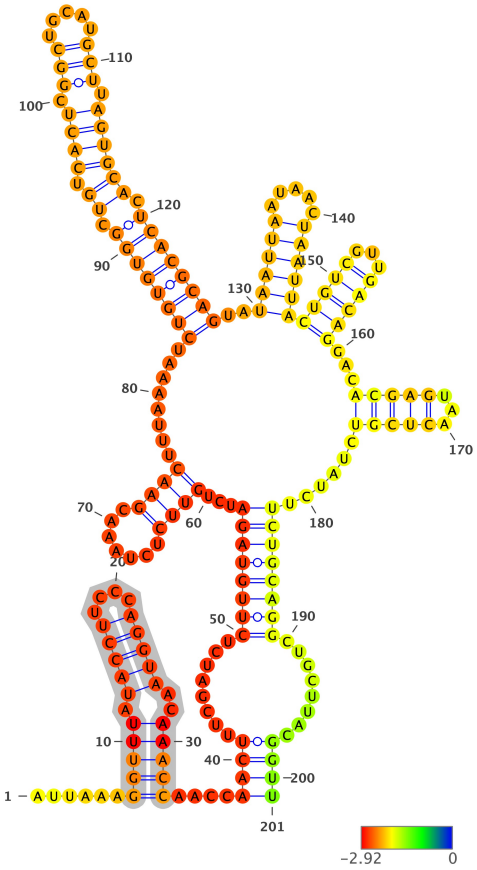
NC_045512.2 (forward strand): Structure number 1 from nt 7 to 33 (nt 7 to 33)

```
5'-GGTTTATACCTTCCCAGGUAACAAACC-3'
5'-(((...(((((....)))))....)))-3'
Motif MFE = -7.0; z-score = -3.41; 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 = -2.76; ED = 24.64
```

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

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

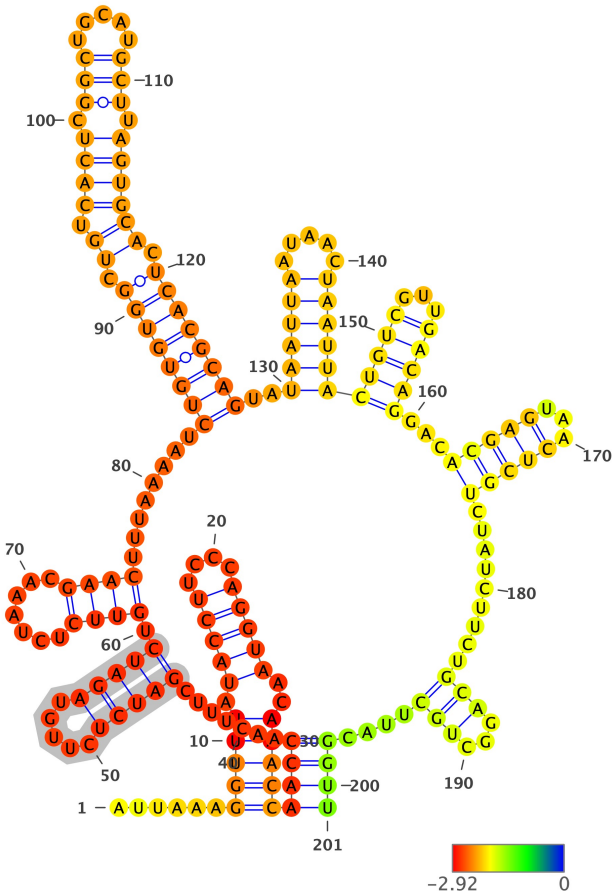
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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

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

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

```
5'-GATCTCTTGTAGAUC-3'
5'-(((((.....)))))-3'
Motif MFE = -2.3; z-score = -2.0; 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 = -2.87; ED = 20.48
```

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

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

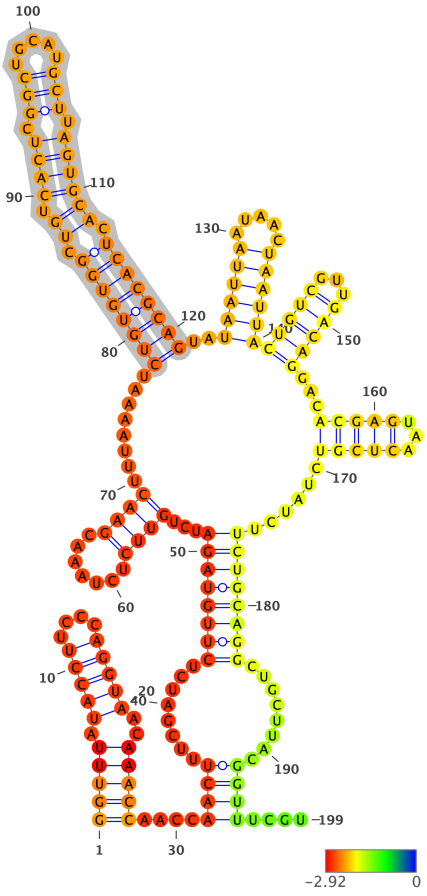
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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

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

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

```
5'-CTGTGTGGCTGTCACTCGGCTGCATGCUTAGUGCACUCACGCAG-3'
5'-((((((((.((.((((.(((.....)).)))))).))))))))-3'
Motif MFE = -20.1; z-score = -3.73; 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 = -2.46; ED = 25.51
```

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

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

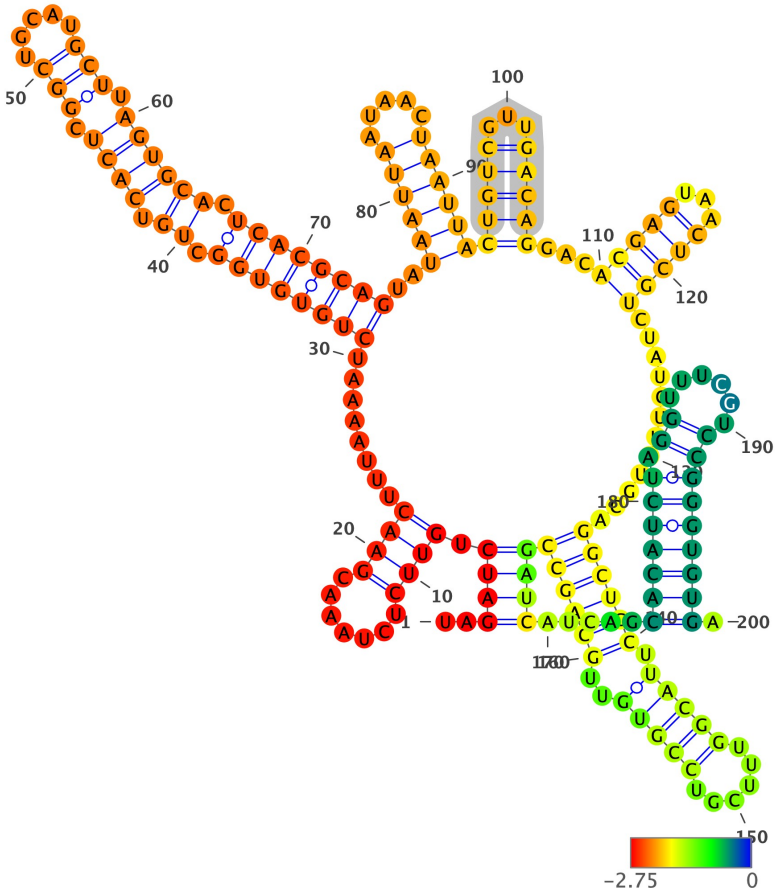
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

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

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

NC_045512.2 (forward strand): Structure number 4 from nt 148 to 158 (nt 95 to 105)

```
5'-TGTCGTTGACA-3'
5'-((.......))-3'
Motif MFE = -0.8; z-score = -3.86; ED = 1.2
```



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

Extracted structure model with flanking nucleotides 54 to 253 (motif highlighted in silver):

```
5'-UAGAUCUGUUCUCUAAACGAACUUUAAAAUCUGUGUGGCUGUCACUCGGCUGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACAC
GAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGCAGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGA-3
5'-..((((.((((.......)))).........((((((((.((.((((.(((.....))).)))))).)))))))..((((((.....))))))(((((...)))))...((
(((...)))))............((((((.(((((......)))))..))))))))))).....(((((((.((......)))))))))).-3'
MFE = -66.3; z-score = -3.55; ED = 8.53
```

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

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

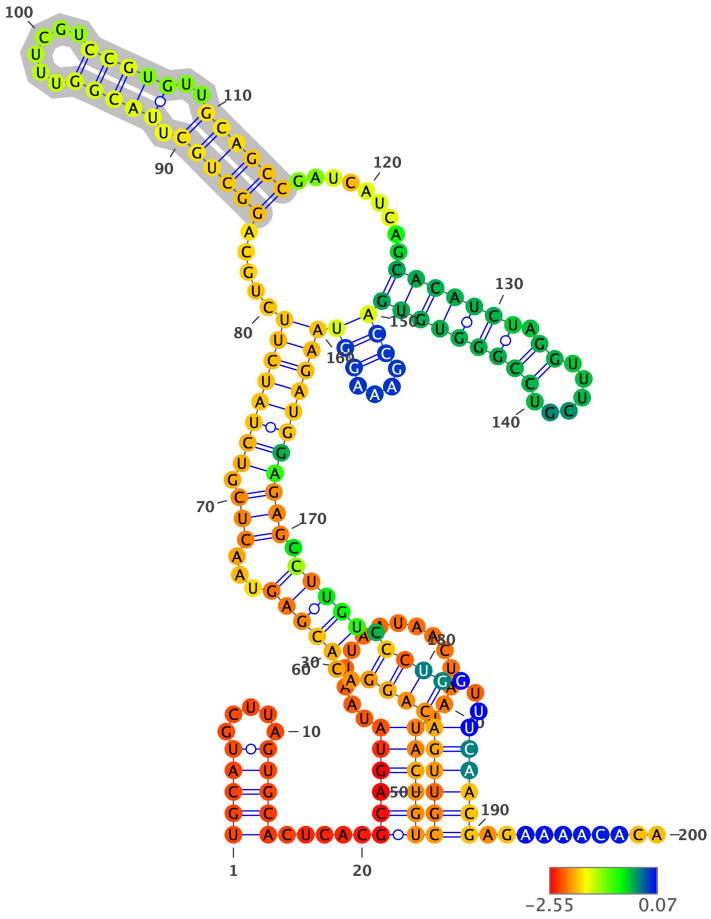
Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--five_prime_UTR, id-NC_045512.2:1..265, 1-265(+)

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

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

```
5'-GGCTGCTTACGGTTTCGTCCGTGTTGCAGCC-3'
5'-((((((...(((......)))....)))))))-3'
Motif MFE = -17.2; z-score = -4.2; ED = 0.19
```



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

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

```
5'-UGCAUGCUUAGUGCACUCACGCAGUAUAAUUAAUAACUAAUUACUGUCGUUGACAGGACACGAGUAACUCGUCUAUCUUCUGCAGGCUGCUUACGGUUUCGUCCGUGUUGC
AGCCGAUCAUCAGCACAUCUAGGUUUCGUCCGGGUGUGACCGAAAGGUAAGAUGGAGAGCCUUGUCCCUGGUUUCAACGAGAAAACACA-3
5'-(((((.....)))))).....((((((..............))))))((((((((((..((((((...(((.(((((((((.....((((((.(((((......)))))).))
))))).........(((((((.((......))))))))))(((....)))))))))))))).)))))...))))))..........-3'
MFE = -66.1; z-score = -3.43; ED = 13.42
```

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

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

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

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

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

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

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

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

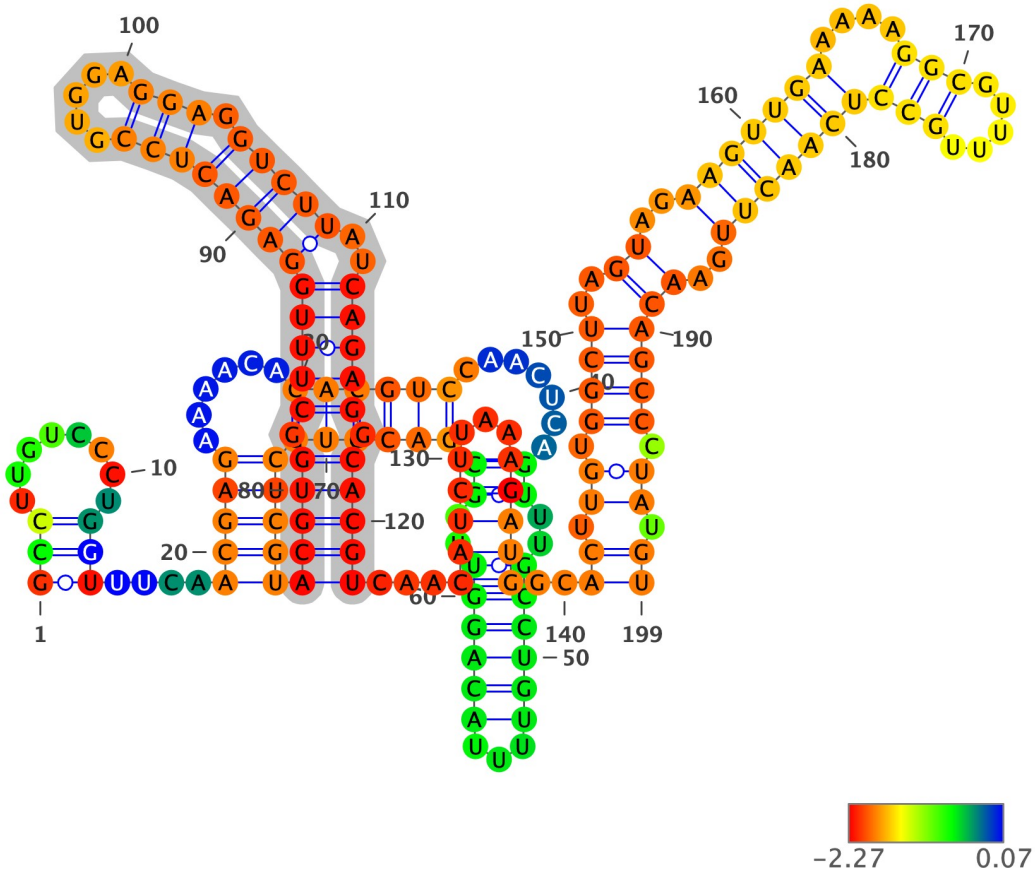
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-ACGTGGCTTTGGAGACTCCGTGGAGGAGGUCUUATCAGAGGCACGU-3'
5'-(((((.(((((((((((((.....))).)))))..)))))).)))))-3'
Motif MFE = -22.1; z-score = -3.94; 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 = -1.48; ED = 15.68
```

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

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

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

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

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

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

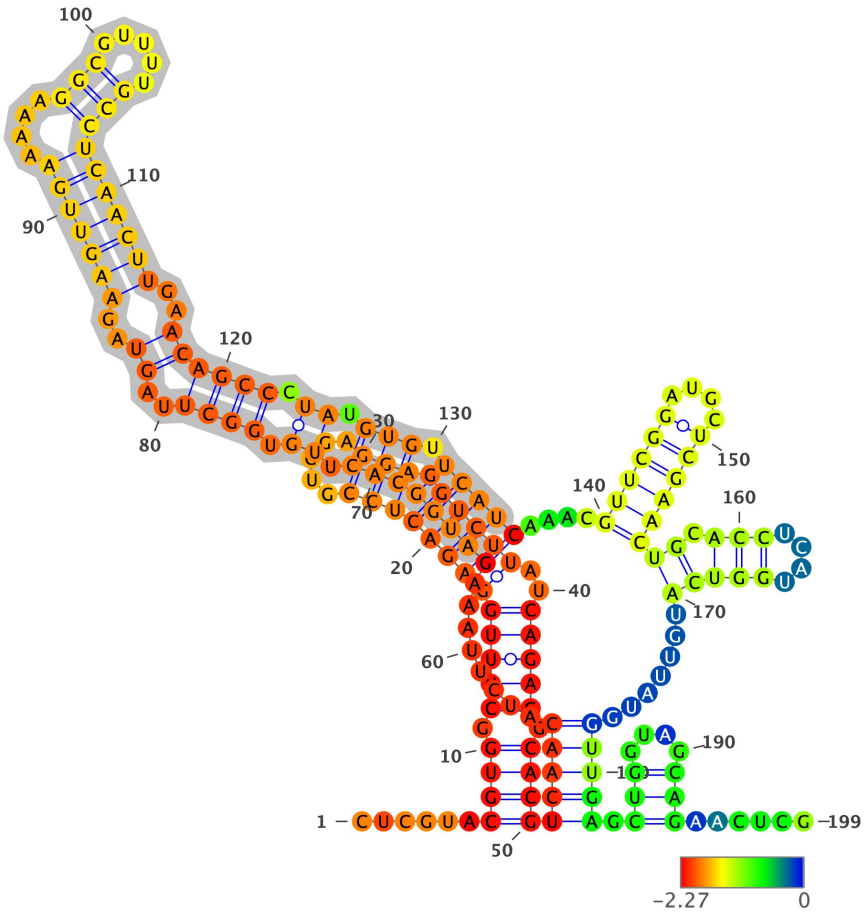
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 7 from nt 408 to 477 (nt 65 to 134)

```
5'-ATGGCACTTGTGGCTTAGTAGAAGTTGAAAAAGGCGTTTTGCCUCAACUTGAACAGCCCUATGUGTUCAU-3'
5'-(((((((.((.((((..((...((((((....(((.....)))))))))...)))))).)).))).))))-3'
Motif MFE = -21.8; z-score = -3.24; ED = 5.84
```



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

Extracted structure model with flanking nucleotides 344 to 542 (motif highlighted in silver):

```
5'-CUCGUACGUGGCUUUGGAGACUCCGUGGAGGAGGUCUUAUCAGAGGCACGUCAACAUCUUAAAGAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAA
CUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCG-3
5'-......((((.(((((((((((((.....))).)))))..)))))).))))(((((........((((((((.((.((((..((..(((((((....(((.....)))))))
)))..)))))).)).))).)))))....((((((....))))))((.(((....)))))).......)))))).(((....))).....-3'
MFE = -62.0; z-score = -1.61; ED = 26.18
```

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

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

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

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

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

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

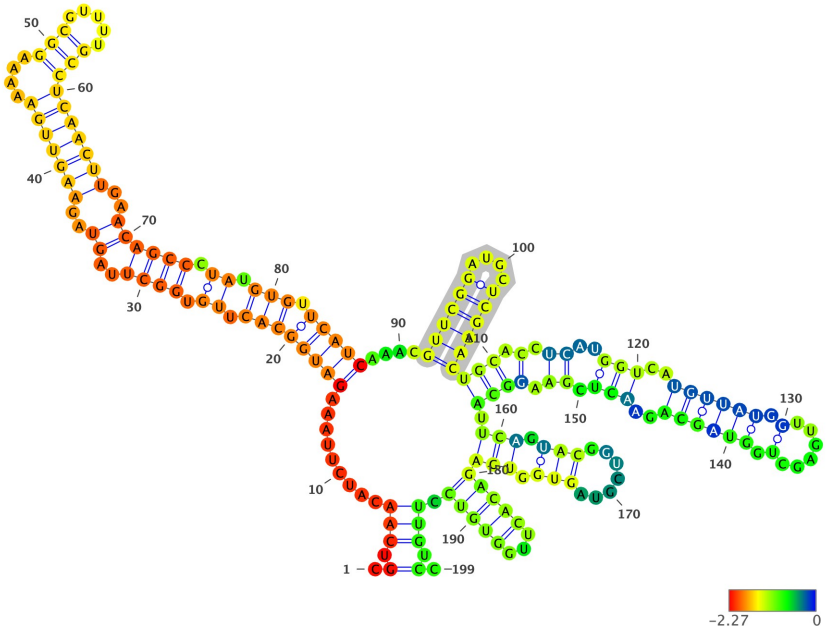
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-GTTCGGATGCUCGAAC-3'
5'-((((((....))))))-3'
Motif MFE = -4.3; z-score = -2.4; 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 = -0.28; ED = 45.83
```

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

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

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

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

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

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

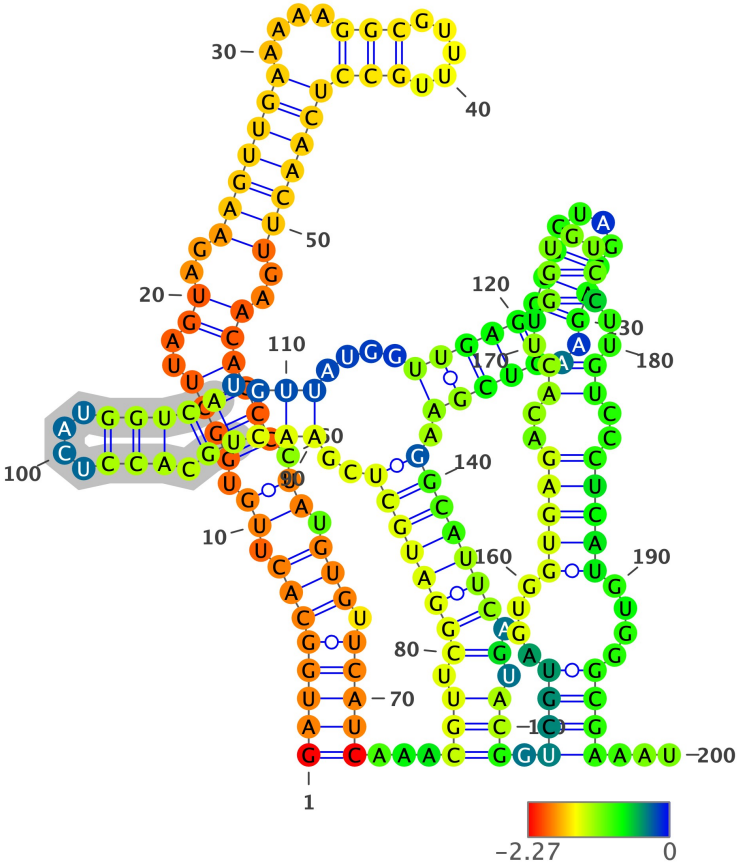
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 9 from nt 499 to 513 (nt 93 to 107)

```
5'-TGCACCTCATGGUCA-3'
5'-((.(((....)))))-3'
Motif MFE = -2.2; z-score = -2.74; ED = 1.08
```



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

Extracted structure model with flanking nucleotides 407 to 606 (motif highlighted in silver):

```
5'-GAUGGCACUUGUGGCUUAGUAGAAGUUGAAAAAGGCGUUUUGCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUU
AUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAU-3
5'-((((((((.((.((((..((..(((((((....(((.....)))))))))..)))))).)).))).)))))...(((.((((((((..(((((.(((....)))))).)))
....((((((((....)))..)))))).))))))).).))).((((....(((((..((..((...))..))..)))))....))))...-3'
MFE = -57.6; z-score = -0.89; ED = 50.62
```

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

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

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

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

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

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

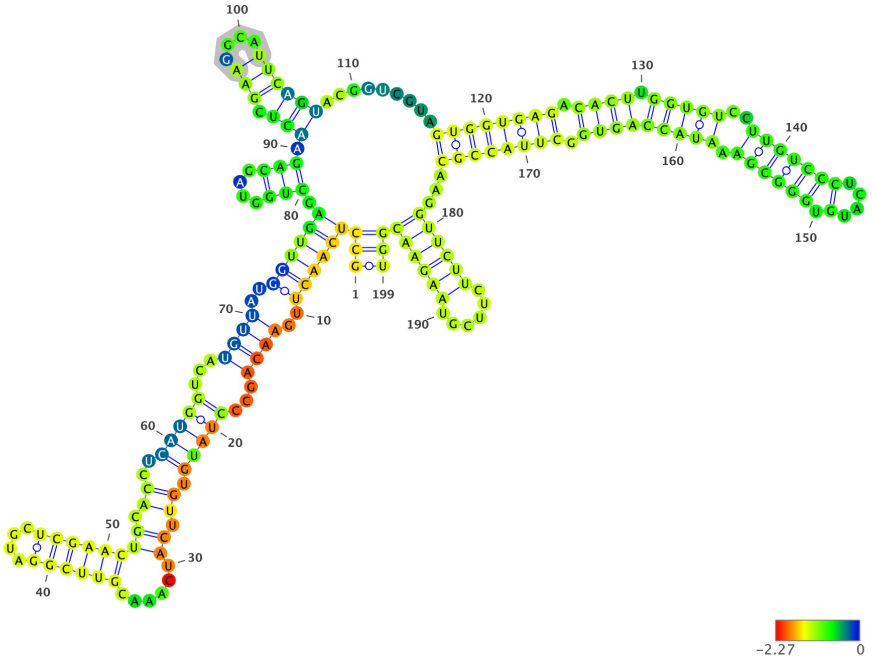
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 10 from nt 544 to 549 (nt 97 to 102)

```
5'-AGGCAU-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 448 to 646 (motif highlighted in silver):

```
5'-GCCUCAACUUGAACAGCCCUAUGUGUUCAUCAAACGUUCGGAUGCUCGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGG
UCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAAAUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGU-3
5'-(((((((((..((((...((((((.((.((......((((((....))))))))).))..))))))...))))).))))))).(((....))).(((.(((....)))))))....
.....(((((((((.((((.((((((..(((((((....).)))))))..)))))))))).)))))))...((((((.....))))))))))-3'
MFE = -60.5; z-score = -1.8; ED = 35.96
```

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

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

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

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

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

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

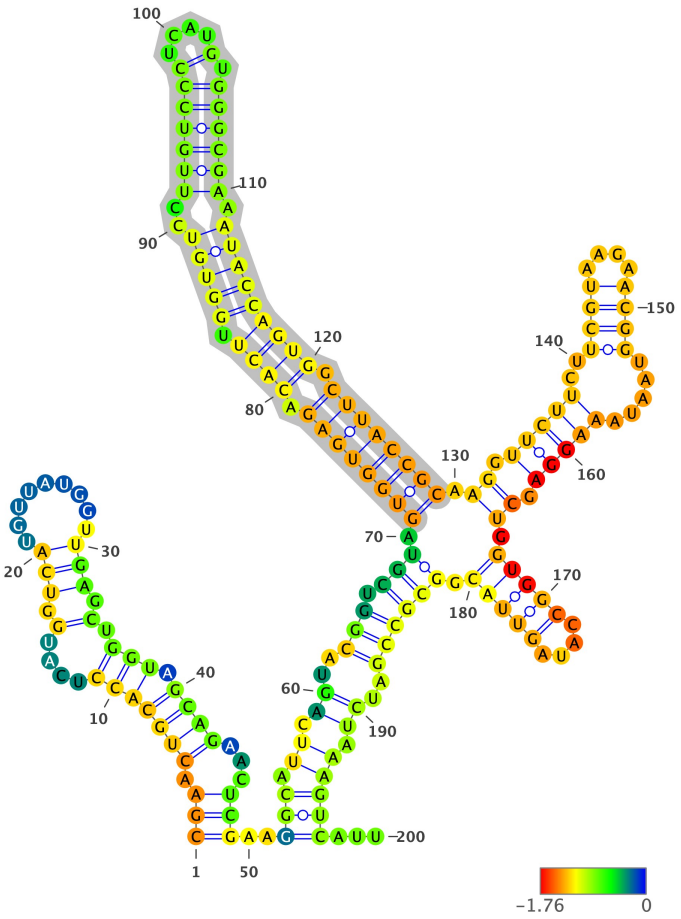
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 11 from nt 564 to 622 (nt 71 to 129)

```
5'-GTGGTGAGACACTTGGTGTCCTTGTCCCTCATGTGGGCGAAAUACCAGUGGCUUACCGC-3'
5'-((((((((.((((.(((((.....................)))))))))).))))))))-3'
Motif MFE = -28.2; z-score = -4.26; ED = 5.09
```



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

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

```
5'-CGAACUGCACCUCAUGGUCAUGUUAUGGUUGAGCUGGUAGCAGAACUCGAAGGCAUUCAGUACGGUCGUAGUGGUGAGACACUUGGUGUCCUUGUCCCUCAUGUGGGCGAA
AUACCAGUGGCUUACCGCAAGGUUCUUCUUCGUAAGAACGGUAAUAAAGGAGCUGGUGGCCAUAGUUACGGCGCCGAUCUAAAGUCAUU-3
5'-(((.(((((((....(.(((.........))).).))).))))...)))..(((.((.((..(((.(((.((((((((.((((.(((((..(((((((....).))))))).
))))))))).))))))))).((.(((((..((((....)))).....))))).)).(((((....)))))).))))))..)).)))))...-3'
MFE = -59.2; z-score = -0.33; ED = 59.24
```

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

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

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

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

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

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

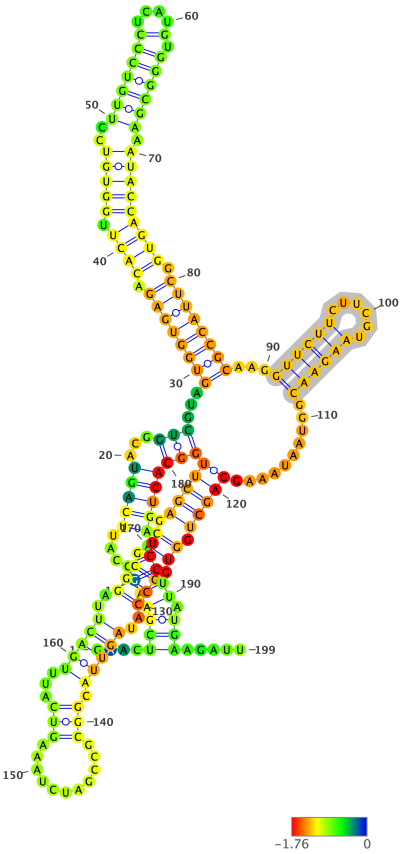
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 12 from nt 626 to 643 (nt 91 to 108)

```
5'-GTTCTTCTTCGTAAGAAC-3'
5'-((((((......))))))-3'
Motif MFE = -3.1; z-score = -3.54; 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 = -2.96; 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(+)

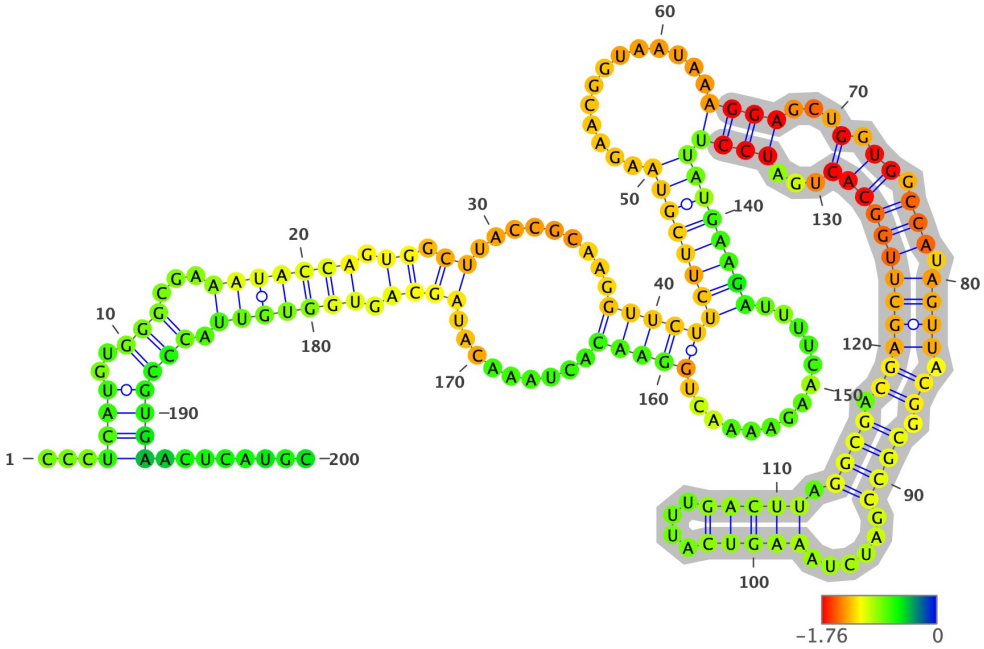
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 13 from nt 653 to 723 (nt 65 to 135)

```
5'-GGAGCTGGTGGCCATAGTTACGGCGCCGATCTAAAGTCATTTGACUUAGGCGACGAGCUUGGCACTGAUCC-3'
5'-(((...(.((.(((.((((.((.((((.....................)))).))))))))))))...)))-3'
Motif MFE = -23.8; z-score = -1.52; 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 = -48.5; z-score = -1.18; ED = 47.39
```

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(+)

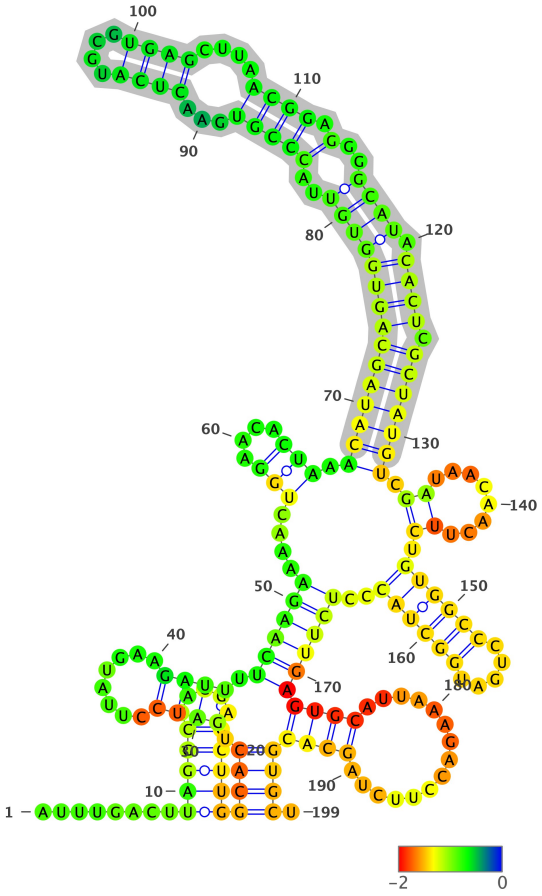
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 14 from nt 758 to 821 (nt 68 to 131)

```
5'-CATAGCAGTGGTGTTACCCGTGAACTCATGCGTGAGCTTAACGGAGGGGCAUACACUCGCUAUG-3'
5'-((((((((((.....................................)))))).)))))))-3'
Motif MFE = -24.4; z-score = -3.03; ED = 3.9
```



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

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

```
5'-AUUUGACUUAGGCGACGAGCUUGGCACUGAUCCUUAUGAAGAUUUUCAAGAAAACUGGAACACUAAACAUAGCAGUGGUGUUACCCGUGAACUCAUGCGUGAGCUUAACGG
AGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCU-3
5'-........(((((.....)))))((((.(((((........)))).((((((....((((....)))).((((((((((((((..(((((...((((....))))....)))))
.)..)))).)))).)))))))).((........)).((((((.....))))))..)))))))(((.............)))))))).-3'
MFE = -52.0; z-score = -0.64; ED = 22.17
```

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

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

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

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

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

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

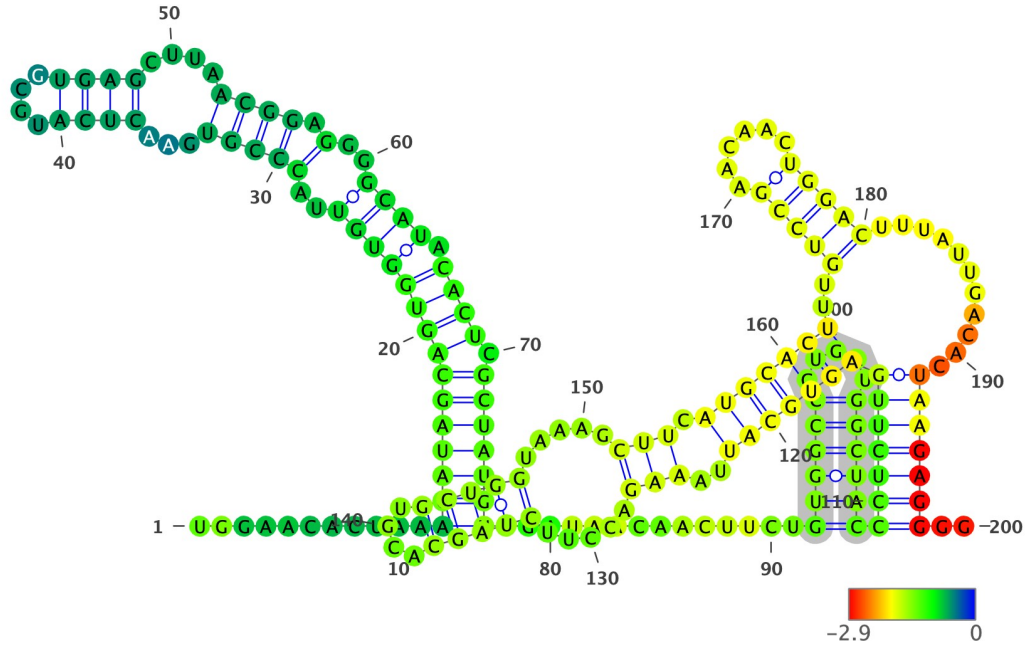
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 15 from nt 837 to 853 (nt 92 to 108)

```
5'-GTGGCCCTGATGGCUAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.1; z-score = -2.93; 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 = -2.4; 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(+)

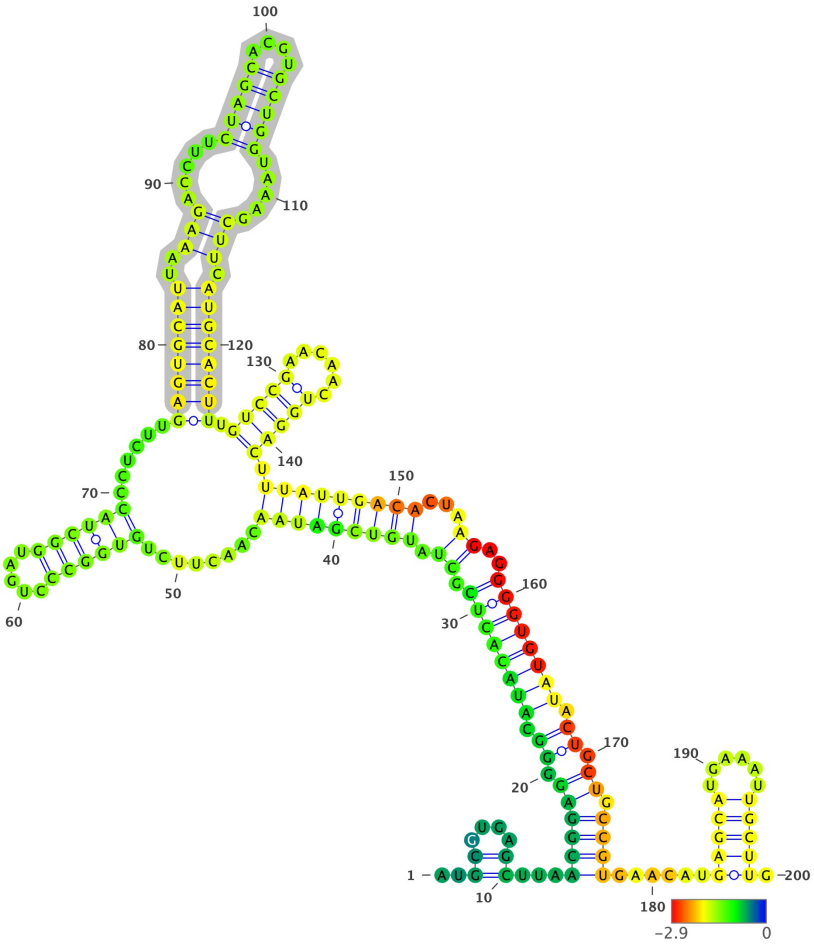
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 16 from nt 861 to 907 (nt 77 to 123)

```
5'-AGTGCATTAAAGACCTTCTAGCACGTGCUGGTAAAGCUUCAUGCACU-3'
5'-(((((((..(((.....(((((....)))))).....))).)))))))-3'
Motif MFE = -15.2; z-score = -2.84; ED = 2.82
```



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

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

```
5'-AUGCGUGAGCUUAACGGAGGGGCAUACACUCGCUAUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAA
GCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUG-3
5'-..((....)).((((((.((.(((((((((.((.(((((((((........((((((.....))))))))).....((((((((..(((.....(((((....)))))).....
.))).)))))))).(((((.....)))))).)))))))))...))..)))))))).)).)).))))......(((((.....))))).-3'
MFE = -65.6; z-score = -2.64; ED = 12.03
```

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

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

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

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

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

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

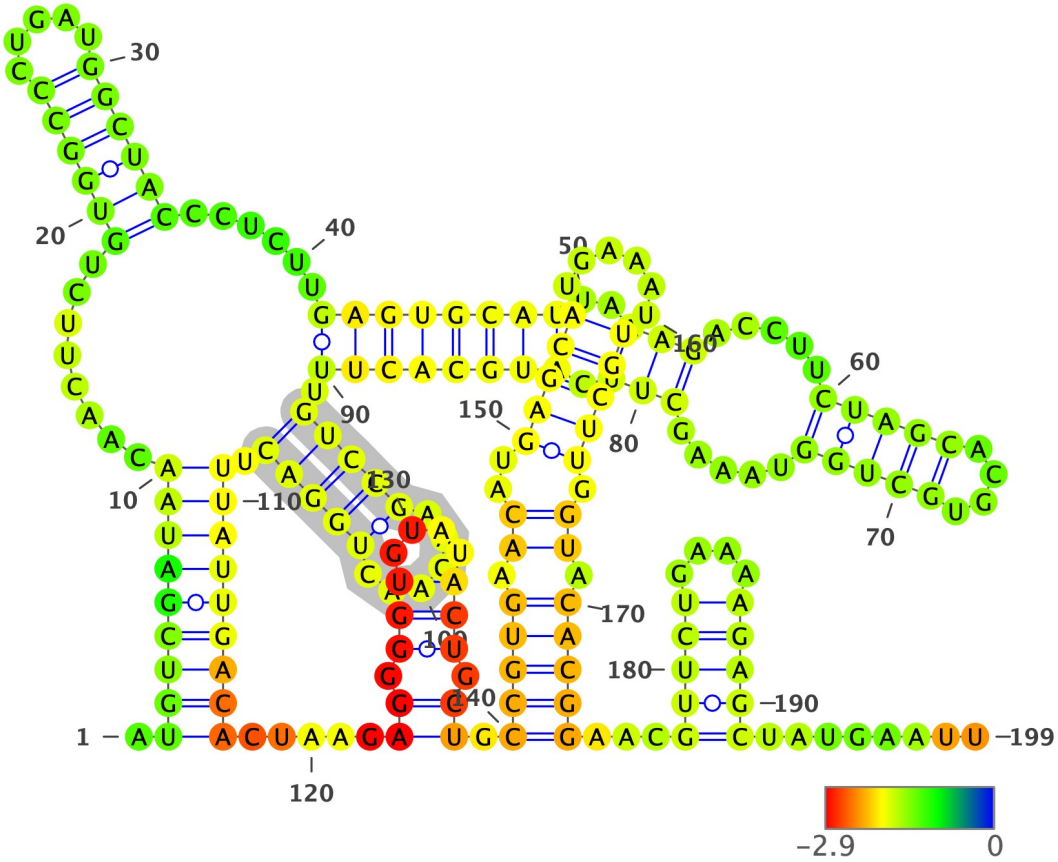
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 17 from nt 910 to 925 (nt 92 to 107)

```
5'-GTCCGAACAACUGGAC-3'
5'-(((((......)))))-3'
Motif MFE = -4.4; z-score = -3.13; ED = 0.56
```



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

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

```
5'-AUGUCGAUAACAACUUCUGUGGCCCUGAUGGCUACCCUCUUGAGUGCAUUAAAGACCUUCUAGCACGUGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUA
UUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACGUUCUGAAAAGAGCUAUGAAUU-3
5'-.(((((((((.........((((((.....))))))......((((((((..(((.....(((((....)))))).....))).)))))))).(((((......))))).)))
))))))).....((.(((....))).)).(((((.((..(((((......))))).)).)))))...(((((....)))))........-3'
MFE = -61.0; z-score = -2.61; ED = 11.08
```

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

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

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

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

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

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

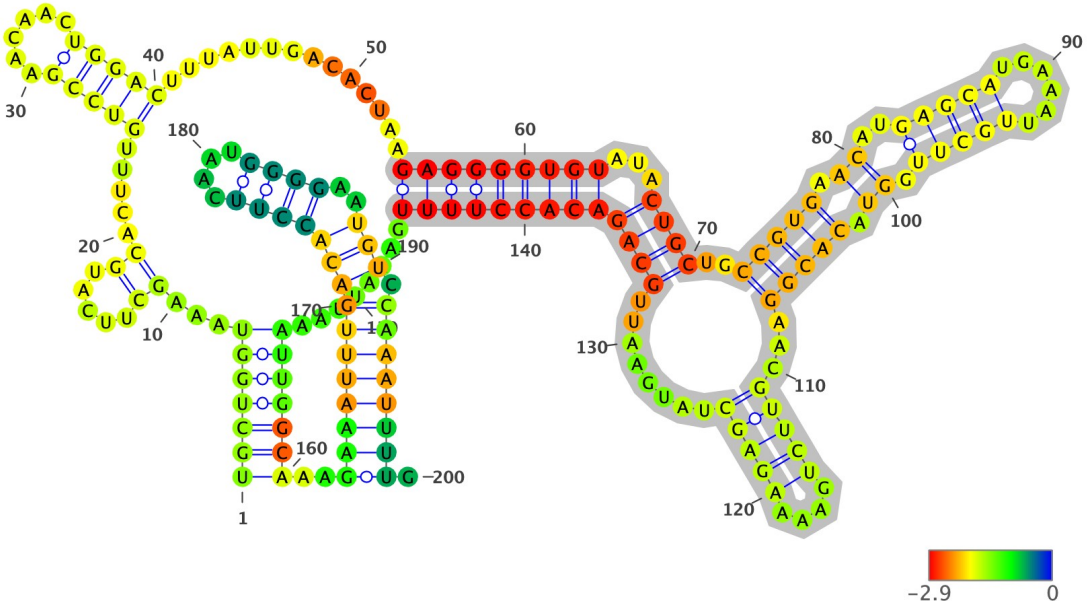
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 18 from nt 940 to 1030 (nt 55 to 145)

```
5'-GAGGGGTGTATACTGCTGCCGTGAACATGAGCATGAAATUGCUUGGUACACGGAACGTTCTGAAAAGAGCTATGAATTGCAGACACCUUUU-3'
5'-((((((((...((((..(((((.((..(((((......))))).)).)))))...(((((....)))))........)))))))))))))-3'
Motif MFE = -32.3; z-score = -3.72; ED = 2.22
```



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

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

```
5'-UGCUGGUAAAGCUUCAUGCACUUUGUCCGAACAACUGGACUUUAUUGACACUAAGAGGGGUGUAUACUGCUGCCGUGAACAUGAGCAUGAAAUUGCUUGGUACACGGAACG
UUCUGAAAAGAGCUAUGAAUUGCAGACACCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUG-3
5'-(((((((...((.....)).....(((((......)))))..............(((((((((...((((..(((((.((..(((((......))))).)).)))))...(
((((....)))))........)))))))))))))........)))))))..((((((((((((((....))))..))).)))))))).-3'
MFE = -52.0; z-score = -1.72; ED = 15.2
```

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

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

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

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

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

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

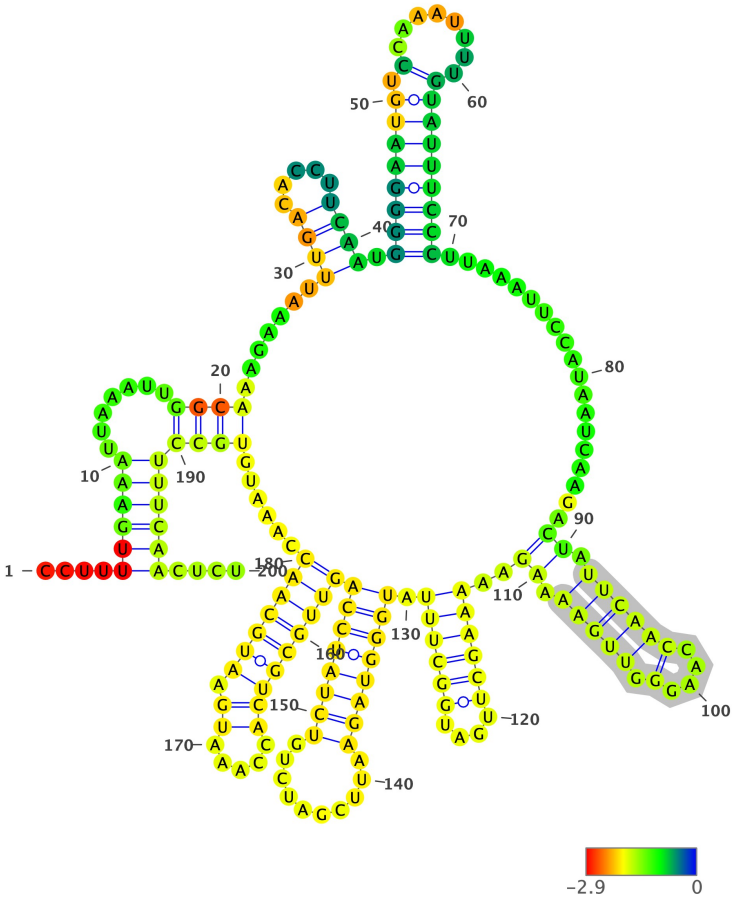
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 19 from nt 1116 to 1132 (nt 92 to 108)

```
5'-TTCAACCAAGGGUUGAA-3'
5'-((((((....).))))))-3'
Motif MFE = -6.0; z-score = -5.7; ED = 0.63
```



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

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

```
5'-CCUUUUGAAAUUAAAUUGGCAAAGAAAUUUGACACCUUCAAUGGGGAAUGUCCAAAUUUUGUAUUUCCCUUAAAUUCCAUAAUCAAGACUAUUCAACCAAGGGUUGAAAAG
AAAAAGCUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCU-3
5'-....((((((.......(((((.......(((((.....)))))..(((((((((.(........)))))))))..................((.((((((....).)))))).))
..((((((....)))))).(((((((((.........)))))))))(((((((((.....)).)))))))......))))))))))....-3'
MFE = -39.8; z-score = -3.15; ED = 29.77
```

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(+)

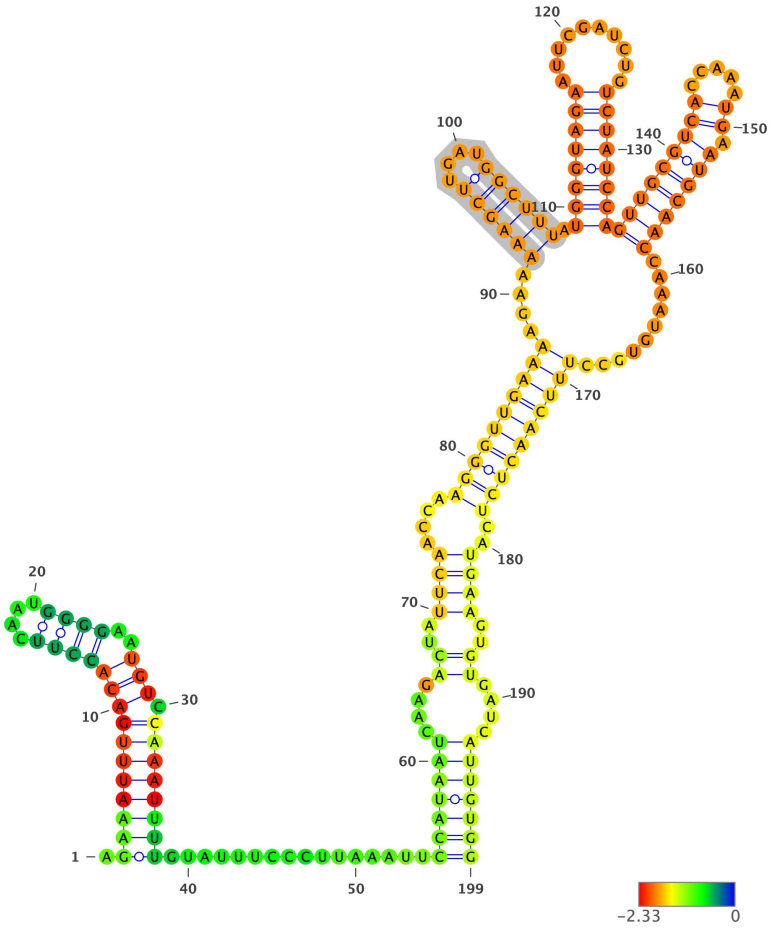
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 20 from nt 1138 to 1153 (nt 92 to 107)

```
5'-AAAGCTTGATGGCUUU-3'
5'-((((((....))))))-3'
Motif MFE = -4.2; z-score = -4.45; 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 = -2.88; 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(+)

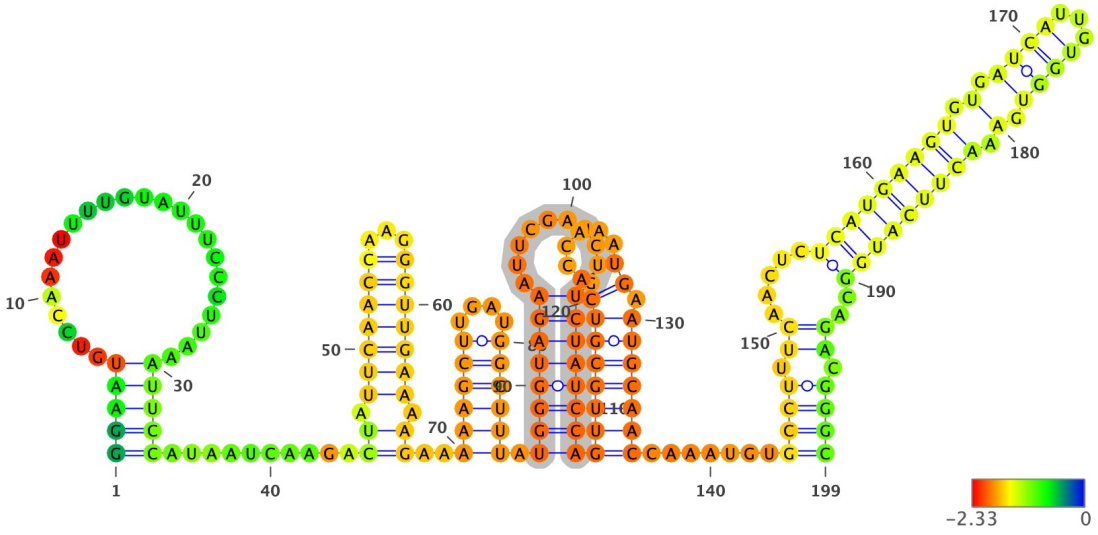
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 21 from nt 1155 to 1180 (nt 87 to 112)

```
5'-TGGGTAGAATTCGATCTGUCUAUCCA-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -7.4; z-score = -2.15; 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 = -2.22; 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(+)

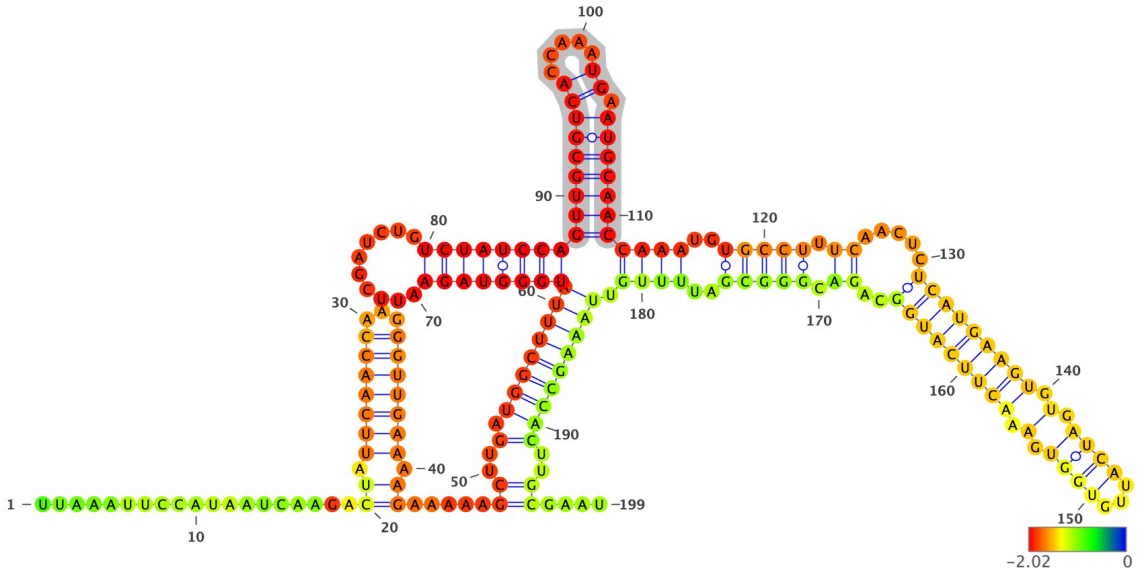
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 22 from nt 1181 to 1204 (nt 88 to 111)

```
5'-GTTGCGTCACCAAAUGAAUGCAAC-3'
5'-((((((((.....)).)))))))-3'
Motif MFE = -6.5; z-score = -2.89; 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 = -3.47; 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(+)

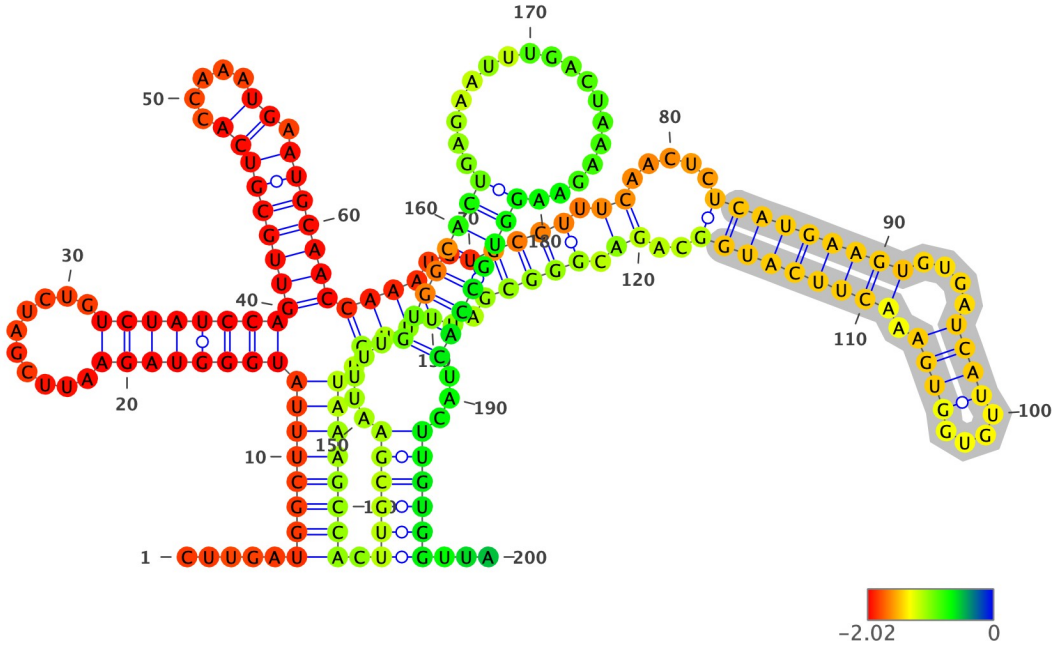
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 23 from nt 1225 to 1257 (nt 84 to 116)

```
5'-CATGAAGTGTGATCATTGTGGUGAAACUUCAUG-3'
5'-(((((((.....(((......)))..)))))))-3'
Motif MFE = -10.8; z-score = -3.45; 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 1142 to 1341 (motif highlighted in silver):

```
5'-CUUGAUGGCUUUAUGGGUAGAAUUCGAUCUGUCUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACU
UCAUGGCAGACGGGCGAUUUUGUUAAAGCCACUUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGUUA-3
5'-.....((((((((((((((((.........))))))))((((((((((.....)).)))))))((((..(((((.((.....((((((((....((((....)))).)))
))))))..)).)))))..)))).)))))))).((((((.....((((((((.................))))))))...))))))...-3'
MFE = -56.8; z-score = -2.17; ED = 16.26
```

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

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

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

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

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

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

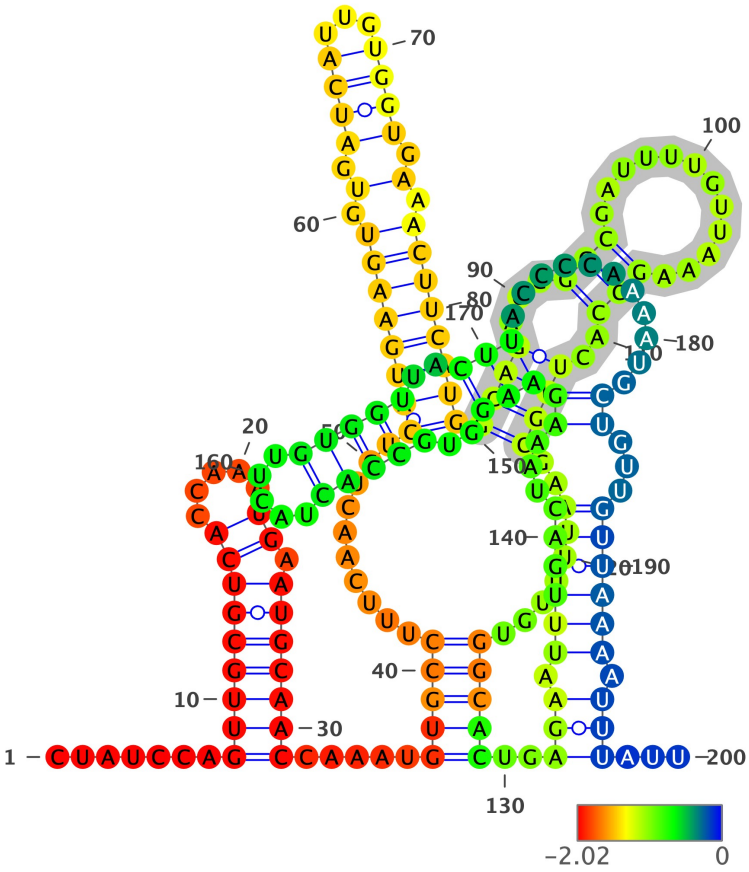
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 1258 to 1288 (nt 85 to 115)

```
5'-GCAGACGGGCGATTTTGTTAAAGCCACUUGC-3'
5'-(((((...(((.............))))..)))))-3'
Motif MFE = -5.6; z-score = -0.22; ED = 2.46
```



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

Extracted structure model with flanking nucleotides 1174 to 1373 (motif highlighted in silver):

```
5'-CUAUCCAGUUGCGUCACCAAAUGAAUGCAACCAAAUGUGCCUUUCAACUCUCAUGAAGUGUGAUCAUUGUGGUGAAACUUCAUGGCAGACGGGCGAUUUUGUUAAAGCCAC
UUGCGAAUUUUGUGGCACUGAGAAUUUGACUAAAGAAGGUGCCACUACUUGUGGUUACUUACCCCAAAAUGCUGUUGUUAAAAUUUAUU-3
5'-.......(((((((((.....)).)))))))).....(((((..........(((((((.(.((((...)))).).)))))))))(((...(((............)))..
))))).........)))))..(((.((((((...((((((..(((((.....)))))..)))).........))...)))))).)))...-3'
MFE = -45.6; z-score = -1.22; 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, 266-13468(+)

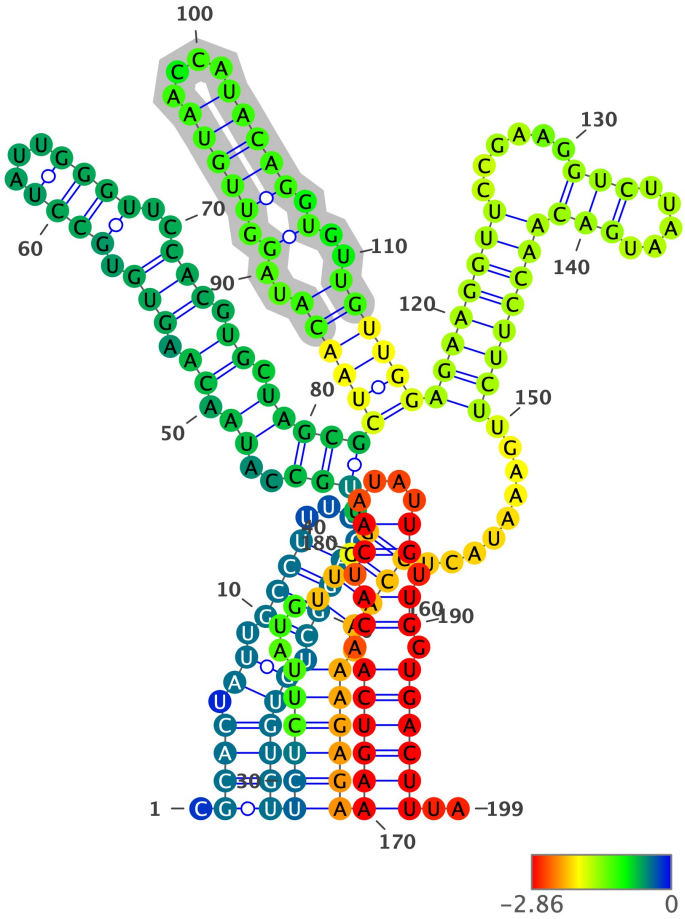
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 1555 to 1580 (nt 87 to 112)

```
5'-CATAGGTTGTAACCAUACAGGUGTUG-3'
5'-((..(.(((((....))))).)..))-3'
Motif MFE = -3.4; z-score = -0.48; ED = 3.49
```



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 1469 to 1667 (motif highlighted in silver):

```
5'-CGCACUAUUGCCUUUGGAGGCUGUGUGUUCUCUUAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUU
GUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUA-3
5'-.((((.((.((((....)))).))))))((((((...((((.(((..((.((.(((.((((...)))).)))).)).)))))((((((..(.(((((....))))).)..)
)))))((((((((.....(((.....)))))))))))).........)))).))))))((((((.((.((....)).)).))))))..-3'
MFE = -51.8; z-score = -2.26; ED = 35.17
```

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(+)

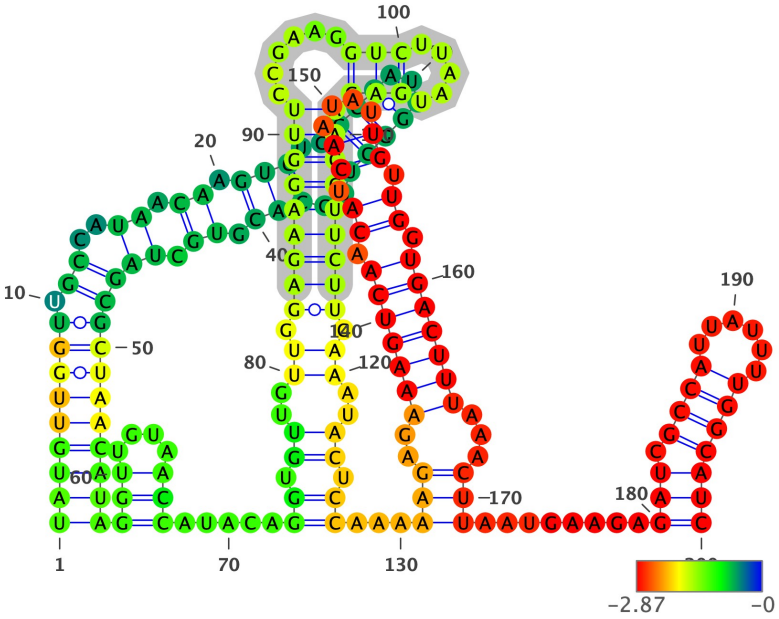
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 26 from nt 1585 to 1617 (nt 84 to 116)

```
5'-AGAAGGTTCCGAAGGTCTTAATGACAACCUUCU-3'
5'-(((((((.....(((.....)))))))))))-3'
Motif MFE = -9.5; z-score = -2.52; 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 1502 to 1701 (motif highlighted in silver):

```
5'-UAUGUUGGUUGCCAUAACAAGUGUGCCUAUUGGGUUCCACGUGCUAGCGCUAACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAAC
CUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUC-3
5'-(((((((((.((..((.((.(((.((((...)))))..))).)).)))))))))))))))(((....))).....((.((..((.(((((((((.....(((.....)))))))
))))))).))..)).))...(((..(((((((.((.((....)).)).)))))))...))).........(((.((((.....)))))))-3'
MFE = -51.5; z-score = -2.14; ED = 26.74
```

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

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

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

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

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

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

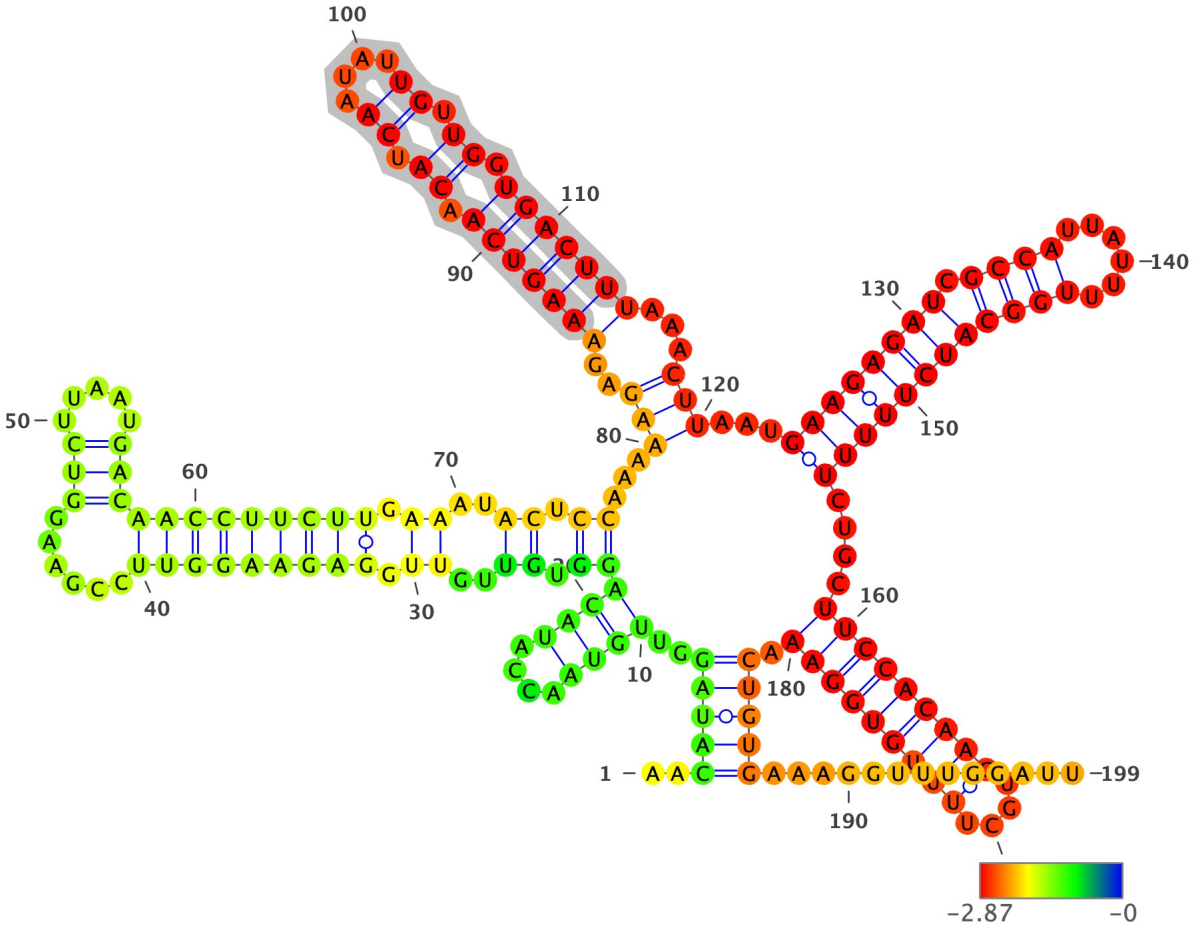
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 27 from nt 1638 to 1665 (nt 86 to 113)

```
5'-AAGTCAACATCAATATUGTUGGUGACUU-3'
5'-((((((.((.((....)).)).))))))-3'
Motif MFE = -6.3; z-score = -2.65; ED = 4.9
```



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

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

```
5'-AACAUAGGUUGUAACCAUACAGGUGUUGUUGGAGAAGGUUCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGAC
UUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUU-3
5'-..(((((..((((....))))((.((..((.((((((((((.....(((.....)))))))))))).))..)).))...(((..(((((((.((.((....)).)).))))
)))...)))...((((((((.((((.....)))))))))))....(((((((((....)))))))))).)))))............-3'
MFE = -56.2; z-score = -3.22; ED = 31.95
```

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

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

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

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

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

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

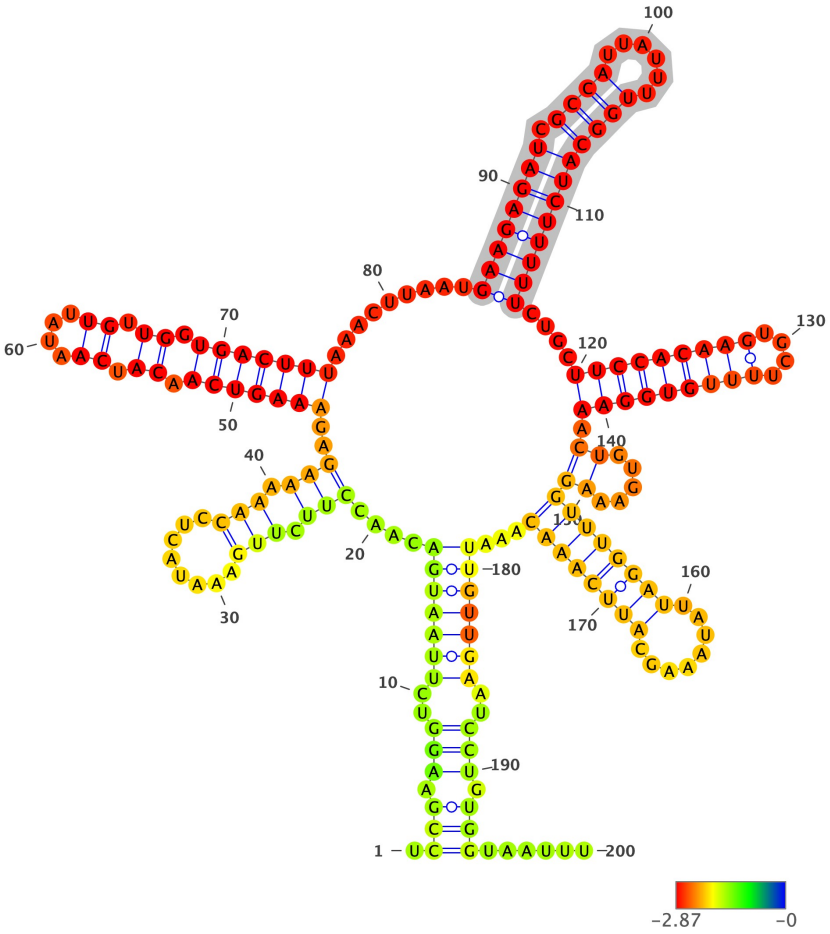
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 28 from nt 1676 to 1706 (nt 85 to 115)

```
5'-GAAGAGATCGCCATTATTTUGGCAUCUUUUU-3'
5'-((((((((.((((......)))))))))))-3'
Motif MFE = -12.1; z-score = -4.44; ED = 0.84
```



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

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

```
5'-UCCGAAGGUCUUAAUGACAACCUUCUUGAAAUACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCU
UUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUU-3
5'-.(((.(((..(((((((....(((.(((........))).)))..(((((((.((.((....)).)).)))))))..........((((((((.((((......))))))))
))))....((((((((((....)))))))))).((.....))((((((((........))))))))...)))))))..))).)))......-3'
MFE = -49.0; z-score = -3.37; ED = 43.74
```

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

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

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

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

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

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

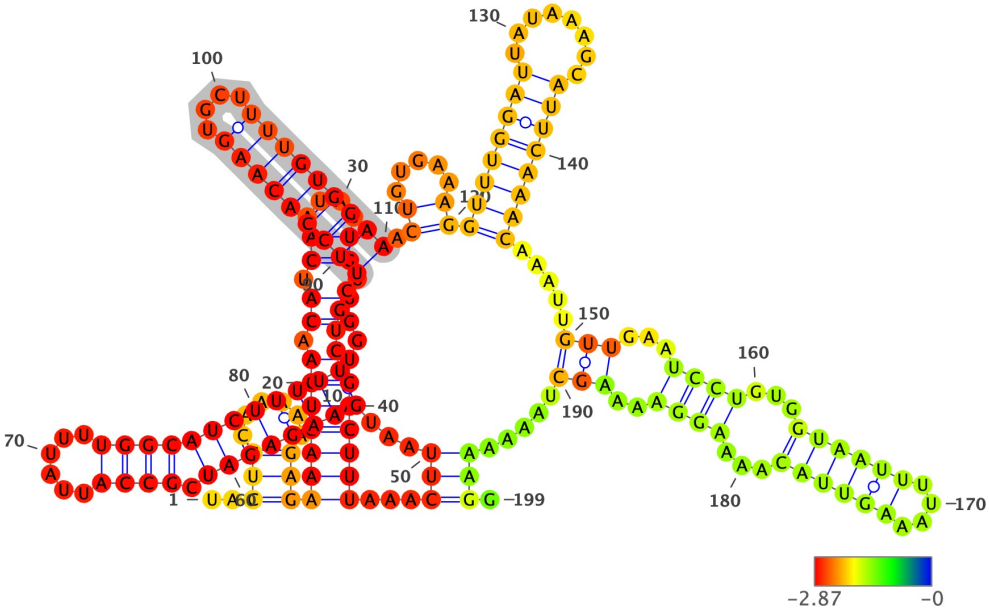
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-TTCCACAAGTGCTTTTGUGGAA-3'
5'-((((((..........))))))-3'
Motif MFE = -9.5; z-score = -4.73; ED = 1.03
```



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

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

```
5'-UACUCCAAAAAGAGAAAGUCAACAUCAAUAUUGUUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAA
CUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGG-3
5'-..(((......)))(((((((.((.((....)).)).)))))))...(((...(((((((((.((((......))))))))))))....((((((((((....)))))))))).
((.....))(((((((((........)))))))))).....(((...((((...((((((....))))))..))))).))).....))).-3'
MFE = -48.5; z-score = -3.23; ED = 33.39
```

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

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

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

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

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

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

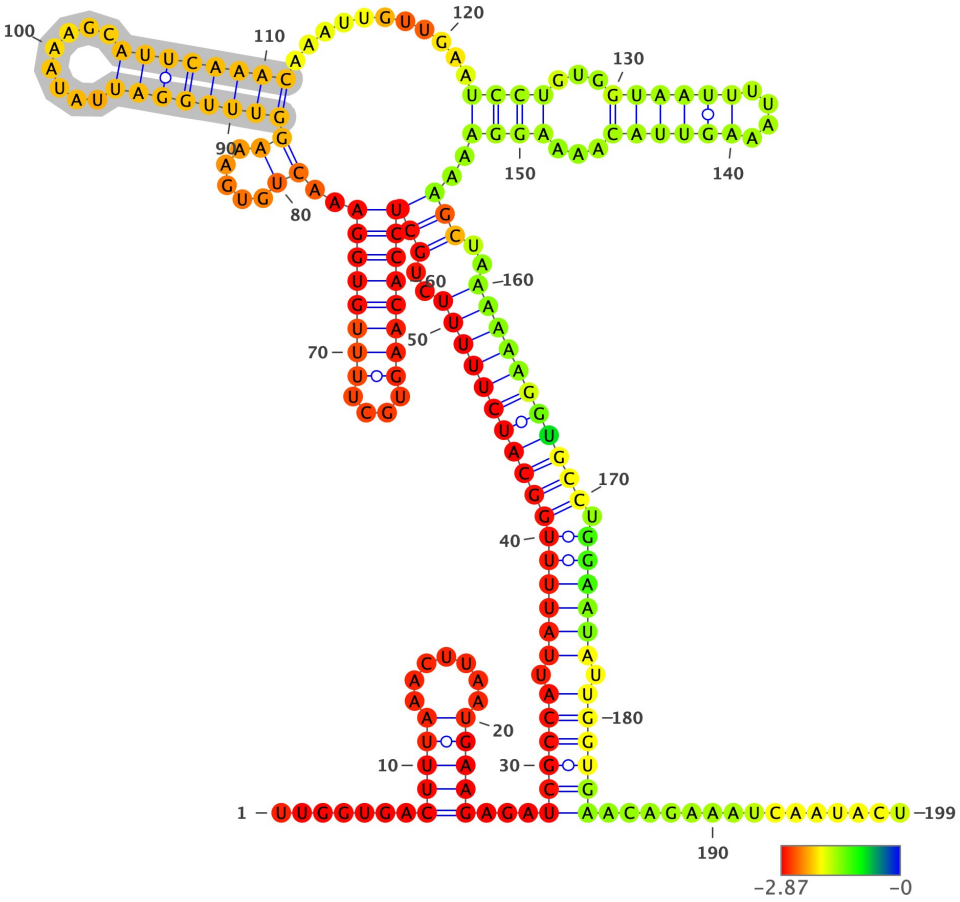
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 30 from nt 1743 to 1766 (nt 88 to 111)

```
5'-GTTTGGATTATAAAGCAUUCAAAC-3'
5'-(((((((.......)))))))-3'
Motif MFE = -4.6; z-score = -3.08; ED = 0.53
```



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

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

```
5'-UUGGUGACUUUAAACUUAAUGAAGAGAUCGCCAUUAUUUUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAAC
AAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAAGGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACU-3
5'-.......(((((.......)))))...((((((.(((((((((((((((..(((((((((((....)))))))))..((.....))(((((((.........)))))))).
..........((((...((((((....))))))...))))..))))..)))))))))))).)))))).)))))).............-3'
MFE = -55.0; z-score = -4.09; 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(+)

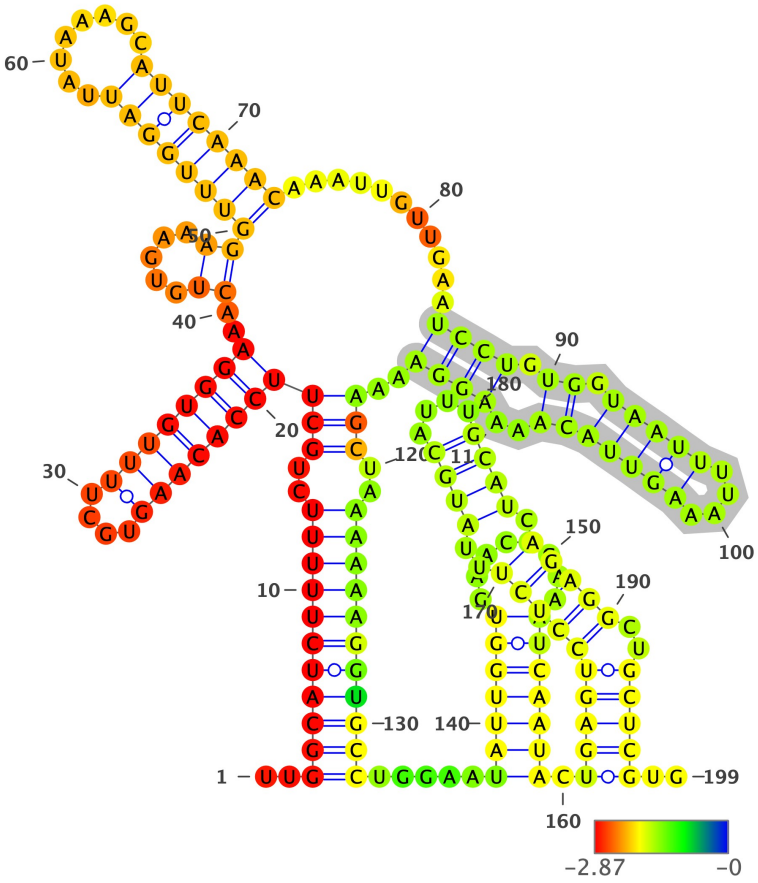
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 1778 to 1807 (nt 85 to 114)

