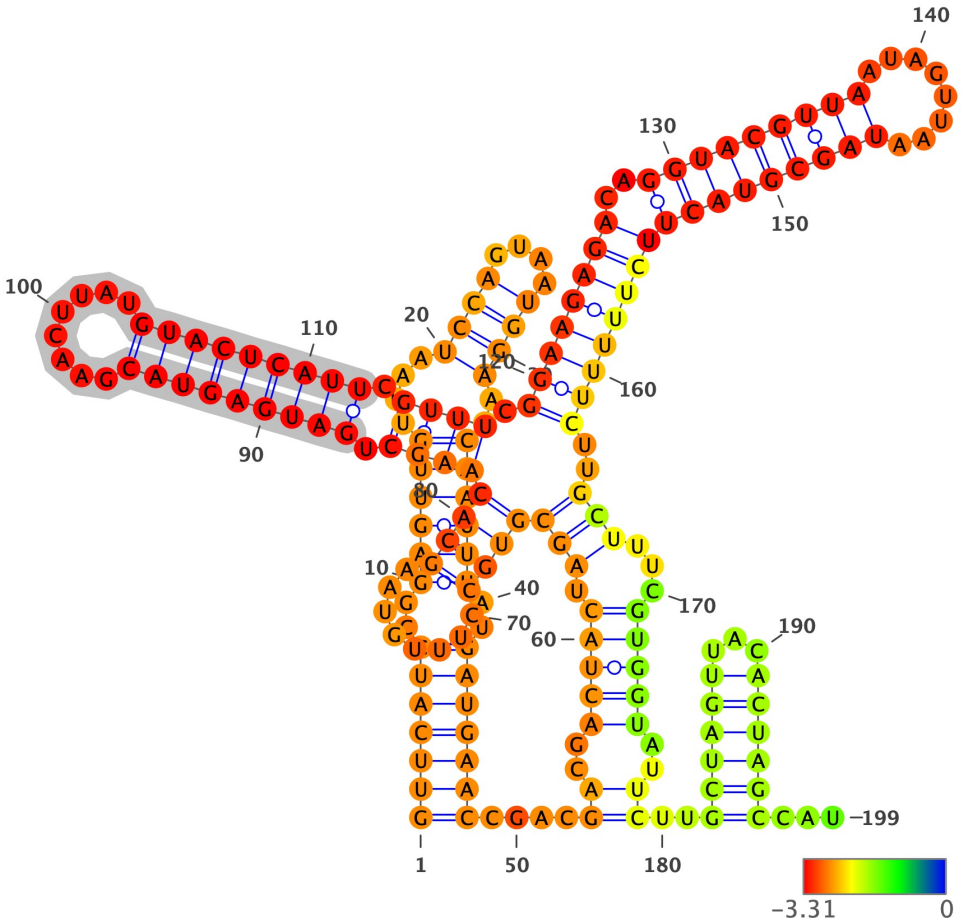
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 143 to 200--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 442 from nt 26230 to 26255 (nt 87 to 112)

```
5'-GAUGAGUACGAACUUAUGUACUCAUU-3'
5'-(((((((((........)))))))))-3'
Motif MFE = -10.2; z-score = -4.64; 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 = -4.37; 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(+)

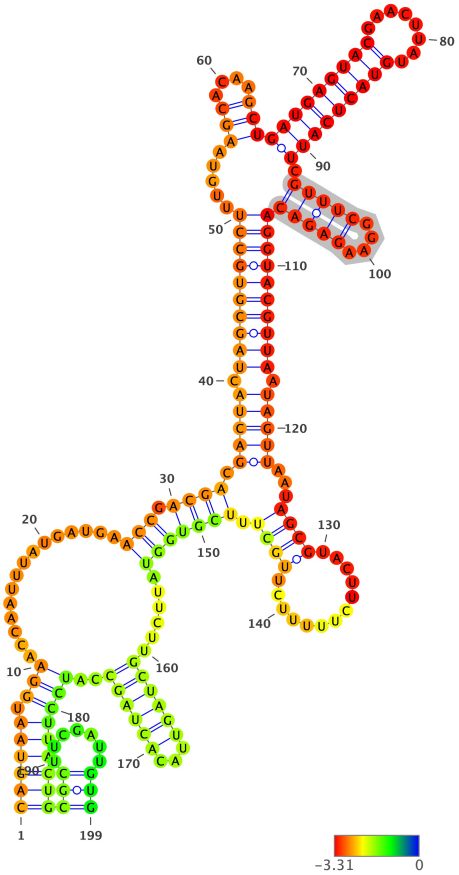
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 443 from nt 26257 to 26270 (nt 93 to 106)

```
5'-GUUUCGGAAGAGAC-3'
5'-(((((....)))))-3'
Motif MFE = -3.2; z-score = -5.23; ED = 0.21
```



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 26165 to 26363 (motif highlighted in silver):

```
5'-CAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUA
CGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUG-3
5'-((((((.(((...............(((.((((.(((((.((((((((((.....(((....)))(((((((((.........))))))))).(((((....))))))))))
))))).)))))...((((.............)))).)))))))......((((((...))))))..))))))))))(((.......)))-3'
MFE = -53.9; z-score = -2.69; ED = 24.07
```

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 56--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 56--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 81 to 199--gene, gene-GU280_gp04, 26245-26472(+)

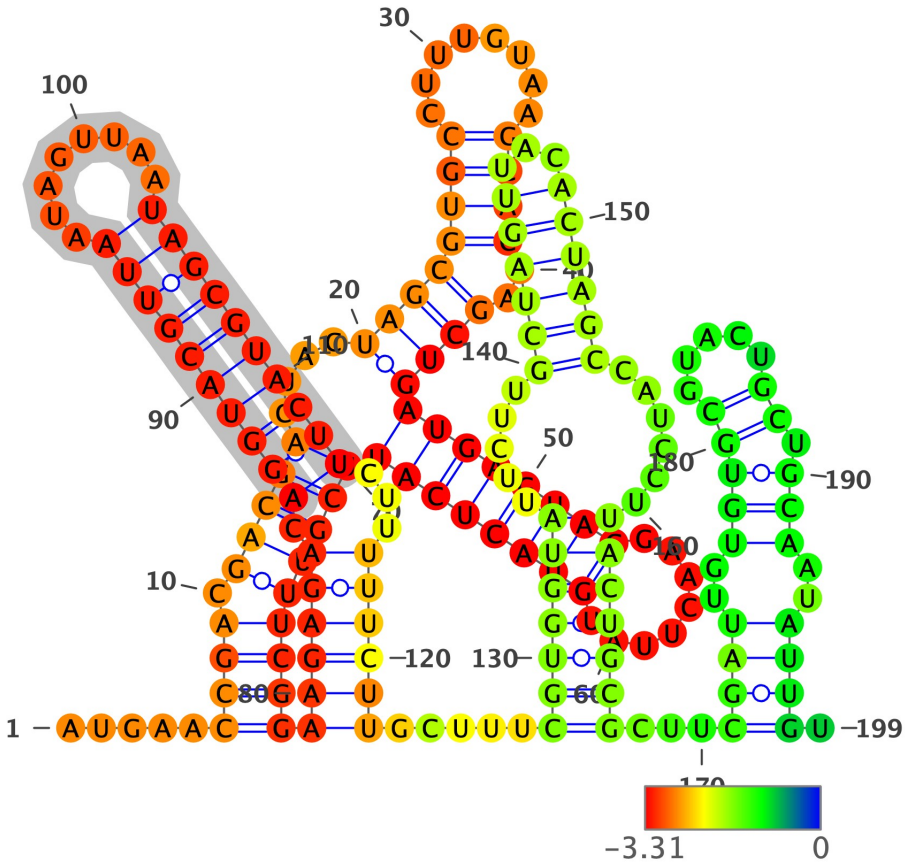
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 81 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 444 from nt 26271 to 26298 (nt 86 to 113)

```
5'-AGGUACGUUAAUAGUUAAUAGCGUACUU-3'
5'-((((((((((........))))))))))-3'
Motif MFE = -9.6; z-score = -3.72; ED = 0.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26186 to 26384 (motif highlighted in silver):

```
5'-AUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUAC
UUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGU-3
5'-.....((((.(((((....((((((((........))))..))))((((((((........)))))))))))))))))((((((.((((((((((........))))))))
))...))))))).....((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..)))).-3'
MFE = -56.3; z-score = -2.58; ED = 24.78
```

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 35--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 35--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 60 to 199--gene, gene-GU280_gp04, 26245-26472(+)

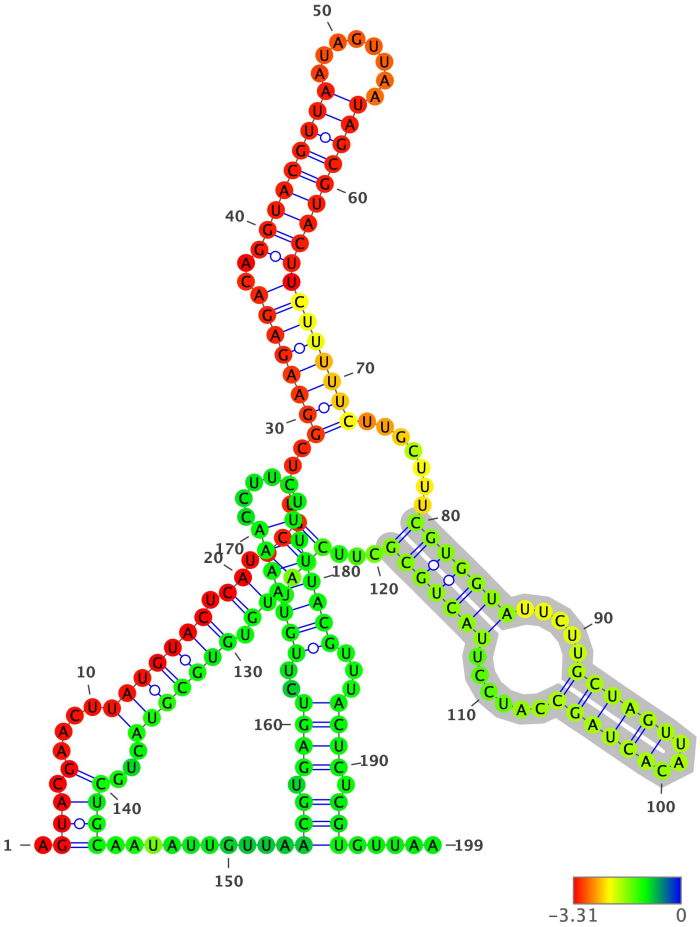
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 60 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 445 from nt 26313 to 26352 (nt 80 to 119)

```
5'-CGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCG-3'
5'-(((((((.....((((((...)))))).....)))))))-3'
Motif MFE = -12.1; z-score = -3.14; 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 = -2.7; 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(+)

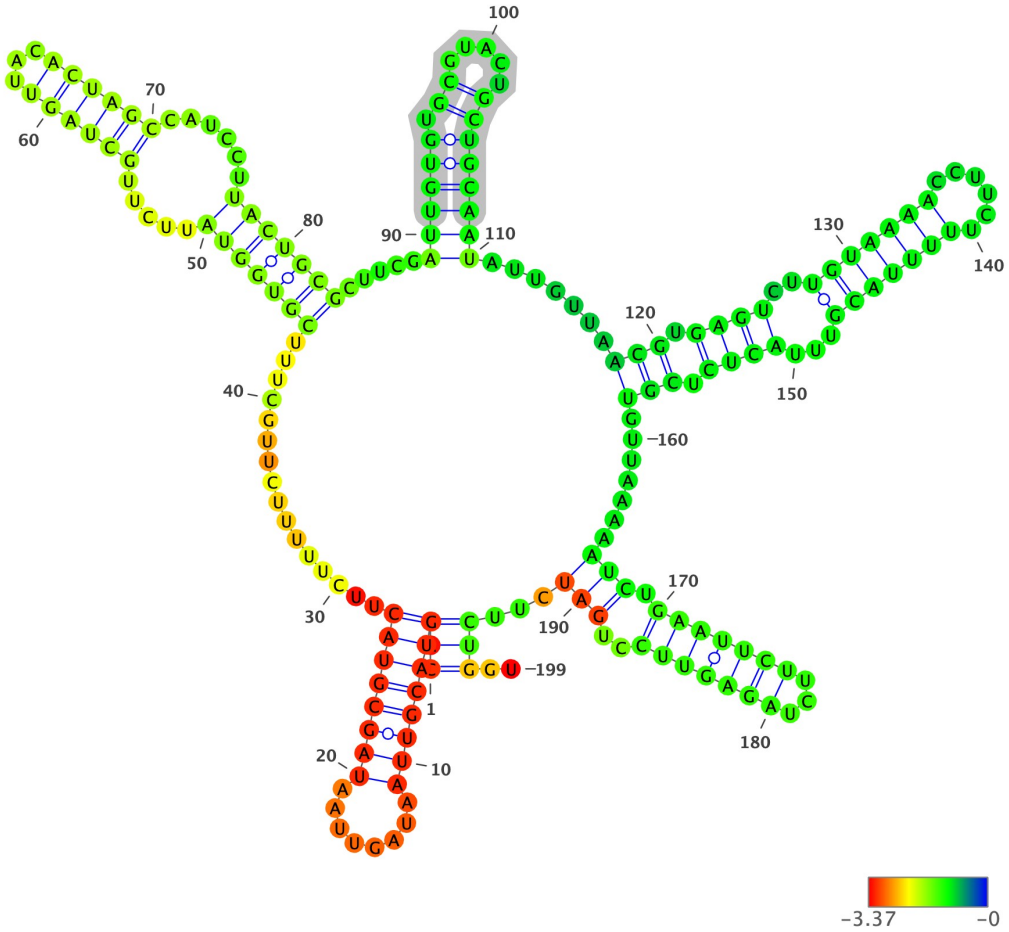
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 446 from nt 26360 to 26377 (nt 91 to 108)

```
5'-UGUGUGCGUACUGCUGCA-3'
5'-(((..((.....)).)))-3'
Motif MFE = -1.5; z-score = 0.14; 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 26270 to 26468 (motif highlighted in silver):

```
5'-CAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUA
UUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGU-3
5'-(((((((((((.......)))))))).................(((((((.....((((((...)))))).....)))))))).....((((((.((.....)))))))).
......(((.((((..(((((((.....)))))))...)))).))).......(((.(((((((...)))))))..)))...)))..-3'
MFE = -45.2; z-score = -2.47; ED = 19.71
```

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_gp04, 26245-26472(+)

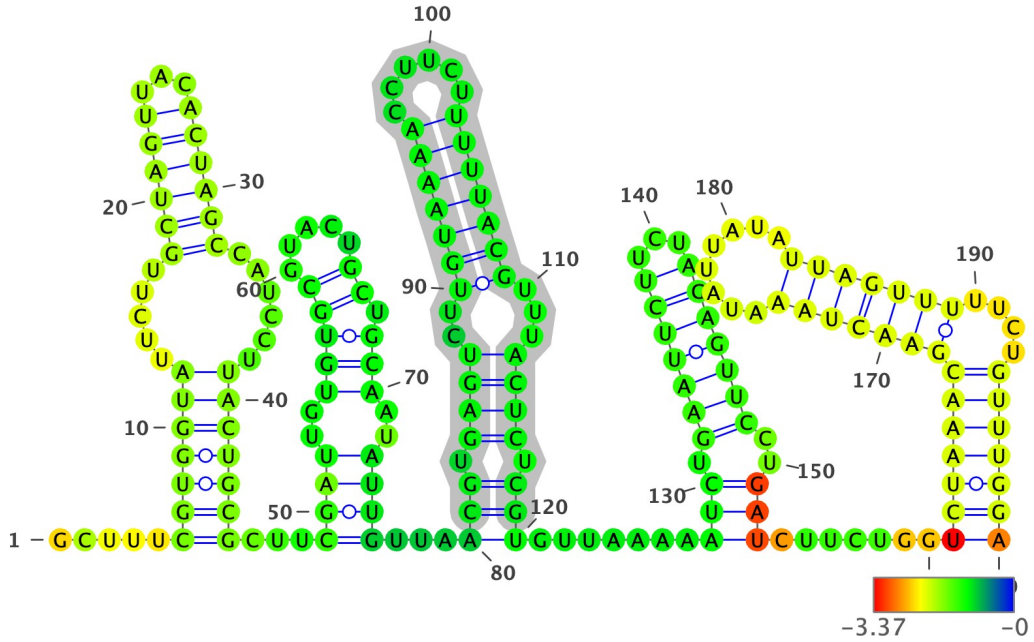
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 447 from nt 26388 to 26426 (nt 81 to 119)

```
5'-CGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCG-3'
5'-((.((((..(((((((.....)))))))...)))).))-3'
Motif MFE = -7.9; z-score = -2.71; 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 = -1.92; 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(+)

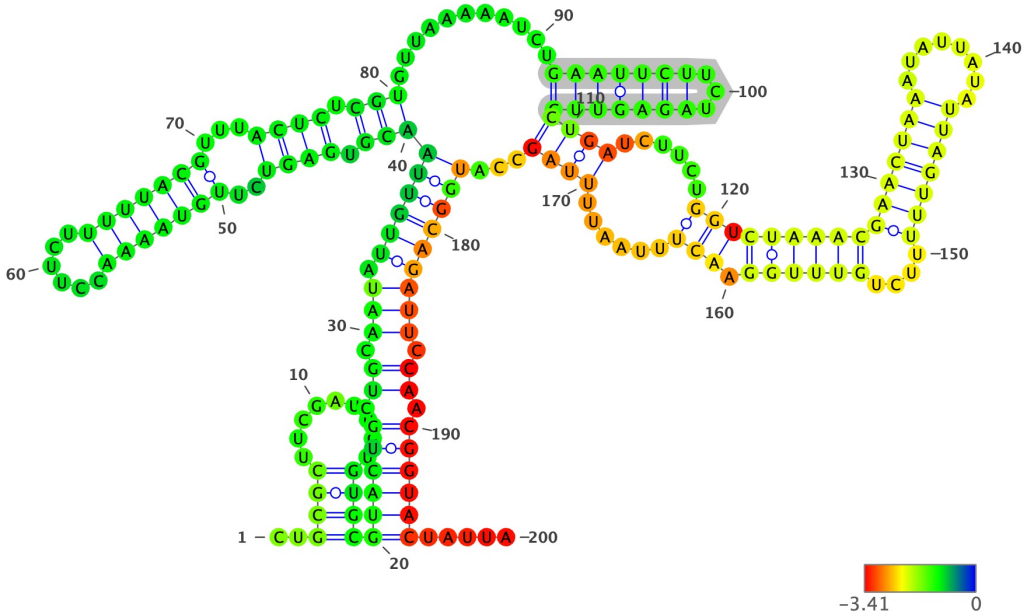
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 448 from nt 26439 to 26455 (nt 92 to 108)

```
5'-GAAUUCUUCUAGAGUUC-3'
5'-(((((((...)))))))-3'
Motif MFE = -3.9; z-score = -4.44; 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 = -2.17; 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(+)

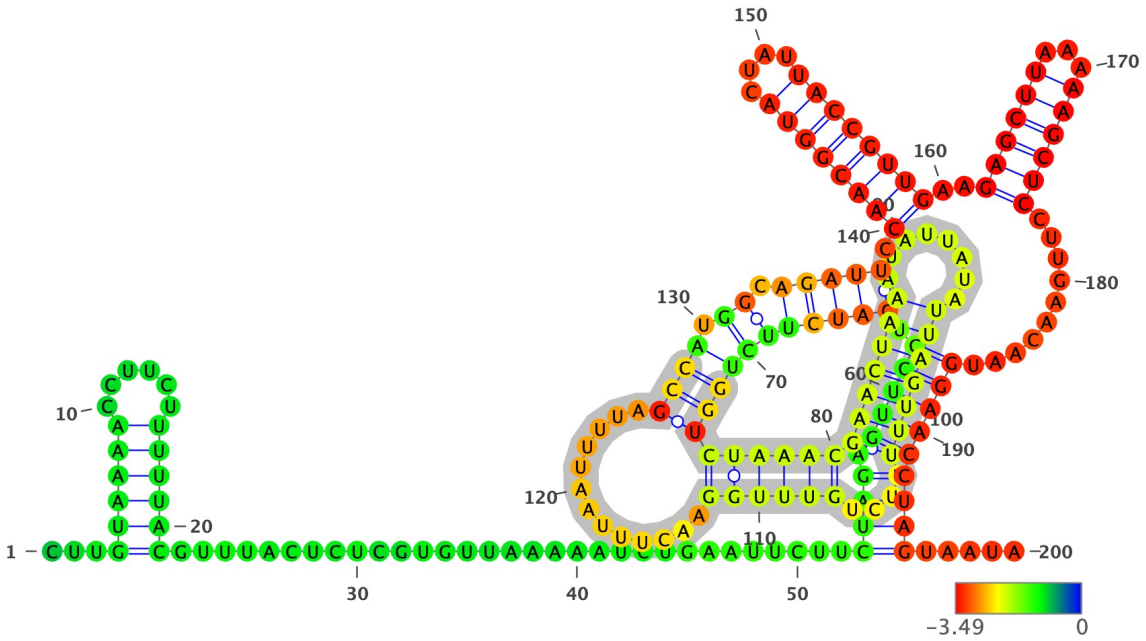
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 449 from nt 26466 to 26522 (nt 72 to 128)

```
5'-GGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCC-3'
5'-((.(((((((((((((.........)))))))....))))))..............))-3'
Motif MFE = -9.2; z-score = -1.31; ED = 5.15
```



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 26395 to 26594 (motif highlighted in silver):

```
5'-CUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUG
GAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUA-3
5'-...((((((.....))))))..............................((((.(((((.(((((((((((((((((((((((.........)))))))....)))))
).............)))).)).))))).((((((((....))))))))..((((((...))))))..........)))))))))).....-3'
MFE = -41.9; z-score = -2.59; ED = 21.22
```

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 78--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 78--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 129 to 200--gene, gene-GU280_gp05, 26523-27191(+)

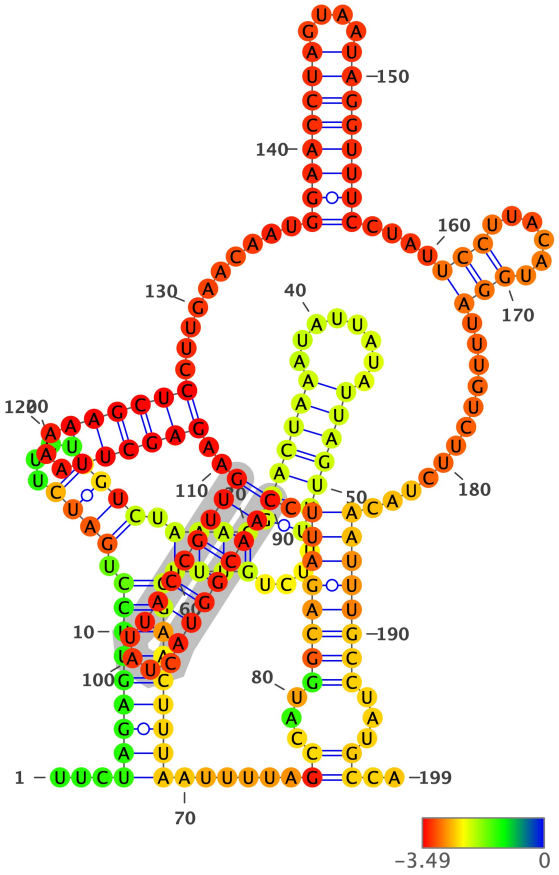
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 129 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 450 from nt 26534 to 26553 (nt 90 to 109)

```
5'-CAACGGUACUAUUACCGUUG-3'
5'-((((((((....))))))))-3'
Motif MFE = -9.0; z-score = -5.0; 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 26445 to 26643 (motif highlighted in silver):