```
5'-TCCTGTGGTAATTTTAAAGUUACAAAAGGA-3'
5'-((((.((.((((......))))))..))))-3'
Motif MFE = -7.4; z-score = -2.96; 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 1694 to 1892 (motif highlighted in silver):

```
5'-UUGGCAUCUUUUUCUGCUUCCACAAGUGCUUUUGUGGAAACUGUGAAAGGUUUGGAUUAUAAAGCAUUCAAACAAAUUGUUGAAUCCUGUGGUAAUUUUAAAGUUACAAAA
GGAAAAGCUAAAAAAGGUGCCUGGAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUG-3
5'-..(((((((((((..(((((((((((....))))))))..((.....))((((((((.........))))))))...........((((.((.(((((....)))))))..)
)))..)))..))))))))))).....(((((((.........)))))))..((((((((((..((((....)))).)))))..)))))..-3'
MFE = -57.1; z-score = -4.49; ED = 17.3
```

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

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

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

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

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

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

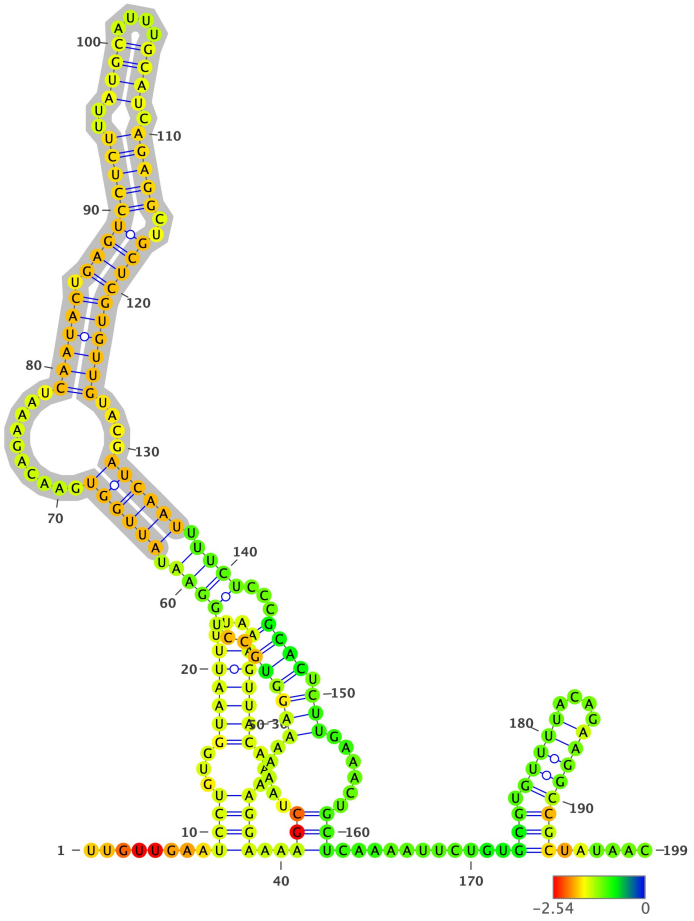
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 32 from nt 1832 to 1905 (nt 63 to 136)

```
5'-ATTGGTGAACAGAAATCAATACTGAGTCCTCTTTATGCATTTGCAUCAGAGGCTGCUCGUGUUGTACGAUCAAU-3'
5'-((((((..........((((((.((((((((((..((((....)))).)))))..))))))))))....))))))-3'
Motif MFE = -20.1; z-score = -2.28; 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 = -1.59; 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(+)

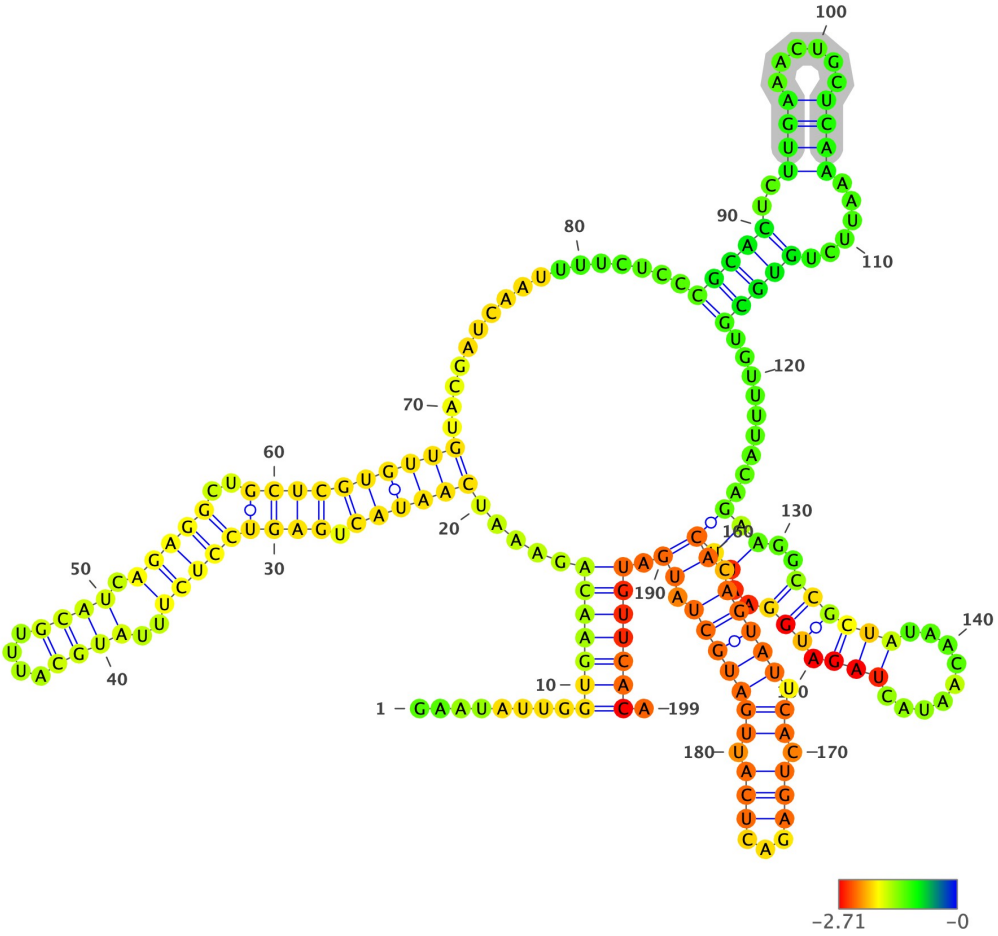
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 1921 to 1932 (nt 94 to 105)

```
5'-TGAAACTGCUCA-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = 0.22; 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 1828 to 2026 (motif highlighted in silver):

```
5'-GAAUAUUGGUGAACAGAAAUCAAUACUGAGUCCUCUUUAUGCAUUUGCAUCAGAGGCUGCUCGUGUUGUACGAUCAAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUC
UGUGCGUGUUUUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACA-3
5'-........(((((((.....((((((.(((((((((..((((....)))).)))))..))))))))))).................(((((..((((......))))).....
.)))))........(((..((((((.........))).)))..)))((.(((((.((.(((...))).)))))))).)).)))))))).-3'
MFE = -44.3; z-score = -1.35; ED = 35.63
```

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(+)

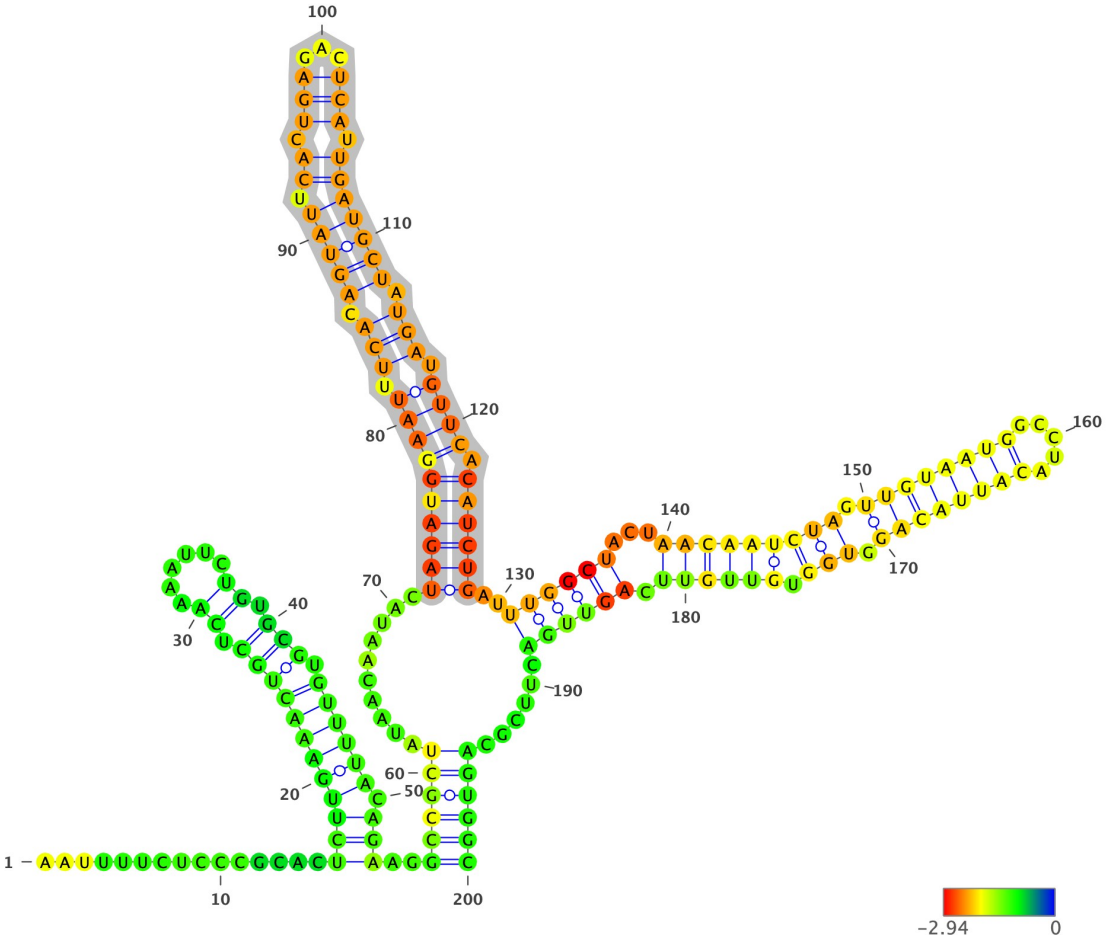
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 34 from nt 1974 to 2030 (nt 72 to 128)

```
5'-TAGATGGAATTTCACAGTATTCACTGAGACUCATUGAUGCUAUGATGUUCACAUCUG-3'
5'-((((.(.(((.(((.(((((.((.(((...))).)))))))).))).)))..).))))-3'
Motif MFE = -17.5; z-score = -3.34; ED = 3.01
```



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

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

```
5'-AAUUUUCUCCCGCACUCUUGAAACUGCUCAAAAUUCUGUGCGUGUUUUACAGAAGGCCGCUAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGC
UAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGC-3
5'-...............((((((((((((.((......)).))).)))))).)))..((((((..........((((((((((.(((.(((((.((.(((...))).))))))
).))).)))).)))))).((((((...((((((((((.((((((((.....)))))))).))).)))))).))))))......))))))-3'
MFE = -52.4; z-score = -2.5; ED = 25.81
```

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

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

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

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

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

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

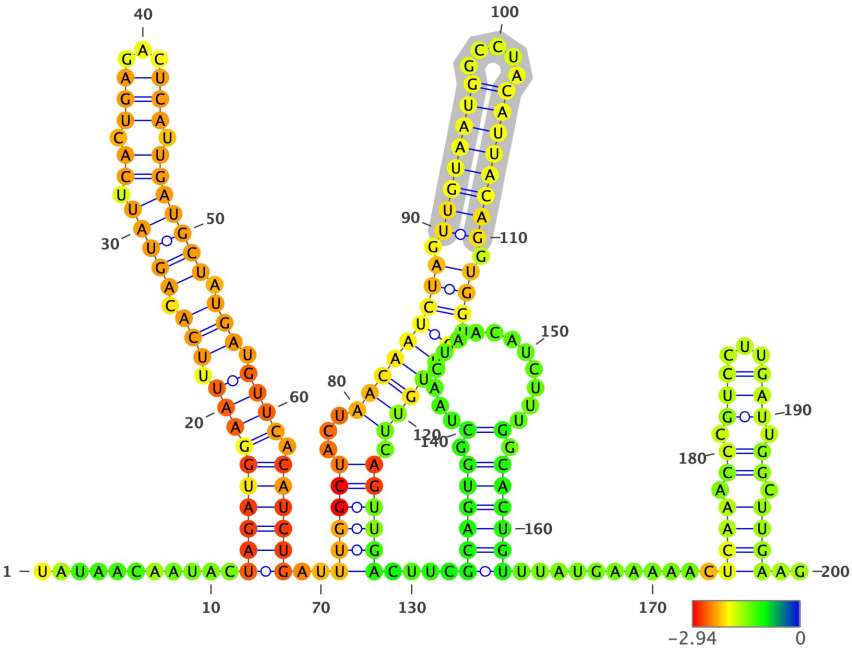
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 35 from nt 2052 to 2072 (nt 90 to 110)

```
5'-TTGTAATGGCCTACAUUACAG-3'
5'-((((((((.....))))))))-3'
Motif MFE = -7.0; z-score = -4.16; 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 1963 to 2162 (motif highlighted in silver):

```
5'-UAUAACAAUACUAGAUGGAAUUUCACAGUAUUCACUGAGACUCAUUGAUGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGG
UGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAG-3
5'-...........(((((((((.(((.(((((.((.(((...))).)))))))).))).)))).)))))).((((((...(((((((((.((((((((.....)))))))).
))).)))))).)))))).....((((((.(..............).)))))).........((((.((.(((...))).)).)))).-3'
MFE = -51.0; z-score = -2.36; ED = 21.48
```

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(+)

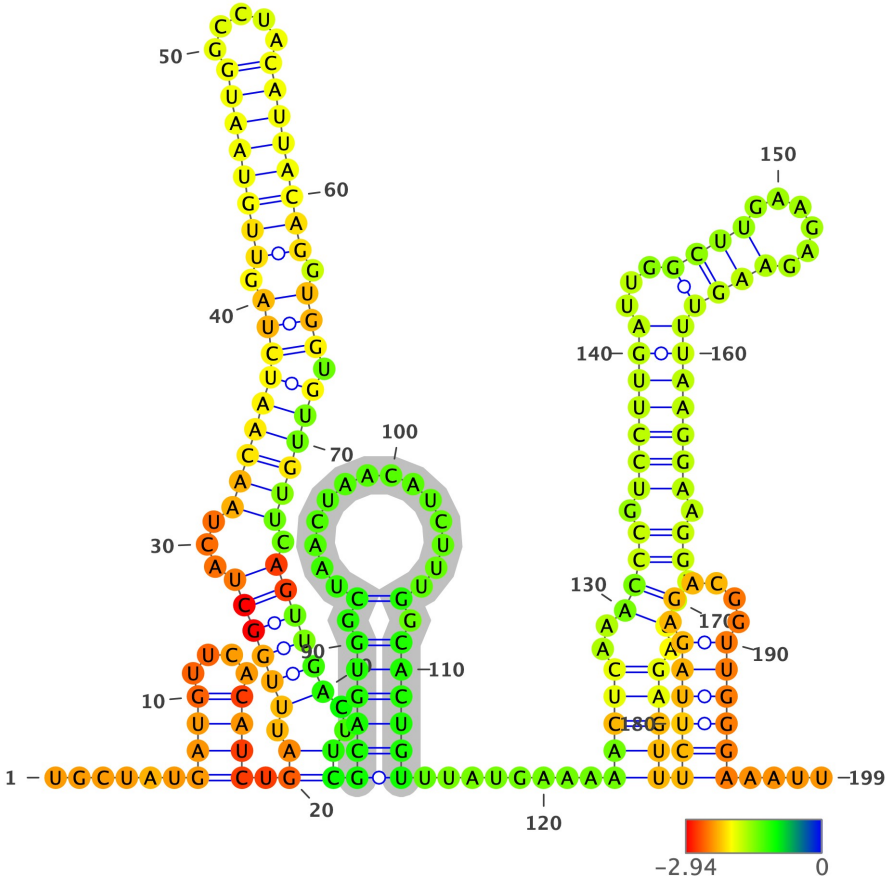
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 36 from nt 2095 to 2124 (nt 85 to 114)

```
5'-GCAGTGGCTAACTAACATCTTTGGCACUGU-3'
5'-((((((.(..............).))))))-3'
Motif MFE = -8.0; z-score = -1.9; ED = 4.07
```



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 2011 to 2209 (motif highlighted in silver):

```
5'-UGCUAUGAUGUUCACAUCUGAUUUGGCUACUAACAAUCUAGUUGUAAUGGCCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCAC
UGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUU-3
5'-......((((....)))).((.((((((...(((((((((.((((((((.....)))))))).))).)))))).))))))..))((((((.(..............).)))
))).......(((((..((((.(((((((...((((......))))))))))).)).)).)))))((((((......))))))....-3'
MFE = -49.3; z-score = -2.74; ED = 37.58
```

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 37 from nt 2136 to 2184 (nt 76 to 124)

```
5'-TCAAACCCGTCCTTGATTGGCTTGAAGAGAAGUUTAAGGAAGGTGTAGA-3'
5'-((....((.((((((((((.............)))).))))).))....))-3'
Motif MFE = -12.7; z-score = -1.97; ED = 6.73
```



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 2061 to 2260 (motif highlighted in silver):

```
5'-CCUACAUUACAGGUGGUGUUGUUCAGUUGACUUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUA
AGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUC-3
5'-..((((.((((((((((((((((.((((.(((....)))))))))).))))))......(((((((.(((.((((((..((((.((((((((((..(((...))).)))).)
)))).)).)).)))))).))).)))))))((((((((....)))).)))))))))))))..))))...(((((....)))))......-3'
MFE = -50.7; z-score = -1.68; ED = 45.88
```

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

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

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

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

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

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

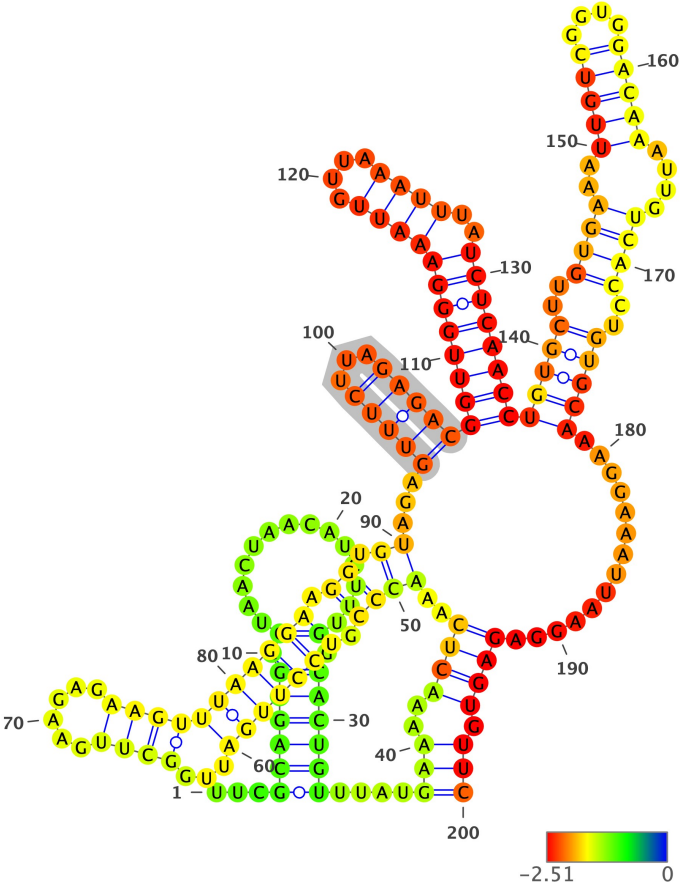
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 38 from nt 2185 to 2197 (nt 94 to 106)

```
5'-GTTTCTTAGAGAC-3'
5'-(((((...)))))-3'
Motif MFE = -1.1; z-score = -3.53; 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 2092 to 2291 (motif highlighted in silver):

```
5'-UUCGCAGUGGCUAACUAACAUCUUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUG
GGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUC-3
5'-...((((((.(..............).))))))....(((..((((..((((.(((((((...((((......)))))))))))).)).))...(((((...)))))(((((
(((((((....))))..))))))))(((((..((((..(((((....)))))....))))..)))))..............)))).)))-3'
MFE = -52.9; z-score = -1.64; ED = 21.09
```

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(+)

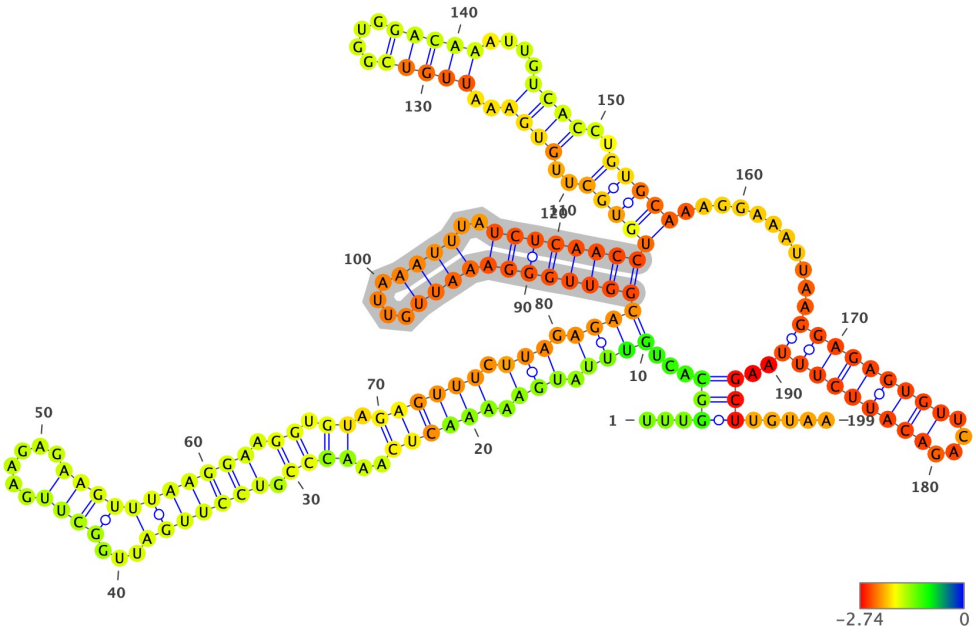
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 39 from nt 2198 to 2227 (nt 85 to 114)

```
5'-GGTTGGGAAATTGTTAAATTTAUCUCAACC-3'
5'-(((((((.............)))))))-3'
Motif MFE = -9.5; z-score = -2.74; ED = 1.98
```



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

Extracted structure model with flanking nucleotides 2114 to 2312 (motif highlighted in silver):

```
5'-UUUGGCACUGUUUAUGAAAAACUCAAACCCGUCCUUGAUUGGCUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCA
ACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAA-3
5'-...(((...((((.(((.((((((..((((.(((((((...((((......)))))))))).)).)).)))))).))).))))((((((((((....)))))..)))))
)))((((((..((((..(((((....)))))....)))))..)))))..........(((((((((....)))))))))..)))).....-3'
MFE = -56.7; z-score = -3.26; ED = 24.02
```

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

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

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

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

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

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

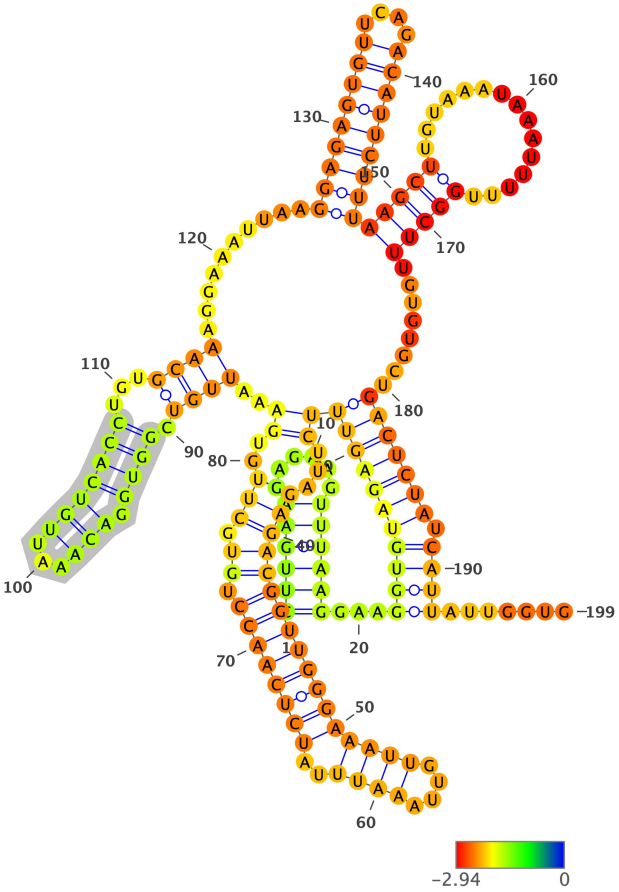
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 40 from nt 2246 to 2263 (nt 91 to 108)

```
5'-GGTGGACAAATUGUCACC-3'
5'-((((.(((...)))))))-3'
Motif MFE = -4.6; z-score = -1.87; ED = 2.46
```



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

Extracted structure model with flanking nucleotides 2156 to 2354 (motif highlighted in silver):

```
5'-CUUGAAGAGAAGUUUAAGGAAGGUGUAGAGUUUCUUAGAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGU
GCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUG-3
5'-((((((......))))))...(((((((((((((...((((((((((((((((....))))..)))))))).)).)))..)).((((.((((.(((...)))))))...
))))..........(((((((((....)))))))))(((((...............)))))........)))))))).))))........-3'
MFE = -43.6; z-score = -1.59; ED = 42.47
```

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(+)

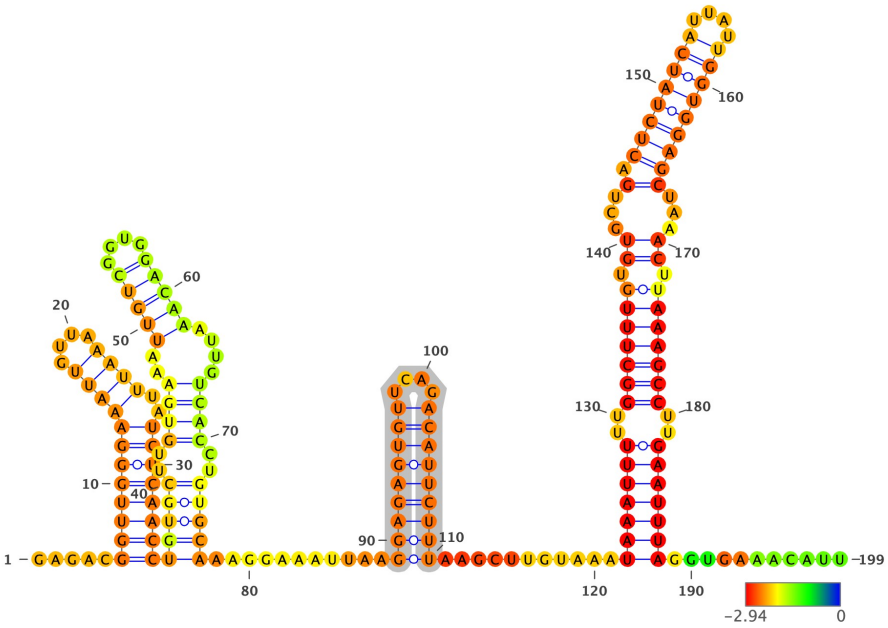
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 41 from nt 2281 to 2302 (nt 89 to 110)

```
5'-GGAGAGTGTTCAGACAUUCUUU-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -6.9; z-score = -3.3; ED = 0.92
```



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

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

```
5'-GAGACGGUUGGGAAAUUGUUAAAUUUAUCUCAACCUGUGCUUGUGAAAUUGUCGGUGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUA
AGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUU-3
5'-.....(((((((((((....))))..))))))))(((((..((((..(((((....)))))....))))..)))))...........(((((((((....))))))))).
..........(((((((..(((((((.((...(.(((((((((....)))))))))...)).)))))))..)))))))...........-3'
MFE = -57.6; z-score = -4.04; ED = 13.49
```

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

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

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

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

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

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

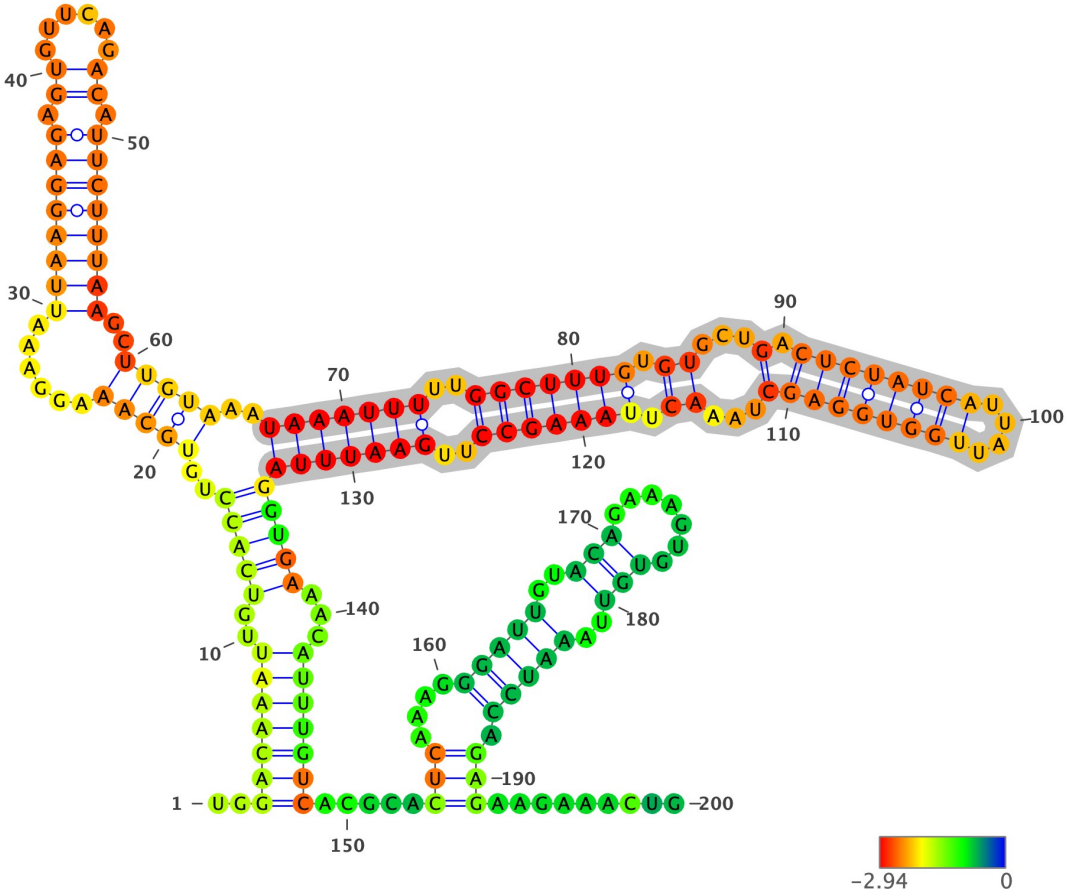
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 2314 to 2380 (nt 67 to 133)

```
5'-TAAATTTTTGGCTTTGTGTGCTGACTCTATCATTATTGGTGGAGCTAAACTTAAAGCCTTGAAUUUA-3'
5'-(((((((..(((((((..((...(.(((((((.....)))))))))...)).)).)))))).)))))))-3'
Motif MFE = -24.1; z-score = -4.59; ED = 2.11
```



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

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

```
5'-UGGACAAAUUGUCACCUGUGCAAAGGAAAUUAAGGAGAGUGUUCAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGC
UAAACUUAAAGCCUUGAAUUUAGGUGAAACAUUUGUCACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUG-3
5'-..(((((((..((((((..((((((.....((((((((.((.....)).)))))))).))))))..))))))..(((((((..(((((((.((...(.(((((((((....)))))))))
...)).)))))))..))))))))))))...)))))))).....(((....((((((..(((.......)))..))))))...))).........-3'
MFE = -52.5; z-score = -3.06; 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(+)

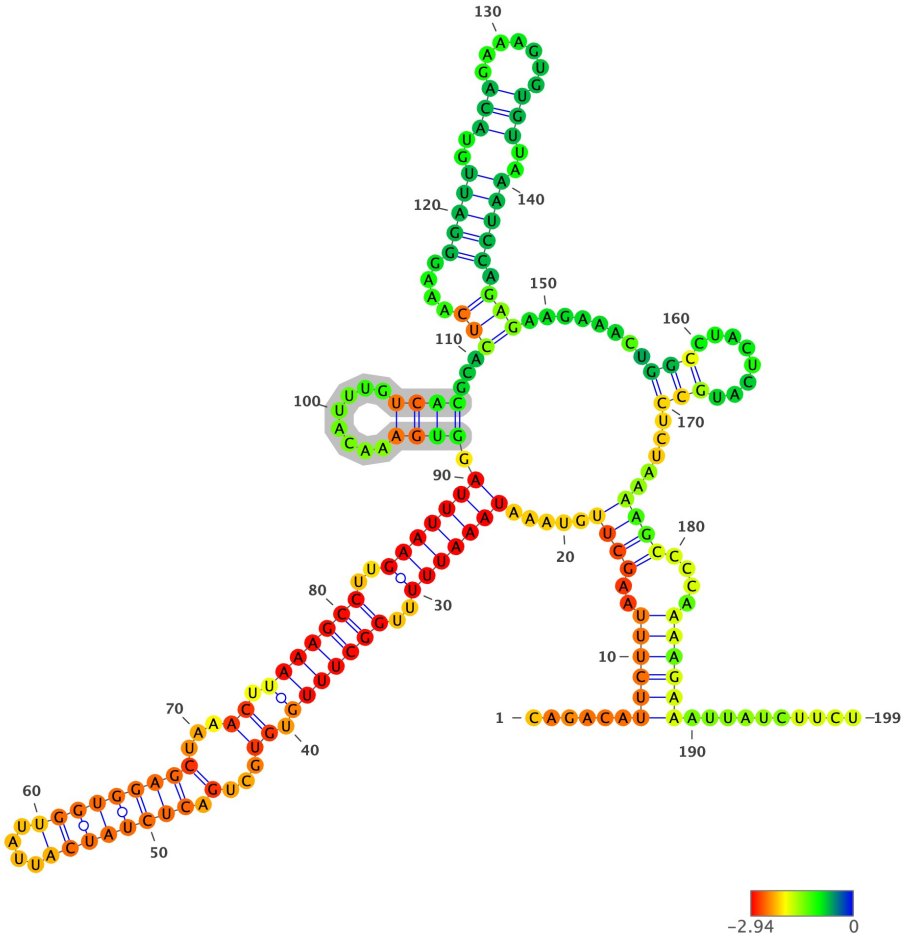
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 43 from nt 2382 to 2397 (nt 92 to 107)

```
5'-GTGAAACATTTGTCAC-3'
5'-((............))-3'
Motif MFE = -1.5; z-score = -1.78; ED = 1.05
```



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

Extracted structure model with flanking nucleotides 2291 to 2489 (motif highlighted in silver):

```
5'-CAGACAUUCUUUAAGCUUGUAAAUAAAUUUUUGGCUUUGUGUGCUGACUCUAUCAUUAUUGGUGGAGCUAAACUUAAAGCCUUGAAUUUAGGUGAAACAUUUGUCACGCAC
UCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCU-3
5'-......((((((..((((.....(((((((..(((((((.((...(.((((((((....)))))))))...)).)))))))..)))))))).((((........))))...(
((....(((((..(((.......)))..))))).)))........(((........)))).....))))....))))))..........-3'
MFE = -45.0; z-score = -1.73; 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(+)

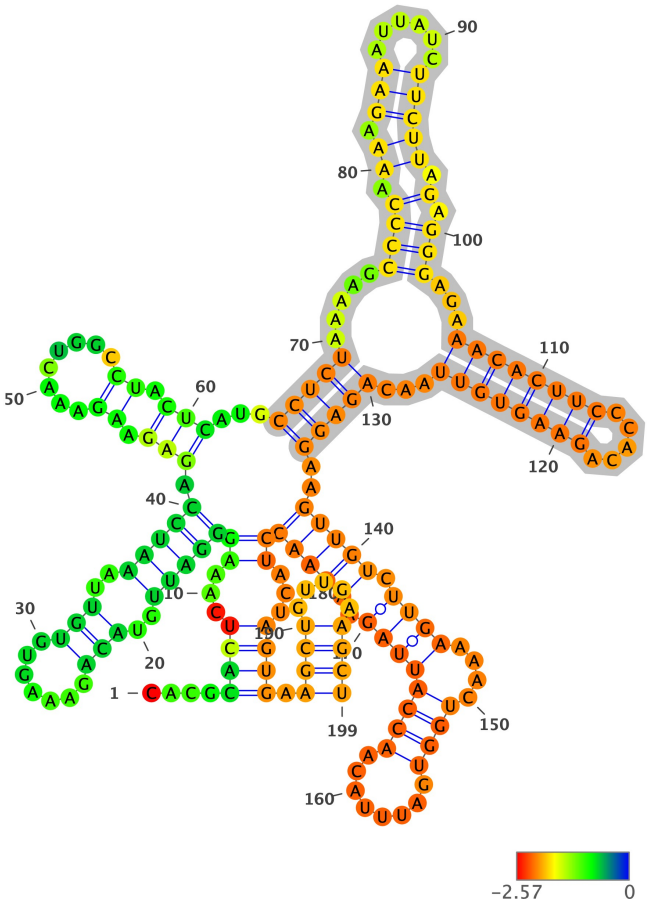
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 44 from nt 2459 to 2528 (nt 65 to 134)

```
5'-CCTCTAAAAGCCCCAAAAGAAATTATCUUCUUAGAGGGAGAAACACTTCCCACAGAAGUGUUAACAGAGG-3'
5'-(((.......((((.((.(((......))))).).)))...((((((((.....))))))))).....)))-3'
Motif MFE = -18.8; z-score = -3.98; ED = 5.36
```



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

Extracted structure model with flanking nucleotides 2395 to 2593 (motif highlighted in silver):

```
5'-CACGCACUCAAAGGGAUUGUACAGAAAGUGUGUUAAAUCCAGAGAAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACU
UCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCU-3
5'-....((((...(((((((..(((.......)))..))))).(((.((........)).)))...(((((.....((((.((.(((......))))).).)))...((((((
((.....))))))))...)))))..(((((.((((....((((........))))))))).)))))))...)))).((((.....))))-3'
MFE = -42.5; z-score = -1.93; ED = 14.95
```

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(+)

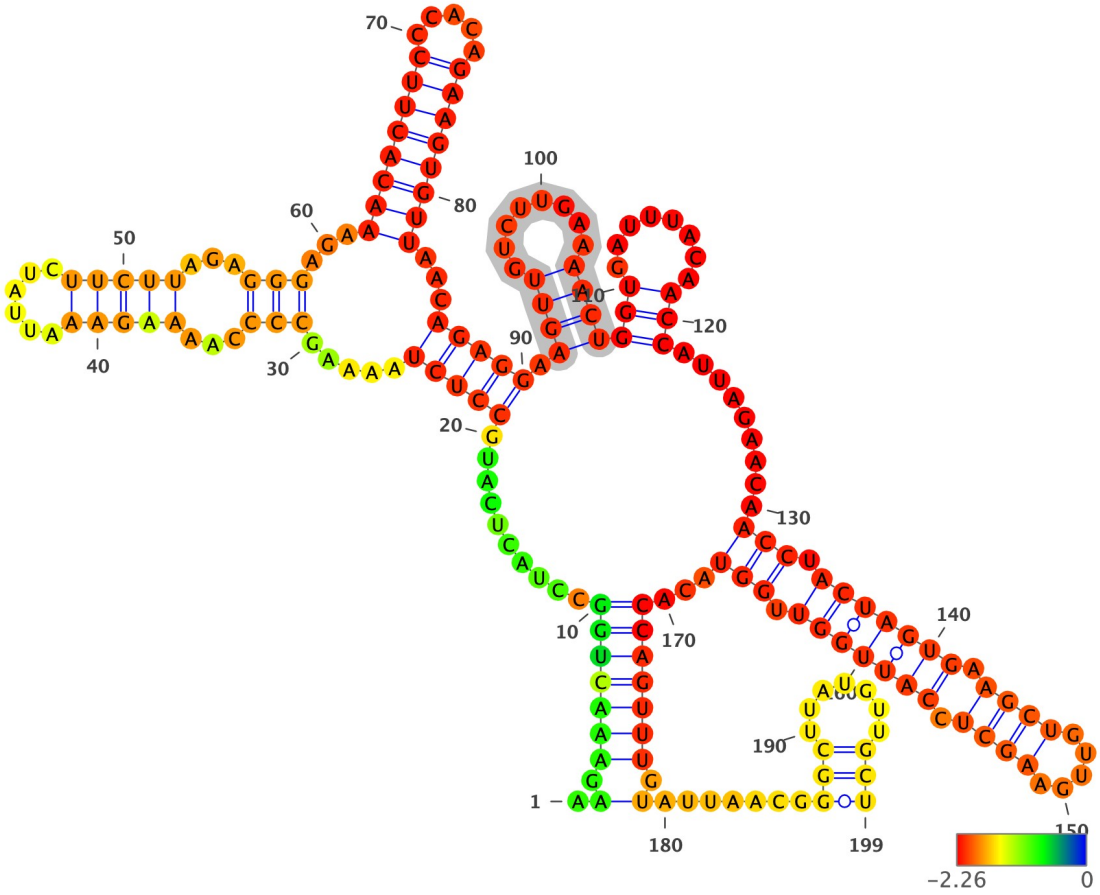
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 45 from nt 2530 to 2545 (nt 92 to 107)

```
5'-AGTTGTCTTGAAAACU-3'
5'-((((........))))-3'
Motif MFE = -0.7; z-score = -0.69; ED = 1.54
```



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

Extracted structure model with flanking nucleotides 2439 to 2637 (motif highlighted in silver):

```
5'-AAGAAACUGGCCUACUCAUGCCUCUAAAAGCCCCAAAAGAAAUUAUCUUCUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUG
AUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCU-3
5'-.(.(((((((..........(((((.....(((...(((((......)))))...)))...((((((((.....))))))))...))))).((((........))))(((.
.......)))........(((.(((((((.((((.....)))).)))))))).)))...)))))))).).......(((.......)))-3'
MFE = -51.8; z-score = -2.69; ED = 24.54
```

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

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

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

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

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

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

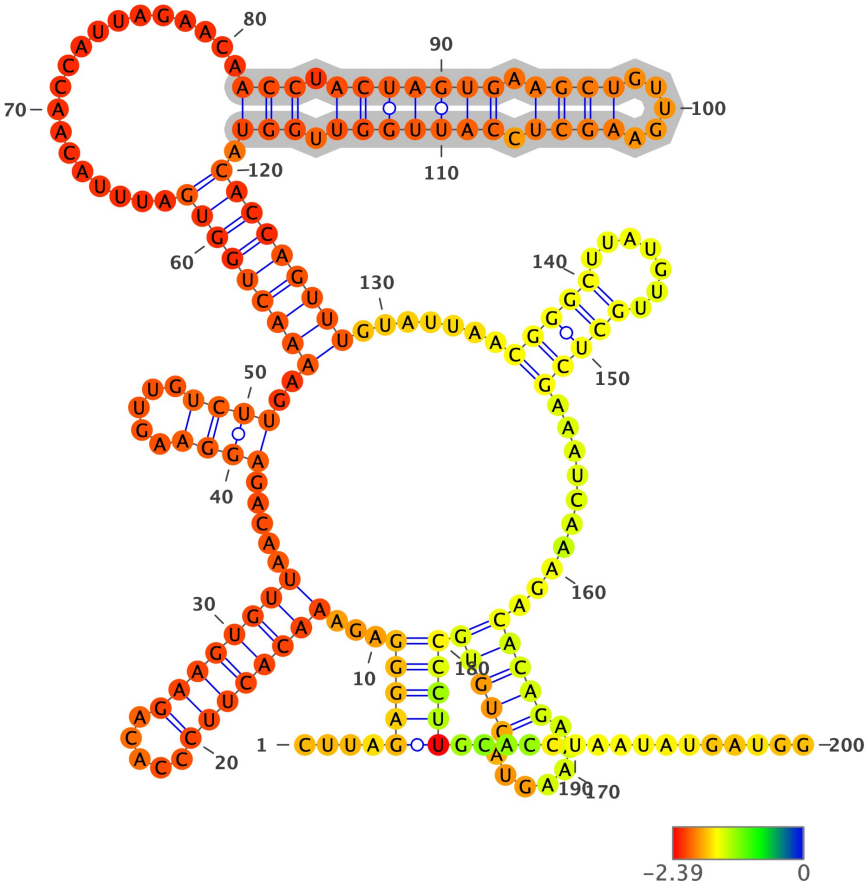
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 46 from nt 2569 to 2605 (nt 82 to 118)

```
5'-ACCTACTAGTGAAGCTGTTGAAGCUCCAUUGGUTGGU-3'
5'-(((.(((((((.((((.....)))).))))))).)))-3'
Motif MFE = -15.4; z-score = -3.93; 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 2488 to 2687 (motif highlighted in silver):

```
5'-CUUAGAGGGAGAAACACUUCCCACAGAAGUGUUAACAGAGGAAGUUGUCUUGAAAACUGGUGAUUUACAACCAUUAGAACAACCUACUAGUGAAGCUGUUGAAGCUCCAUU
GGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGG-3
5'-....(((((...((((((((.....))))))))).....((((.....)))).((((((((((.....................(((.(((((((.((((.....)))).))))
))).))).))))))))).......(((((.......)))))..........(((((.......)))))))))).................-3'
MFE = -53.0; z-score = -2.11; ED = 19.41
```

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(+)

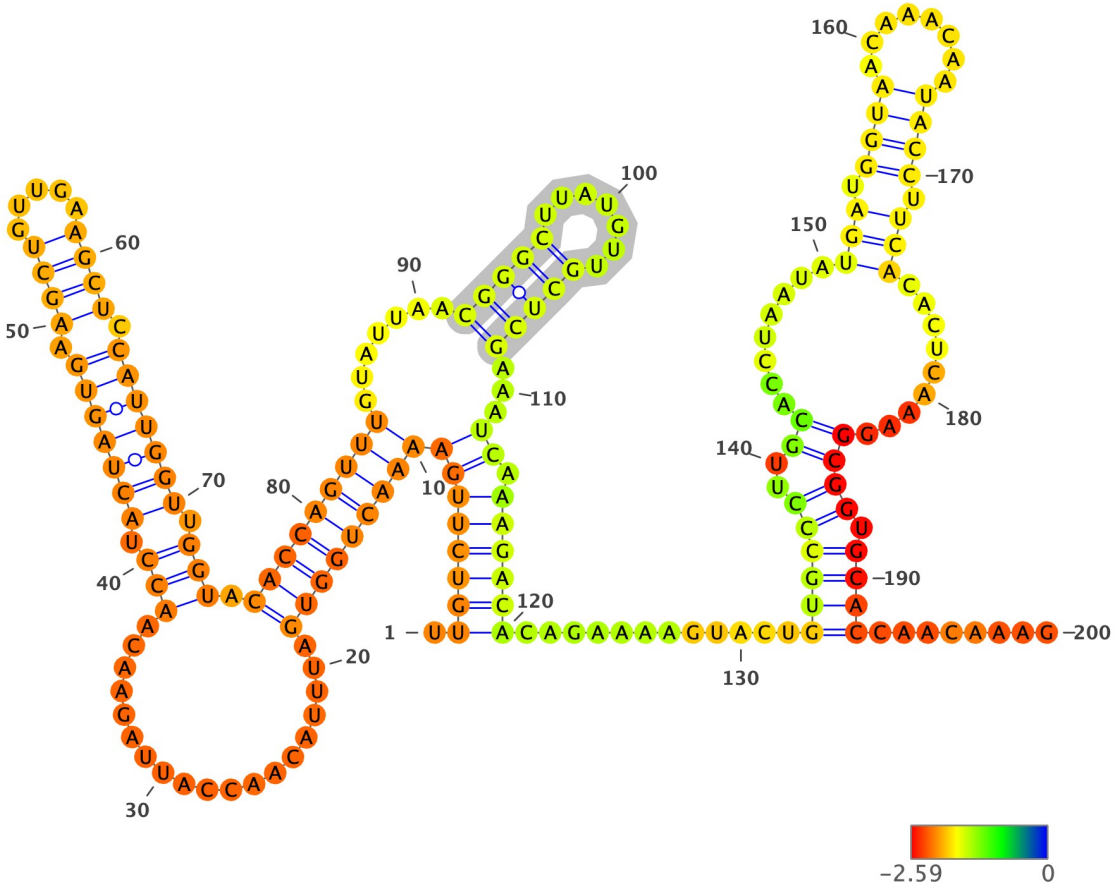
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 47 from nt 2623 to 2639 (nt 92 to 108)

```
5'-CGGGCTTATGTTGCUCG-3'
5'-(((((.......)))))-3'
Motif MFE = -5.5; z-score = -2.91; 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 = -2.86; 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(+)

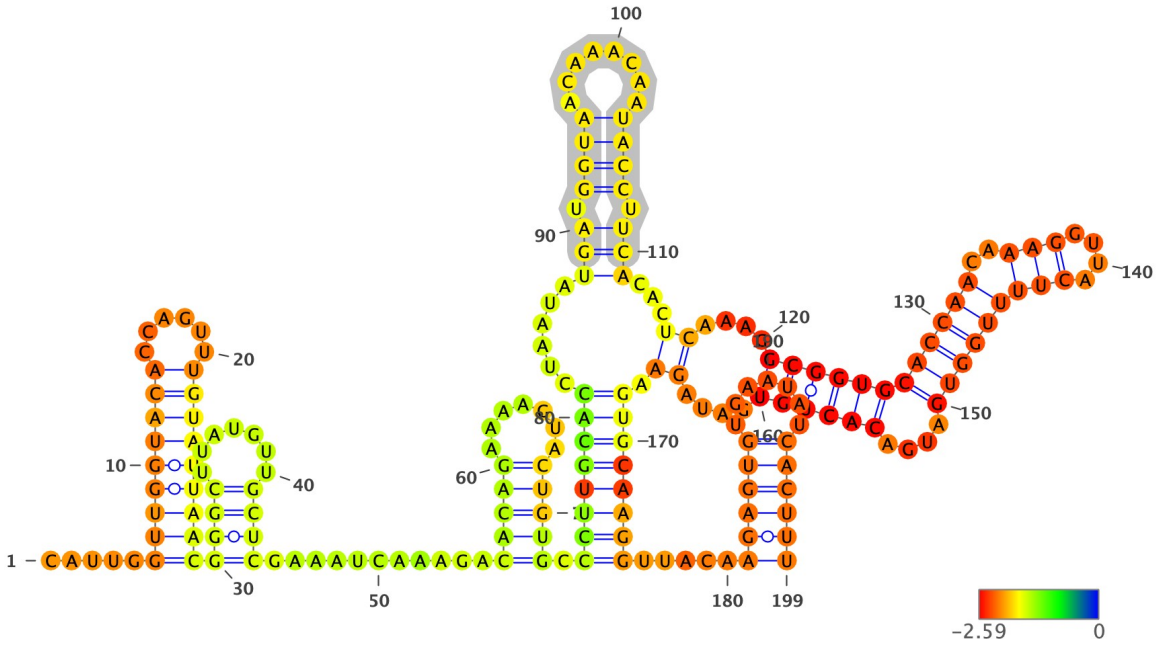
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 48 from nt 2683 to 2704 (nt 89 to 110)

```
5'-GATGGTAACAAACAAUACCTUC-3'
5'-((.((((........)))).))-3'
Motif MFE = -3.2; z-score = -2.4; ED = 1.12
```



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

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

```
5'-CAUUGGUUGGUACACCAGUUUGUAUUAACGGGCUUAUGUUGCUCGAAAUCAAAGACACAGAAAAGUACUGUGCCCUUGCACCUAAUAUGAUGGUAACAAACAAUACCUUCA
CACUCAAAGGCGGUGCACCAACAAAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUU-3
5'-.....((((((((((......))))))))))(((.......))))..........(((((.......))))).(((((((((......(((.((((........)))).)))
...((....((((((((((((..(((....)))))))))....))))))....)).)))))))).....((((((.......))))))-3'
MFE = -52.2; z-score = -2.57; 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(+)

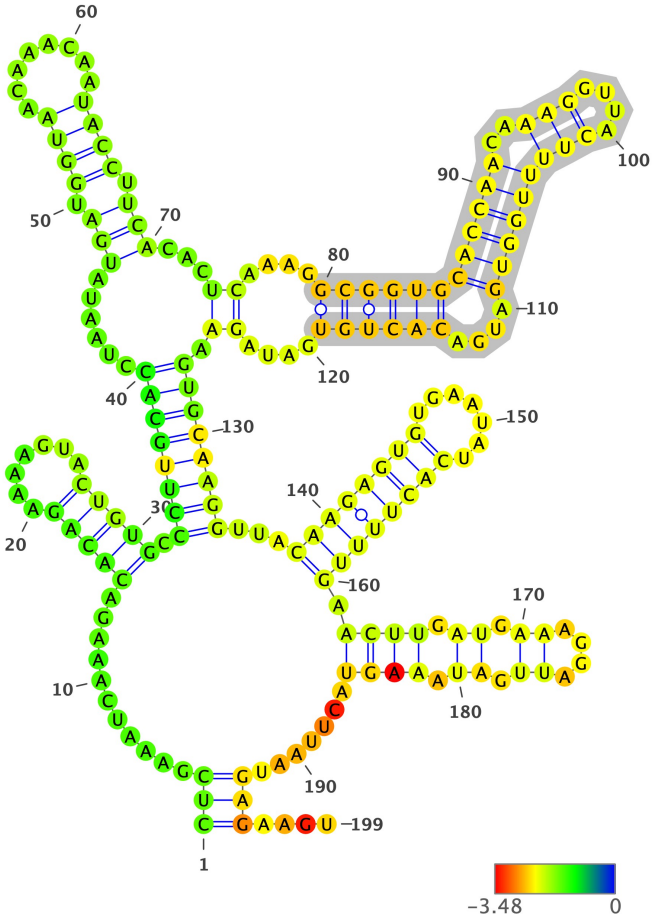
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-GCGGTGCACCAACAAAGGTTACUUUUGGUGATGACACUGU-3'
5'-(((((((((((((..(((....)))))))))....))))))-3'
Motif MFE = -12.9; z-score = -2.64; 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 = -2.68; 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(+)

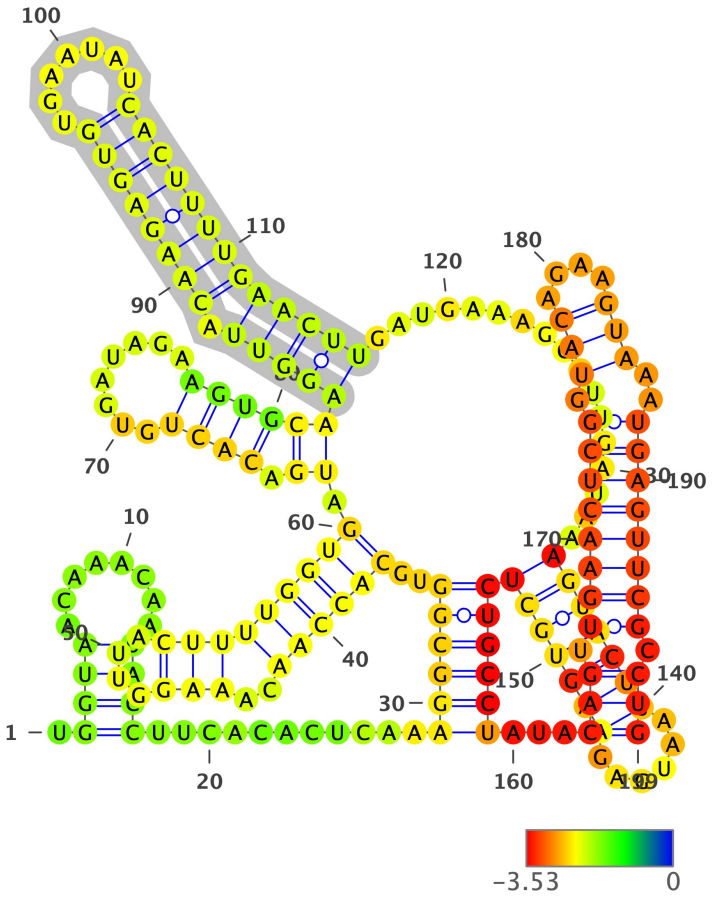
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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'-AGGTTACAAGAGTGTGAATATCACUUUUGAACUU-3'
5'-(((((.(((((((((.......)))))))))))))))-3'
Motif MFE = -10.9; z-score = -3.86; 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 = -3.23; 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(+)

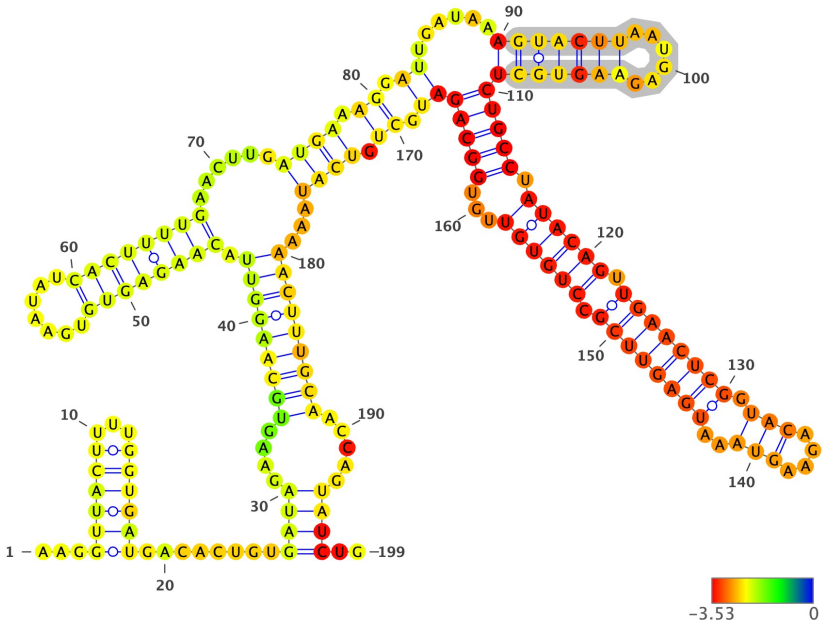
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 2819 to 2836 (nt 91 to 108)

```
5'-GTACTTAATGAGAAGUGC-3'
5'-(((............)))-3'
Motif MFE = -3.8; z-score = -3.13; 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 2729 to 2927 (motif highlighted in silver):

```
5'-AAGGUUACUUUUGGUGAUGACACUGUGAUAGAAGUGCAAGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCU
GCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUG-3
5'-...((((((...))))))........((((....(((((((((.((((((((.......))))))))......((((.((.((......(((((((......)))))))((
(((.((((((.((((((((.(((....)))..)))))))).))))))...)))))))).)).))))...))))))))).....))))..-3'
MFE = -57.2; z-score = -3.93; ED = 41.48
```

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(+)

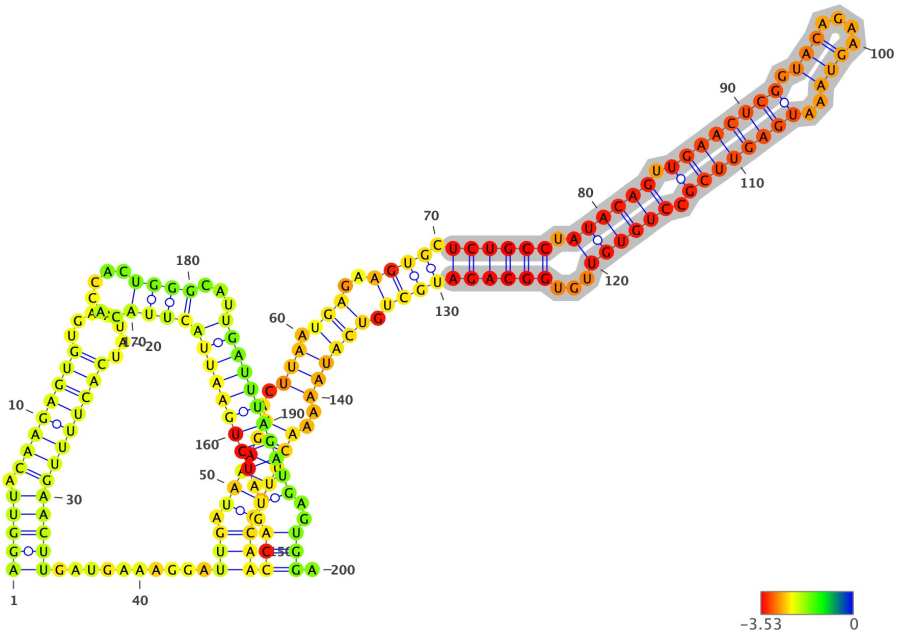
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 52 from nt 2837 to 2895 (nt 71 to 129)

```
5'-TCTGCCTATACAGTTGAACTCGGTACAGAAGTAAAUGAGUUCGCCUGUGUTGTGGCAGA-3'
5'-((((((.(((((((.(((((((((.............)))))))))..)))))))...)))))))-3'
Motif MFE = -27.0; z-score = -5.31; ED = 1.66
```



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

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

```
5'-AGGUUACAAGAGUGUGAAUAUCACUUUUGAACUUGAUGAAAGGAUUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUU
CGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGA-3
5'-(((((.(((((((((.......)))))))))))))).........(((.(((((((..(((.(((..(((((.(((((((.(((((((.(((((((((.(((....))))..)))))))
)).)))))))...)))))))))).)))))))..))))))))))(((.((((((((((((((((.....)))))...))))))))))))..))).-3'
MFE = -60.4; z-score = -3.6; ED = 18.7
```

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, 266-13468(+)

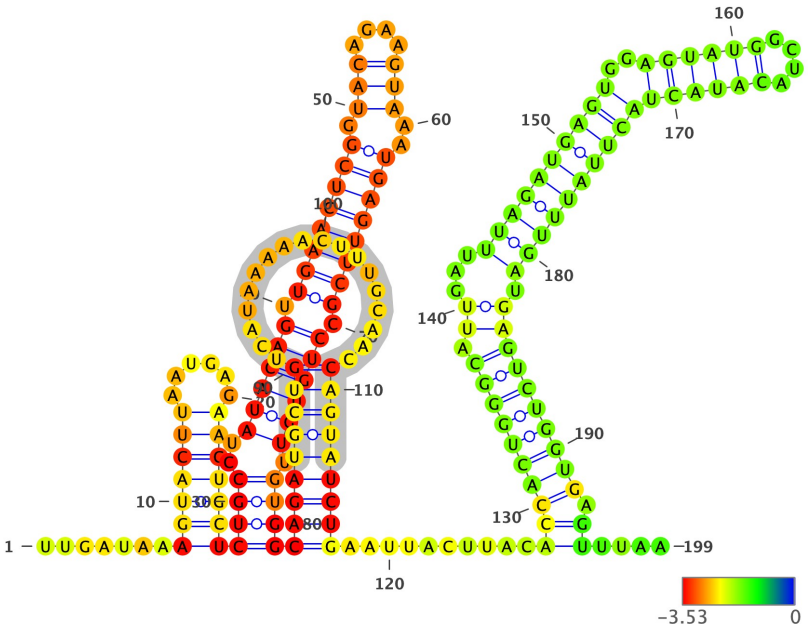
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 2896 to 2923 (nt 86 to 113)

```
5'-TGCTGTCATAAAAACTTTGCAACCAGUA-3'
5'-((((.....................))))-3'
Motif MFE = -1.1; z-score = 0.07; ED = 5.79
```



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

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

```
5'-UUGAUAAAGUACUUAAUGAGAAGUGCUCUGCCUAUACAGUUGAACUCGGUACAGAAGUAAAUGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAG
UAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUACUUAUUUGAUGAGUCUGGUGAGUUUAA-3
5'-.......(((((((......)))))))((((..((((((.((((((((.(((....)))..)))))))).)))))).))))((((((((.................)))
))))))..........((((((((((.((...((((((((((..((((((....)))))))))))))))).))))))))))).))....-3'
MFE = -60.2; z-score = -4.21; ED = 20.49
```

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

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

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

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

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

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

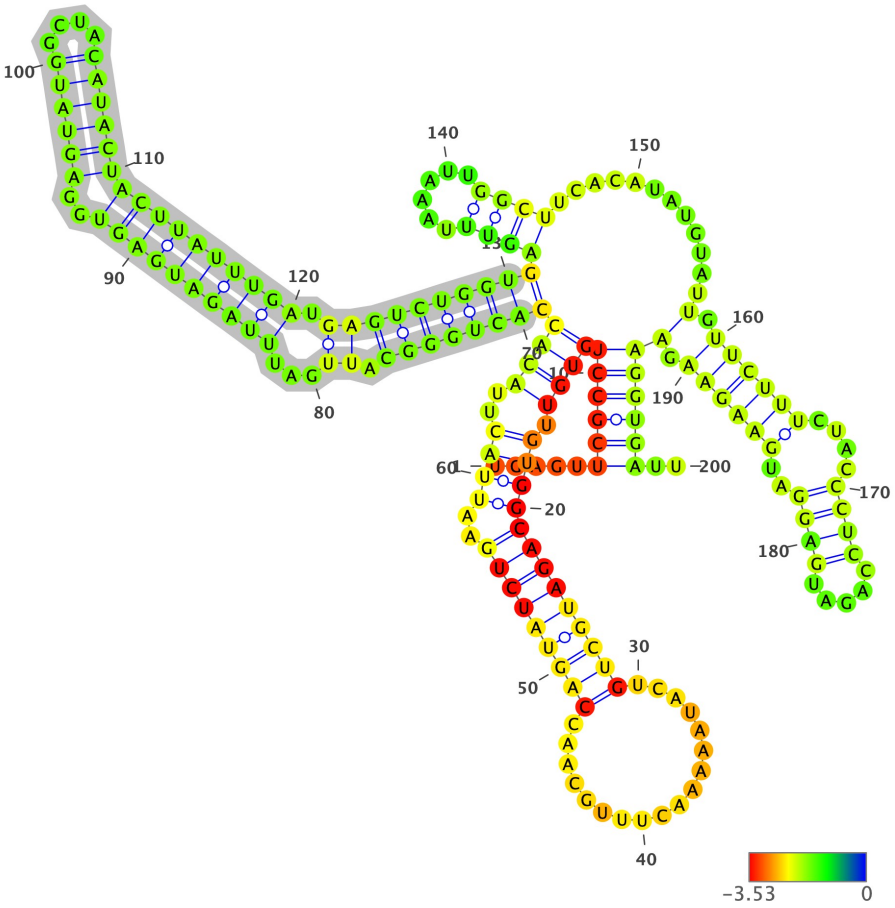
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 54 from nt 2941 to 3001 (nt 70 to 130)

```
5'-ACTGGGCATTGATTTAGATGAGTGGAGTATGGCTACAUACUACUUAUUUGAUGAGUCUGGU-3'
5'-(((((((...(...((((((((((..(((((......)))))))))))))))).)..)))))))-3'
Motif MFE = -19.3; z-score = -3.48; ED = 5.78
```



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

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

```
5'-UGAGUUCGCCUGUGUUGUGGCAGAUGCUGUCAUAAAAACUUUGCAACCAGUAUCUGAAUUACUUACACCACUGGGCAUUGAUUUAGAUGAGUGGAGUAUGGCUACAUACUA
CUUAUUUGAUGAGUCUGGUGAGUUUAAAUUGGCUUCACAUAUGUAUUGUUCUUUCUACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUU-3
5'-.....((((((((((.((((((((((((.................))))))))).))))..))))((((((((.((...((((((((((..((((((....))))))))))))))))))))))))))))).)))))))))).(((((((((((((.....)))).............(.((((((....((((.....))))).))))))).)))))))..-3'
MFE = -54.6; z-score = -2.53; ED = 22.59
```

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

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

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

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

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

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

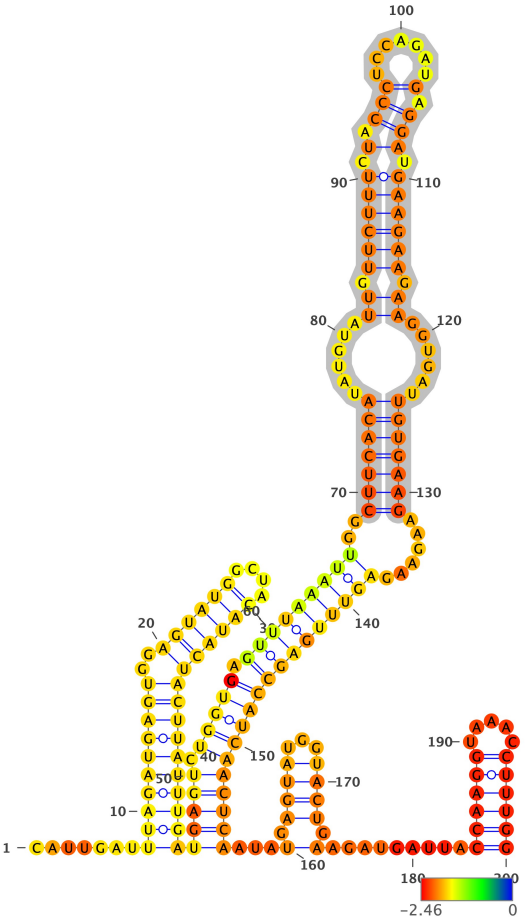
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 55 from nt 3015 to 3077 (nt 69 to 131)

```
5'-CTTCACATATGTATTGTTCTTTCTACCCTCCAGATGAGGATGAAGAAGAAGGTGATUGUGAAG-3'
5'-(((((((.....((.(((((((.(.(((.......).))).))))))).))).....)))))))-3'
Motif MFE = -17.5; z-score = -2.49; 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 = -52.1; z-score = -3.11; ED = 19.42
```

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

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

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

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

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

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

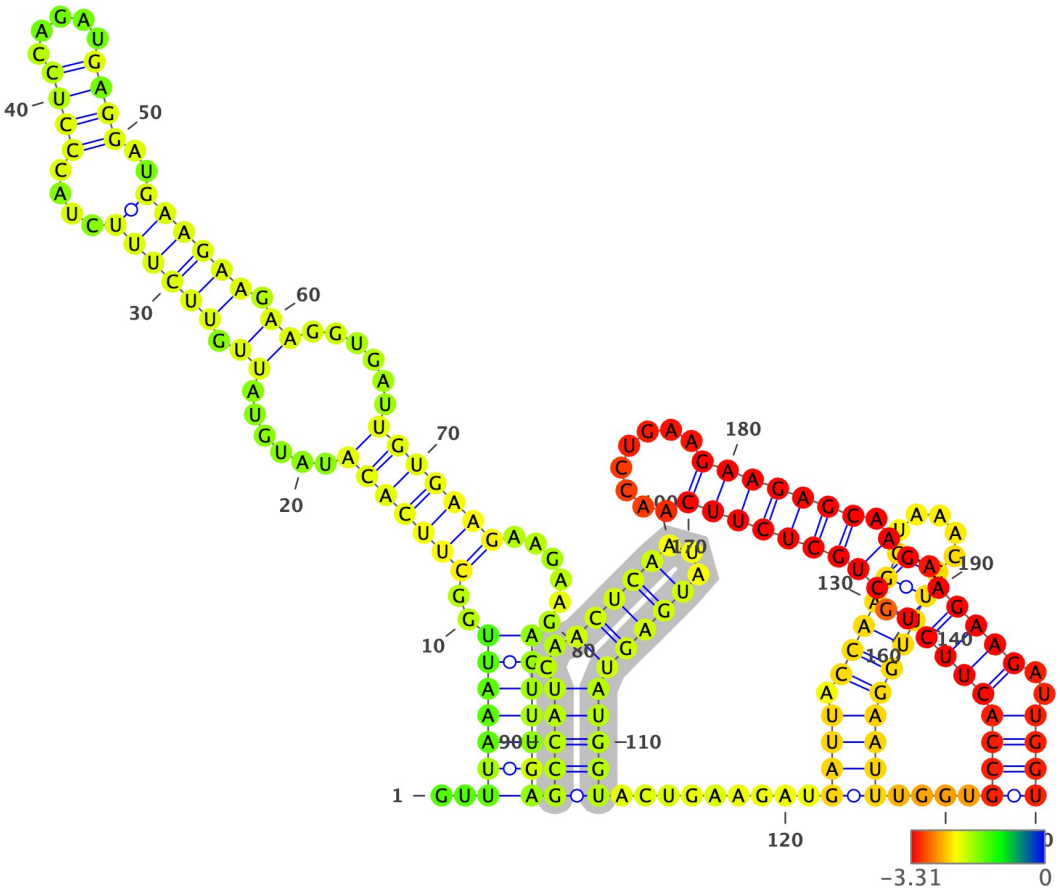
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-GCCATCAACTCAATAUGAGUAUGGU-3'
5'-(((((..(((((...)))))))))-3'
Motif MFE = -7.6; z-score = -3.47; 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 = -4.09; 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(+)

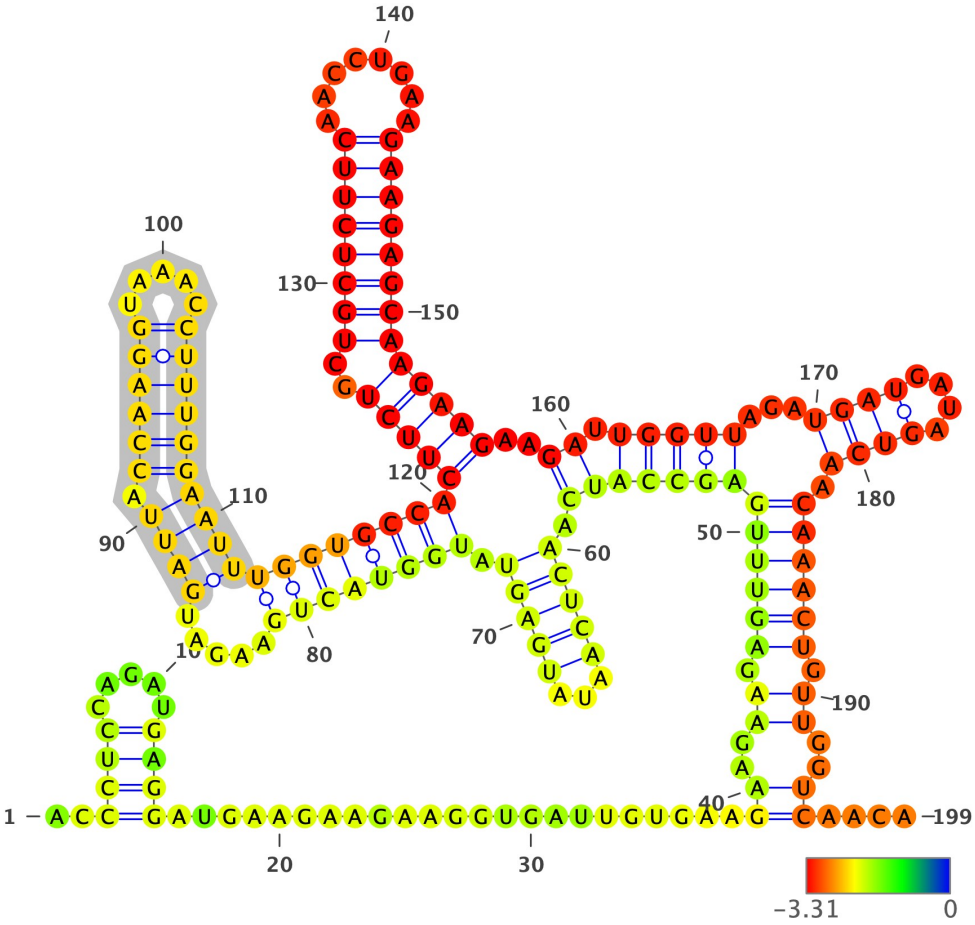
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 3125 to 3150 (nt 87 to 112)

```
5'-GATTACCAAGGTAAACCUUUGGAAUU-3'
5'-((((.((((((.....))))))))))-3'
Motif MFE = -5.7; z-score = -2.66; ED = 5.17
```



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 3039 to 3237 (motif highlighted in silver):

```
5'-ACCCUCCAGAUGAGGAUGAAGAAGAAGGUGAUUGUGAAGAAGAAGAGUUUGAGCCAUCAACUCAAUAUGAGUAUGGUACUGAAGAUGAUUACCAAGGUAAACCUUUGGAAU
UUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACA-3
5'-..((((.....)))).......................((..((.(((((((((((((.(((((...))))).((((((((.....((((.((((((.....)))))))))
))))))))))(((((..((((((((........)))))))))))))..)).)))))...((((....)))).)))))).))..)).....-3'
MFE = -50.5; z-score = -2.48; ED = 43.07
```

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

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

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

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

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

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

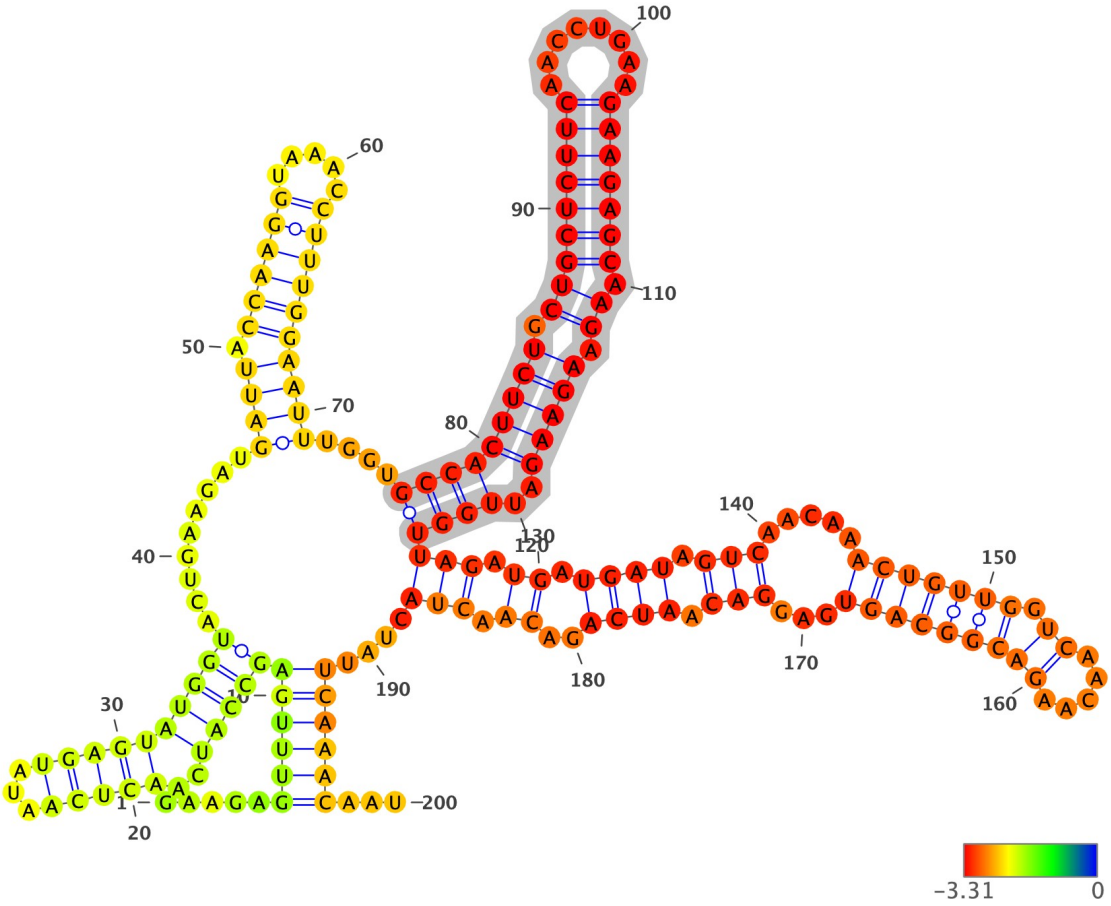
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-GCCACTTCTGCTGCTCTTCAACCTGAAGAAGAGCAAGAAGAAGATUGGU-3'
5'-(((((((((.((((((((((........)))))))).)).)))))..))))-3'
Motif MFE = -20.1; z-score = -4.33; 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 = -4.3; ED = 17.48
```

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(+)

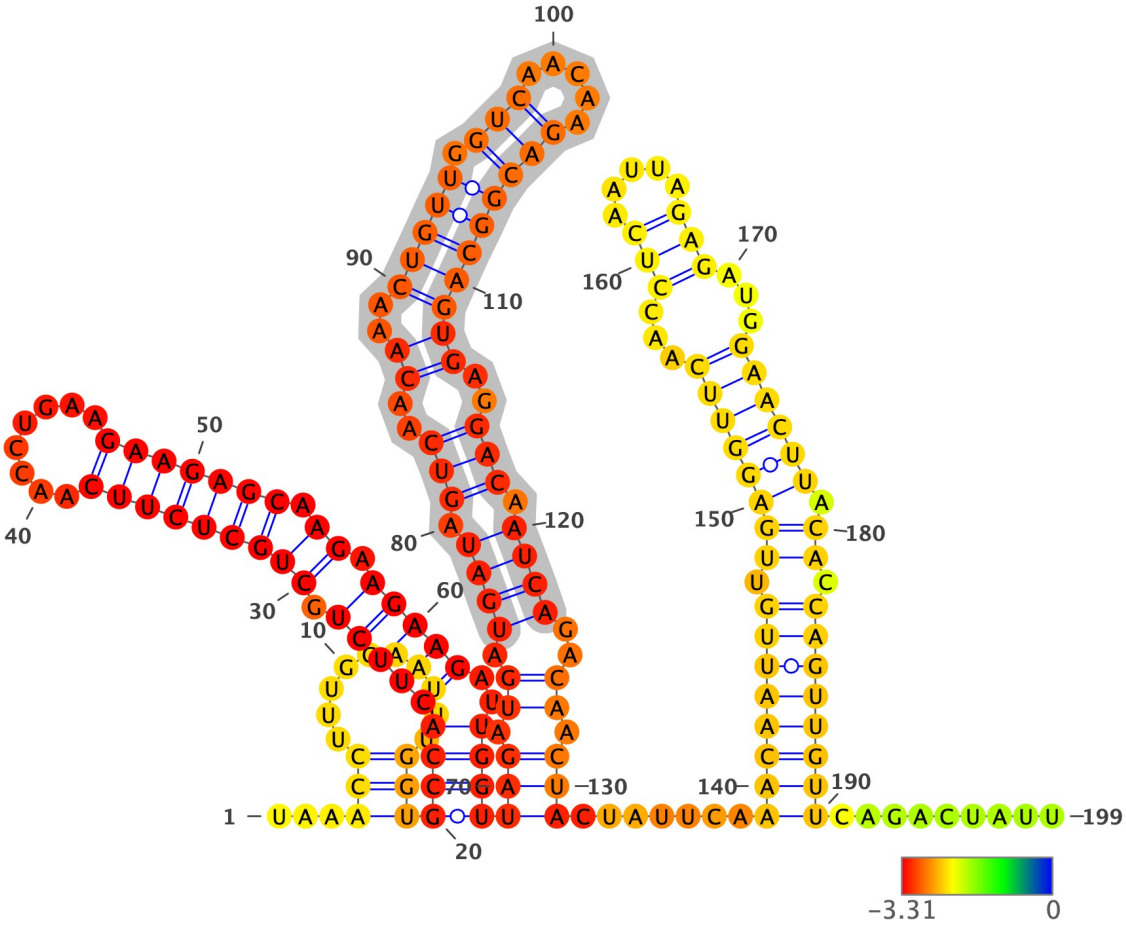
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 59 from nt 3211 to 3258 (nt 76 to 123)

```
5'-TGATAGTCAACAAACTGTTGGTCAACAAGACGGCAGUGAGGACAAUCA-3'
5'-((((.(((..((..(((((.(((.....)))))))))..))).))))-3'
Motif MFE = -13.5; z-score = -3.06; ED = 3.99
```



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 3136 to 3334 (motif highlighted in silver):

```
5'-UAAACCUUUGGAAUUUGGUGCCACUUCUGCUGCUCUUCAACCUGAAGAAGAGCAAGAAGAAGAUUGGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAG
UGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUU-3
5'-...(((..........)))(((((((((.((((((((((........)))))))).)).)))))..))))(((.((.((((.(((..((..(((((.(((.....))))))))
))..))).))))..)).)))......((((((((.((((((((...(((.....)))...)))))).)).))))))))..........-3'
MFE = -55.1; z-score = -3.5; ED = 43.5
```

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(+)

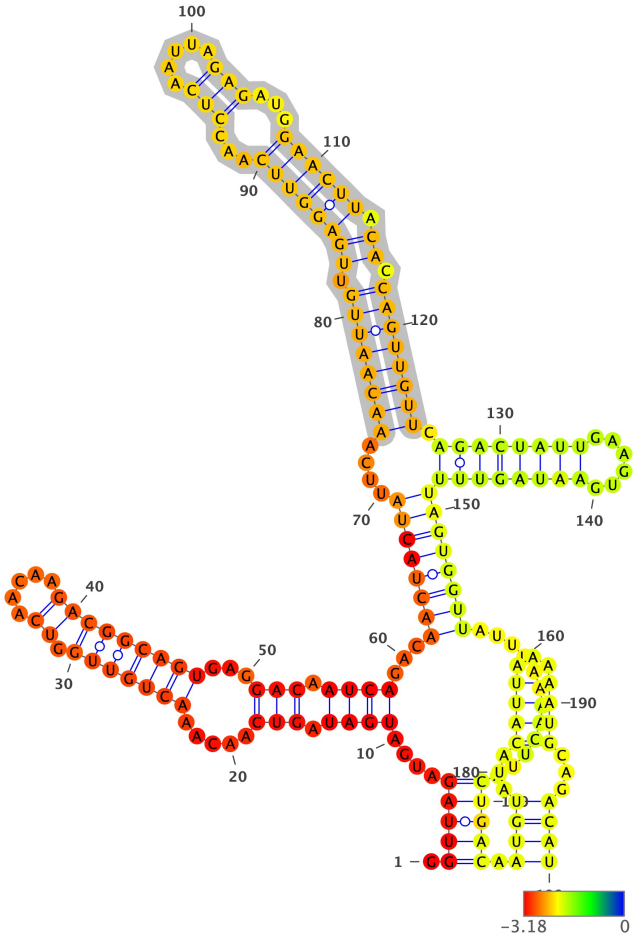
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 60 from nt 3274 to 3325 (nt 74 to 125)

```
5'-AACAATTGTTGAGGTTCAACCTCAATTAGAGATGGAACUUACACCAGUUGUU-3'
5'-(((((((((.(((((((((...(((.....)))...)))))))).)).)))))))-3'
Motif MFE = -16.5; z-score = -4.04; ED = 1.36
```



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

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

```
5'-GGUUAGAUGAUGAUAGUCAACAAACUGUUGGUCAACAAGACGGCAGUGAGGACAAUCAGACAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAAC
UUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAU-3
5'-.(((((....((((.(((.....(((((((.((.....)))))))))...)))).)))))...(((((((((....(((((((.(((((((((...(((.....)))...)))))
))).)).)))))))).(((((((.....)))))))))))))))).....)))))).((((...((((...))))...))))-3'
MFE = -47.0; z-score = -3.39; ED = 24.66
```

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

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

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

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

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

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

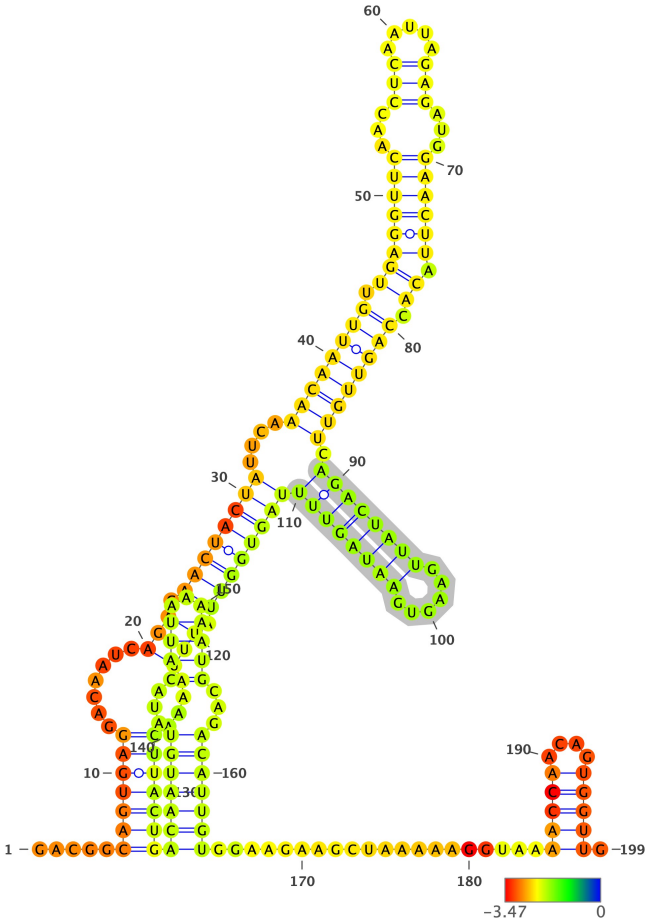
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 61 from nt 3327 to 3348 (nt 89 to 110)

```
5'-AGACTATTGAAGTGAAUAGUUU-3'
5'-((((((.(......).))))))-3'
Motif MFE = -5.2; z-score = -4.51; 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 = -3.3; 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(+)

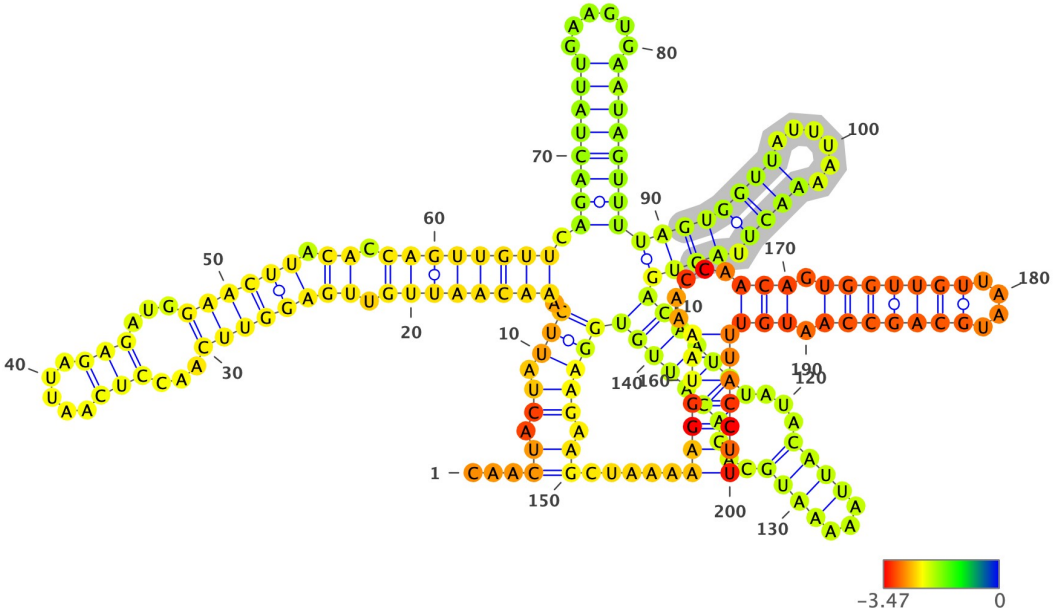
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 3351 to 3369 (nt 91 to 109)

```
5'-GTGGTTATTTAAAACUTAC-3'
5'-((((((......)))).))-3'
Motif MFE = -0.3; z-score = 0.09; 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 3261 to 3460 (motif highlighted in silver):

```
5'-CAACUACUAUUCAAACAAUUGUUGAGGUUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUG
ACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUU-3
5'-...((.((.(((.((((((((.((((((((...(((.....)))...)))))).)).))))))))).((((((((......))))))))((((((((......)))).))))
(((((((...((((...))))...)))))))))))).)).....(((((((.....(((.(((((((....)))))))).))))))))))-3'
MFE = -50.8; z-score = -4.51; ED = 16.77
```

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(+)

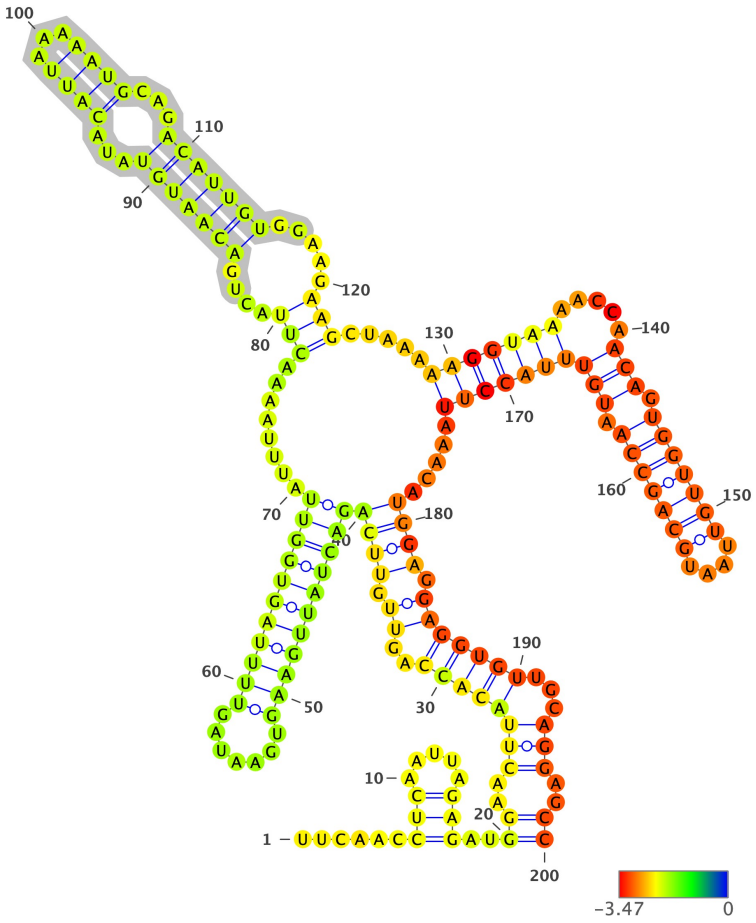
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 63 from nt 3370 to 3404 (nt 83 to 117)

```
5'-TGACAATGTATACATTAAAAAUGCAGACAUUGUGG-3'
5'-(.(((((((...((.......))...)))))))).)-3'
Motif MFE = -7.6; z-score = -2.39; 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 3288 to 3487 (motif highlighted in silver):

```
5'-UUCAACCUCAAUUAGAGAUGGAACUUACACCAGUUGUUCAGACUAUUGAAGUGAAUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACA
UUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCC-3
5'-......((.....)))..((..(((((((((..((.(((((((((((((((.......)))))))))))).........(((....(((((((...(((((...)))))...)))
))))).....)))).....(((((((.....(((.(((((((....)))))))..)))))))))).....)))).)))))))...))))..))-3'
MFE = -43.9; z-score = -2.08; ED = 40.32
```

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

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

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

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

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

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

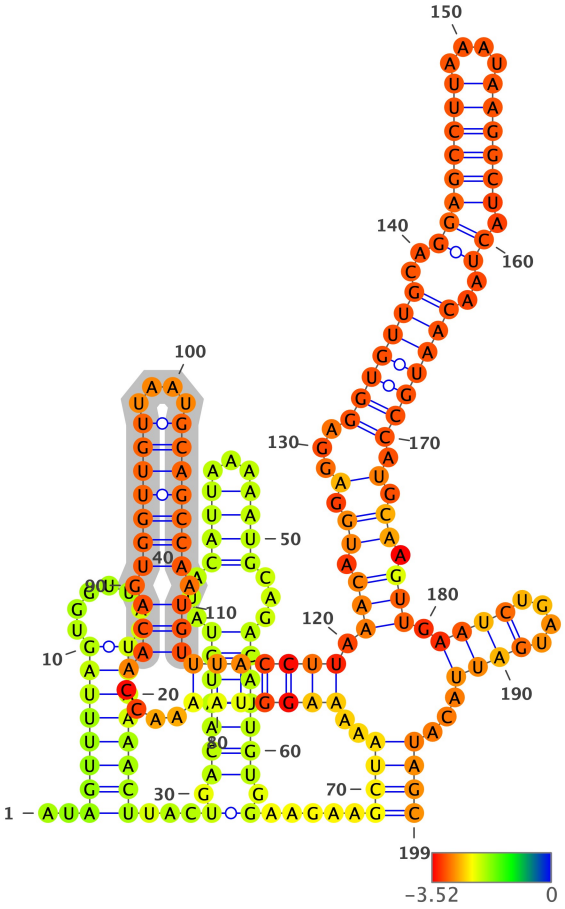
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 64 from nt 3428 to 3453 (nt 87 to 112)

```
5'-ACAGTGGTTGTTAATGCAGCCAAUGU-3'
5'-(((.(((((((....)))))))).)))-3'
Motif MFE = -10.3; z-score = -4.76; 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 3342 to 3540 (motif highlighted in silver):

```
5'-AUAGUUUUAGUGGUUAUUUAAAACUUACUGACAAUGUAUACAUUAAAAAUGCAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUG
UUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGC-3
5'-..((((((((.......))))))))...(.(((((((...((((...))))...)))))))).).....((((..(((((((.....(((.(((((((....)))))))).))
))))))))).(((.((.(...(((((((..((((((((....)))))).))..)))))))).).)).))).((((....))))...))))-3'
MFE = -50.7; z-score = -3.6; ED = 35.82
```

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(+)

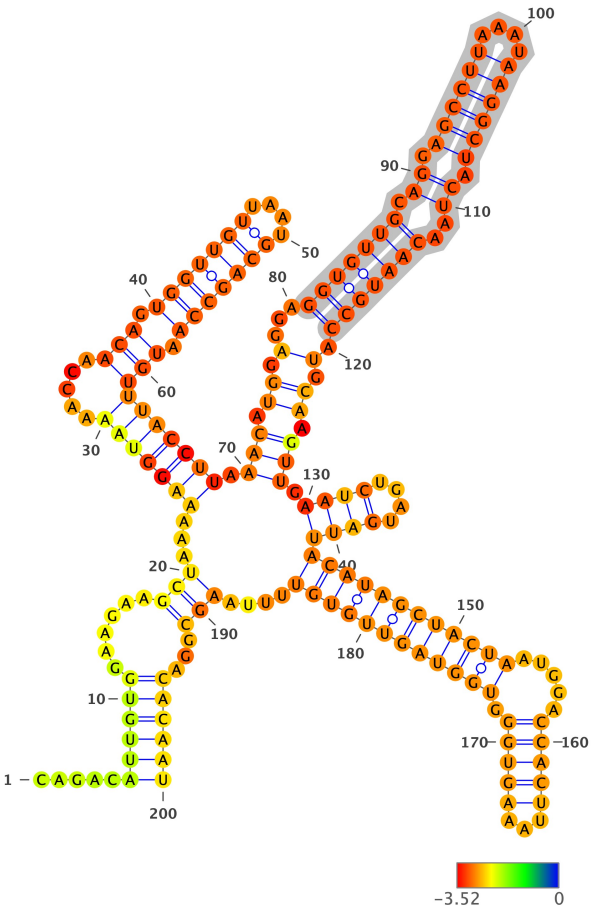
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 65 from nt 3473 to 3511 (nt 81 to 119)

```
5'-GGTGTTGCAGGAGCCTTAAATAAGGCTACUAACAAUGCC-3'
5'-(((((((.((...((((....))))...))..)))))))-3'
Motif MFE = -15.6; z-score = -4.21; ED = 1.87
```



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

Extracted structure model with flanking nucleotides 3393 to 3592 (motif highlighted in silver):

```
5'-CAGACAUUGUGGAAGAAGCUAAAAAGGUAAAACCAACAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUA
ACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAU-3
5'-.....((((((......(((...(((((((.....(((.(((((((....)))))))).))))))))))).(((.((.(...(((((((.((.((((((....)))))).)).
.)))))))).).)).))).((((....))))((((((((((((.....(((((...)))))).)))))))))))....)))...))))))-3'
MFE = -60.2; z-score = -4.63; ED = 19.18
```

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

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

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

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

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

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

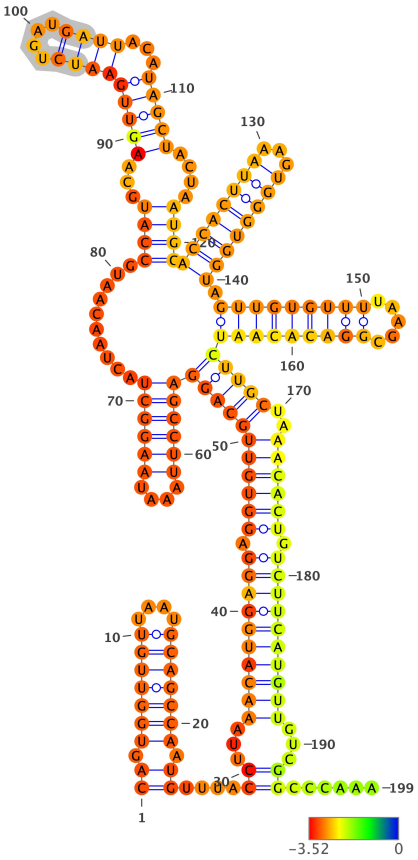
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 66 from nt 3524 to 3531 (nt 96 to 103)

```
5'-TCTGATGA-3'
5'-(......)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 3429 to 3627 (motif highlighted in silver):

```
5'-CAGUGGUUGUUAAUGCAGCCAAUGUUUACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAG
CUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAA-3
5'-((.(((((((....)))))))).))....((...((((((((((.(((((((((((((((((....))))))..........((((...(((((((((....))))))..)))
))....))))(((((((((...)))))))))..(((((((((.....)))))))))))))))..)))))).))))))))...))......-3'
MFE = -66.0; z-score = -4.86; ED = 15.38
```

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(+)

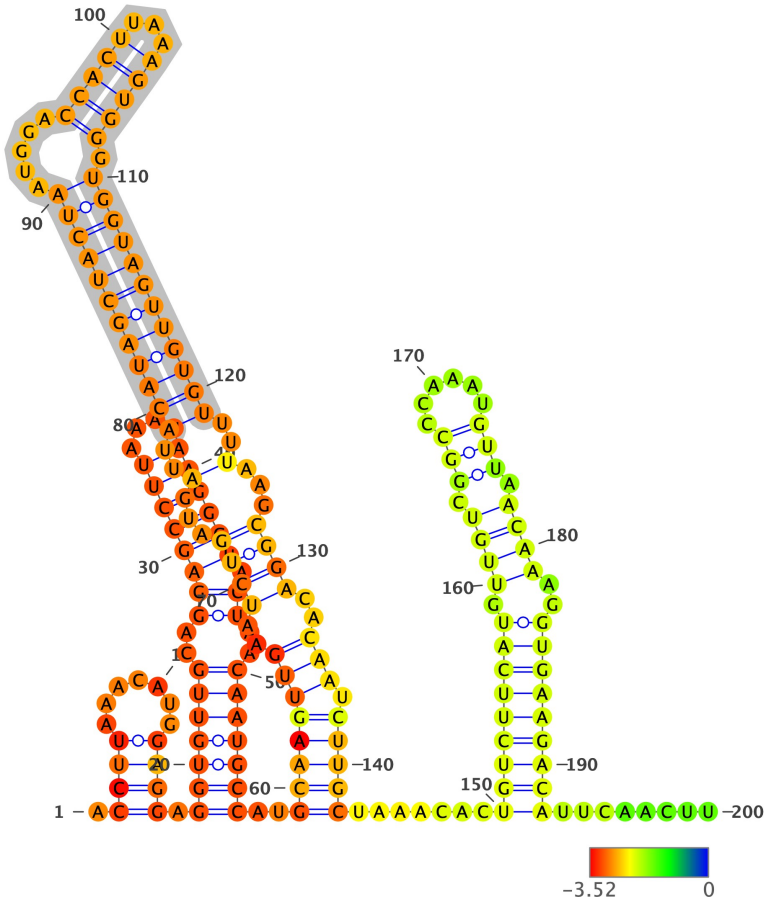
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 67 from nt 3534 to 3576 (nt 79 to 121)

```
5'-ACATAGCTACTAATGGACCACTTAAAGUGGGUGGUAGUUGUGU-3'
5'-(((((((((((((.....((((.....)))).))))))))))))-3'
Motif MFE = -16.7; z-score = -3.91; 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 3456 to 3655 (motif highlighted in silver):

```
5'-ACCUUAAACAUGGAGGAGGUGUUGCAGGAGCCUUAAAUAAGGCUACUAACAAUGCCAUGCAAGUUGAAUCUGAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUG
GUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUU-3
5'-.((((.......)))).(((((((..((((((((....)))))).))..)))))))..((((((((..((((...(..(((((((((((.....(((((...))))).))
))))))))))..)...))))..))).)))))).......(((((((((.((((.(((......))).))))..)))))))))........-3'
MFE = -64.9; z-score = -4.64; ED = 12.32
```

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

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

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

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

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

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

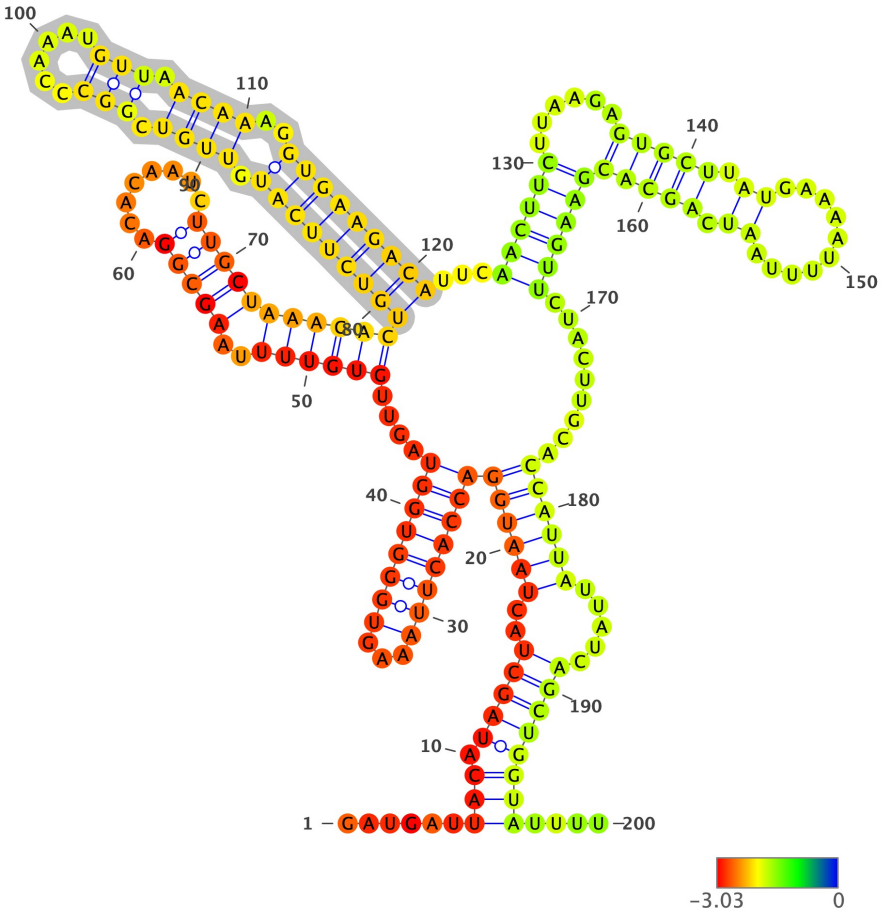
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 68 from nt 3605 to 3647 (nt 79 to 121)

```
5'-TGTCTTCATGTTGTCGGCCCAAATGUTAACAAAGGUGAAGACA-3'
5'-((((((((((.((((..((......))..)))))..))))))))))-3'
Motif MFE = -14.2; z-score = -3.01; ED = 2.86
```



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

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

```
5'-GAUGAUUACAUAGCUACUAAUGGACCACUUAAAGUGGGUGGUAGUUGUGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAA
GGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUU-3
5'-......(((.((((((..(((((((((((((((...)))))))))....((((((..(((((........)))))))))))))))))))))))).(((((.(((......))).)))))
.))))))))))...((((((.....((((((.((..........)).))))))))))).........))))))).....)))))))).....-3'
MFE = -49.8; z-score = -2.31; ED = 32.88
```

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

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

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

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

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

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

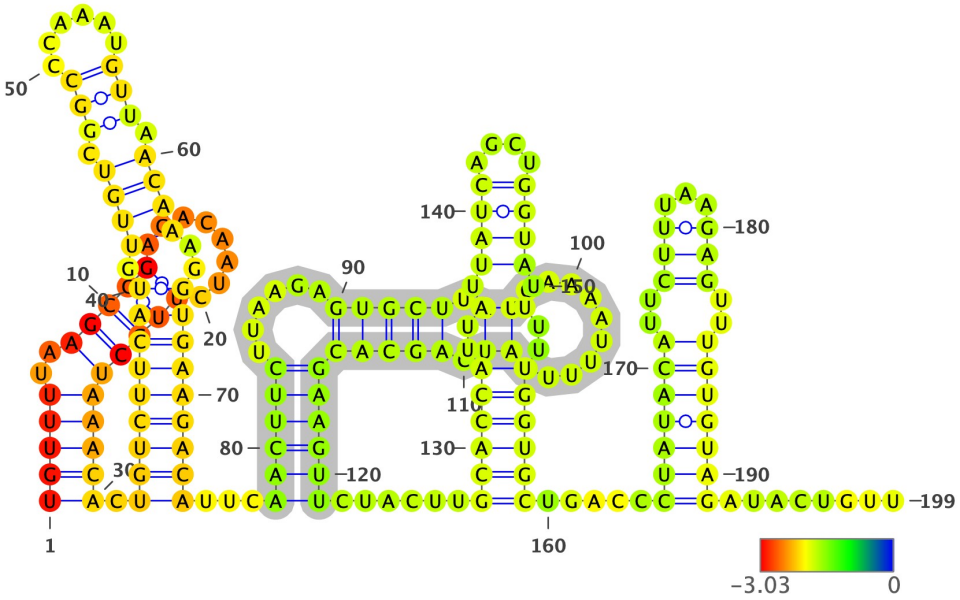
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 69 from nt 3651 to 3694 (nt 78 to 121)

```
5'-AACTTCTTAAGAGTGCTTATGAAAATTTTAATCAGCACGAAGUU-3'
5'-((((((......(((((..............)))))))))))-3'
Motif MFE = -7.6; z-score = -1.8; ED = 4.36
```



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

Extracted structure model with flanking nucleotides 3574 to 3772 (motif highlighted in silver):

```
5'-UGUUUUAAGCGGACACAAUCUUGCUAAACACUGUCUUCAUGUUGUCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCA
GCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUU-3
5'-(((((..(((((........)))))))))).((((((((((.((((.(((......))).)))).))))))))))...((((((......(((((.(..........)).)
))))))))))......((((((..(.((((....)))).).))))))).....(((((((..(((...))))..)))))))........-3'
MFE = -49.4; z-score = -2.74; ED = 15.76
```

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(+)

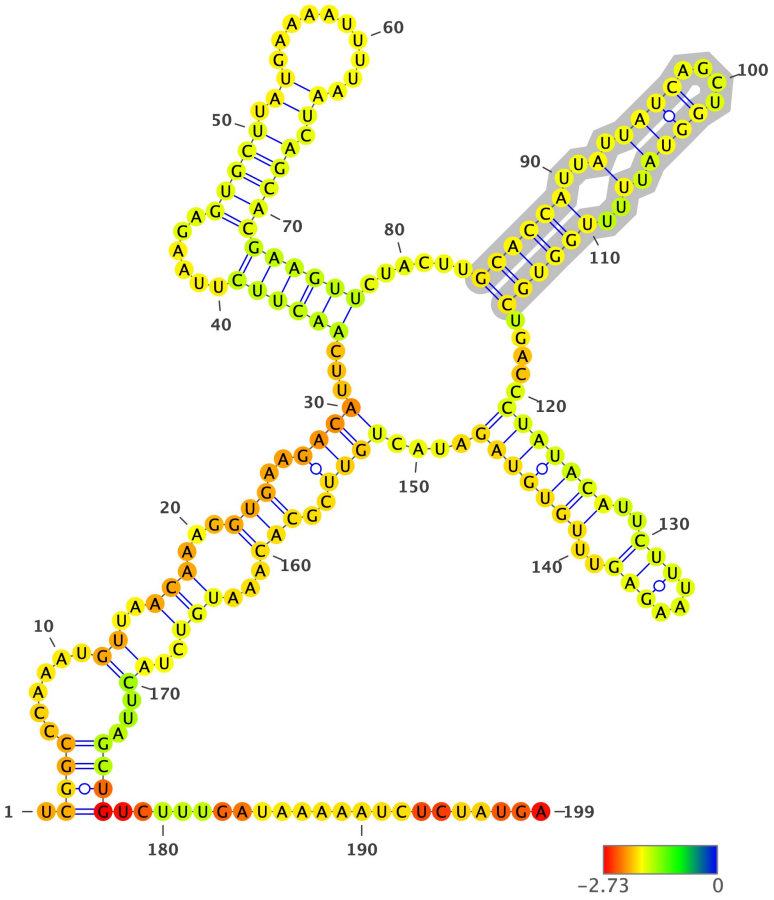
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 70 from nt 3701 to 3732 (nt 84 to 115)

```
5'-GCACCATTATTATCAGCTGGUATUTTUGGUGC-3'
5'-((((((..(..(((....)))..)..)))))))-3'
Motif MFE = -11.2; z-score = -4.08; ED = 0.68
```



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

Extracted structure model with flanking nucleotides 3618 to 3816 (motif highlighted in silver):

```
5'-UCGGCCCAAAUGUUAACAAAGGUGAAGACAUUCAACUUCUUAAGAGUGCUUAUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUG
GUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGA-3
5'-.((((......((..(((...(((..(((((...((((((......(((((.((..........)).)))))))))))).....((((((..(.((((....)))))..))
))))).....(((((((..(((...)))..)))))))....)))))..)))...)))..))...))))......................-3'
MFE = -40.6; z-score = -1.03; ED = 36.24
```

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

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

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

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

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

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

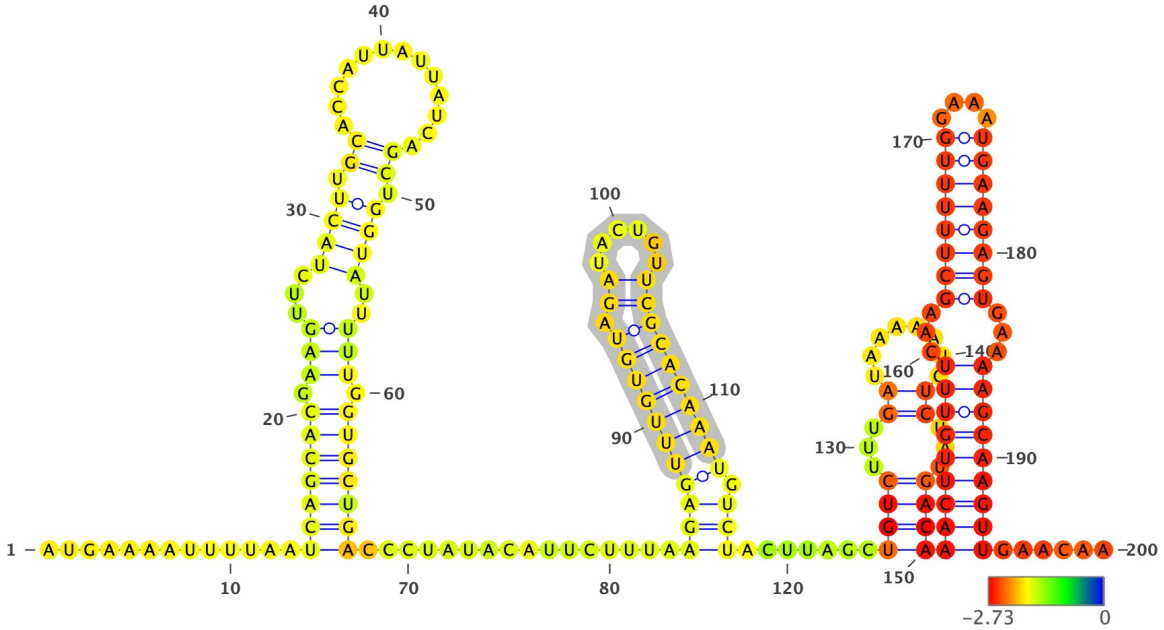
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 71 from nt 3756 to 3780 (nt 88 to 112)

```
5'-TTTGTGTAGATACTGTUCGCACAAA-3'
5'-(((((((.((.....)))))))))-3'
Motif MFE = -6.1; z-score = -2.58; ED = 2.6
```



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

Extracted structure model with flanking nucleotides 3669 to 3868 (motif highlighted in silver):

```
5'-AUGAAAAUUUUAAUCAGCACGAAGUUCUACUUGCACCAUUAUUAUCAGCUGGUAUUUUUGGUGCUGACCCUAUACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAA
AUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAA-3
5'-.............(((((((.(((...((((.((.............)).)))))..))))..)))))))................((((((((((.((.....)))))))))
)).)))......((((...((........))...))))((((((((((...(((((((((....)))))))))...))))))))).....-3'
MFE = -43.7; z-score = -2.69; ED = 30.6
```

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

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

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

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

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

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

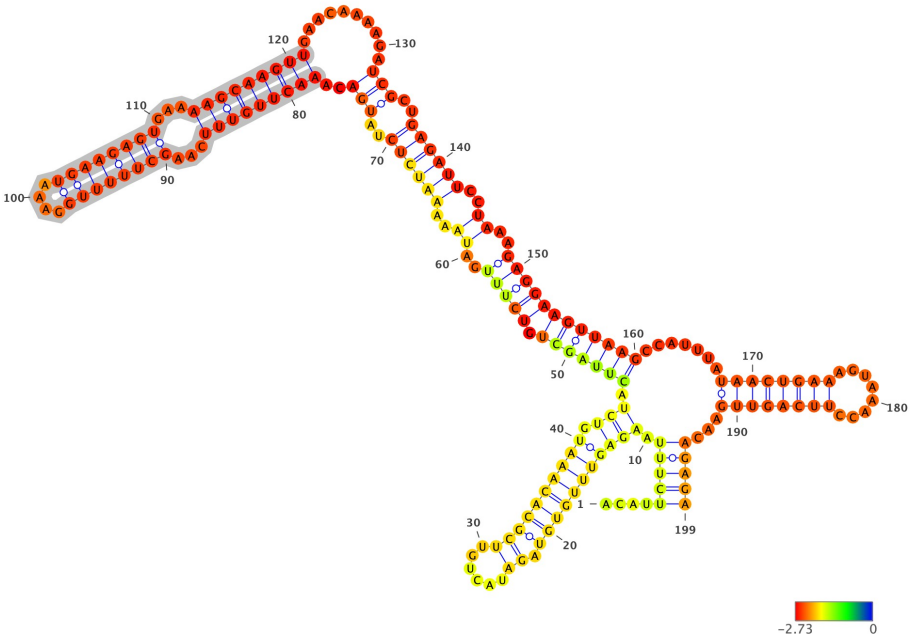
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 72 from nt 3819 to 3862 (nt 78 to 121)

```
5'-AACTTGTTTCAAGCTTTTTGGAAAUGAAGAGUGAAAAGCAAGUU-3'
5'-((((((((((...((((((((....))))))))...)))))))))-3'
Motif MFE = -13.1; z-score = -4.36; ED = 3.73
```



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

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

```
5'-ACAUUCUUUAAGAGUUUGUGUAGAUACUGUUCGCACAAAUGUCUACUUAGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGA
AAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGA-3
5'-....(((((.(((((((((((.((......)))))))))).))).(((((((.(((((..((..((((((..(((..(((((((((...((((((((....))))))))..
.)))))))))..........)))..))))))..))..))))))))))))).......((((((((........))))))))...)))))-3'
MFE = -47.3; z-score = -2.84; 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(+)

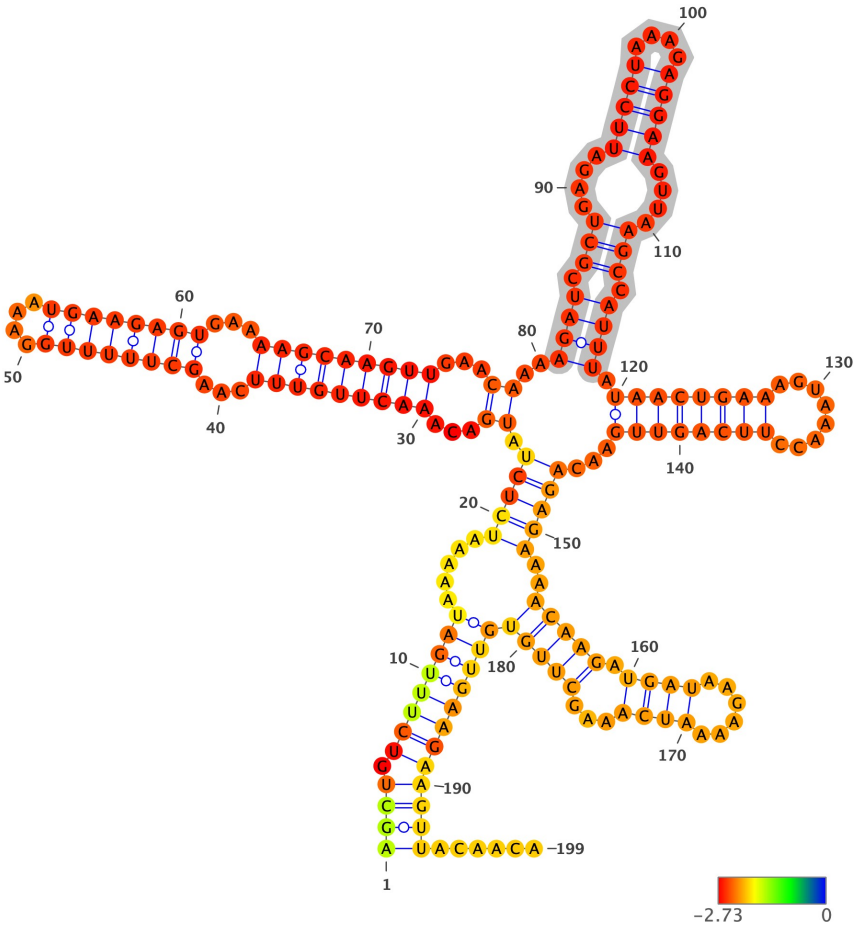
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

```
5'-AGATCGCTGAGATTCCTAAAGAGGAAGTTAAGCCAUUU-3'
5'-((((.(((....(((((....))))).....))).))))-3'
Motif MFE = -8.8; z-score = -2.19; ED = 3.01
```



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

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

```
5'-AGCUGUCUUUGAUAAAAAUCUCUAUGACAAACUUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAA
GCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACA-3
5'-((((.((((((((.....(((((.((...((((((((((...((((((((....))))))))...))))))))))...))..((((.(((....(((((....)))))....)
)).)))).((((((((.........))))))))...)))))..(((((.((((......))))...))))))))))))))))).....-3'
MFE = -45.2; z-score = -3.92; ED = 13.37
```

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

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

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

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

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

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

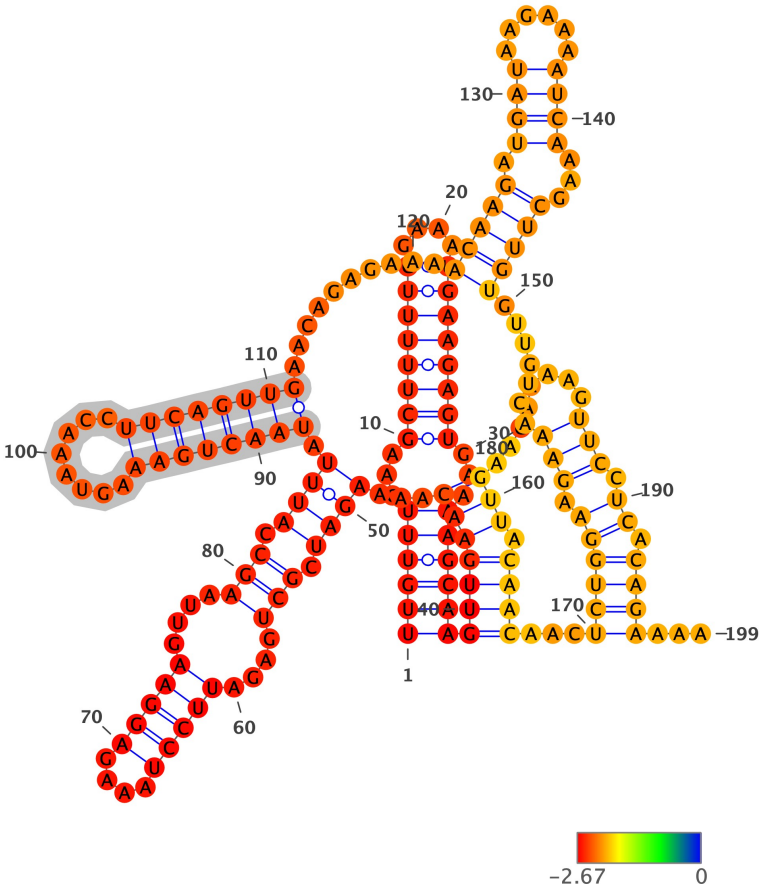
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 74 from nt 3909 to 3932 (nt 88 to 111)

```
5'-TAACTGAAAGTAAACCUUCAGUUG-3'
5'-((((((((........))))))))-3'
Motif MFE = -6.1; z-score = -4.56; ED = 2.04
```



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

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

```
5'-UUGUUUCAAGCUUUUUGGAAAUGAAGAGUGAAAAGCAAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUG
AACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAA-3
5'-((((((...((((((((....))))))))...))))))(((((((...((((.(((....(((((....)))))....))).)))).((((((((........))))))))
..........(((((.((((......))))...)))))..........))).))))...((((((.(((......))).)).))))...-3'
MFE = -40.6; z-score = -3.37; ED = 27.97
```

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

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

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

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

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

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

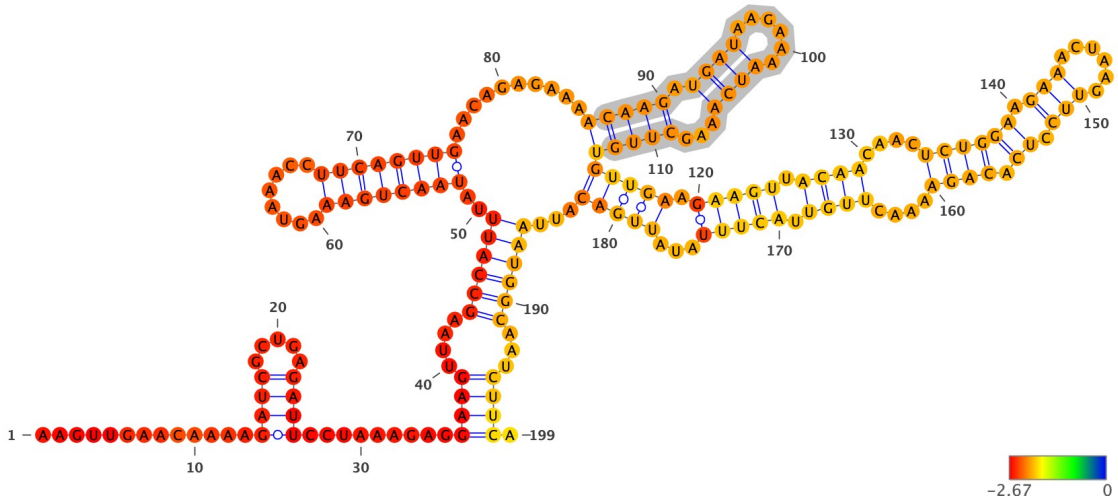
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 75 from nt 3944 to 3969 (nt 87 to 112)

```
5'-CAAGATGATAAGAAAAUCAAAGCUUG-3'
5'-((((..(((......)))....))))-3'
Motif MFE = -2.8; z-score = -2.01; ED = 1.23
```



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 3858 to 4056 (motif highlighted in silver):

```
5'-AAGUUGAACAAAAGAUCGCUGAGAUUCCUAAAGAGGAAGUUAAGCCAUUUAUAACUGAAAGUAAACCUUCAGUUGAACAGAGAAAACAAGAUGAUAAGAAAAUCAAAGCUU
GUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCA-3
5'-.............((((.....)))).........((((....((((((..((((((((.........))))))))..........(((((.((((......))))...)))
))(((((.(((((.((((....((((((.(((......))).)).))))....)))).)))))...)))))...))))))...)))).-3'
MFE = -37.5; z-score = -2.22; ED = 33.39
```

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

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

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

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

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

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

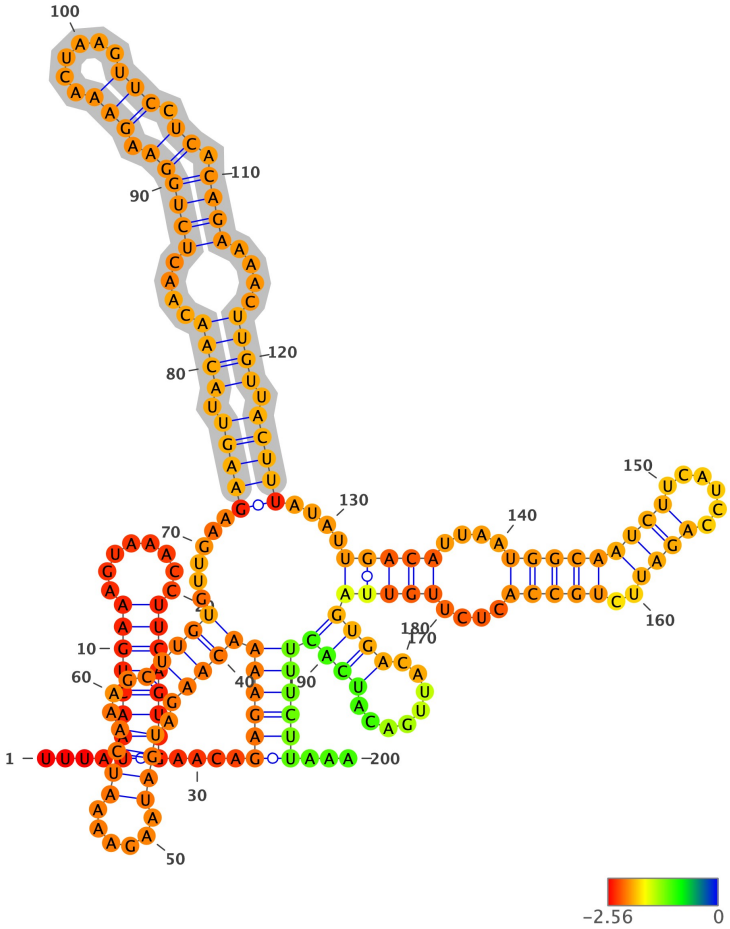
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 76 from nt 3978 to 4030 (nt 74 to 126)

```
5'-AAGTTACAACAACTCTGGAAGAAACTAAGUUCCUCACAGAAAACUUGUTACUU-3'
5'-((((.((((....((((((.(((......))).)).)))).....)))).))))-3'
Motif MFE = -10.0; z-score = -2.65; 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 = -2.86; 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(+)

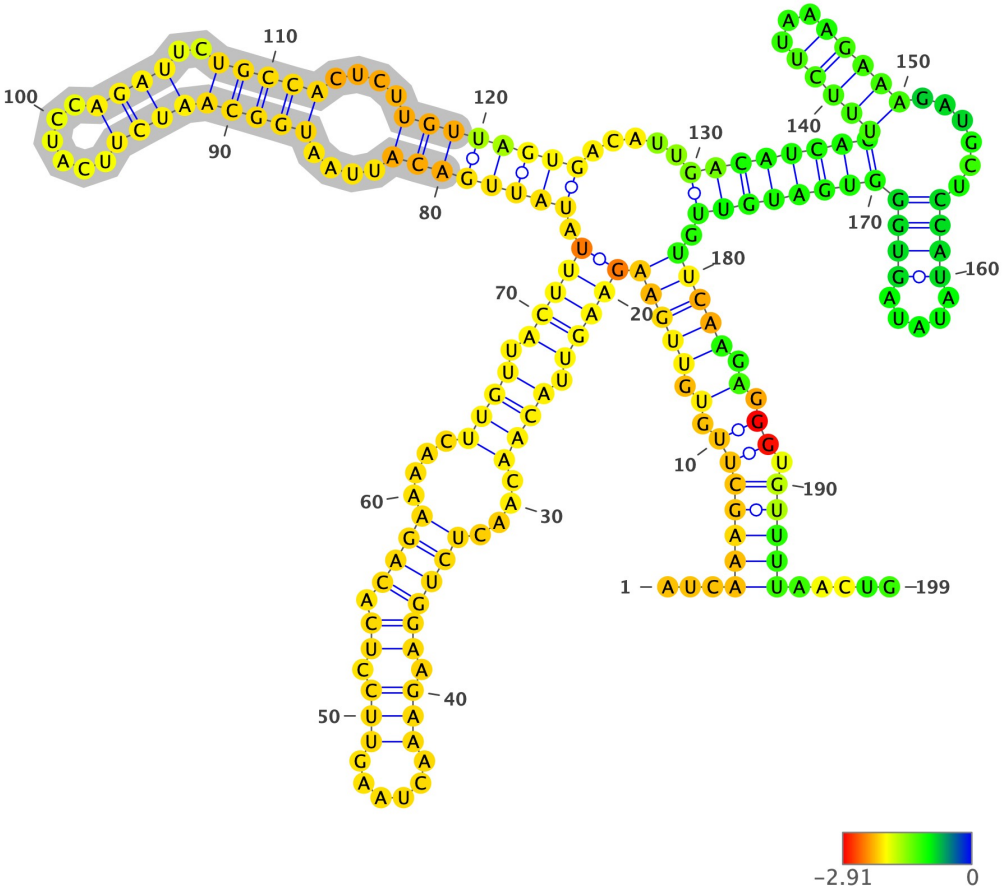
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4038 to 4077 (nt 80 to 119)

```
5'-ACATTAATGGCAATCTTCATCCAGAUTCUGCCACTCTUGU-3'
5'-(((....((((((((((......))))..)))))....)))-3'
Motif MFE = -8.1; z-score = -3.37; ED = 3.25
```



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

Extracted structure model with flanking nucleotides 3959 to 4157 (motif highlighted in silver):

```
5'-AUCAAAGCUUGUGUUGAAGAAGUUACAACAACUCUGGAAGAAACUAAGUUCCUCACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCC
ACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUAGUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUG-3
5'-...(((((((.(.(((((((((((.((((....((((((.(((......))).)).))))....)))).))))).((((((((....((((((((((......))))..))))
)....))))))))).....((((((((((((((...)))))......((((.....))))))))))))).))))).).)).)))))).....-3'
MFE = -44.4; z-score = -1.72; ED = 34.85
```

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

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

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

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

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

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

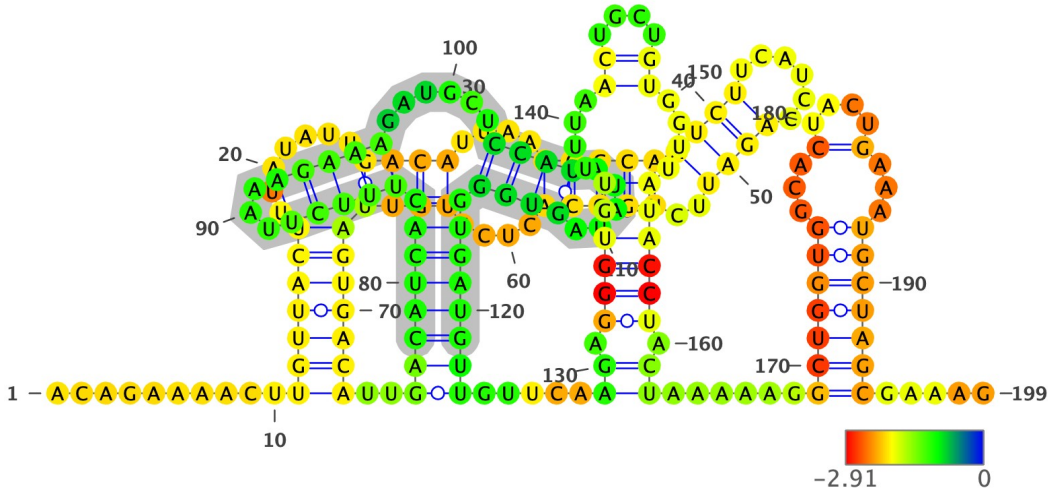
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 78 from nt 4090 to 4133 (nt 78 to 121)

```
5'-CATCACTTTCTTAAAGAAAGATGCTCCATATATAGUGGGUGAUG-3'
5'-((((((((((.....))))).................))))))-3'
Motif MFE = -8.3; z-score = -1.21; ED = 9.16
```



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 4013 to 4211 (motif highlighted in silver):

```
5'-ACAGAAAACUUGUUACUUUAUAUUGACAUUAAUGGCAAUCUUCAUCCAGAUUCUGCCACUCUUGUUAGUGACAUUGACAUCACUUUCUUAAAGAAAGAUGCUCCAUAUAUA
GUGGGUGAUGUUGUUCAAGAGGGUGUUUUAACUGCUGUGGUUAUACCUACUAAAAAGGCUGGUGGCACUACUGAAAUGCUAGCGAAAG-3
5'-..........(((((((.......((((....((((((((((......))))..))))))....))))))))))..((((((((((((...))))))......((((.....
))))))))))))).....((.(((((((....((....)).....))))))).)).....(((((((...(....)...)))))))).....-3'
MFE = -42.4; z-score = -0.35; ED = 29.78
```

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

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

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

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

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

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

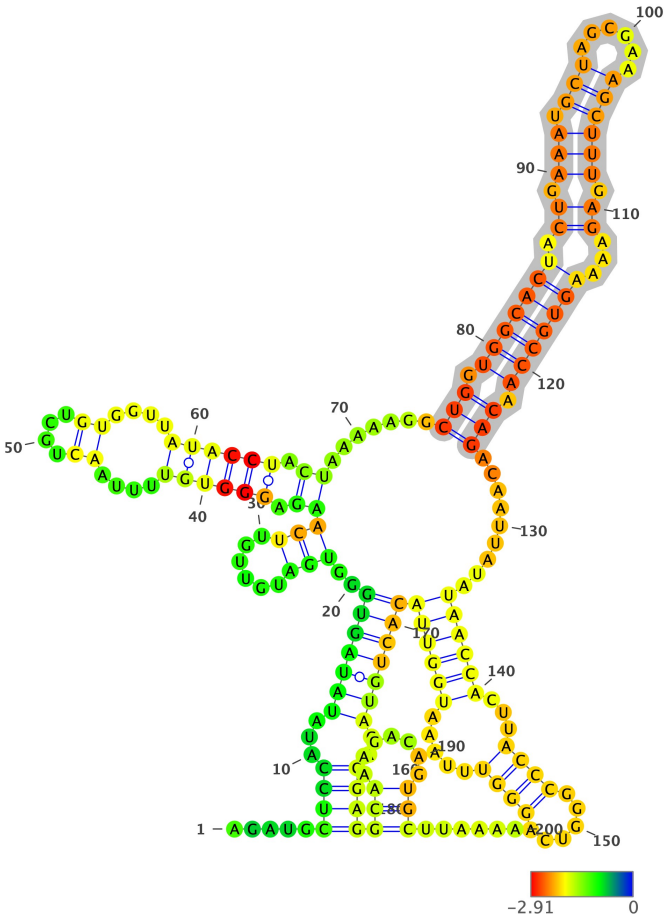
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 79 from nt 4182 to 4232 (nt 75 to 125)

```
5'-CTGGTGGCACTACTGAAATGCTAGCGAAAGCUUUGAGAAAAGUGCCAACAG-3'
5'-(((.((((((..((.(((.(((......)))))).))....)))))).)))-3'
Motif MFE = -18.7; z-score = -3.63; 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 = -2.94; ED = 18.14
```

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

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

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

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

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

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

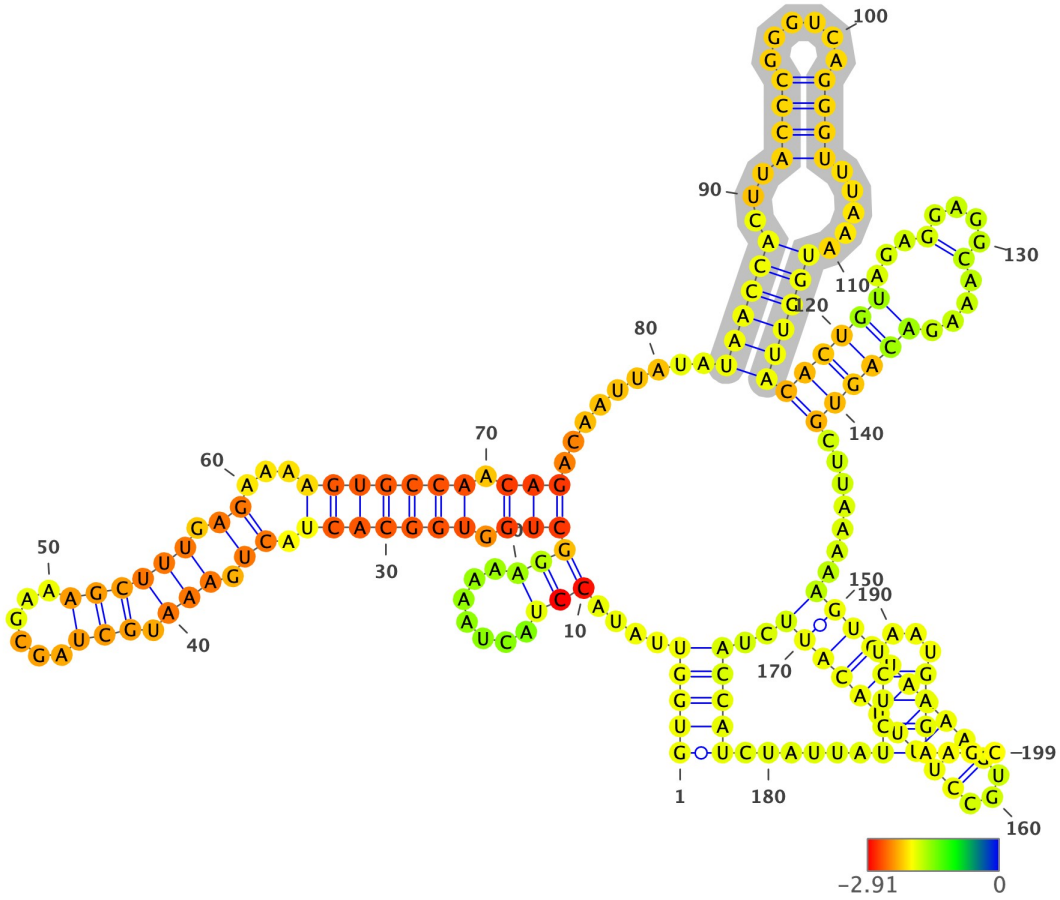
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 80 from nt 4242 to 4275 (nt 83 to 116)

```
5'-TAACCACTTACCCGGGTCAGGGUTTAAAUGGUUA-3'
5'-((((((...((((......))))).....))))))-3'
Motif MFE = -10.7; z-score = -3.35; 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 = -3.55; 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(+)

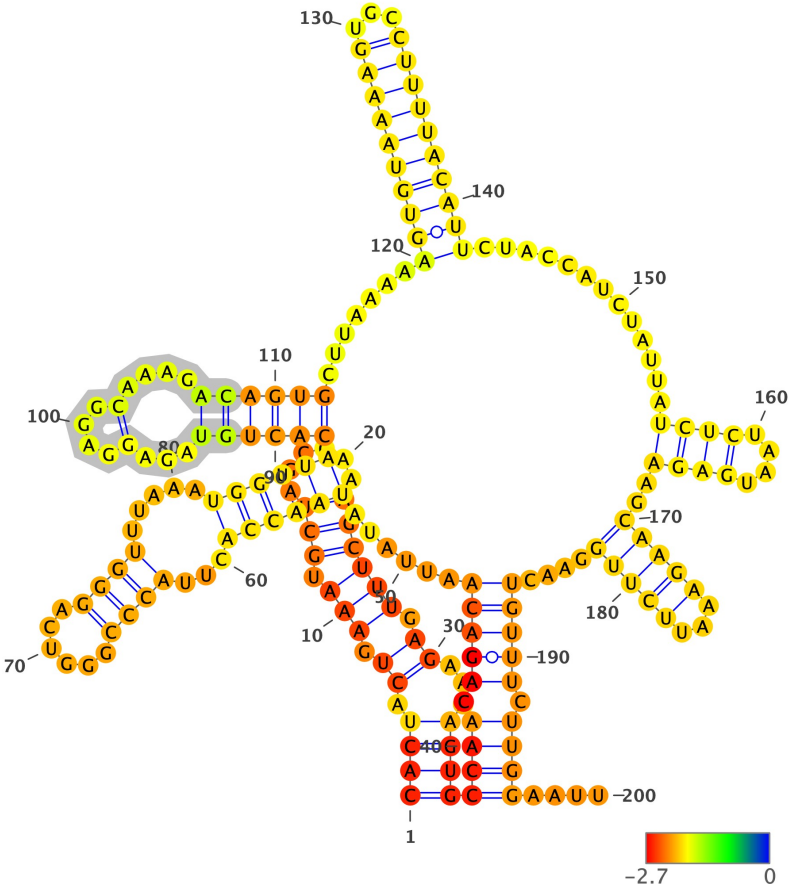
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 4280 to 4296 (nt 92 to 108)

```
5'-GTAGAGGAGGCAAAGAC-3'
5'-((.............))-3'
Motif MFE = 0.0; z-score = 0.36; 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 4189 to 4388 (motif highlighted in silver):

```
5'-CACUACUGAAAUGCUAGCGAAAGCUUUGAGAAAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGU
GCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUU-3
5'-((((.((.(((.(((......))))))).))...))))((((.(((((......((((((...((((......))))).....))))))((((((...(....)....)))))
).......((((((((((...))))))))))).............((((....))))..(((((...)))))....)))))).))))....-3'
MFE = -46.8; z-score = -2.44; ED = 10.08
```

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

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

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

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

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

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

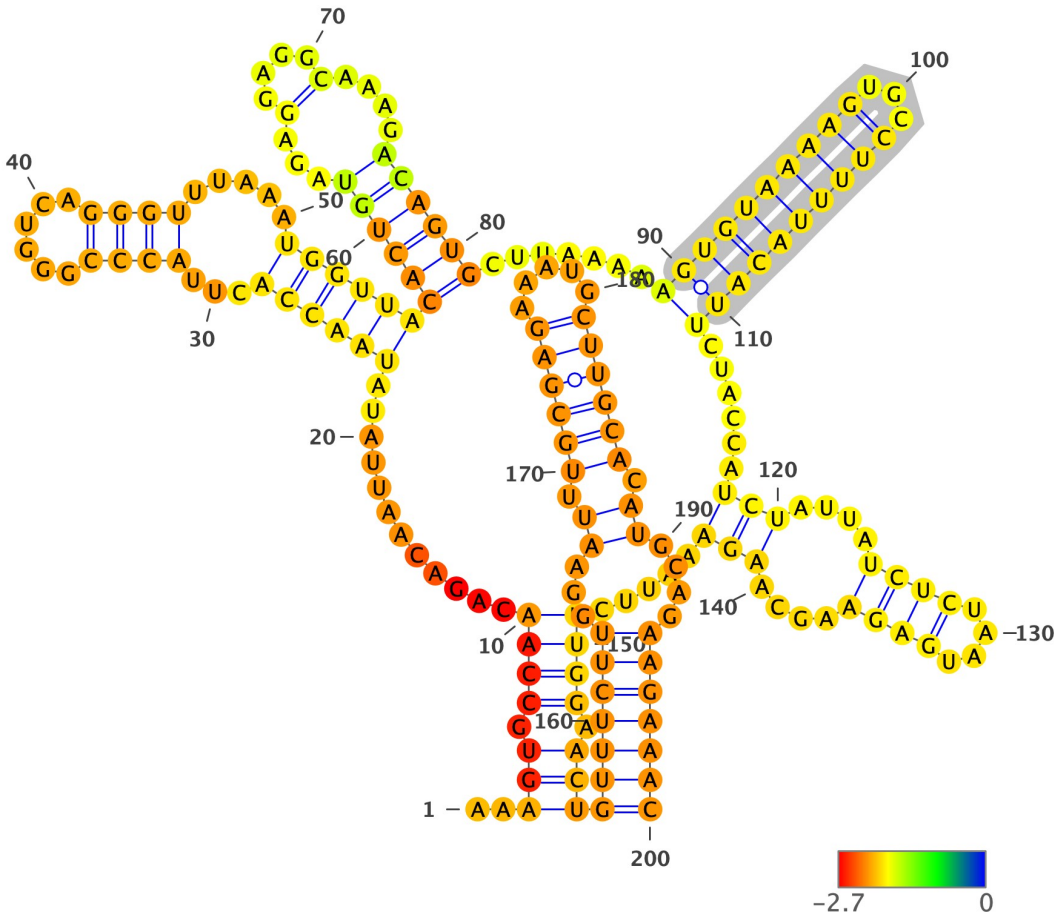
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 82 from nt 4309 to 4329 (nt 90 to 110)

```
5'-GTGTAAAAGTGCCUUUUACAU-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -5.9; z-score = -3.43; ED = 0.65
```



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

Extracted structure model with flanking nucleotides 4220 to 4419 (motif highlighted in silver):

```
5'-AAAGUGCCAACAGACAAUUAUAUAACCACUUACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUU
CUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAAC-3
5'-..(((.((((.............((((((...((((......)))).....))))))((((((...(....)....))))))).......((((((((((...))))))))))
......(((....((((....))))....))).....)))).)))(((((((...((.((((((.....)))))).))....)))))))-3'
MFE = -46.6; z-score = -2.16; ED = 32.14
```

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

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

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

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

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

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

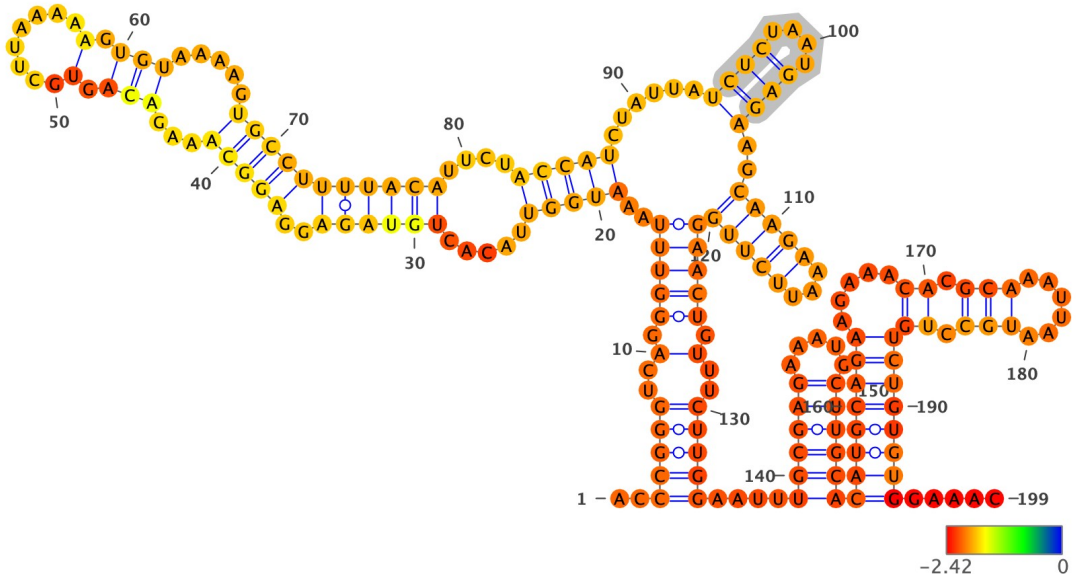
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 83 from nt 4345 to 4354 (nt 95 to 104)

```
5'-CTCTAATGAG-3'
5'-(((....)))-3'
Motif MFE = -1.0; z-score = -7.86; ED = 0.91
```



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

Extracted structure model with flanking nucleotides 4251 to 4449 (motif highlighted in silver):

```
5'-ACCCGGGUCAGGGUUUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAG
AAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAAC-3
5'-..((((((..(.((((((..((((((.....((((((..((((((...(((.(........).))).....))))))))))))....))))))......((((....)))))..((((
(...))))))))))..)..))))))....((((((.....))))))(((((((((.....((.(((......))).))))))))))).....-3'
MFE = -50.7; z-score = -2.54; ED = 51.44
```

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

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

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

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

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

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

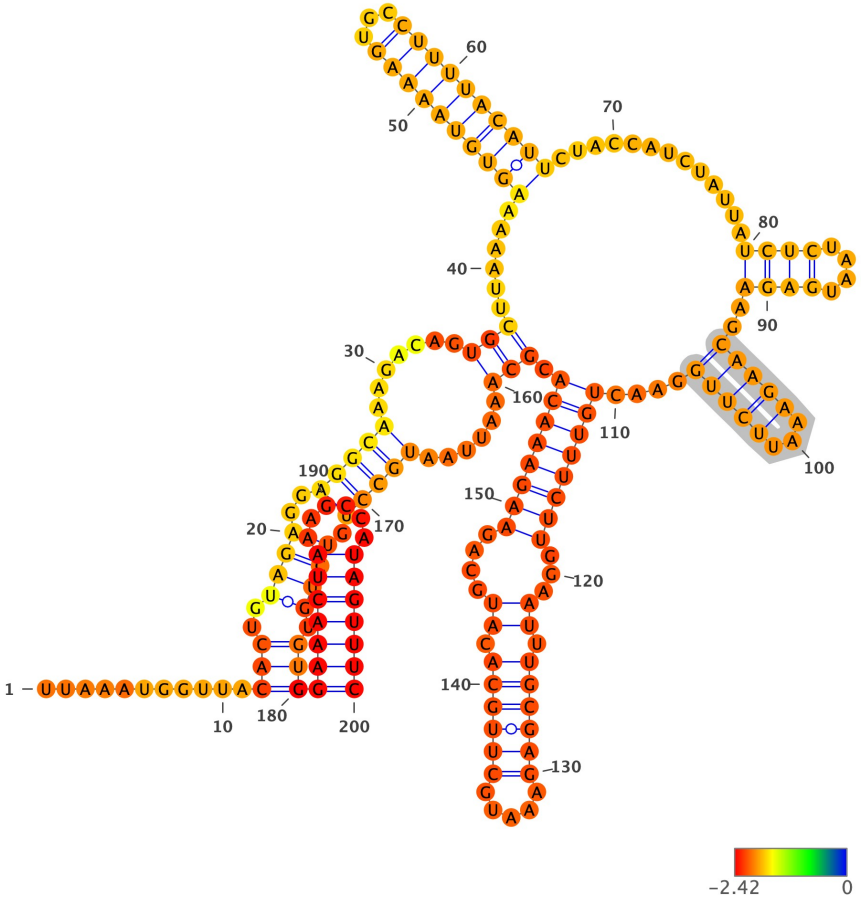
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 84 from nt 4358 to 4370 (nt 94 to 106)

```
5'-CAAGAAATUCUUG-3'
5'-(((((...)))))-3'
Motif MFE = -1.6; z-score = -7.71; ED = 0.92
```



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

Extracted structure model with flanking nucleotides 4265 to 4464 (motif highlighted in silver):

```
5'-UUAAAUGGUUACACUGUAGAGGAGGCAAAGACAGUGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACU
GUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUC-3
5'-...........(((..((((..(((((.......(((......((((((((((...)))))))))).............((((....)))).(((((...))))).....(
(((((((...((.((((((.....)))))).))....)))))))).)))......))))).)))).)))(((((((......)))))))-3'
MFE = -48.9; z-score = -2.71; ED = 42.24
```

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

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

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

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

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

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

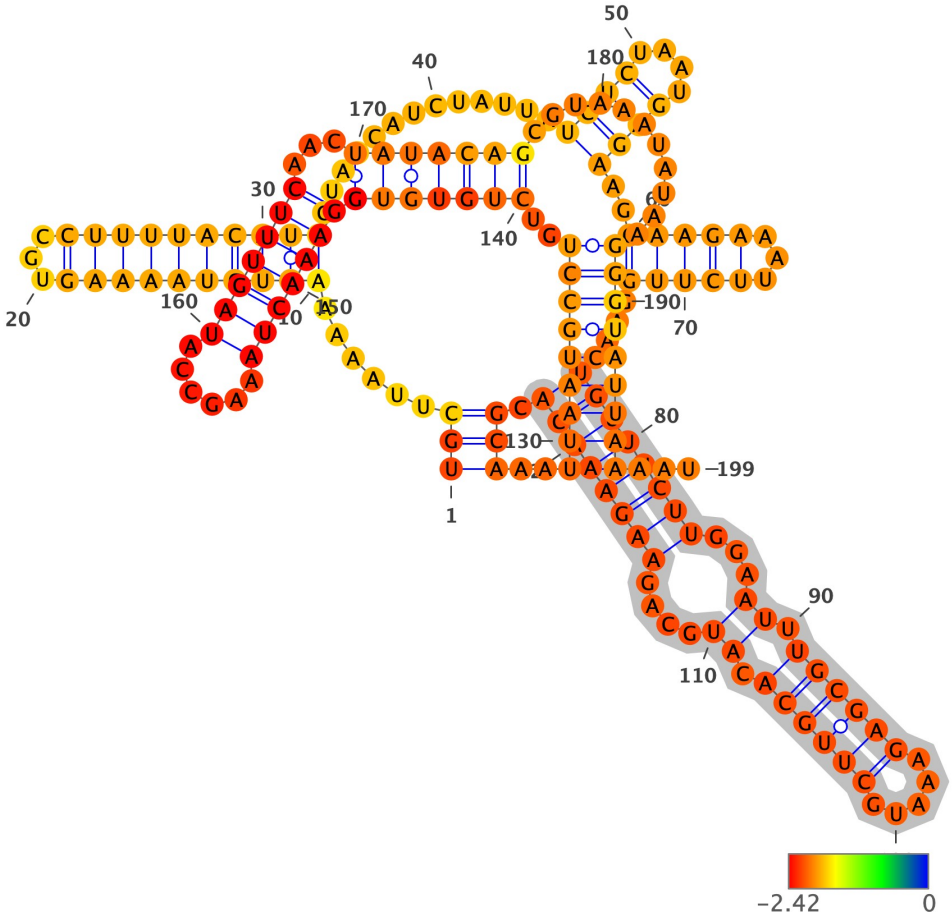
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 85 from nt 4375 to 4420 (nt 77 to 122)

```
5'-TGTTTCTTGGAATTTGCGAGAAATGCUUGCACAUGCAGAAGAAACA-3'
5'-(((((((((...((.((((((.....)))))).))....)))))))))-3'
Motif MFE = -14.0; z-score = -3.22; ED = 2.53
```



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

Extracted structure model with flanking nucleotides 4299 to 4497 (motif highlighted in silver):

```
5'-UGCUUAAAAAGUGUAAAAGUGCCUUUUACAUUCUACCAUCUAUUAUCUCUAAUGAGAAGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUG
CAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAU-3
5'-(((.....(((((((((...)))))))))).............((((....)))))..(((((...)))))....(((((((...((.((((((.....)))))).)).
...)))))))).)))..(((((((((..(((((((((((((.....)))))))))...)))))))).....)))))))))...-3'
MFE = -49.7; z-score = -3.2; ED = 10.02
```

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

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

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

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

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

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

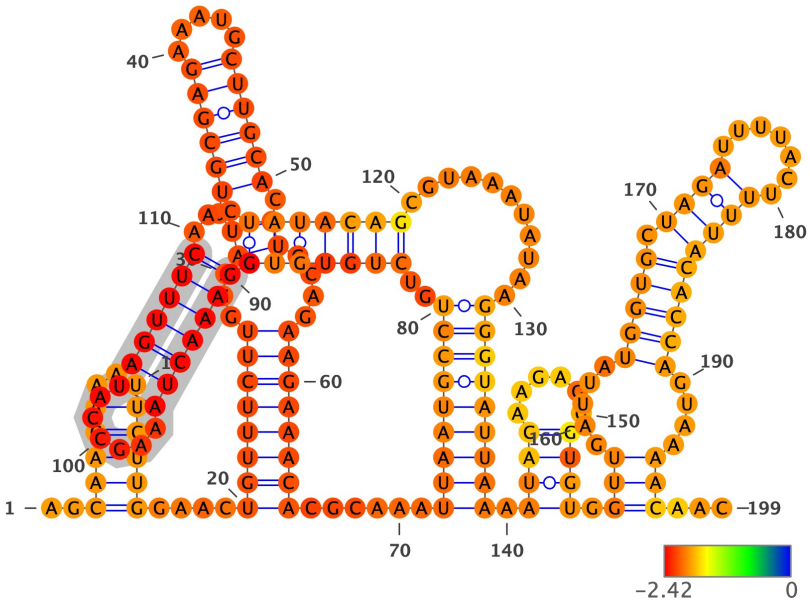
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 86 from nt 4445 to 4464 (nt 90 to 109)

```
5'-GAAACTAAAGCCAUAGUUUC-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.7; z-score = -3.96; ED = 0.29
```



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

Extracted structure model with flanking nucleotides 4356 to 4554 (motif highlighted in silver):

```
5'-AGCAAGAAAUUCUUGGAACUGUUUCUUGGAAUUUGCGAGAAAUGCUUGCACAUGCAGAAGAAACACGCAAAUUAAUGCCUGUCUGUGUGGAAACUAAAGCCAUAGUUUCAA
CUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAAC-3
5'-..(((((...)))))....(((((((((...((.((((((.....)))))).)).....)))))))))......(((((((((..((((((((((((((.....)))))))))))))..
.)))))))).....)))))))).((((.....)))).(((.....(((((.(((((.....)))))))))....))))...-3'
MFE = -46.2; z-score = -2.24; ED = 29.11
```

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

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

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

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

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

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

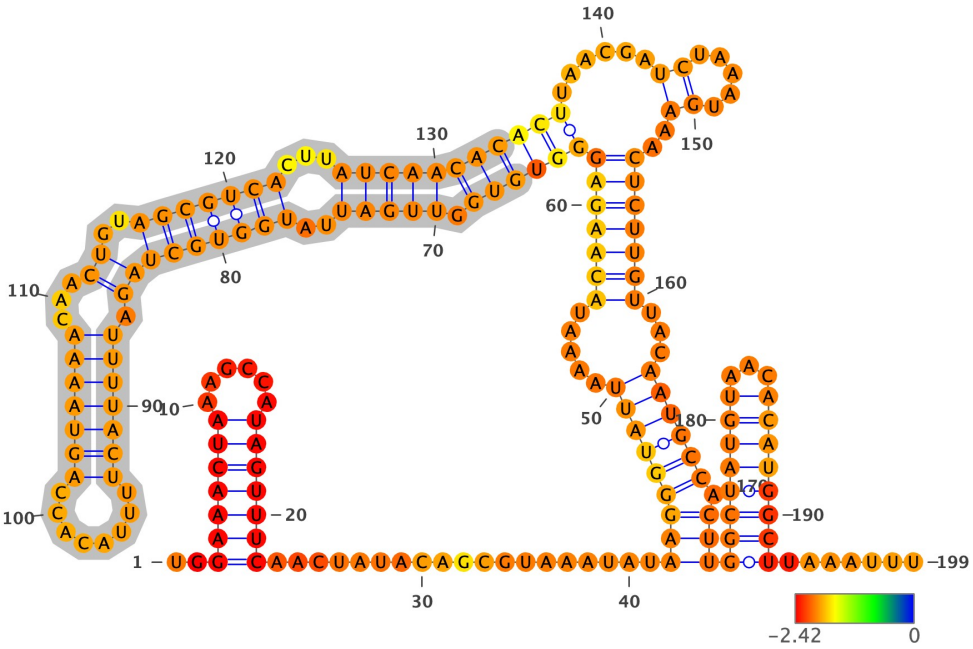
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 87 from nt 4508 to 4575 (nt 66 to 133)

```
5'-GTGGTTGATTATGGTGCTAGATTTTACTTTTACACCAGUAAAACAACUGTAGCGUCACTTAUCAACAC-3'
5'-(((.((((((..((((((((((.(((((((........)))))))...))..)))))))...)))))))))-3'
Motif MFE = -15.9; z-score = -2.25; ED = 10.43
```



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 4443 to 4641 (motif highlighted in silver):

```
5'-UGGAAACUAAAGCCAUAGUUUCAACUAUACAGCGUAAAUAUAAGGGUAUUAAAAUACAAGAGGGUGUGGUUGAUUAUGGUGCUAGAUUUUACUUUUACACCAGUAAAACAA
CUGUAGCGUCACUUAUCAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUU-3
5'-..(((((((......)))))))...................(((((((((.....((((((((((((.(((((..(((((((((.(((((((........)))))))...
))..)))))))...)))))))))))).....((.....))..)))))))...)))))).)))(((((((((...)))))))))........-3'
MFE = -46.9; z-score = -3.64; ED = 19.85
```

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(+)

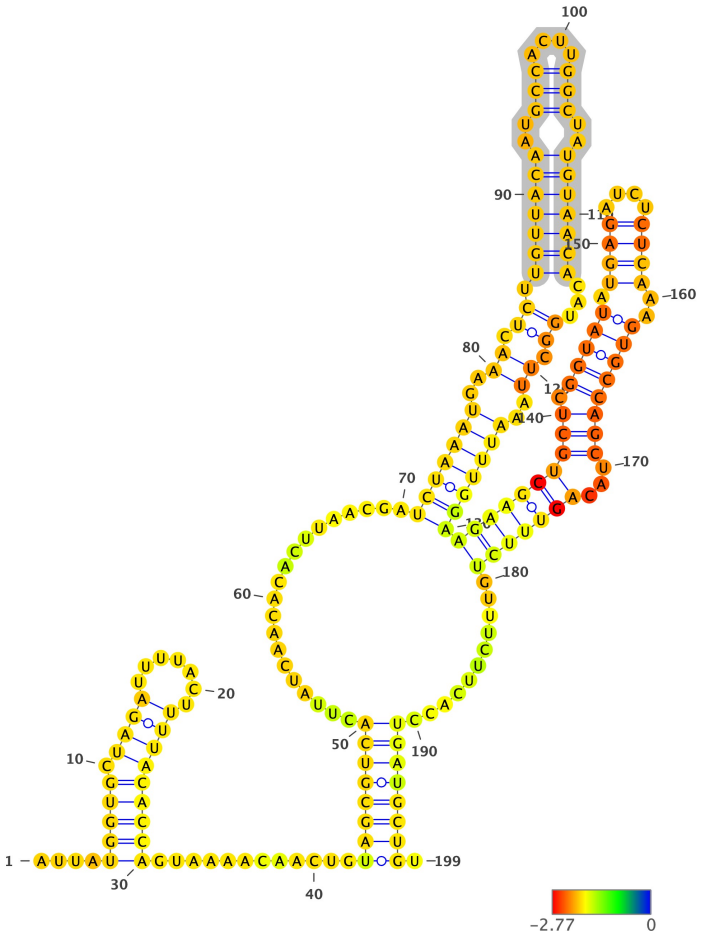
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 88 from nt 4600 to 4627 (nt 86 to 113)

```
5'-TGTTACAATGCCACTTGGCTAUGUAACA-3'
5'-(((((((..(((....)))..)))))))-3'
Motif MFE = -11.1; z-score = -5.13; 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 = -3.33; 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(+)

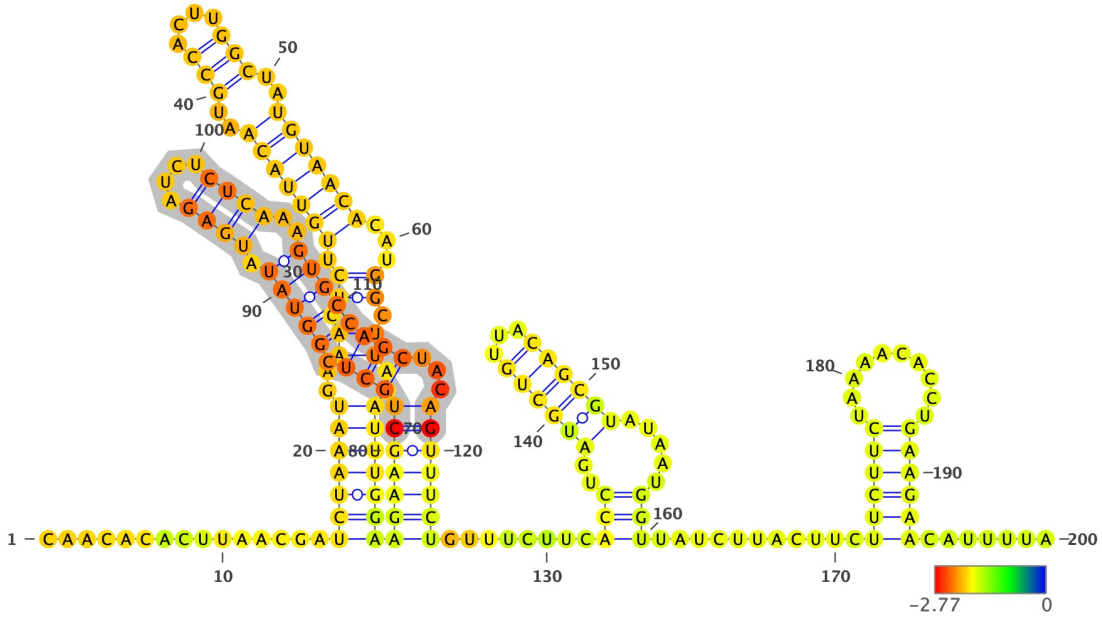
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 89 from nt 4650 to 4688 (nt 81 to 119)

```
5'-CTGCTCGGTATATGAGATCTCUCAAAGUGCCAGCTACAG-3'
5'-(.(((.(((((...((....)).....)))))))).....)-3'
Motif MFE = -12.0; z-score = -2.47; 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 4570 to 4769 (motif highlighted in silver):