```
5'-UUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAA
GAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCA-3
5'-...(((((((((.((((....)))).(((((((((((.........)))))))....))))))))))))).....((...((((((((.((((((((....))))))))..
((((((...)))))).........((((((((....))))))))....(((......))).............))))))))...))..-3'
MFE = -55.1; z-score = -4.87; 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(+)

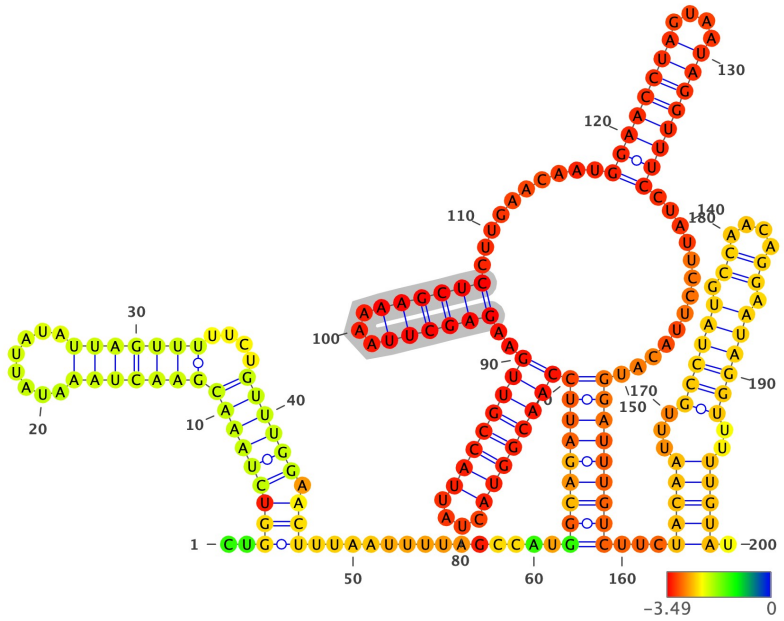
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 451 from nt 26556 to 26570 (nt 93 to 107)

```
5'-GAGCUUAAAAAGCUC-3'
5'-((((((...))))))-3'
Motif MFE = -5.0; z-score = -6.44; 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 = -4.33; 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(+)

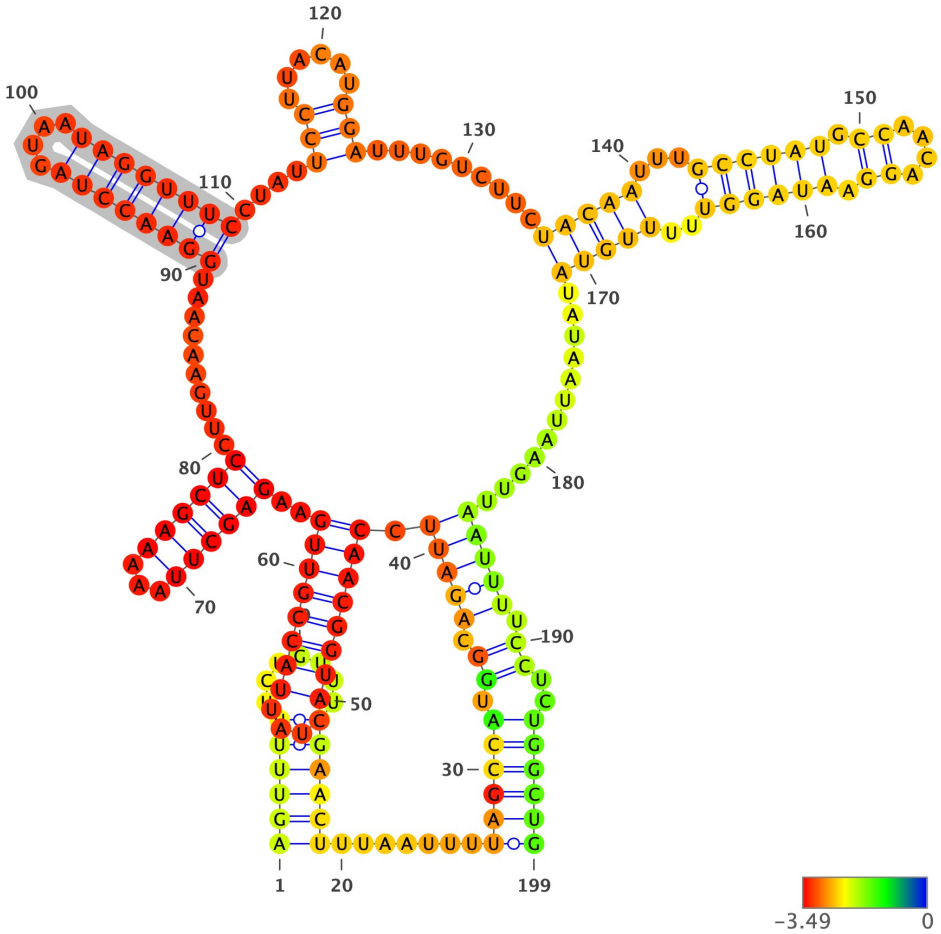
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 452 from nt 26581 to 26600 (nt 90 to 109)

```
5'-GGAACCUAGUAAUAGGUUUC-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.2; z-score = -5.03; 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 = -3.77; 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(+)

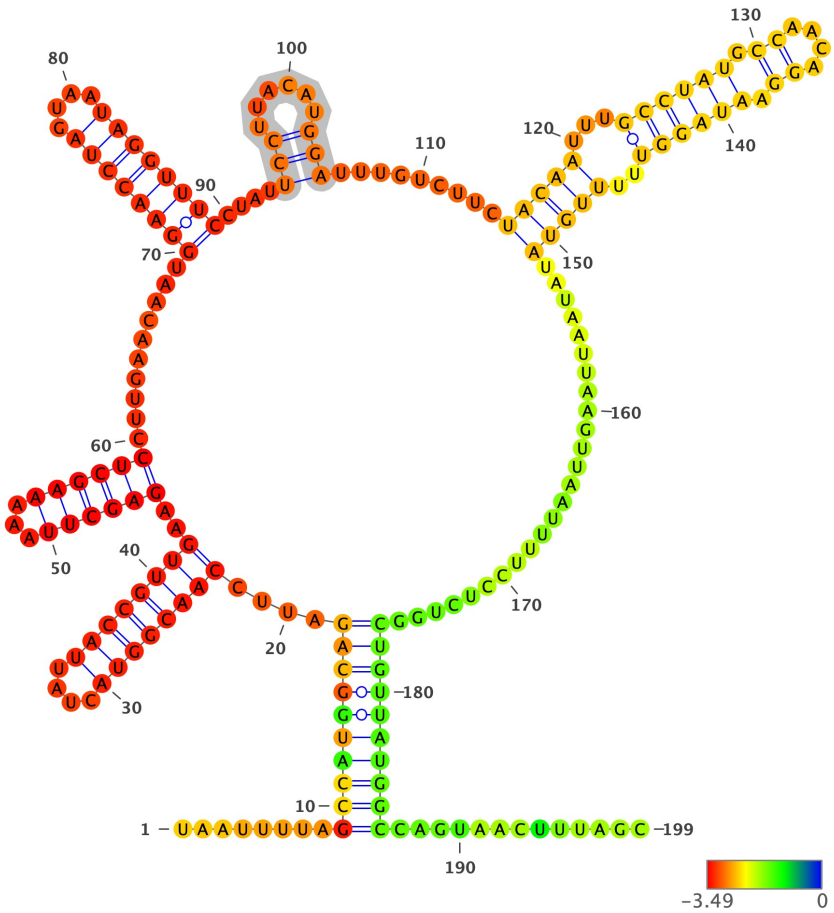
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 453 from nt 26605 to 26616 (nt 94 to 105)

```
5'-UCCUUACAUGGA-3'
5'-(((......)))-3'
Motif MFE = -1.9; z-score = -6.83; 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 = -4.23; 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(+)

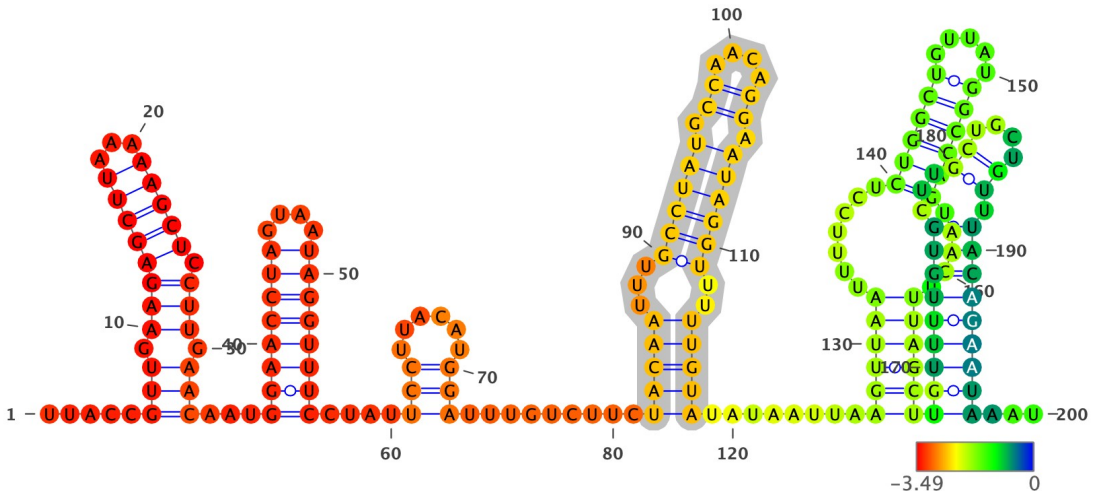
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 454 from nt 26626 to 26662 (nt 82 to 118)

```
5'-UACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUA-3'
5'-(((((...((((((.((....)).))))))..)))))-3'
Motif MFE = -10.9; z-score = -3.21; 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 = -2.99; 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(+)

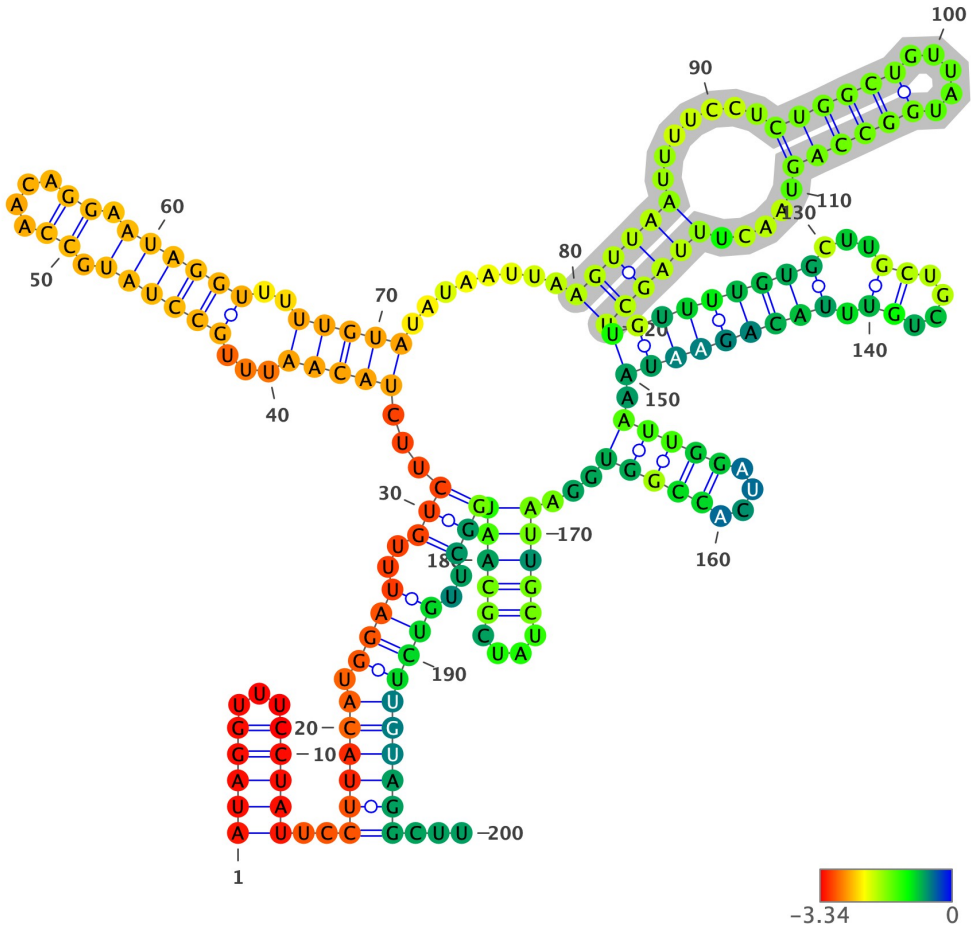
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 455 from nt 26671 to 26711 (nt 80 to 120)

```
5'-AGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCU-3'
5'-(((((........((((((.....))))))......)))))-3'
Motif MFE = -11.1; z-score = -2.87; ED = 2.17
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26592 to 26791 (motif highlighted in silver):

```
5'-AUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUA
ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUU-3
5'-(((((...)))))..((((((.((((..(((...(((((...((((((.((....)).))))))..)))))........((((((.......((((((.....))))))..
...))))))((((((((...((....)).))))))))).(((((....)))))...(((((....)))))))..))))))))))...-3'
MFE = -50.2; z-score = -2.28; ED = 38.53
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

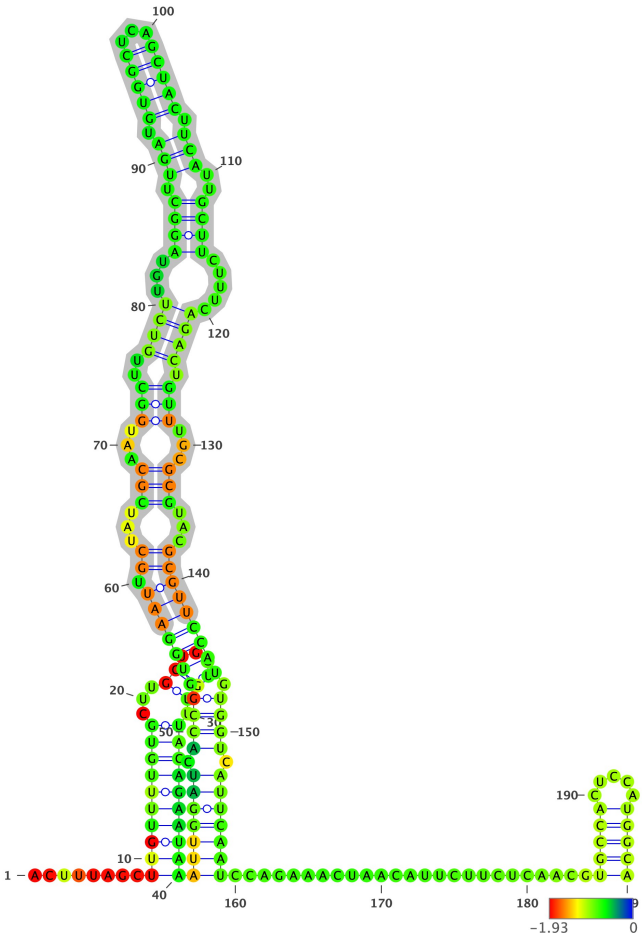
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 456 from nt 26759 to 26844 (nt 57 to 142)

```
5'-AAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUUGCUUCUUUCAGACUGUUUGCGCGUACGCGUU-3'
5'-(((.((....((...(.......................................................)...)).....)))))-3'
Motif MFE = -22.3; z-score = -1.3; ED = 16.33
```



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 26703 to 26901 (motif highlighted in silver):

```
5'-ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUU
GCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCA-3
5'-........((((((((((...((....)).)))))))))(((((((.(((((((((((.((...(((...(((..(((((...((((.(((.((((((...)))))).))).
)))).....)))).))).))...)))...)))))))))).)))).)))))))).......................(((((.....)))))-3'
MFE = -51.1; z-score = -1.45; ED = 18.23
```

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_gp05, 26523-27191(+)

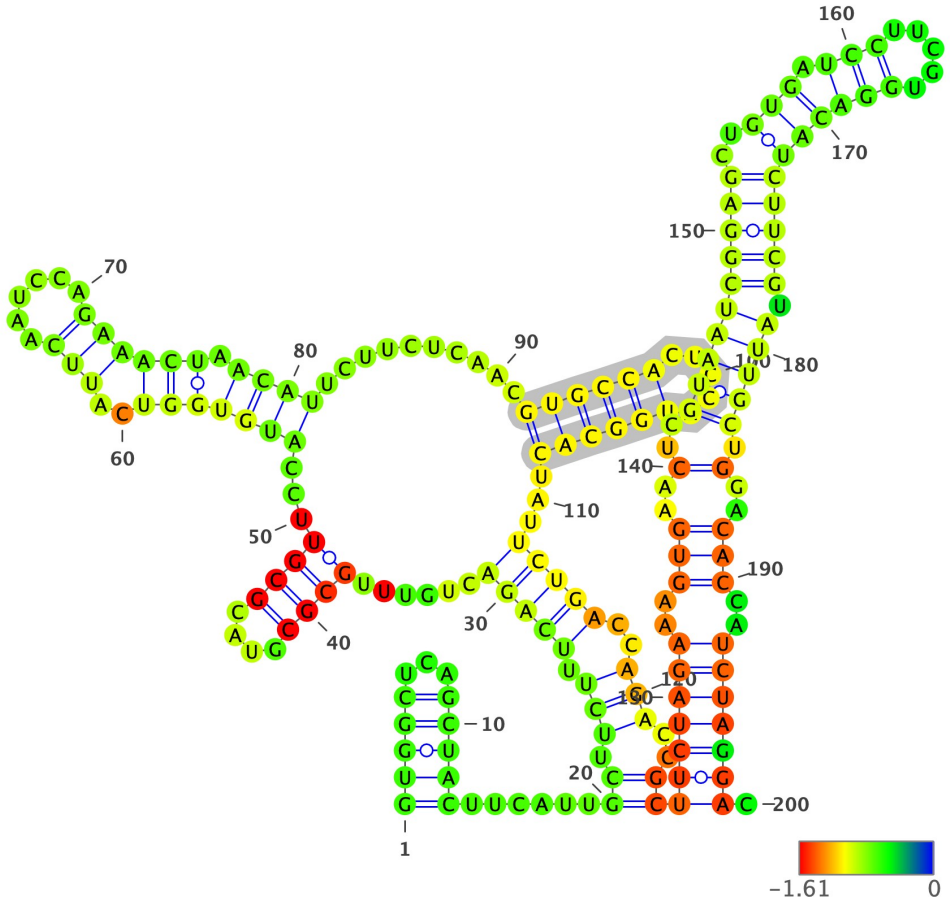
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 457 from nt 26886 to 26902 (nt 92 to 108)

```
5'-GUGCCACUCCAUGGCAC-3'
5'-(((((.......)))))-3'
Motif MFE = -7.5; z-score = -4.18; 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 = -1.07; 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(+)

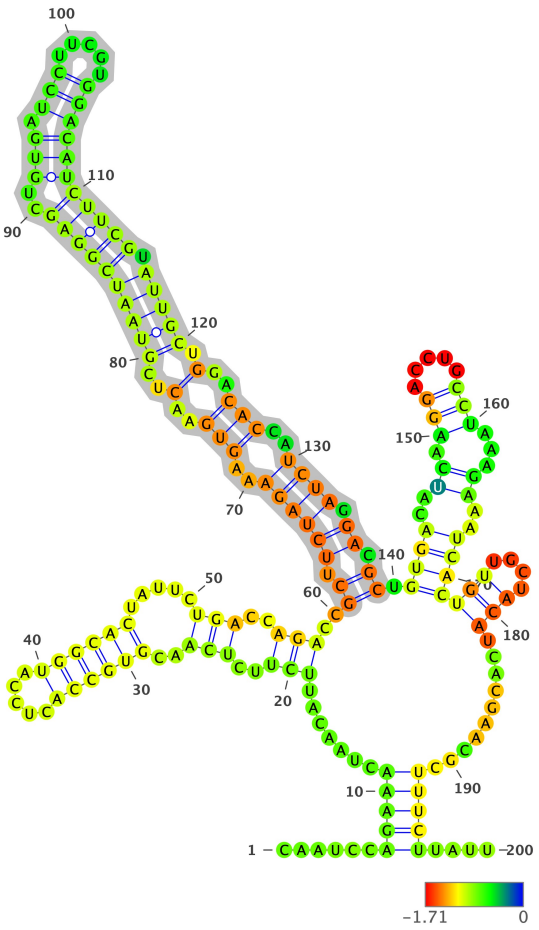
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 458 from nt 26918 to 26996 (nt 61 to 139)

```
5'-GCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGC-3'
5'-((.((((((..(((..(.........................................)..)))..)))).)).))-3'
Motif MFE = -25.9; z-score = -2.58; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26858 to 27057 (motif highlighted in silver):

```
5'-CAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAUUCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCU
UCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUU-3
5'-......(((((.......(((..(((..((((((.....))))))).....)))..)))..((.((((((..(((..(..(((((((((((..(((.(((.....))))))))
))).))))).)..)))..)))).)).)).((((..((.(((.....)))...))..))))(((....)))..........)))))....-3'
MFE = -40.6; z-score = -0.88; ED = 23.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

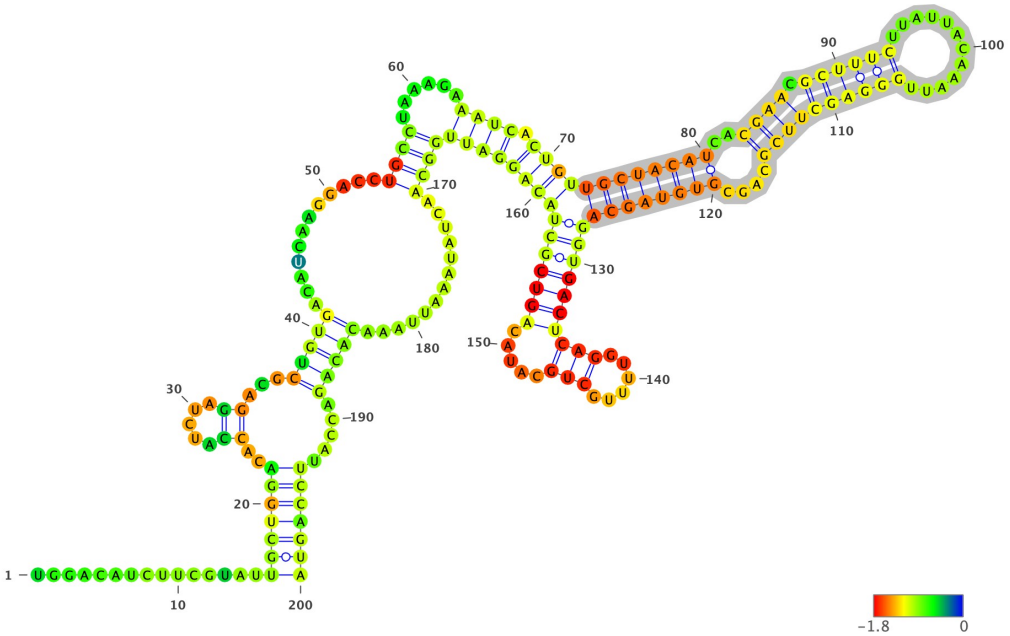
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 459 from nt 27032 to 27086 (nt 73 to 127)