```
5'-CAACACACUUAACGAUCUAAAUGAAACUCUUGUUACAAUGCCACUUGGCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCC
AGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUA-3
5'-...............(((((((..((.((.(((((((..(((....))))..)))))))...)).)).)).)))))(((((((((.(((((.((((....)))))..)))))
))))...)))))))........(((..((((((...))))))).....))).....((((((.........))))))........-3'
MFE = -44.8; z-score = -2.65; ED = 22.58
```

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(+)

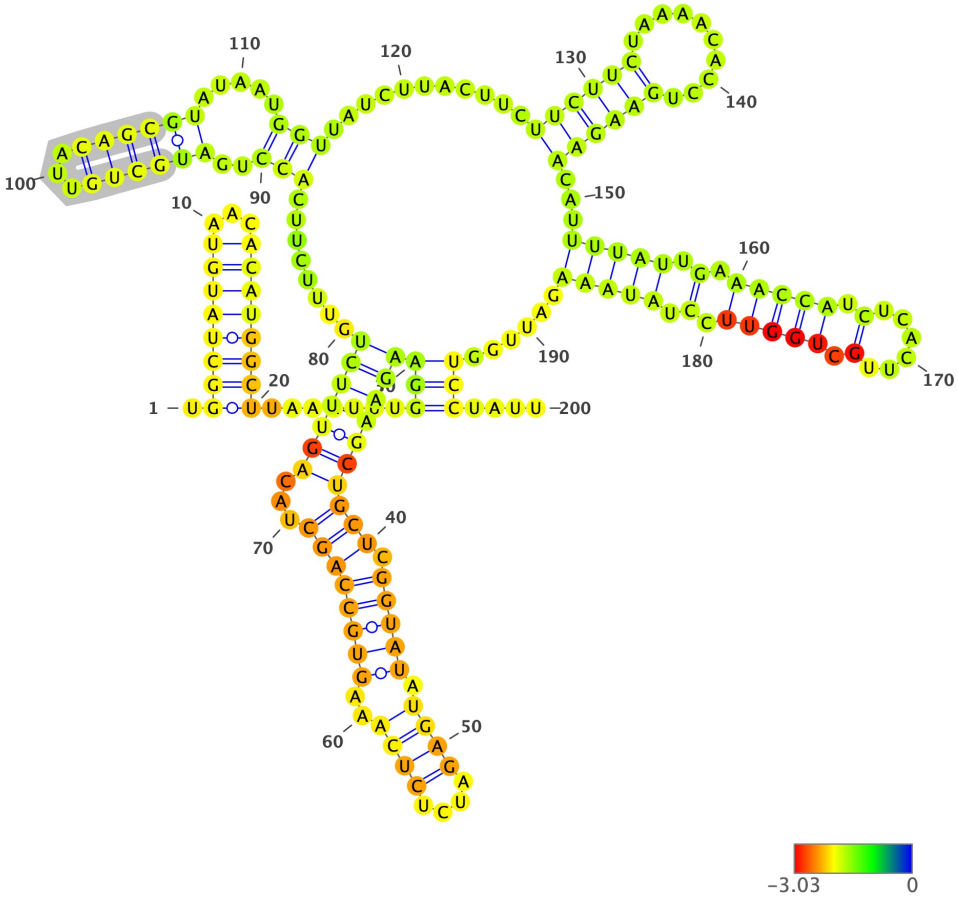
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 90 from nt 4709 to 4719 (nt 95 to 105)

```
5'-GCTGTTACAGC-3'
5'-((((...))))-3'
Motif MFE = -0.7; z-score = -2.28; 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 4615 to 4814 (motif highlighted in silver):

```
5'-UGGCUAUGUAACACAUGGCUUAAAUUUGGAAGAAGCUGCUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAA
UGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAACAUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUU-3
5'-.((((((((...))))))))).......(((((((((((((.(((((.((((....)))).)))))))))...)))))))........(((..((((((...))))))....
.))).........((((((.........))))))...(((((.(.(((((.(......).)))))).).)))))......)))....-3'
MFE = -45.5; z-score = -2.03; ED = 26.27
```

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(+)

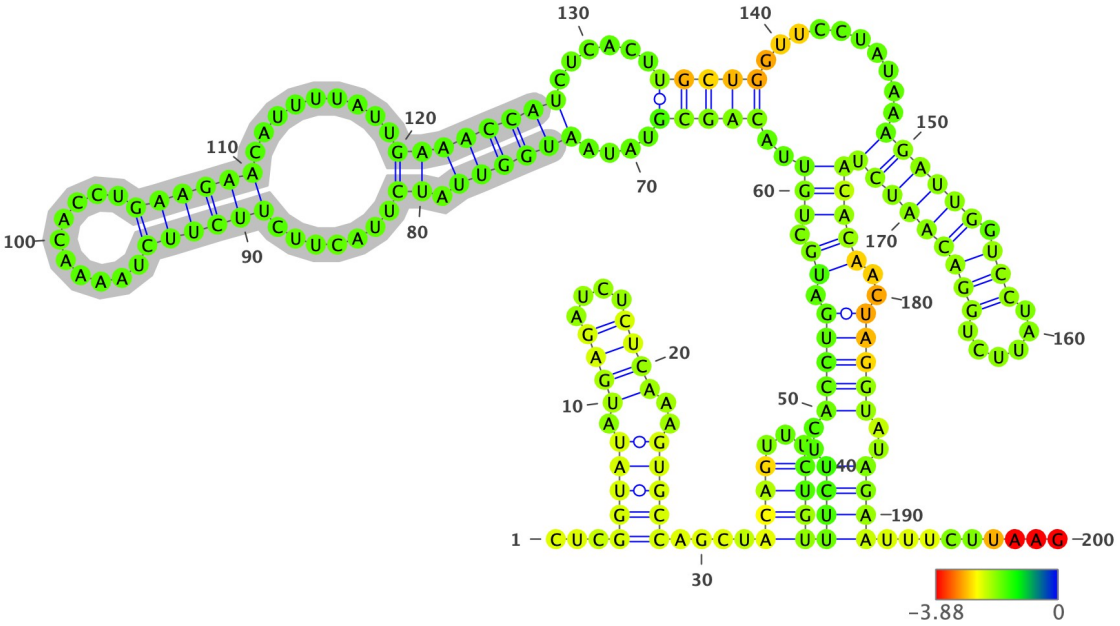
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 91 from nt 4726 to 4778 (nt 74 to 126)

```
5'-TGGTTATCTTACTTCTTCTTCTAAAACACCTGAAGAACATTTTATTGAAACCA-3'
5'-(((((..........((((((..........))))))...........)))))-3'
Motif MFE = -7.5; z-score = -2.27; ED = 4.63
```



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

Extracted structure model with flanking nucleotides 4653 to 4852 (motif highlighted in silver):

```
5'-CUCGGUAUAUGAGAUCUCUCAAAGUGCCAGCUACAGUUUCUGUUUCUUCACCUGAUGCUGUUACAGCGUAUAAUGGUUAUCUUACUUCUUCUUCUAAAACACCUGAAGAAC
AUUUUAUUGAAACCAUCUCACUUGCUGGUUCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAG-3
5'-...(((((.((((....))))..)))))....((((...))))((((..(((((.((.(((..(((((....((((((.((.......((((((..........)))))).
........))))))))......)))))..........((((((.(((......)))))))))))))))..)))))..))))..........-3'
MFE = -41.5; z-score = -2.57; ED = 22.13
```

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(+)

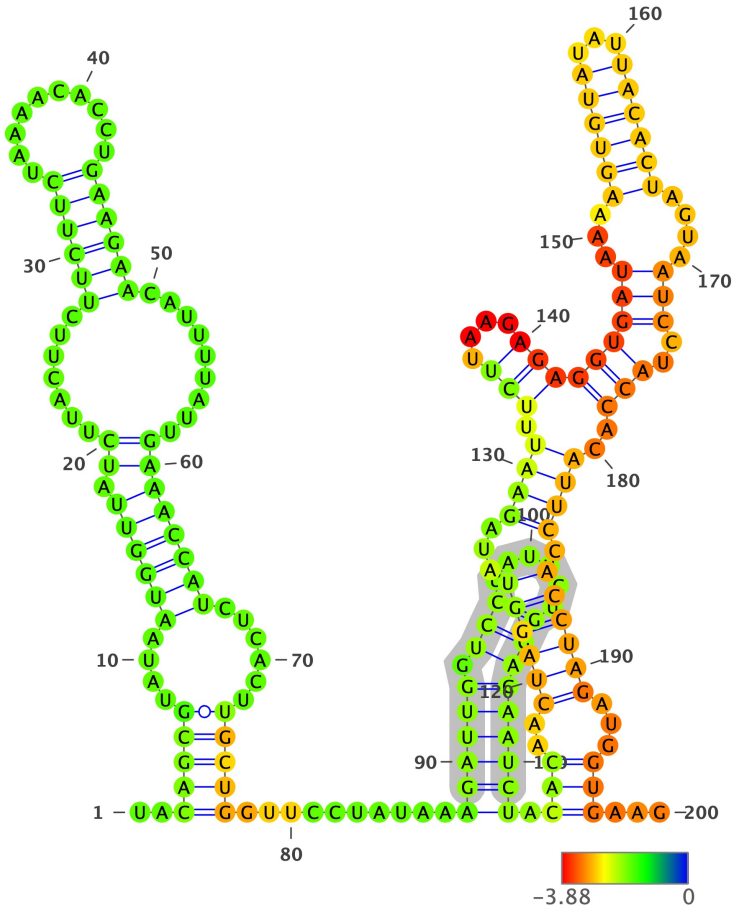
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 92 from nt 4802 to 4824 (nt 89 to 111)

```
5'-GATTGGTCCTATTCTGGACAAUC-3'
5'-(((((.(((......))))))))-3'
Motif MFE = -7.3; z-score = -3.8; 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 = -2.06; ED = 37.16
```

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(+)

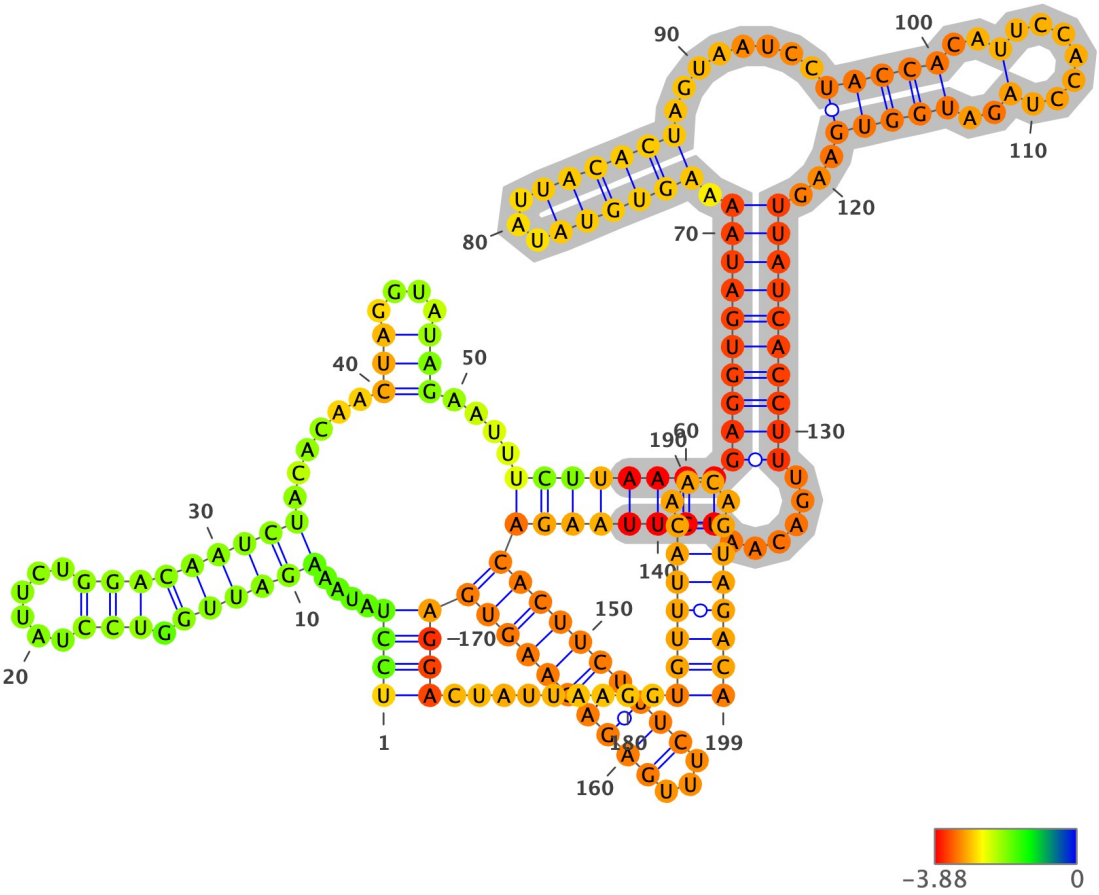
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 93 from nt 4850 to 4933 (nt 58 to 141)

```
5'-AAGAGAGGTGATAAAAGTGTATATUACACUAGTAATCCTACCACATTCCACCTAGAUGGUGAAGUUAUCACCUUTGACAAUCUU-3'
5'-(((((((((((((.((((((...))))))........((((((..........).)))))...)))))))))).....))))-3'
Motif MFE = -22.0; z-score = -3.63; ED = 8.98
```



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

Extracted structure model with flanking nucleotides 4793 to 4991 (motif highlighted in silver):

```
5'-UCCUAUAAAGAUUGGUCCUAUUCUGGACAAUCUACACAACUAGGUAUAGAAUUUCUUAAGAGAGGUGAUAAAAGUGUAUAUUACACUAGUAAUCCUACCACAUUCCACCUA
GAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACA-3
5'-((((....((((((.(((......)))))))))......(((....)))....(((((((((((((((((.((((((...))))))........(((((..(.......)
..)))))...)))))))))).....))))))))((((((((((...)))))))))))))).........(((((((....)))))))-3'
MFE = -55.2; z-score = -5.32; ED = 17.59
```

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

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

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

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

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

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

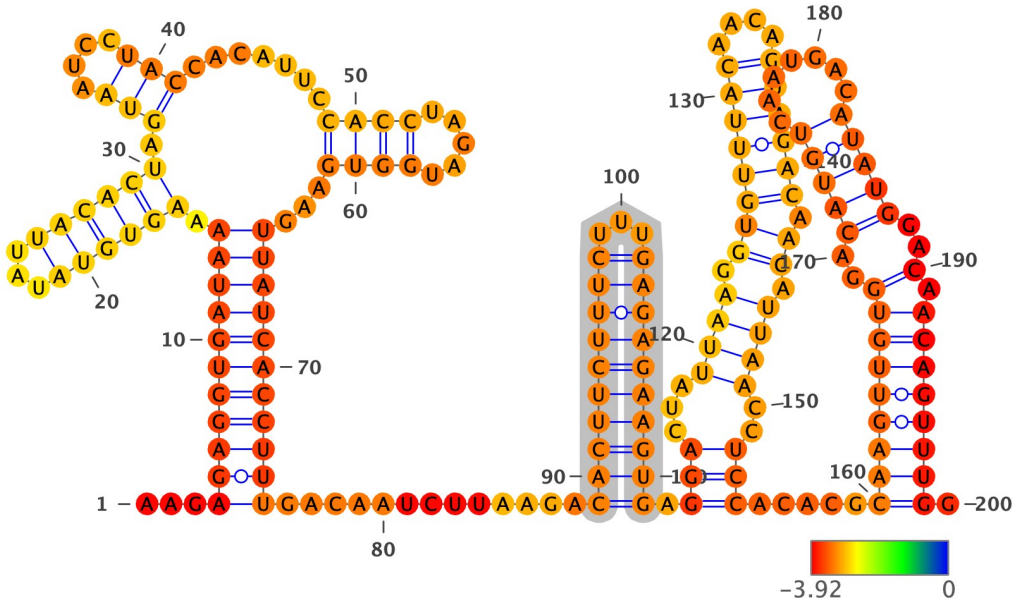
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 94 from nt 4938 to 4960 (nt 89 to 111)

```
5'-CACTTCTTTCTTTGAGAGAAGUG-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -10.7; z-score = -5.49; 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 = -3.48; 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(+)

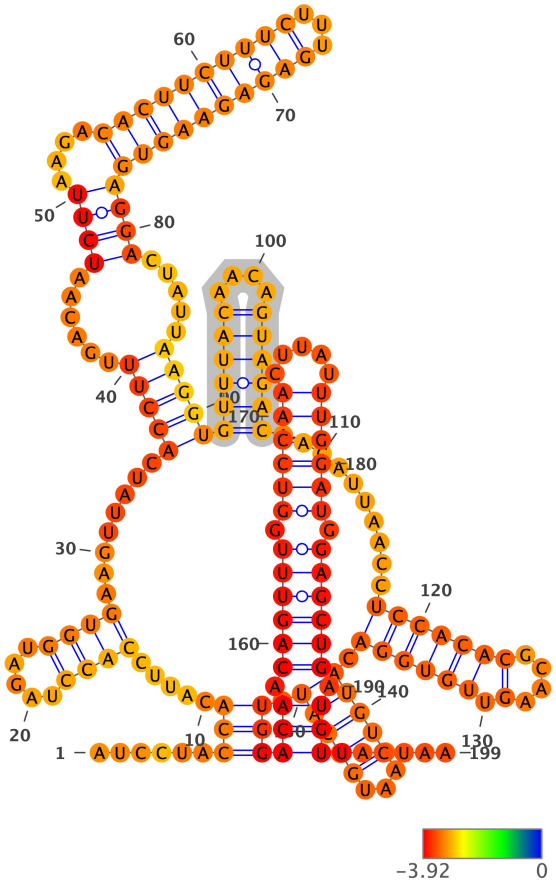
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 95 from nt 4975 to 4990 (nt 92 to 107)

```
5'-GTTTACAACAGUAGAC-3'
5'-((((((....))))))-3'
Motif MFE = -3.5; z-score = -6.2; ED = 0.18
```



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

Extracted structure model with flanking nucleotides 4884 to 5082 (motif highlighted in silver):

```
5'-AUCCUACCACAUUCCACCUAGAUGGUGAAGUUAUCACCUUUGACAAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACA
UUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAA-3
5'-......(((.....((((.....))))........(((((......((((....((((((((((...)))))))))))))).....)))))((((((....))))))....
......(((((((....).)))))).(((((...))))).)))(((.((((((.((((((.....)))))).)))))).)))......-3'
MFE = -57.0; z-score = -4.1; ED = 32.95
```

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

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

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

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

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

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

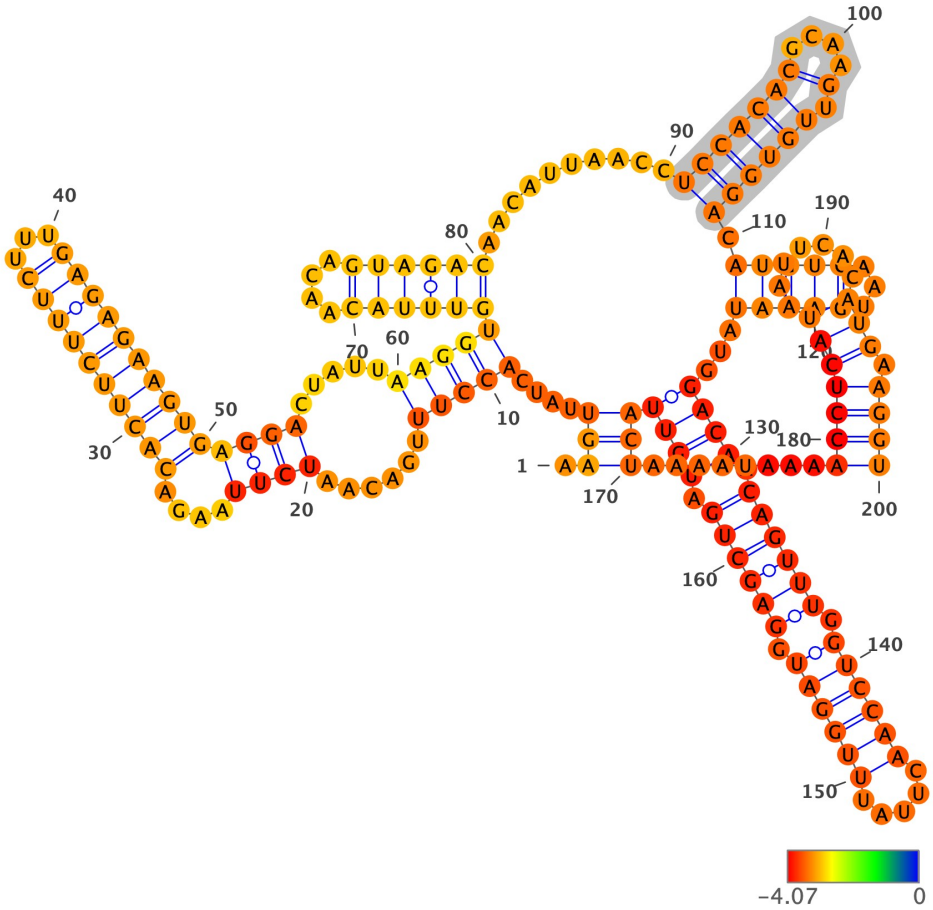
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 96 from nt 5001 to 5019 (nt 91 to 109)

```
5'-TCCACACGCAAGTUGUGGA-3'
5'-(((((((....).))))))-3'
Motif MFE = -6.7; z-score = -3.24; 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 = -4.25; 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(+)

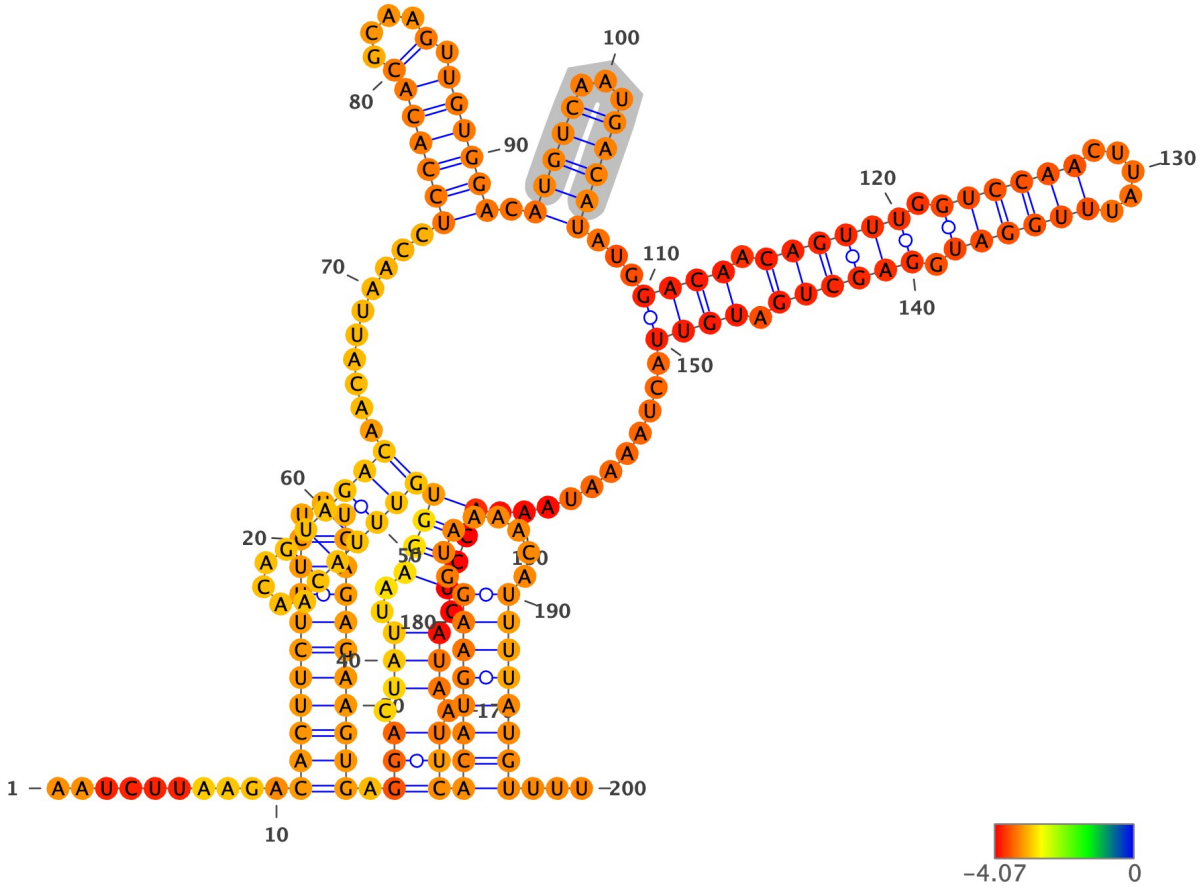
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 97 from nt 5022 to 5032 (nt 95 to 105)

```
5'-TGTCAATGACA-3'
5'-((((...))))-3'
Motif MFE = -0.8; z-score = -10.1; 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 4928 to 5127 (motif highlighted in silver):

```
5'-AAUCUUAAGACACUUCUUUCUUUGAGAGAAGUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGA
CAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUU-3
5'-..........((((((((((...)))))))))).(((.(((..((((((((((....))))))..........(((((((....).)))))).(((((...)))))...((
((.((((((.((((((.....)))))).)))))).)))).....)))).))).)))((((((((.......))))))))...-3'
MFE = -55.1; z-score = -4.34; ED = 31.25
```

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

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

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

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

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

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

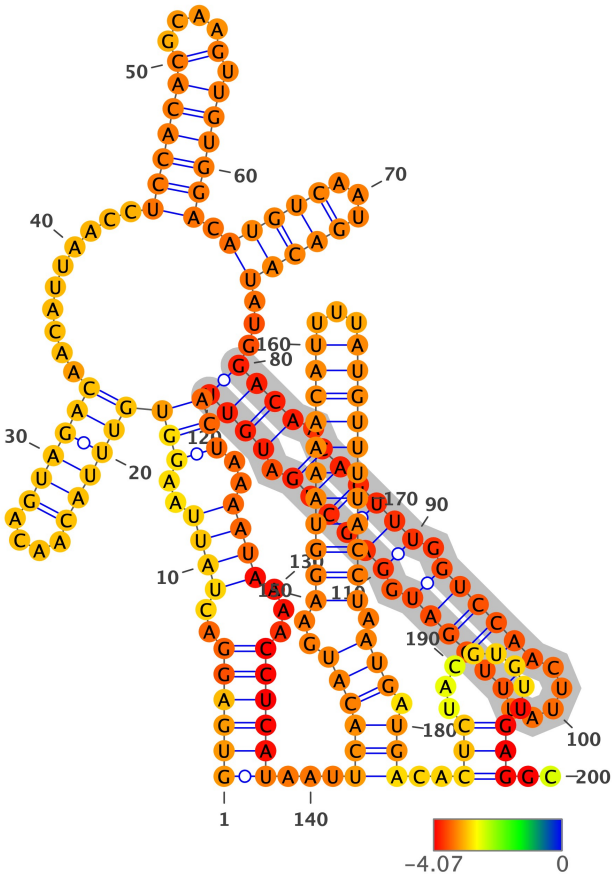
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 5037 to 5077 (nt 80 to 120)

```
5'-GACAACAGTTTGGTCCAACTTATUUGGAUGGAGCUGAUGUU-3'
5'-((((.((((((.((((((.....)))))).)))))).))))-3'
Motif MFE = -17.8; z-score = -4.86; ED = 0.99
```



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

Extracted structure model with flanking nucleotides 4958 to 5157 (motif highlighted in silver):

```
5'-GUGAGGACUAUUAAGGUGUUUACAACAGUAGACAACAUUAACCUCCACACGCAAGUUGUGGACAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGA
GCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGGC-3
5'-((((((..((((..((((((((((....))))))..........(((((((....).)))))).(((((...)))))...((((.((((((.((((((.....)))))).))
)))).)))))))..))))...))))))...((((((..((((((((((((...)))))))))))).))).))).(((........)))..-3'
MFE = -60.4; z-score = -4.61; 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(+)

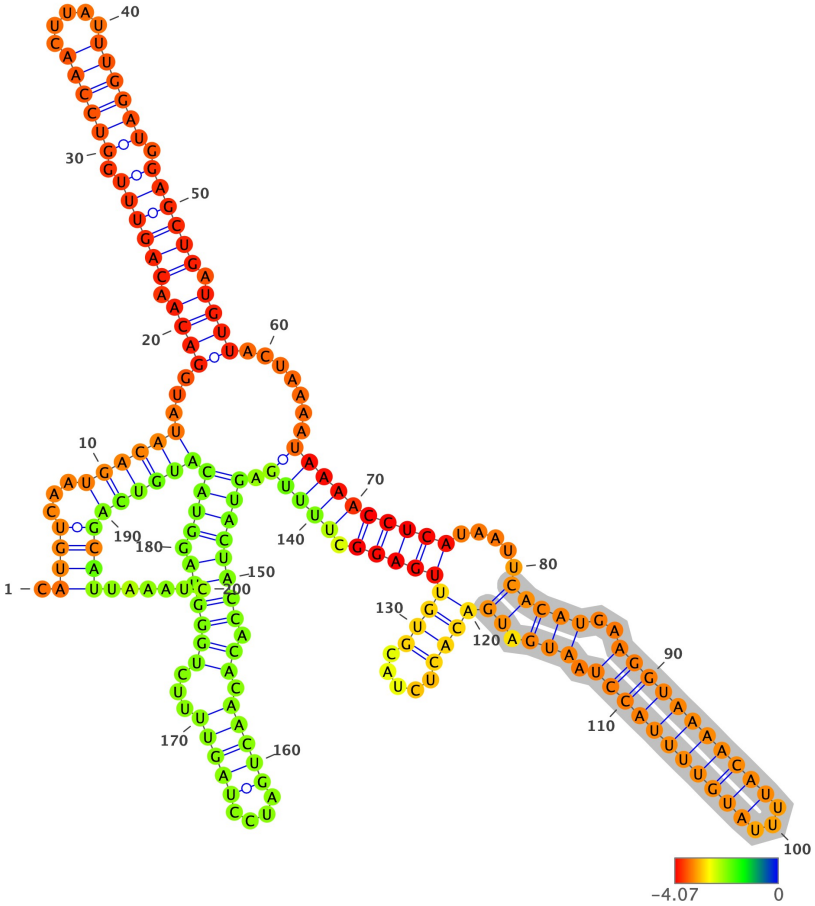
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 99 from nt 5100 to 5138 (nt 81 to 119)

```
5'-CACATGAAGGTAAAACATTTTAUGUUUUACCUAAUGAUG-3'
5'-(((((..(((((((((((...)))))))))))).))).))-3'
Motif MFE = -12.8; z-score = -4.45; ED = 3.26
```



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

Extracted structure model with flanking nucleotides 5020 to 5219 (motif highlighted in silver):

```
5'-CAUGUCAAUGACAUAUGGACAACAGUUUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACC
UAAUGAUGACACUCUACGUGUUGAGGCUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUC-3
5'-.((((...((((((...((((.((((((.((((((.....)))))).)))))).)))).......((((((((((.....(((((..((((((((((((...)))))))))))
).))).))((((.....)))))))))).))))).((((((((.((.(((((....)))))...)))))).))))))))))))))).....-3'
MFE = -57.9; z-score = -4.39; ED = 15.18
```

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

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

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

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

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

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

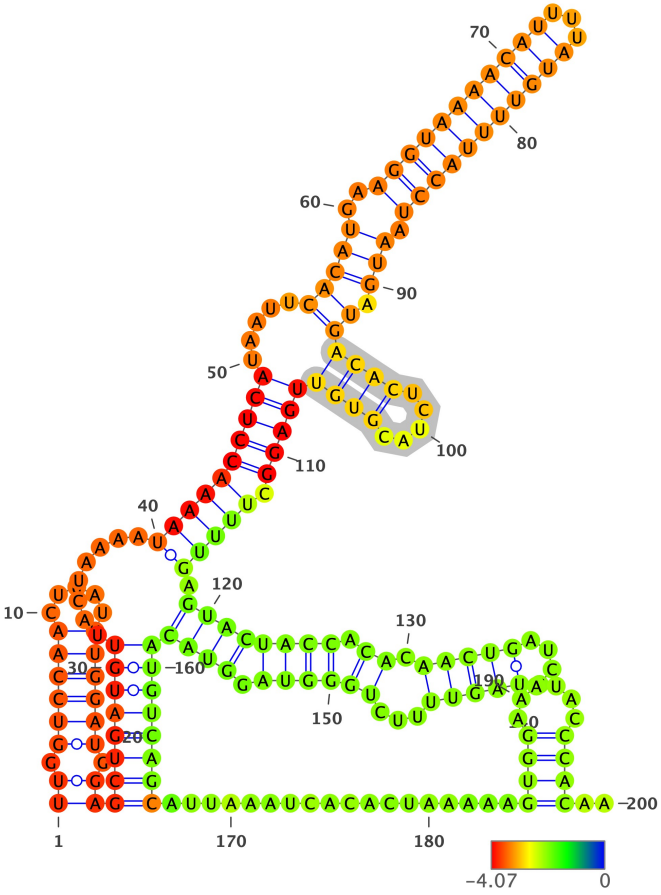
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 100 from nt 5139 to 5151 (nt 94 to 106)

```
5'-ACACTCTACGUGU-3'
5'-((((.....))))-3'
Motif MFE = -1.7; z-score = -7.32; ED = 0.73
```



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

Extracted structure model with flanking nucleotides 5046 to 5245 (motif highlighted in silver):

```
5'-UUGGUCCAACUUAUUUGGAUGGAGCUGAUGUUACUAAAAUAAAACCUCAUAAUUCACAUGAAGGUAAAACAUUUUAUGUUUUACCUAAUGAUGACACUCUACGUGUUGAGG
CUUUUGAGUACUACCACACAACUGAUCCUAGUUUUCUGGGUAGGUACAUGUCAGCAUUAAAUCACACUAAAAAGUGGAAAUACCCACAA-3
5'-((.((((((.....)))))).))((((((((.........((((((((((.....(((((..((((((((((((...)))))))))))).))).))((((.....)))))))))
.))))).((((((((.((.(((((....)))))...)))))).))))))))))))).................((((......))))..-3'
MFE = -52.5; z-score = -3.85; ED = 20.73
```

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

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

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

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

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

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

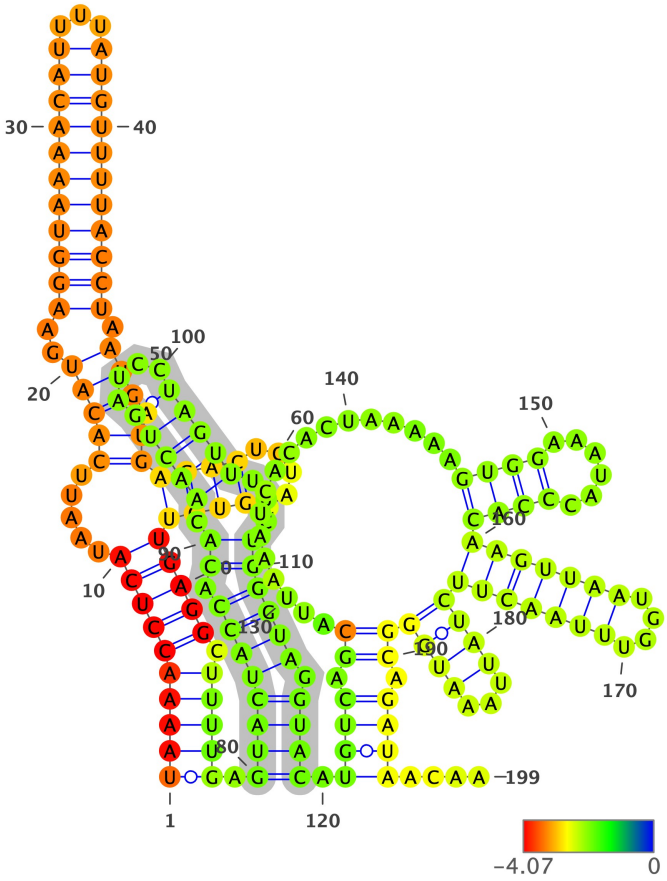
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 101 from nt 5164 to 5203 (nt 80 to 119)

```
5'-GTACTACCACACAACTGATCCUAGUUTTCUGGGUAGGUAC-3'
5'-((((((((.((.(((((....)))))...)))))).))))-3'
Motif MFE = -9.8; z-score = -2.36; 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 = -3.22; ED = 36.54
```

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

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

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

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

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

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

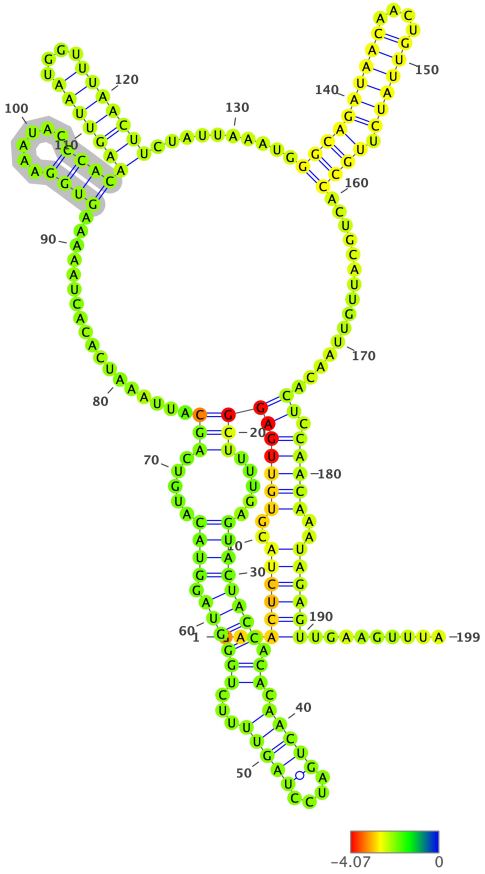
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 102 from nt 5230 to 5243 (nt 93 to 106)

```
5'-GTGGAAATACCCAC-3'
5'-((((.....))))-3'
Motif MFE = -3.7; z-score = -4.25; 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 = -2.81; 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(+)

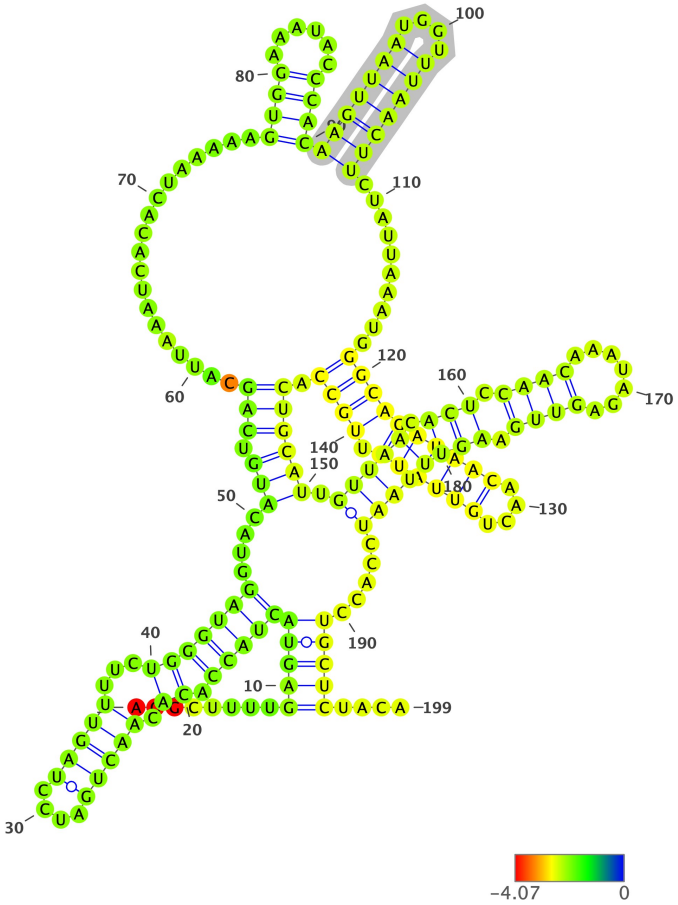
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 103 from nt 5244 to 5261 (nt 91 to 108)

```
5'-AAGTTAATGGTUUAACUU-3'
5'-(((((((....)))))))-3'
Motif MFE = -3.4; z-score = -4.05; 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 = -2.53; 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(+)

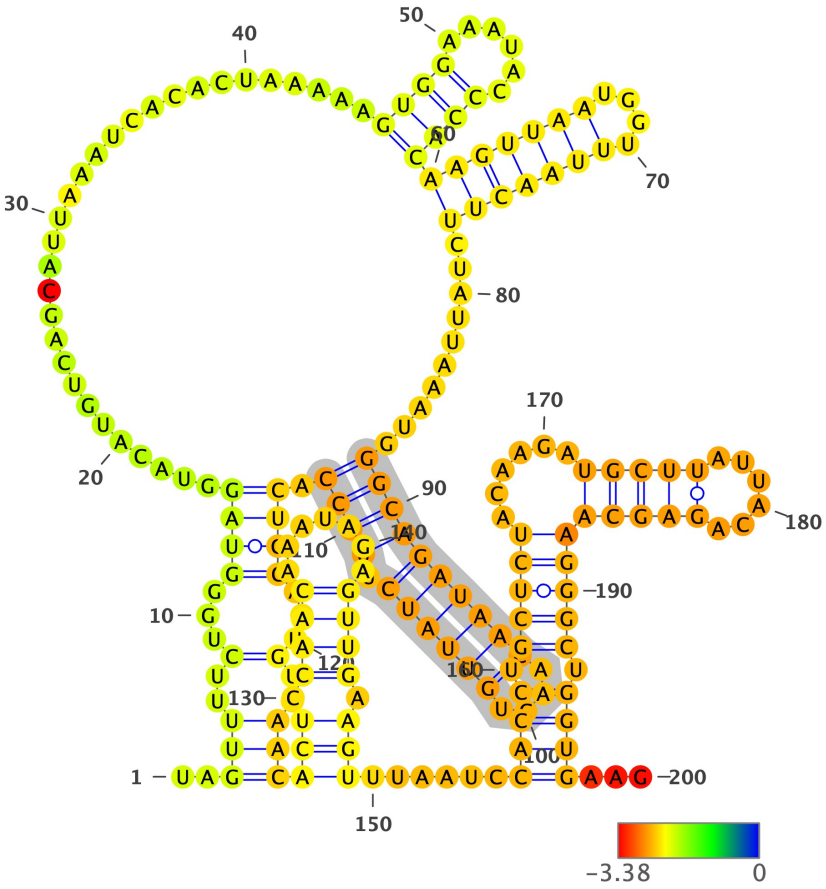
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 104 from nt 5272 to 5296 (nt 88 to 112)

```
5'-GGCAGATAACAACTGUUAUCTUGCC-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -10.9; z-score = -4.64; 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 = -1.96; 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(+)

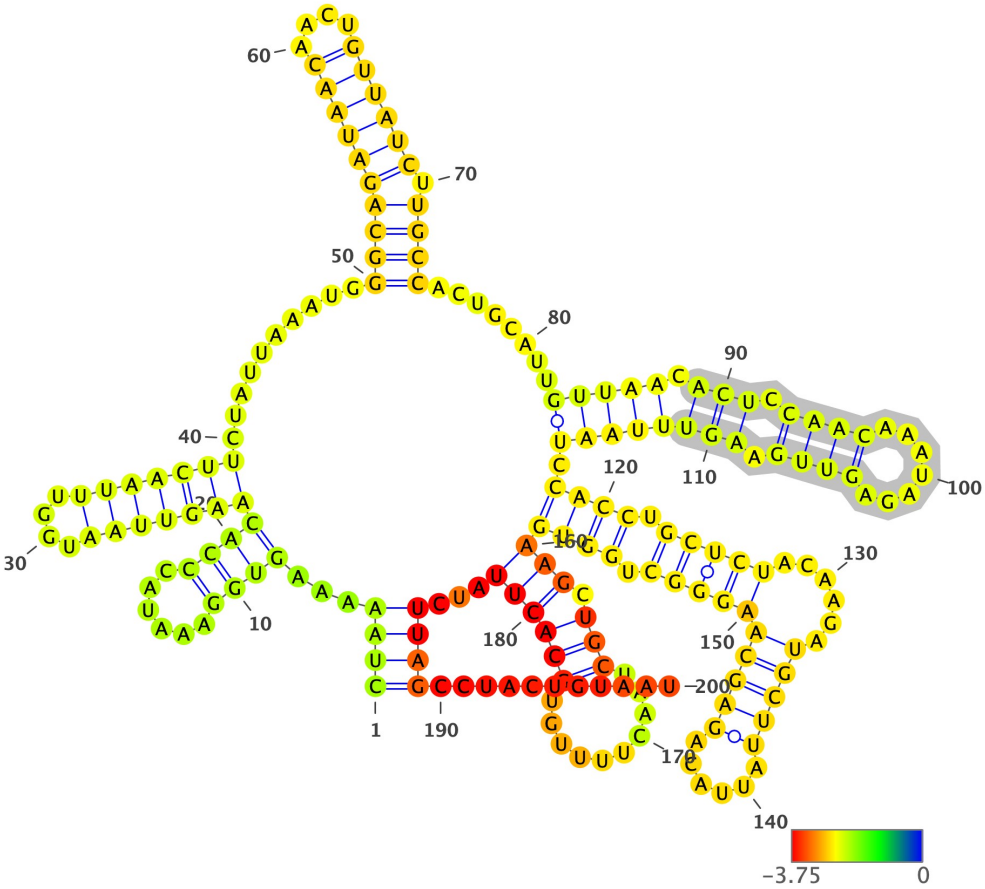
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 105 from nt 5311 to 5333 (nt 89 to 111)

```
5'-ACTCCAACAAATAGAGUUGAAGU-3'
5'-(((.((((.......)))).)))-3'
Motif MFE = -3.3; z-score = -2.99; 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 = -3.04; ED = 38.6
```

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

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

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

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

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

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

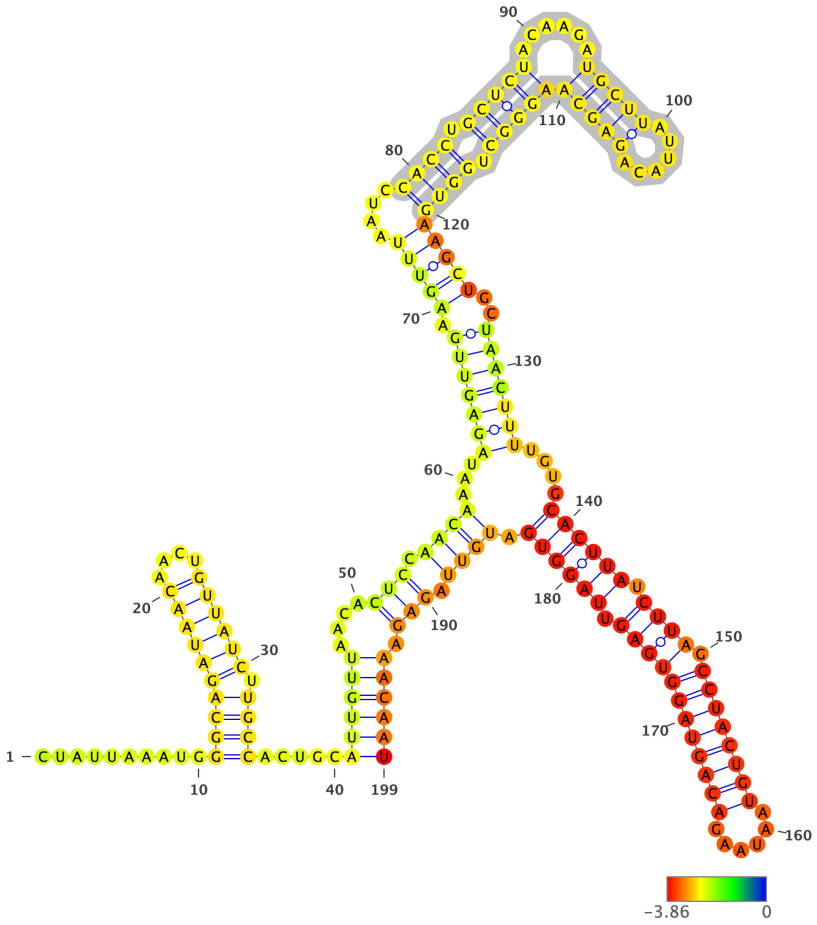
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 106 from nt 5340 to 5381 (nt 79 to 120)

```
5'-CACCTGCTCTACAAGATGCTTATTACAGAGCAAGGGCTGGUG-3'
5'-((((.((((.......(((((......))))).)))).))))-3'
Motif MFE = -14.9; z-score = -2.68; ED = 0.36
```



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

Extracted structure model with flanking nucleotides 5262 to 5460 (motif highlighted in silver):

```
5'-CUAUUAAAUGGGCAGAUAACAACUGUUAUCUUGCCACUGCAUUGUUAACACUCCAACAAAUAGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAA
GGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAU-3
5'-..........(((((((((....)))))).))))).....((((((....(((.((((...(((((((.(((((....((((.(((((......(((((......))))))
)))).))))))))..))))))).....((((((.((((.((((((((......))))))))))))).)))))).)))).))).))))))-3'
MFE = -61.4; z-score = -4.28; ED = 17.84
```

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

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

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

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

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

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

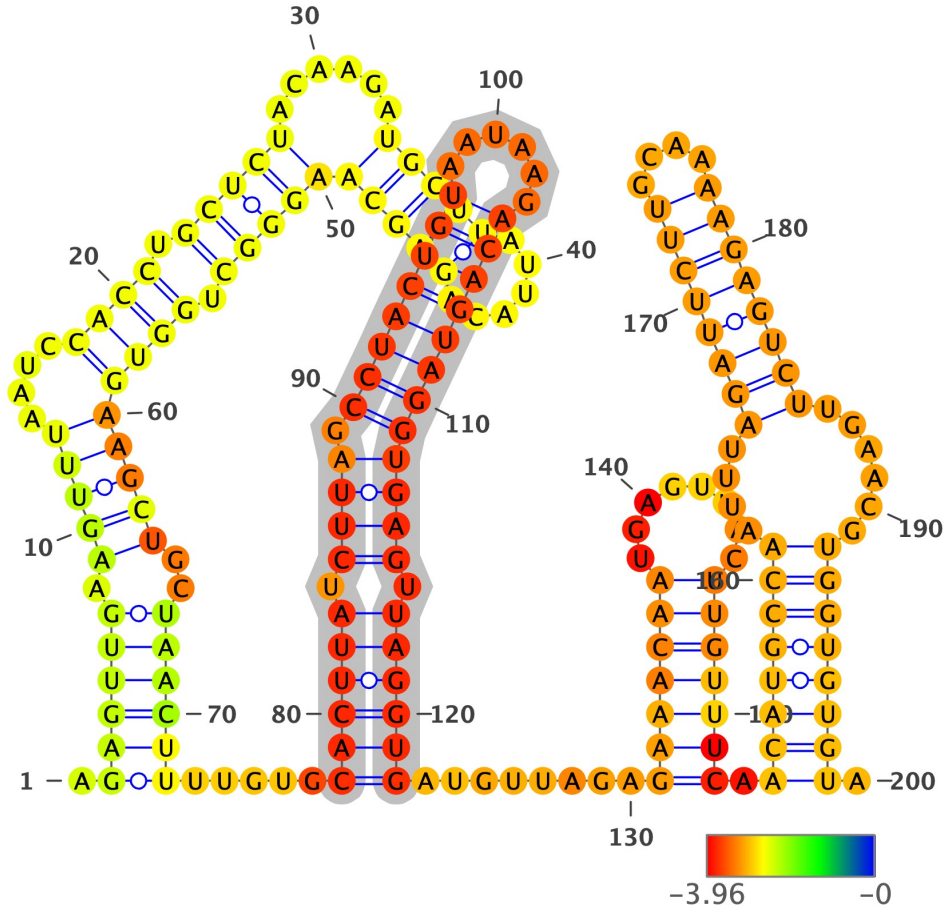
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 107 from nt 5400 to 5444 (nt 78 to 122)

```
5'-CACTTATCTTAGCCTACTGTAATAAGACAGUAGGTGAGTUAGGUG-3'
5'-((((((.(((..((((((((......))))))))).))).))))))-3'
Motif MFE = -20.7; z-score = -5.36; ED = 1.77
```



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

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

```
5'-AGAGUUGAAGUUUAAUCCACCUGCUCUACAAGAUGCUUAUUACAGAGCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGG
UGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUA-3
5'-.((((((.(((((....((((.(((((......(((((......)))))))))).))))))))).)))))).....((((((.((((.((((((((......))))))))
)))).)))))).......((((((.........)))))).((((((((....((((((((....))))))))......))))))))).-3'
MFE = -67.6; z-score = -5.21; ED = 12.19
```

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

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

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

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

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

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

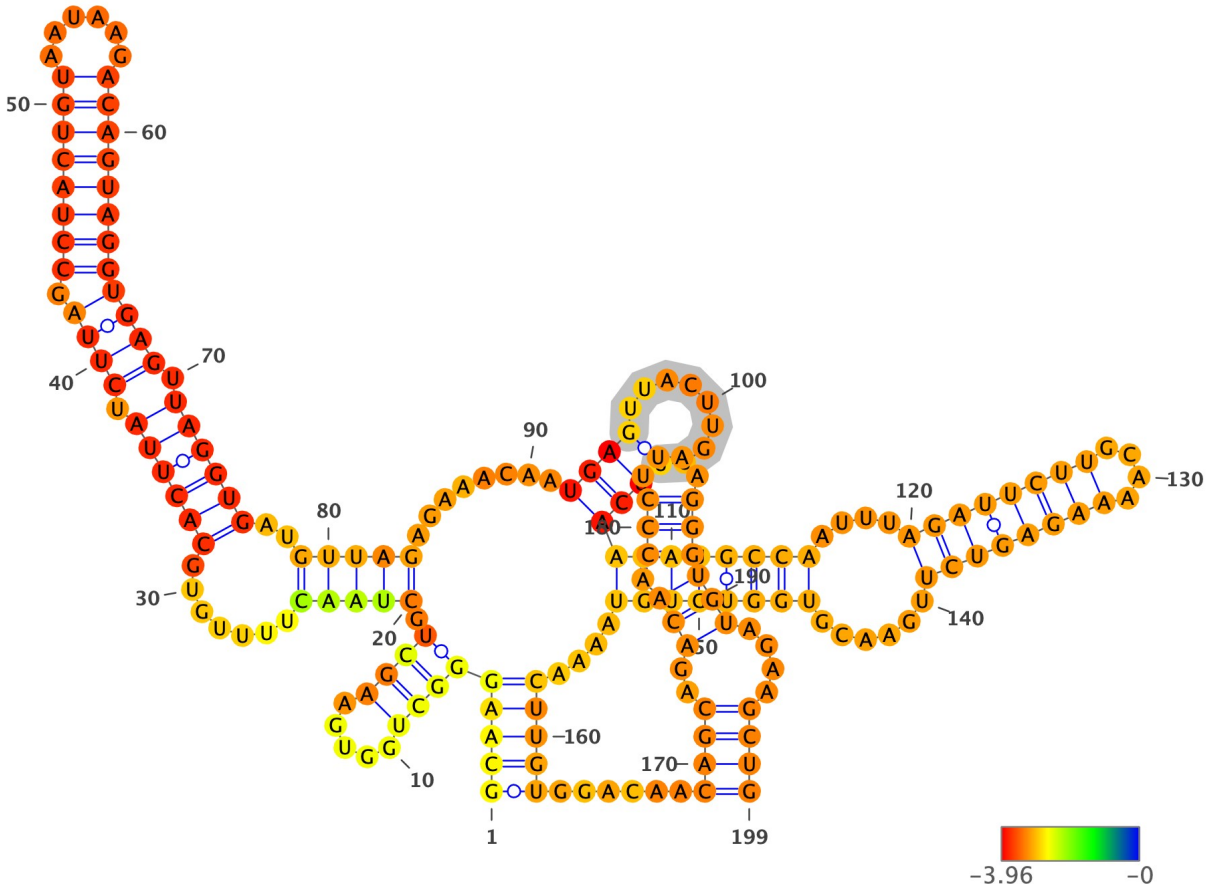
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 108 from nt 5463 to 5472 (nt 95 to 104)

```
5'-GTTACTTGTU-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 5369 to 5567 (motif highlighted in silver):

```
5'-GCAAGGGCUGGUGAAGCUGCUAACUUUUGUGCACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAU
GCCAAUUUAGAUUCUUGCAAAAGAGUCUUGAACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUG-3
5'-(((((((((.....)))).(((((.......((((((.((((.((((((((.....))))))))))))).))))))..)))))........((((........))))((((
((((....((((((((....))))))))......))))))))....)))))......((((..(((.(((....))))))....))))-3'
MFE = -61.3; z-score = -4.03; ED = 19.0
```

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

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

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

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

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

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

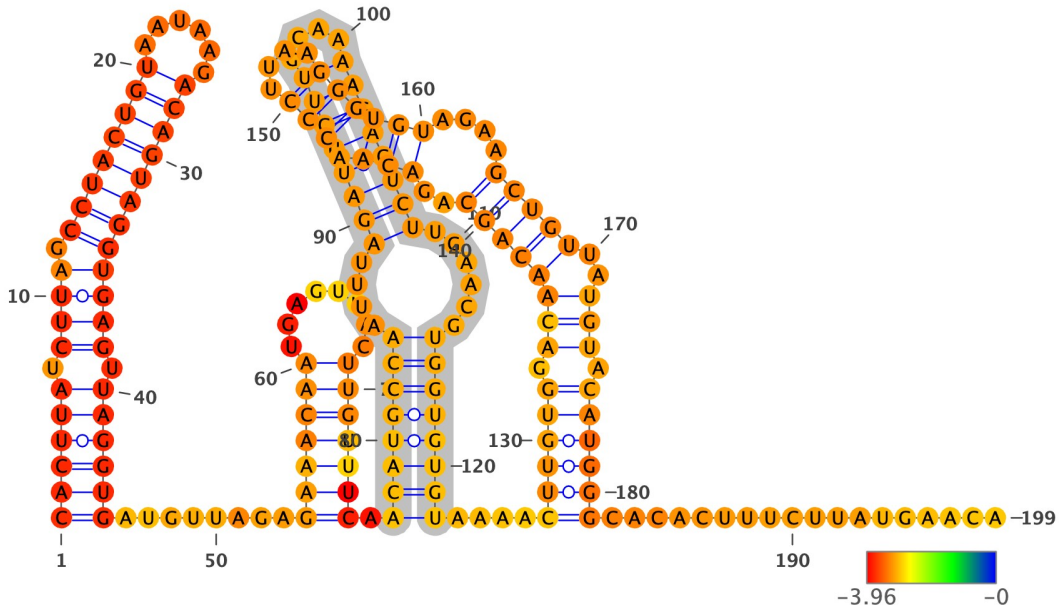
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 109 from nt 5476 to 5521 (nt 77 to 122)

```
5'-ACATGCCAATTTAGATTCTTGCAAAAGAGUCUTGAACGUGGUGUGU-3'
5'-(((((((((....(((((((((....)))))))))......)))))))))-3'
Motif MFE = -16.9; z-score = -4.15; ED = 3.32
```



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

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

```
5'-CACUUAUCUUAGCCUACUGUAAUAAGACAGUAGGUGAGUUAGGUGAUGUUAGAGAAACAAUGAGUUACUUGUUUCAACAUGCCAAUUUAGAUUCUUGCAAAAGAGUCUUGA
ACGUGGUGUGUAAAACUUGUGGACAACAGCAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACA-3
5'-((((((.((((.(((((((((.....)))))))))))).)))))).......(((((((........)))))))..(((((((((....(((((((((....)))))))))...
...)))))))))....((((((.(((((((((..(((.(((....)))))))....))))))..))).)))))).................-3'
MFE = -63.0; z-score = -4.65; ED = 24.97
```

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

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

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

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

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

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

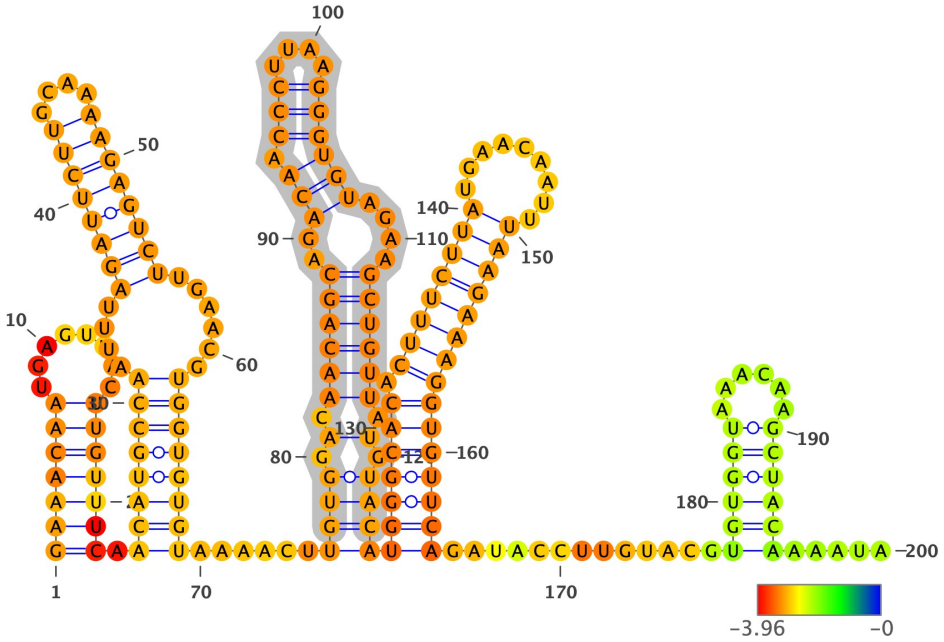
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 110 from nt 5529 to 5575 (nt 77 to 123)

```
5'-GTGGACAACAGCAGACAACCCTTAAGGGUGUAGAAGCUGUUAUGUAC-3'
5'-(((.(.(((((((..(((.(((....)))))))....)))))))).).)))-3'
Motif MFE = -14.3; z-score = -2.48; 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(+)

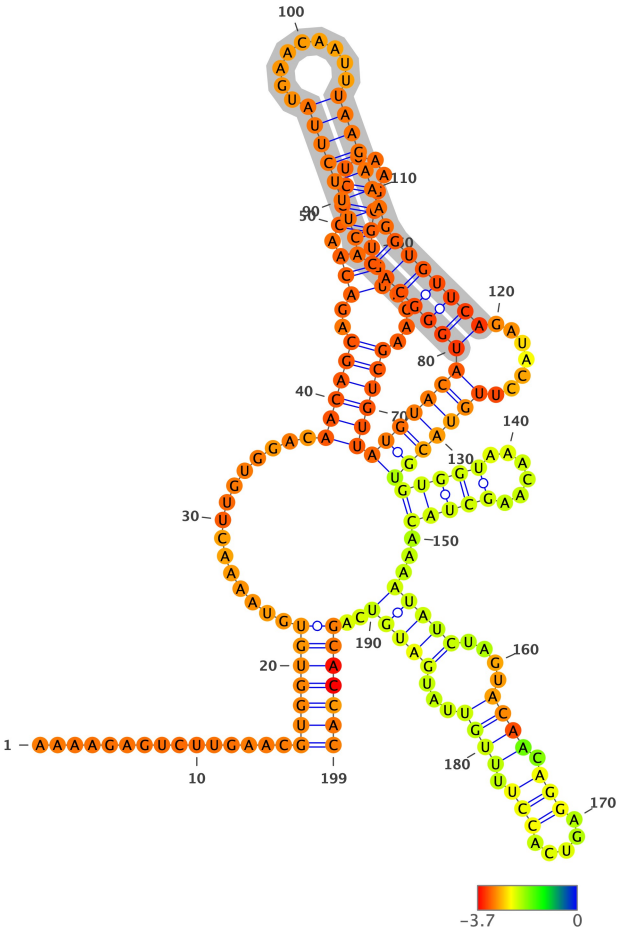
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 111 from nt 5577 to 5616 (nt 80 to 119)

```
5'-TGGGCACACTTTCTTATGAACAATTUAAGAAAGGUGUUCA-3'
5'-(((((((.(((((((((.........)))))))))))))))-3'
Motif MFE = -15.3; z-score = -4.52; 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 = -3.58; 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(+)

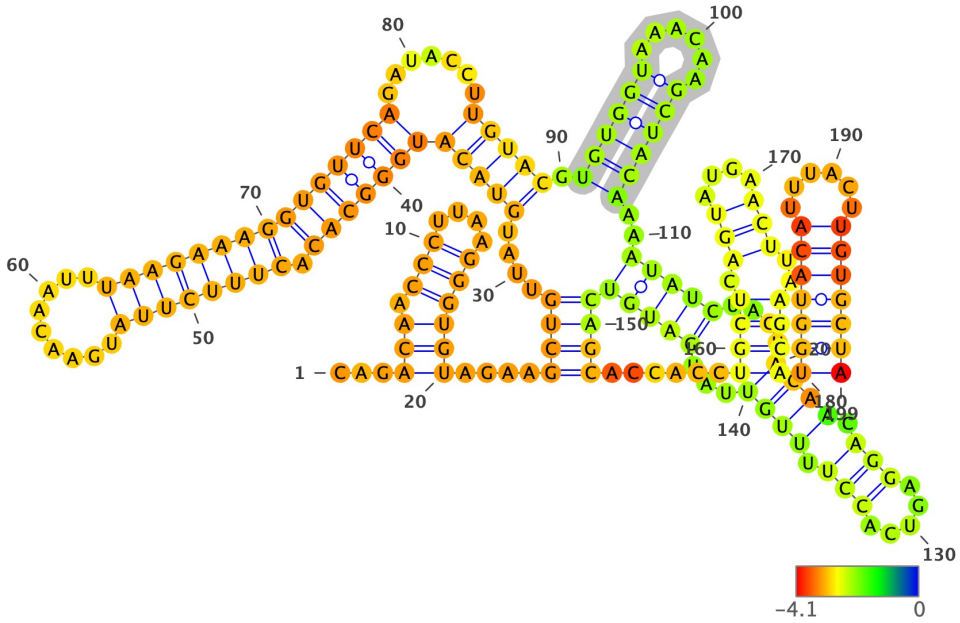
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 112 from nt 5630 to 5647 (nt 91 to 108)

```
5'-TGTGGTAAACAAGCUACA-3'
5'-((((((......))))))-3'
Motif MFE = -4.5; z-score = -3.84; ED = 0.6
```



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

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

```
5'-CAGACAACCCUUAAGGGUGUAGAAGCUGUUAUGUACAUGGGCACACUUUCUUAUGAACAAUUUAAGAAAGGUGUUCAGAUACCUUGUACGUGUGGUAAACAAGCUACAAAA
UAUCUAGUACAACAGGAGUCACCUUUUGUUAUGAUGUCAGCACCACCUGCUCAGUAUGAACUUAAGCAUGGUACAUUUACUUGUGCUA-3
5'-...(((.(((....))))))....((((....((((((((((((.((((((((.........)))))))))))))))).......))))).((((((......))))))..(
((((....((((.(((.....)).))))...)))))))))......((((.(((....)))..))))(((((((......)))))))-3'
MFE = -52.1; z-score = -2.98; ED = 34.29
```

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

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

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

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

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

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

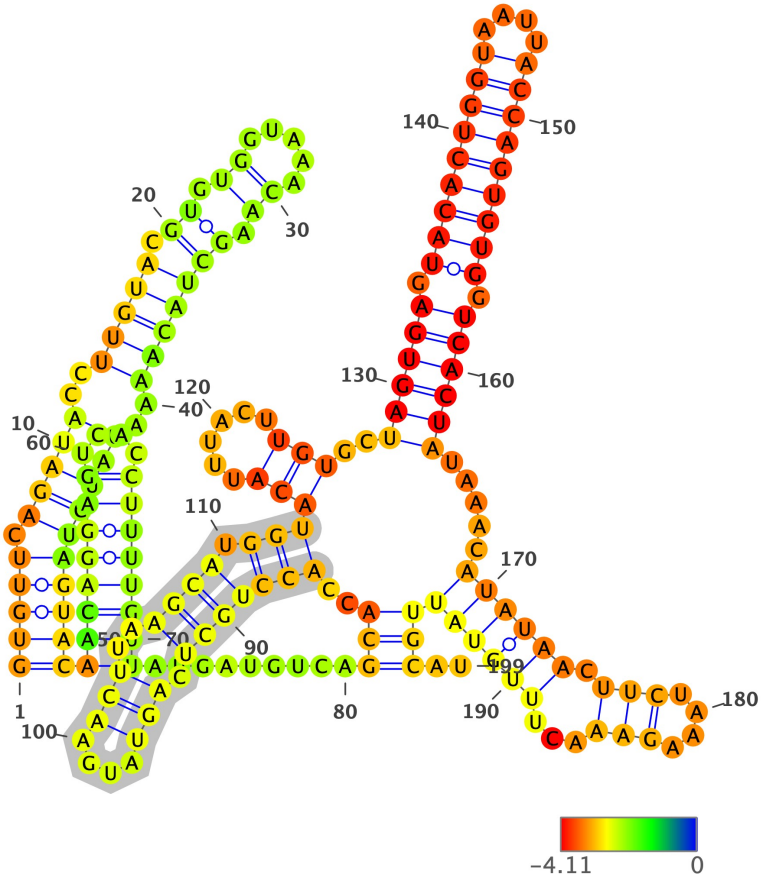
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

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

```
5'-ACCTGCTCAGTATGAACUTAAGCATGGU-3'
5'-(((((((.(((....)))..)))).)))-3'
Motif MFE = -6.4; z-score = -1.82; 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 = -2.81; 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(+)

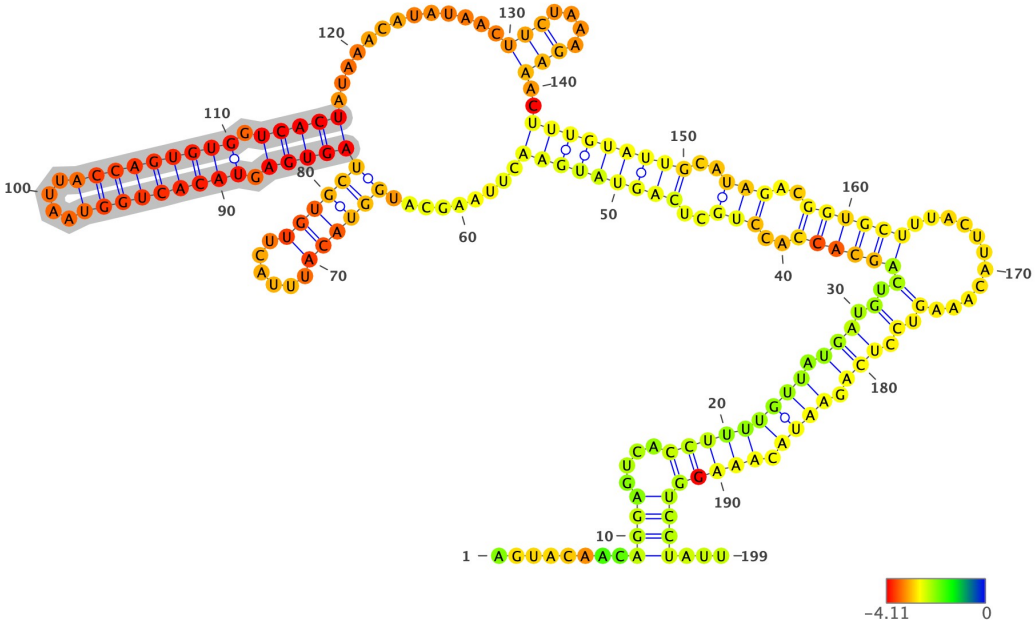
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 114 from nt 5738 to 5771 (nt 83 to 116)

```
5'-AGTGAGTACACTGGTAATTACCAGUGUGGUCACU-3'
5'-(((((.(((((((((......)))))))).)))))-3'
Motif MFE = -20.9; z-score = -6.02; 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 = -3.18; 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(+)

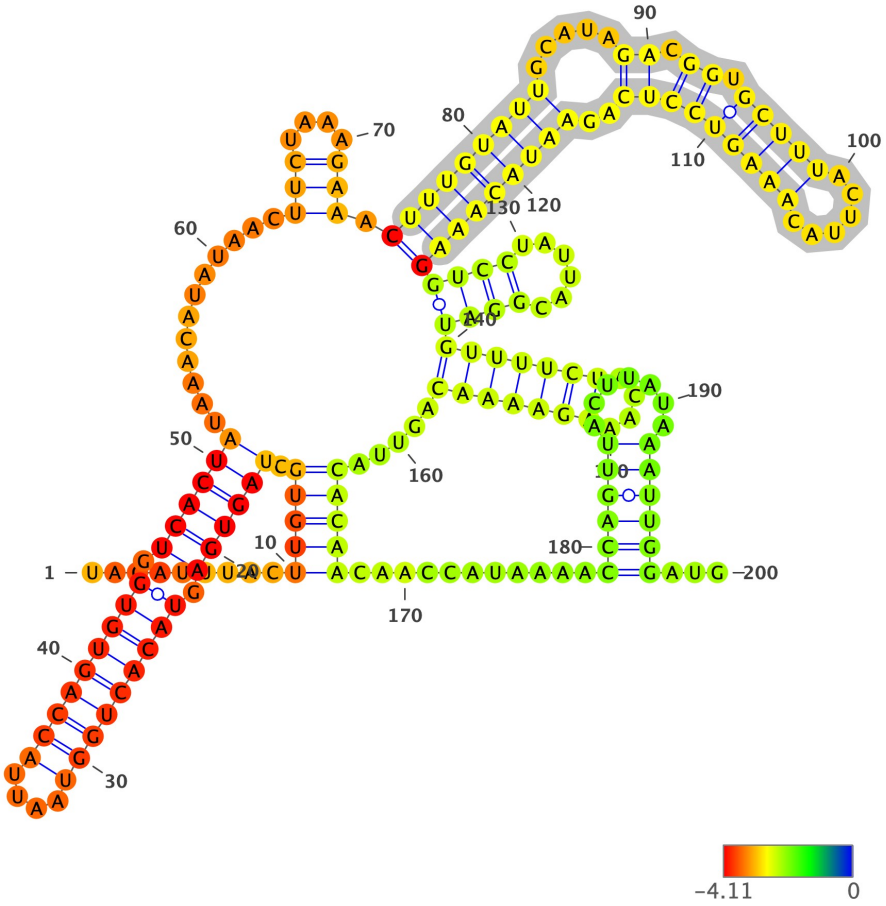
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 115 from nt 5797 to 5845 (nt 76 to 124)

```
5'-TTTGTATTGCATAGACGGTGCTTTACTTACAAAGUCCUCAGAAUACAAA-3'
5'-((((((((.....((.((.(((((.....)))))))))..))))))))-3'
Motif MFE = -8.4; z-score = -1.44; ED = 6.66
```



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

Extracted structure model with flanking nucleotides 5722 to 5921 (motif highlighted in silver):

```
5'-UACAUUUACUUGUGCUAGUGAGUACACUGGUAAUUACCAGUGUGGUCACUAUAAACAUAUAACUUCUAAAGAAACUUUGUAUUGCAUAGACGGUGCUUUACUUACAAAGUC
CUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUG-3
5'-.........(((((.((((((.(((((((((....)))))))))).))))))............(((....))).(((((((((.....((.((.(((((.....))))))
)))..)))))))))((((.....))))(((((((....)))))))).....)))))...........((((((.......))))))...-3'
MFE = -52.5; z-score = -4.56; ED = 15.14
```

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(+)

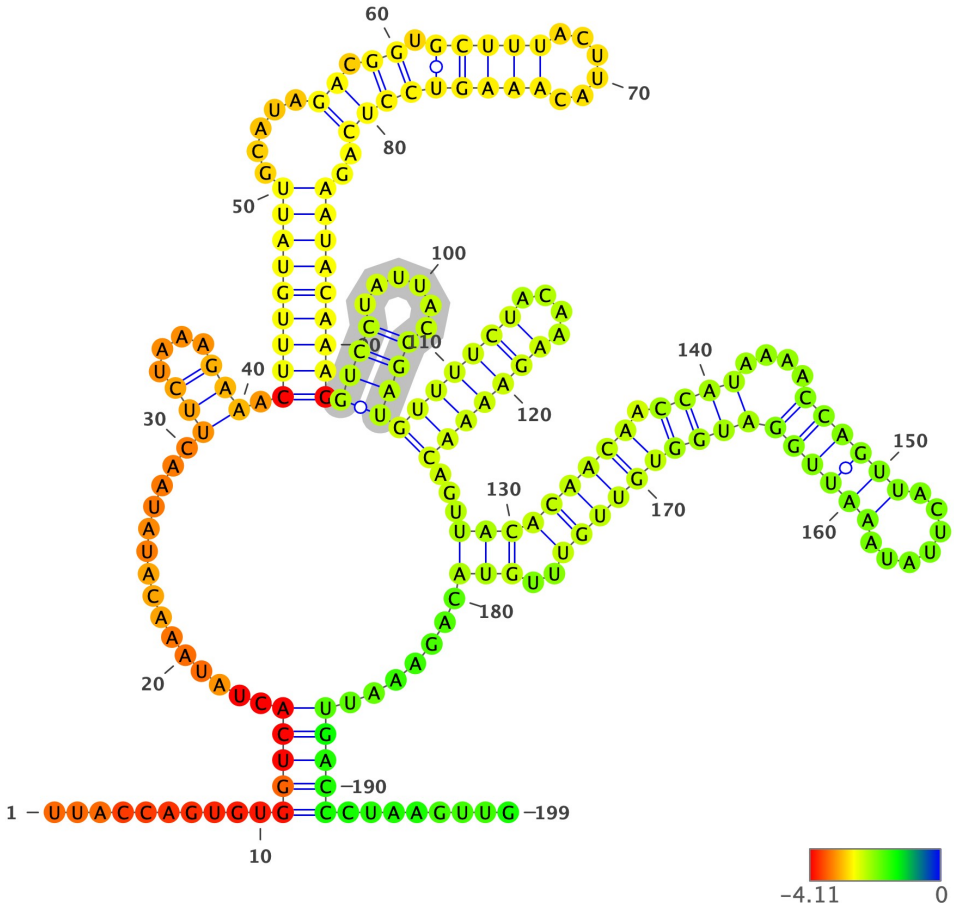
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 116 from nt 5847 to 5860 (nt 93 to 106)

```
5'-GTCCTATTACGGAU-3'
5'-((((......))))-3'
Motif MFE = -2.6; z-score = -3.44; 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 = -2.23; 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(+)

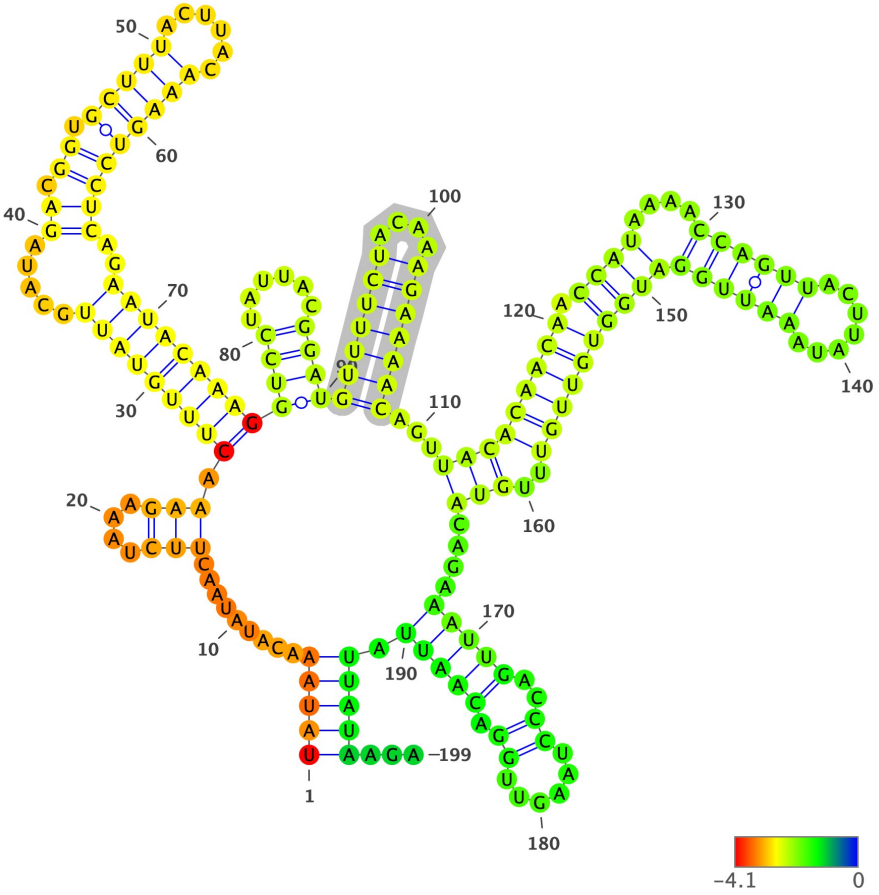
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 117 from nt 5861 to 5878 (nt 91 to 108)

```
5'-GTTTTCTACAAAGAAAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -7.72; 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 = -2.8; 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(+)

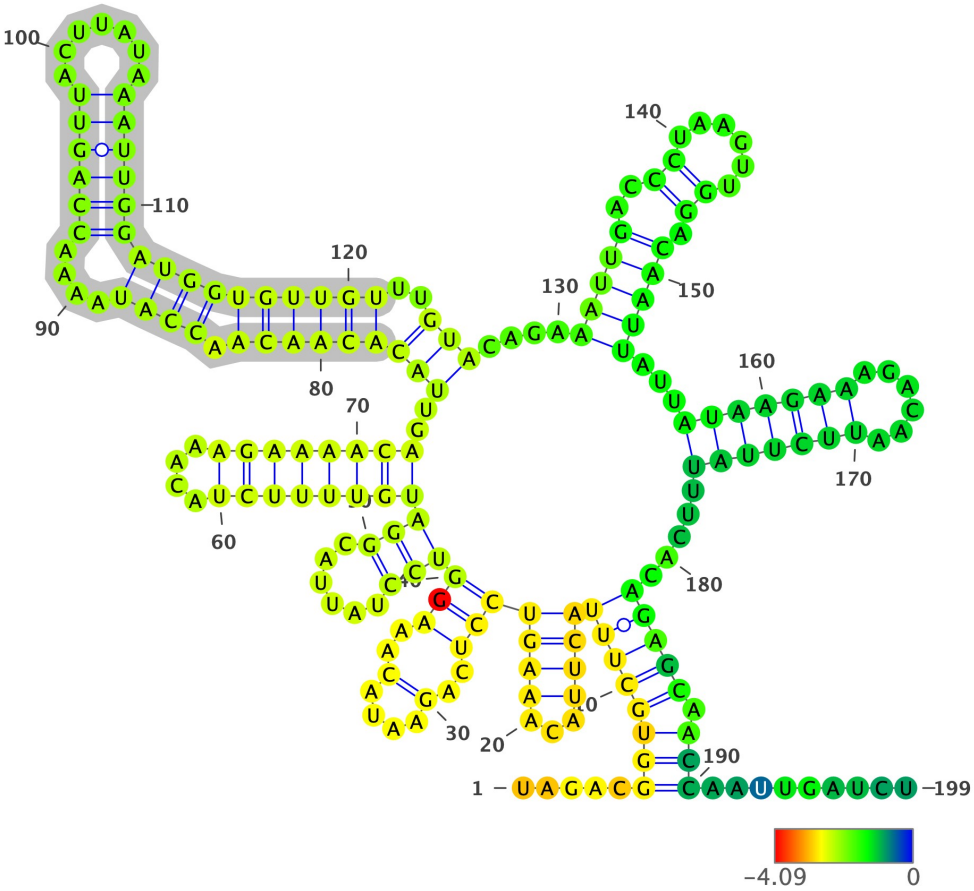
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 118 from nt 5885 to 5928 (nt 78 to 121)

```
5'-ACAACAACCATAAAACCAGTTACTTATAAAUUGGAUGGUGUUGU-3'
5'-((((((.((((....((((..........))))))))))))))-3'
Motif MFE = -12.6; z-score = -3.95; ED = 2.01
```



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

Extracted structure model with flanking nucleotides 5808 to 6006 (motif highlighted in silver):

```
5'-UAGACGGUGCUUUACUUACAAAGUCCUCAGAAUACAAAGGUCCUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGG
AUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCU-3
5'-.....((((((((((((...))))))((..(....)..))))((......)))(((((((((....)))))))))..((((((((((.((((....((((((.......))))))
))))))))))..))).....((((((..((.......)).))))))...(((((((.....)))))))).....))))).)))).........-3'
MFE = -39.1; z-score = -2.27; ED = 19.95
```

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

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

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

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

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

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

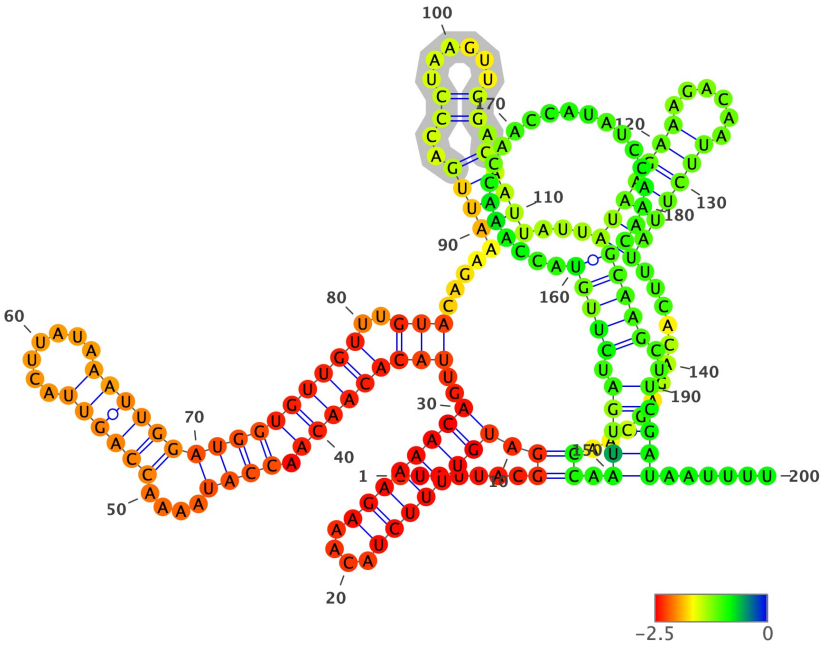
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 119 from nt 5942 to 5956 (nt 93 to 107)

```
5'-GACCCTAAGTTGGAC-3'
5'-(..((......)).)-3'
Motif MFE = -1.5; z-score = -1.15; ED = 0.73
```



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

Extracted structure model with flanking nucleotides 5850 to 6049 (motif highlighted in silver):

```
5'-CUAUUACGGAUGUUUUCUACAAAGAAAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUU
AUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUU-3
5'-.......((.(((((((((....)))))))))..((((((((((.((((....((((((.......))))))))))))))))))..))).....(((((..((......)).)))))
...(((((((......)))))))............)).(((((.(((((.....................)))))..)))))......-3'
MFE = -33.2; z-score = -1.86; ED = 34.74
```

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

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

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

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

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

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

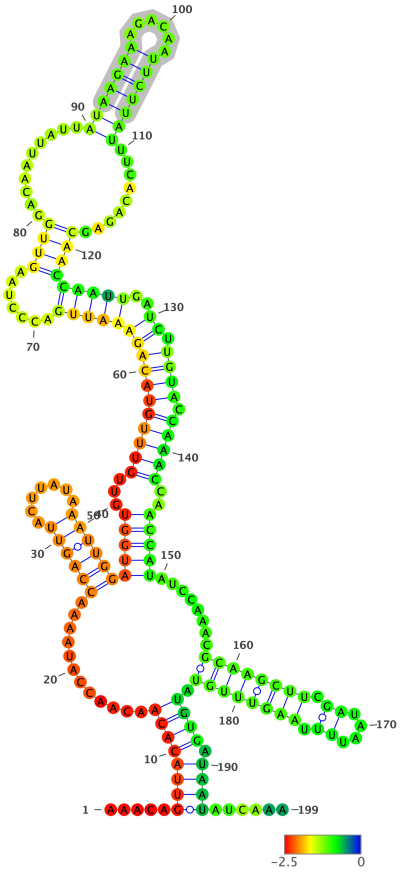
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 120 from nt 5966 to 5981 (nt 92 to 107)

```
5'-AAGAAAGACAAUUCUU-3'
5'-(((((......)))))-3'
Motif MFE = -0.7; z-score = -2.64; ED = 3.0
```



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

Extracted structure model with flanking nucleotides 5875 to 6073 (motif highlighted in silver):

```
5'-AAACAGUUACACAACAACCAUAAAACCAGUUACUUAUAAAUUGGAUGGUGUUGUUUGUACAGAAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUU
CACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUGUAUGUGAUAAUAUCAAA-3
5'-.....((((((((.............((((((.......))))))(((((...((((((((((((((((.......((((..........(((((((......)))))))..
.......))))))))).))).)))).)))))..)))))........((((((((.((....)).)))))))).)))).))))......-3'
MFE = -34.7; z-score = -2.15; ED = 45.16
```

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

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

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

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

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

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

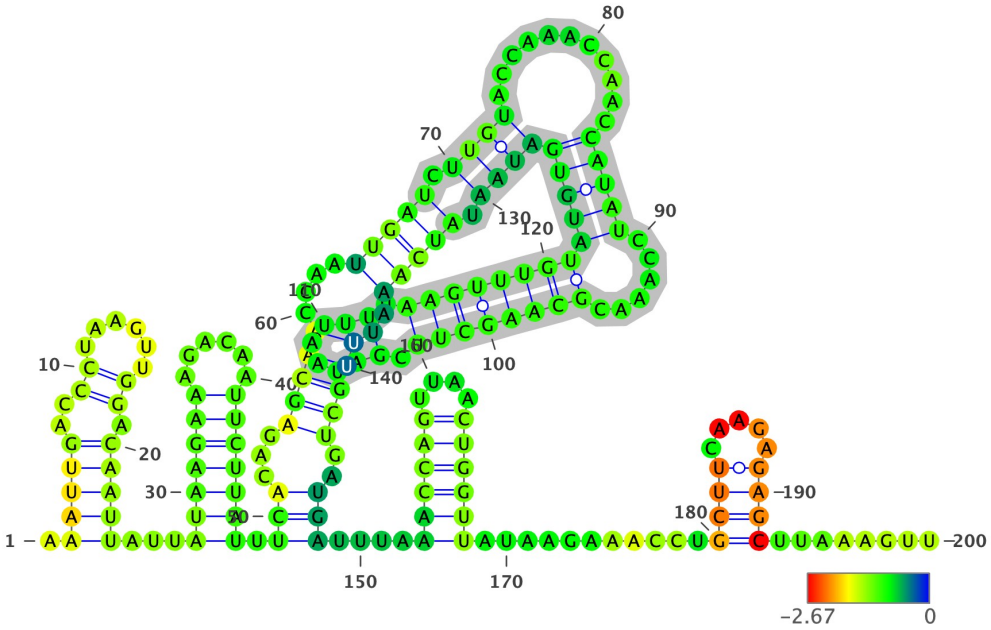
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 121 from nt 6004 to 6068 (nt 68 to 132)

```
5'-TCTTGTACCAAACCAACCATATCCAAACGCAAGCTTCGATAATTTTAAGUUUGUATGTGATAATA-3'
5'-(.........................(((((((..........)))))))).........)-3'
Motif MFE = -9.6; z-score = -1.51; ED = 6.36
```



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 5937 to 6136 (motif highlighted in silver):

```
5'-AAAUUGACCCUAAGUUGGACAAUUAUUAUAAGAAAGACAAUUCUUAUUUCACAGAGCAACCAAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUU
UUAAGUUUGUAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUU-3
5'-.(((((..((......)).))))))...(((((((......))))))).(((...(((((....(((((.((((..........(((((......((((((((.((....)
).)))))))))))))))).))))))..))))))..)))....((((((....))))))..........((((.....)))).........-3'
MFE = -30.5; z-score = -0.21; 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, 266-13468(+)

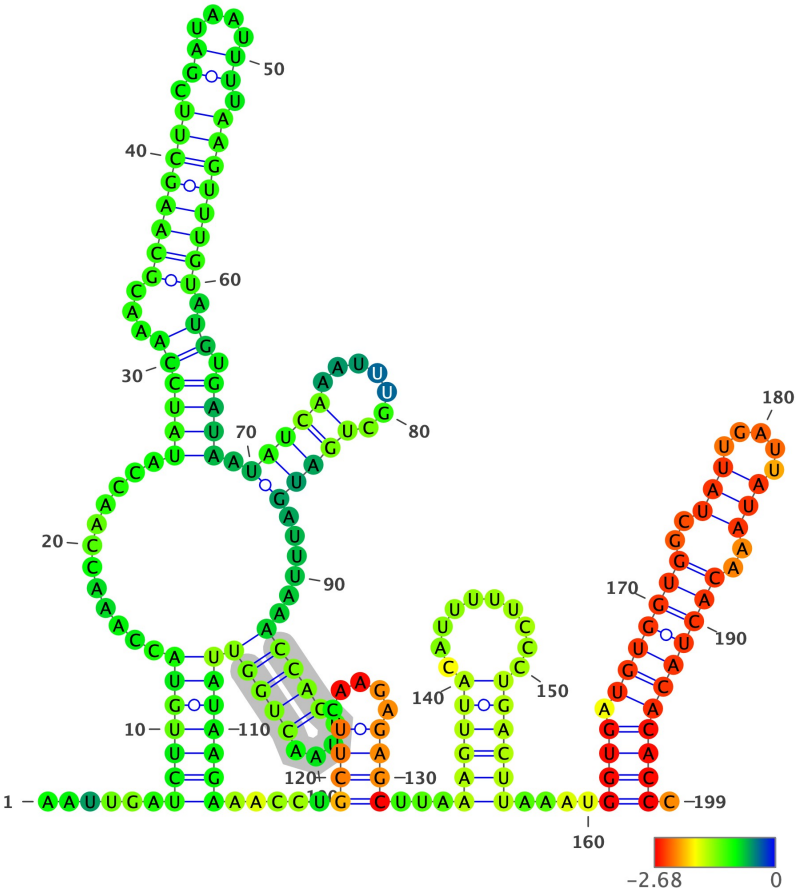
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 6091 to 6102 (nt 94 to 105)

```
5'-CCAGTTAACUGG-3'
5'-((((....))))-3'
Motif MFE = -3.0; z-score = -5.27; ED = 0.2
```



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

Extracted structure model with flanking nucleotides 5998 to 6196 (motif highlighted in silver):

```
5'-AAUUGAUCUUGUACCAAACCAACCAUAUCCAAACGCAAGCUUCGAUAAUUUUAAGUUUGUAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAA
GAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCC-3
5'-......(((((((.............((((((...(((((((((.((....)).)))))))))..)).))))).(((((.......)))))).....(((((....)))))))))
))).....(((.....)))))...((((((..........))))))....((((.(((((((..(((.....)))..))))))))))).-3'
MFE = -40.1; z-score = -2.09; ED = 32.13
```

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

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

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

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

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

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

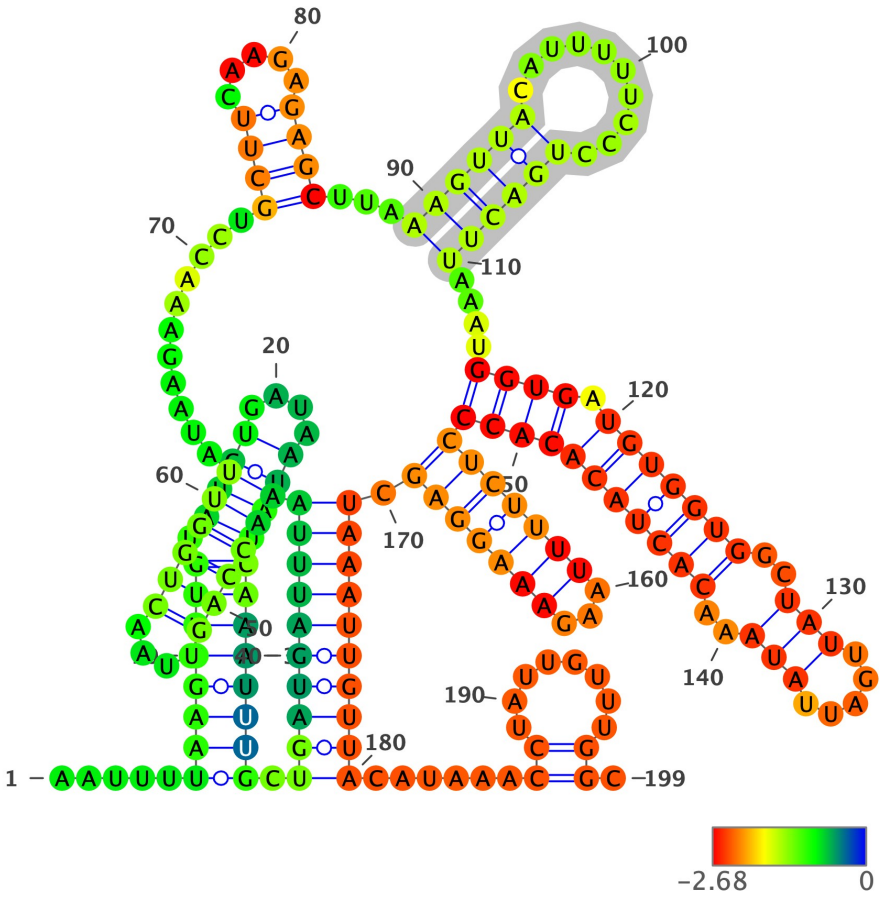
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 123 from nt 6132 to 6153 (nt 89 to 110)

```
5'-AAGTTACATTTTTCCCUGACUU-3'
5'-((((((..........))))))-3'
Motif MFE = -0.7; z-score = -0.73; ED = 2.16
```



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

Extracted structure model with flanking nucleotides 6044 to 6242 (motif highlighted in silver):

```
5'-AAUUUUAAGUUUGUAUGUGAUAAUAUCAAAUUUGCUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUA
AAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGC-3
5'-.....((((((((.((((....)))))))))))).((((((((((((((((....))))))...........((((.....))))...((((((..........)))))).
...((((.(((((((..(((.....)))..)))))))))))(((((((...)))))))).))))))))))......((........)).-3'
MFE = -43.4; z-score = -1.92; ED = 41.04
```

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

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

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

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

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

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

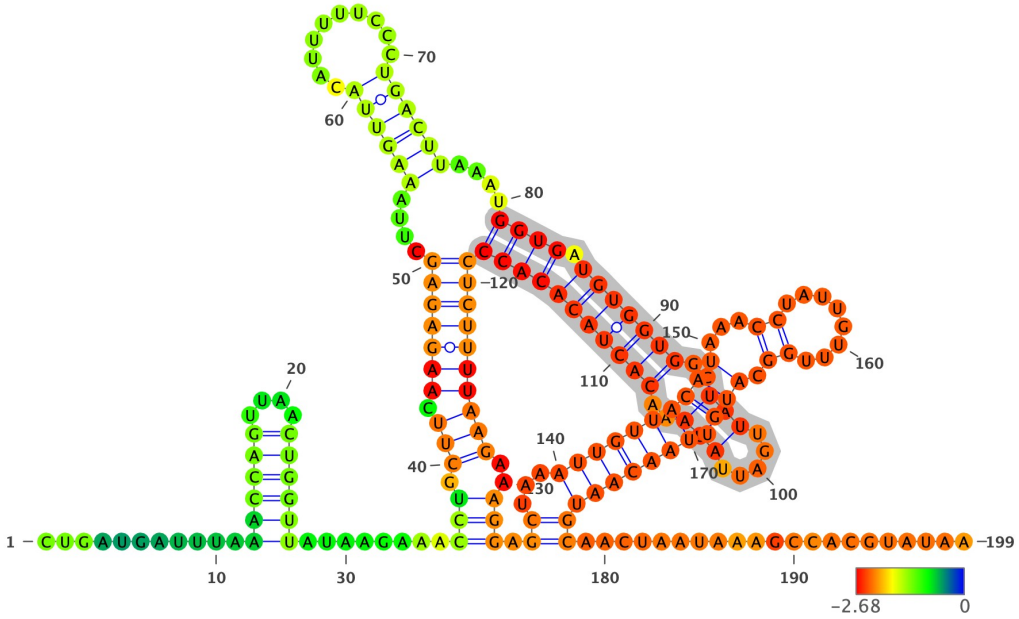
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 6158 to 6195 (nt 81 to 118)

```
5'-GGTGATGTGGTGGCTATTGATTAUAAACACUACACACC-3'
5'-((((.(((((((..(((.....)))..)))))))))))-3'
Motif MFE = -15.3; z-score = -3.89; ED = 0.39
```



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

Extracted structure model with flanking nucleotides 6078 to 6276 (motif highlighted in silver):

```
5'-CUGAUGAUUUAAACCAGUUAACUGGUUAUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACU
ACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAA-3
5'-...........((((((....))))))........(((.(((.(((((((....((((((..........))))))....((((.(((((((..(((.....)))..))))
))))))))))))))))..))).((...((((((((((...((........)).))).)))))))))......................-3'
MFE = -41.2; z-score = -1.89; ED = 50.41
```

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(+)

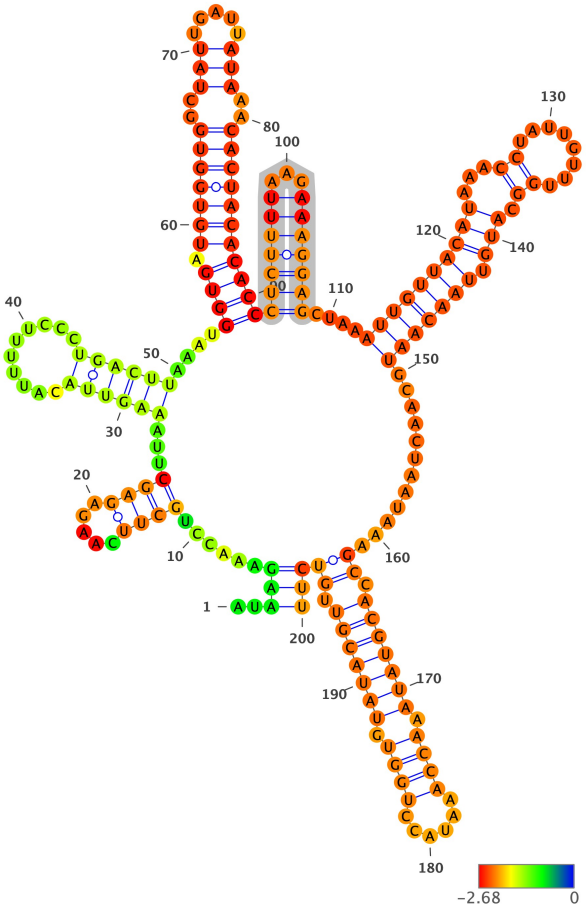
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 125 from nt 6196 to 6212 (nt 92 to 108)

```
5'-CTCTTTTAAGAAAGGAG-3'
5'-(((((.......)))))-3'
Motif MFE = -3.1; z-score = -3.35; 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 6105 to 6304 (motif highlighted in silver):

```
5'-AUAAGAAACCUGCUUCAAGAGAGCUUAAAGUUACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUA
AAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUU-3
5'-..(((......((((.....)))))...((((((..........))))))....(((((.(((((((..(((.....))).))))))))))))(((((((...)))))))...
.((((((((((...((........)).))).)))))))............((.(((((((.((((......)))).)))))))..)))))-3'
MFE = -45.7; z-score = -3.01; ED = 22.07
```

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(+)

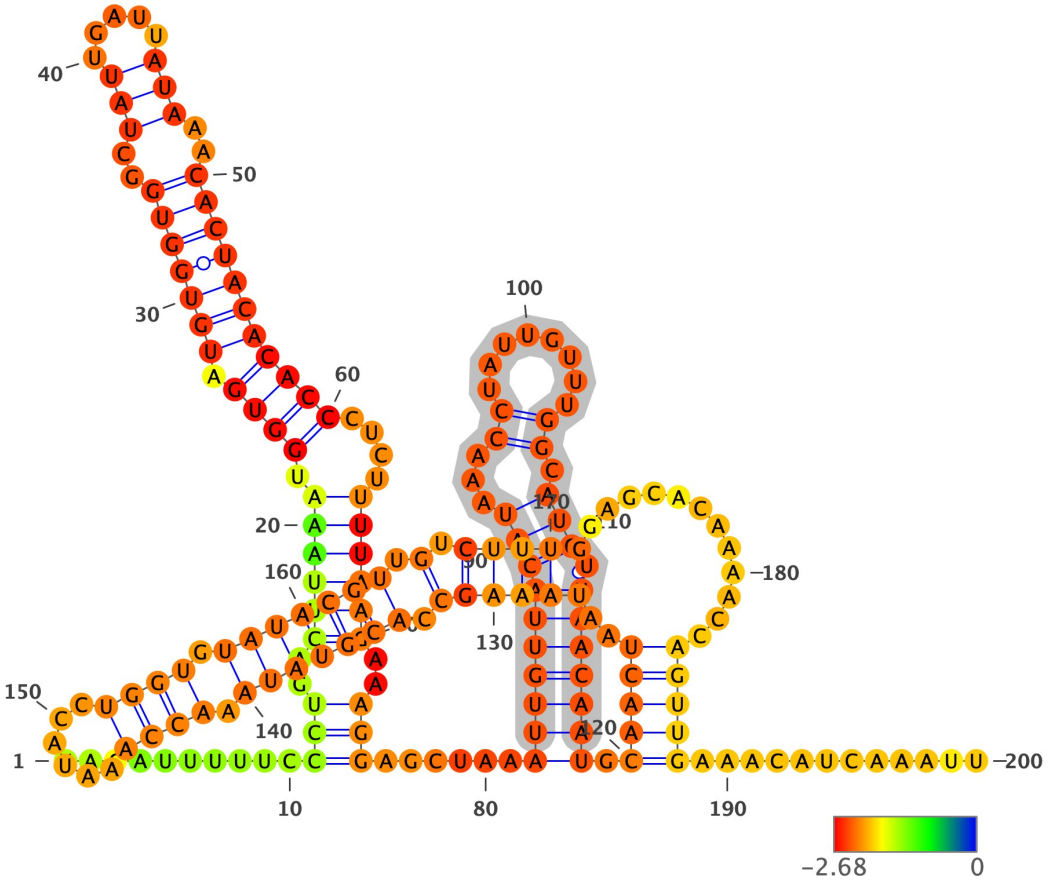
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 126 from nt 6218 to 6252 (nt 83 to 117)

```
5'-TTGTTACATAAACCTATTGTTTGGCAUGTUAACAA-3'
5'-(((((((....((........))..))).)))))-3'
Motif MFE = -5.5; z-score = -1.65; ED = 3.87
```



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

Extracted structure model with flanking nucleotides 6136 to 6335 (motif highlighted in silver):

```
5'-UACAUUUUUCCCUGACUUAAAUGGUGAUGUGGUGGCUAUUGAUUAUAAACACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGU
UAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUU-3
5'-..........(((..((((((.((((.(((((((..(((.....))).)))))))))))....))))))..))).....((((((((((...((........)).))))
)))))))).((((((..((((((.(((((((.(((((.....))))).)))))))).).)))))...........)))))...........-3'
MFE = -47.2; z-score = -3.25; ED = 24.29
```

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

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

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

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

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

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

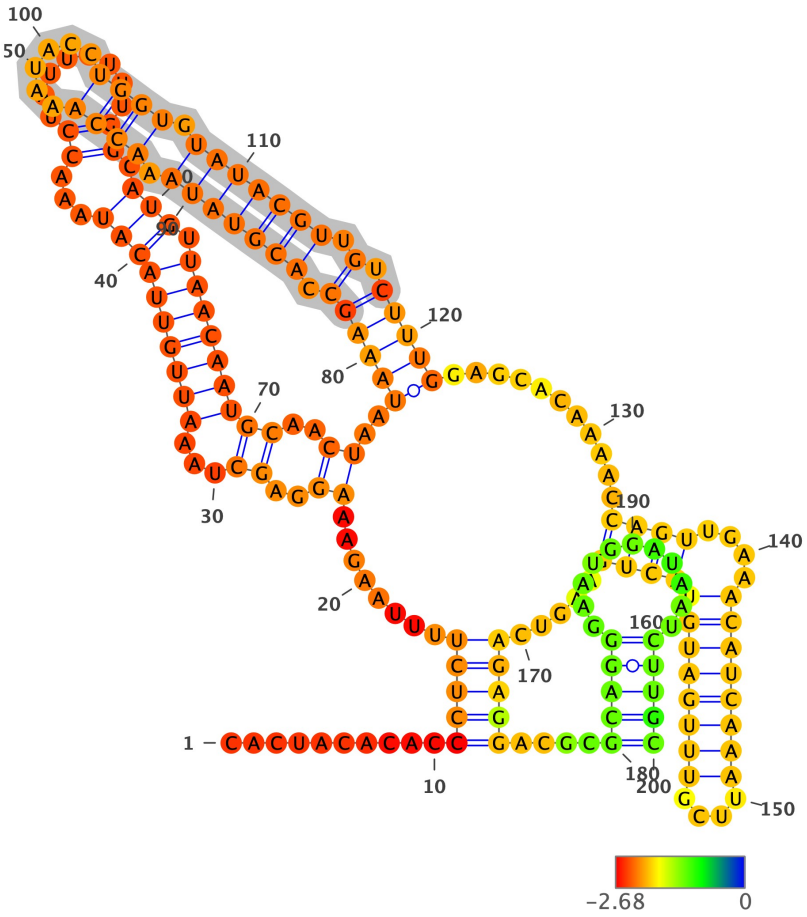
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 127 from nt 6266 to 6302 (nt 82 to 118)

```
5'-GCCACGTATAAACCAAATACCUGGUGUAUACGUTGTC-3'
5'-((.(((((((.((((......)))).)))))))).).)-3'
Motif MFE = -12.2; z-score = -3.4; ED = 1.96
```



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

Extracted structure model with flanking nucleotides 6185 to 6384 (motif highlighted in silver):

```
5'-CACUACACACCCUCUUUUAAGAAAGGAGCUAAAUUGUUACAUAAACCUAUUGUUUGGCAUGUUAACAAUGCAACUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUA
CGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGC-3
5'-..........(((((........((..((...((((((((((...((........)).))).)))))))))..))..((((((.(((((((.((((......)))).))))
))).).)))))...........((((....((((((((....))))))))))))).....)))))....(((((...........)))))-3'
MFE = -43.0; z-score = -1.8; ED = 31.53
```

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

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

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

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

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

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

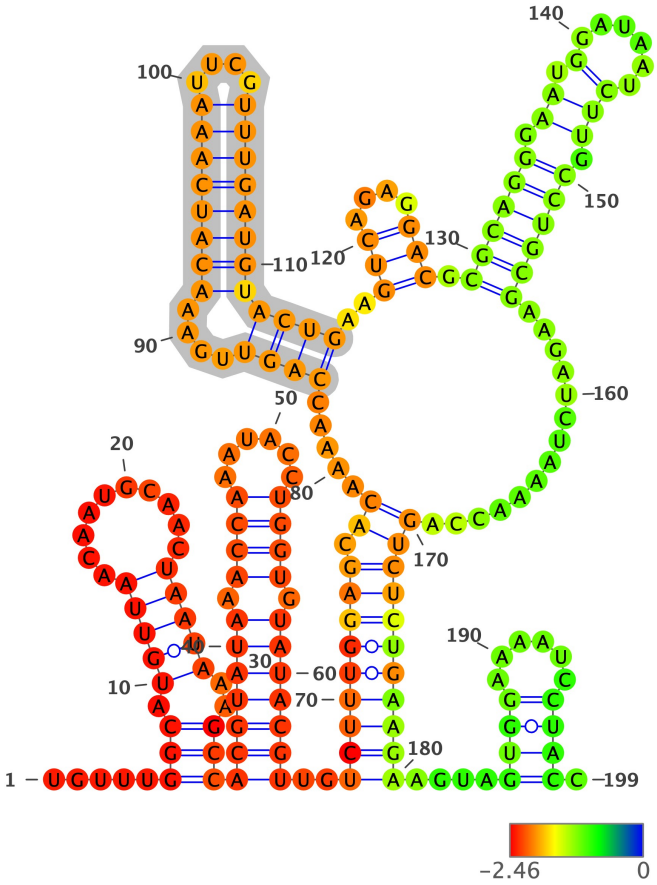
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 128 from nt 6318 to 6349 (nt 84 to 115)

```
5'-CAGTTGAAACATCAAATTCGUUUGAUGTACUG-3'
5'-((((.....(((((((....)))))))).))))-3'
Motif MFE = -8.0; z-score = -2.38; 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 = -2.41; ED = 27.43
```

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(+)

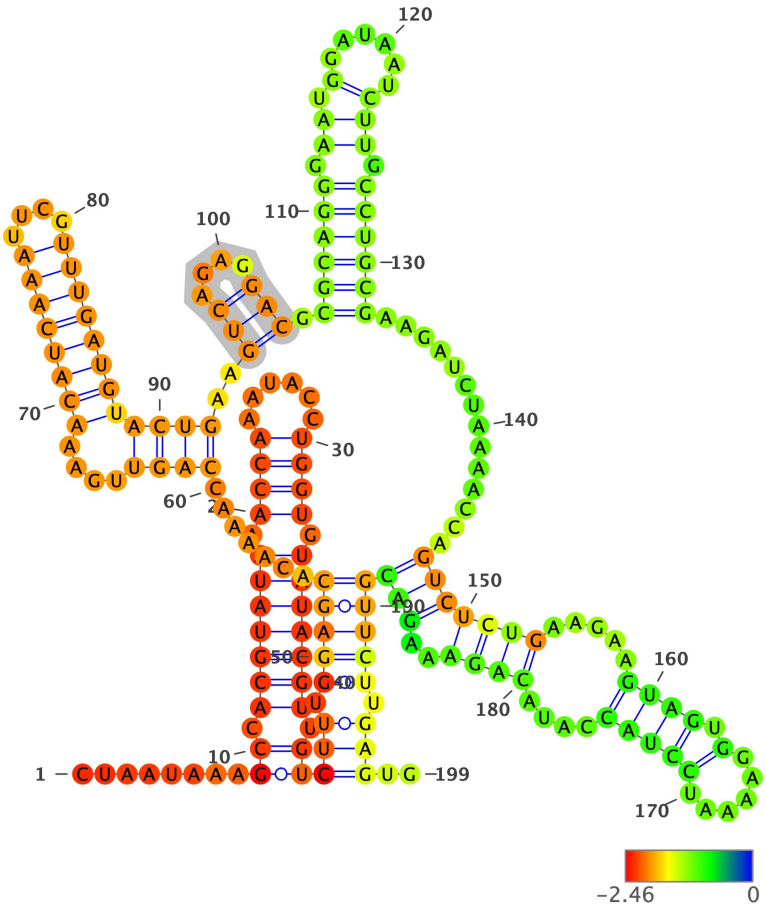
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 129 from nt 6352 to 6361 (nt 95 to 104)

```
5'-GTCAGAGGAC-3'
5'-(((....)))-3'
Motif MFE = -0.4; z-score = -3.1; ED = 1.36
```



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

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

```
5'-CUAAUAAAGCCACGUAUAAACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGG
GAAUGGAUAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUG-3
5'-........((.(((((((.((((......)))).)))))))).))(((.(((((.......((((....((((((((....)))))))))))))..(((....))).((((((
.((.(......))).))))))..............(((((((.....((((.(......)))))....))))..)))))))).)))..-3'
MFE = -49.4; z-score = -1.88; ED = 28.44
```

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(+)

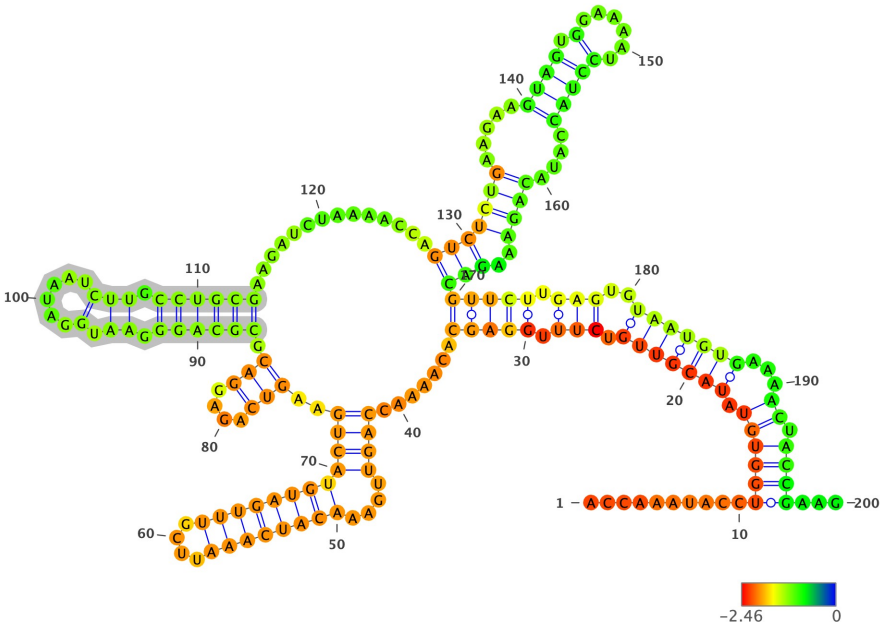
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 130 from nt 6363 to 6389 (nt 87 to 113)

```
5'-CGCAGGGAATGGATAATCUUGCCUGCG-3'
5'-((((((.((.(.....))).)))))))-3'
Motif MFE = -10.0; z-score = -2.33; ED = 3.35
```



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

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

```
5'-ACCAAAUACCUGGUGUAUACGUUGUCUUUGGAGCACAAAACCAGUUGAAACAUCAAAUUCGUUUGAUGUACUGAAGUCAGAGGACGCGCAGGGAAUGGAUAAUCUUGCCUG
CGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAG-3
5'-..........((((((.(((((((.(((.(((((.......(((((....(((((((((....)))))))))))))..(((....))).((((((.((.(......))).))))
)).............(((((((.....((((.(......))))))....))))..)))))))).))))..)))))))...)).))))...-3'
MFE = -45.8; z-score = -0.98; 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(+)

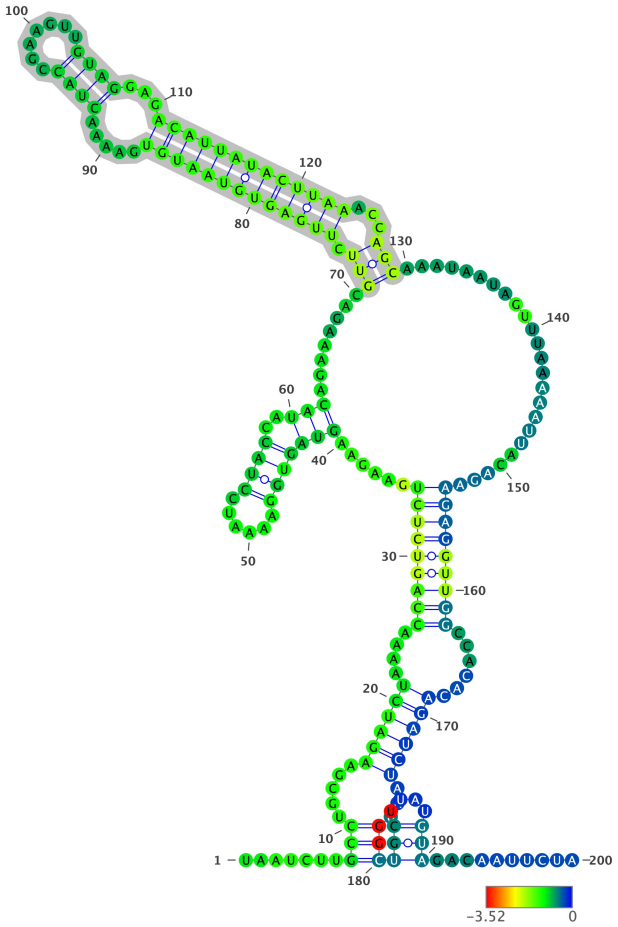
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 131 from nt 6446 to 6504 (nt 71 to 129)

```
5'-GTTCTTGAGTGTAATGTGAAAACTACCGAAGTTGUAGGAGACAUUAUACUUAAACCAGC-3'
5'-(((.((((((((((((.....................))))))))))))...)))-3'
Motif MFE = -16.2; z-score = -2.92; ED = 2.83
```



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

Extracted structure model with flanking nucleotides 6376 to 6575 (motif highlighted in silver):

```
5'-UAAUCUUGCCUGCGAAGAUCUAAAACCAGUCUCUGAAGAAGUAGUGGAAAAUCCUACCAUACAGAAAGACGUUCUUGAGUGUAAUGUGAAAACUACCGAAGUUGUAGGAGA
CAUUAUACUUAAACCAGCAAAUAAUAGUUUAAAAAUUACAGAAGAGGUUGGCCACACAGAUCUAAUGGCUGCUUAUGUAGACAAUUCUA-3
5'-.......(((.....(((((((....((((((((((......(((((((......)))))..)))).......(((.((((((((((((.....((((.......))))))...)
))))))))))))...)))).....................))))))))).....))))))...))))(((....))).........-3'
MFE = -37.0; z-score = -0.85; ED = 37.76
```

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(+)

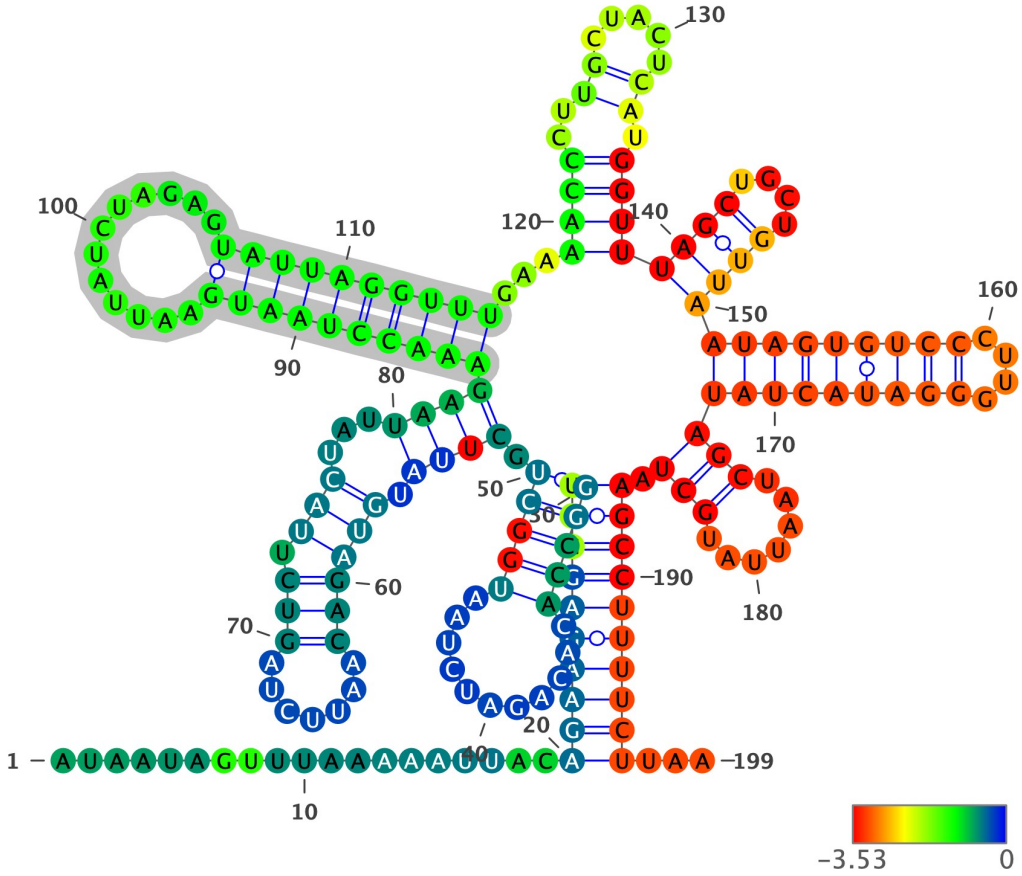
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 132 from nt 6590 to 6621 (nt 84 to 115)

```
5'-AAACCTAATGAATTATCTAGAGUAUUAGGUUU-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -6.8; z-score = -3.15; 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 = -3.11; 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(+)

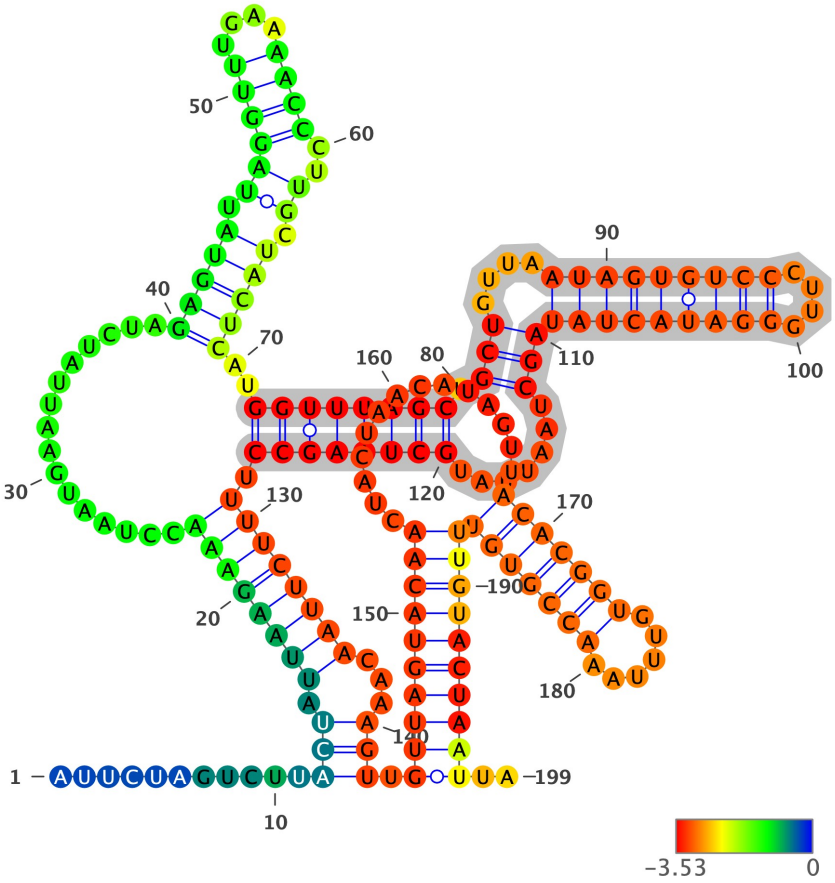
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 133 from nt 6641 to 6696 (nt 72 to 127)

```
5'-GGTTTAGCTGCTGTTAATAGTGTCCCTTGGGAUACUAUAGCTAATTATGCUAAGCC-3'
5'-(((((((((.(((....((((((((((....)))))))))))).......)))))))))-3'
Motif MFE = -21.7; z-score = -3.56; ED = 4.77
```



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

Extracted structure model with flanking nucleotides 6570 to 6768 (motif highlighted in silver):

```
5'-AUUCUAGUCUUACUAUUAAGAAACCUAAUGAAUUAUCUAGAGUAUUAGGUUUGAAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAG
CUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUA-3
5'-...........(((.(((((((((.................(((((.((((((....)))))..)).)))))..(((((((((.(((....((((((((((....))))))))))
).......)))))))).)))))))...))).((((((((((.............(((((((......)))))))))))))))))..-3'
MFE = -49.6; z-score = -4.37; ED = 39.3
```

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

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

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

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

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

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

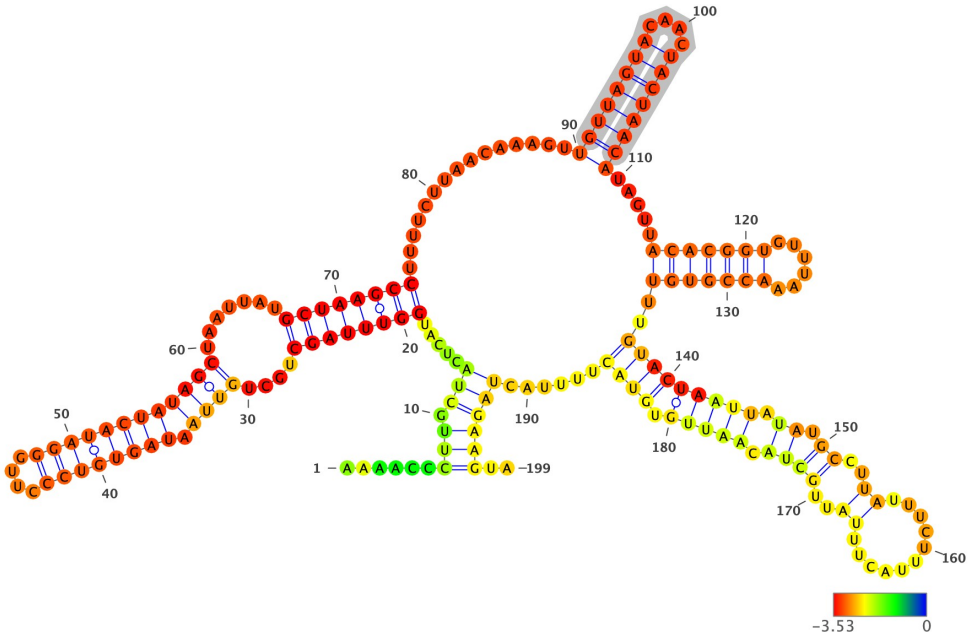
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 134 from nt 6713 to 6730 (nt 91 to 108)

```
5'-GTTAGTACAACUACUAAC-3'
5'-(((((((....)))))))-3'
Motif MFE = -4.6; z-score = -6.41; 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 6623 to 6821 (motif highlighted in silver):

```
5'-AAAACCCUUGCUACUCAUGGUUUAGCUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUA
GUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUA-3
5'-......(((.(((.....(((((((((....(((((.(((((((((....)))))))))))).......)))))))).............(((((((....)))))))))..
...(((((((......))))))).(((((((((.((.((..((...........)).))))).)))))).)))).....))))))..-3'
MFE = -46.9; z-score = -3.75; ED = 26.46
```

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

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

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

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

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

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

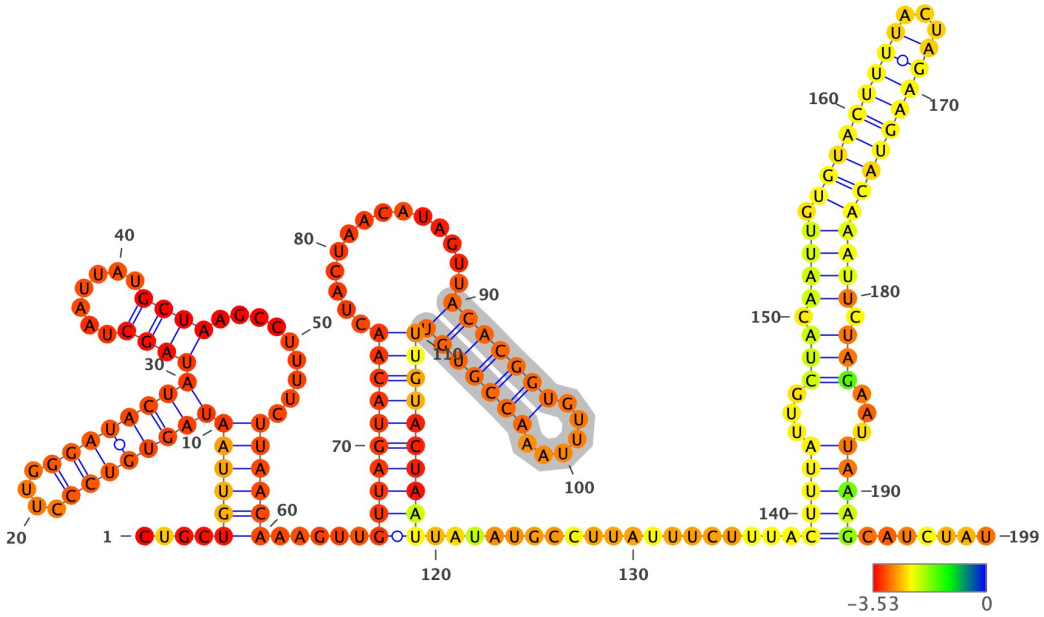
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 6737 to 6756 (nt 90 to 109)

```
5'-ACACGGTGTTTAAACCGUGU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -10.0; z-score = -5.28; ED = 0.44
```



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

Extracted structure model with flanking nucleotides 6648 to 6846 (motif highlighted in silver):

```
5'-CUGCUGUUAAUAGUGUCCCUUGGGAUACUAUAGCUAAUUAUGCUAAGCCUUUUCUUAACAAAGUUGUUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUU
GUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAU-3
5'-....((((((((((((((....))))))))))(((.......)))).........))))).....((((((((((.............(((((((.....)))))))))
))))))))...................(((((...(((.((((.((((((((((...)))))))))))))).)))...)))))).......-3'
MFE = -45.9; z-score = -4.22; 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(+)

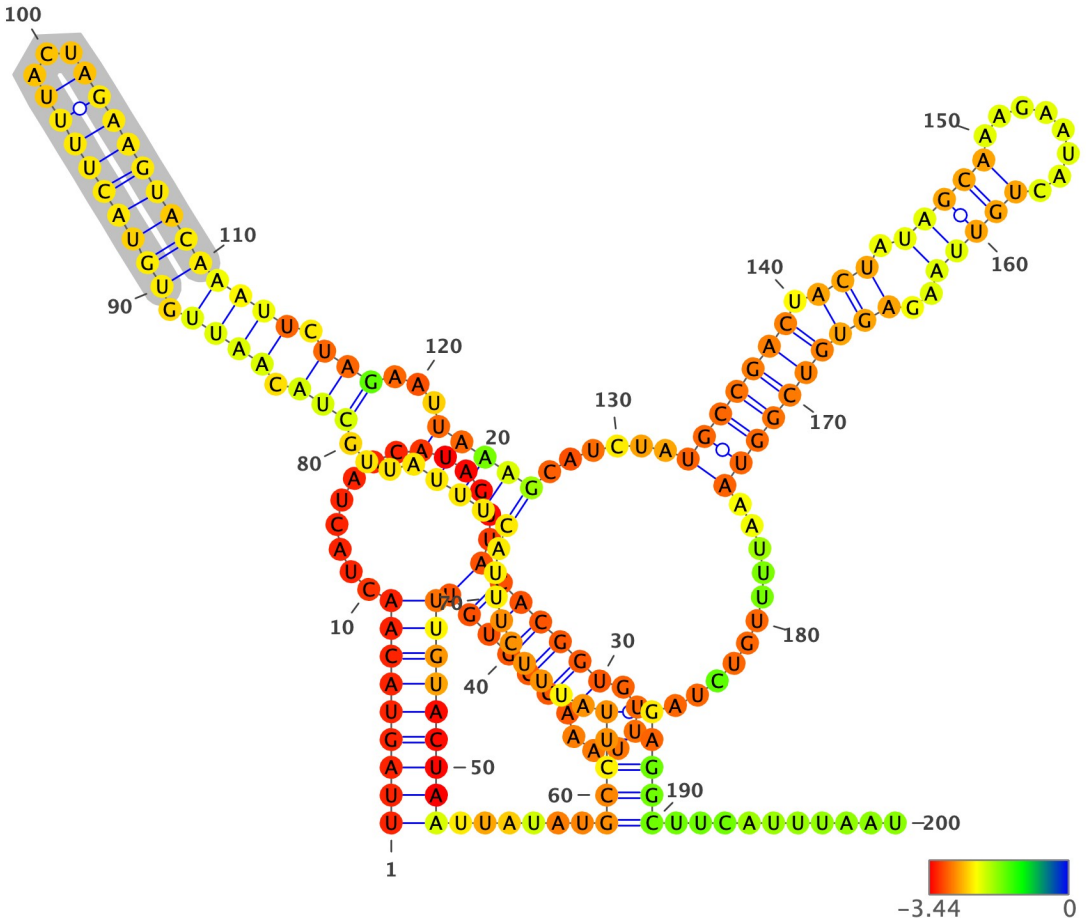
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 136 from nt 6803 to 6823 (nt 90 to 110)

```
5'-TGTACTTTTACTAGAAGUACA-3'
5'-((.((((((.....)))))).))-3'
Motif MFE = -6.3; z-score = -4.73; 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 6714 to 6913 (motif highlighted in silver):

```
5'-UUAGUACAACUACUAACAUAGUUACACGGUGUUUAAACCGUGUUUGUACUAAUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAA
AUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUAAGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAU-3
5'-((((((((((.............(((((((......))))))))))))))))).....(((((.........(((((...(((.((((.((((((((((...)))))))))).
)))).)))...)))))).....(((((((.(((.(((((.........)))))..)))))))))).........)))))..........-3'
MFE = -51.4; z-score = -4.59; ED = 12.28
```

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

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

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

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

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

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

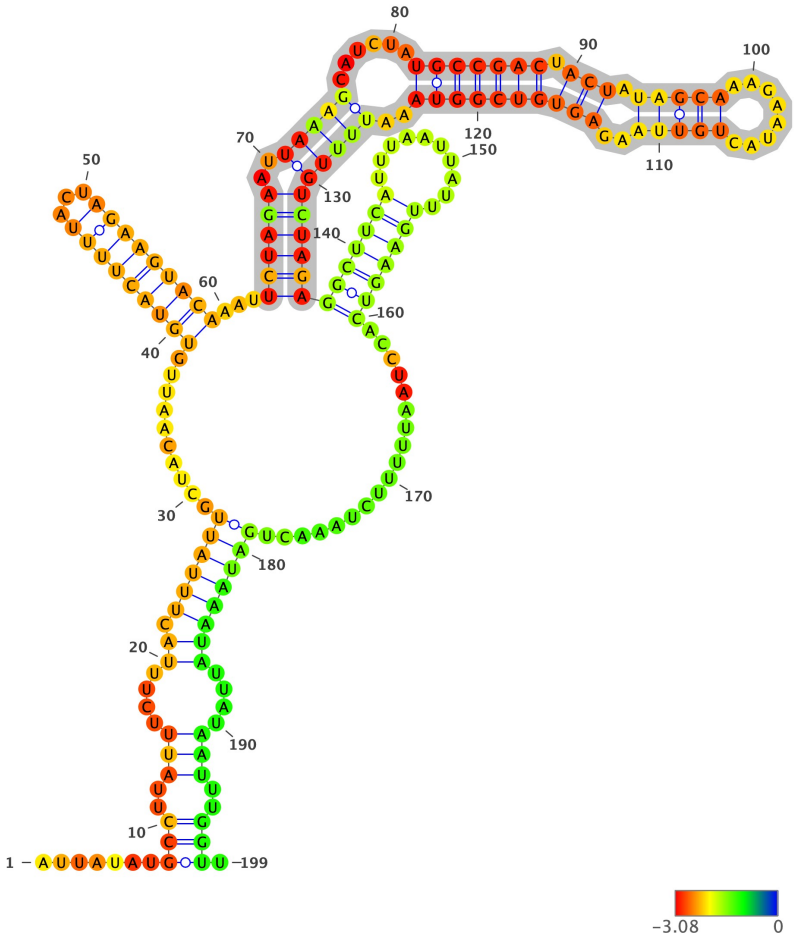
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 137 from nt 6827 to 6900 (nt 63 to 136)

```
5'-TCTAGAATTAAAGCATCTATGCCGACTACTATAGCAAAGAATACUGUTAAGAGUGUCGGUAAATTTUGUCUAGA-3'
5'-(.((.(..((.........(((((((.(((...(((........)))....)))))))))).....))).)).)-3'
Motif MFE = -18.6; z-score = -2.93; ED = 6.82
```



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 6765 to 6963 (motif highlighted in silver):

```
5'-AUUAUAUGCCUUAUUUCUUUACUUUAUUGCUACAAUUGUGUACUUUUACUAGAAGUACAAAUUCUAGAAUUAAAGCAUCUAUGCCGACUACUAUAGCAAAGAAUACUGUUA
AGAGUGUCGGUAAAUUUUGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUU-3
5'-.......(((..(((....((.((((((..........(((((((((...)))))))))...((((((..(((((......(((((((.(((.(((((........)))))
..))))))))))..))))))))))))(((((((..........)))))))).................)))))))).....)))..))).-3'
MFE = -38.1; z-score = -3.14; ED = 21.41
```

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(+)

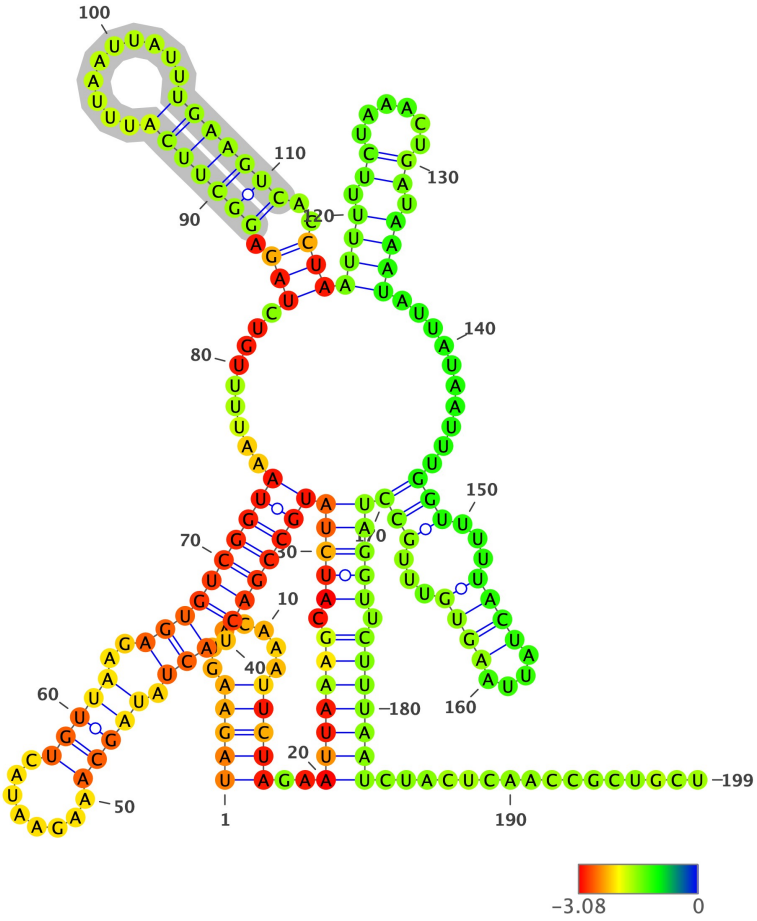
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 138 from nt 6901 to 6924 (nt 88 to 111)

```
5'-GGCTTCATTTAATTATTTGAAGUC-3'
5'-((((((...........))))))-3'
Motif MFE = -6.2; z-score = -4.2; 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 = -2.22; ED = 45.48
```

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

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

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

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

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

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

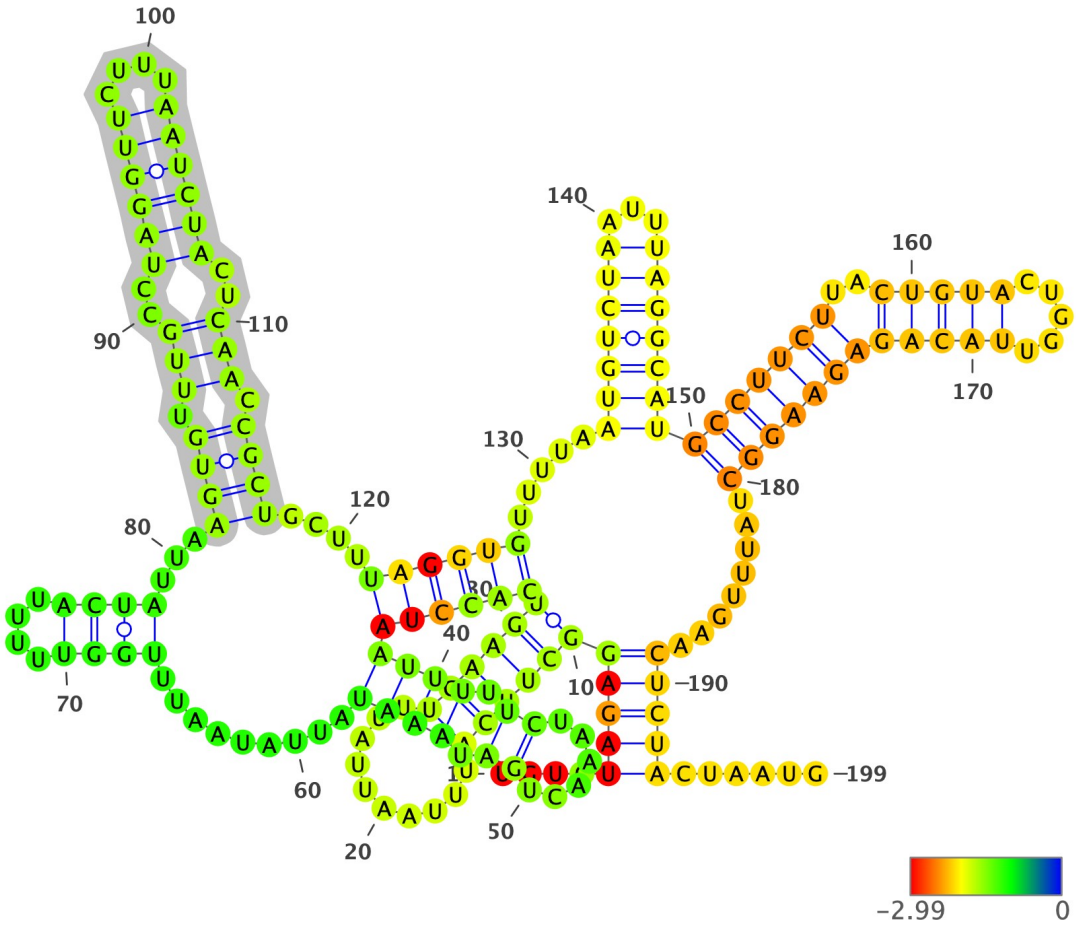
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 139 from nt 6974 to 7009 (nt 82 to 117)

```
5'-AGTGTTTGCCTAGGTTCTTTAAUCUACTCAACCGCU-3'
5'-((((.(((..((((((....))))))..))).))))-3'
Motif MFE = -7.2; z-score = -1.86; ED = 1.28
```



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

Extracted structure model with flanking nucleotides 6893 to 7091 (motif highlighted in silver):

```
5'-UGUCUAGAGGCUUCAUUUAAUUAUUUGAAGUCACCUAAUUUUUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCA
ACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUG-3
5'-....(((((((((((.........))))))((((((((((.((......)).))))).........((((....))))...((((.(((..((((((....))))))..))
).))))....))))))).....(((((((...)))))))(((((((..(((((.....)))))))))))).........)))))......-3'
MFE = -46.1; z-score = -3.24; ED = 19.3
```

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

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

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

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

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

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

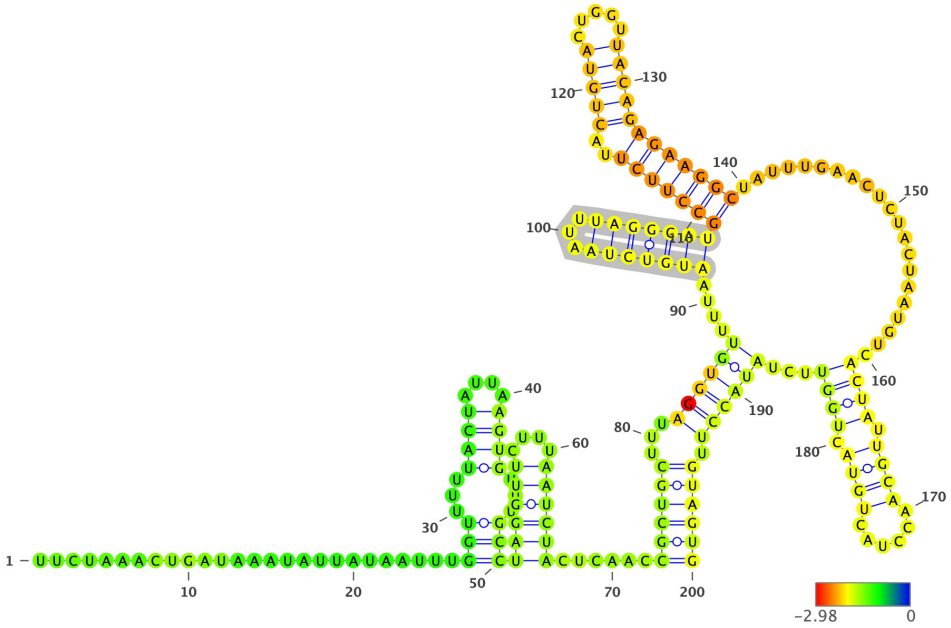
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 140 from nt 7025 to 7041 (nt 92 to 108)

```
5'-ATGTCTAATTTAGGCAU-3'
5'-((((((.....))))))-3'
Motif MFE = -4.2; z-score = -4.84; ED = 1.02
```



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

Extracted structure model with flanking nucleotides 6934 to 7133 (motif highlighted in silver):

```
5'-UUCUAAACUGAUAAAUAUUAUAAUUUGGUUUUUACUAUUAAGUGUUUGCCUAGGUUCUUUAAUCUACUCAACCGCUGCUUUAGGUGUUUUAAUGUCUAAUUUAGGCAUGCC
UUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUG-3
5'-.........................(((...((((....))))...)))((((((....))))))......((((((...((((((....(((((((...)))))))))(((
((((..((((((.....))))))))))))).....................((((.((((......)))))..))))...)))))).)))))-3'
MFE = -41.7; z-score = -2.0; 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(+)

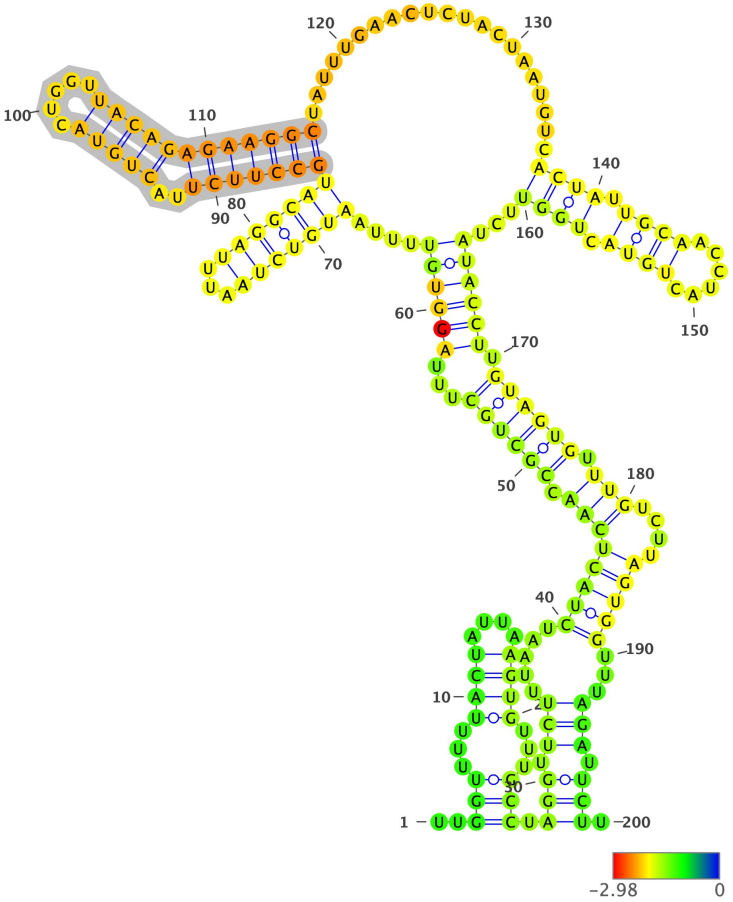
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 141 from nt 7042 to 7072 (nt 85 to 115)

```
5'-GCCTTCTTACTGTACTGGTUACAGAGAAGGC-3'
5'-(((((((..(((((.....)))))))))))-3'
Motif MFE = -13.1; z-score = -4.21; 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 = -3.3; 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(+)

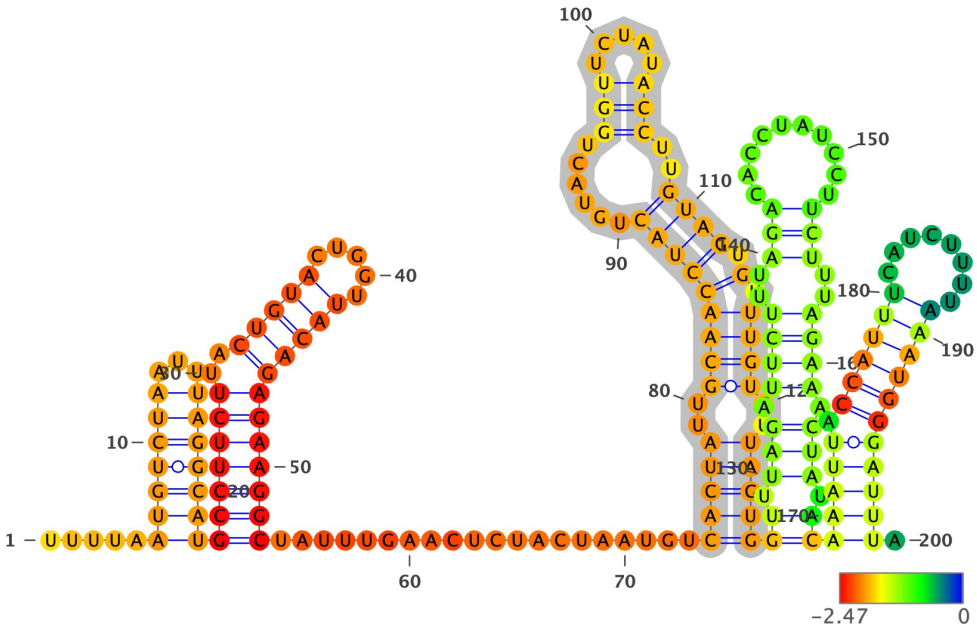
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 142 from nt 7093 to 7145 (nt 74 to 126)

```
5'-CACTATTGCAACCTACTGTACTGGTTCTATACCTTGUAGTGTUUGUCTUAGUG-3'
5'-(((((..((((((((((...................)))).).))))..)))))-3'
Motif MFE = -12.3; z-score = -1.69; ED = 8.53
```



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

Extracted structure model with flanking nucleotides 7020 to 7219 (motif highlighted in silver):

```
5'-UUUUAAUGUCUAAUUUAGGCAUGCCUUCUUACUGUACUGGUUACAGAGAAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUA
GUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAGAAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUA-3
5'-.....(((((((...)))))))(((((((..(((((.....)))))))))))).....................(((((..(((((((((......(((.....)))..)))
).).))))..)))))((.(((.((((..(((..........)))..)))).))).))(((((.((((((........)))))))))).-3'
MFE = -45.1; z-score = -3.31; 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(+)

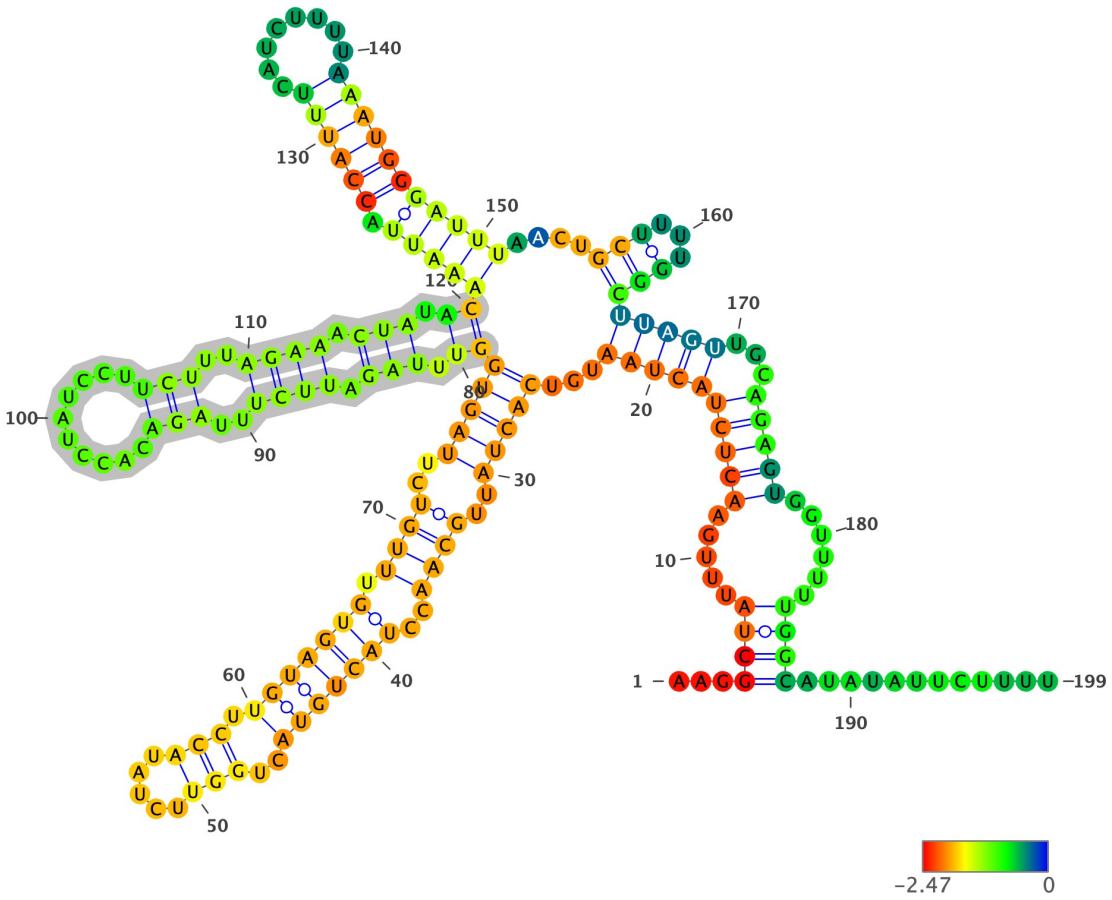
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 143 from nt 7146 to 7187 (nt 79 to 120)

```
5'-GTTTAGATTCTTTAGACACCTATCCTTCUTTAGAAACUATAC-3'
5'-(..(((.((((..((............))..)))).)))..)-3'
Motif MFE = -5.4; z-score = -1.83; ED = 3.91
```



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

Extracted structure model with flanking nucleotides 7068 to 7266 (motif highlighted in silver):

```
5'-AAGGCUAUUUGAACUCUACUAAUGUCACUAUUGCAACCUACUGUACUGGUUCUAUACCUUGUAGUGUUUGUCUUAGUGGUUUAGAUUCUUUAGACACCUAUCCUUCUUUAG
AAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUU-3
5'-...((((.....((((((((((...(((((..((((..(((((((..(((.....))).)))))))).))))..)))))((.(((.((((..(((..........)))..))
)).))).))(((((.((((((........))))))))))....(((...)))))))...)))))......))))............-3'
MFE = -37.9; z-score = -1.21; 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_gp01, 266-21555(+)

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

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

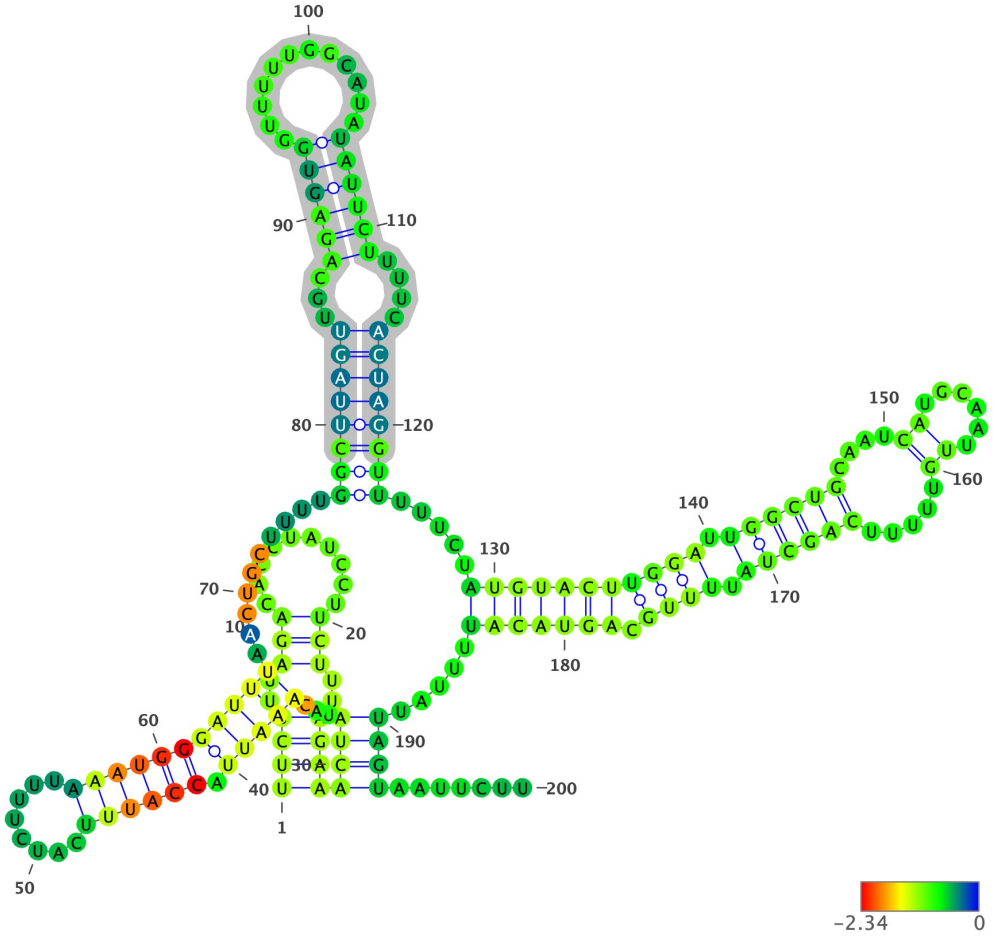
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 7231 to 7273 (nt 79 to 121)

```
5'-CTTAGTTGCAGAGTGGTTUUUGGCATATATTCTTTTCACTAGG-3'
5'-(.........................................)-3'
Motif MFE = -6.0; z-score = 0.03; ED = 6.38
```



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 7153 to 7352 (motif highlighted in silver):

```
5'-UUCUUUAGACACCUAUCCUUCUUUAGAAACUAUACAAAUUACCAUUUCAUCUUUUAAAUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCU
UUUCACUAGGUUUUUCUAUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAGCUAUUUUGCAGUACAUUUUAUUAGUAAUUCUU-3
5'-((((..(((..........)))..))))((((...(((((.((((((........)))))))))))..........((((((((...((((((.............))))))
....))))))))).....((((((((((.((((((....((......)).....)))))).)))).)))))))).....))))........-3'
MFE = -32.5; z-score = -1.03; ED = 29.67
```

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

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

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

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

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

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

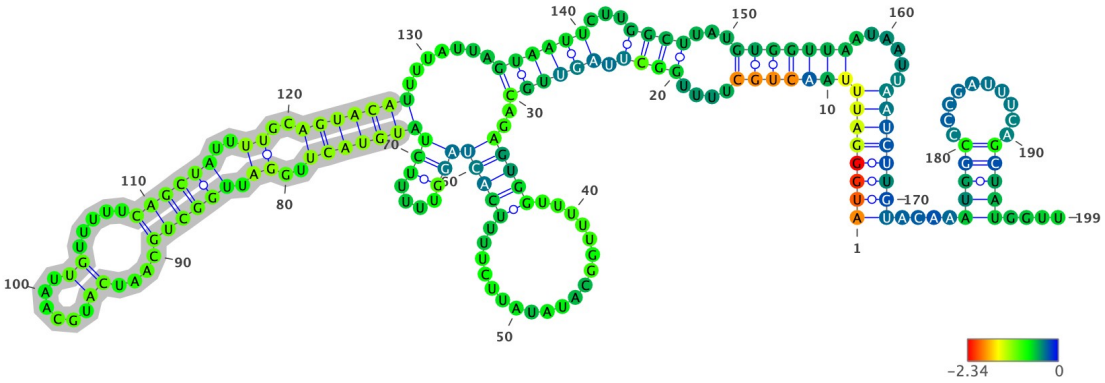
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 145 from nt 7282 to 7335 (nt 73 to 126)

```
5'-TGTACTTGGATTGGCTGCAATCATGCAATUGTTTTTCAGCUATTUUGCAGUACA-3'
5'-((((((..((..(((((....((.....)).....)))))...)).)))))))-3'
Motif MFE = -13.4; z-score = -2.18; ED = 8.01
```



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 7210 to 7408 (motif highlighted in silver):

```
5'-AUGGGAUUUAACUGCUUUUGGCUUAGUUGCAGAGUGGUUUUUGGCAUAUAUUCUUUUCACUAGGUUUUUCUAUGUACUUGGAUUGGCUGCAAUCAUGCAAUUGUUUUUCAG
CUAUUUUGCAGUACAUUUUAUUAGUAAUUCUUGGCUUAUGUGGUUAAUAAUUAAUCUUGUACAAAUGGCCCCGAUUUCAGCUAUGGUU-3
5'-((((((((((((((((....((((.((((((..(((((.....................)))))(((....)))(((((((..((.(((((((....((......)).....)))
))))..))..)))))))).......))))))...)))))...)))))))......)))))))....(((((..........)))))....-3'
MFE = -33.8; z-score = 0.19; ED = 63.36
```

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(+)

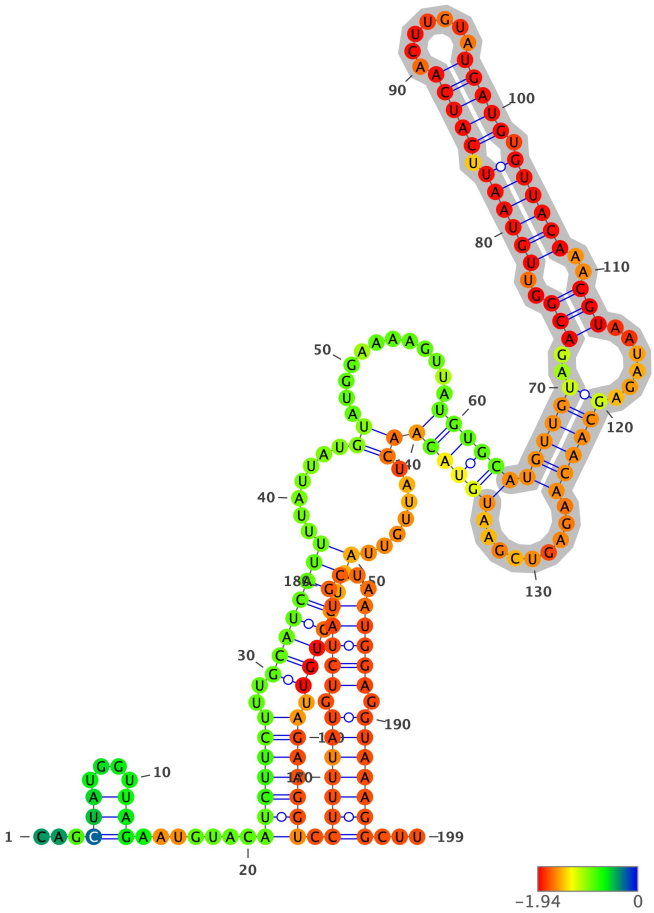
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 146 from nt 7461 to 7532 (nt 64 to 135)

```
5'-ATGTTGTAGACGGTTGTAATTCATCAACTTGTAUGAUGTGUUACAAACGUAATAGAGCAACAAGAGTCGAAU-3'
5'-((((((...(((..((((((.(((((.......))))).))))))..)))).......)))))..........)-3'
Motif MFE = -18.7; z-score = -2.77; ED = 7.13
```



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

Extracted structure model with flanking nucleotides 7398 to 7596 (motif highlighted in silver):