```
5'-UGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAGCUUCGCAGCGUGUAGCA-3'
5'-(((((((((..(((((.(((((((.............))))))))))....))))))))-3'
Motif MFE = -18.4; z-score = -3.49; 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 = -0.8; 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(+)

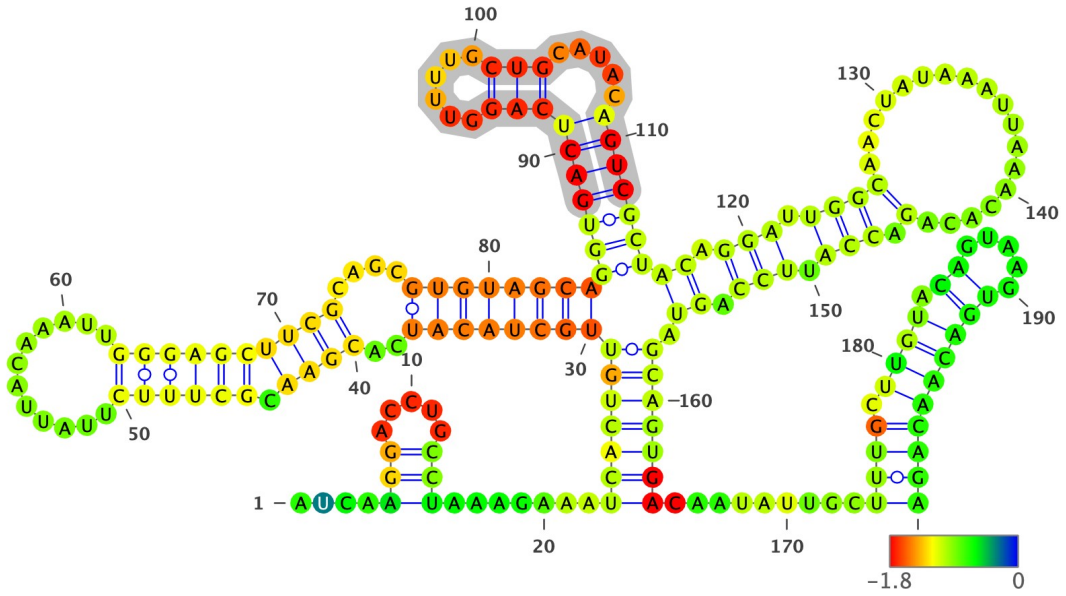
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 460 from nt 27090 to 27114 (nt 88 to 112)

```
5'-GACUCAGGUUUUGCUGCAUACAGUC-3'
5'-(((.(((......)))......)))-3'
Motif MFE = -3.2; z-score = -0.27; ED = 5.08
```



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 27003 to 27202 (motif highlighted in silver):

```
5'-AUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAGCUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGU
CGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUAGCAGUGACAAUAUUGCUUUGCUUGUACAGUAAGUGACAACAGA-3
5'-....(((.....)))......((((((((((((((..((((.((((((.............))))))))))....))))))))((((((((((......)))).....)))
))))((.(((.((((.................).))).))).)).)))))))).........((((.((((.((.....)))))))))-3'
MFE = -47.4; z-score = -2.05; ED = 30.23
```

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 189--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 189--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 200 to 200--gene, gene-GU280_gp06, 27202-27387(+)

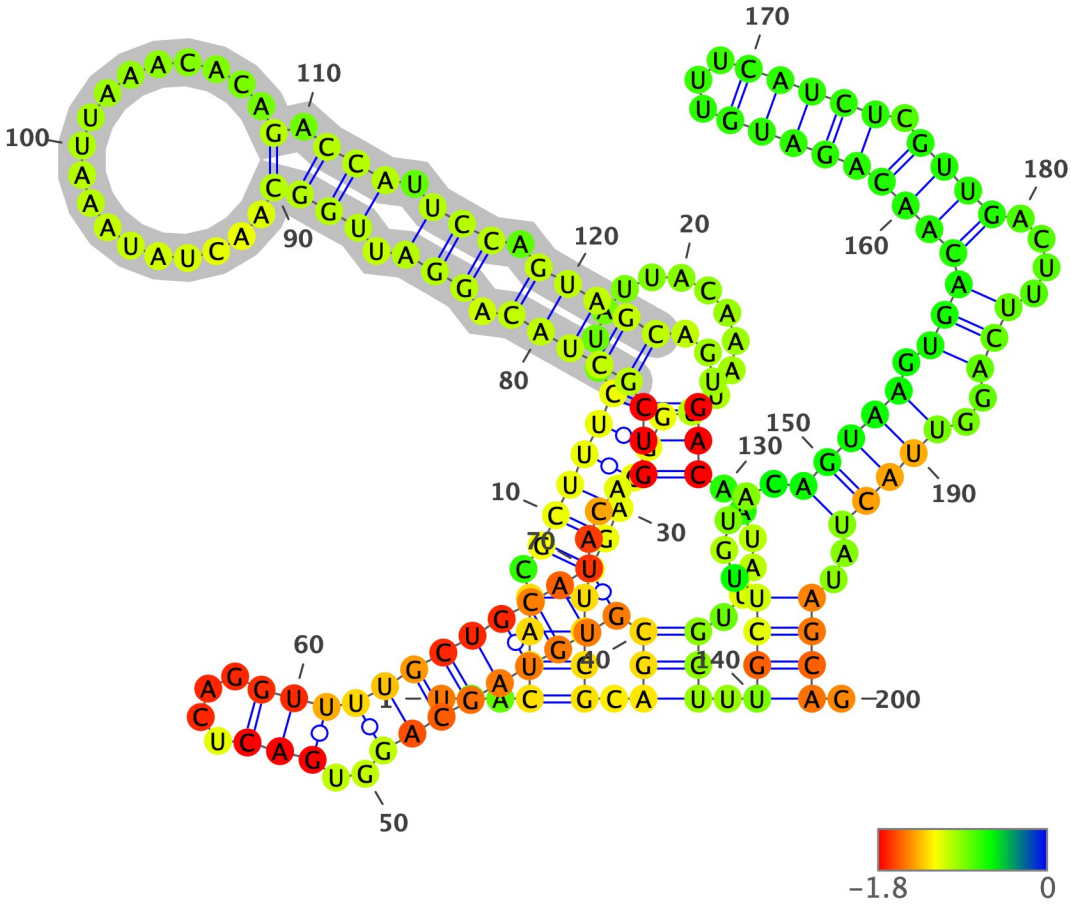
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 200 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 461 from nt 27115 to 27161 (nt 77 to 123)

```
5'-GCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGUAGC-3'
5'-(((((.(((.((((.................).))).))).)))))-3'
Motif MFE = -12.0; z-score = -3.51; 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 = -0.97; ED = 28.84
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 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(+)

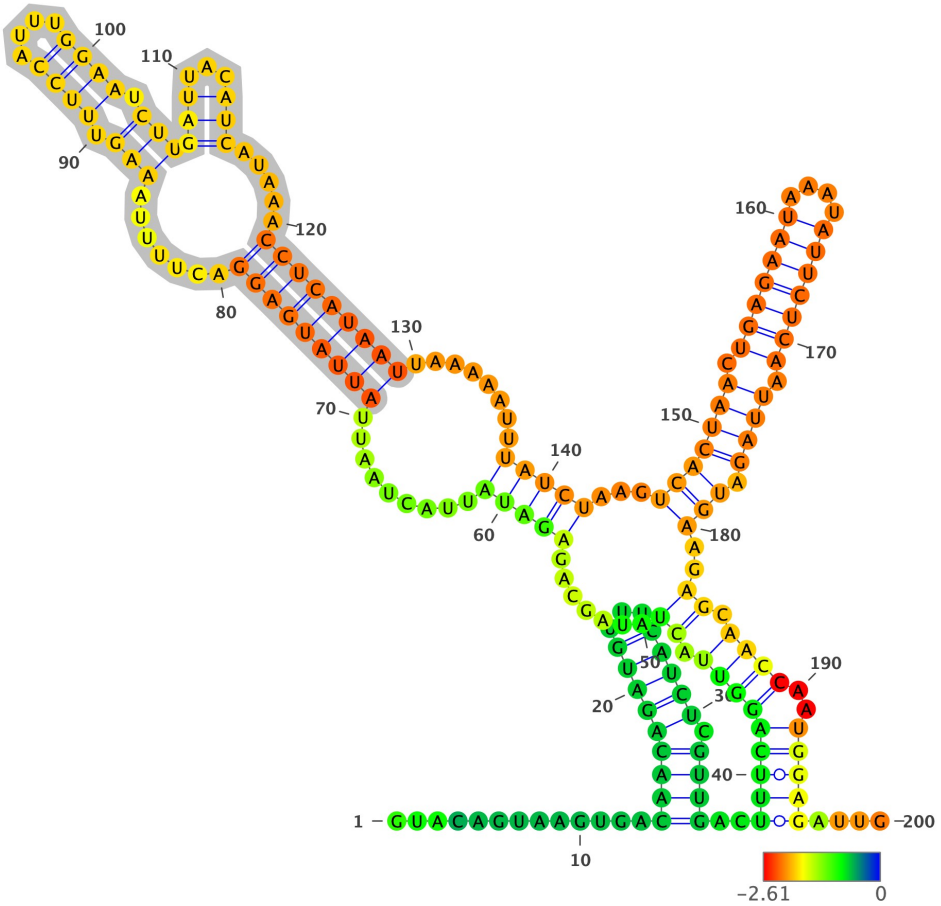
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

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 462 from nt 27253 to 27311 (nt 71 to 129)

```
5'-AUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUACAUCAUAAACCUCAUAAU-3'
5'-(((((((((.......(((.((((....)))).)))..............)))))))))-3'
Motif MFE = -12.7; z-score = -2.89; 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 = -1.65; ED = 25.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 9--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 9--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

4-- nt 20 to 200--gene, gene-GU280_gp06, 27202-27387(+)

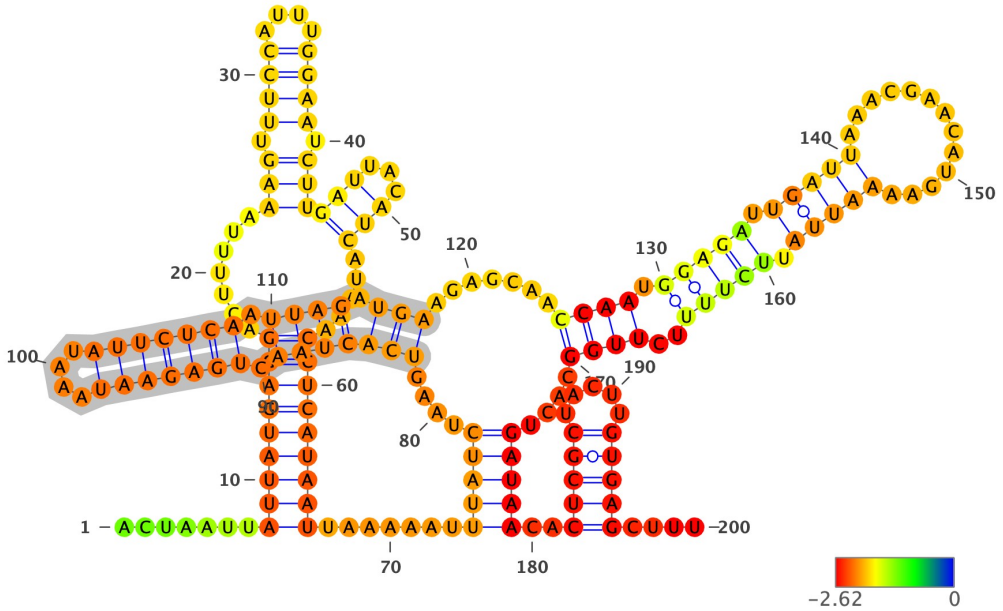
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 20 to 200--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

NC_045512.2 (forward strand): Structure number 463 from nt 27328 to 27362 (nt 83 to 117)

```
5'-UCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGA-3'
5'-(((((((.(((((((....)))))))).)))).)))-3'
Motif MFE = -10.5; z-score = -5.4; 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 = -2.64; 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(+)

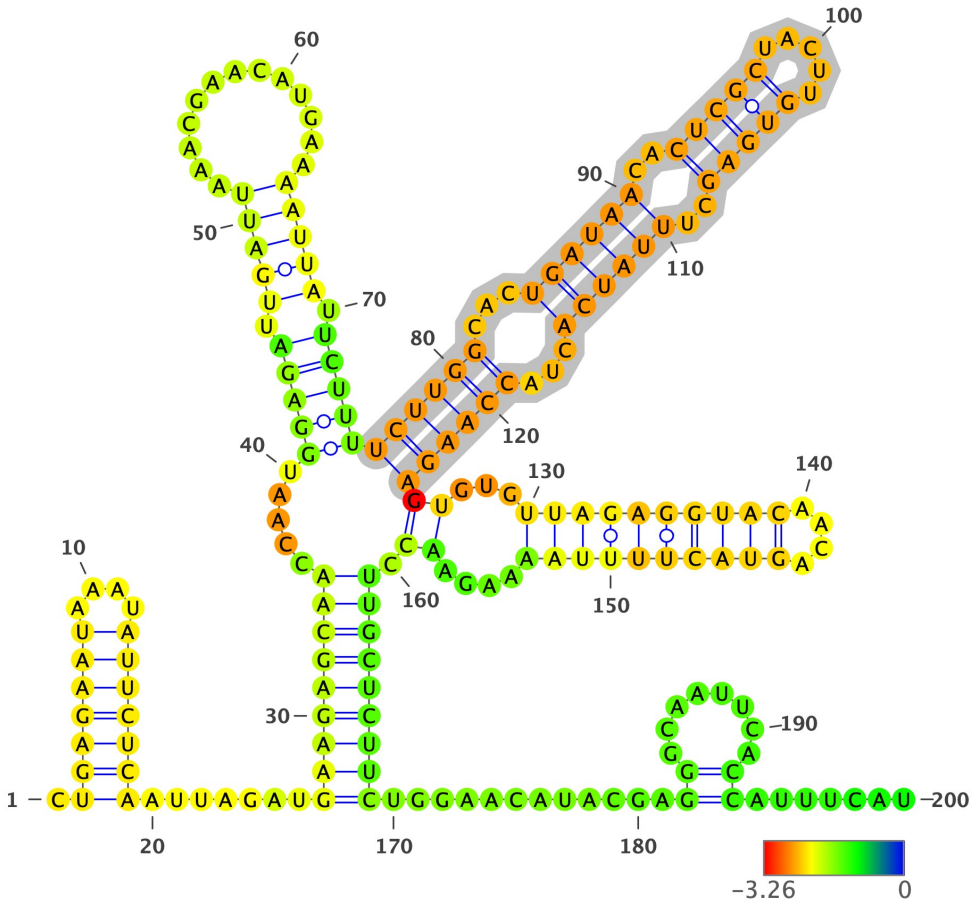
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 464 from nt 27410 to 27458 (nt 76 to 124)

```
5'-UCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGA-3'
5'-((((((...((((((..(((((.....)))))..))))))...))))))-3'
Motif MFE = -18.5; z-score = -4.48; 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 = -3.7; 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(+)

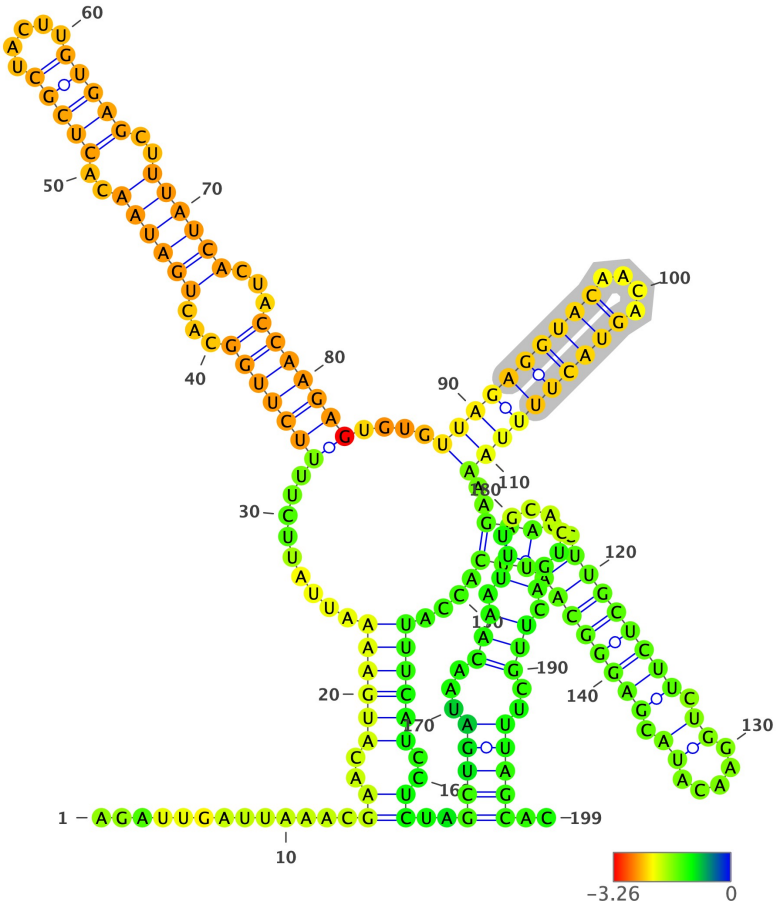
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 465 from nt 27468 to 27483 (nt 92 to 107)

```
5'-AGGUACAACAGUACUU-3'
5'-((((((....))))))-3'
Motif MFE = -3.9; z-score = -5.64; ED = 0.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27377 to 27575 (motif highlighted in silver):

```
5'-AGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAA
AAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCAC-3
5'-.............((..((((((.........(((((((...((((((..(((((.....)))))..))))))...)))))))....((((((((((....))))))))))
..(((..((((((((.((.....)).))))))))))....))))))..))..(((((...(((.((......)).)))..)))))..-3'
MFE = -44.6; z-score = -2.43; ED = 22.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 11--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 11--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 18 to 199--gene, gene-GU280_gp07, 27394-27759(+)

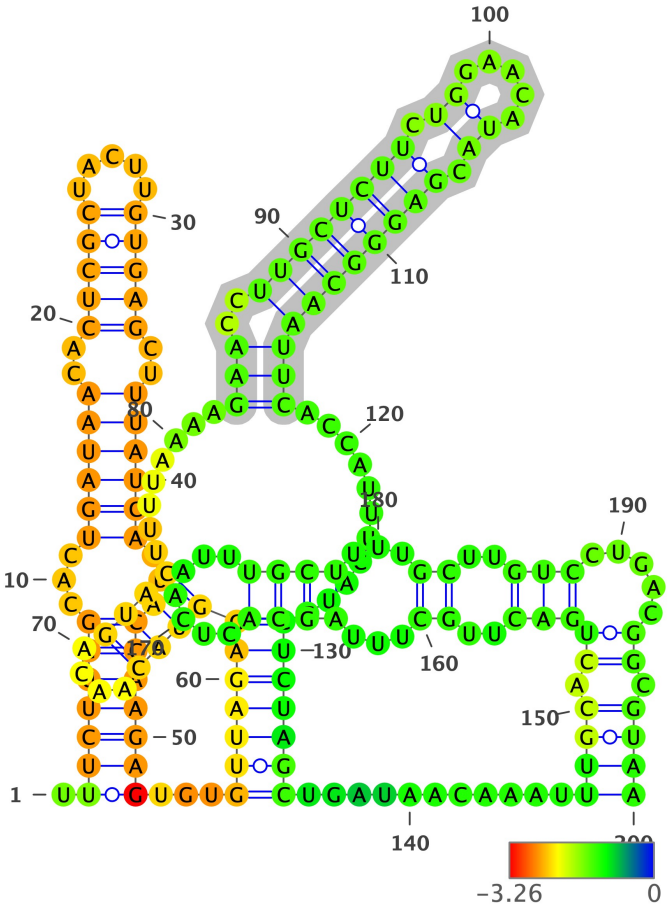
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 18 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 466 from nt 27490 to 27524 (nt 83 to 117)

```
5'-GAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUC-3'
5'-(((..((((((((...........)))))))))))-3'
Motif MFE = -8.1; z-score = -1.47; 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 = -2.32; ED = 27.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp07, 27394-27759(+)

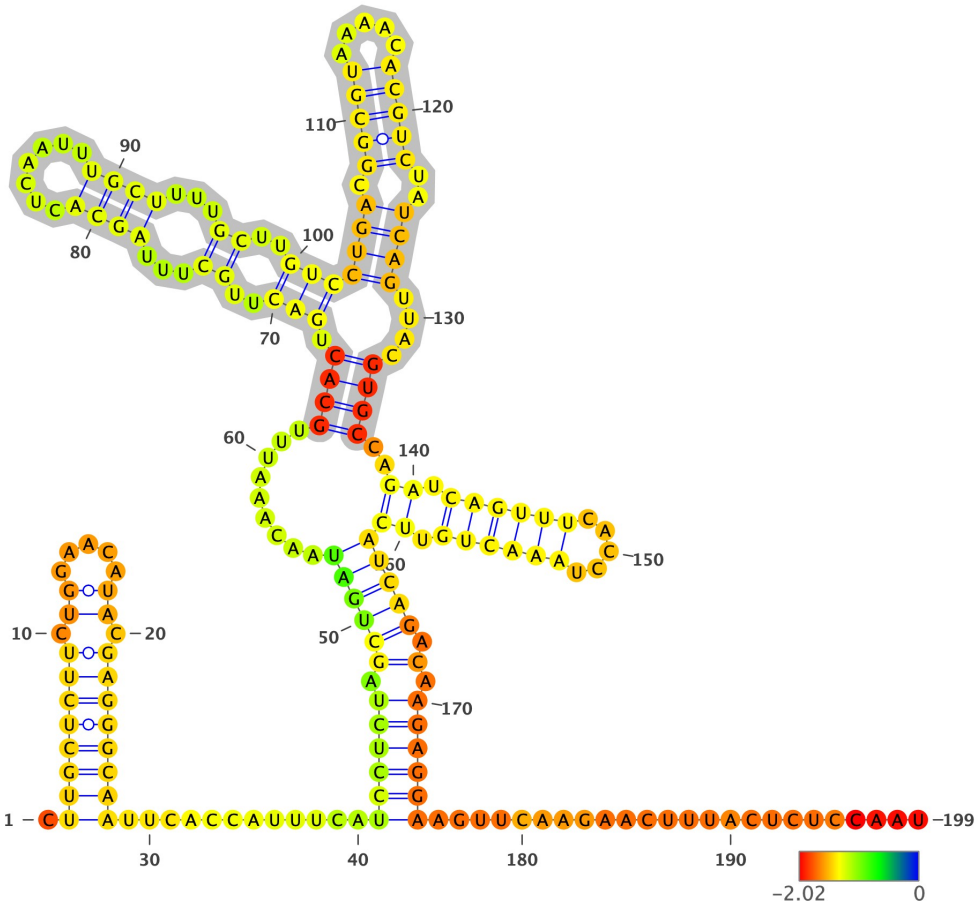
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 467 from nt 27556 to 27629 (nt 63 to 136)

```
5'-GCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCGUAAAACACGUCUAUCAGUUACGUGC-3'
5'-((((.(((..((...((((.......))))...))..)))((((.(((((.....)))))..))))....))))-3'
Motif MFE = -19.8; z-score = -2.27; ED = 1.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27494 to 27692 (motif highlighted in silver):

```
5'-CUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCACUCAAUUUGCUUUUGCUUGUCCUGACGGCG
UAAAACACGUCUAUCAGUUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAU-3
5'-.((((((((.((.....)).)))))))).............((((((.((((((.........((((.(((..((...((((.......))))...))..)))((((.((((
(.....)))))..))))....))))..((.((((((.....)))))).)))))))).).))))))........................-3'
MFE = -46.7; z-score = -2.73; ED = 13.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp07, 27394-27759(+)

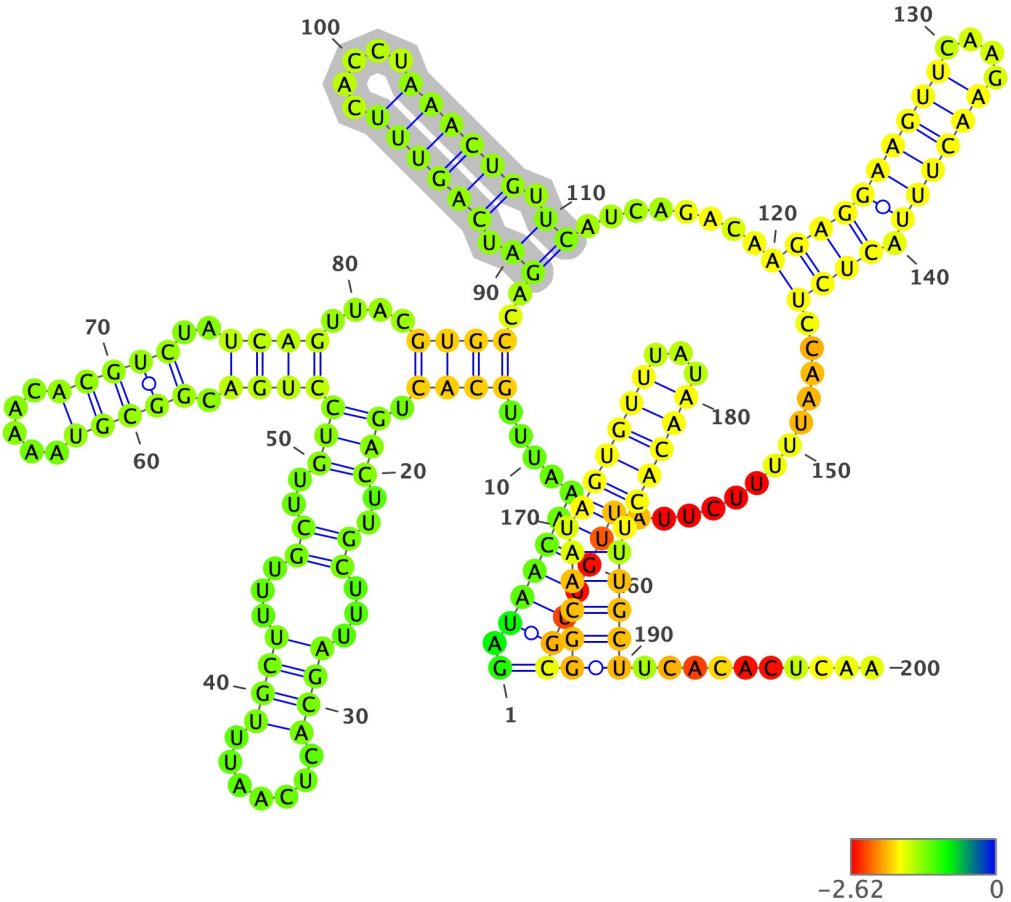
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 468 from nt 27632 to 27654 (nt 89 to 111)

```
5'-GAUCAGUUUCACCUAAACUGUUC-3'
5'-((.((((((.....)))))).))-3'
Motif MFE = -4.1; z-score = -3.96; 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 = -2.18; 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(+)

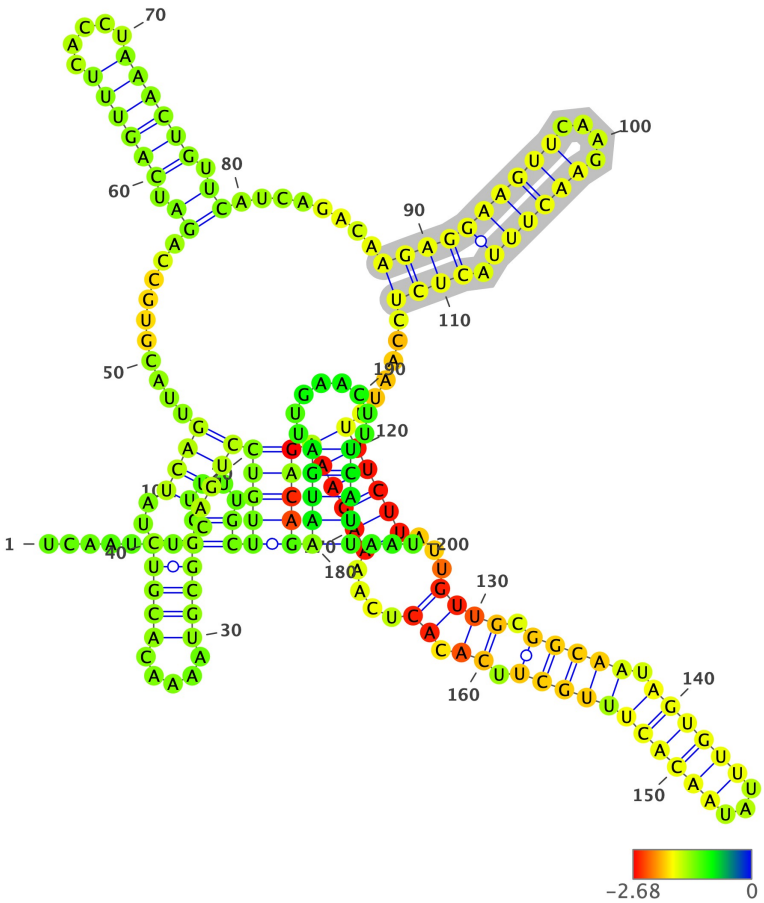
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 469 from nt 27663 to 27687 (nt 88 to 112)

```
5'-AGAGGAAGUUCAAGAACUUUACUCU-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -5.8; z-score = -3.01; 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 = -2.77; 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(+)

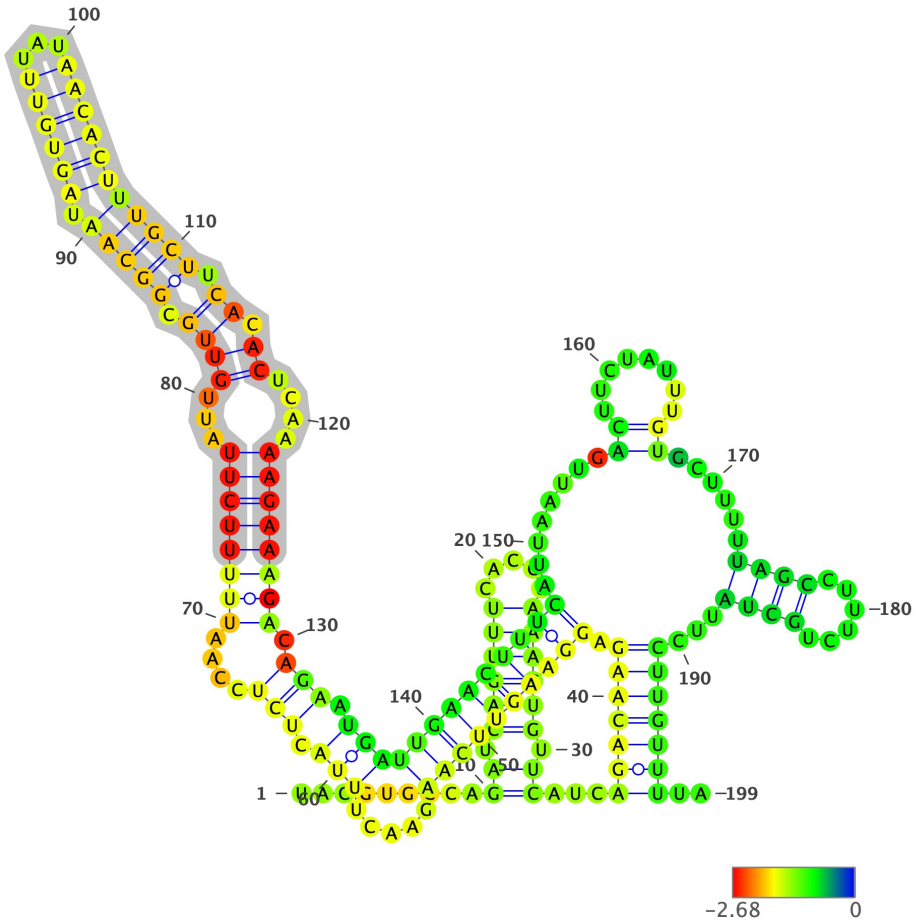
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 470 from nt 27695 to 27748 (nt 73 to 126)

```
5'-UUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCUUCACACUCAAAAGAA-3'
5'-(((((...((((.((((..((((((...)))))).)))).)).)).....)))))-3'
Motif MFE = -12.5; z-score = -2.98; 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 27623 to 27821 (motif highlighted in silver):

```
5'-UACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCU
UCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUA-3
5'-.........((.((((((.....)))))).))...(((((((.((((((((((.....(((.(((....((((((((...((((.(((((.((((((...)))))))))))
.)).)).....)))))))).))).))))))))))))).........((........)).....((((......))))...)))))))..-3'
MFE = -38.9; z-score = -2.3; ED = 29.35
```

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 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(+)

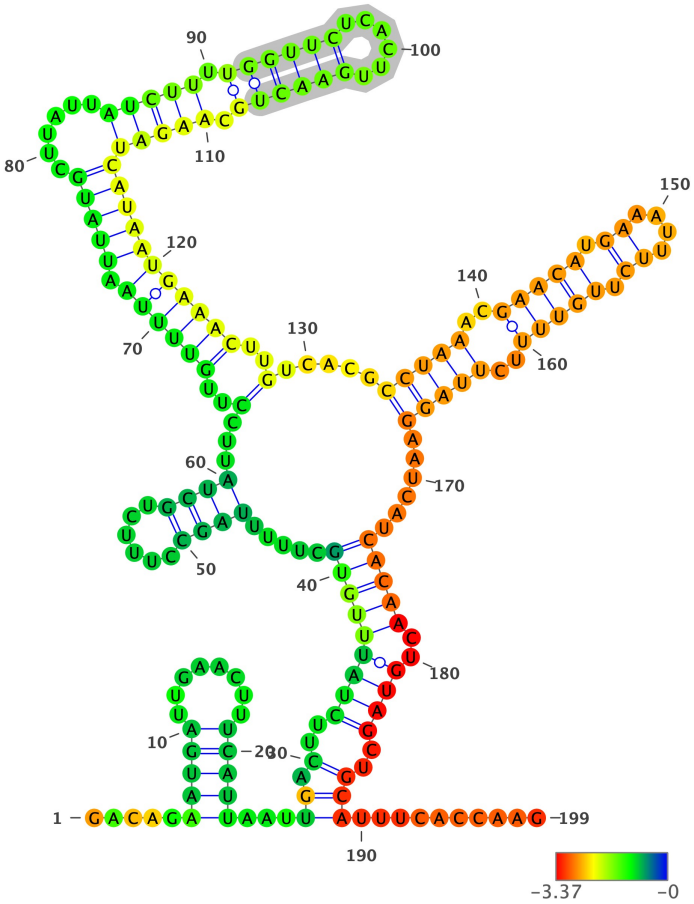
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 471 from nt 27841 to 27856 (nt 92 to 107)

```
5'-GGUUCUCACUUGAACU-3'
5'-(((((......)))))-3'
Motif MFE = -3.8; z-score = -3.65; 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 27750 to 27948 (motif highlighted in silver):

```
5'-GACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAA
GAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAG-3
5'-.....(((((........)))))...((.(..(((((((((.....((((......))))...(..((((((.(((((......(((((.((((((......))))))).))
))))))))))))))..).....(((((..(((((.((....)).)))))..)))))......)))))..))))..))).........-3'
MFE = -33.5; z-score = -1.29; ED = 24.99
```

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 10--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 10--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 7 to 138--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 7 to 138--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

6-- nt 145 to 199--gene, gene-GU280_gp09, 27894-28259(+)

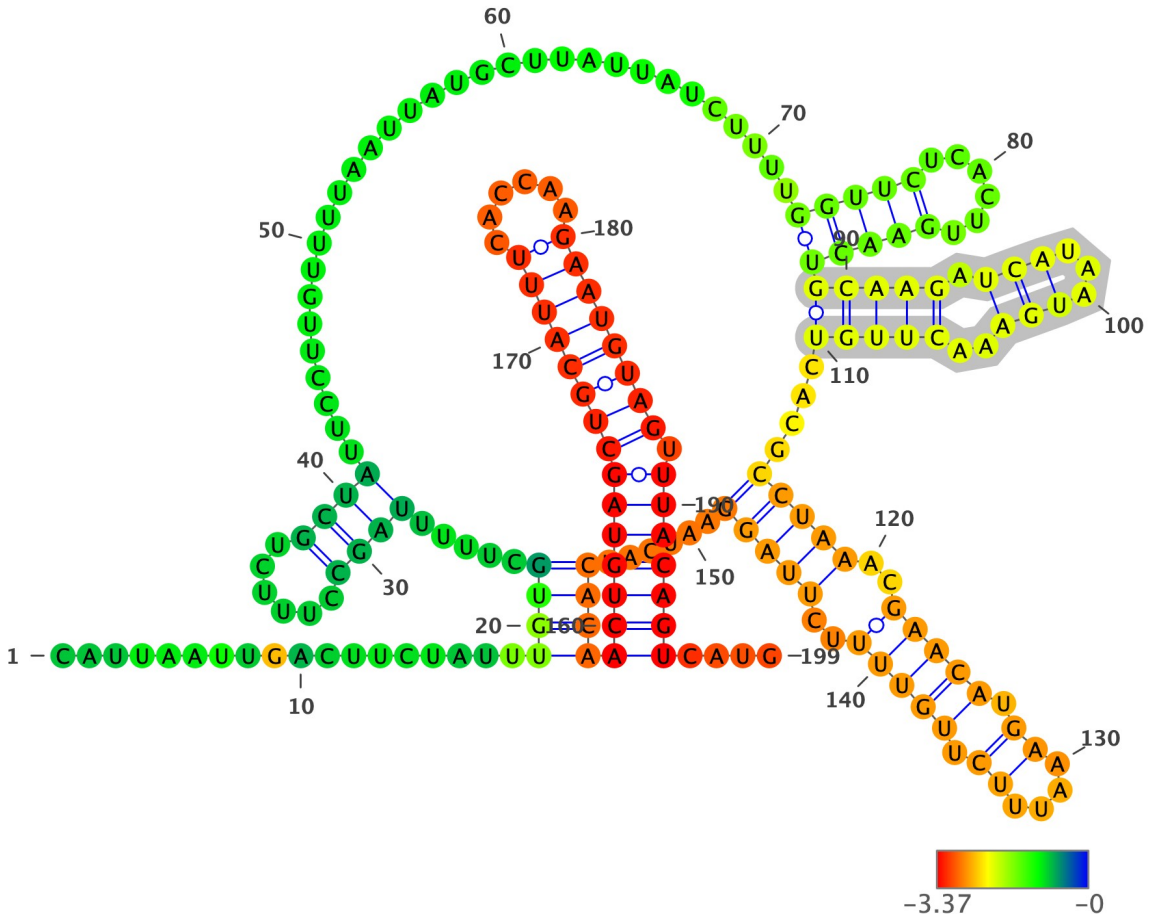
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 145 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 472 from nt 27857 to 27878 (nt 89 to 110)

```
5'-GCAAGAUCAUAAUGAAACUUGU-3'
5'-(((((.((.....)).)))))-3'
Motif MFE = -2.7; z-score = -1.35; ED = 1.48
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27769 to 27967 (motif highlighted in silver):

```
5'-CAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUC
ACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUG-3
5'-...................((((.....((((......))))..............................(((((......)))))(((((.(((...)))..))))).
...(((((..(((((.((....)).)))))..)))))......))))((((((((((((((.....))))))))).)))))))....-3'
MFE = -37.4; z-score = -3.2; ED = 18.71
```

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 119--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 119--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 126 to 199--gene, gene-GU280_gp09, 27894-28259(+)

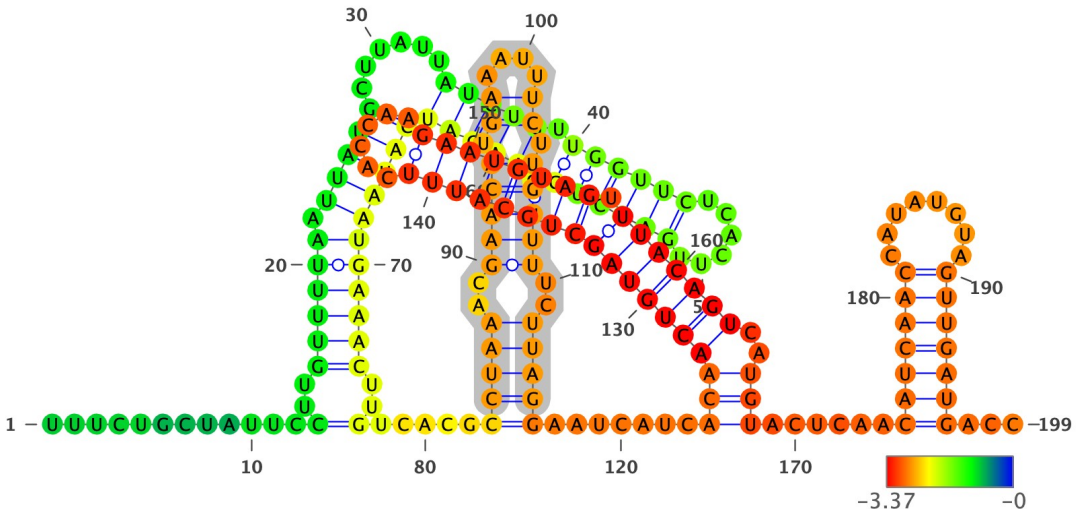
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 126 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 473 from nt 27884 to 27915 (nt 84 to 115)

```
5'-CUAAACGAACAUGAAAUUUCUUGUUUUCUUAG-3'
5'-((((..(((((.(......).)))))..))))-3'
Motif MFE = -4.7; z-score = -2.1; ED = 1.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27801 to 27999 (motif highlighted in silver):

```
5'-UUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUC
UUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACC-3
5'-............(..((((((.(((((......(((((.((((((......))))))).))))))))))))))))..).....(((((..(((((.((....)).)))))..
)))))).......((((((((((((((((((.....)))))))).)))))))..))).....(((((((........)))))))...-3'
MFE = -46.6; z-score = -3.74; ED = 12.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 87--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 87--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 94 to 199--gene, gene-GU280_gp09, 27894-28259(+)

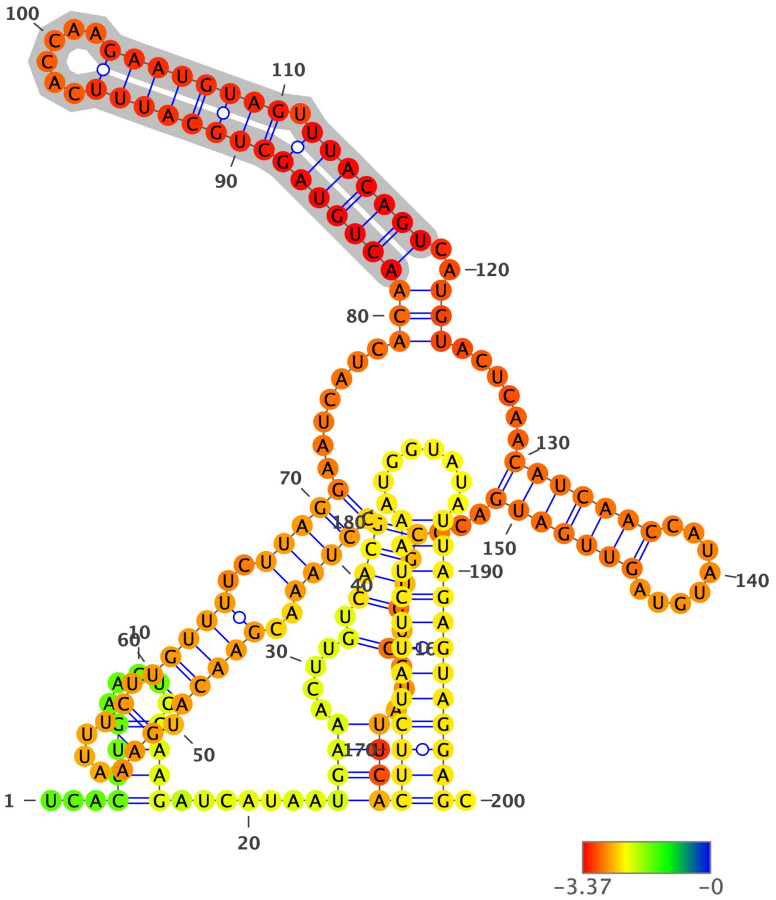
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 94 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 474 from nt 27927 to 27963 (nt 82 to 118)

```
5'-ACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGU-3'
5'-(((((((((((((((.....)))))))))).)))))))-3'
Motif MFE = -14.5; z-score = -4.92; 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 27846 to 28045 (motif highlighted in silver):