```
5'-CAGCUAUGGUUAGAAUGUACAUCUUCUUUGCAUCAUUUUAUUAUGUAUGGAAAAGUUAUGUGCAUGUUGUAGACGGUUGUAAUUCAUCAACUUGUAUGAUGUGUUACAAAC
GUAAUAGAGCAACAAGAGUCGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUU-3
5'-...(((....)))........(((((((..((((((((.......((............((((((((((((..(((..((((((.(((((.......))))).))))))..)
))......))))))..........))))))))).......))))))))).)))))))).(((((((.(((((....))))).)))))))...-3'
MFE = -46.6; z-score = -1.98; ED = 22.04
```

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(+)

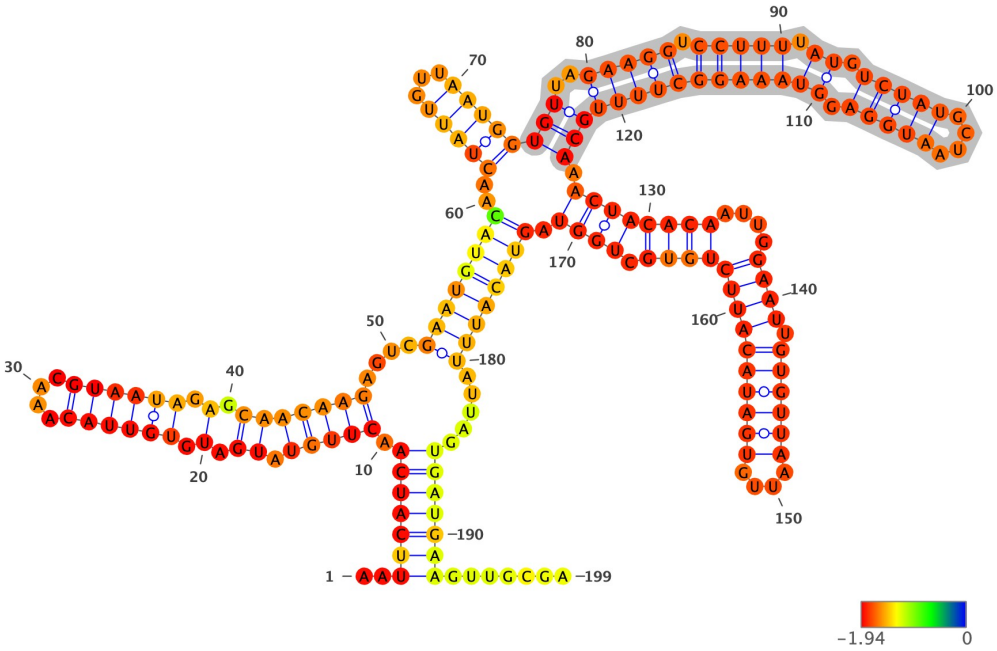
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 147 from nt 7552 to 7601 (nt 75 to 124)

```
5'-TGTTAGAAGGTCCTTTTATGTCTATGCTAAUGGAGGUAAAGGCUUUUGCA-3'
5'-(((..(((((.(((((.((.((((......)))).))))))))))))))-3'
Motif MFE = -14.1; z-score = -3.01; 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 = -2.96; ED = 37.98
```

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(+)

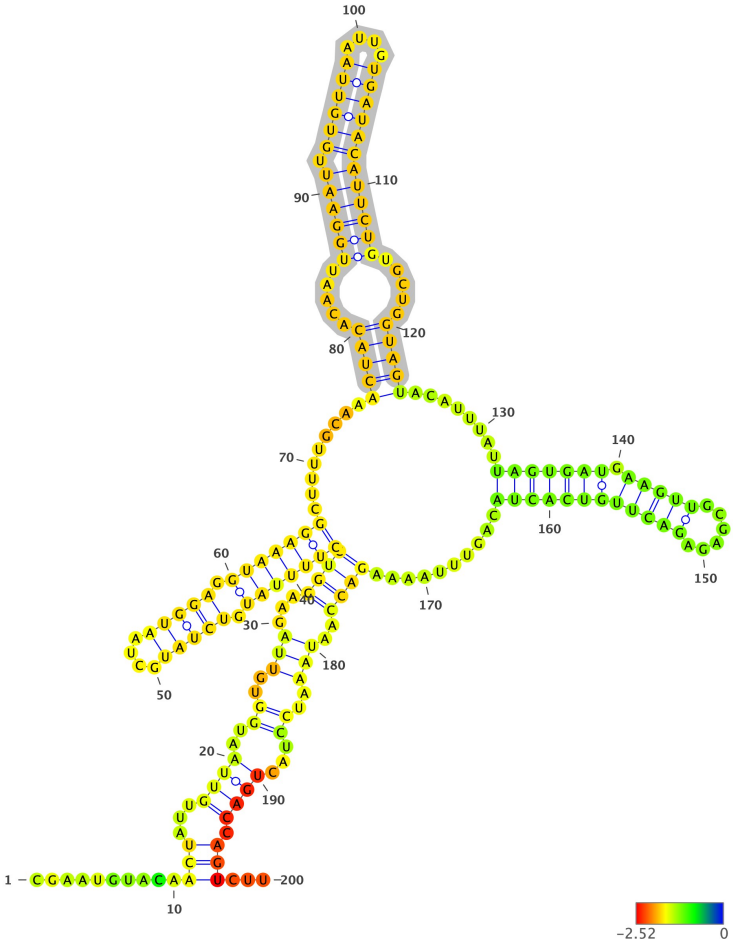
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 148 from nt 7604 to 7650 (nt 77 to 123)

```
5'-CTACACAATTGGAATTGTGTTAATTGTGAUACAUUCUGTGCUGGUAG-3'
5'-((((.((...((((((.(((((((....)))))))))))....))))))-3'
Motif MFE = -9.9; z-score = -1.22; ED = 5.9
```



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

Extracted structure model with flanking nucleotides 7528 to 7727 (motif highlighted in silver):

```
5'-CGAAUGUACAACUAUUGUUAAUGGUGUUAGAAGGUCCUUUUAUGUCUAUGCUAAUGGAGGUAAAGGCUUUUGCAAACUACACAAUUGGAAUUGUGUUAAUUGUGAUACAUU
CUGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUU-3
5'-..........(((...(((((..((..(((...((((((((((((.(((((....)))))).)))))))).........((((.....((((((.(((((((....)))))))))
)))).....)))))).........(((((((.(((((.....)))))))))))).........))))..))))..))...)))))).)))...-3'
MFE = -43.5; z-score = -2.65; ED = 49.57
```

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(+)

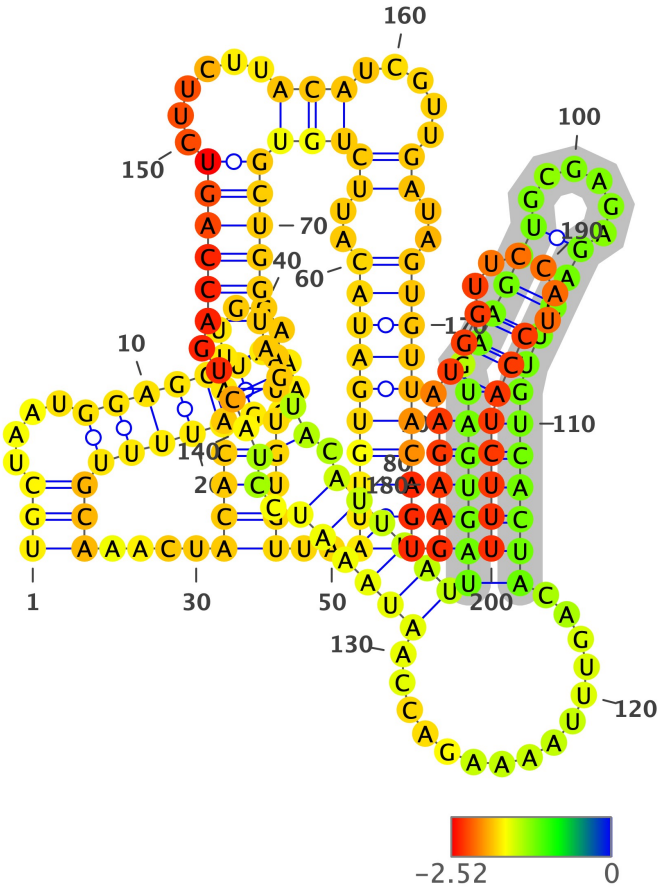
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 149 from nt 7660 to 7690 (nt 85 to 115)

```
5'-TAGTGATGAAGTTGCGAGAGACUUGUCACUA-3'
5'-(((((((.(((((.....)))))))))))))-3'
Motif MFE = -10.2; z-score = -2.99; ED = 2.13
```



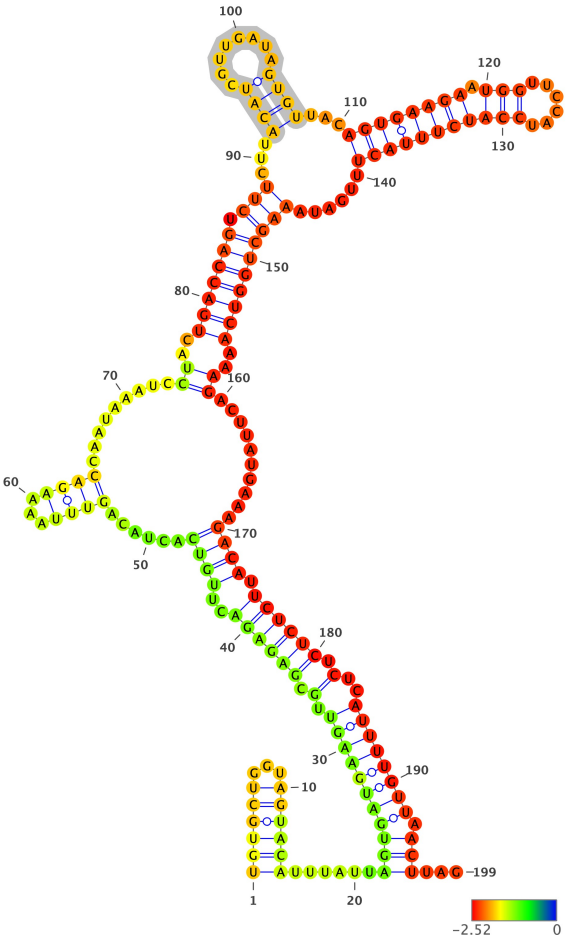
Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

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

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

NC_045512.2 (forward strand): Structure number 150 from nt 7731 to 7746 (nt 92 to 107)

```
5'-ACATCGTTGATAGUGU-3'
5'-((((........))))-3'
Motif MFE = 0.0; z-score = 0.61; 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 7640 to 7838 (motif highlighted in silver):

```
5'-UGUGCUGGUAGUACAUUUAUUAGUGAUGAAGUUGCGAGAGACUUGUCACUACAGUUUAAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACA
GUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAAAGACAUUCUCUCUCUCAUUUUGUUAACUUAG-3
5'-((((((...))))))......(((((((((((.(.((((((..((((......((((...))))..........((..(((((((.(((...((((........))))...(
(((((((.(((......)))))))))))......)))))))))))..))..........)))).)))))).)..)))))))).)))...-3'
MFE = -42.0; z-score = -1.43; ED = 32.38
```

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(+)

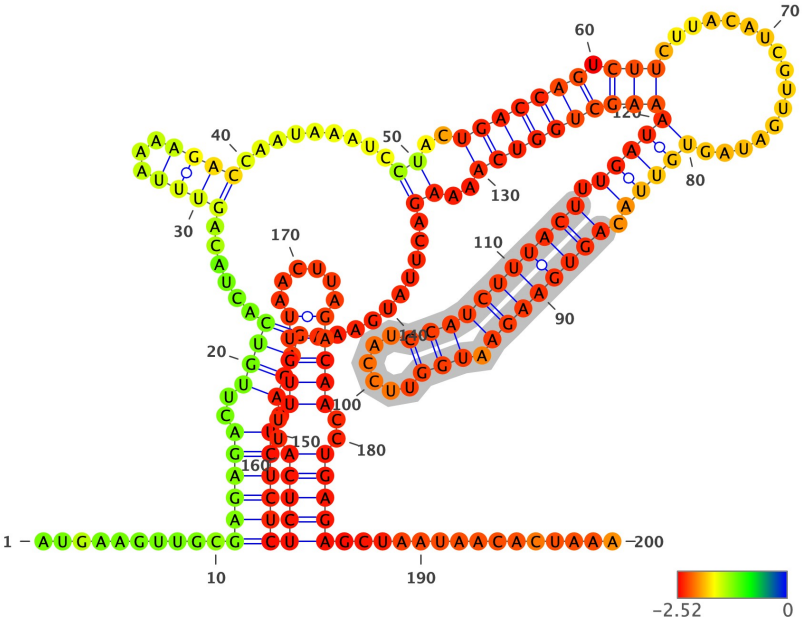
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 151 from nt 7750 to 7778 (nt 86 to 114)

```
5'-AGTGAAGAATGGTTCCATCCAUCUUUACU-3'
5'-((((((((.(((......)))))))))))-3'
Motif MFE = -10.4; z-score = -4.18; 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 = -3.28; 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(+)

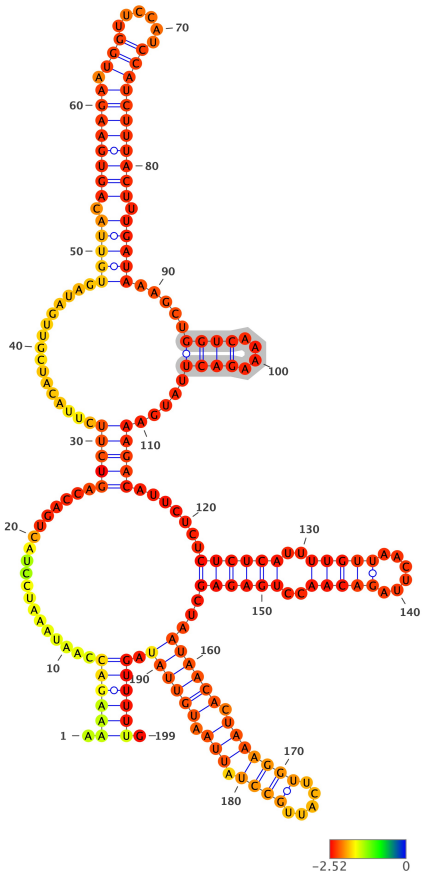
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 152 from nt 7790 to 7801 (nt 94 to 105)

```
5'-GGTCAAAAGACU-3'
5'-((((....))))-3'
Motif MFE = -2.1; z-score = -5.31; ED = 0.57
```



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

Extracted structure model with flanking nucleotides 7697 to 7895 (motif highlighted in silver):

```
5'-AAAAGACCAAUAAAUCCUACUGACCAGUCUUCUUACAUCGUUGAUAGUGUUACAGUGAAGAAUGGUUCCAUCCAUCUUUACUUUGAUAAAGCUGGUCAAAAGACUUAUGAA
AGACAUUCUCUCUCUCAUUUUGUUAACUUAGACAACCUGAGAGCUAAUAACACUAAAGGUUCAUUGCCUAUUAAUGUUAUAGUUUUUG-3
5'-.((((((...................(((((.............(((((.(((((((((.(((.....)))))))))))).)))))).....((((....)))).....)
))))).......((((((..((((((.....))))))..))))))...((((((.(((((((.....)))).))).)))))).)))))).-3'
MFE = -40.5; z-score = -3.63; ED = 26.15
```

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

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

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

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

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

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

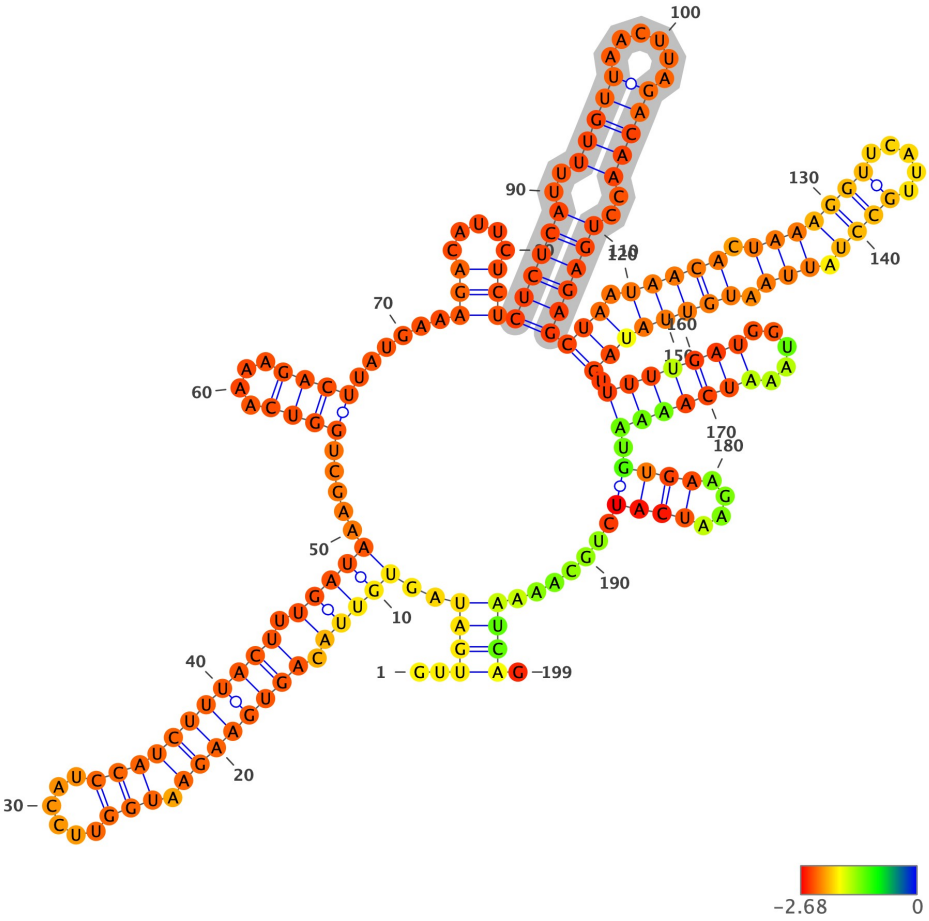
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 153 from nt 7819 to 7850 (nt 84 to 115)

```
5'-CTCTCATTTTGTTAACTTAGACAACCUGAGAG-3'
5'-((((((..(((..........)))..))))))-3'
Motif MFE = -10.3; z-score = -3.91; 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 = -2.47; ED = 30.66
```

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

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

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

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

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

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

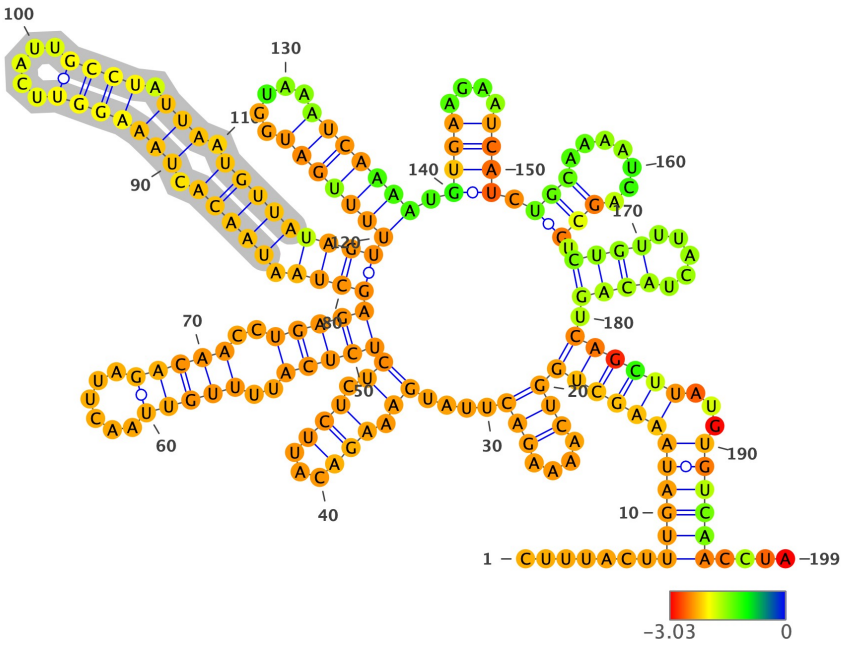
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 154 from nt 7855 to 7886 (nt 84 to 115)

```
5'-TAACACTAAAGGTTCATTGCCUAUUAAUGUUA-3'
5'-(((((.(((((((.....)))).))).)))))-3'
Motif MFE = -6.5; z-score = -3.0; 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 = -2.41; 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(+)

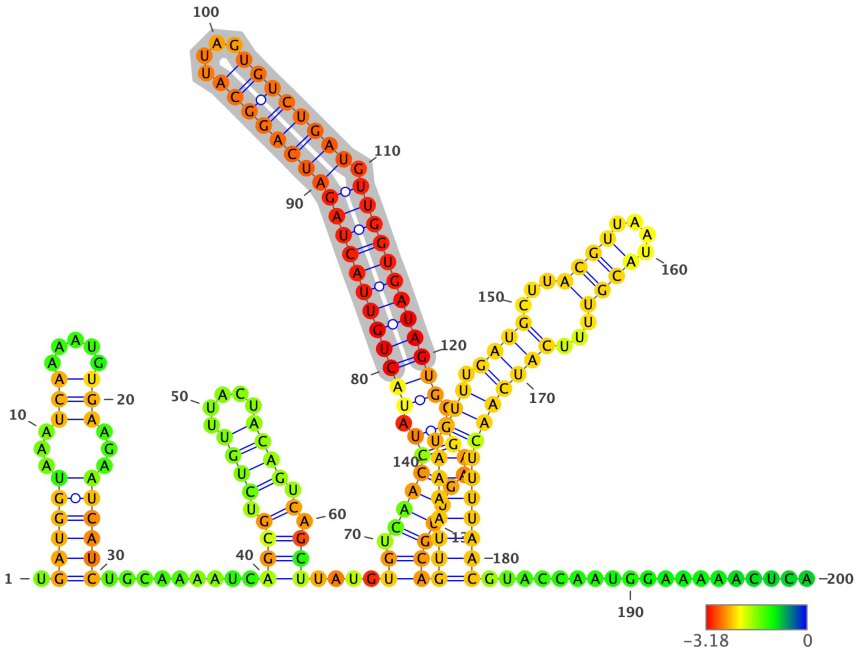
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 155 from nt 7973 to 8013 (nt 80 to 120)

```
5'-CTGTTACTAGATCAGGCATTAGUGUCUGAUGUUGGUGAUAG-3'
5'-(((((((((((((((((....)))))))).))))))))))-3'
Motif MFE = -18.5; z-score = -5.57; 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 7894 to 8093 (motif highlighted in silver):

```
5'-UGAUGGUAAAUCAAAAUGUGAAGAAUCAUCUGCAAAAUCAGCGUCUGUUUACUACAGUCAGCUUAUGUGUCAACCUAUACUGUUACUAGAUCAGGCAUUAGUGUCUGAUGU
UGGUGAUAGUGCGGAAGUUGCAGUUAAAAUGUUUGAUGCUUACGUUAAUACGUUUUCAUCAACUUUUAACGUACCAAUGGAAAAACUCA-3
5'-.((((((...(((.....)))...))))))........((((.((((.....)))).).)))....((.((((((.((((((((((((((((((((....)))))))).)
))))))))))).))..))))))(((((((.(((.((((...((((....))))...)))))))))))))).....................-3'
MFE = -51.9; z-score = -2.71; ED = 28.46
```

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(+)

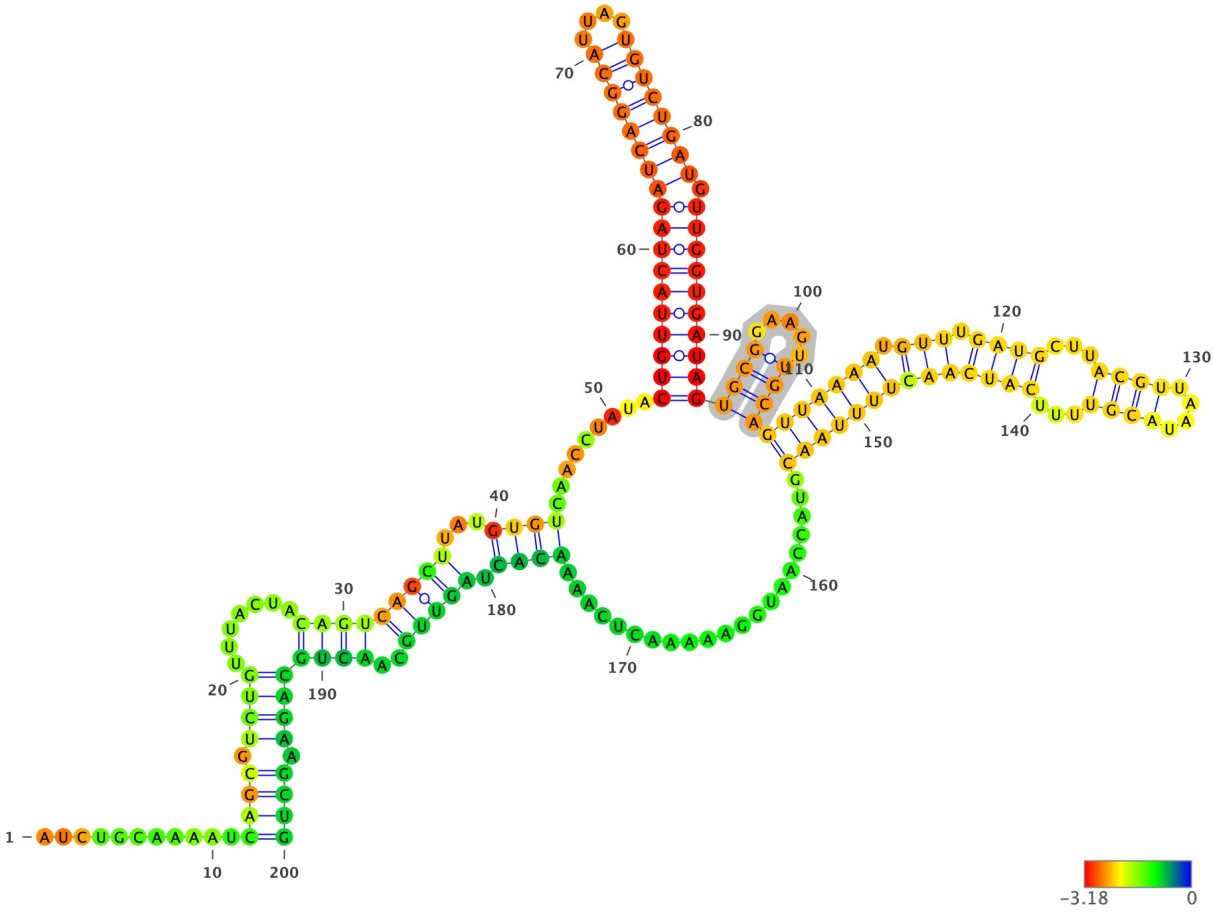
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 156 from nt 8014 to 8026 (nt 94 to 106)

```
5'-TGCGGAAGTUGCA-3'
5'-((((.....))))-3'
Motif MFE = -1.2; z-score = -1.63; 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 = -3.76; 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(+)

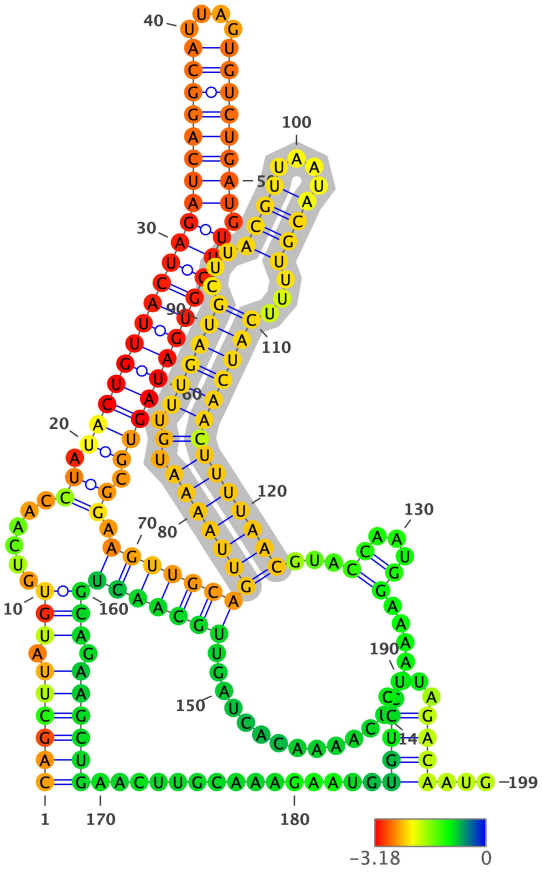
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 157 from nt 8027 to 8074 (nt 76 to 123)

```
5'-GTTAAAATGTTTGATGCTTACGTTAATACGUTTTCAUCAACUUUUAAC-3'
5'-(((((((...((((((...(((......)))...)))))).)))))))-3'
Motif MFE = -12.4; z-score = -4.13; 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 = -2.91; ED = 17.02
```

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

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

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

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

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

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

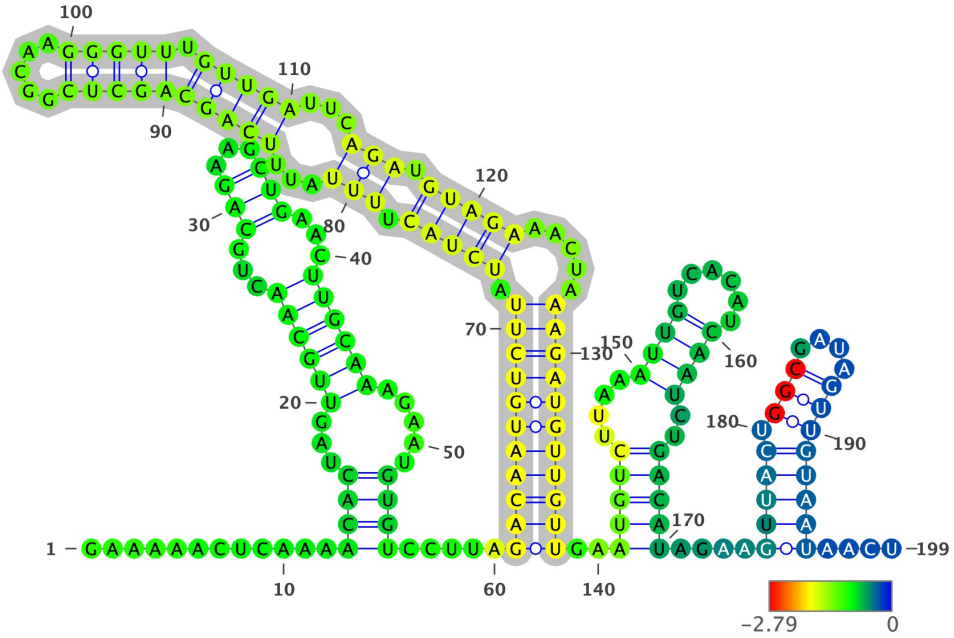
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein',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

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

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

NC_045512.2 (forward strand): Structure number 158 from nt 8144 to 8221 (nt 61 to 138)

```
5'-GACAATGTCTTATCTACTTTTATTTCAGCAGCTCGGCAAGGGUUTGUUGATTCAGATGUAGAAACTAAAGAUGUUGUU-3'
5'-(((((((((((.(((((.(((...((((((((((.....))))).))))))...))).)))))).....)))))))))))-3'
Motif MFE = -23.6; z-score = -3.38; 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 8084 to 8282 (motif highlighted in silver):

```
5'-GAAAAACUCAAAACACUAGUUGCAACUGCAGAAGCUGAACUUGCAAAGAAUGUGUCCUUAGACAAUGUCUUAUCUACUUUUAUUUCAGCAGCUCGGCAAGGGUUUGUUGAU
UCAGAUGUAGAAACUAAAGAUGUUGUUGAAUGUCUUAAAUUGUCACAUCAAUCUGACAUAGAAGUUACUGGCGAUAGUUGUAAUAACU-3
5'-............((((...((((((...(((...)))...))))))).....)))).....(((((((((((.(((((.(((...((((((((((.....))))).))))).
..))).))))).....))))))))))..(((((....((((......))))..))))).....(((((.(((....))))))))....-3'
MFE = -43.2; z-score = -1.72; ED = 37.93
```

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

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

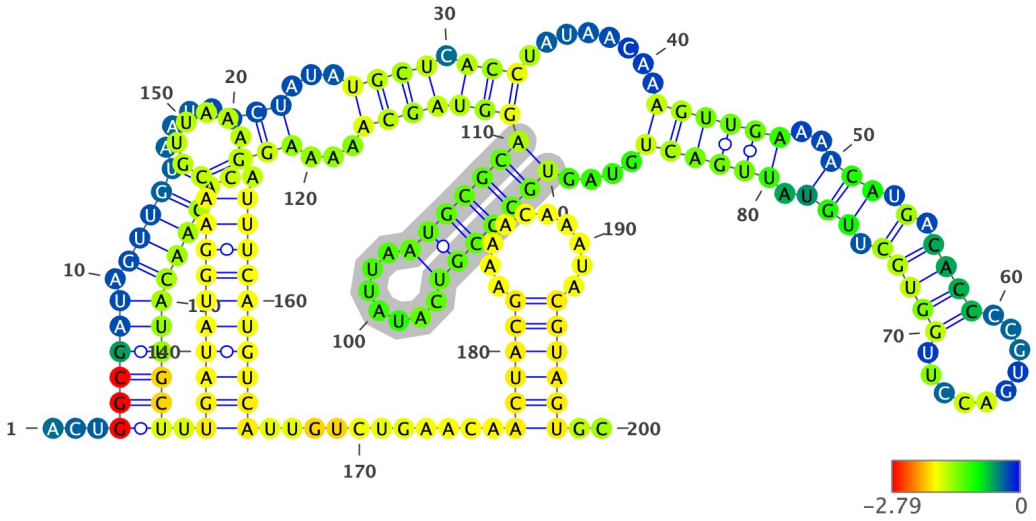
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 159 from nt 8350 to 8370 (nt 90 to 110)

```
5'-TGCGCGTCATATTAAUGCGCA-3'
5'-(((((((.......)))))))-3'
Motif MFE = -7.8; z-score = -3.4; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8261 to 8460 (motif highlighted in silver):

```
5'-ACUGGCGAUAGUUGUAAUAACUAUAUGCUCACCUAUAACAAAGUUGAAAACAUGACACCCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAG
GUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGC-3
5'-...((((((.(((((....(((...((((.(((........((((((..(((.(.((((..........)))))).))).))))))....(((((((.......)))))))
))))))...))).)))))))))).((((((((((.....).)))))))))..........((((((.........))))))..-3'
MFE = -47.6; z-score = -2.33; 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(+)

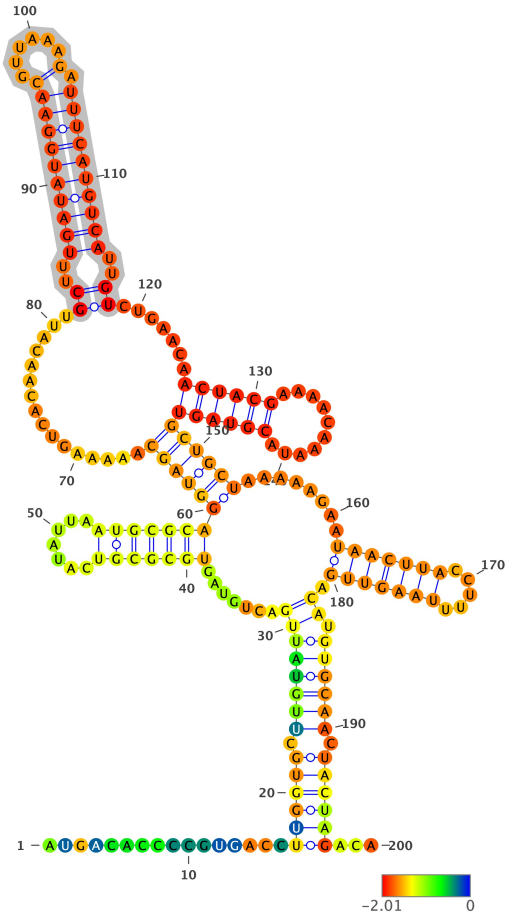
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 160 from nt 8393 to 8429 (nt 82 to 118)

```
5'-GCTTTGATATGGAACGTTAAAGAUUUCAUGUCATTGU-3'
5'-((..((((((((((.........))))))))))..))-3'
Motif MFE = -11.0; z-score = -3.7; 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'-AUGACACCCGUGACCUUGGUGCUUGUAUUGACUGUAGUGCGCGUCAUAUUAAUGCGCAGGUAGCAAAAAGUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUG
UCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGACAUGUGCAACUACUAGACA-3
5'-.................((((((.(((((((((.......(((((((.......)))))))(((((.................((..((((((((((.....).)))))))
))))..))).......((((((..........))))))))))).......(((((((.....)))))))..)).)))))).))))))...-3'
MFE = -42.4; z-score = -0.79; ED = 44.0
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

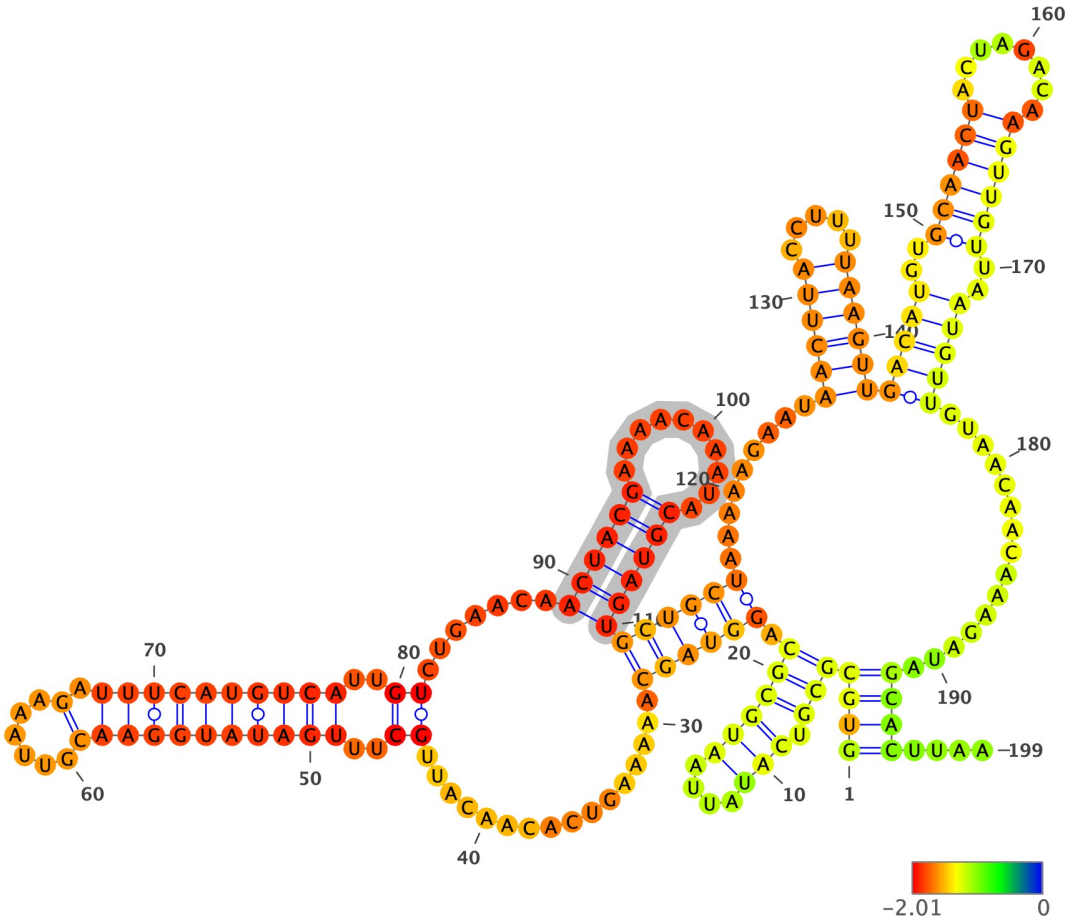
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 161 from nt 8437 to 8458 (nt 89 to 110)

```
5'-ACTACGAAAACAAATACGUAGU-3'
5'-((((((..........))))))-3'
Motif MFE = -4.3; z-score = -5.27; 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 = -2.91; ED = 37.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

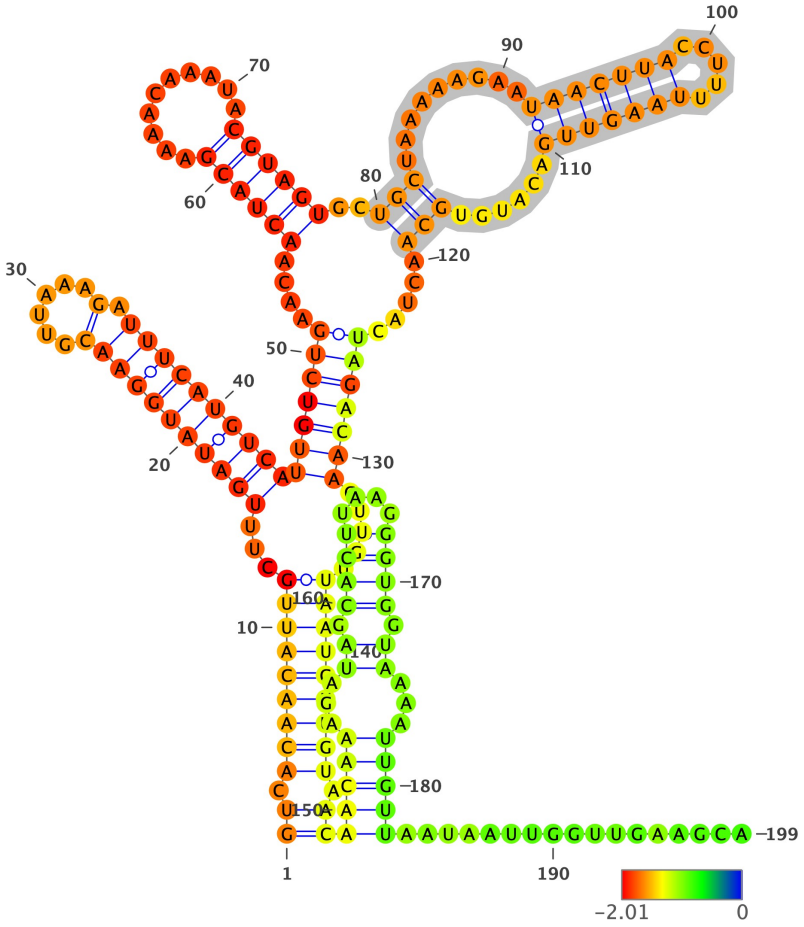
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 8461 to 8500 (nt 80 to 119)

```
5'-TGCTAAAAAGAATAACTTACCTTTUAAGUUGACATGTGCA-3'
5'-(((.........(((((((.....)))))))).....)))-3'
Motif MFE = -3.1; z-score = 0.15; ED = 4.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8382 to 8580 (motif highlighted in silver):

```
5'-GUCACAACAUUGCUUUGAUAUGGAACGUUAAAGAUUUCAUGUCAUUGUCUGAACAACUACGAAAACAAAUACGUAGUGCUGCUAAAAAGAAUAACUUACCUUUUAAGUUGA
CAUGUGCAACUACUAGACAAGUUGUUAAUGUUGUAACAACAAAGAUAGCACUUAAGGGUGGUAAAAUUGUUAAUAAUUGGUUGAAGCA-3
5'-((.((((((((((...((((((((((.....).)))))))))))(((((((....((((((..........))))))..(((.........(((((((.....)))))))).
.....))).....)))))))).....)))))))).))((((((...((.((((....)))).)).)...)))))..................-3'
MFE = -38.6; z-score = -1.92; ED = 37.24
```

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(+)

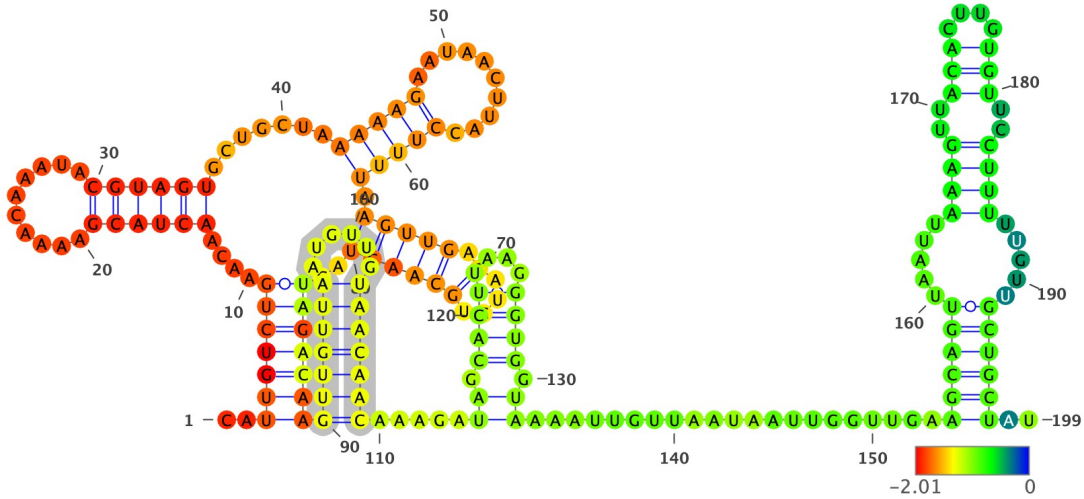
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 163 from nt 8513 to 8532 (nt 90 to 109)

```
5'-GTTGTTAATGTTGUAACAAC-3'
5'-(((((((......)))))))-3'
Motif MFE = -4.5; z-score = -5.49; 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 = -1.0; 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(+)

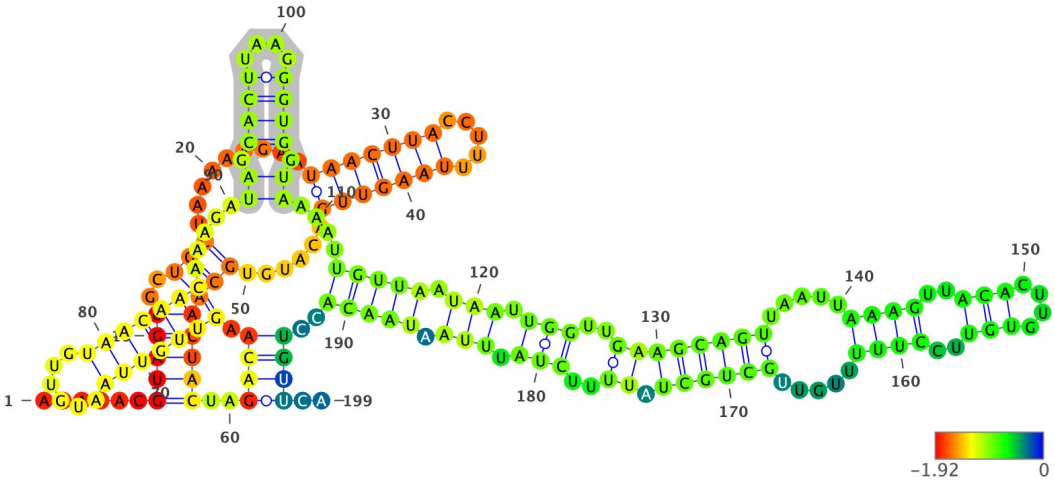
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 164 from nt 8538 to 8555 (nt 91 to 108)

```
5'-TAGCACTTAAGGGUGGUA-3'
5'-((.((((....)))).))-3'
Motif MFE = -3.2; z-score = -2.61; 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(+)

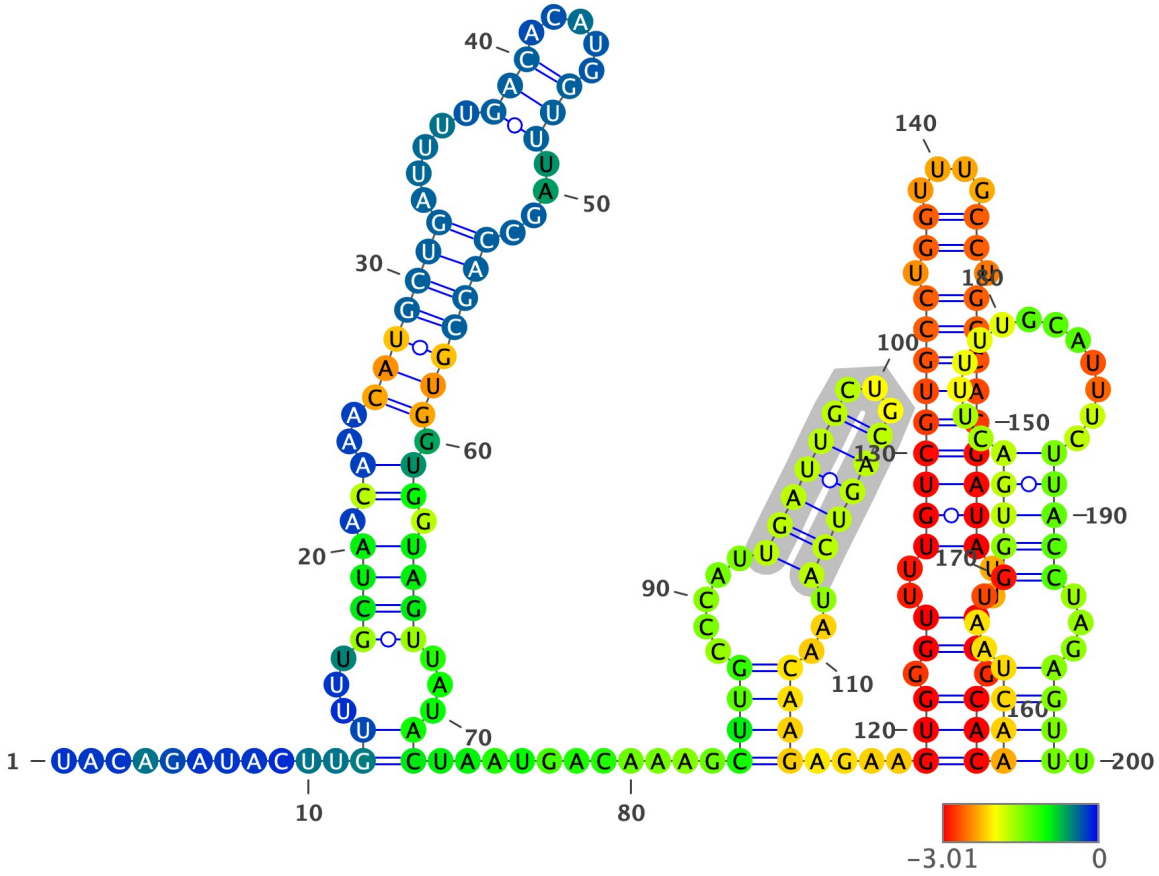
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 165 from nt 8823 to 8837 (nt 93 to 107)

```
5'-TGATTGCTGCAGUCA-3'
5'-(((((((...)))))))-3'
Motif MFE = -2.7; 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 8731 to 8930 (motif highlighted in silver):

```
5'-UACAGAUACUUGUUUUGCUAACAAACAUGCUGAUUUUGACACAUGGUUUAGCCAGCGUGGUGGUAGUUAUACUAAUGACAAAGCUUGCCCAUUGAUUGCUGCAGUCAUAAC
AAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUU-3
5'-...........((...((((.((..(((((((.....(((.....)))....)))))))).)).))))...)).........((((.....((((((...))))))...)
))).....(((.((..((((((((((.((....)).)))))))))..)).)))(((...(((((.............)))))...)))).-3'
MFE = -51.9; z-score = -2.44; 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(+)

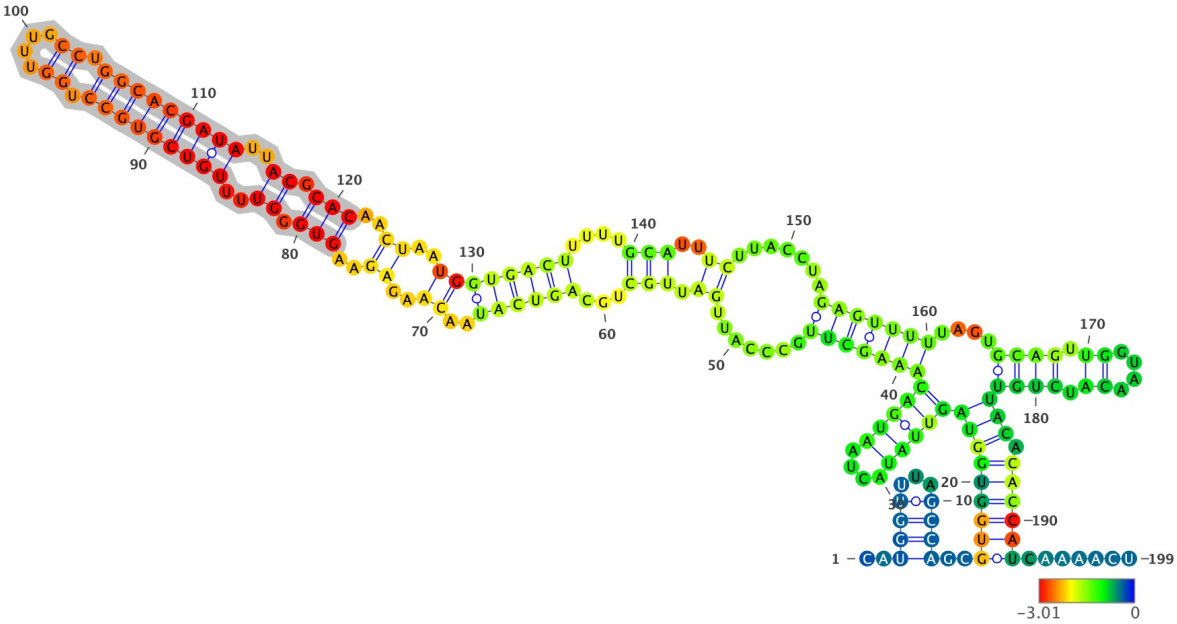
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 166 from nt 8849 to 8892 (nt 78 to 121)

```
5'-GTGGGTTTTGTCGTGCCTGGTTTGCCTGGCACGAUATTACGCAC-3'
5'-(((.((..((((((((((.((....)).)))))))))..)).)))-3'
Motif MFE = -24.5; z-score = -4.91; 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 = -2.73; 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(+)

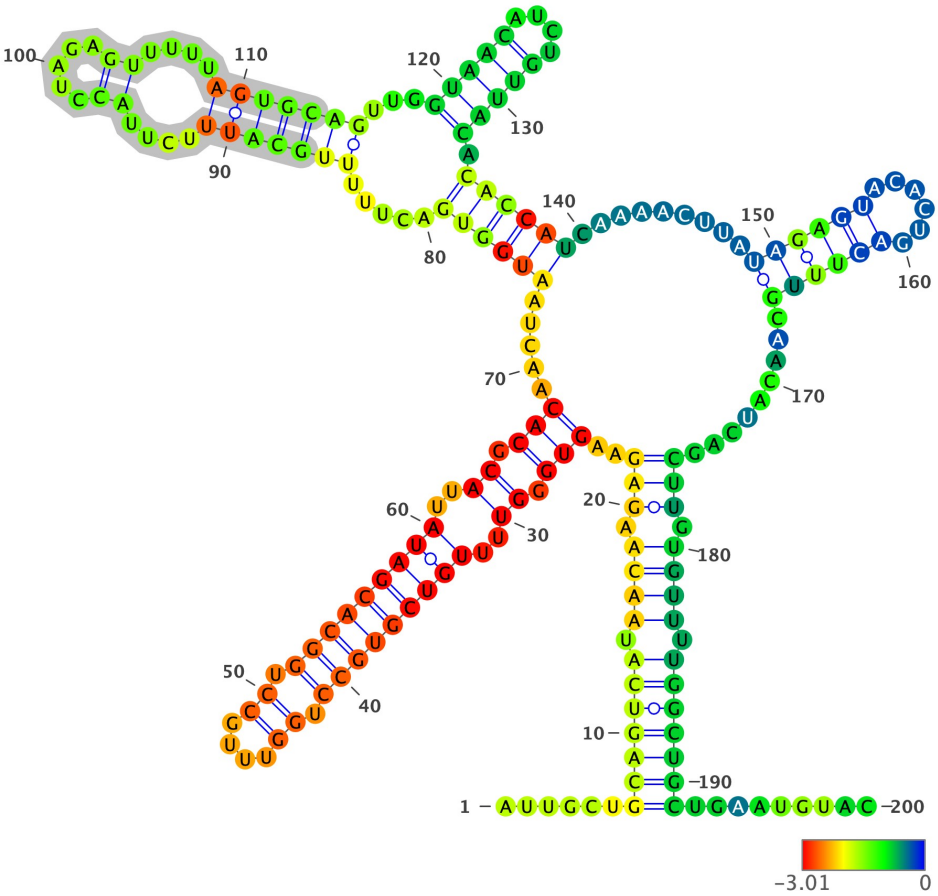
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 167 from nt 8911 to 8937 (nt 87 to 113)

```
5'-GCATTTCTTACCTAGAGTTTTTAGUGC-3'
5'-(((.....................)))-3'
Motif MFE = -2.5; z-score = -0.9; ED = 4.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8825 to 9024 (motif highlighted in silver):

```
5'-AUUGCUGCAGUCAUAACAAGAGAAGUGGGUUUUGUCGUGCCUGGUUUGCCUGGCACGAUAUUACGCACAACUAAUGGUGACUUUUUGCAUUUCUUACCUAGAGUUUUUAGU
GCAGUUGGUAACAUCUGUUACACACCAUCAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUAC-3
5'-......(((((((.((((.(((..(((.((..(((((((((.((....)).))))))))).)).))).....((((((.....(((((((....((.....)).....)))
))))...(((((....))))).))))))..........((((((......))))))..........))).)))).)))))))..........-3'
MFE = -58.8; z-score = -3.14; ED = 23.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

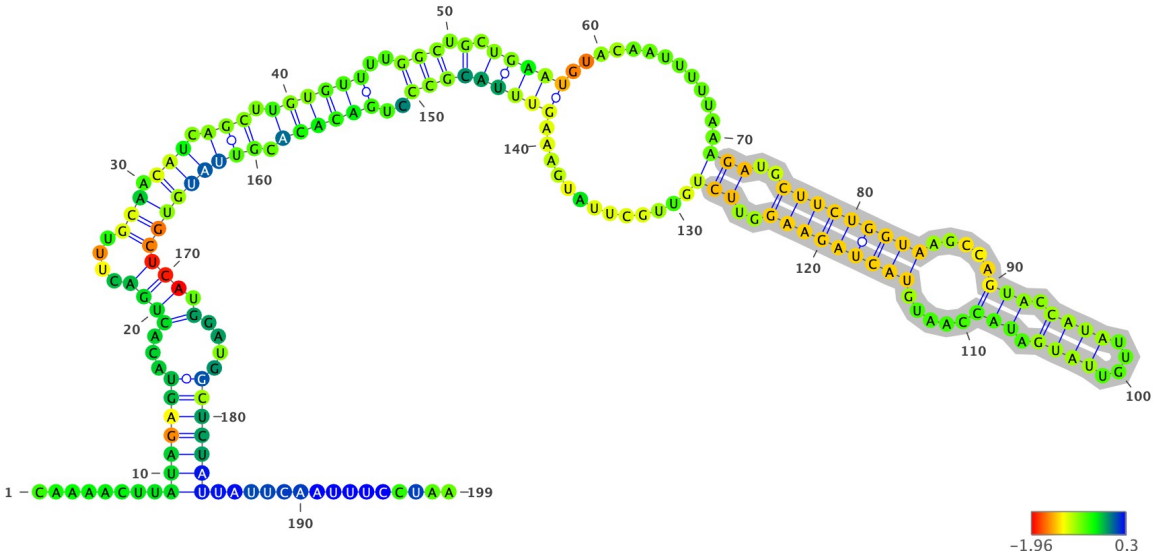
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 168 from nt 9035 to 9090 (nt 72 to 127)

```
5'-GATGCTTCTGGTAAGCCAGTACCATATTGTUAUGATACCAATGUACUAGAAGGTUC-3'
5'-((..((((((((((.............................)))))))))..))-3'
Motif MFE = -15.8; z-score = -2.67; ED = 1.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 8964 to 9162 (motif highlighted in silver):

```
5'-CAAAACUUAUAGAGUACACUGACUUUGCAACAUCAGCUUGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCA
AUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGCCCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAA-3
5'-........(((((((...((((....(((.(((.(((((((..(((.(.(((((.............(((..(((((((((.....(((.((((....)))).)))..
...)))))))))..)))............)))))))))..)))))).))))))))))))).)....)))))))................-3'
MFE = -46.2; z-score = -2.03; ED = 18.2
```

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(+)

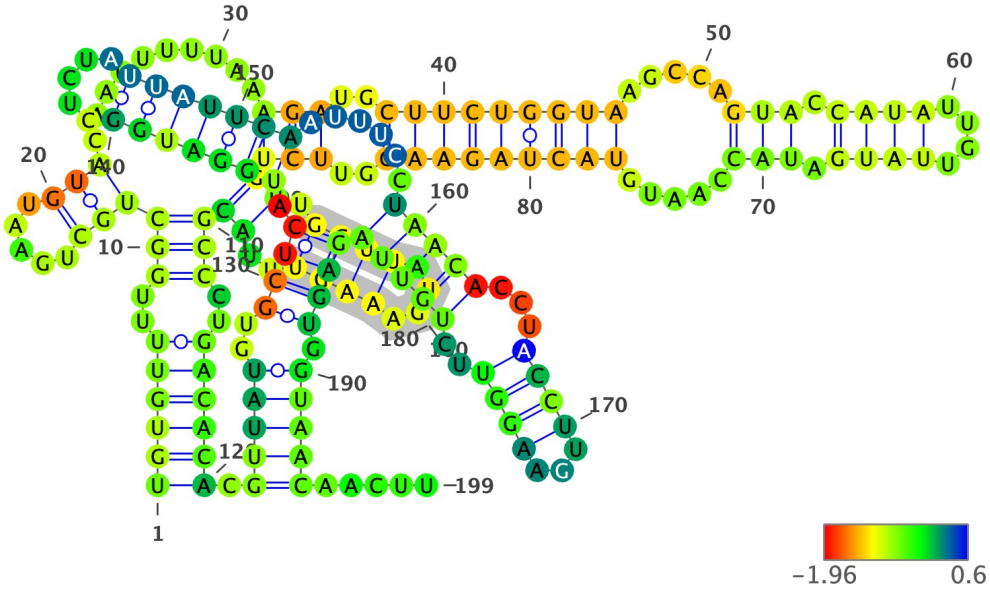
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 169 from nt 9095 to 9106 (nt 94 to 105)

```
5'-GCTTATGAAAGU-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = 0.1; 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 9002 to 9200 (motif highlighted in silver):

```
5'-UGUGUUUUGGCUGCUGAAUGUACAAUUUUUAAAGAUGCUUCUGGUAAGCCAGUACCAUAUUGUUAUGAUACCAAUGUACUAGAAGGUUCUGUUGCUUAUGAAAGUUUACGC
CCUGACACACGUUAUGUGCUCAUGGAUGGCUCUAUUAUUCAAUUUCCUAACACCUACCUUGAAGGUUCUGUUAGAGUGGUAACAACUU-3
5'-((((((..((((((.....)))).........(((..(((((((((.....(((.((((....)))).))).....)))))))))..))))((.((((....)))))..))))
)..)))))).((((((..((((.(((((((.....)))))))).....((((((...((((...))))..))))))))).)))))).....-3'
MFE = -43.7; z-score = -0.85; ED = 27.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

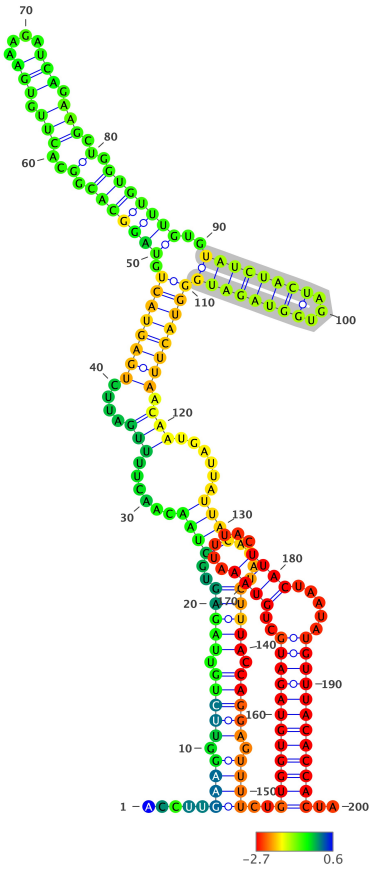
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 9258 to 9276 (nt 91 to 109)

```
5'-TATCTACTAGTGGUAGAUG-3'
5'-(((((((.....)))))))-3'
Motif MFE = -5.8; z-score = -3.96; 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 9168 to 9367 (motif highlighted in silver):

```
5'-ACCUUGAAGGUUCUGUUAGAGUGGUAACAACUUUUGAUUCUGAGUACUGUAGGCACGGCACUUGUGAAAGAUCAGAAGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGG
UACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUA-3
5'-.....((((.(((((.(((((..((((......(((....(((((((((.(((((((.(..(((.(((....))).))).).)))))))..(((((((((...)))))))))
))))))).))).....))))....))))).)))))..((((((((((((..((((......)))).....))))))))))))..-3'
MFE = -50.1; z-score = -1.49; ED = 56.68
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

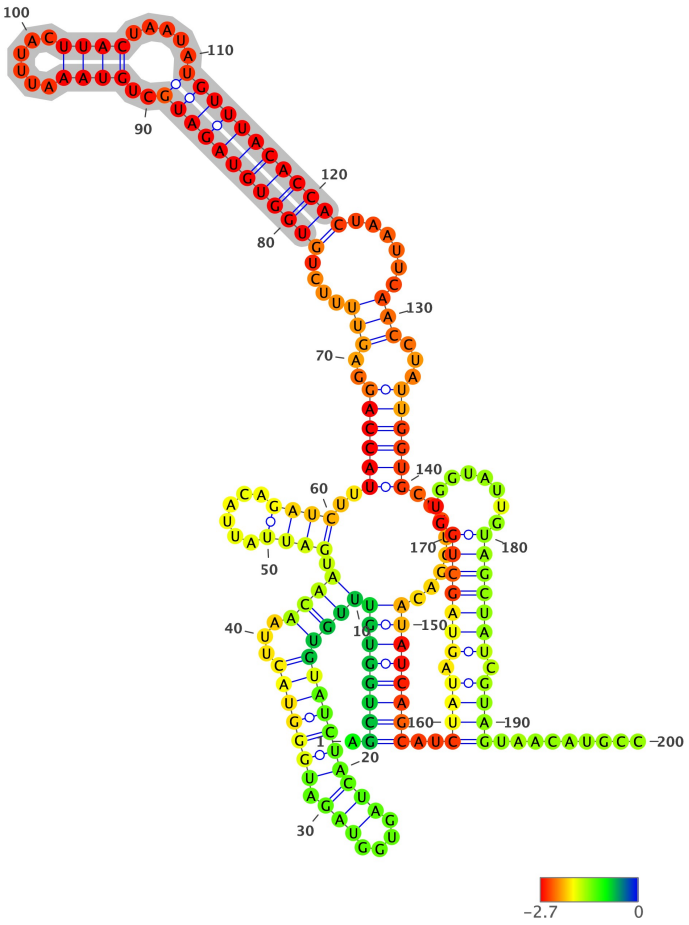
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 171 from nt 9322 to 9364 (nt 79 to 121)

```
5'-TGGTGTAGATGCTGTAAATTTACUUACTAATATGUUUACACCA-3'
5'-((((((((((...((((......))))......))))))))))-3'
Motif MFE = -11.2; z-score = -2.86; ED = 2.53
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9244 to 9443 (motif highlighted in silver):

```
5'-AGCUGGUGUUUGUGUAUCUACUAGUGGUAGAUGGGUACUUAACAAUGAUUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAU
GUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCC-3
5'-.((((((((((((((((((((((....))).)))))))...)))).((((......))))..((((((..(((....(((((((((((..((((......))))).....)
))))))))))).....)))...))))))........))))))))..((((.(((((((.........)))))))).))))..........-3'
MFE = -48.5; z-score = -2.42; ED = 60.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

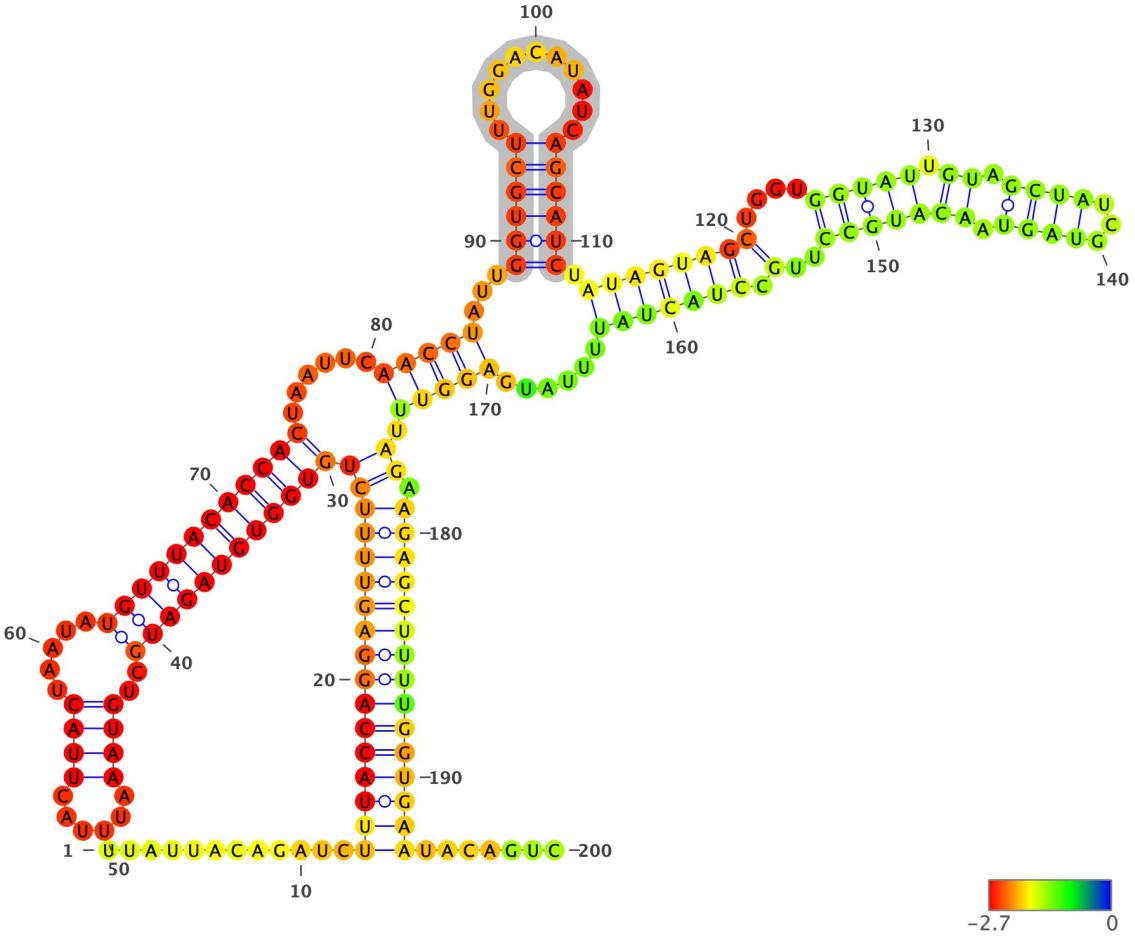
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 172 from nt 9380 to 9402 (nt 89 to 111)

```
5'-GGTGCTTTGGACATATCAGCAUC-3'
5'-((((.(..........).))))-3'
Motif MFE = -4.0; z-score = -0.79; ED = 2.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9292 to 9491 (motif highlighted in silver):

```
5'-UUAUUACAGAUCUUUACCAGGAGUUUUCUGUGGUGUAGAUGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUC
UAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUC-3
5'-............(((((((((((((((((((((((((((..((((......))))).....)))))))))))))).....((((((...((((((..........))))))
.(((((((((....((((((.((.((((...)))).)))))))..).)))))))......)))))).)).)))))))))))))).......-3'
MFE = -52.1; z-score = -3.53; ED = 24.36
```

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(+)

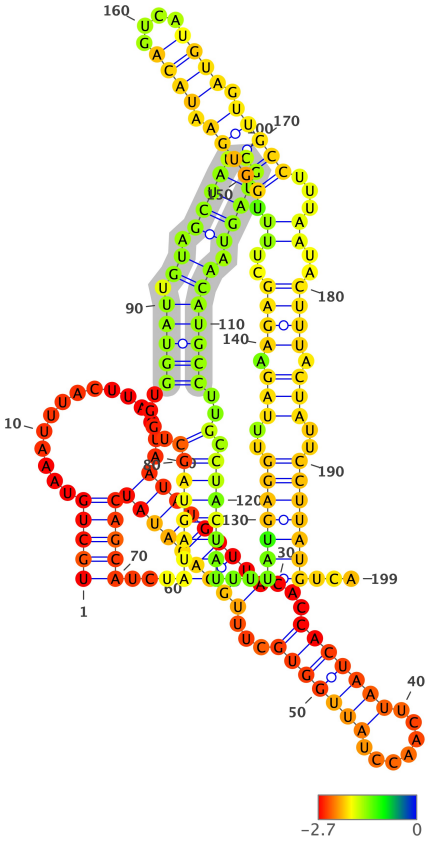
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 173 from nt 9416 to 9443 (nt 86 to 113)

```
5'-GGTATTGTAGCTATCGUAGUAACAUGCC-3'
5'-(((((.((.((((...)))).)))))))-3'
Motif MFE = -6.5; z-score = -1.92; ED = 1.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9331 to 9529 (motif highlighted in silver):

```
5'-UGCUGUAAAUUUACUUACUAAUAUGUUUACACCACUAAUUCAACCUAUUGGUGCUUUGGACAUAUCAGCAUCUAUAGUAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUG
CCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCA-3
5'-(((((...............(((((((((...(((((((.......)))))))...))))))))))))))...((((((((....(((((.((.((((...)))).)))))
))..).)))))))..(((((((..(((.((((..((.(((((.((((....)))).)))))...))..)))).)))..)))))))...-3'
MFE = -49.6; z-score = -3.25; ED = 16.08
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

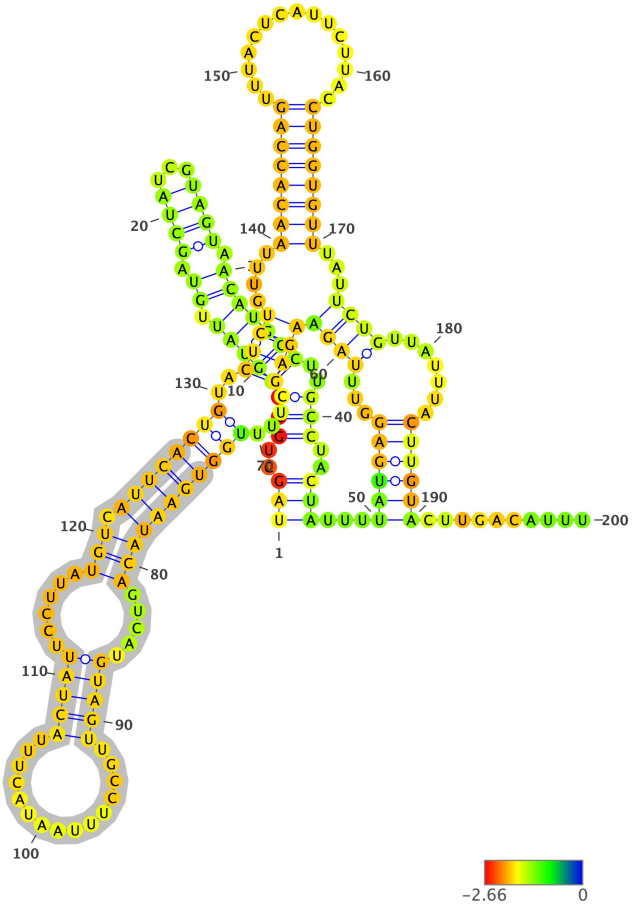
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 174 from nt 9481 to 9533 (nt 74 to 126)

```
5'-TGAATACAGTCATGTAGTTGCCTTTAATACTTTACUATTCCTTATGUCATTCA-3'
5'-(...(((.......(((.................)))........)).)...)-3'
Motif MFE = -5.8; z-score = -1.34; ED = 1.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9408 to 9607 (motif highlighted in silver):

```
5'-UAGCUGGUGGUAUUGUAGCUAUCGUAGUAACAUGCCUUGCCUACUAUUUUAUGAGGUUUAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAU
UCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUU-3
5'-(((..((((((((.((.((((...)))).)))))))..)))..)))...((((((...((((((((....((((((((((.....(((((.................)))))
......))).))))))))..)))))....((((((((.................))))))))...))))).......))))))..........-3'
MFE = -36.8; z-score = -2.13; ED = 36.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

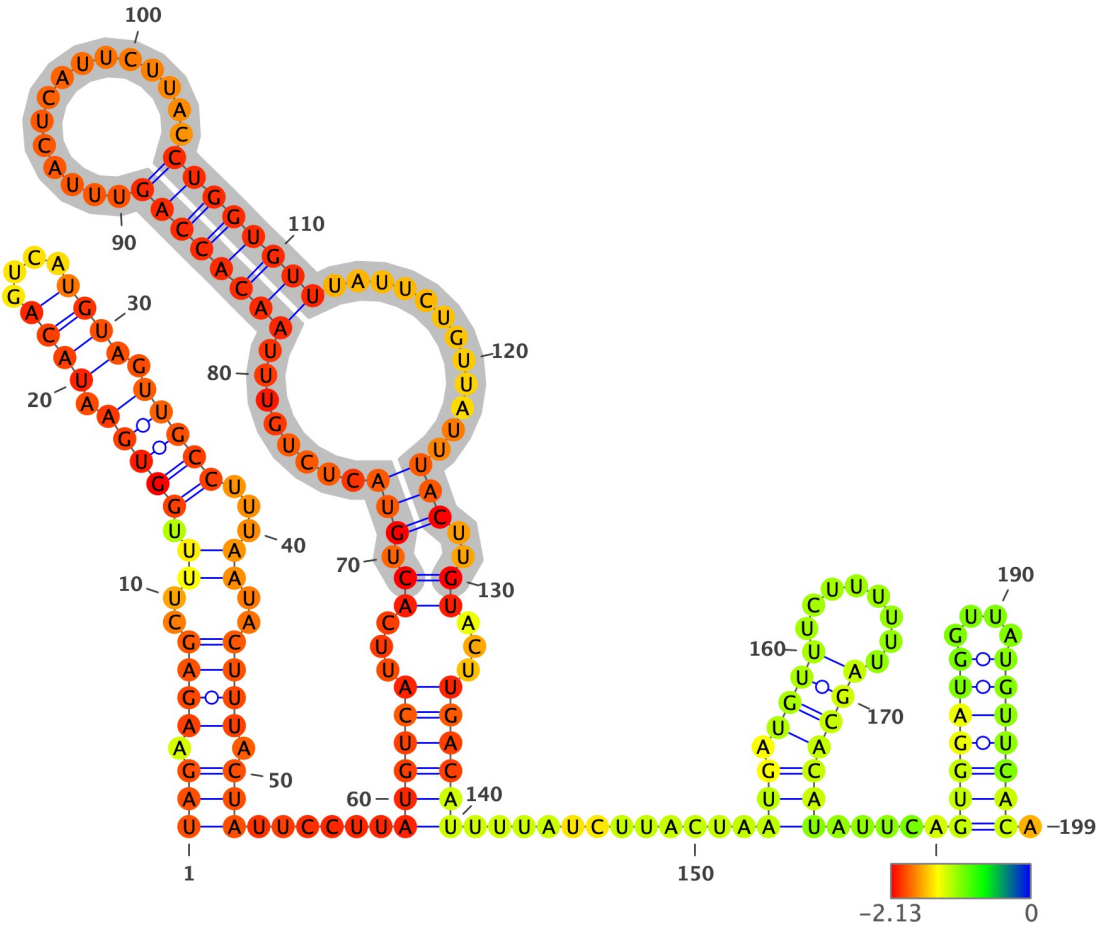
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 175 from nt 9534 to 9595 (nt 69 to 130)

```
5'-CTGTACTCTGTTTAACACCAGTTTACTCATTCTTACCUGGUGUUTATTCTGTTATTTACTTG-3'
5'-(.(..........((((((((...............))))))))..............)..)-3'
Motif MFE = -9.0; z-score = -2.11; ED = 5.94
```



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 9466 to 9664 (motif highlighted in silver):

```
5'-UAGAAGAGCUUUUGGUGAAUACAGUCAUGUAGUUGCCUUUAAUACUUUACUAUUCCUUAUGUCAUUCACUGUACUCUGUUUAACACCAGUUUACUCAUUCUUACCUGGUGU
UUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACA-3
5'-(((.((((..((.(((((.((((....)))).)))))...))..)))).))).....((((((...((.(((........((((((((...............)))))))
).............)))..))...))))))............(((.((((........)))))))).....(((((((....)))))))).-3'
MFE = -31.1; z-score = -1.39; ED = 36.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

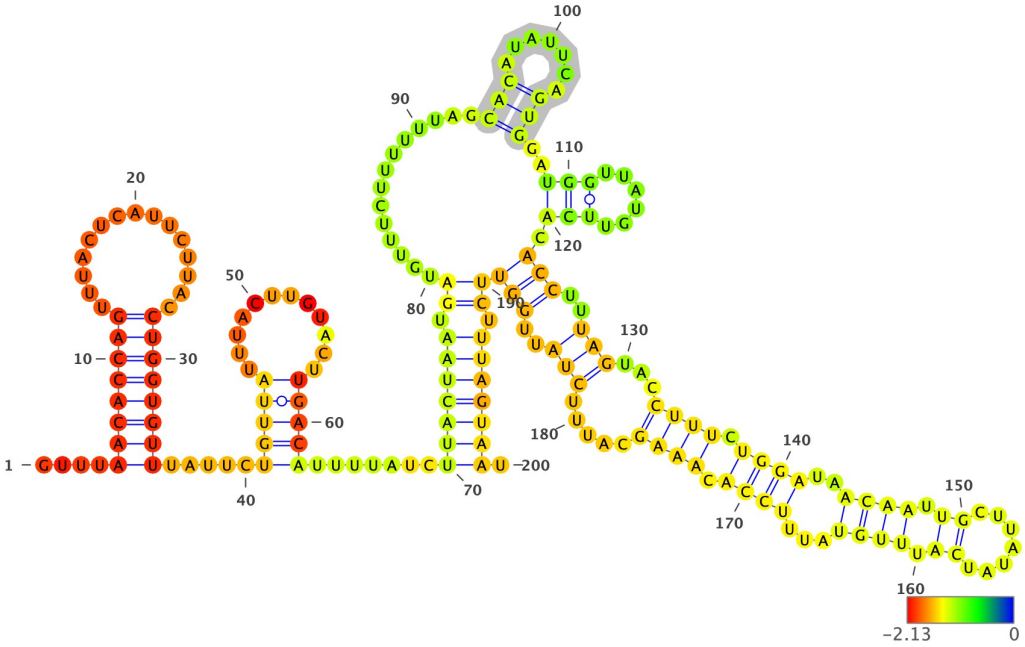
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 176 from nt 9636 to 9648 (nt 94 to 106)

```
5'-CACATATTCAGUG-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.23; 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 9543 to 9742 (motif highlighted in silver):

```
5'-GUUUAACACCAGUUUACUCAUUCUUACCUGGUGUUUAUUCUGUUAUUUACUUGUACUUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGG
UUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAU-3
5'-....((((((((.............))))))))).....(((((.............))))).......(((((((.((.............(((.......)))..(((
......))).(((..(((...((((.((((..((((.((.......)).))))...)))).)))).....)))..))))).))))))).-3'
MFE = -28.8; z-score = -2.59; ED = 20.72
```

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(+)

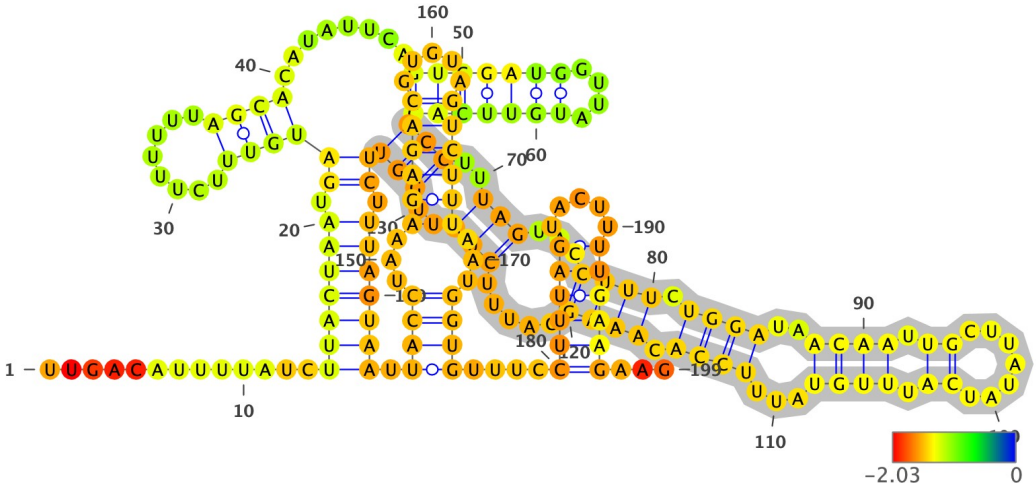
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 177 from nt 9664 to 9731 (nt 66 to 133)