```
5'-UCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGU
UUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGC-3
5'-...((((.....)))).......((((....(.(((((((((..(((((.((....)).)))))..)))))).......((((((((((((((((.....)))))))))).
)))))))..)))......(((((((.......)))))))...)))))).)...))))((((((((((((.......)))))))))))).-3'
MFE = -51.6; z-score = -3.81; ED = 18.08
```

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 42--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 42--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 49 to 200--gene, gene-GU280_gp09, 27894-28259(+)

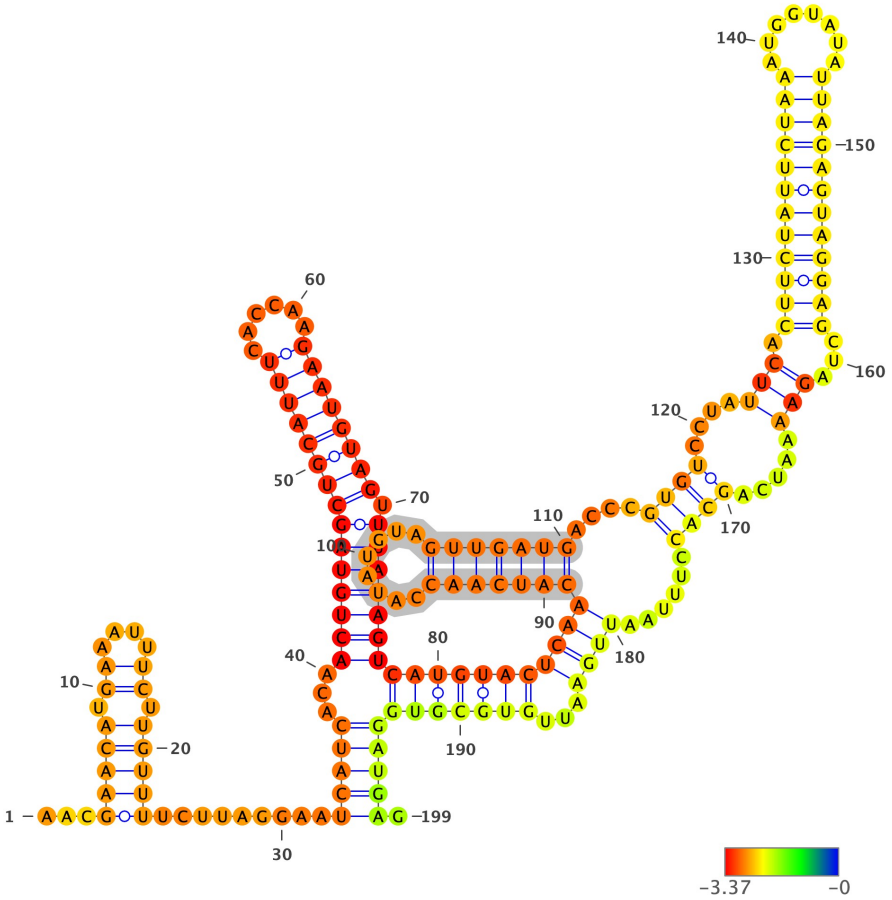
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 49 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 475 from nt 27975 to 27996 (nt 89 to 110)

```
5'-CAUCAACCAUAUGUAGUUGAUG-3'
5'-(((((((........)))))))-3'
Motif MFE = -6.3; z-score = -4.44; 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 = -3.25; 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(+)

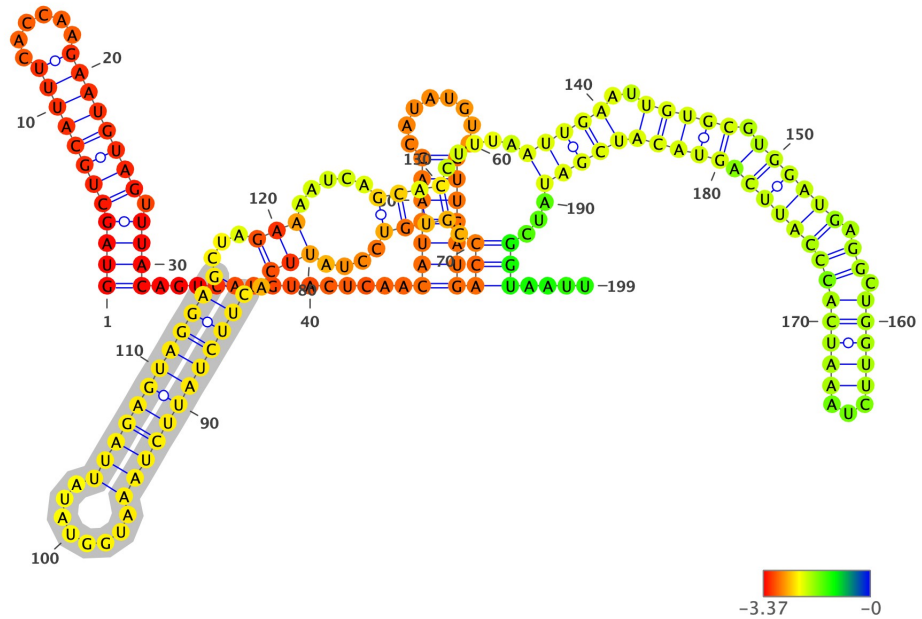
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 476 from nt 28013 to 28044 (nt 84 to 115)

```
5'-CUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAG-3'
5'-(((((((((((.........))))))))))))-3'
Motif MFE = -11.8; z-score = -4.41; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27930 to 28128 (motif highlighted in silver):

```
5'-GUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUA
GGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAUAUCGGUAAUU-3
5'-(((((((((((.......)))))))).))))..............(((((((.........)))))))(((.((((....(((.(((((((((((.........))))))))
))))...)))).....)))).....(((((..(((((.((((((.((.(((((...)))))))))))))))))))))))...)))....-3'
MFE = -52.9; z-score = -2.75; ED = 31.69
```

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_gp09, 27894-28259(+)

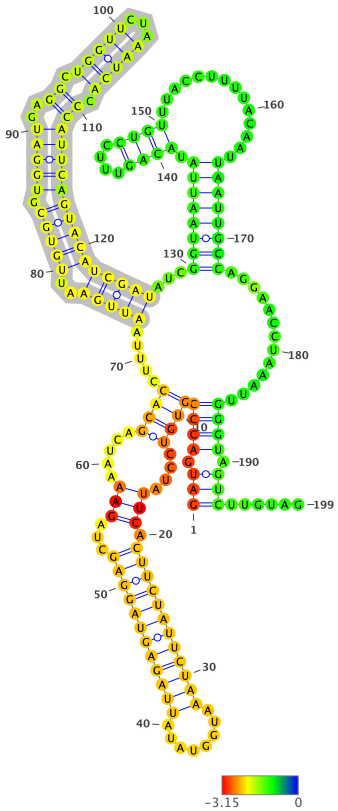
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 477 from nt 28065 to 28118 (nt 73 to 126)

```
5'-AUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCAUUCAGUACAUCGAU-3'
5'-(((((..(((((..((((..((.(((((...))))).))))))).))))))))))-3'
Motif MFE = -17.3; z-score = -3.3; 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 = -44.8; z-score = -2.0; ED = 30.95
```

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_gp09, 27894-28259(+)

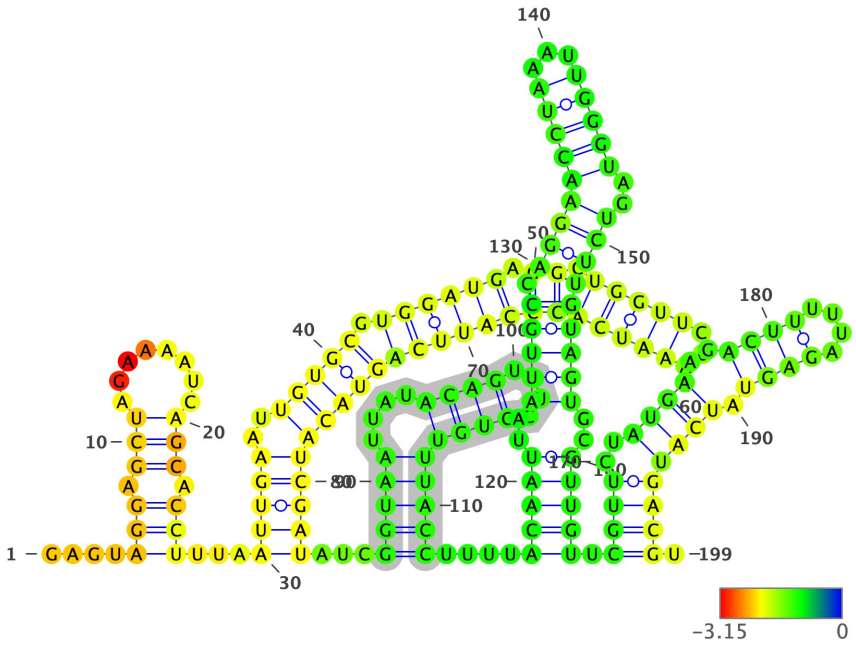
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 478 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 = -1.11; 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(+)

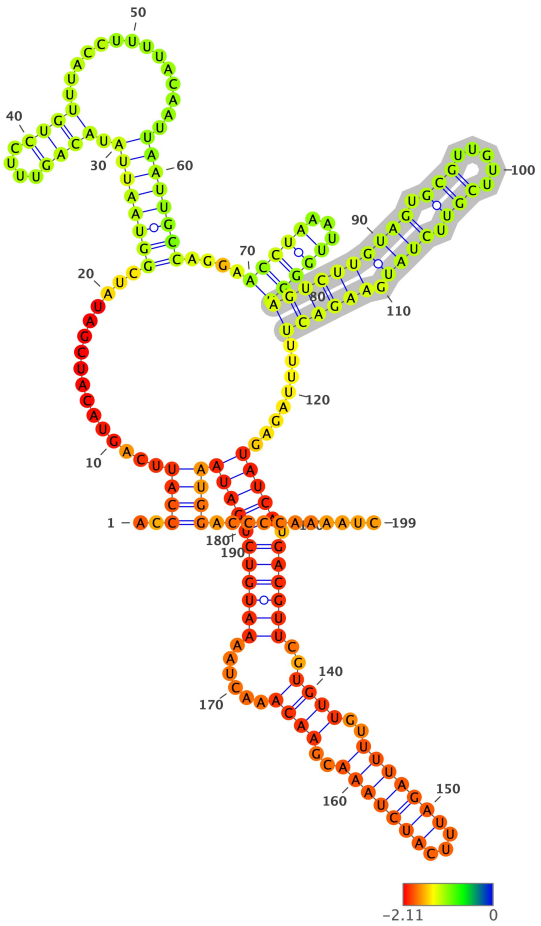
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 479 from nt 28182 to 28215 (nt 83 to 116)

```
5'-AGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACU-3'
5'-((((((((((.(((.....))).)))).))))))-3'
Motif MFE = -11.3; z-score = -3.21; 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 = -1.8; 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(+)

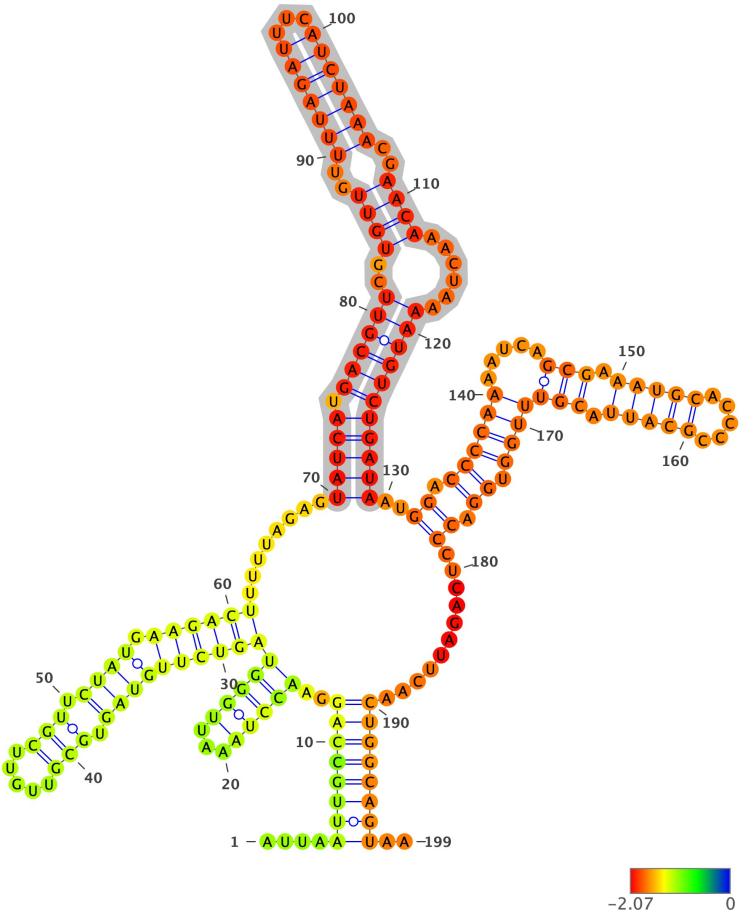
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 480 from nt 28224 to 28283 (nt 70 to 129)

```
5'-UAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUA-3'
5'-(((((.(((((((..(((((..(((((((...)))))))..))))......)))))))))))-3'
Motif MFE = -14.7; z-score = -3.23; ED = 9.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28155 to 28353 (motif highlighted in silver):

```
5'-AUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAAC
AAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAA-3
5'-....((((((((..(((((...)))))((((((((((.(((.....))).)))).))))))........(((((.((((((..((((..(((((((...)))))))..)))
).....)))))))))))..((.((((((.....(((.(((((.....))))).)))))))).)).)).........))))))))..-3'
MFE = -57.2; z-score = -3.72; ED = 15.97
```

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 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(+)

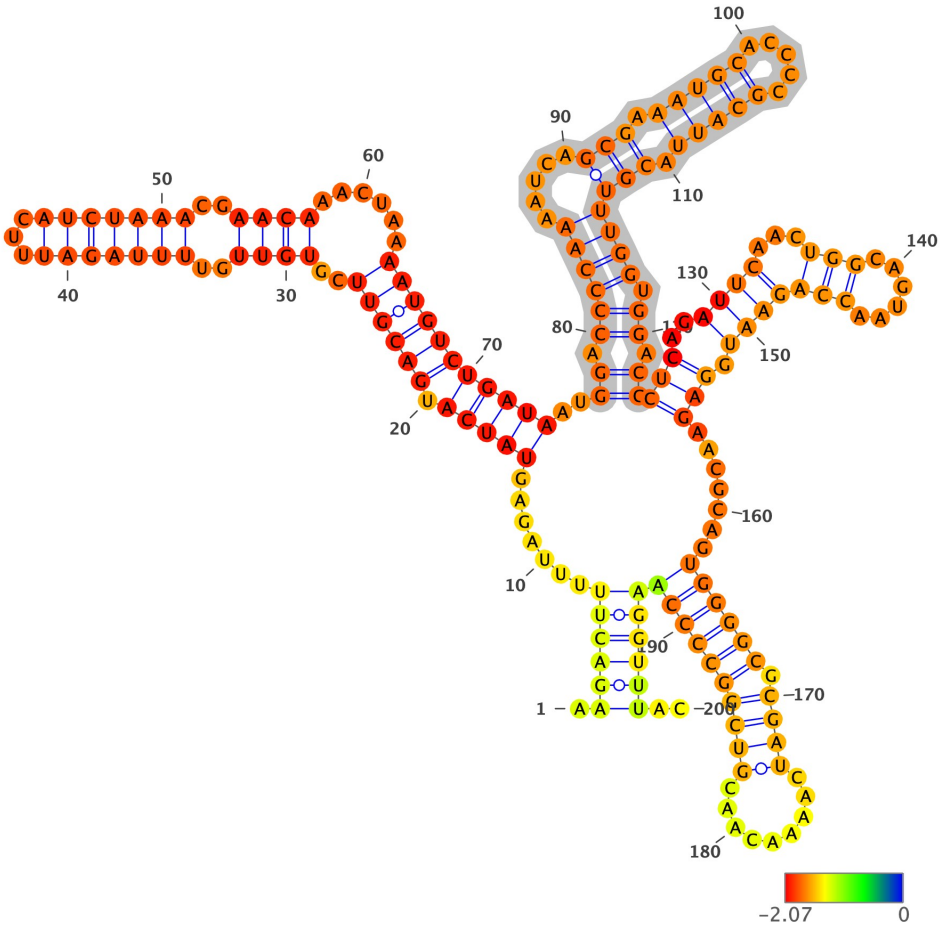
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 481 from nt 28286 to 28332 (nt 77 to 123)

```
5'-GGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACC-3'
5'-((.((((((.....((...((((.....))))...)))))).)).))-3'
Motif MFE = -13.6; z-score = -1.95; 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 = -2.17; 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(+)

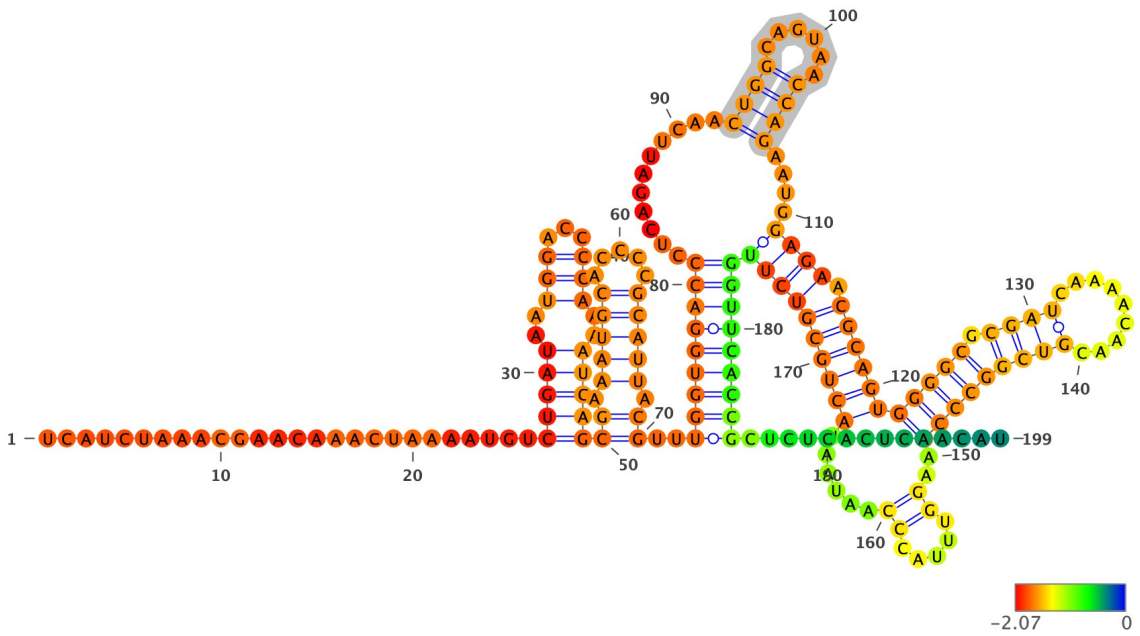
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 482 from nt 28344 to 28357 (nt 93 to 106)

```
5'-CUGGCAGUAACCAG-3'
5'-((((.....))))-3'
Motif MFE = -3.2; z-score = -2.81; ED = 0.23
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28252 to 28450 (motif highlighted in silver):

```
5'-UCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGG
AGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAU-3
5'-.........................(((((..(((...)))..)))))((.(((((.....))))).))..(((((((((..........((((......)))).....(
(((.((((((((((.((((.........)))))))))..((.....)).....))))))))))))))))))).............-3'
MFE = -51.7; z-score = -2.74; ED = 25.97
```

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 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(+)

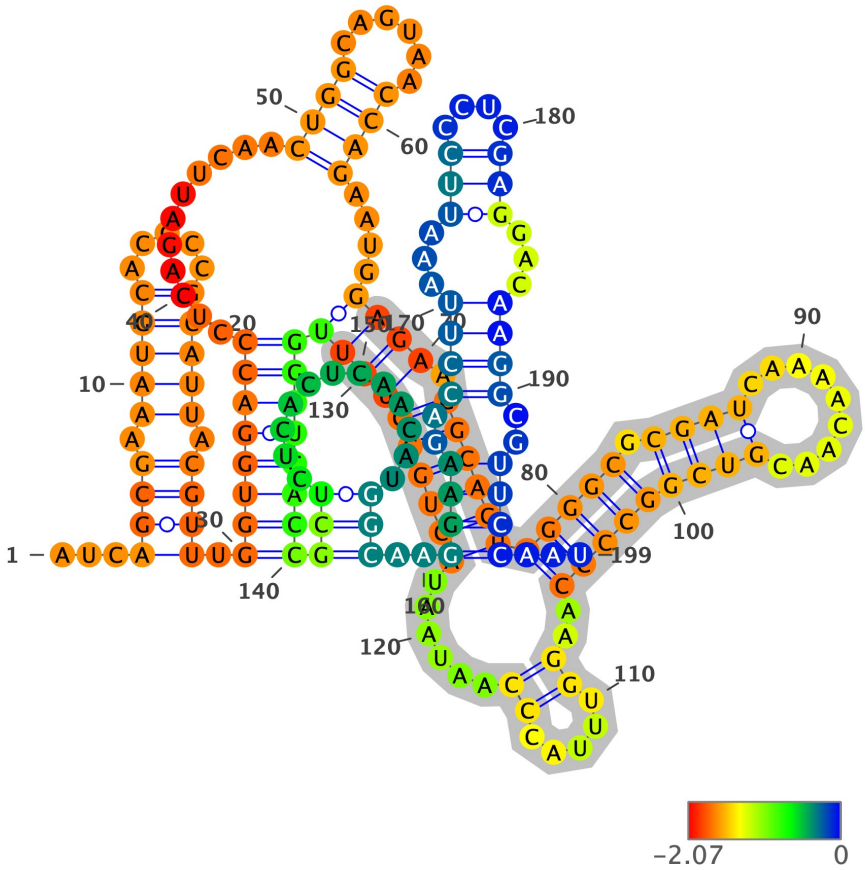
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 483 from nt 28363 to 28426 (nt 68 to 131)

```
5'-AGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCCAAUAAUACUGCGUCU-3'
5'-(((.(((((((((((.((((.........)))))))))..((.....)).....))))))))-3'
Motif MFE = -22.6; z-score = -3.51; ED = 5.89
```



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 28296 to 28494 (motif highlighted in silver):

```
5'-AUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUU
UACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAU-3
5'-...((((.(((((.....))))).)))).((((((((...........((((......))))....((((.(((((((((((.((((.........)))))))))..((..
...)).....))))))))))))))))))(((............)))..((((..((((...(((....)))...))))..))))...-3'
MFE = -59.0; z-score = -2.01; ED = 11.96
```

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_gp10, 28274-29533(+)

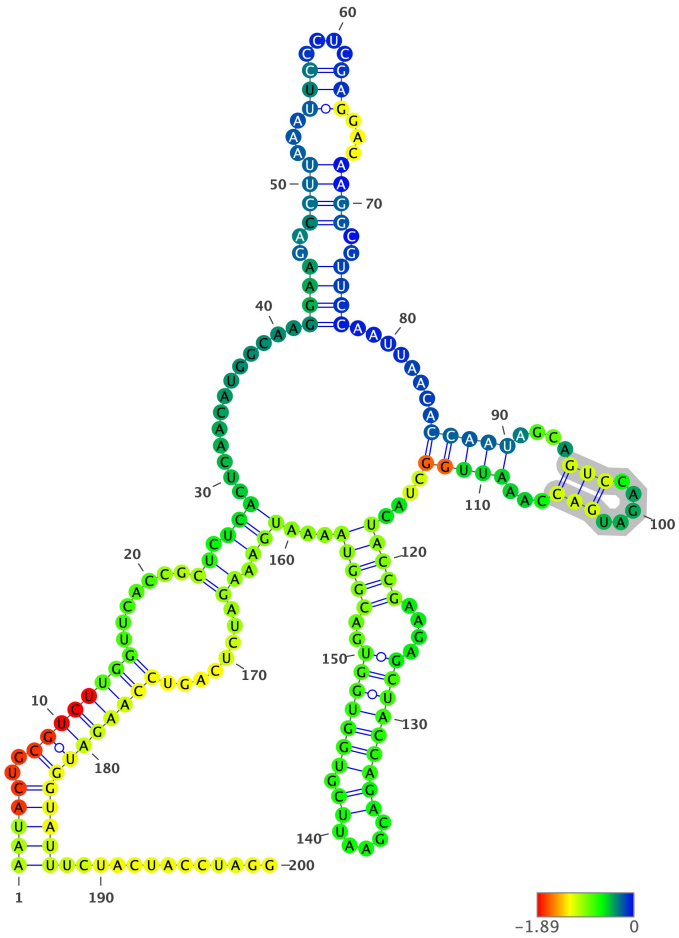
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 484 from nt 28509 to 28519 (nt 95 to 105)

```
5'-GUCCAGAUGAC-3'
5'-(((.....)))-3'
Motif MFE = 0.0; z-score = 0.29; 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 28415 to 28614 (motif highlighted in silver):

```
5'-AAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAUUAACACCAAUAGCAGUCCAGAUGACCAAAUU
GGCUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGG-3
5'-(((((..((((((((.......((.(((.............((((..((((...(((....)))...))))..))))........(((((....(((.....)))...)))
))....(((((....((((((((.....)).)))))))..)))))...))).)).......))))))))))))).............-3'
MFE = -43.3; z-score = -0.05; ED = 23.82
```

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_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']

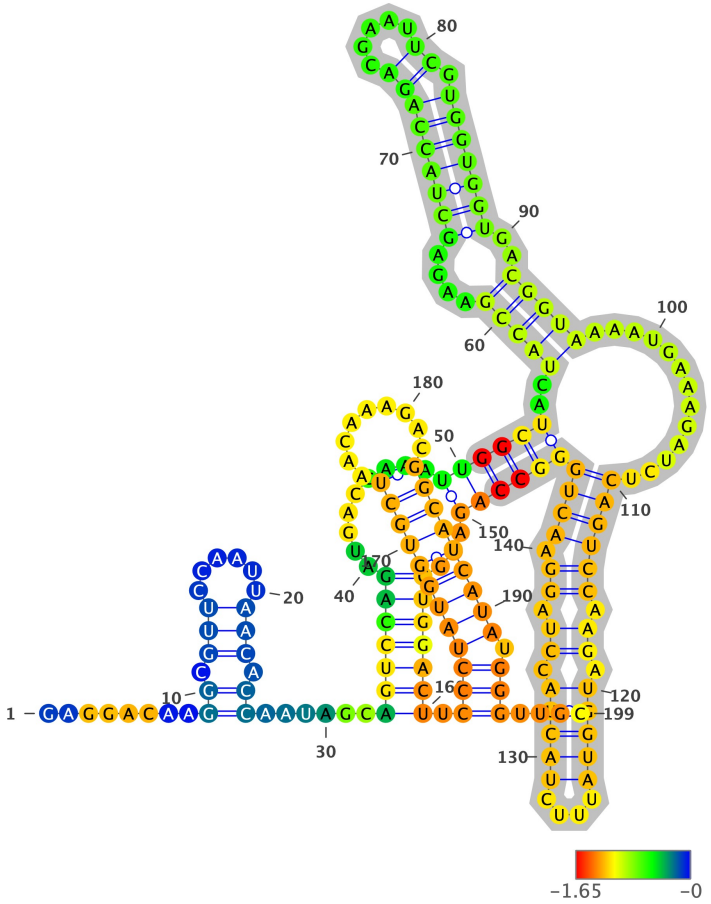
3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

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 485 from nt 28526 to 28623 (nt 51 to 148)

```
5'-GGCUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCC-3'

5'-((.......................................................((((((....(((((....)))))....)).)))))..))-3'
Motif MFE = -28.8; z-score = -2.38; ED = 8.35
```



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 28476 to 28674 (motif highlighted in silver):

```
5'-GAGGACAAGGCGUUCCAAUUAACACCAAUAGCAGUCCAGAUGACCAAAUUGGCUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCA
GUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGC-3
5'-........((.(((......))).))......(((((((.........((((((..(((((....(((((((((.....)).)))))))..)))))..............((
((((.((.(((((....)))))).)).)).))))))))))...)))))))).((((((((((((.........))))))))).)))....-3'
MFE = -57.6; z-score = -2.14; ED = 15.19
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

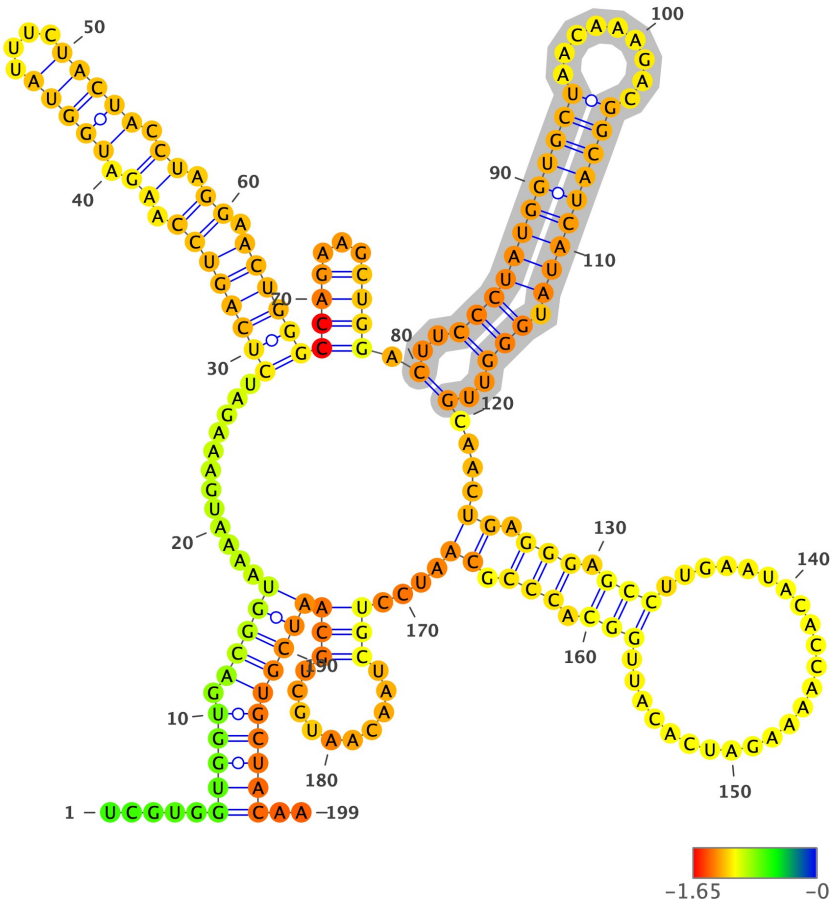
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 486 from nt 28634 to 28673 (nt 80 to 119)

```
5'-CUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUG-3'
5'-(..((((((((((((.........))))))))).)))..)-3'
Motif MFE = -14.5; z-score = -3.25; 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 = -1.42; 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(+)

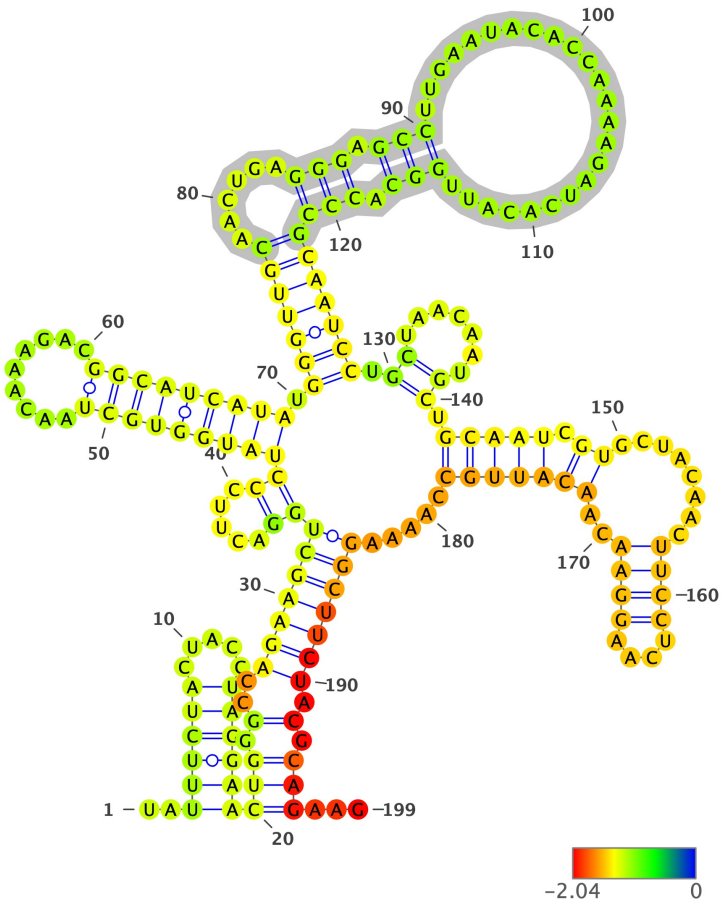
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 487 from nt 28674 to 28719 (nt 77 to 122)

```
5'-CAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCG-3'
5'-(......(((.(((.......................))).))))-3'
Motif MFE = -8.5; z-score = -1.28; ED = 2.33
```



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 28598 to 28796 (motif highlighted in silver):

```
5'-UAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCAC
AUUGGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAG-3
5'-..((((((.....))))))(((.(..((((((((((.....))(((((((((.........)))))))))).(((((((......(((.(((.....................
...))).))))))))))).((.......)).(((((.((........((((....))))..)))))))).....)))))))).).)))...-3'
MFE = -46.9; z-score = -1.32; ED = 35.52
```

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_gp10, 28274-29533(+)

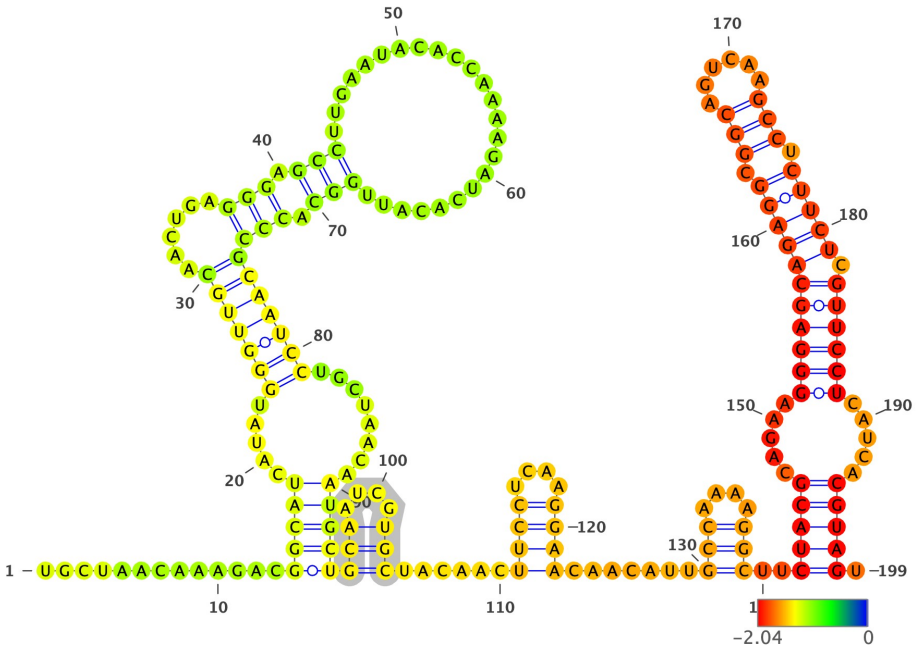
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 488 from nt 28739 to 28748 (nt 95 to 104)

```
5'-GCAAUCGUGC-3'
5'-(((....)))-3'
Motif MFE = -0.2; z-score = -0.62; 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 = -1.71; 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(+)

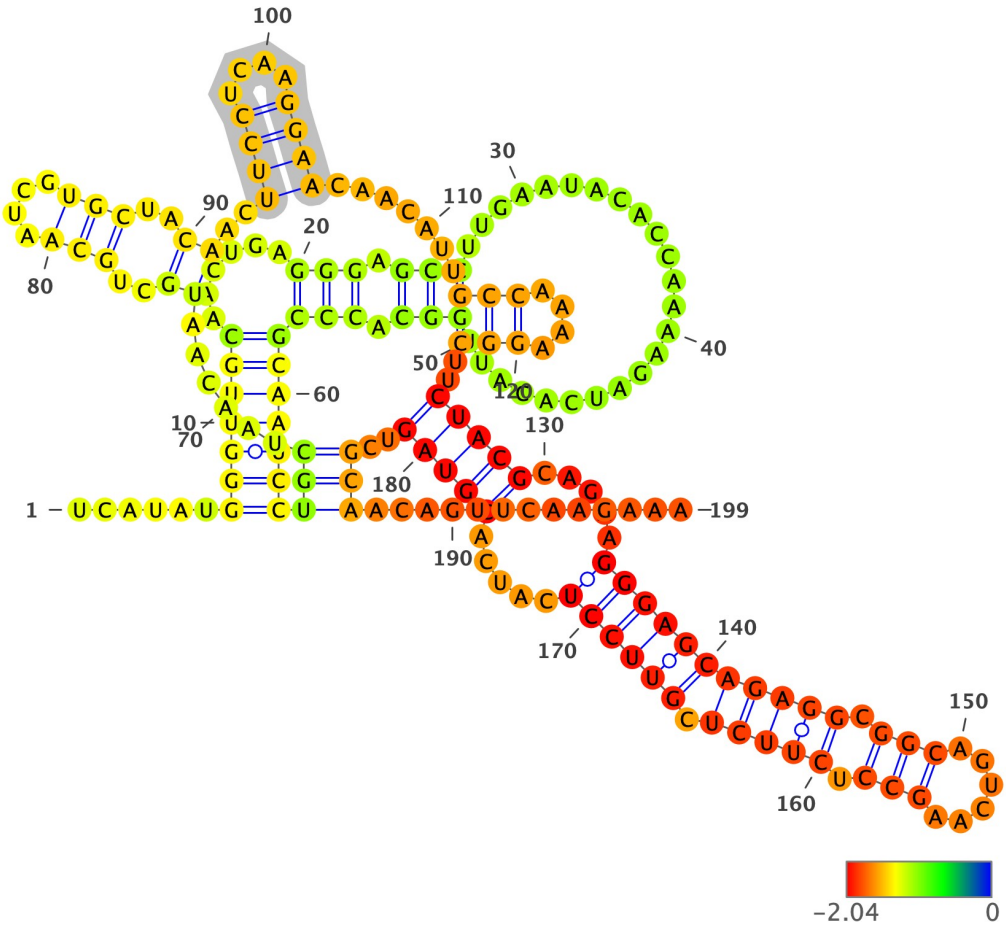
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 489 from nt 28755 to 28766 (nt 94 to 105)

```
5'-UUCCUCAAGGAA-3'
5'-((((....))))-3'
Motif MFE = -1.6; z-score = -5.35; 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 = -1.72; 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(+)

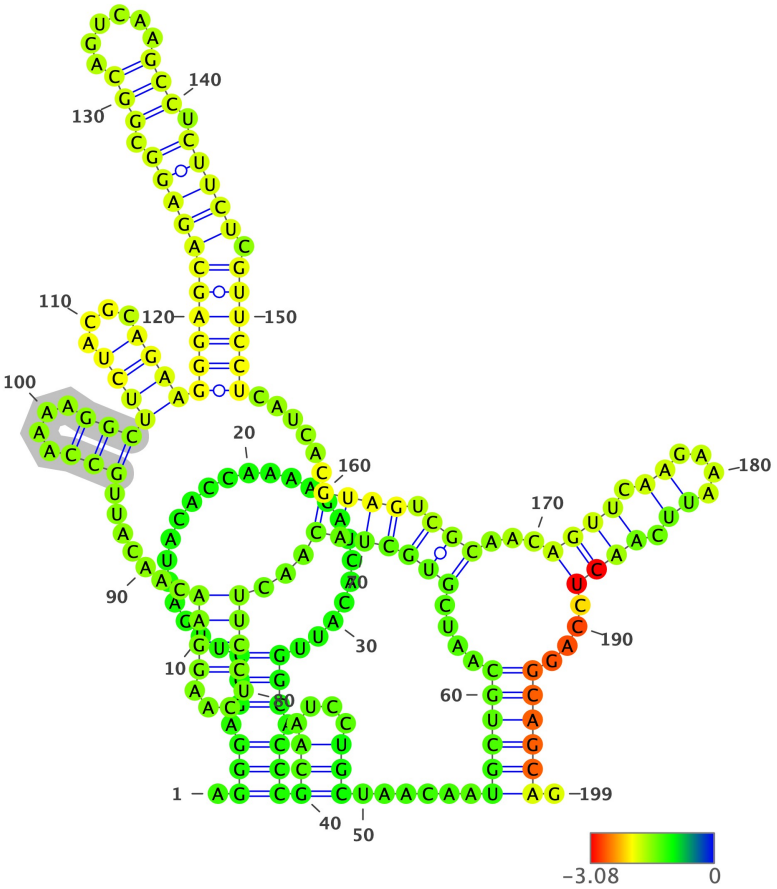
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 490 from nt 28774 to 28783 (nt 95 to 104)

```
5'-GCCAAAAGGC-3'
5'-(((....)))-3'
Motif MFE = -2.6; z-score = -9.73; 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 = -2.16; 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(+)

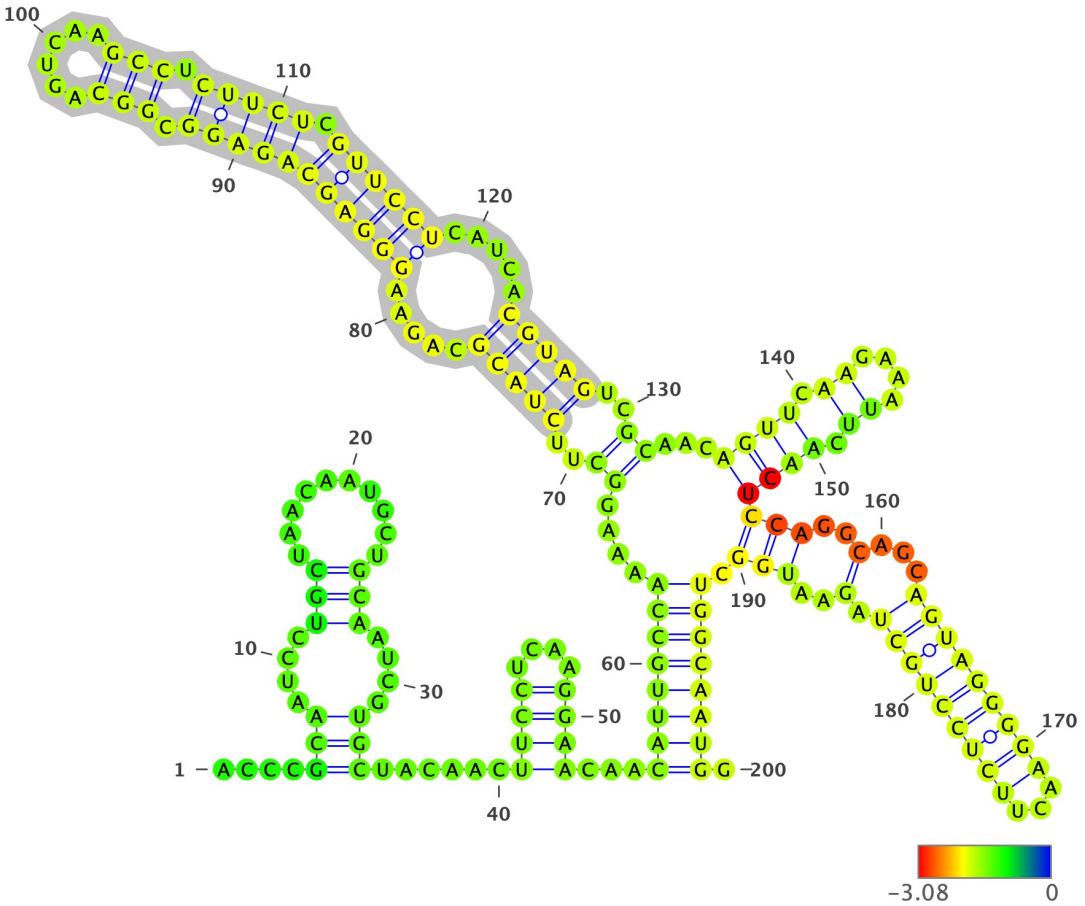
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 491 from nt 28786 to 28842 (nt 72 to 128)

```
5'-CUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAG-3'
5'-(((((.....((((((((((.(((......))).)))))).)))))).....)))))-3'
Motif MFE = -24.0; z-score = -3.09; 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 = -2.64; 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(+)