```
5'-ACCTTTAGTACCTTTCTGGATAACAATTGCTTATATCATUUGUATTUCCACAAAGCATTTCUATTGGU-3'
5'-(((..((....((((.((((..((((.((.......)).))))...)))).)))).....))..)))-3'
Motif MFE = -12.1; z-score = -2.48; ED = 2.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9599 to 9797 (motif highlighted in silver):

```
5'-UUGACAUUUUAUCUUACUAAUGAUGUUUCUUUUUUAGCACAUAUUCAGUGGAUGGUUAUGUUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUU
UCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAG-3
5'-.............(((((((.((((((........))))........(((((((....)))))))(((..(((...((((.((((..((((.((.......)).))))...
)))).))))).....)))..))))).))))))).((((...((((((.....))))))...))))....((((((.....))))))...-3'
MFE = -36.1; z-score = -1.07; ED = 51.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

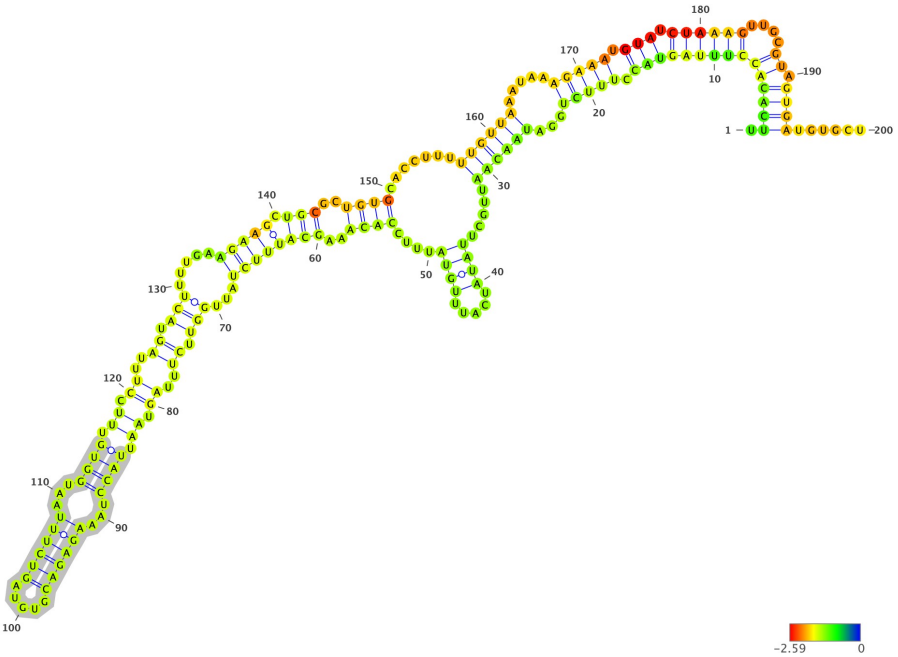
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 178 from nt 9743 to 9773 (nt 85 to 115)

```
5'-TACCTAAAGAGACGTGTAGUCUUTAATGGUG-3'
5'-((((....(((((.....)))))....))))-3'
Motif MFE = -9.1; z-score = -3.04; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9659 to 9858 (motif highlighted in silver):

```
5'-UUCACACCUUUAGUACCUUUCUGGAUAACAAUUGCUUAUAUCAUUUGUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAU
GGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCU-3
5'-.(((((((((((((((.(((((...((((((.....((((.....))))....((((..((((((((...(((.((..((.((.((((...((((((.....))))))...
)))).)).))..)).)))).....))))).)))..))))).......))))))).....))))).))).))))))....)).))))......-3'
MFE = -40.2; z-score = -1.35; ED = 54.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

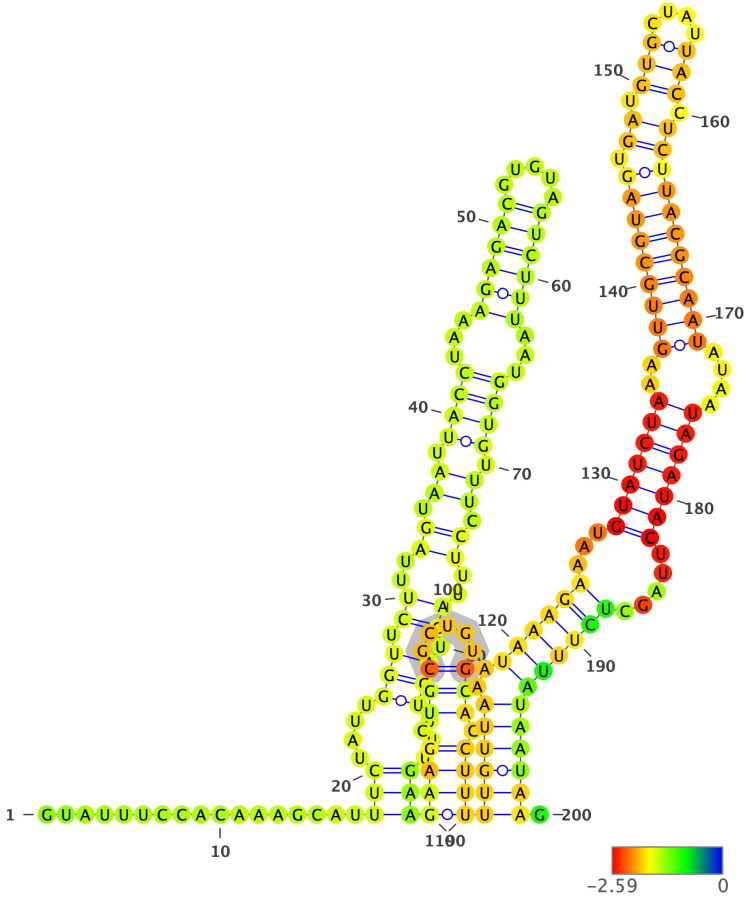
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 9801 to 9807 (nt 97 to 103)

```
5'-CGCTGTG-3'
5'-(.....)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9705 to 9904 (motif highlighted in silver):

```
5'-GUAUUUCCACAAAGCAUUUCUAUUGGUUCUUUAGUAAUUACCUAAAGAGACGUGUAGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUU
UGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUACGCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAG-3
5'-.................(((....(((.((..(((.((.((((...((((((.....))))))...)))))..)).))..)).)))...)))(((((.(((.....))).)))))(
((((((..(((((((...(((((((..((((((((((.((.(((....))).)))))))))))....)))))))).....))))))))))).-3'
MFE = -44.1; z-score = -3.02; ED = 32.34
```

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(+)

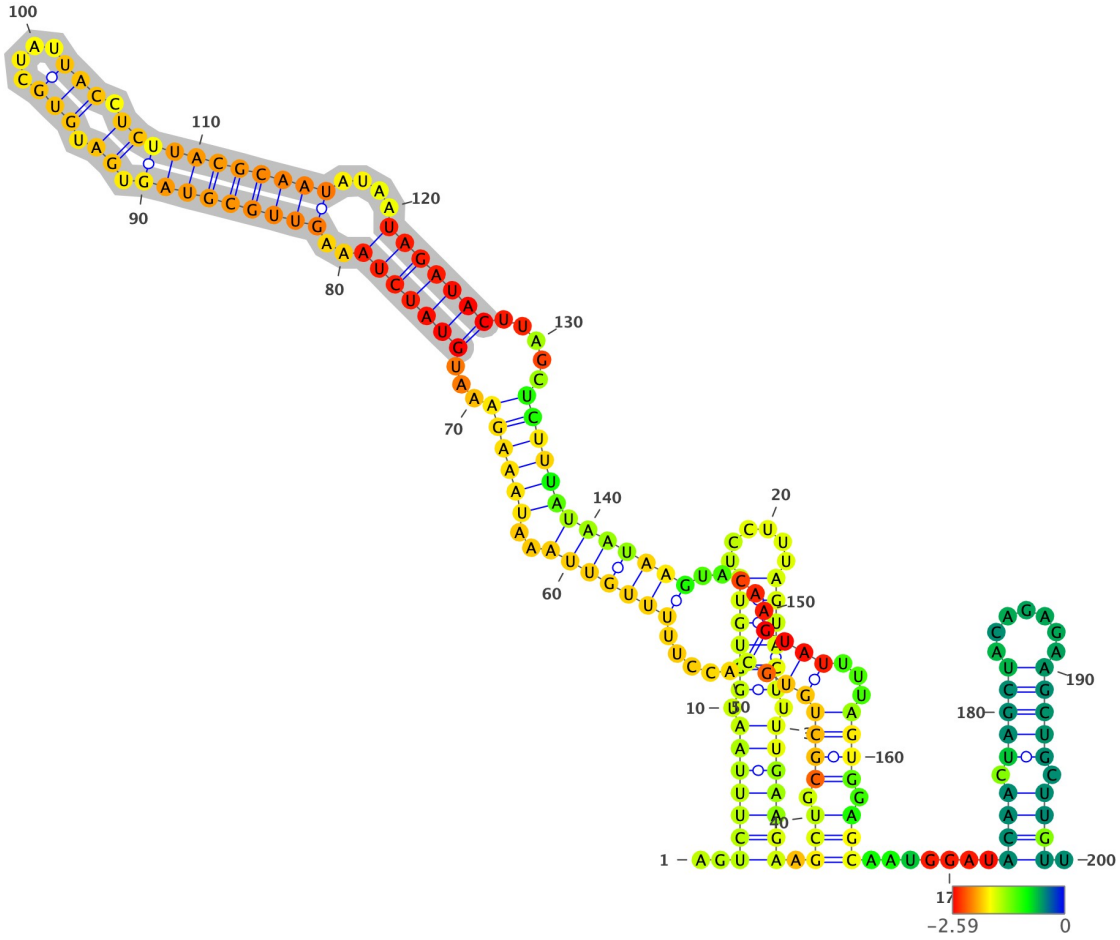
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 180 from nt 9832 to 9886 (nt 73 to 127)

```
5'-GTATCTAAAGTTGCGTAGTGATGTGCTATUACCUCTUACGCAAUATAAUAGAUAC-3'
5'-(((((((..(((((((((..((.(((....))).)).))))))))....)))))))-3'
Motif MFE = -17.4; z-score = -3.77; ED = 3.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 9760 to 9959 (motif highlighted in silver):

```
5'-AGUCUUUAAUGGUGUUUCCUUUAGUACUUUUGAAGAAGCUGCGCUGUGCACCUUUUUGUUAAAUAAAGAAAUGUAUCUAAAGUUGCGUAGUGAUGUGCUAUUACCUCUUAC
GCAAUAUAAUAGAUACUUAGCUCUUUAUAAUAAGUACAAGUAUUUUAGUGGAGCAAUGGAUACAACUAGCUACAGAGAAGCUGCUUGUU-3
5'-..(((((((.((((((......)))))).)))))))).(((.(((((((((.....(((((((..((((((...(((((((..((((((((((.((.(((....))).))))))
))))).....)))))))).....))))))))))))).....))))...)))).))).......((((.(((((.......))))).)))).-3'
MFE = -50.0; z-score = -2.68; ED = 14.76
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

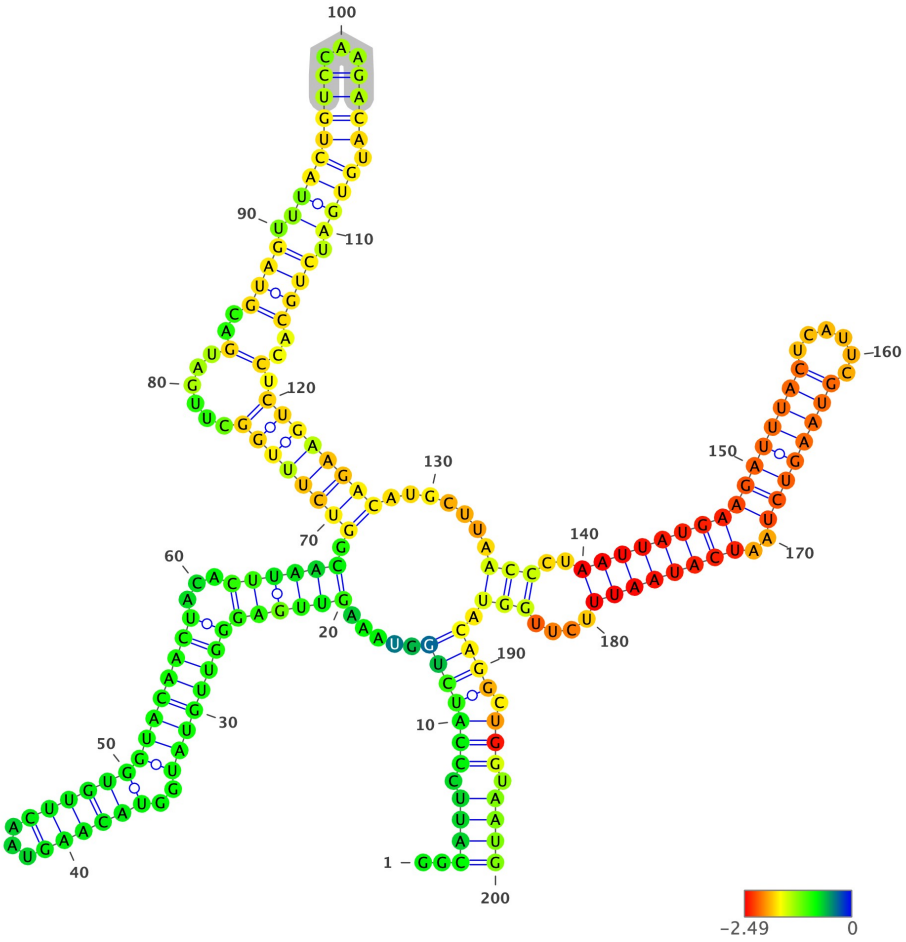
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 181 from nt 10168 to 10174 (nt 97 to 103)

```
5'-TCCAAGA-3'
5'-((...))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10072 to 10271 (motif highlighted in silver):

```
5'-GGCAUUCCCAUCUGGUAAAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAU
CUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUG-3
5'-..((((.(((((((.....((((((((((((((..((((((...)))))))))))))))...)))))).((((((((......(..((((.((((((((...)))).)))).
))))..).))))))))).......(((..((((((((((((((((.....))))))))..))))))))....))).)))).))).))))-3'
MFE = -55.2; z-score = -2.57; ED = 16.4
```

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(+)

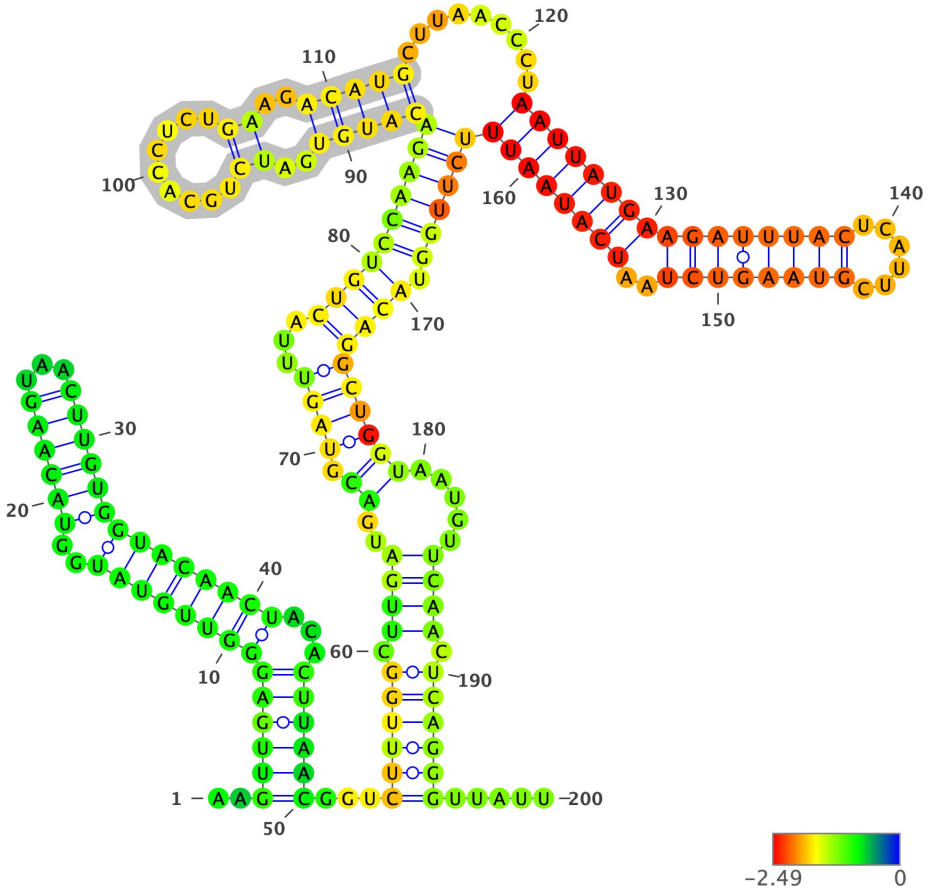
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 182 from nt 10175 to 10201 (nt 87 to 113)

```
5'-CATGTGATCTGCACCTCTGAAGACATG-3'
5'-(..((...(.........)...))..)-3'
Motif MFE = -4.4; z-score = -0.67; ED = 2.56
```



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 10089 to 10288 (motif highlighted in silver):

```
5'-AAGUUGAGGGUUGUAUGGUACAAGUAACUUGUGGUACAACUACACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACA
UGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUU-3
5'-..(((((((((((((..((((((...))))))))))))))...))))))...((((((.((((..((.((((...(((((((((((((((..((.........))..)))
))).........((((((((((((((((......)))))))).)))))))))))))).))))))))))).....)))).))))))).....-3'
MFE = -53.8; z-score = -2.87; ED = 15.48
```

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(+)

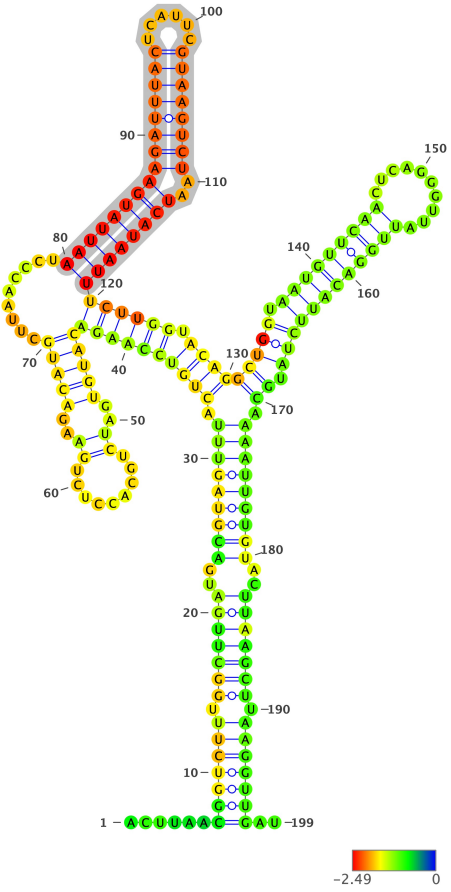
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 183 from nt 10211 to 10250 (nt 80 to 119)

```
5'-AATTATGAAGATTTACTCATTCGUAAGUCUAAUCAUAAUU-3'
5'-(((((((((((((((.....)))))))).)))))))-3'
Motif MFE = -12.4; z-score = -5.47; ED = 1.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10132 to 10330 (motif highlighted in silver):

```
5'-ACUUAACGGUCUUUGGCUUGAUGACGUAGUUUACUGUCCAAGACAUGUGAUCUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAA
UCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAU-3
5'-......(((((((.(((((((..(((((((((.((((((((((((((..((.........))..)))))).........((((((((((((((((.....)))))))).
))))))))))))))).))))(((((.(((((((((.........))))))))))))).)).))))))))..)))))))).)))))))..-3'
MFE = -53.8; z-score = -2.92; ED = 12.45
```

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(+)

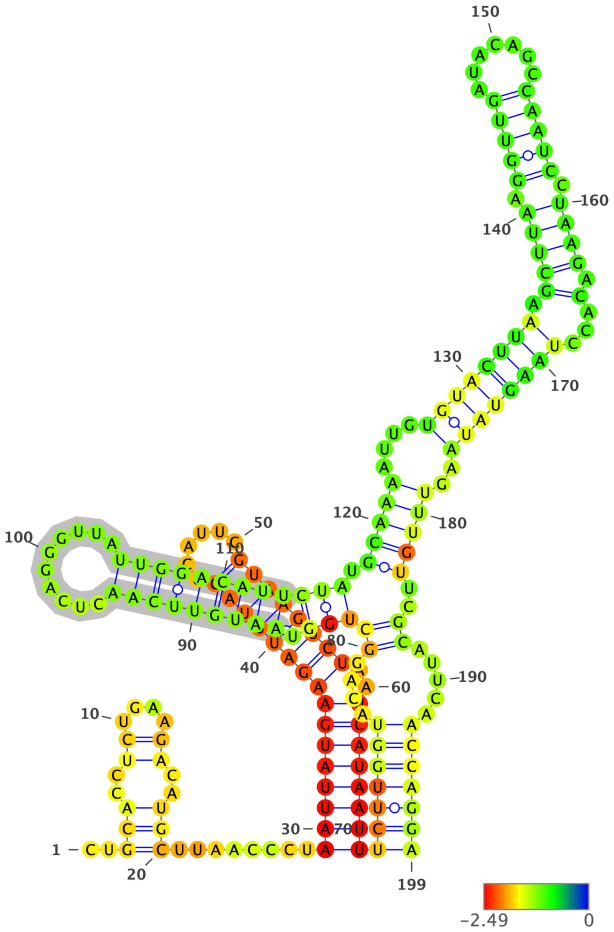
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 184 from nt 10268 to 10295 (nt 86 to 113)

```
5'-AATGTTCAACTCAGGGTTAUUGGACAUU-3'
5'-((((((((((.........))))))))))-3'
Motif MFE = -5.2; z-score = -1.46; ED = 3.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10183 to 10381 (motif highlighted in silver):

```
5'-CUGCACCUCUGAAGACAUGCUUAACCCUAAUUAUGAAGAUUUACUCAUUCGUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACA
UUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGA-3
5'-..(((..((....))..))).........(((((((((((((((.....))))))))..))))))))(((((((....(((((.((((((((.........)))))))
))))).(((((....((((((((.(((((.(((((.......))))).)))).)...))))))))..)))))..))).....)))))))-3'
MFE = -45.2; z-score = -2.06; ED = 39.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

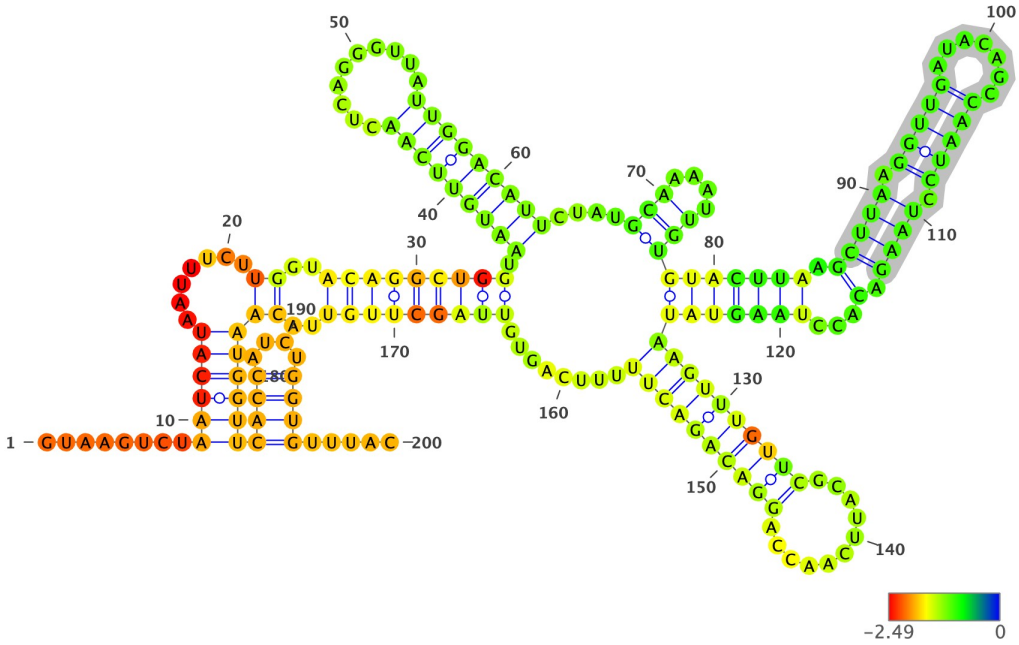
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 185 from nt 10319 to 10345 (nt 87 to 113)

```
5'-CTTAAGGTTGATACAGCCAAUCCUAAG-3'
5'-((((.(((((.......))))).))))-3'
Motif MFE = -4.6; z-score = -1.69; 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 10233 to 10432 (motif highlighted in silver):

```
5'-GUAAGUCUAAUCAUAAUUUCUUGGUACAGGCUGGUAAUGUUCAACUCAGGGUUAUUGGACAUUCUAUGCAAAAUUGUGUACUUAAGCUUAAGGUUGAUACAGCCAAUCCUA
AGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUAC-3
5'-........((((((.......((..(((((((((.(((((((((.........)))))))))....(((....)))(((((((.(((((.(((((.......))))).))
)).)...)))))))((((((((((.........))))))))))........))))))))..)))))))((((....))))).....-3'
MFE = -43.7; z-score = -0.81; ED = 21.78
```

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(+)

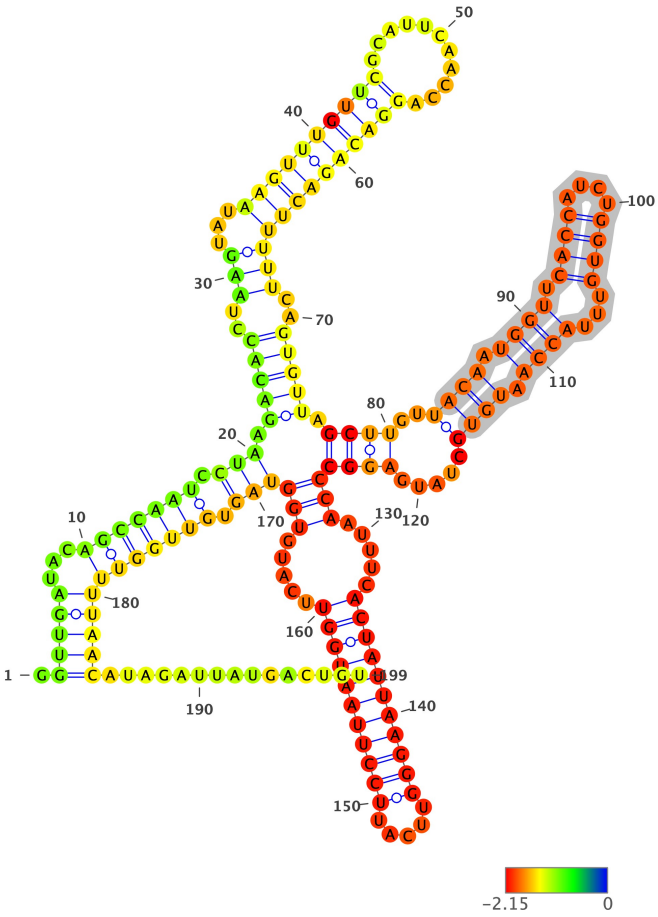
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 186 from nt 10407 to 10438 (nt 84 to 115)

```
5'-ACAATGGTTCACCATCTGGUGTTTACCAAUGU-3'
5'-(((.((((.((((....))))...)))).)))-3'
Motif MFE = -10.0; z-score = -3.06; 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 10324 to 10522 (motif highlighted in silver):

```
5'-GGUUGAUACAGCCAAUCCUAAGACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCA
AUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGU-3
5'-.(((((...(((((((.(((.(((((..(((...((((((((((.....))))))))))))..))))).((((..((((.((((.((((....))))...))))
.))))).....))))(((.....((((((((((.....))))))))))).....)))))).))))))))))))...............-3'
MFE = -53.4; z-score = -2.49; ED = 24.94
```

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(+)

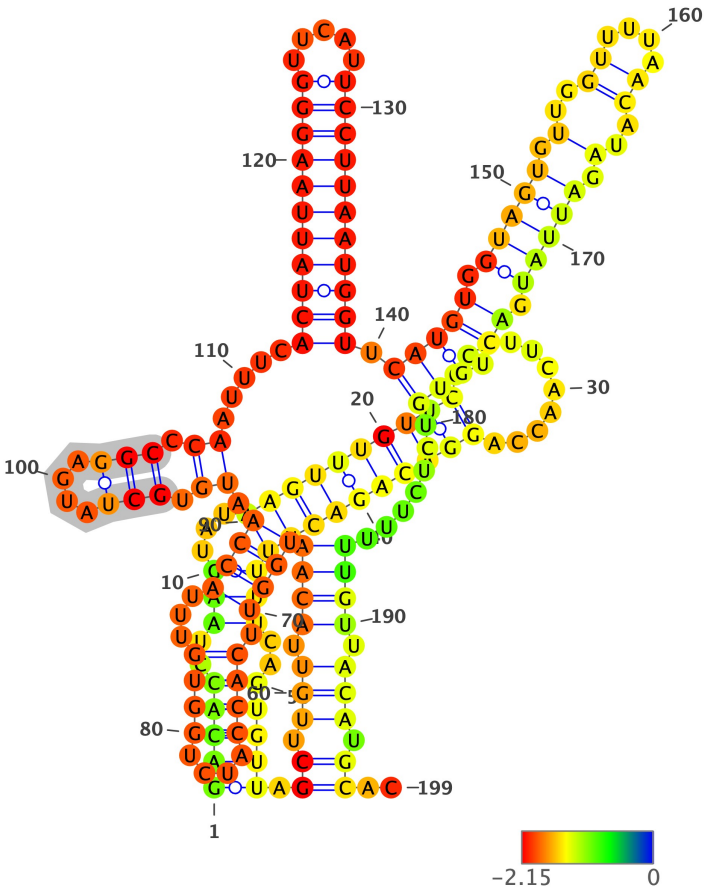
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 187 from nt 10439 to 10448 (nt 95 to 104)

```
5'-GCTATGAGGC-3'
5'-((......))-3'
Motif MFE = -0.4; z-score = -1.68; ED = 1.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10345 to 10543 (motif highlighted in silver):

```
5'-GACACCUAAGUAUAAGUUUGUUCGCAUUCAACCAGGACAGACUUUUUCAGUGUUAGCUUGUUACAAUGGUUCACCAUCUGGUGUUUACCAAUGUGCUAUGAGGCCCAAUUU
CACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUGCAC-3
5'-(((((..(((...(((((((((((...........))))))))))))..))))).((.(((.((((((((.((((....))))...)))).((.(((....))).)).....
.((((((((((.....))))))))))).(((((.(((((.(..((....))..).))))).)).))).......)))).))).))..-3'
MFE = -50.1; z-score = -2.59; 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, 266-13468(+)

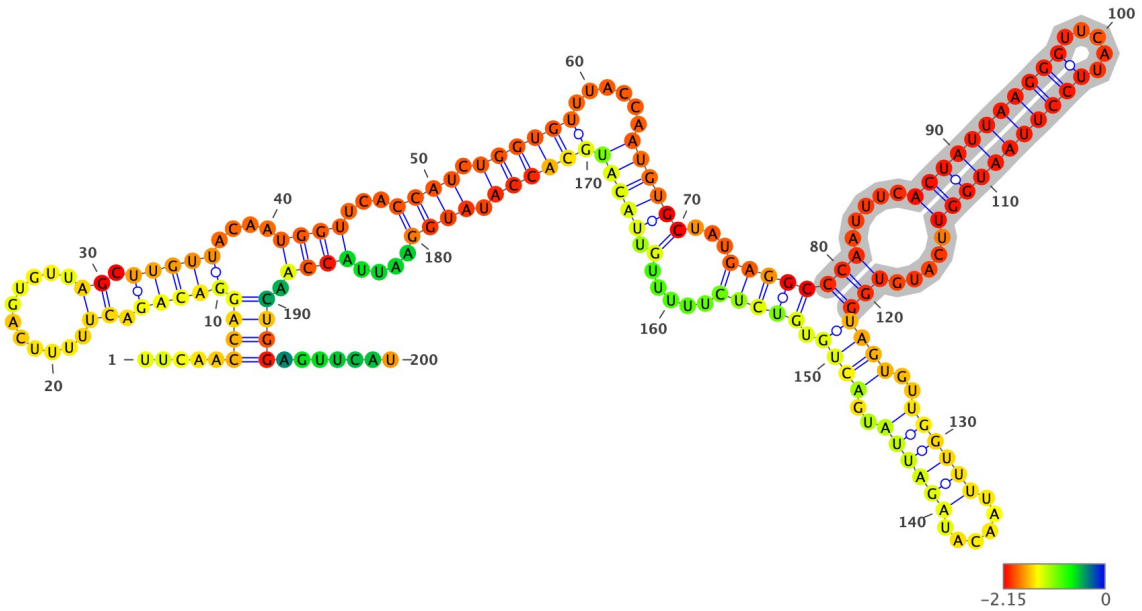
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 10449 to 10491 (nt 79 to 121)

```
5'-CCAATTTCACTATTAAGGGTTCATUCCUUAAUGGUTCATGUGG-3'
5'-(((.....(((((((((((.....)))))))))))).....)))-3'
Motif MFE = -14.0; z-score = -4.21; 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 = -1.7; 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(+)

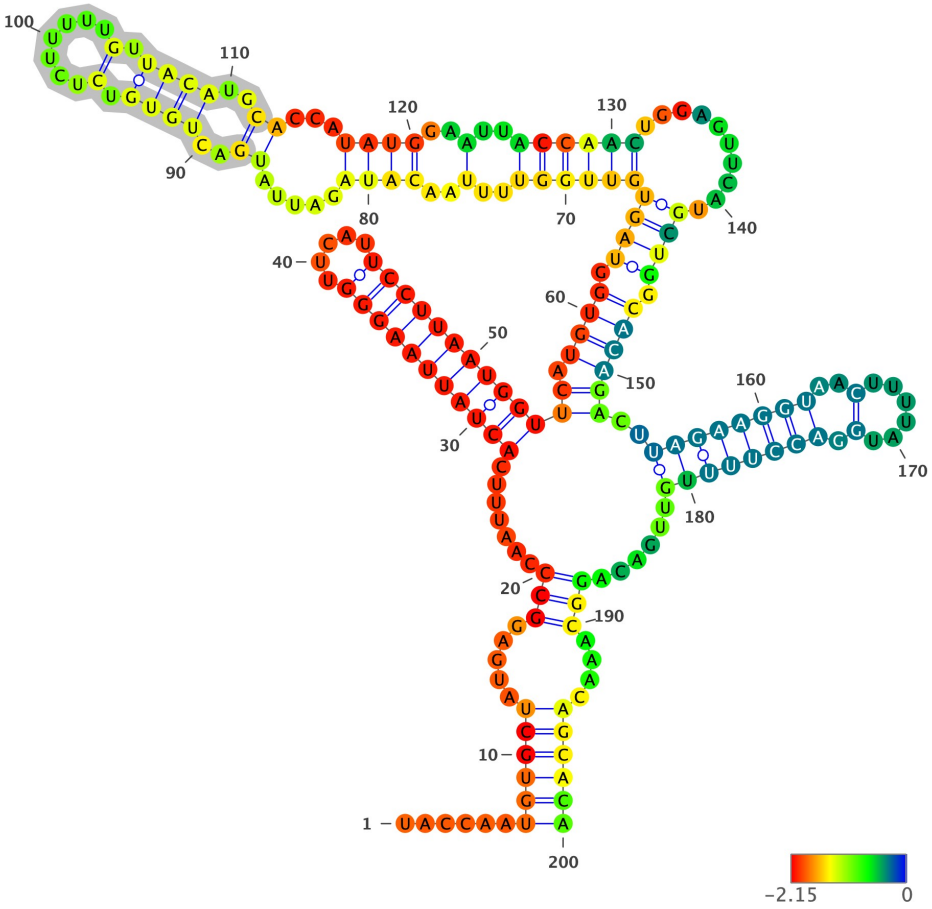
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 189 from nt 10517 to 10541 (nt 88 to 112)

```
5'-GACTGTGTCTCTTTTTGTUACATGC-3'
5'-(..((((.(.......).)))))..)-3'
Motif MFE = -1.6; z-score = -0.35; ED = 4.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10430 to 10629 (motif highlighted in silver):

```
5'-UACCAAUGUGCUAUGAGGCCCAAUUUCACUAUUAAGGGUUCAUUCCUUAAUGGUUCAUGUGGUAGUGUUGGUUUUAACAUAGAUUAUGACUGUGUCUCUUUUUGUUACAUG
CACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACA-3
5'-......((((((.....(((.......((((((((((.....))))))))))))).(((((.((((((((((..(..((((.....((..((((.(.......).)))))..
))...))))..)..)))))).........))))).)))))).((((((((..(......).)))))))).....)))....)))))-3'
MFE = -49.1; z-score = -1.86; ED = 32.1
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

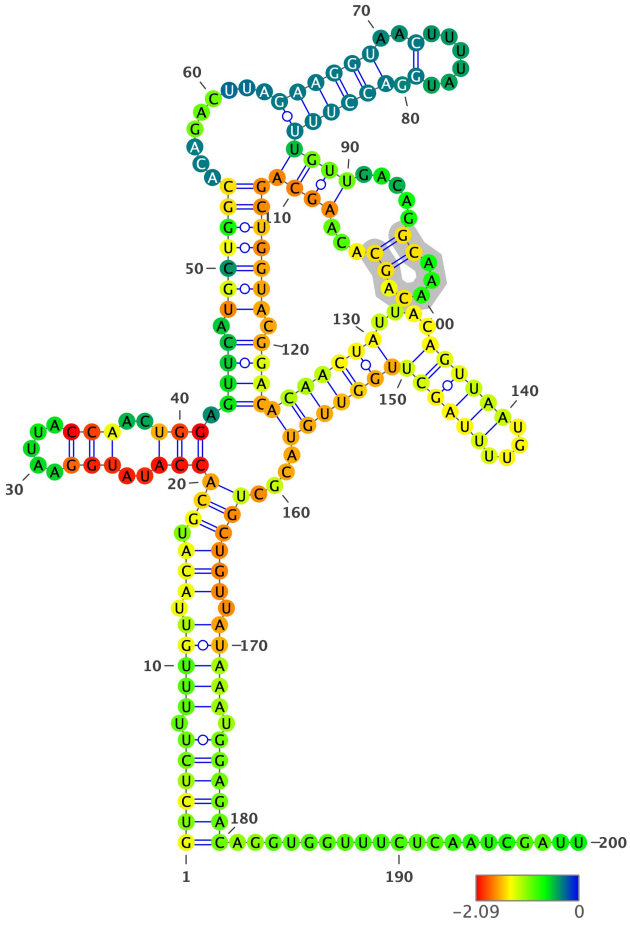
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 190 from nt 10618 to 10626 (nt 96 to 104)

```
5'-GCAAACAGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10523 to 10722 (motif highlighted in silver):

```
5'-GUCUCUUUUUGUUACAUGCACCAUAUGGAAUUACCAACUGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCA
GCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGCUUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUU-3
5'-((((((.(((((.(((.((((((..(((.....)))..))).((((.(((((((.........((((((..(......).))))))((((.....((.....))...))))
))))))).))))(((((((....((((((....))))))))))))....)))))).))))).))))))....................-3'
MFE = -48.6; z-score = -1.44; 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(+)

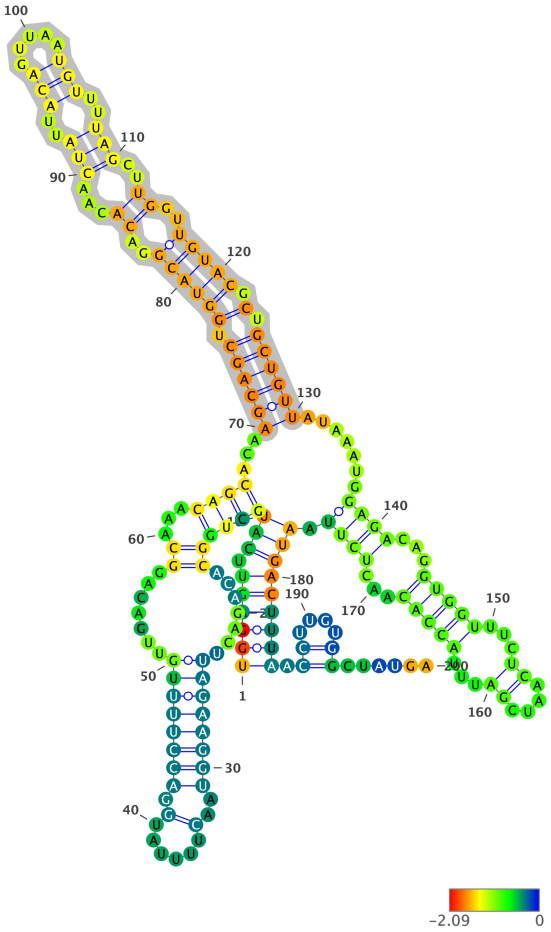
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 191 from nt 10630 to 10690 (nt 70 to 130)

```
5'-AGCAGCTGGTACGGACACAACTATTACAGTTAAUGUTTUAGCTUGGTUGUACGCTGCUGUU-3'
5'-((((((.(((((((..((...((((..(((.....)))).))))..)).))..)))))).).)))))-3'
Motif MFE = -20.6; z-score = -3.61; ED = 7.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10561 to 10760 (motif highlighted in silver):

```
5'-UGGAGUUCAUGCUGGCACAGACUUAGAAGGUAACUUUUAUGGACCUUUUGUUGACAGGCAAACAGCACAAGCAGCUGGUACGGACACAACUAUUACAGUUAAUGUUUUAGC
UUGGUUGUACGCUGCUGUUAUAAAUGGAGACAGGUGGUUUCUCAAUCGAUUUACCACAACUCUUAAUGACUUUAACCUUGUGGCUAUGA-3
5'-((((((.((((((((((.......(((((((((..(......).))))))))).......))...)))))...((((((.((((((..((...((((..(((.....)))).))))..)))).
.))..))))))).).))))))).......((((...((((((...((....))...))))))...)))))..)))))))))..((....)).......-3'
MFE = -46.3; z-score = -0.85; ED = 21.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

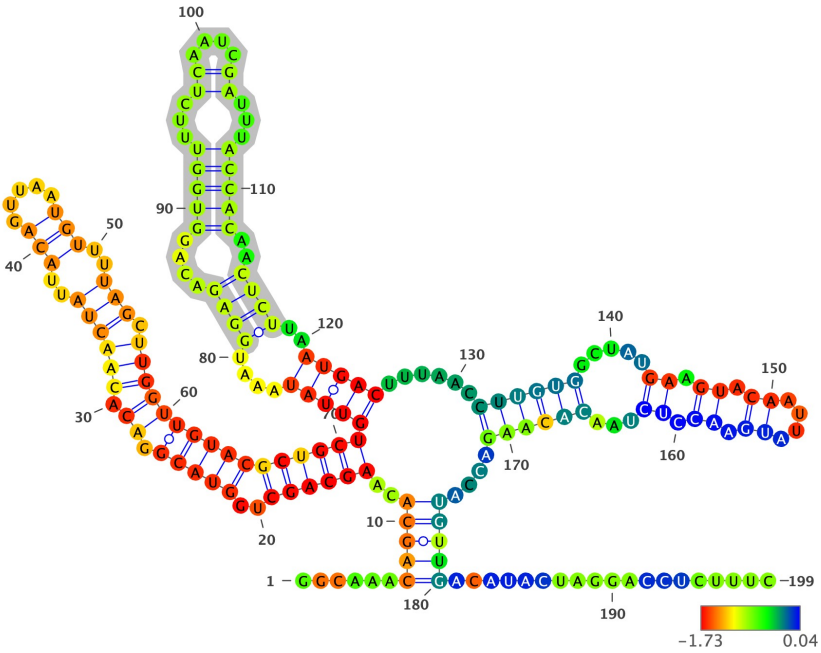
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 192 from nt 10697 to 10734 (nt 81 to 118)

```
5'-GGAGACAGGTGGTTTCTCAATCGATTTACCACAACUCU-3'
5'-(.....................................)-3'
Motif MFE = -9.0; z-score = -1.49; 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 = -1.11; ED = 16.56
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

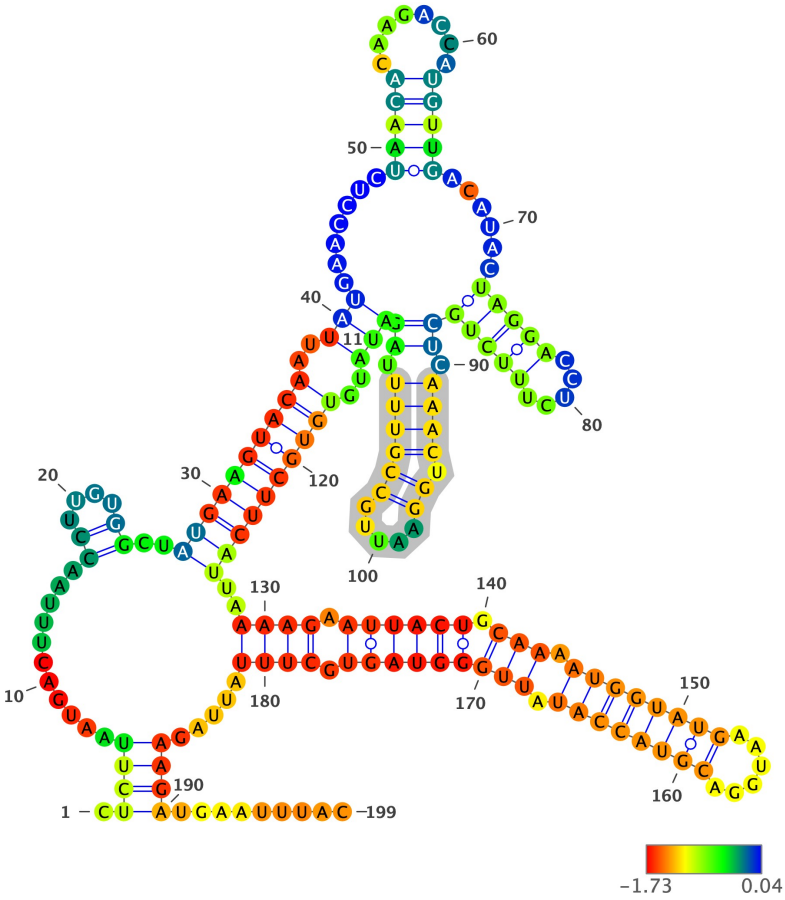
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 10821 to 10838 (nt 91 to 108)

```
5'-AAACTGGAATTGCCGUUU-3'
5'-((((.((.....))))))-3'
Motif MFE = -1.0; z-score = -0.27; ED = 2.94
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10731 to 10929 (motif highlighted in silver):

```
5'-CUCUUAAUGACUUUAACCUUGUGGCUAUGAAGUACAAUUAUGAACCUCUAACACAAGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAG
AUAUGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAUAUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUAC-3
5'-.((((...........((....))..((((((((((..(((.......(((((........)))))......(((((.....)))))((.((((.((.....))))))).))
)))..)))))))))))..((((.((((((.(((.((((((((......)))))))).))))))))).))))).....))))........-3'
MFE = -37.2; z-score = -0.73; ED = 35.11
```

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(+)

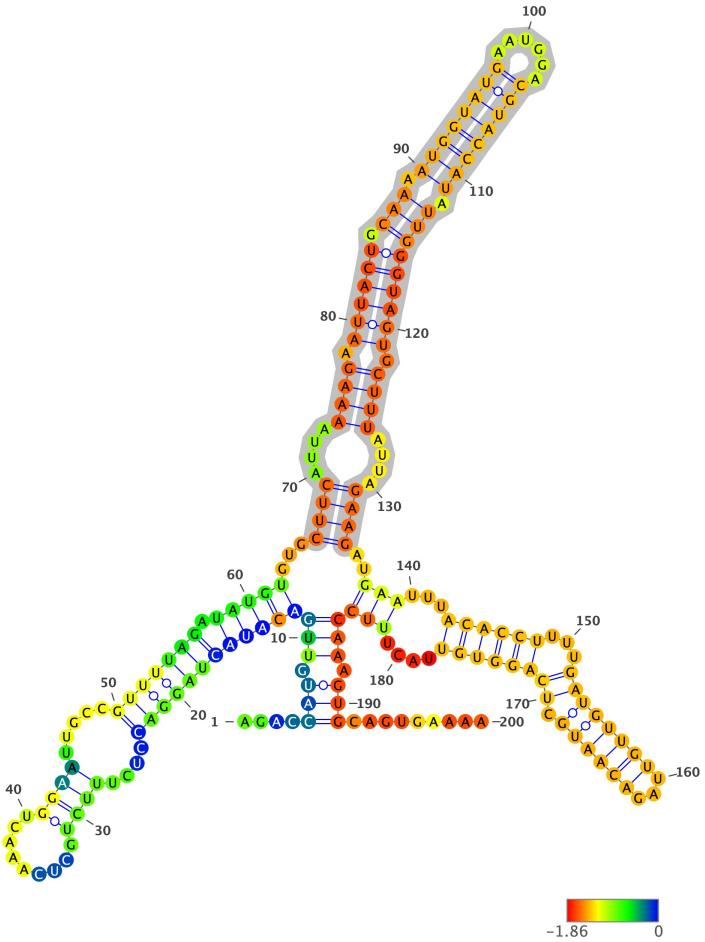
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 194 from nt 10851 to 10919 (nt 66 to 134)

```
5'-CTTCATTAAAAGAATTACTGCAAAATGGTATGAATGGACGUACCAUAUUGGGUAGUGCUUUATTAGAAG-3'
5'-((((....((((.((((((.(((.((((((((.....))))))))).))))))))).))))....))))-3'
Motif MFE = -20.0; z-score = -3.88; ED = 3.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10786 to 10985 (motif highlighted in silver):

```
5'-AGACCAUGUUGACAUACUAGGACCUCUUUCUGCUCAAACUGGAAUUGCCGUUUUAGAUAUGUGUGCUUCAUUAAAAGAAUUACUGCAAAAUGGUAUGAAUGGACGUACCAU
AUUGGGUAGUGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAA-3
5'-....(((.((((((((((((((....((((.........))))).....)))))))).)))))...((((....((((.((((((.(((.((((((((.....))))))))
.)))))))))).))))....))))..(((...((((((...((((((((...)))))).))))))))....)))))).)))........-3'
MFE = -42.2; z-score = -0.43; ED = 25.94
```

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(+)

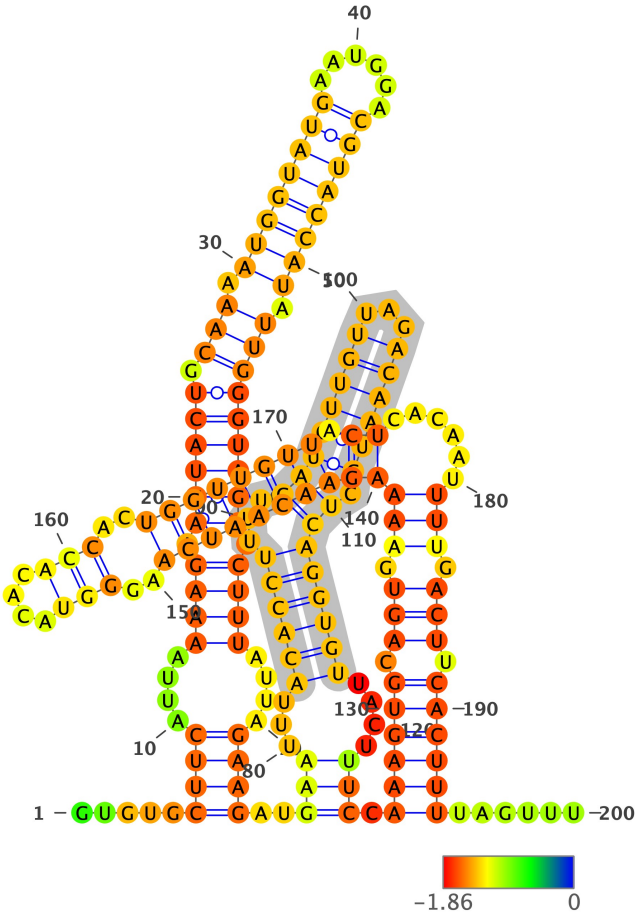
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 195 from nt 10928 to 10962 (nt 83 to 117)

```
5'-ACACCTTTTGATGTTGTTAGACAAUGCTCAGGUGU-3'
5'-((((((......((((.....)))).....))))))-3'
Motif MFE = -8.1; z-score = -1.73; 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 = -2.24; ED = 27.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

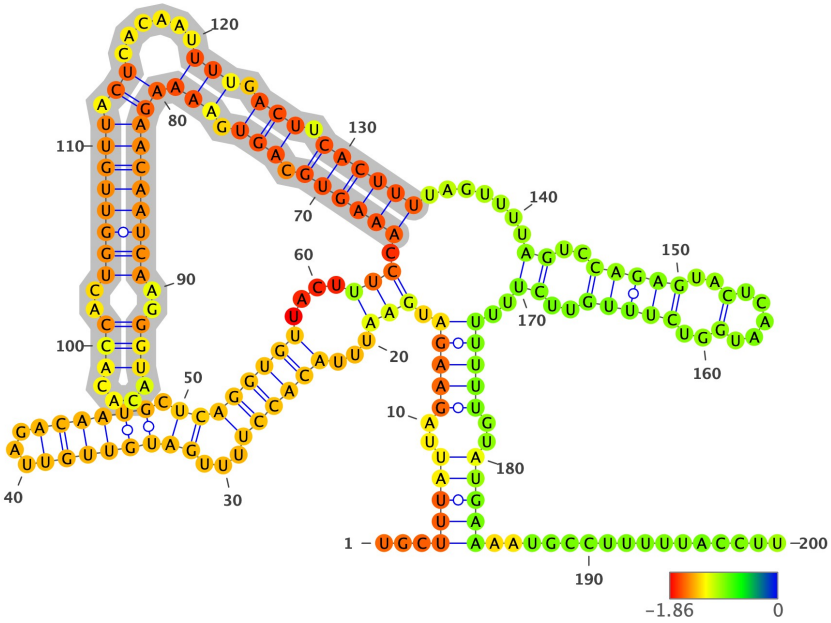
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 196 from nt 10971 to 11039 (nt 66 to 134)

```
5'-AAAGTGCAGTGAAAAGAACAATCAAGGGTACACACCACUGGUUGUUACUCACAATUUTGACUTCACUUU-3'
5'-((((((.(((..(((((((((((((..(........)..)))))))).))......))..))).))))))-3'
Motif MFE = -19.0; z-score = -3.66; ED = 4.8
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 10906 to 11105 (motif highlighted in silver):

```
5'-UGCUUUAUUAGAAGAUGAAUUUACACCUUUUGAUGUUGUUAGACAAUGCUCAGGUGUUACUUUCCAAAGUGCAGUGAAAAGAACAAUCAAGGGUACACACCACUGGUUGUU
ACUCACAAUUUUGACUUCACUUUUAGUUUUAGUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUU-3
5'-...(((((..(((((.(((...((((((...((((((((...))))))).))))))))....))).((((((.(((.((((((((((((..(((....)))..)))))))))
.)).....))).))).))))))).......((..(((((..(.....)..)))))..))..)))))..)))))................-3'
MFE = -38.2; z-score = -0.87; ED = 36.6
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

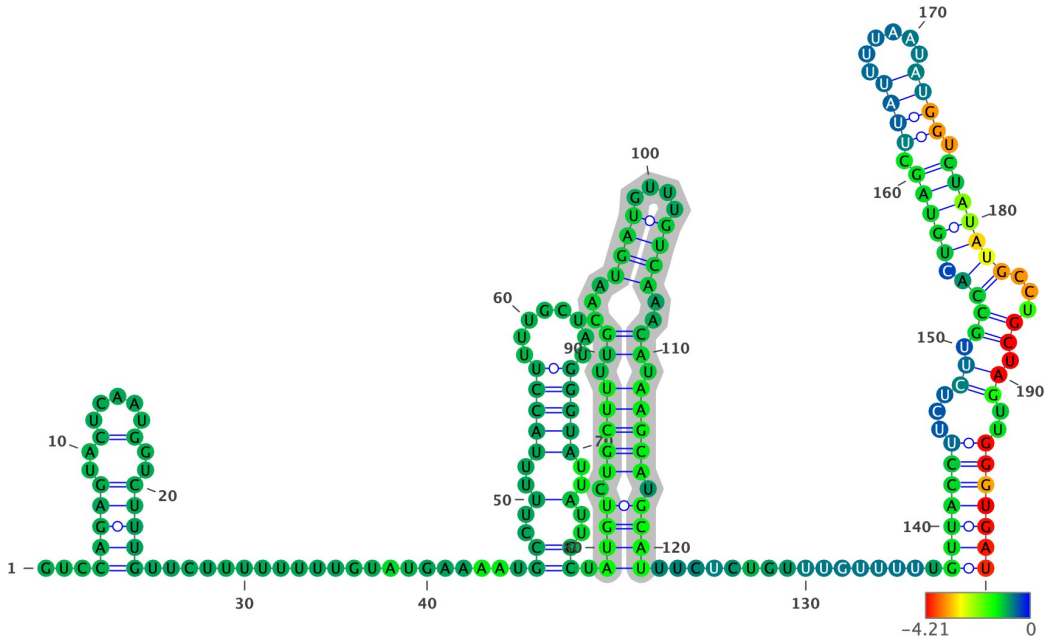
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 197 from nt 11126 to 11168 (nt 79 to 121)

```
5'-ATGTCTGCTTTTGCAATGATGTTTGUCAAACATAAGCATGCAU-3'
5'-((((.(((((......((((....)))).....))))).))))-3'
Motif MFE = -9.7; z-score = -1.99; ED = 7.49
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11048 to 11247 (motif highlighted in silver):

```
5'-GUCCAGAGUACUCAAUGGUCUUUGUUCUUUUUUUUGUAUGAAAAUGCCUUUUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAU
AAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAU-3
5'-...(((((..(.....)..)))))......................((..(..(((((........)))))..)..)).((((.(((((.((...((((....))))..)).
))))).))))................(((((((...((.((((.(((((.((((......)))).)))))))...)).))..)))))))-3'
MFE = -33.8; z-score = -2.03; ED = 35.33
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

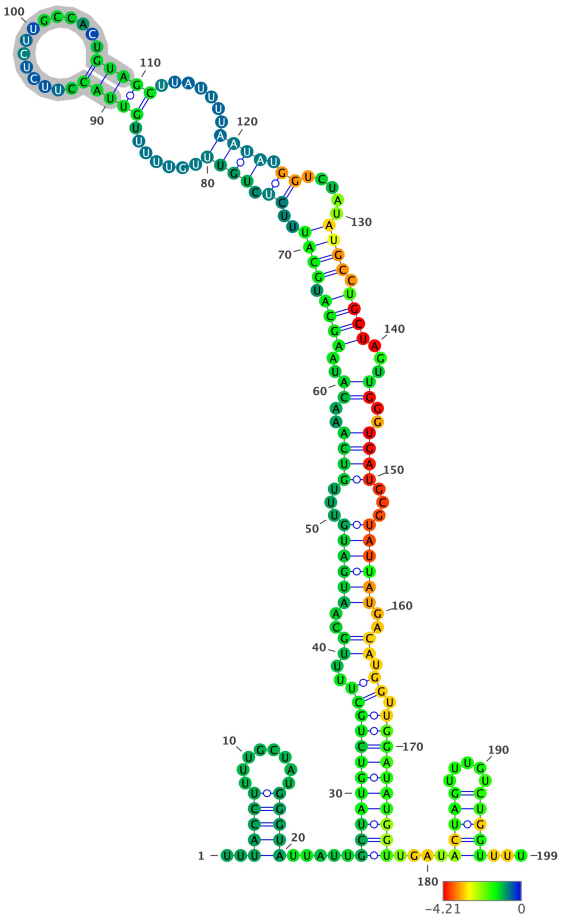
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 11187 to 11206 (nt 90 to 109)

```
5'-TACCTTCTCTTGCCACTGUA-3'
5'-(((..............)))-3'
Motif MFE = 0.0; z-score = 0.38; 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 11098 to 11296 (motif highlighted in silver):

```
5'-UUUACCUUUUGCUAUGGGUAUUAUUGCUAUGUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGC
UUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUU-3
5'-..(((((........)))))).....((((((((((((..((..((((((...(((((..((..((((.((((..((.((((.......(((((.............)))))
.......)))).))).....)))).))))...))..))))...)))))))..)).)).)))))))))))....(((((.....)))))).-3'
MFE = -38.3; z-score = -1.14; ED = 35.72
```

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(+)

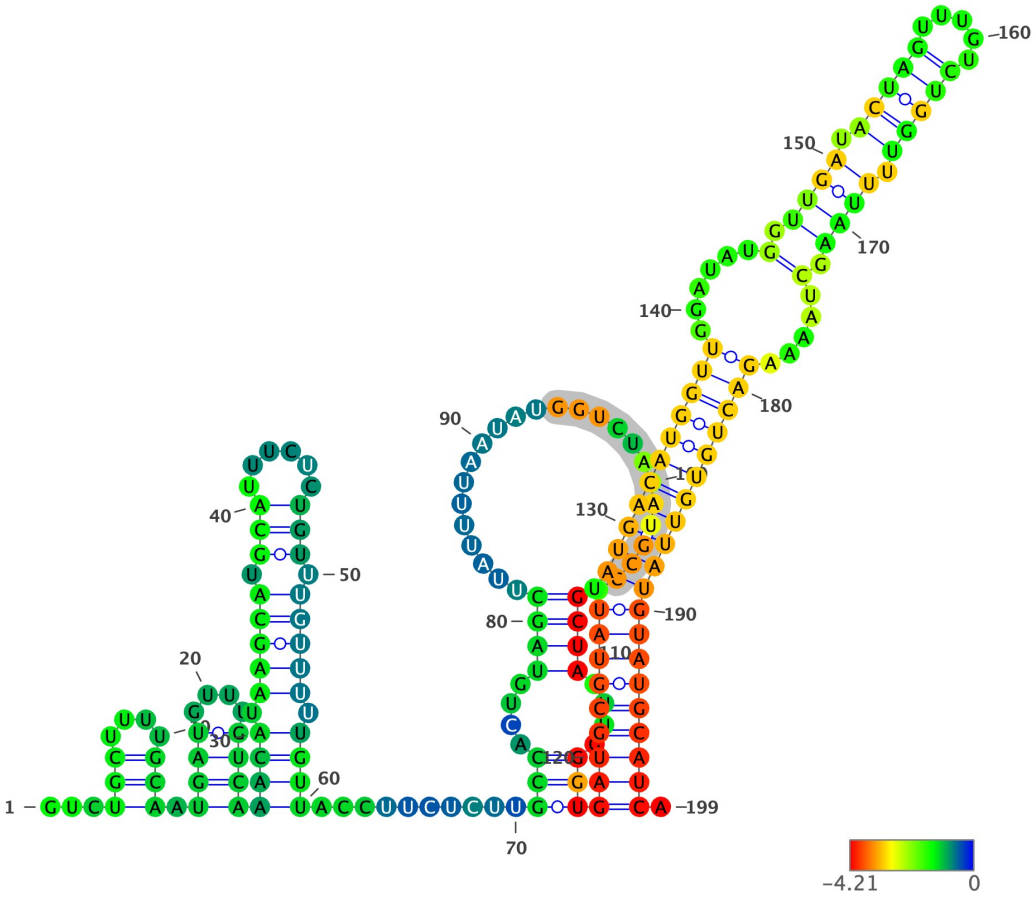
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 199 from nt 11221 to 11232 (nt 94 to 105)

```
5'-GGTCTATATGCC-3'
5'-(((......)))-3'
Motif MFE = -0.4; z-score = -1.59; ED = 1.51
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11128 to 11326 (motif highlighted in silver):

```
5'-GUCUGCUUUUGCAAUGAUGUUUGUCAAACAUAAGCAUGCAUUUCUCUGUUUGUUUUUGUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAG
UUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUUUAAGCUAAAAGACUGUGUUAUGUAUGCAUCA-3
5'-...(((....))).((((....))))((((.(((((.(((......))).))))).))))..........(((....((((.........................)))).
...)))(((((((((.(((((((((((......(.((((.(((((.....))))).)))).).....))))))))))))))))))).-3'
MFE = -49.6; z-score = -3.01; ED = 29.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

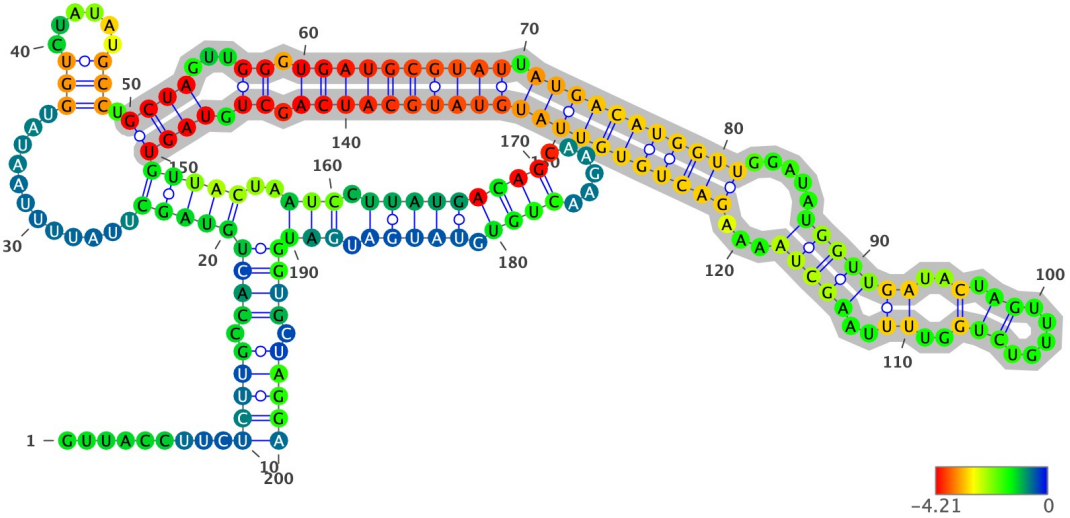
4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 200 from nt 11234 to 11334 (nt 50 to 150)

```
5'-GCTAGTTGGGTGATGCGTATTATGACATGGTTGGATATGGTTGATACTAGTTTGTCTGGTUUTAAGCTAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGU-3'

5'-((((...((.((((((((((.((((((((((.........((..(.........)..)).........)))))))))))))))))))))).)).))))-3'
Motif MFE = -37.5; z-score = -5.06; ED = 7.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11185 to 11384 (motif highlighted in silver):

```
5'-GUUACCUUCUCUUGCCACUGUAGCUUAUUUUAAUAUGGUCUAUAUGCCUGCUAGUUGGGUGAUGCGUAUUAUGACAUGGUUGGAUAUGGUUGAUACUAGUUUGUCUGGUUU
UAAGCUAAAAGACUGUGUUAUGUAUGCAUCAGCUGUAGUGUUACUAAUCCUUAUGACAGCAAGAACUGUGUAUGAUGAUGGUGCUAGGA-3
5'-.........(((((.(((((((((.............(((......))).(((((...((.((((((((((.(((((((((((.....(((((((..(.((.....)))..))
..)))))...)))))))))))))))))))).)).)))))))))..(((.(((((((((.....)))))).)))))).)))))))).))))-3'
MFE = -46.8; z-score = -2.36; ED = 33.92
```

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(+)

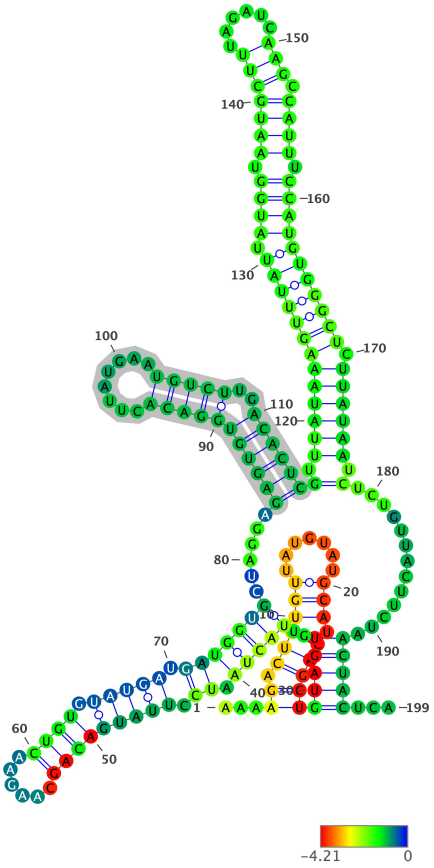
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 201 from nt 11385 to 11416 (nt 84 to 115)

```
5'-GAGTGTGGACACTTATGAAUGUCUTGACACUC-3'
5'-(((((((((((.........)))))..))))))-3'
Motif MFE = -10.6; z-score = -3.02; 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 = -0.6; ED = 20.34
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

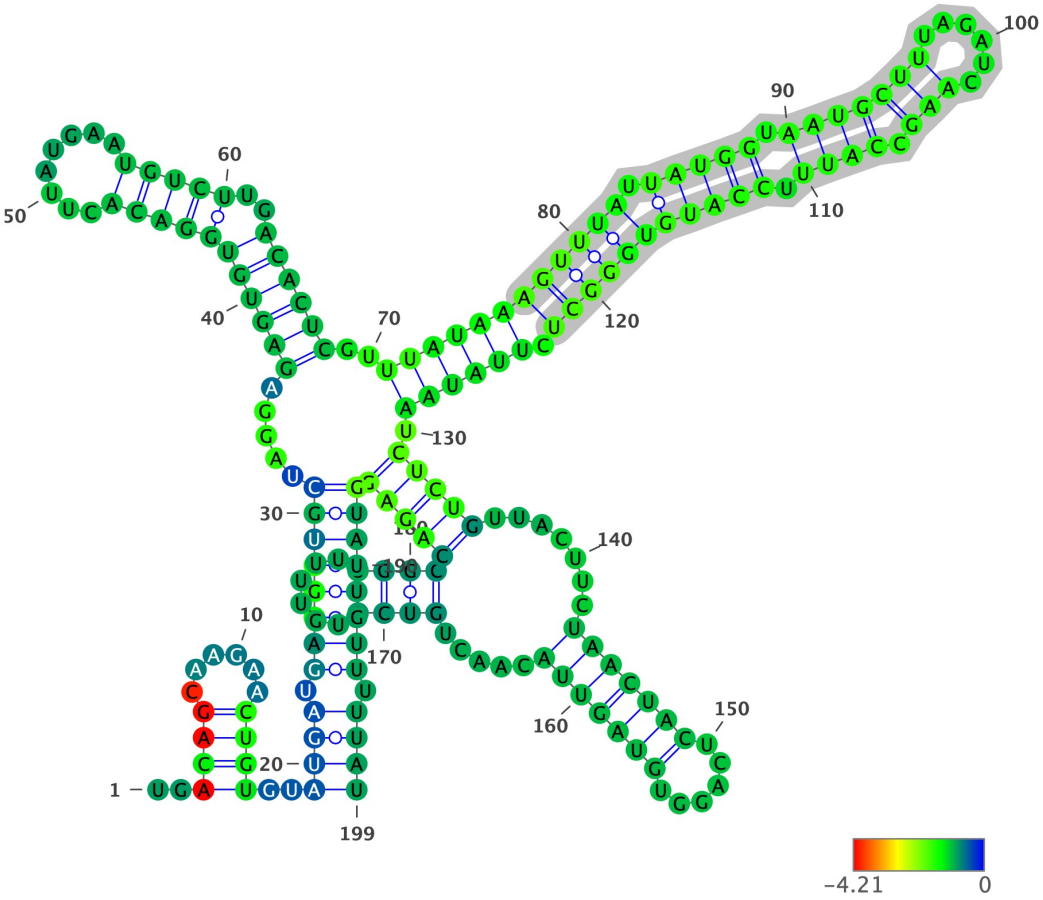
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 202 from nt 11425 to 11470 (nt 77 to 122)

```
5'-AGTTTATTATGGTAATGCTTTAGATCAAGCCAUUTCCAUGTGGGCU-3'
5'-(((((...((((((.(((((((.....))).))))).))))))..))))-3'
Motif MFE = -11.4; z-score = -2.29; 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 = -1.12; 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(+)

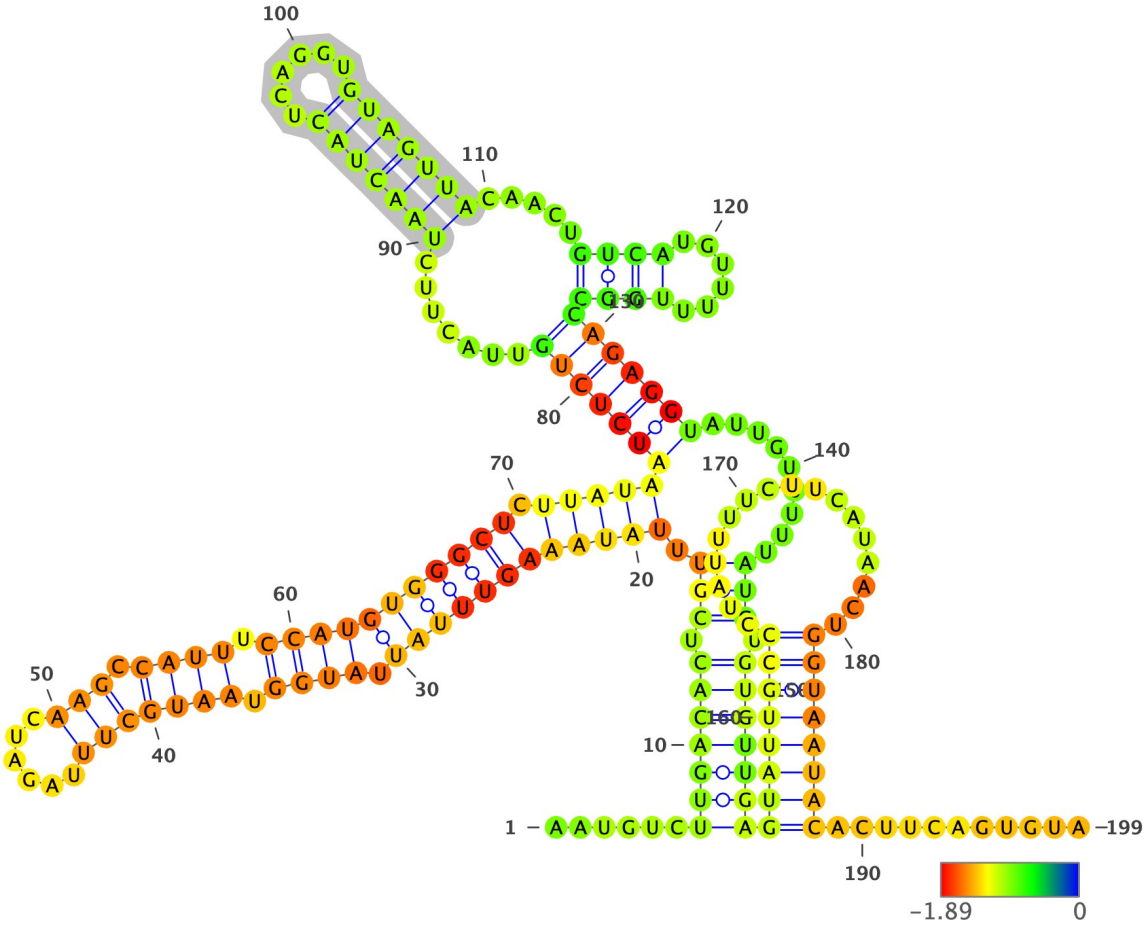
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 203 from nt 11491 to 11510 (nt 90 to 109)

```
5'-TAACTACTCAGGTGUAGUUA-3'
5'-(((((((.....)))))))-3'
Motif MFE = -6.2; z-score = -5.01; 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 = -1.72; ED = 20.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

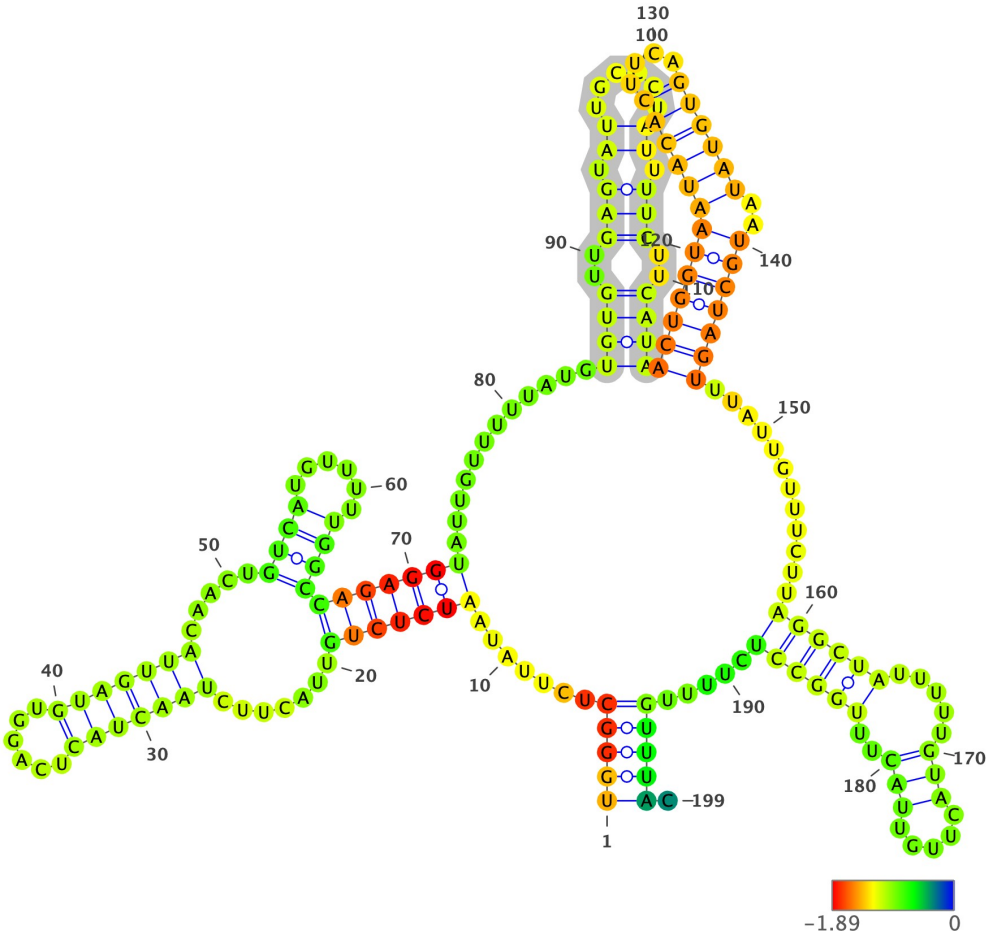
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 204 from nt 11549 to 11578 (nt 85 to 114)

```
5'-TGTGTTGAGTATTGCCCTATTUUCTTCAUA-3'
5'-(((((..(((.............))))..))))-3'
Motif MFE = -2.6; z-score = -0.7; ED = 2.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11465 to 11663 (motif highlighted in silver):

```
5'-UGGGCUCUUAUAAUCUCUGUUACUUCUAACUACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUC
AUAACUGGUAAUACACUUCAGUGUAUAAUGCUAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUAC-3
5'-(((((.......(((((((.......(((((((.......)))))))).....((((......))))))))))).............((((..((((.((......)).)))).))
)))(((((((((((((....)))))))..)))))))............((((((.....(((.....)))).)))))).....))))).-3'
MFE = -38.5; z-score = -2.33; ED = 35.4
```

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(+)

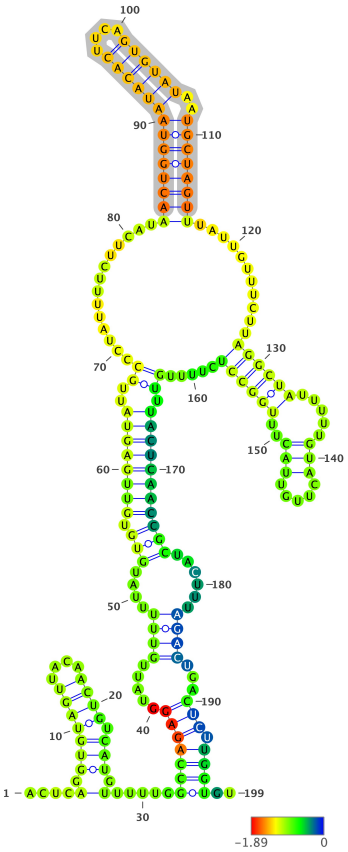
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 205 from nt 11579 to 11610 (nt 84 to 115)

```
5'-ACTGGTAATACACTTCAGUGUAUAAUGCUAGU-3'
5'-(((((((((((((....))))))..)))))))-3'
Motif MFE = -10.9; z-score = -3.75; ED = 1.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11496 to 11694 (motif highlighted in silver):

```
5'-ACUCAGGUGUAGUUACAACUGUCAUGUUUUUGGCCAGAGGUAUUGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGC
UAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGGCCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGU-3
5'-....(.(((((((....)))).))).).....(((((((.....((((....(((.((((((((..((..............((((((((((((((....))))))..)))
)))))..........((((((.....(((.....)))..))))))).....)).)))))))))))).....))))...))).))))..-3'
MFE = -42.0; z-score = -2.05; ED = 31.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

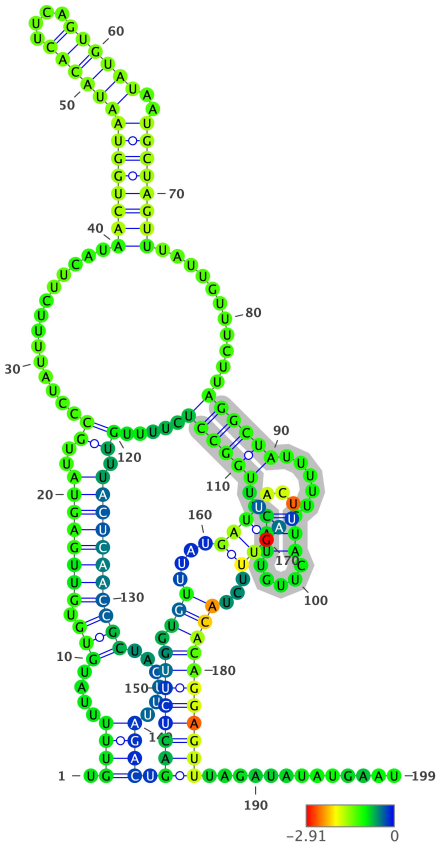
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 206 from nt 11624 to 11651 (nt 86 to 113)

```
5'-GGCTATTTTTGTACTTGTTACTTTGGCC-3'
5'-((((....................))))-3'
Motif MFE = -4.4; z-score = -1.41; ED = 1.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11539 to 11737 (motif highlighted in silver):

```
5'-UGUUUUUAUGUGUGUUGAGUAUUGCCCUAUUUUCUUCAUAACUGGUAAUACACUUCAGUGUAUAAUGCUAGUUUAUUGUUUCUUAGGCUAUUUUUGUACUUGUUACUUUGG
CCUCUUUUGUUUACUCAACCGCUACUUUAGACUGACUCUUGGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAU-3
5'-.((((....(((.(((((((((..((..............((((((((((((((....))))))..))))))))...........((((((.....(((.....)))..)))
)))).....)).))))))))))).....)))).((((((((.(((....((((....))))...)))))))))))..............-3'
MFE = -41.8; z-score = -2.48; ED = 23.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

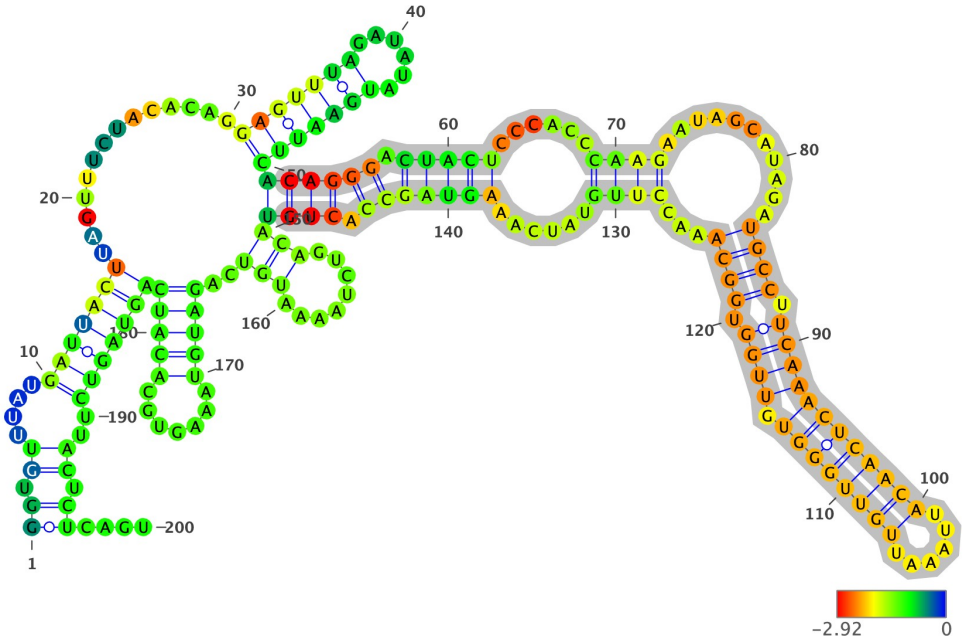
4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 207 from nt 11741 to 11837 (nt 52 to 148)