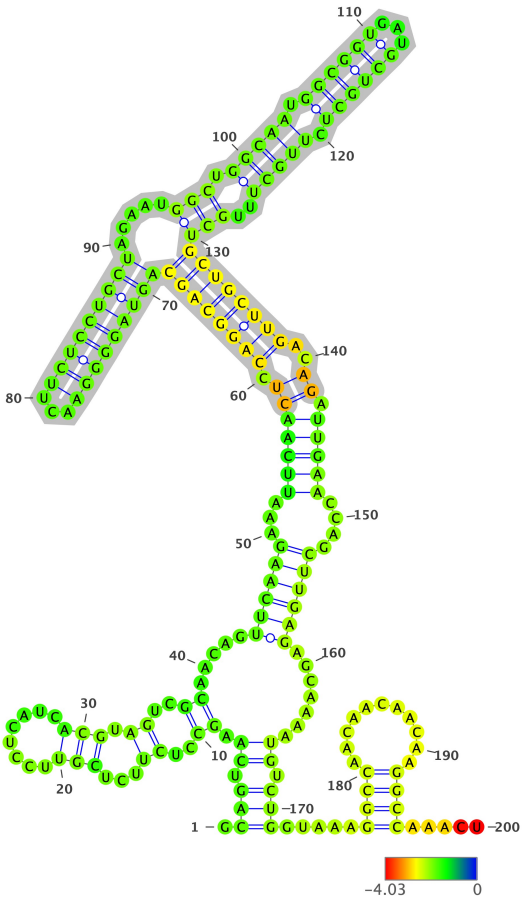
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 492 from nt 28866 to 28950 (nt 58 to 142)

```
5'-CUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAG-3'
5'-((.(((((((((((((((.....))))))))).....(((.(((((.((((((...)))))).)))))..))))))))))))..))-3'
Motif MFE = -39.4; z-score = -4.17; ED = 9.29
```



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 28809 to 29008 (motif highlighted in silver):

```
5'-GCAGUCAAGCCUCUUCUCGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAAUUCAACUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUG
AUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAAACU-3
5'-.(((.((.((..((...(((.........))).))..)).....((((((...(((((((.((((((((((((((((...)))))))))).....(((.(((((.((((((.
..)))))).)))))..))))))))))))..)).)))))....))))))........)).)))).....((((...........))))).....-3'
MFE = -59.2; z-score = -1.98; ED = 26.67
```

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_gp10, 28274-29533(+)

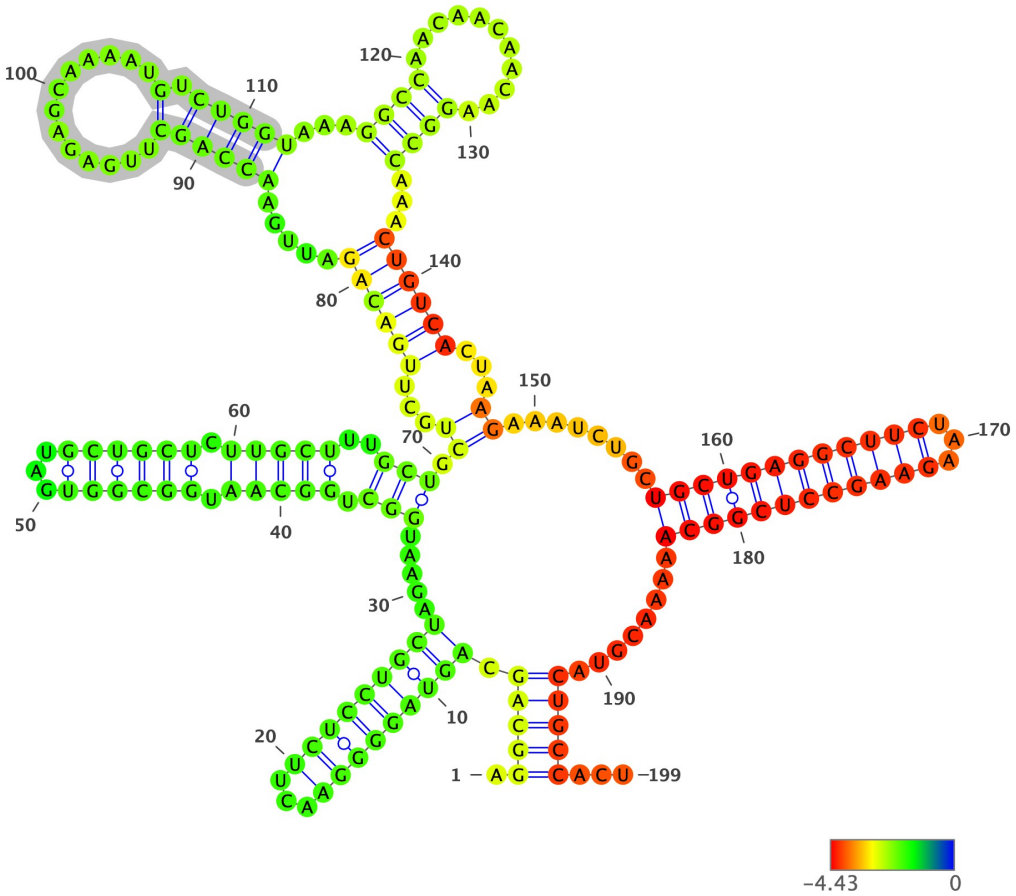
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 493 from nt 28957 to 28980 (nt 88 to 111)

```
5'-CCAGCUUGAGAGCAAAAUGUCUGG-3'
5'-(((((.............).))))-3'
Motif MFE = -2.4; z-score = 0.3; ED = 4.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28870 to 29068 (motif highlighted in silver):

```
5'-AGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGG
UAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACU-3
5'-.(((((.((((((((((...)))))))))).....(((.(((((.((((((...)))))).)))))..))).((...((((((.....((((((.............).))))
)...((((...........))))...))))))...))........((((((((((((...)))))))))))).........)))))...-3'
MFE = -74.5; z-score = -4.05; ED = 16.01
```

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_gp10, 28274-29533(+)

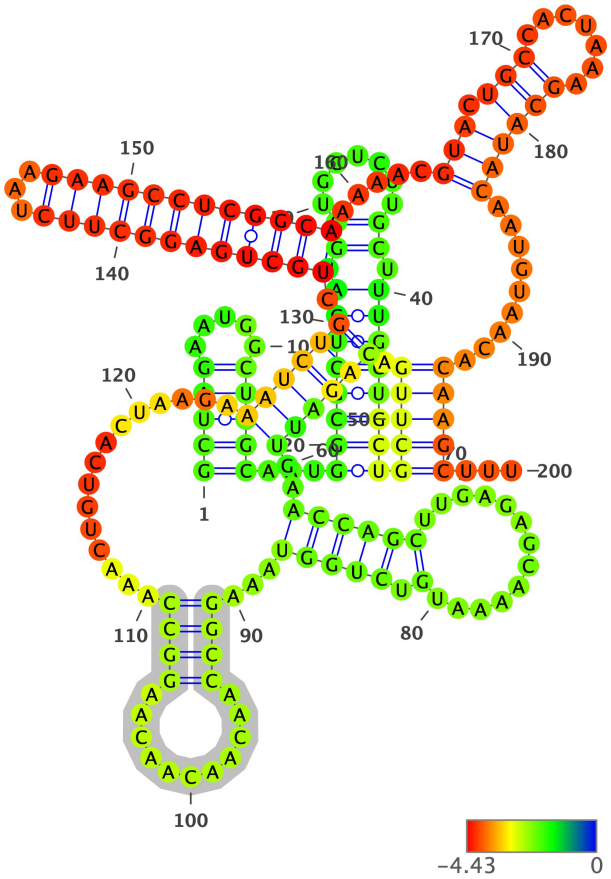
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 494 from nt 28985 to 29003 (nt 91 to 109)

```
5'-GGCCAACAACAACAAGGCC-3'
5'-((((...........))))-3'
Motif MFE = -4.9; z-score = -4.41; 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 = -3.37; 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(+)

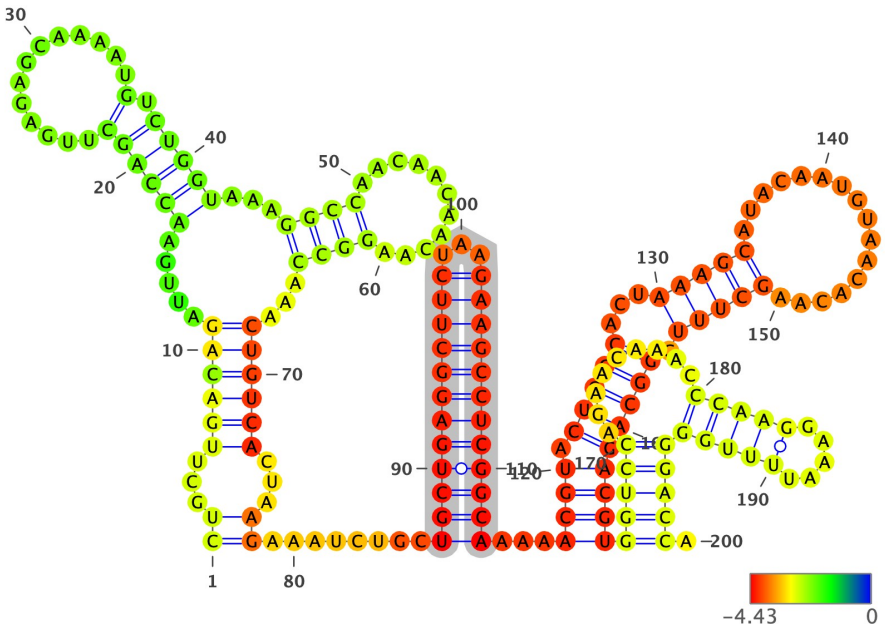
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 495 from nt 29026 to 29052 (nt 87 to 113)

```
5'-UGCUGAGGCUUCUAAGAAGCCUCGGCA-3'
5'-(((((((((((...)))))))))))-3'
Motif MFE = -19.7; z-score = -6.33; ED = 0.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28940 to 29139 (motif highlighted in silver):

```
5'-CUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGGUAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGG
CAAAAACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCA-3
5'-((...((((((.....((((((.............).)))))...((((...........))))...))))))...)).........(((((((((((...)))))))))))
))...((((.(((((...(((((................))))).))))))))))(((((.........(((((.....)))))))))).-3'
MFE = -63.7; z-score = -4.73; 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(+)

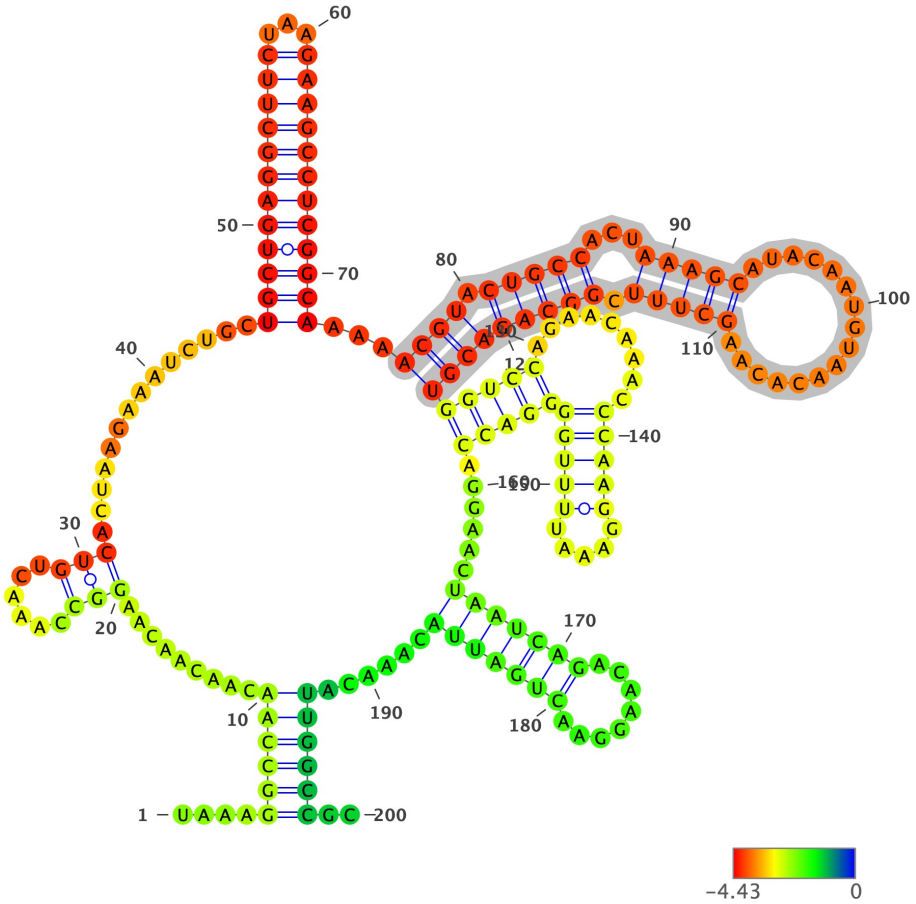
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 496 from nt 29056 to 29104 (nt 76 to 124)

```
5'-ACGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGU-3'
5'-((((.(((((...(((((................))))).)))))))))-3'
Motif MFE = -14.6; z-score = -3.63; 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 = -5.14; 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(+)

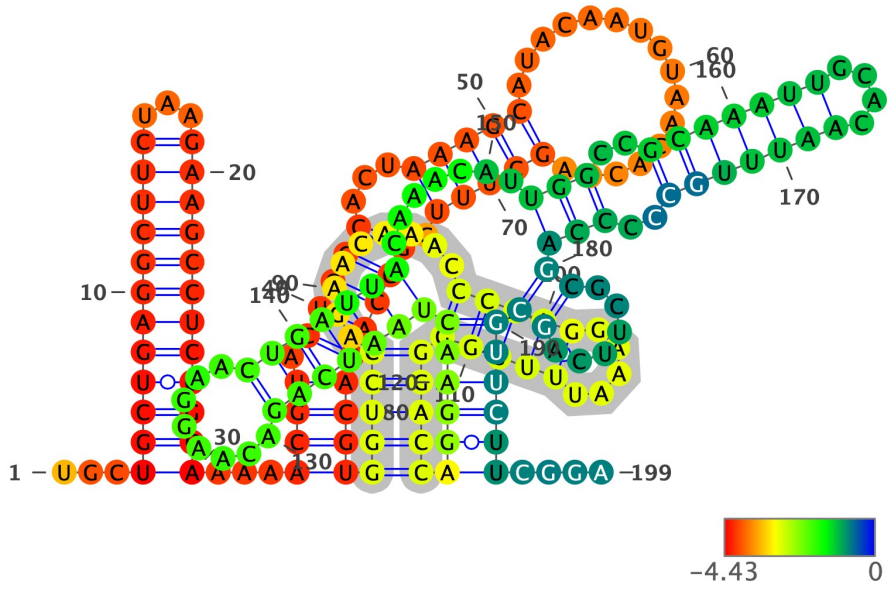
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 497 from nt 29105 to 29138 (nt 83 to 116)

```
5'-GGUCCAGAACAAACCCAAGGAAAUUUUGGGGACC-3'
5'-(((((.........((((.......)))))))))-3'
Motif MFE = -8.1; z-score = -1.65; 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 = -4.31; ED = 11.59
```

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_gp10, 28274-29533(+)

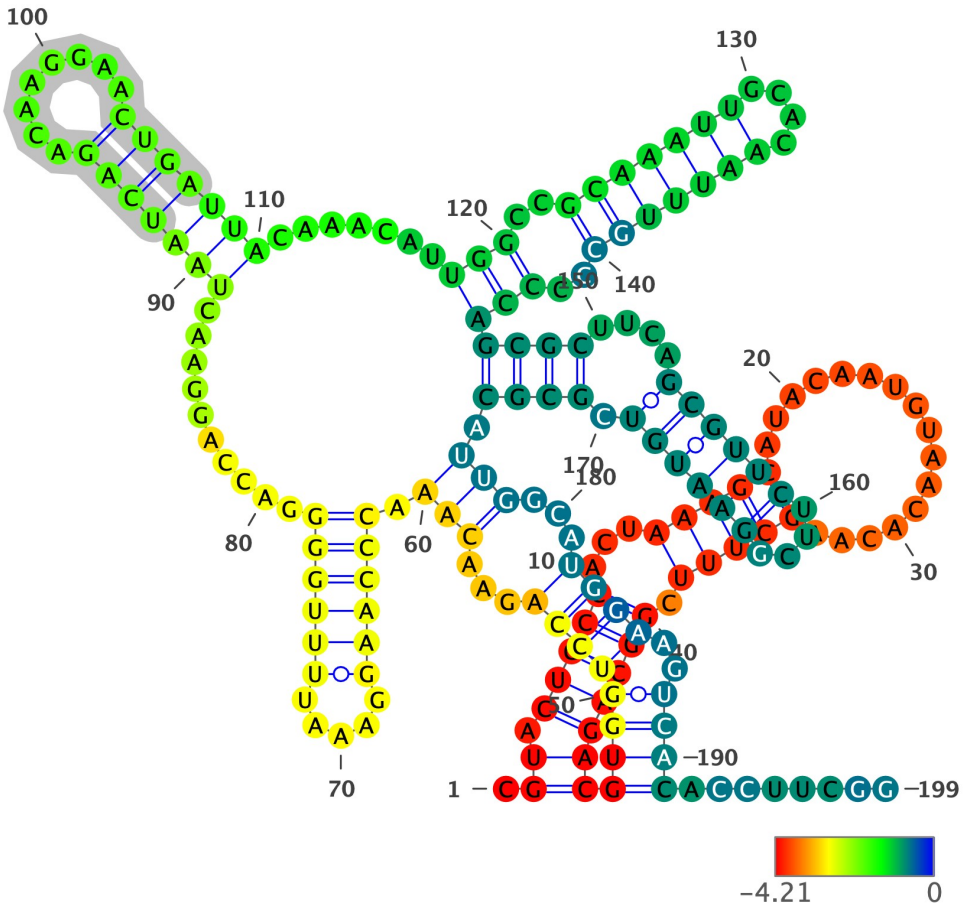
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 29148 to 29163 (nt 92 to 107)

```
5'-UCAGACAAGGAACUGA-3'
5'-((((........))))-3'
Motif MFE = -1.7; z-score = -1.9; ED = 0.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29057 to 29255 (motif highlighted in silver):

```
5'-CGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUAC
AAACAUUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGG-3
5'-.((.(((((...(((((.................))))).)))))))((((((((...(((.((((((.....))))))..........(((((((........)))))))).
......(((..(((((((....)))))))..)))((((....((((((....))))))).)))).)))...))))..))))........-3'
MFE = -53.1; z-score = -1.71; ED = 28.25
```

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_gp10, 28274-29533(+)

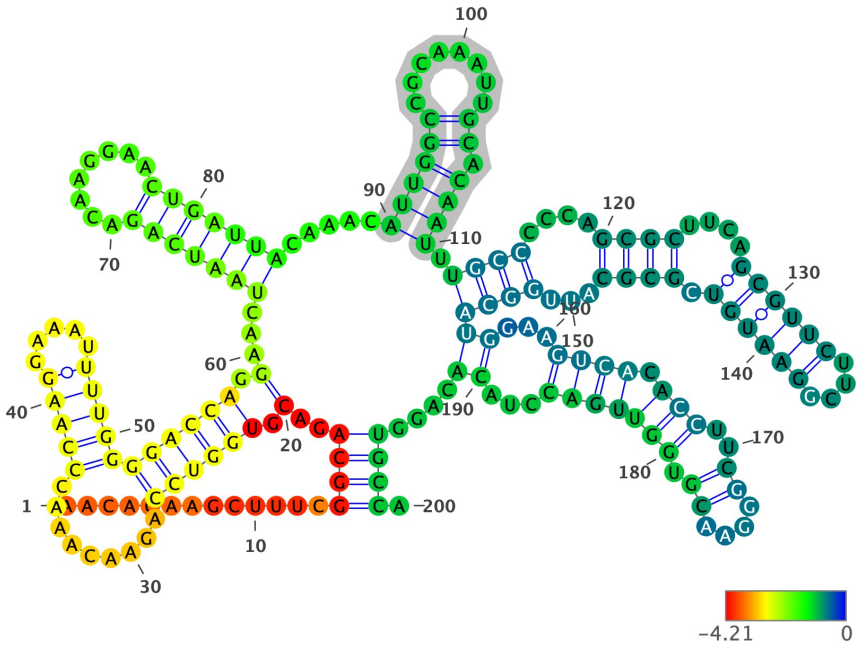
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 29172 to 29192 (nt 90 to 110)

```
5'-AUUGGCCGCAAAUUGCACAAU-3'
5'-((((((........)).))))-3'
Motif MFE = -1.8; z-score = -0.41; 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 29083 to 29282 (motif highlighted in silver):

```
5'-AACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUU
UGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCA-3
5'-............((((..(.((((((.........(((((.....)))))))))))).)...(((((((.......)))))))).....((((((........)).)))).
((((....((((....((((((....)))))).)))).....)))))((...((((.(((..((....)).)))))))...)).....)))).-3'
MFE = -51.8; z-score = -1.13; ED = 25.51
```

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_gp10, 28274-29533(+)

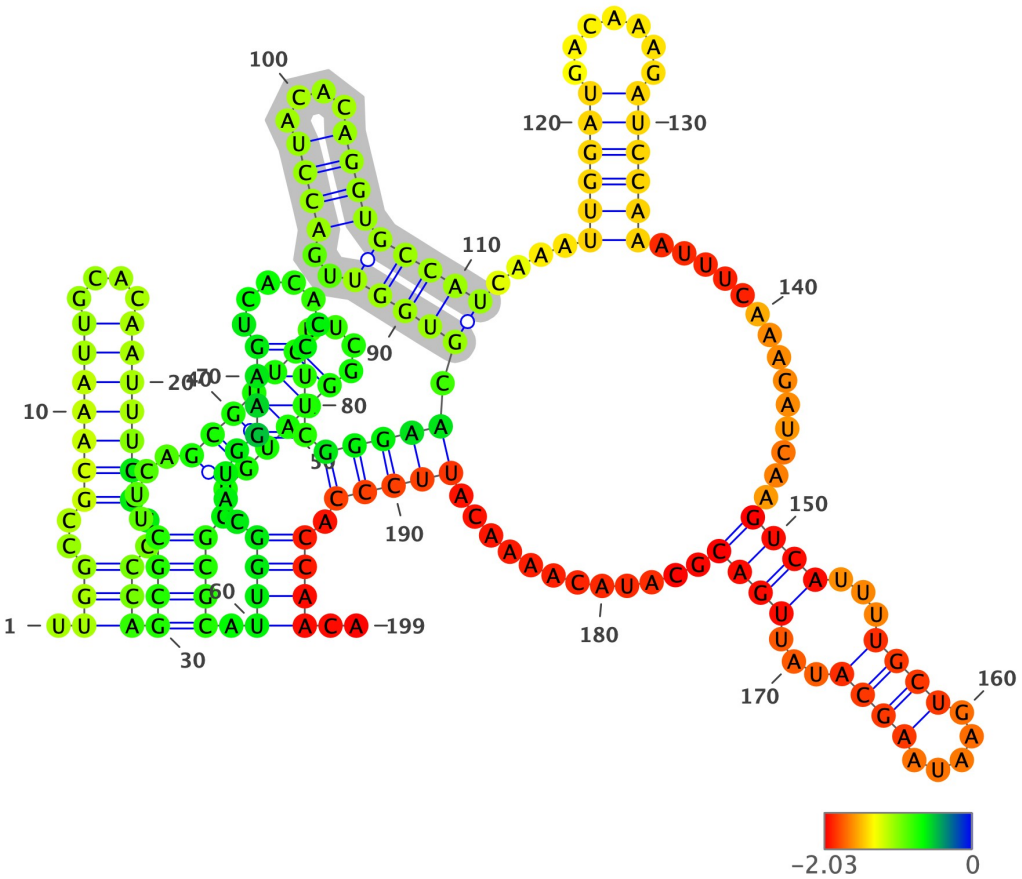
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 29260 to 29283 (nt 88 to 111)

```
5'-GUGGUUGACCUACACAGGUGCCAU-3'
5'-(((((..((((....)))))))))-3'
Motif MFE = -7.3; z-score = -2.41; 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 = -2.16; 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(+)

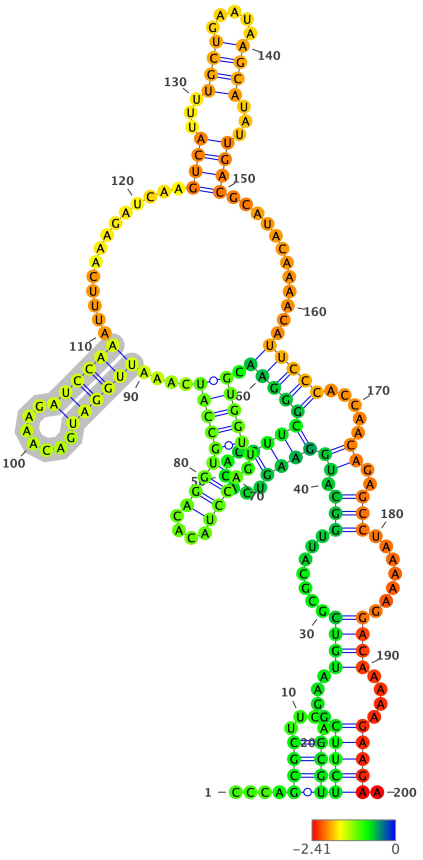
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 501 from nt 29288 to 29306 (nt 91 to 109)

```
5'-UUGGAUGACAAAGAUCCAA-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -3.92; 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 = -2.13; 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(+)

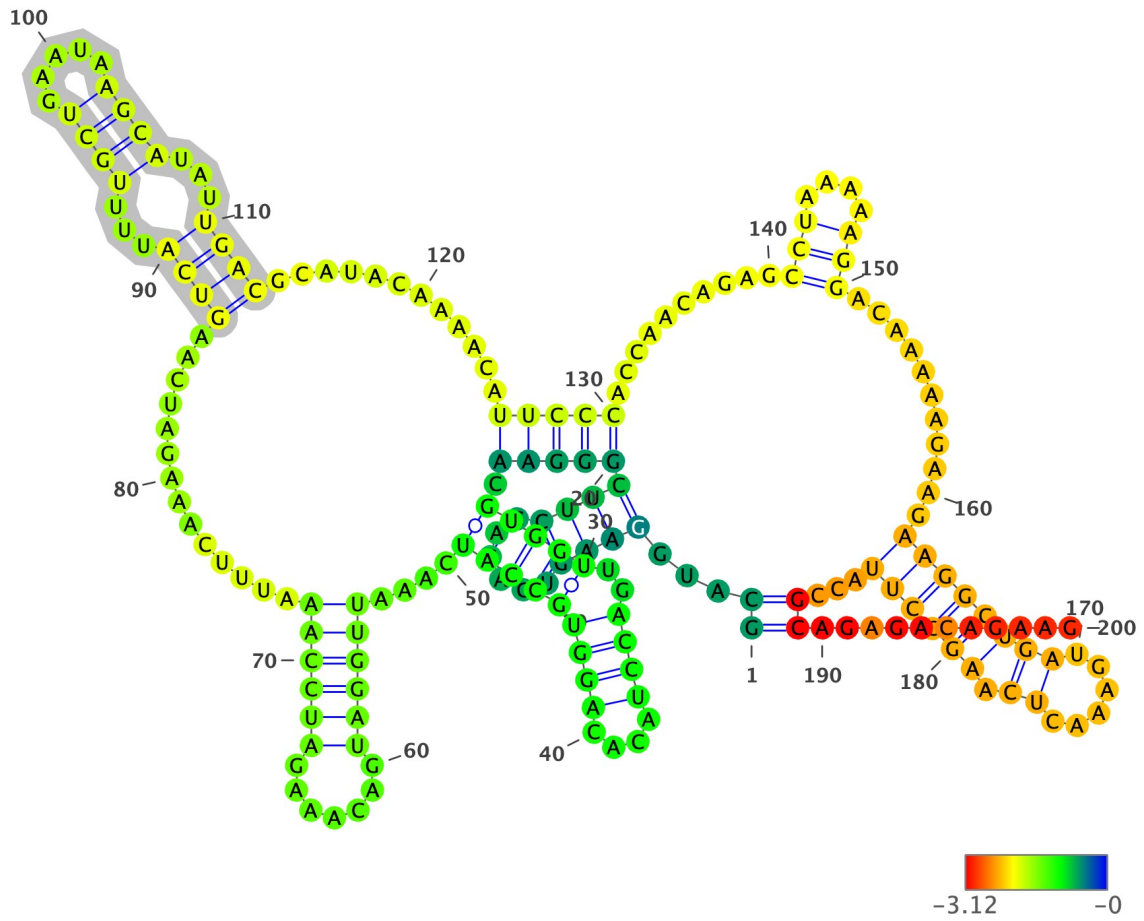
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 502 from nt 29321 to 29347 (nt 87 to 113)

```
5'-GUCAUUUUGCUGAAUAAGCAUAUUGAC-3'
5'-(((((...((((.....))))...)))))-3'
Motif MFE = -7.9; z-score = -3.64; 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 = -1.89; 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(+)

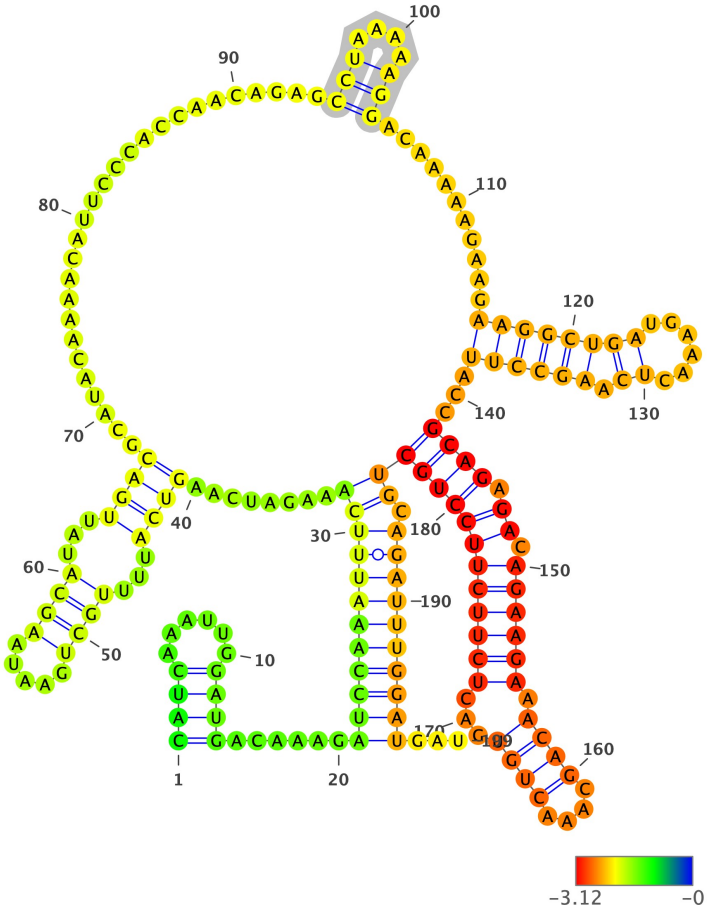
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 503 from nt 29375 to 29384 (nt 95 to 104)

```
5'-CCUAAAAAGG-3'
5'-((......))-3'
Motif MFE = -0.3; z-score = -9.58; 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 = -4.37; ED = 15.28
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

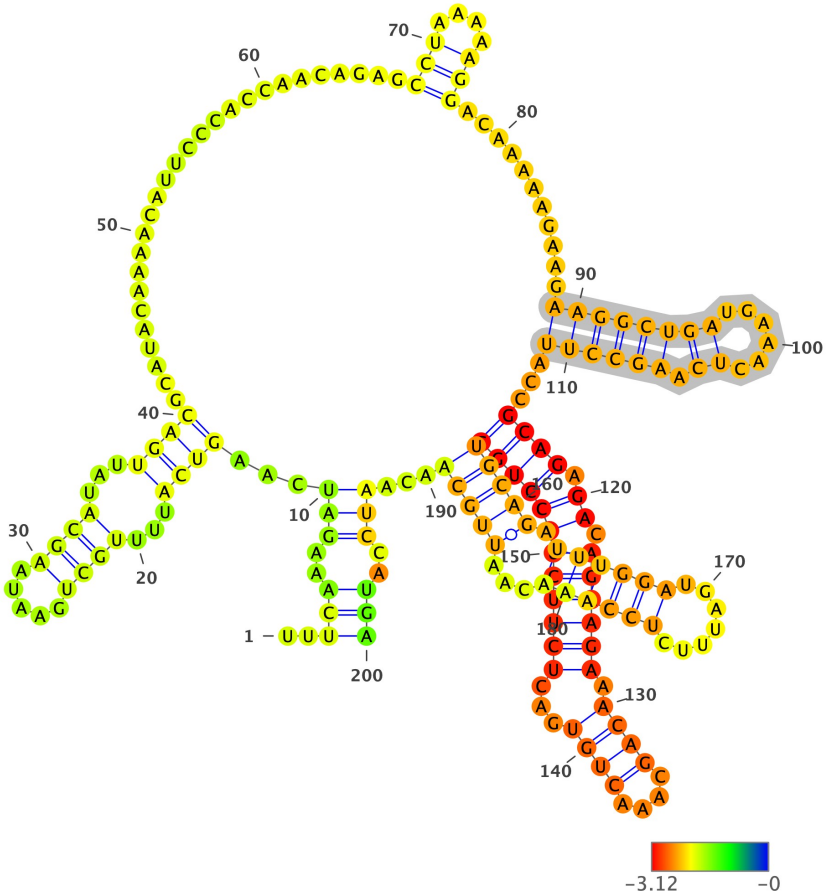
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 504 from nt 29396 to 29418 (nt 89 to 111)

```
5'-AAGGCUGAUGAAACUCAAGCCUU-3'
5'-((((((((......)).))))))-3'
Motif MFE = -6.9; z-score = -3.59; 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(+)

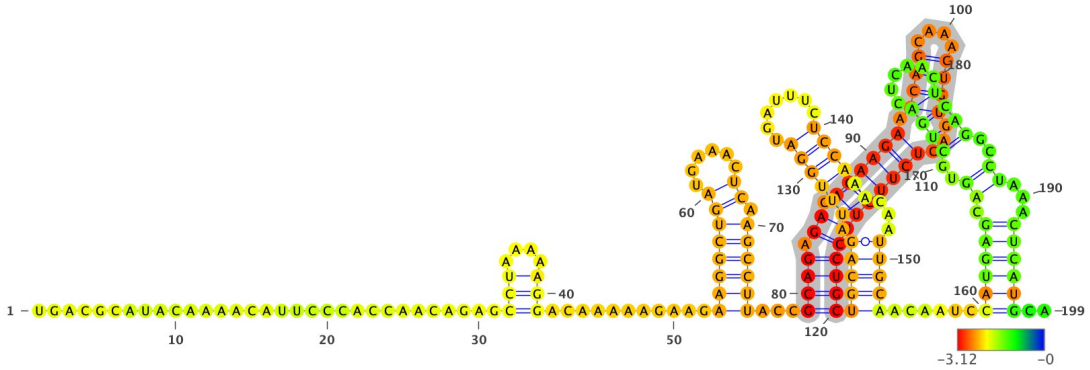
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 505 from nt 29422 to 29463 (nt 79 to 120)

```
5'-GCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGC-3'
5'-((((.((.(((((((.((((....))))...))))))))))))-3'
Motif MFE = -14.7; z-score = -4.27; 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 = -2.96; 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(+)

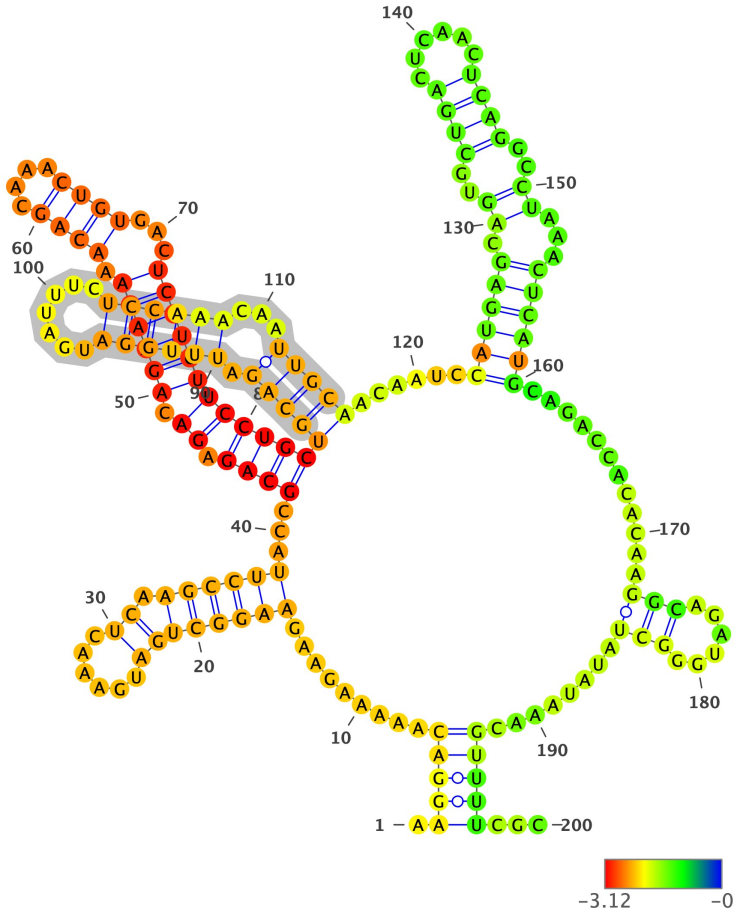
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 506 from nt 29465 to 29495 (nt 85 to 115)

```
5'-GCAGAUUUGGAUGAUUUCUCCAAACAAUUGC-3'
5'-((((....(((.......)))......))))-3'
Motif MFE = -6.3; z-score = -1.78; ED = 1.65
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29381 to 29580 (motif highlighted in silver):

```
5'-AAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAA
UUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGC-3
5'-.(((((.........((((((((......)).))))))...((((.((.((((((.((((....))))...))))))))))))(((((.((((((.......))))))...
)))))......((((((.((..((((......))))..))...))))))............(((......)))........)))))...-3'
MFE = -48.8; z-score = -2.55; ED = 29.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 153--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 153--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 178 to 200--gene, gene-GU280_gp11, 29558-29674(+)

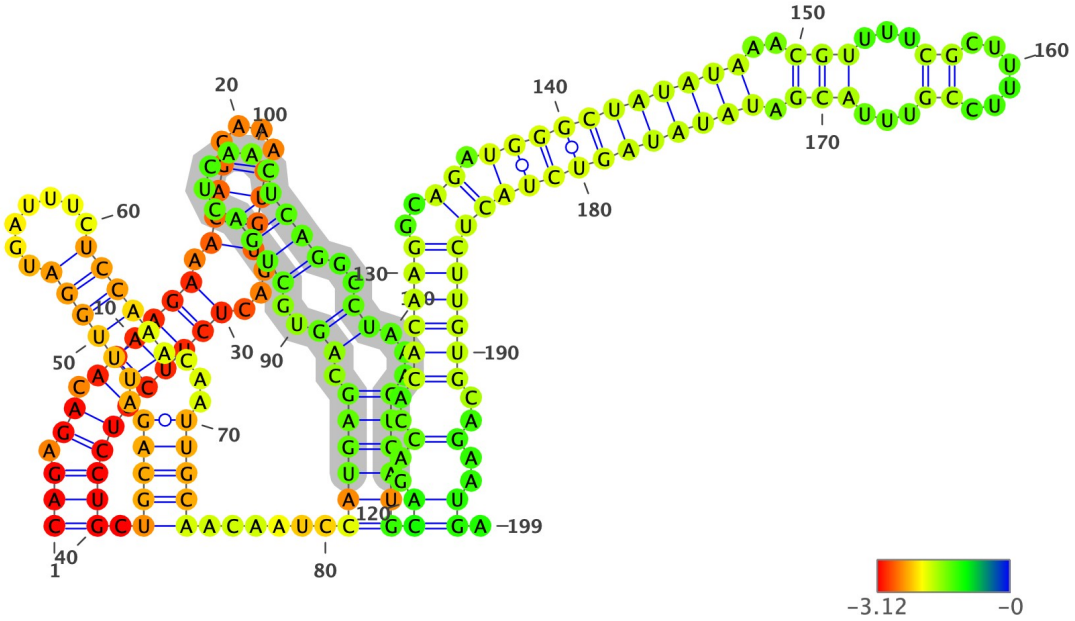
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 178 to 200--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

NC_045512.2 (forward strand): Structure number 507 from nt 29505 to 29538 (nt 83 to 116)

```
5'-UGAGCAGUGCUGACUCAACUCAGGCCUAAACUCA-3'
5'-((((..(..((((......))))..)....))))-3'
Motif MFE = -7.0; z-score = -2.01; ED = 2.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29423 to 29621 (motif highlighted in silver):

```
5'-CAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAA
ACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGA-3
5'-(((.((.((((((.((((....))))...)))))))))))).(((((.((((((.......))))))...)))))......((((((.((..((((......))))..))..
.))))))((..(..((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))..)..)).-3'
MFE = -53.2; z-score = -3.23; ED = 12.25
```

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 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(+)

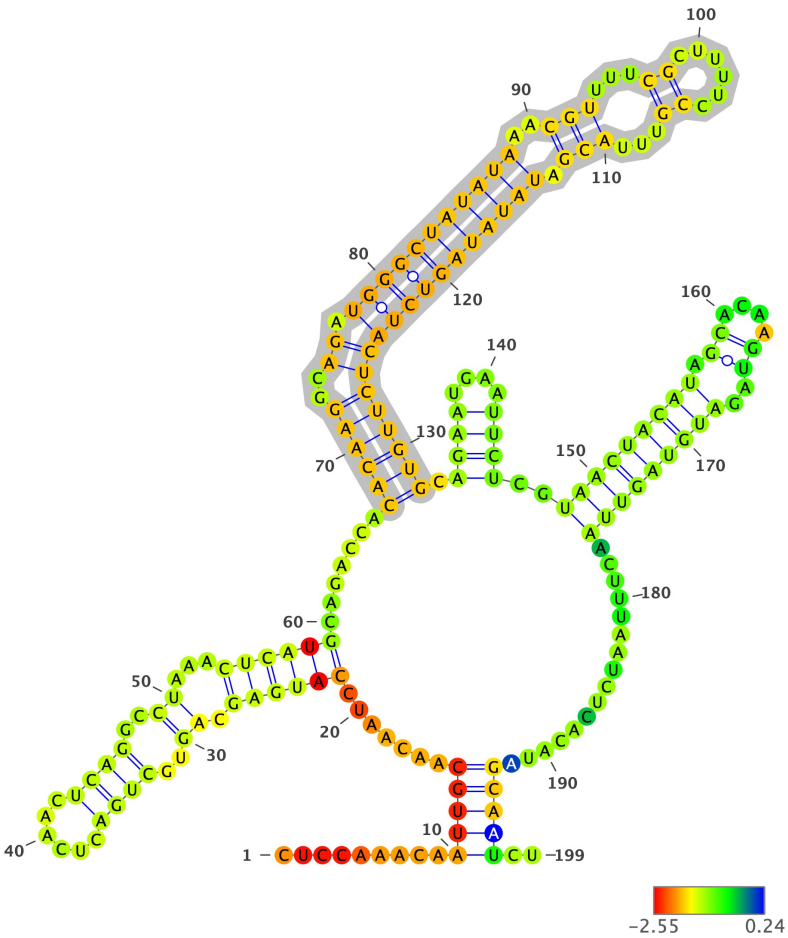
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

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 508 from nt 29548 to 29613 (nt 67 to 132)

```
5'-CACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUG-3'
5'-((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))-3'
Motif MFE = -19.7; z-score = -3.15; 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 = -3.23; 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(+)

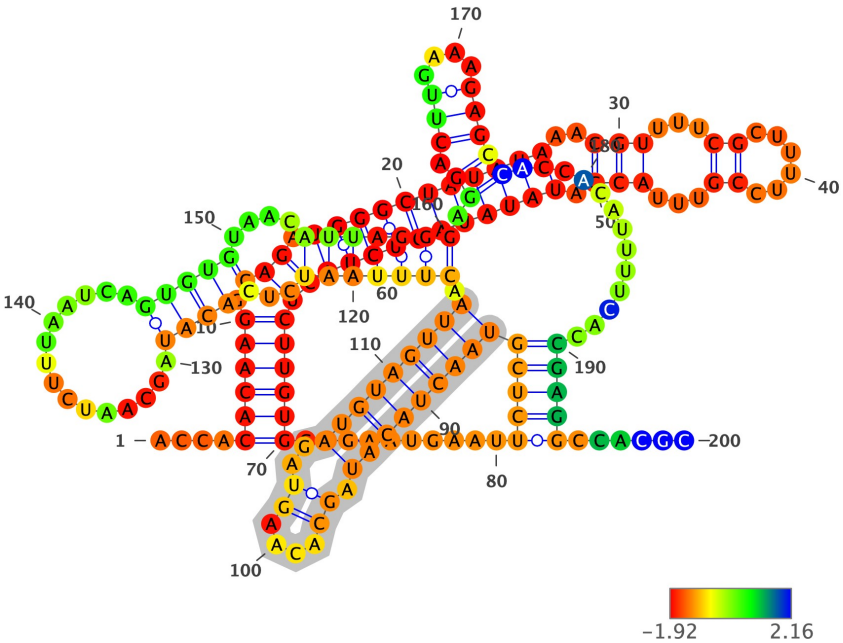
Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

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 509 from nt 29629 to 29657 (nt 86 to 114)

```
5'-UAACUACAUAGCACAAGUAGAUGUAGUUA-3'
5'-(((((((((..........)))))))))-3'
Motif MFE = -8.5; z-score = -3.89; 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 = -1.24; 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 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"]