```
5'-CAGGGACTACTCCCACCCAAGAATAGCATAGATGCCTTCAAACTCAACATTAAATUGUUGGGUGUUGGTGGCAAACCTTGTATCAAAGTAGCCACUG-3'

5'-((.............................((((.(((((((((((.....)))))))).)))).))))......................))-3'
Motif MFE = -27.6; z-score = -2.71; 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 11690 to 11889 (motif highlighted in silver):

```
5'-GGUGUUUAUGAUUACUUAGUUUCUACACAGGAGUUUAGAUAUAUGAAUUCACAGGGACUACUCCCACCCAAGAAUAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUG
GGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGU-3
5'-((.((....(((((((.............(((((((......)))))))((((((.(((((......((((...........((((.(((((((((((.....)))))
))).)))).))))...))))......))))))).))))(((........)))..(((((.......))))))))))))..)).)).....-3'
MFE = -45.1; z-score = -1.29; ED = 22.41
```

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(+)

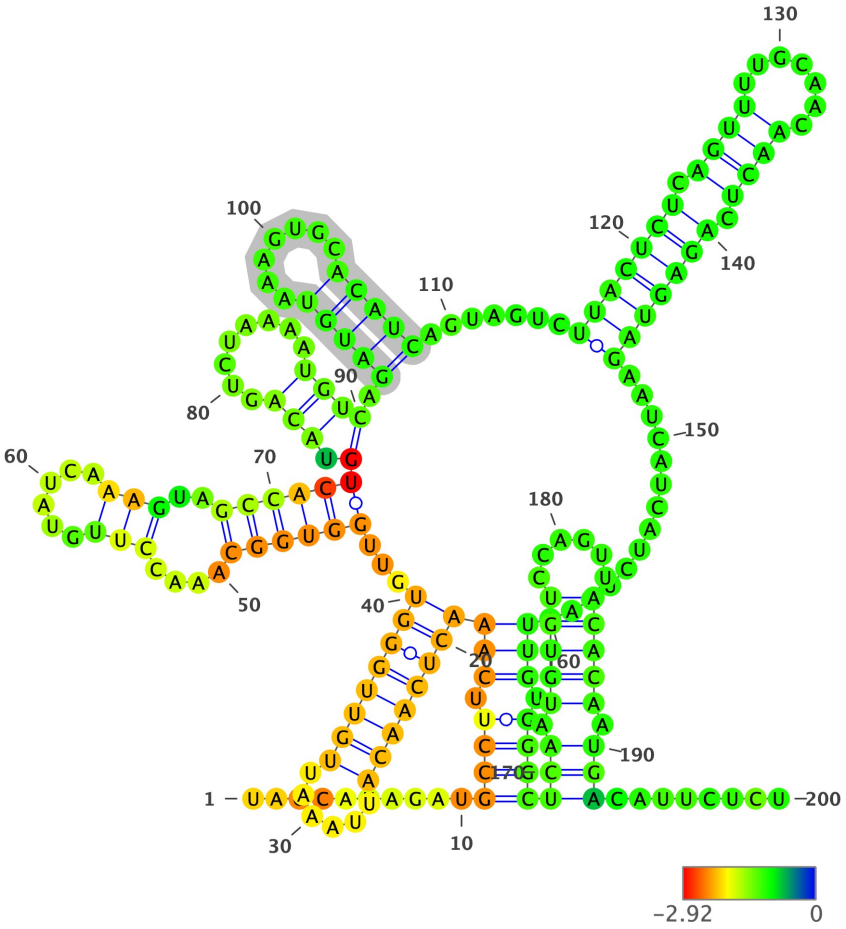
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 208 from nt 11855 to 11871 (nt 92 to 108)

```
5'-GATGTAAAGTGCACAUC-3'
5'-((((.........))))-3'
Motif MFE = -2.1; z-score = -2.3; ED = 1.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11764 to 11963 (motif highlighted in silver):

```
5'-UAGCAUAGAUGCCUUCAAACUCAACAUUAAAUUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGU
AGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCU-3
5'-..........((((.(((((((((((......))))))))...((((((....(((......)))..))))))(.(((........)))).(((((.......)))))...
....(((((((.((((.......)))).)))))))..............))).))))(((.(((((......))))).))).........-3'
MFE = -45.8; z-score = -1.95; ED = 42.42
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

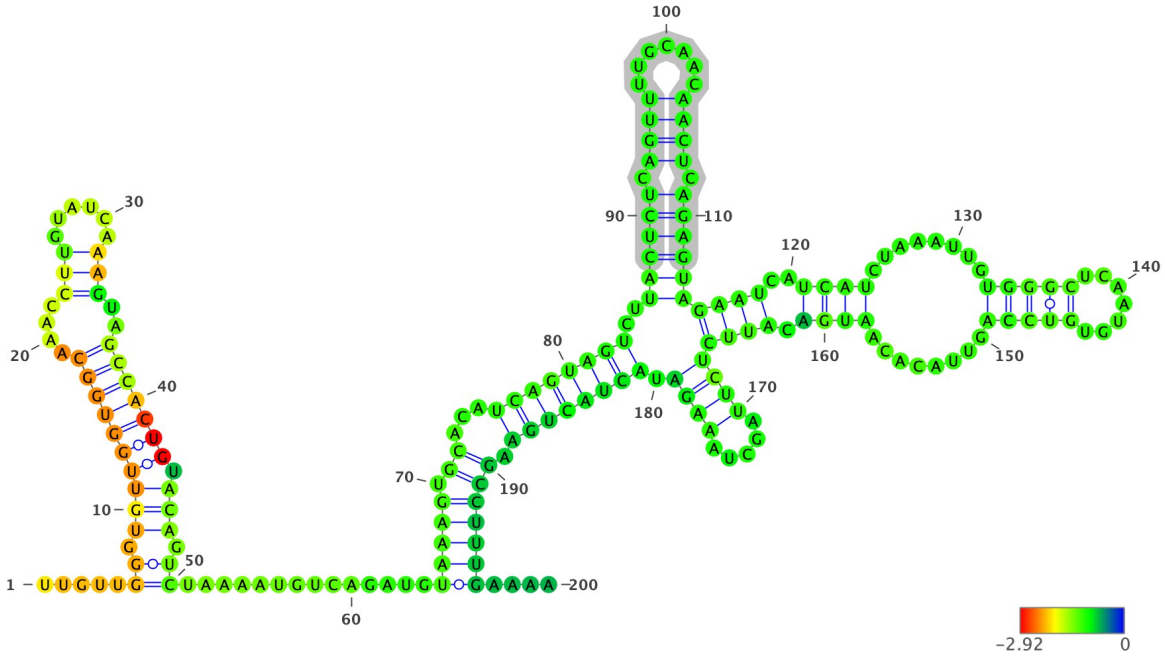
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 209 from nt 11882 to 11906 (nt 88 to 112)

```
5'-CTCTCAGTTTTGCAACAACUCAGAG-3'
5'-((((.((((.......)))).))))-3'
Motif MFE = -4.0; z-score = -1.84; ED = 1.18
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11795 to 11994 (motif highlighted in silver):

```
5'-UUGUUGGGUGUUGGUGGCAAACCUUGUAUCAAAGUAGCCACUGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGA
GUAGAAUCAUCAUCUAAAUUGUGGGCUCAAUGUGUCCAGUUACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAA-3
5'-.....((.(((((((((((....(((.....)))..)))))))).))).))..............(((((.((...((((((((..((((((.((((.......)))).)))
)))((((..((((........(((((.......)))))........)))).))))((((.....)))).))))))))).)))))))....-3'
MFE = -45.6; z-score = -1.15; ED = 33.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

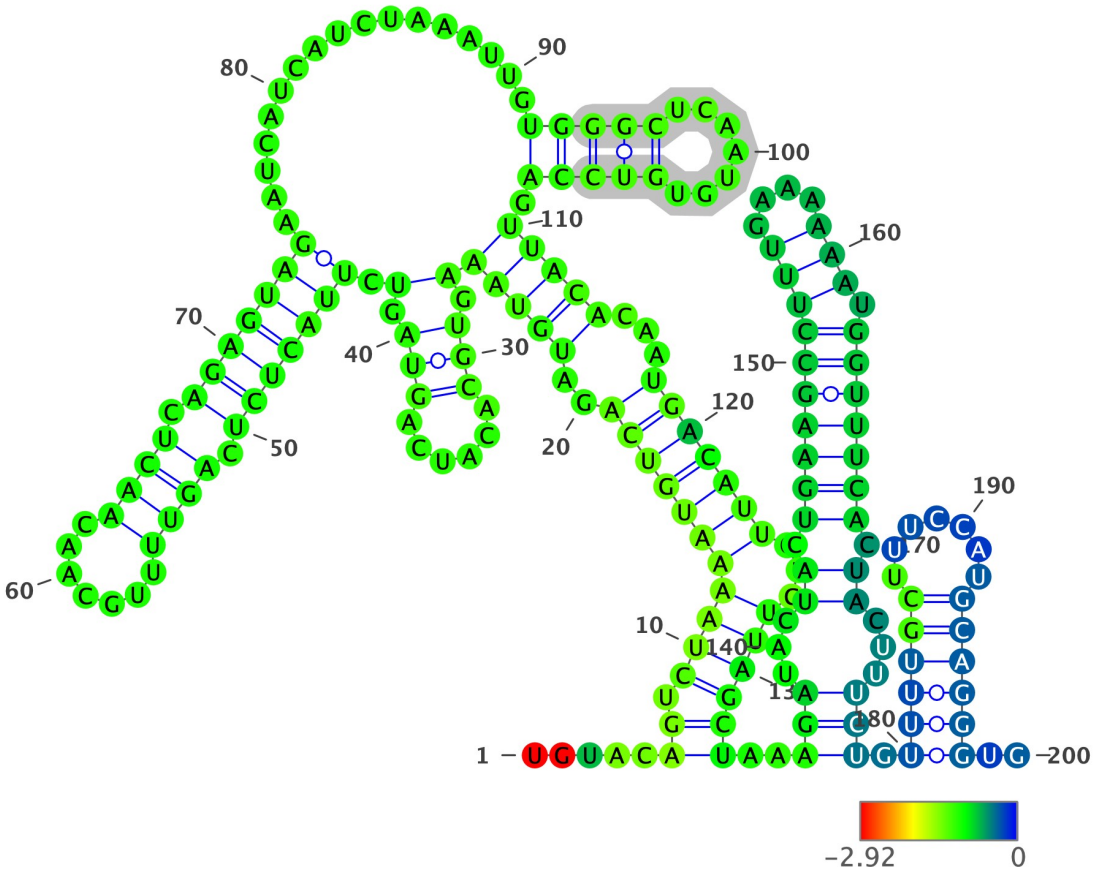
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 210 from nt 11929 to 11941 (nt 94 to 106)

```
5'-GGCTCAATGTGUC-3'
5'-(((.......)))-3'
Motif MFE = -0.1; z-score = 0.4; ED = 1.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 11836 to 12035 (motif highlighted in silver):

```
5'-UGUACAGUCUAAAAUGUCAGAUGUAAAGUGCACAUCAGUAGUCUUACUCUCAGUUUUGCAACAACUCAGAGUAGAAUCAUCAUCUAAAAUUGUGGGCUCAAUGUGUCCAGUU
ACACAAUGACAUUCUCUUAGCUAAAGAUACUACUGAAGCCUUUGAAAAAAUGGUUUCACUACUUUCUGUUUUGCUUUCCAUGCAGGGUG-3
5'-.....((.(((((((((((..((((((.(((.....))).).(((((((.(((.....)))).)))))))).................(((((.....)))))).))
)))...)))))))...))))))..(((...((.((((((((((....))).)))))))..))...))).((((((.....))))))..-3'
MFE = -38.8; z-score = -0.69; ED = 44.04
```

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, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

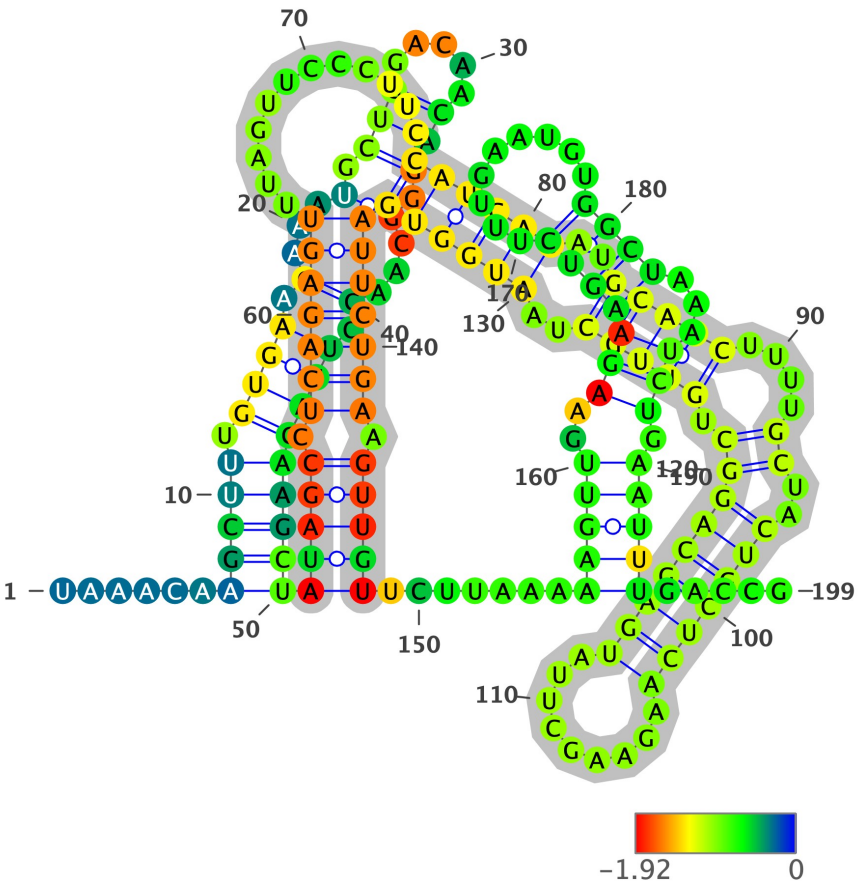
4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 12095 to 12192 (nt 51 to 148)

```
5'-ATAGCCTCAGAGTTTAGTTCCCTTCCATCATATGCAGCTTTTGCTACTGCTCAAGAAGCTTATGAGCAGGCTGUUGCTAAUGGUGAUUCUGAAGUUGU-3'

5'-(.(((.(((((((.............((((((..(((((....((..((((((...........))))))))).)))))..))))))))))))).))).)-3'
Motif MFE = -29.1; z-score = -2.33; ED = 8.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12045 to 12243 (motif highlighted in silver):

```
5'-UAAACAAGCUUUGUGAAGAAAUGCUGGACAACAGGGCAACCUUACAAGCUAUAGCCUCAGAGUUUAGUUCCCUUCCAUCAUAUGCAGCUUUUGCUACUGCUCAAGAAGCUU
AUGAGCAGGCUGUUGCUAAUGGUGAUUCUGAAGUUGUUCUUAAAAAGUUGAAGAAGUCUUUGAAUGUGGCUAAAUCUGAAUUUGACCG-3
5'-......(((((.((((.(...(.(((.....))).)...).)))))))))(((((.(((((((.............((((((..(((((....((..(((((((........
.)))))))))).)))))..))))))))))))).)))))).......(((((..(((((((.........))))...))).)))))).....-3'
MFE = -43.8; z-score = -0.36; ED = 27.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

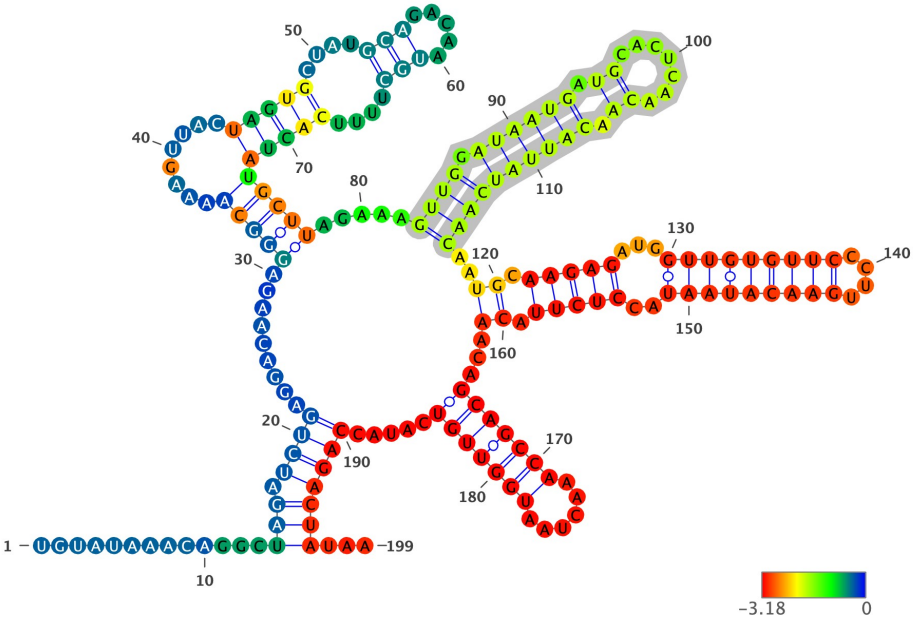
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 212 from nt 12382 to 12415 (nt 83 to 116)

```
5'-GTTGGATAATGATGCACTCAACAACAUUAUCAAC-3'
5'-((((.((((((.((.......)).))))))))))-3'
Motif MFE = -6.3; z-score = -2.9; 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 = -2.19; ED = 26.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

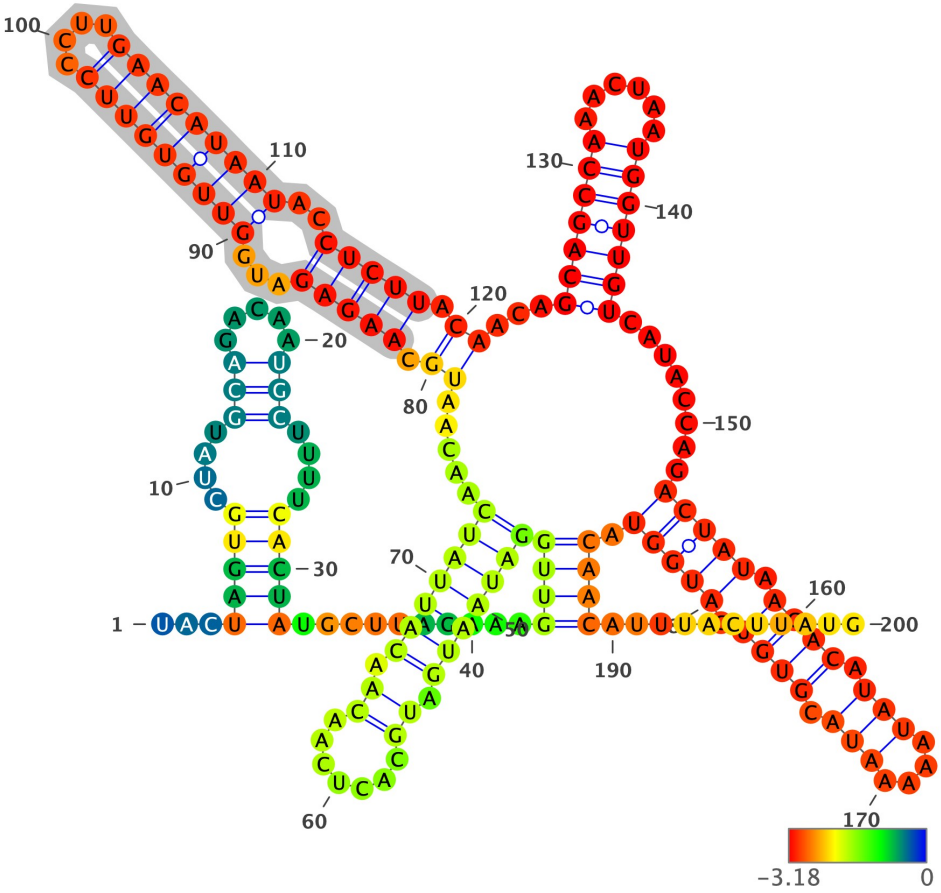
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 213 from nt 12421 to 12457 (nt 82 to 118)

```
5'-AAGAGATGGTTGTGTTCCCTTGAACAUAAUACCUCUU-3'
5'-((((((...((((((((((....))))))))))..))))))-3'
Motif MFE = -11.7; z-score = -3.47; ED = 5.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12340 to 12539 (motif highlighted in silver):

```
5'-UACUAGUGCUAUGCAGACAAUGCUUUUCACUAUGCUUAGAAAGUUGGAUAAUGAUGCACUCAACAACAUUAUCAACAAUGCAAGAGAUGGUUGUGUUCCCUUGAACAUAAU
ACCUCUUACAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUG-3
5'-...((((((....(((.....)))....)))))).........((((((((((.((.......)).)))))))).....((.((((((...((((((((((....))))))))))
..))))))..))...(((((((.....)))))))........((((.((((.(((....))).)))).)))))..))))..........-3'
MFE = -46.4; z-score = -3.78; ED = 16.72
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

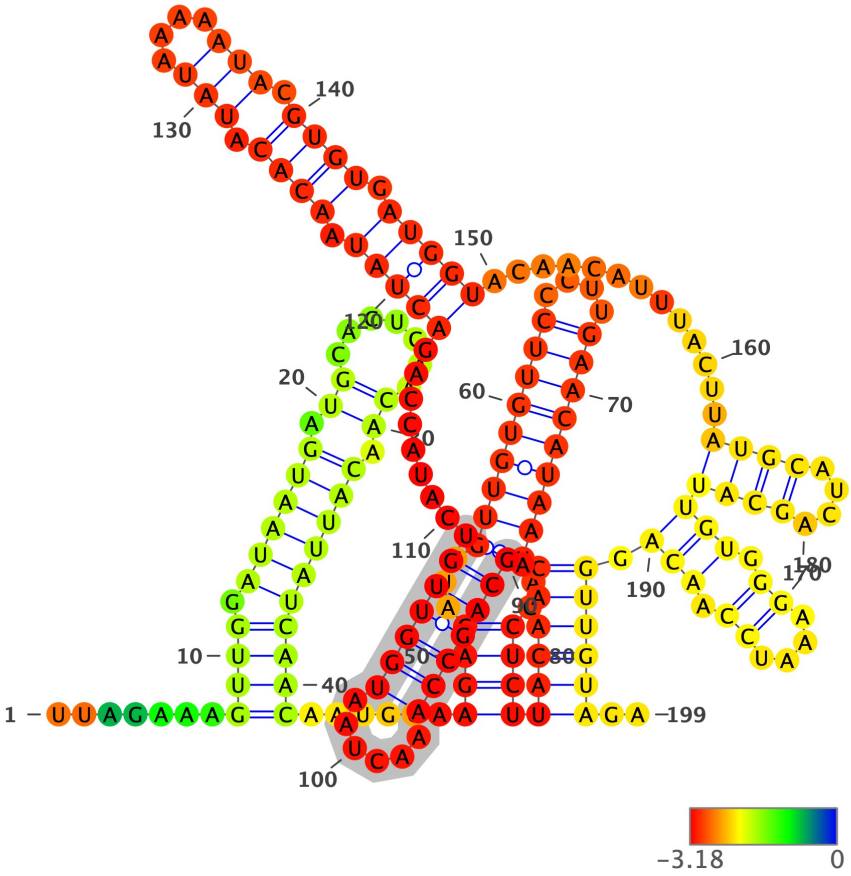
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 214 from nt 12464 to 12483 (nt 90 to 109)

```
5'-GCAGCCAAACTAAUGGUUGU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -7.5; z-score = -3.56; 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 = -3.05; 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(+)

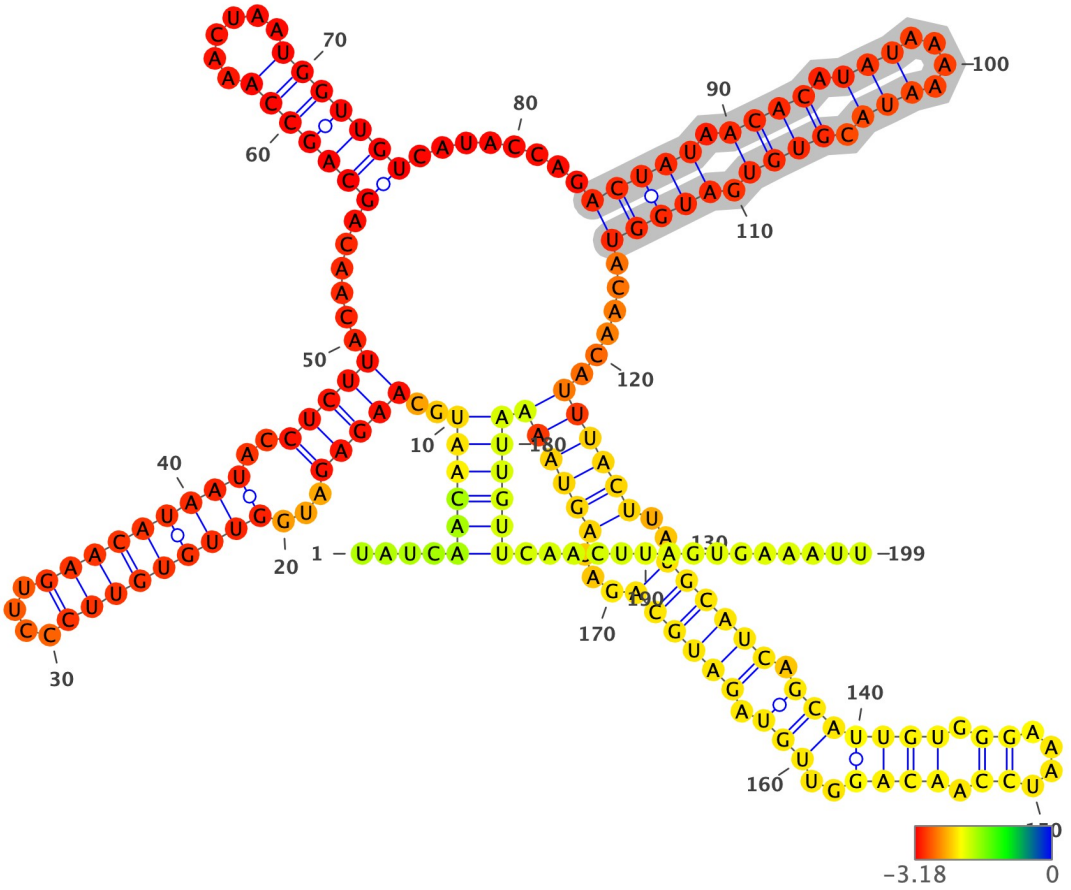
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 215 from nt 12492 to 12523 (nt 84 to 115)

```
5'-ACTATAACACATATAAAAATACGUGUGAUGGU-3'
5'-(((((.((((............)))).)))))-3'
Motif MFE = -6.6; z-score = -2.8; 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 = -3.65; 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(+)

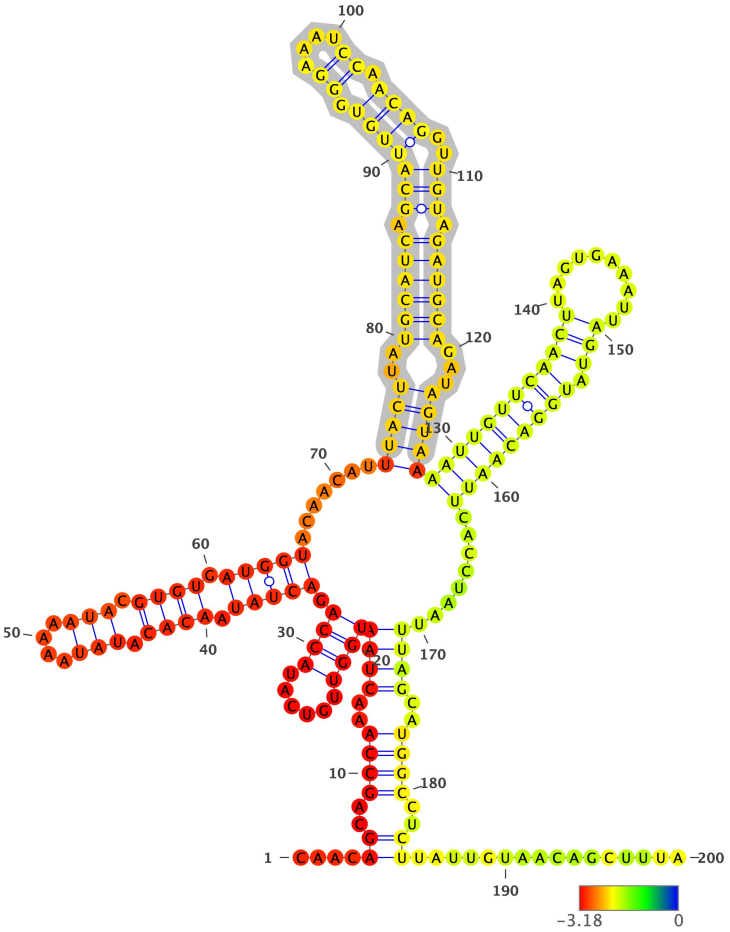
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 216 from nt 12532 to 12584 (nt 74 to 126)

```
5'-TACTTATGCATCAGCATTGTGGGAAATCCAACAGGTUGUAGAUGCAGATAGUA-3'
5'-((((..((((((.(((((((.((....)).))))..))).))))))...))))-3'
Motif MFE = -15.1; z-score = -2.71; ED = 7.87
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12459 to 12658 (motif highlighted in silver):

```
5'-CAACAGCAGCCAAACUAAUGGUUGUCAUACCAGACUAUAACACAUAUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUG
UAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUA-3
5'-....((..((((..((((((((.....)))).(((((.((((.(((....))).)))).)))))).......(((((..((((((.(((((((.((....)).))))..))
).))))))...)))))((((((((((((.........))).))))))))).........))))..))))..)).................-3'
MFE = -44.0; z-score = -2.4; ED = 25.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

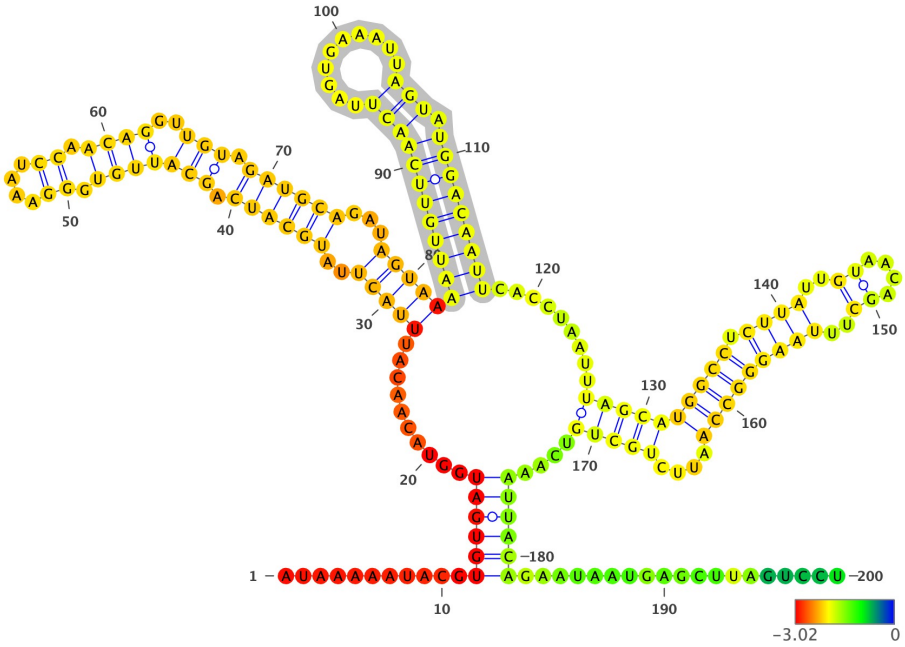
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 217 from nt 12586 to 12620 (nt 83 to 117)

```
5'-AATTGTTCAACTTAGTGAAATTAGUAUGGACAAUU-3'
5'-((((((((((((.........))).)))))))))-3'
Motif MFE = -7.4; z-score = -2.74; ED = 4.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12504 to 12703 (motif highlighted in silver):

```
5'-AUAAAAAUACGUGUGAUGGUACAACAUUUACUUAUGCAUCAGCAUUGUGGGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGG
ACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGCCAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCU-3
5'-...........((((((..........((((((..((((((.(((((((.((....)).)))))..)))).))))))...))))))((((((((((.........)))).)))
))))))).........((((((((((.((((..((....))..))))))))).....))))))....))))))...................-3'
MFE = -45.3; z-score = -1.7; 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(+)

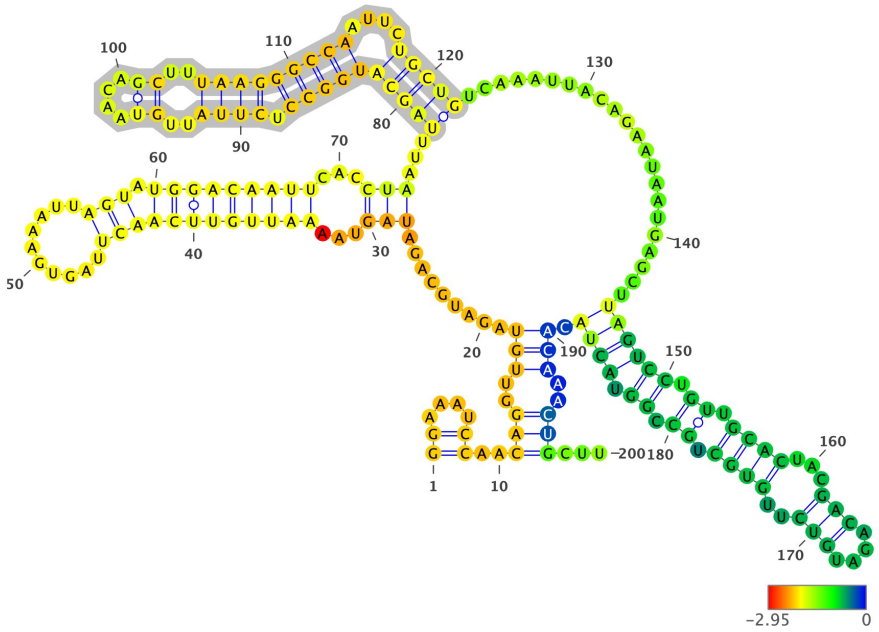
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 218 from nt 12630 to 12674 (nt 78 to 122)

```
5'-TAGCATGGCCTCTTATTGTAACAGCTTUAAGGGCCAATTCUGCTG-3'
5'-(.((((((((.((((..(......)..))))))))).....))).)-3'
Motif MFE = -16.7; z-score = -4.13; 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 12553 to 12752 (motif highlighted in silver):

```
5'-GGAAAUCCAACAGGUUGUAGAUGCAGAUAGUAAAAUUGUUCAACUUAGUGAAAUUAGUAUGGACAAUUCACCUAAUUUAGCAUGGCCUCUUAUUGUAACAGCUUUAAGGGC
CAAUUCUGCUGUCAAAUUACAGAAUAAUGAGCUUAGUCCUGUUGCACUACGACAGAUGUCUUGUGCUGCCGGUACUACACAAACUGCUU-3
5'-((....))..(((..(((.........(((...(((((((((((((.........))).)))))))))...)))...((((((((((.((((..((....))..)))))))
))....)))))......................((((((.((.((((...(((....)))..)))).)).)).)))).)))..)))...-3'
MFE = -45.8; z-score = -2.51; ED = 42.72
```

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(+)

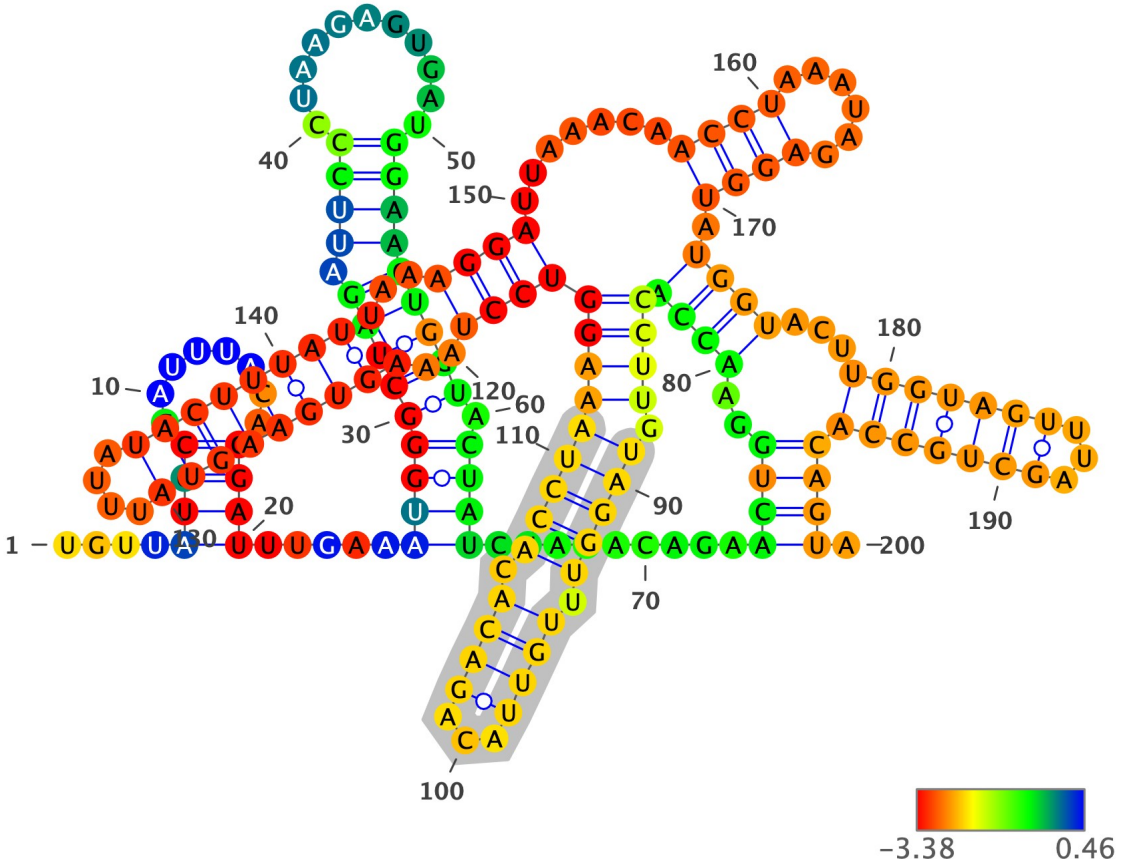
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 219 from nt 12904 to 12926 (nt 89 to 111)

```
5'-TAGGTTTGTTACAGACACACCUA-3'
5'-(((((.(((((...))))).)))))-3'
Motif MFE = -6.2; z-score = -3.53; 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 12816 to 13015 (motif highlighted in silver):

```
5'-UGUUAUCCGAUUUACAGGAUUUGAAAUGGGCUAGAUUCCCUAAGAGUGAUGGAACUGGUACUAUCUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUA
AAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUA-3
5'-....((((........))))....(((((((((.((((..........))))))))).))))........((((..(((((((((.(((((.((((...)))).)))))
))))(((((..((((((((((....))))))))))..))))).....((((.....)))).))))...(((((((...)))))))))).-3'
MFE = -49.6; z-score = -2.38; ED = 37.73
```

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(+)

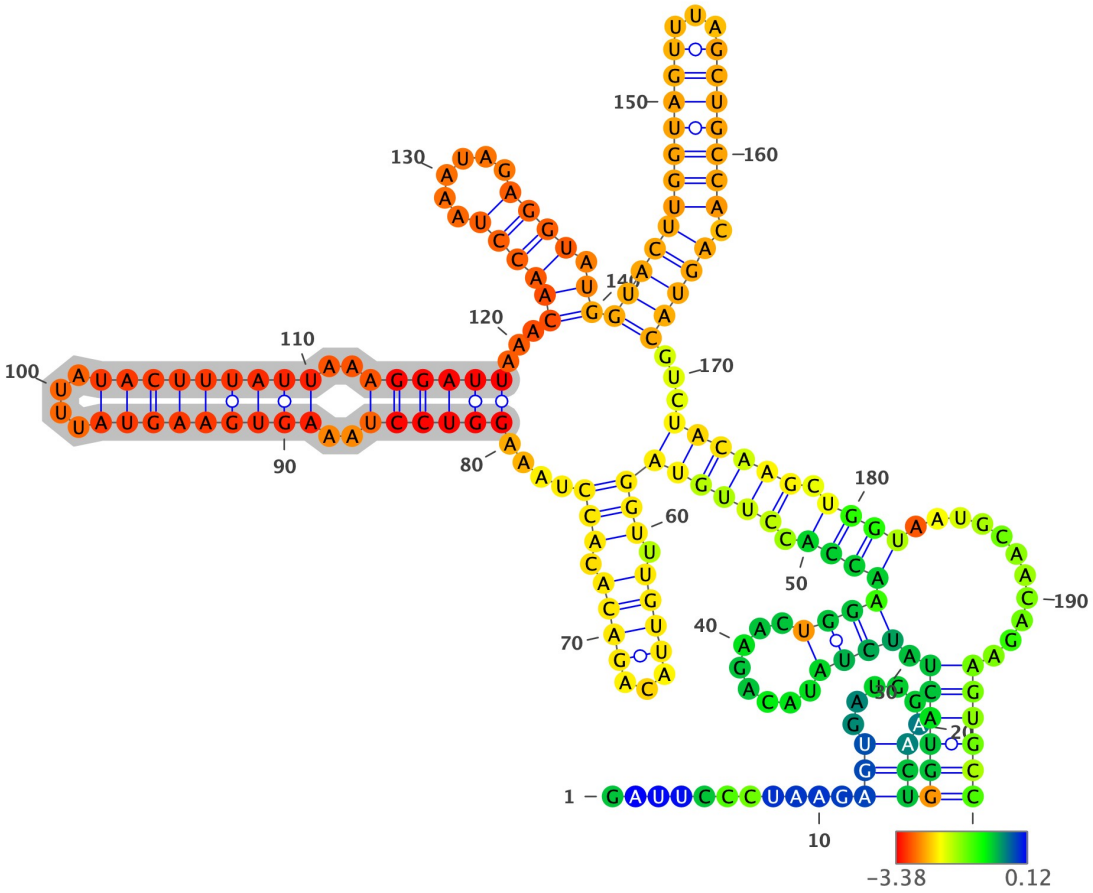
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 220 from nt 12929 to 12966 (nt 81 to 118)

```
5'-GGTCCTAAAGTGAAGTATTTAUACUUUAUUAAAGGAUU-3'
5'-((((((...((((((((((....))))))))))...))))))-3'
Motif MFE = -11.9; z-score = -3.93; 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 = -3.06; ED = 24.37
```

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(+)

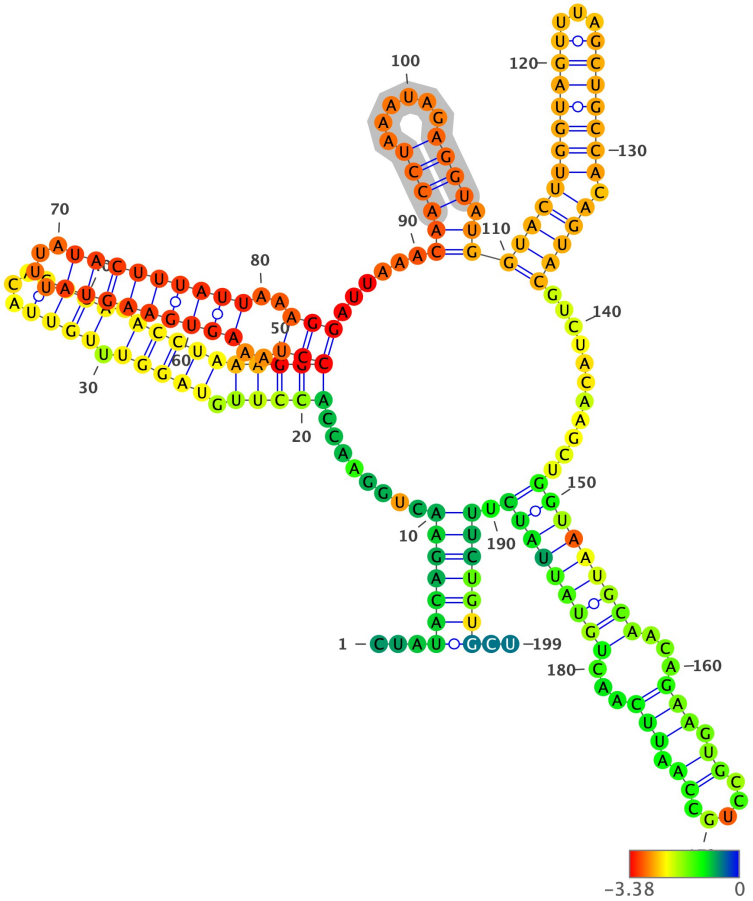
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 221 from nt 12972 to 12985 (nt 93 to 106)

```
5'-ACCTAAATAGAGGU-3'
5'-((((......))))-3'
Motif MFE = -2.2; z-score = -6.89; ED = 0.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 12880 to 13078 (motif highlighted in silver):

```
5'-CUAUACAGAACUGGAACCACCUUGUAGGUUUGUUACAGACACACCUAAAGGUCCUAAAGUGAAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGU
ACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCCAAUUCAACUGUAUUAUCUUUCUGUGCU-3
5'-...(((((((.........(((((.(((((.((((...)))).))))))))))(((..((((((((((....)))))))))..)))......((((((......)))).))((
((((((((((...)))))))).)))))...........((((((((...(((.((.....)).)))...))))))))).)))))))..-3'
MFE = -55.3; z-score = -4.09; ED = 29.18
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 266-13468(+)

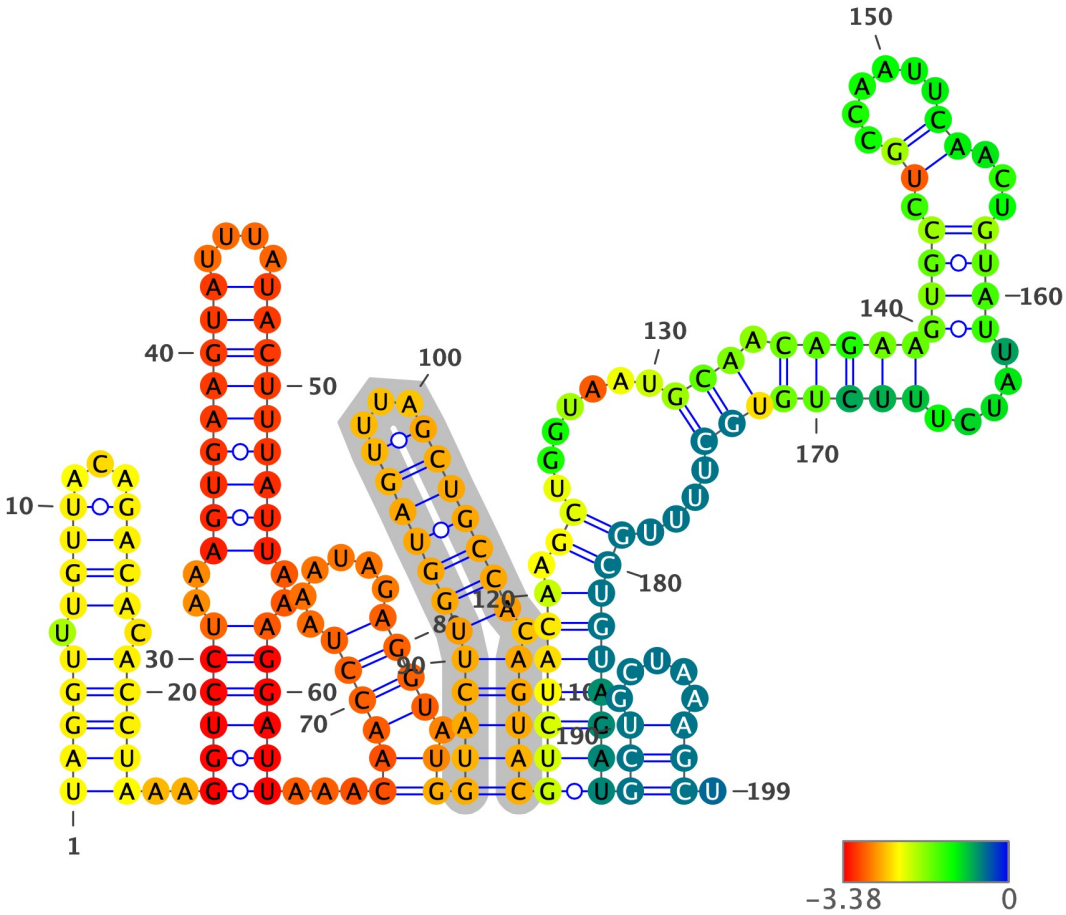
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 199--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 222 from nt 12989 to 13016 (nt 86 to 113)

```
5'-GTACTTGGTAGTTTAGCUGCCACAGUAC-3'
5'-((((((((((.......))))).)))))-3'
Motif MFE = -12.5; z-score = -4.05; 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 = -3.71; 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(+)

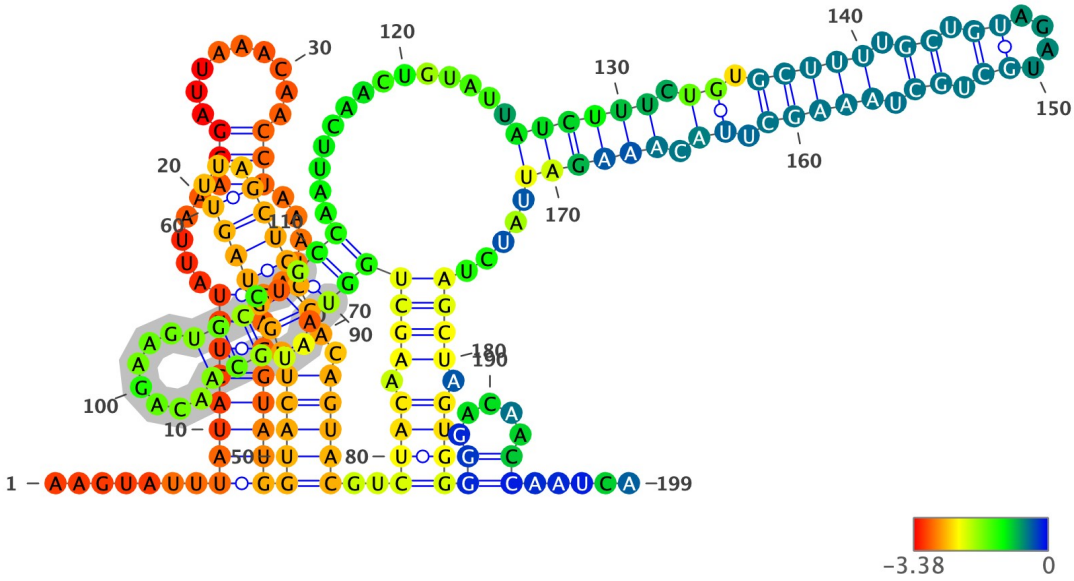
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 223 from nt 13030 to 13049 (nt 90 to 109)

```
5'-TAATGCAACAGAAGTGCCTG-3'
5'-(..................)-3'
Motif MFE = -0.8; z-score = 0.17; 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 12941 to 13139 (motif highlighted in silver):

```
5'-AAGUAUUUAUACUUUAUUAAAGGAUUAAACAACCUAAAUAGAGGUAUGGUACUUGGUAGUUUAGCUGCCACAGUACGUCUACAAGCUGGUAAUGCAACAGAAGUGCCUGCC
AAUUCAACUGUAUUAUCUUUCUGUGCUUUUGCUGUAGAUGCUGCUAAAGCUUACAAAGAUUAUCUAGCUAGUGGGGGACAACCAAUCA-3
5'-.......(((((((((.....(((.........))).....)))))))))((((((((((((...)))))))).))))..((((.(((((((((..(((.......))).)))))
.............((((((.(.((((((.((.((....)).)).)))))).)).)))))).....))))).)))))((.....)).....-3'
MFE = -45.6; z-score = -1.87; ED = 32.39
```

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(+)

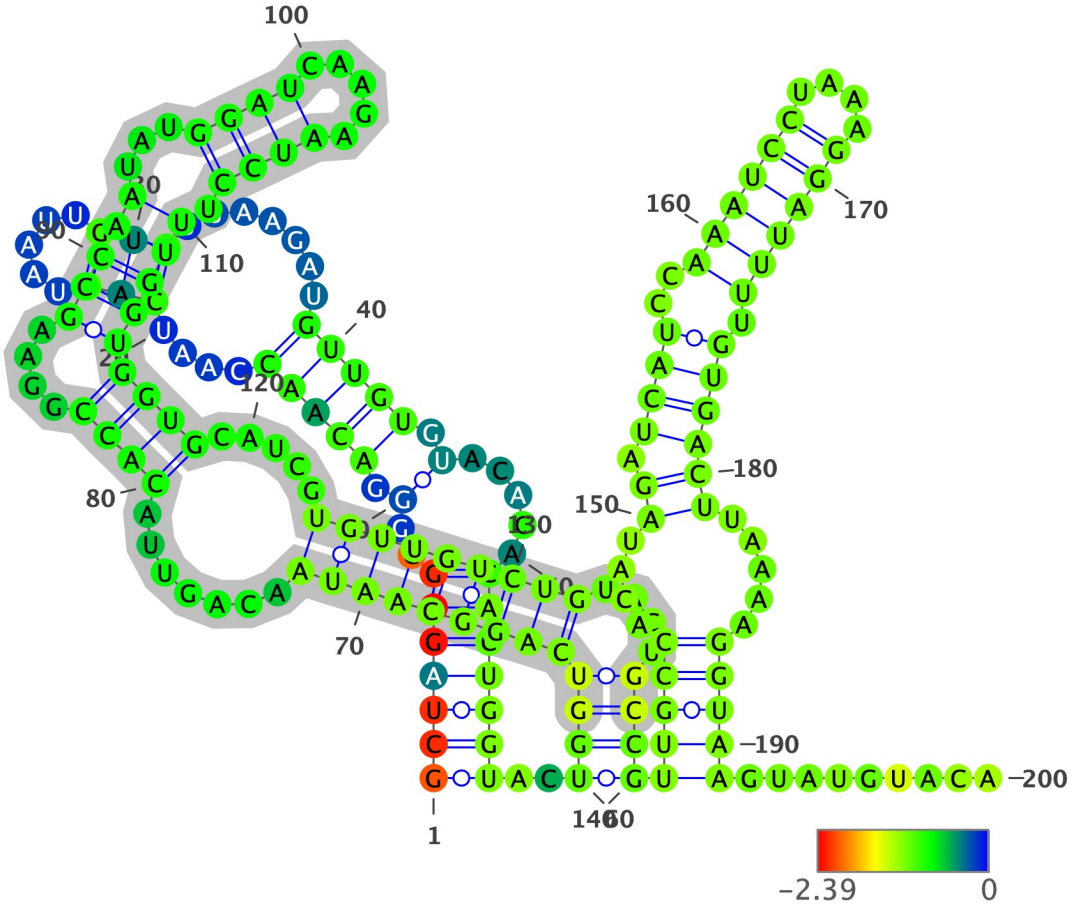
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 224 from nt 13179 to 13255 (nt 62 to 138)

```
5'-GTCAGGCAATAACAGTTACACCGGAAGCCAATATGGATCAAGAAUCCTUUGGUGGUGCATCGUGUUGUCUGTACTGC-3'
5'-((((.((((((.....................................................))))))).))....))-3'
Motif MFE = -22.4; z-score = -1.55; ED = 9.6
```



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 13118 to 13317 (motif highlighted in silver):

```
5'-GCUAGUGGGGGACAACCAAUCACUAAUUGUGUUAAGAUGUUGUGUACACACACUGGUACUGGUCAGGCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUU
GGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACA-3
5'-(((((((..(.(((((....(((.....)))).......)))))).).....)))))))..((((((((((((.......((((....(((((...((((.....)))).))
)))))))).....)))))))))....))))(((((....((.((((..((((((....))))))).))))))).....)))))..........-3'
MFE = -49.8; z-score = -0.84; ED = 42.46
```

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(+)

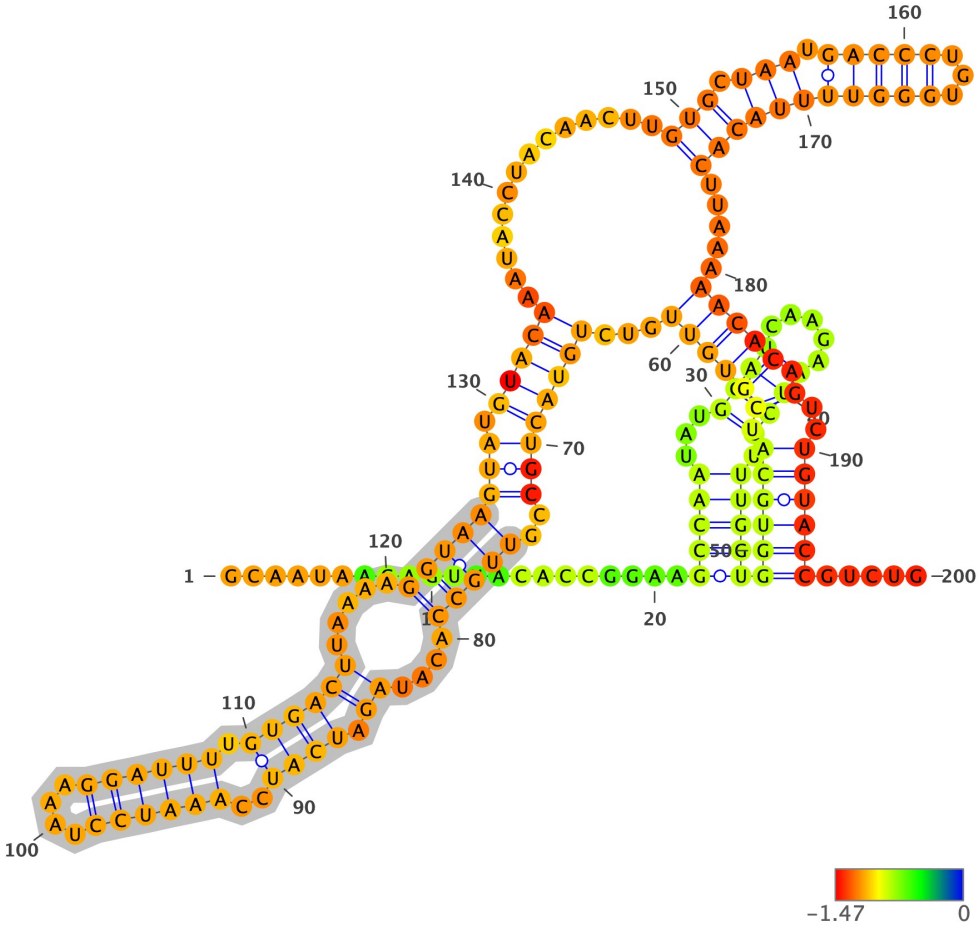
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 225 from nt 13258 to 13308 (nt 75 to 125)

```
5'-TTGCCACATAGATCATCCAAATCCTAAAGGAUUUTGUGACUTAAAAGGUAA-3'
5'-(((((....((.(((((..((((((....)))))).)))))).....)))))-3'
Motif MFE = -10.9; z-score = -2.63; ED = 4.73
```



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 13184 to 13383 (motif highlighted in silver):

```
5'-GCAAUAACAGUUACACCGGAAGCCAAUAUGGAUCAAGAAUCCUUUGGUGGUGCAUCGUGUUGUCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGU
GACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUG-3
5'-....................(((((...((((.....)))).)))))((((((.((((((...(((((((((..(((((....((.((((..((((((....)))))))..))
))))).....)))))))).)))))..............(((.(((.((((((...))))))))))).....))))).)..)))))).....-3'
MFE = -43.2; z-score = -0.51; ED = 40.01
```

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(+)

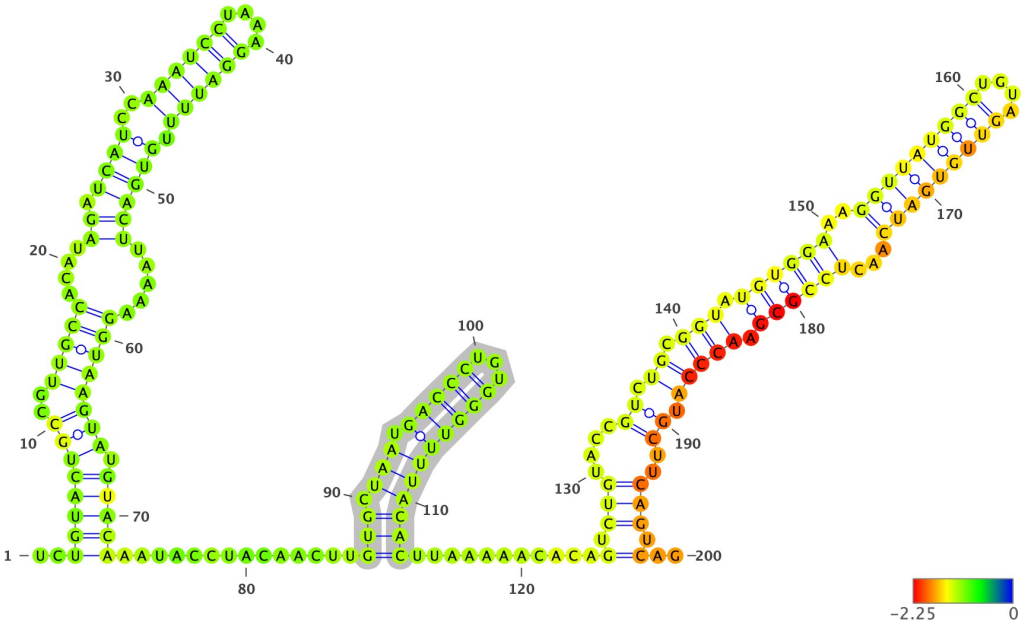
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 226 from nt 13332 to 13358 (nt 87 to 113)

```
5'-GTGCTAATGACCCTGTGGGUUUUACAC-3'
5'-(((.(((.(((((...)))))))))))-3'
Motif MFE = -6.4; z-score = -1.38; 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 13246 to 13445 (motif highlighted in silver):

```
5'-UCUGUACUGCCGUUGCCACAUAGAUCAUCCAAAUCCUAAAGGAUUUUGUGACUUAAAAGGUAAGUAUGUACAAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUAC
ACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAG-3
5'-..((((((((..(((((....((.((((..((((((....)))))).))))))).....)))))))).))))).............(((.(((.(((((...)))))))))
)).........(.(((....((.((.(((.((((((..(((((((((....)))))))))...)))))).)))))).))..))).)..-3'
MFE = -47.6; z-score = -1.06; ED = 54.89
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 266-13468(+)

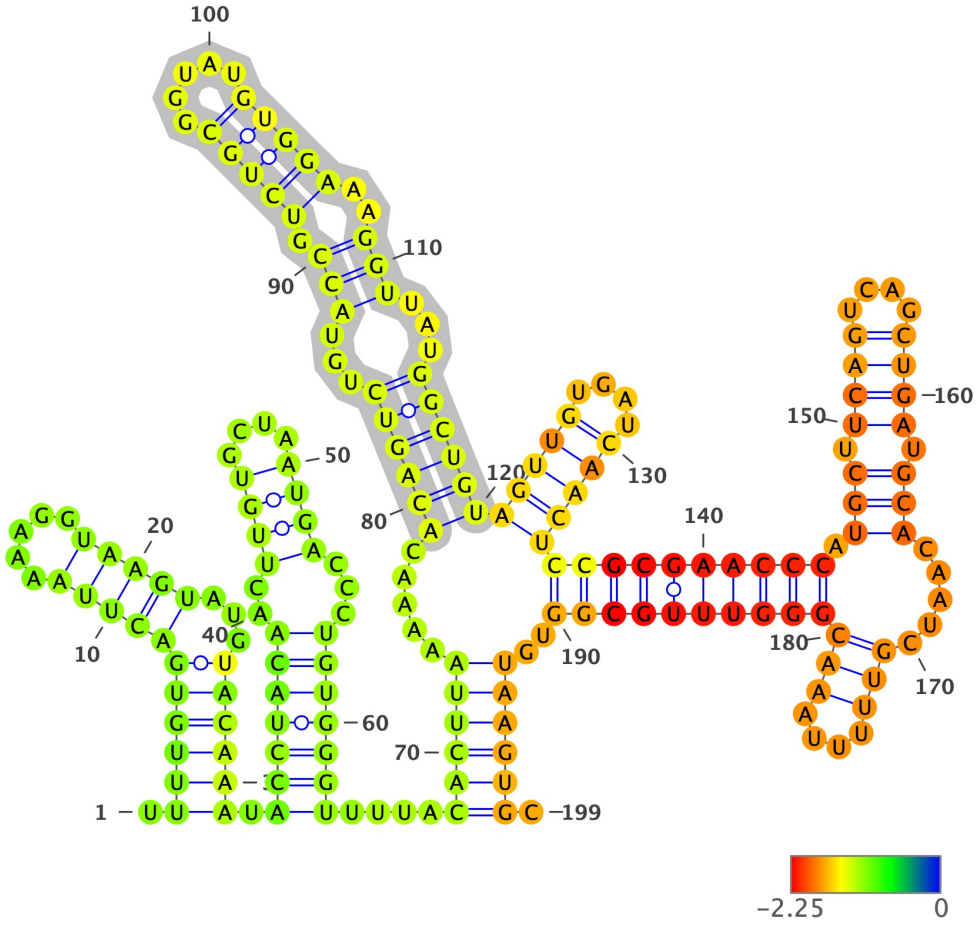
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 1 to 200--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 13367 to 13408 (nt 79 to 120)

```
5'-ACAGTCTGTACCGTCTGCGGTATGTGGAAAGGUTATGGCUGU-3'
5'-((((((...(((.(((.........)))..)))...))))))-3'
Motif MFE = -14.5; z-score = -2.52; 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 = -2.35; 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(+)

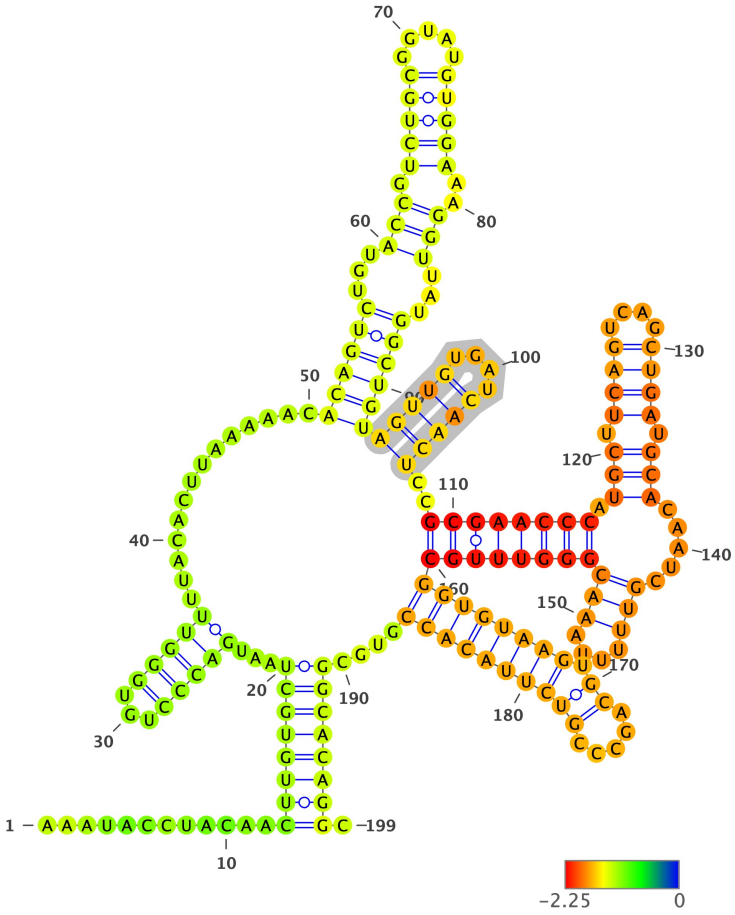
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 228 from nt 13409 to 13422 (nt 93 to 106)

```
5'-AGTTGTGATCAACU-3'
5'-(((.(....).)))-3'
Motif MFE = -2.8; z-score = -3.94; 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 13317 to 13515 (motif highlighted in silver):

```
5'-AAAUACCUACAACUUGUGCUAAUGACCCUGUGGGUUUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCG
AACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGC-3
5'-...........(((((((((...((((((...)))))).............(((((((...(((.(((((.....))))))..)))...)))))))(((((....))))))..(((
(((((.(((.((((....)))).))).....((((....))))))))))))))(((((((.((.....))))))))))....)))))))).-3'
MFE = -65.3; z-score = -2.67; ED = 26.18
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 152--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 152 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

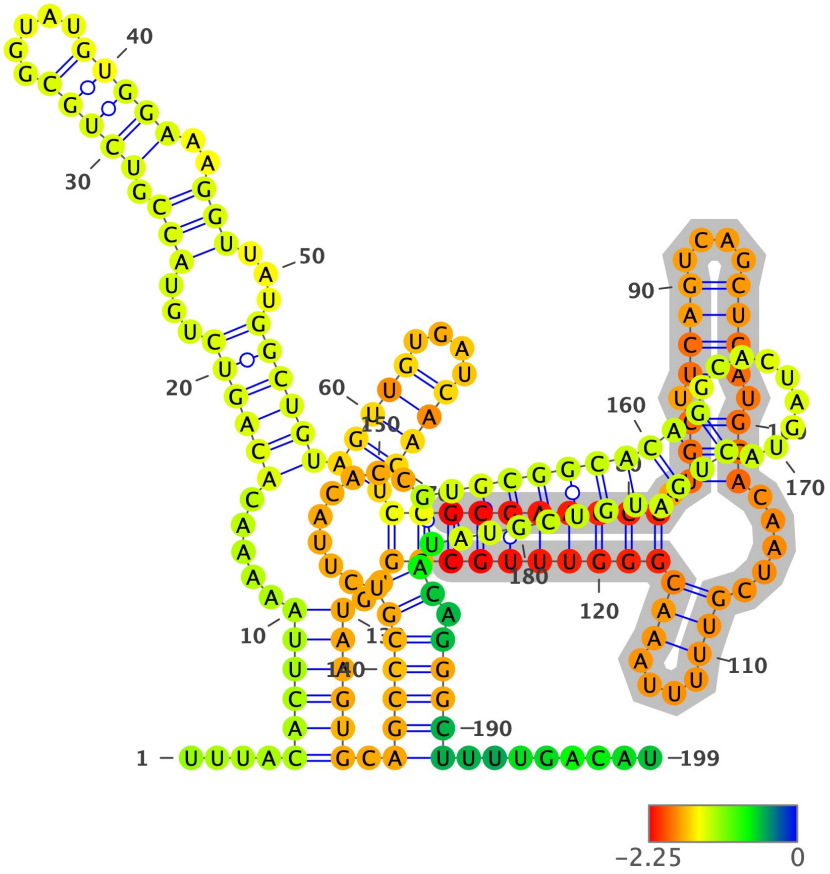
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 167--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=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 13425 to 13476 (nt 74 to 125)

```
5'-GCGAACCCATGCTTCAGTCAGCTGATGCACAATCGTTTTTAAACGGGUUUGC-3'
5'-(((((((((.(((.((........)).))).....................)))))))))-3'
Motif MFE = -16.8; z-score = -2.96; ED = 2.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13352 to 13550 (motif highlighted in silver):

```
5'-UUUACACUUAAAAACACAGUCUGUACCGUCUGCGGUAUGUGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUU
UUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAU-3
5'-....((((((.....((((((...(((.(((((.....)))))..)))...)))))))((((....))))))((((((((((.(((.((((....)))).))).....(((.
...))))))))))))..)))))).(((((((........((((((((((.........))).)))))))))).)))))........-3'
MFE = -65.5; z-score = -2.91; ED = 20.32
```

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 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(+)

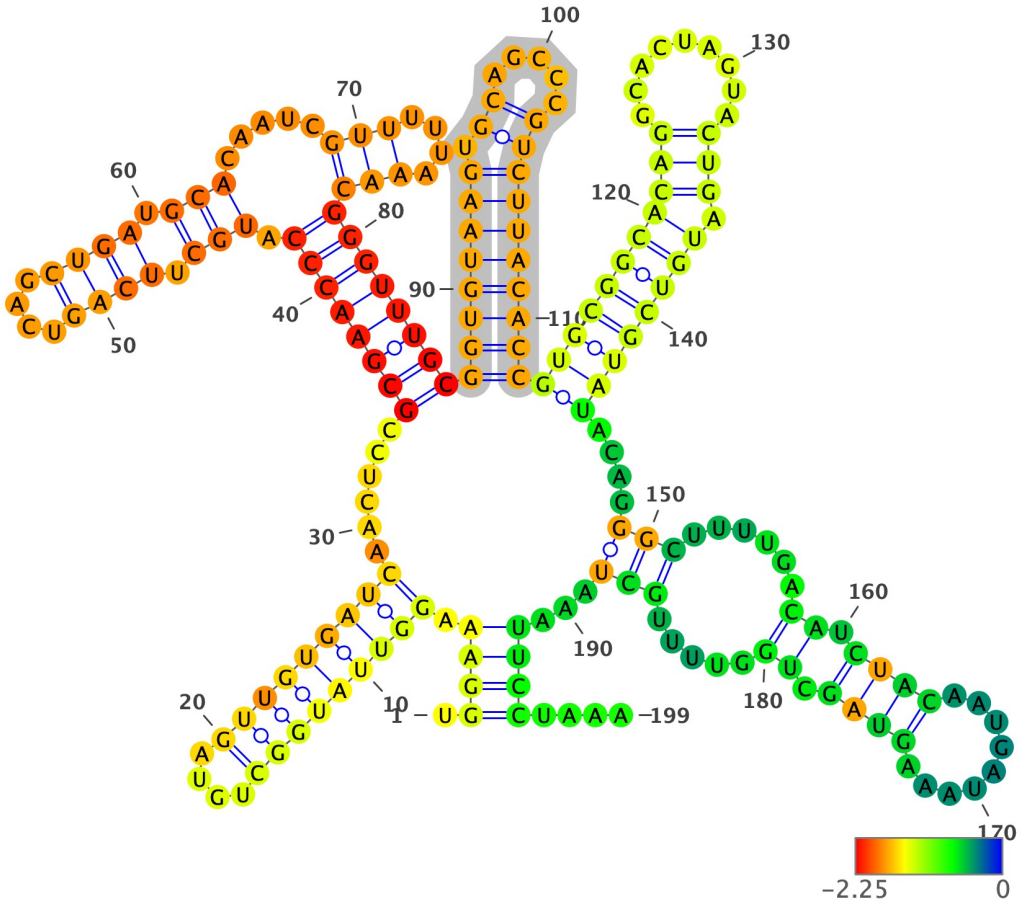
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 230 from nt 13477 to 13502 (nt 87 to 112)

```
5'-GGTGTAAGTGCAGCCCGUCUUACACC-3'
5'-(((((((((.((.....)))))))))))-3'
Motif MFE = -10.1; z-score = -2.6; ED = 1.5
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13391 to 13589 (motif highlighted in silver):

```
5'-UGGAAAGGUUAUGGCUGUAGUUGUGAUCAACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACAC
CGUGCGGCACAGGCACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAA-3
5'-.((((.((((((((((....))))))))).....(((((((.(((.((((....)))).))).....(((....)))))))))))(((((((.((.....)))))))))
)((((((((((.........))).)))))))....(((......((.((((.........)))).))).....)))...))))....-3'
MFE = -58.8; z-score = -2.31; ED = 38.45
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 78--CDS, cds-YP_009724389.1, 266-13468(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

4-- nt 78 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

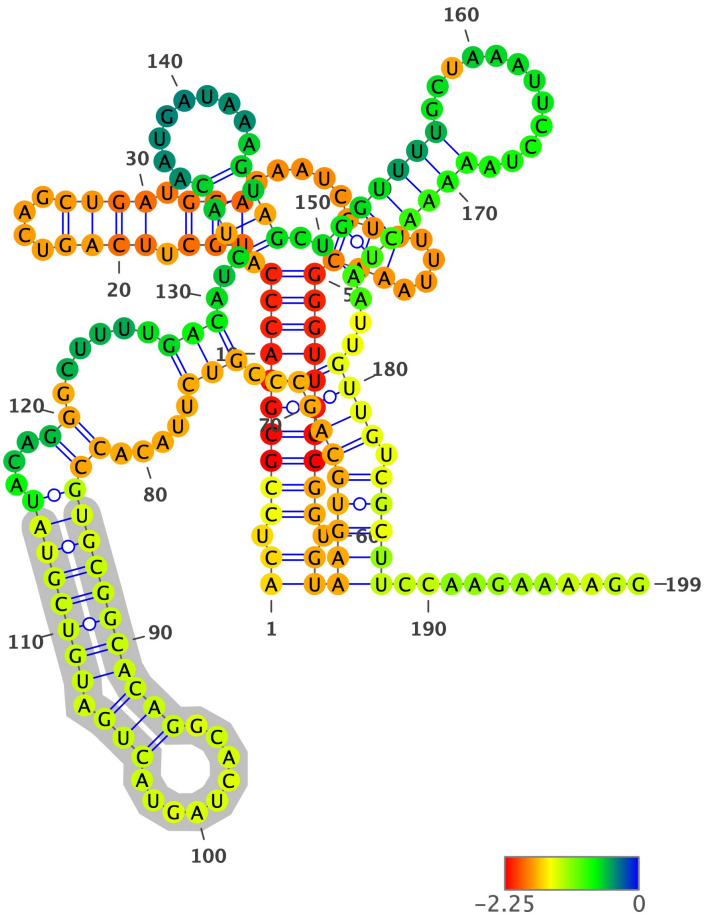
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

5-- nt 1 to 93--CDS, cds-YP_009725295.1, 266-13483(+)

Attributes: ['ID=cds-YP_009725295.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009725295.1,GeneID:43740578', 'Name=YP_009725295.1', 'Note=pp1a', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1a polyprotein', 'protein_id=YP_009725295.1']

NC_045512.2 (forward strand): Structure number 231 from nt 13504 to 13533 (nt 85 to 114)

```
5'-TGCGGCACAGGCACTAGTACUGAUGUCGUA-3'
5'-((((((((((.........))).)))))))-3'
Motif MFE = -10.2; z-score = -2.06; 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 13420 to 13618 (motif highlighted in silver):

```
5'-ACUCCGCGAACCCAUGCUUCAGUCAGCUGAUGCACAAUCGUUUUUAAACGGGUUUGCGGUGUAAGUGCAGCCCGUCUUACACCGUGCGGCACAGGCACUAGUACUGAUGUC
GUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGG-3
5'-((.((((((((((.(((.((((....)))).))).....(((....)))))))))))))).))((((((((((..(((.....((((((((((((.........))).))))
))))...))......)))..((((.........)))).(((((((.............)))))))...)))).)))))...........-3'
MFE = -52.5; z-score = -1.22; ED = 45.1
```

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 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(+)

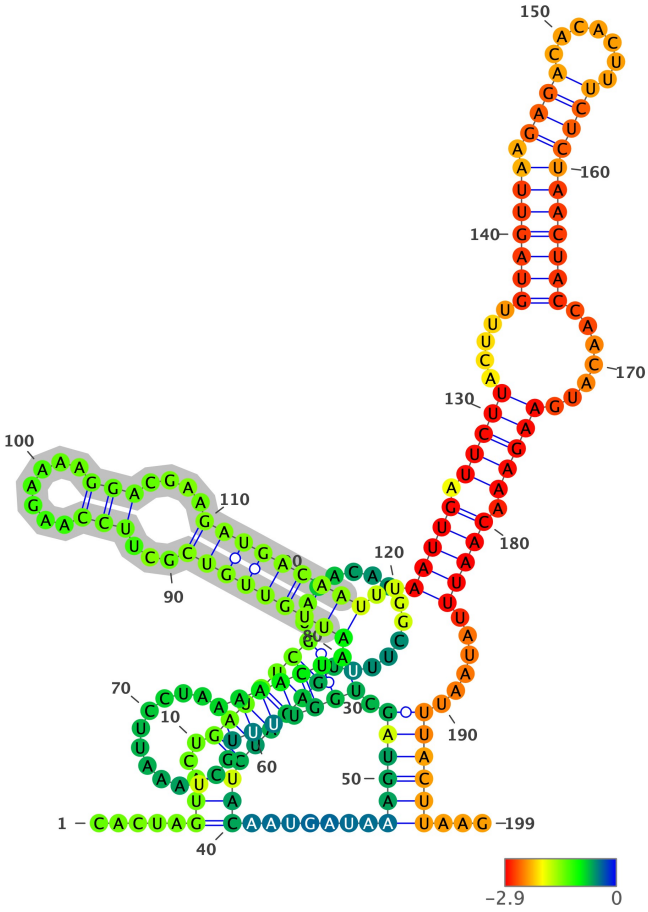
Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', '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 232 from nt 13596 to 13631 (nt 82 to 117)

```
5'-TTGTTGTCGCTTCCAAGAAAAGGACGAAGAUGACAA-3'
5'-((((((((...(((.......)))....))))))))-3'
Motif MFE = -8.4; z-score = -2.36; ED = 5.33
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13515 to 13713 (motif highlighted in silver):

```
5'-CACUAGUACUGAUGUCGUAUACAGGGCUUUUGACAUCUACAAUGAUAAAGUAGCUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGA
UGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACUACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAG-3
5'-.....(((..(((((((.............))))))))).......((((((.(((((((.............)))))))(((((((((...(((.......)))....))
)))))))..(((((.(((((.....(((((((.((((.......)))))))))))).......))))).)))))......))))))...-3'
MFE = -38.7; z-score = -2.14; ED = 27.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

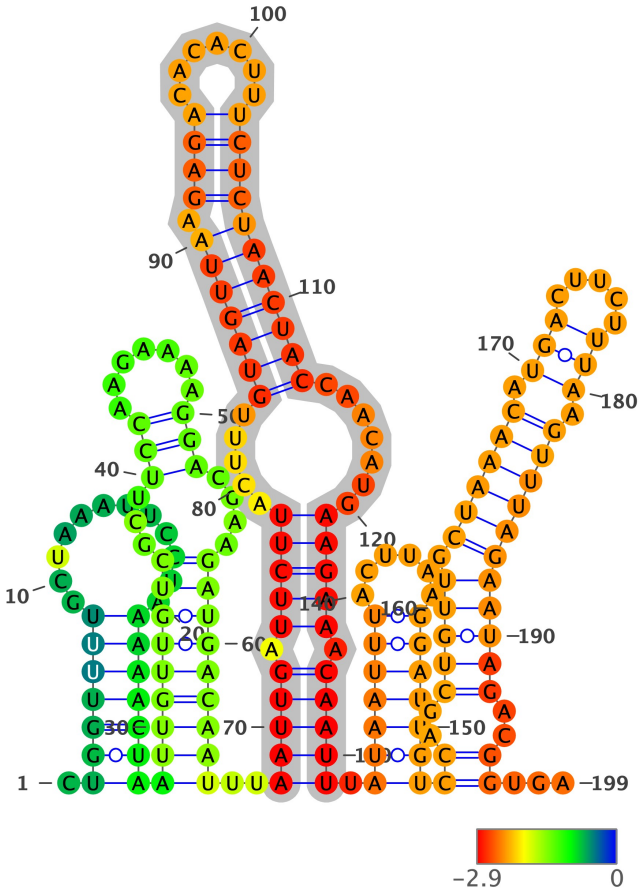
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 233 from nt 13635 to 13698 (nt 68 to 131)

```
5'-AATTGATTCTTACTTTGTAGTTAAGAGACACACTTTCUCTAACUACCAACATGAAGAAACAAUU-3'
5'-(((((.(((((.....(((((((..(((.........))).)))))))).....))))).)))))-3'
Motif MFE = -15.2; z-score = -4.13; ED = 6.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13568 to 13766 (motif highlighted in silver):

```
5'-CUGGUUUUGCUAAAUUCCUAAAAACUAAUUGUUGUCGCUUCCAAGAAAAGGACGAAGAUGACAAUUUAAUUGAUUCUUACUUUGUAGUUAAGAGACACACUUUCUCUAACU
ACCAACAUGAAGAAACAAUUUAUAAUUUACUUAAGGAUUGUCCAGCUGUUGCUAAACAUGACUUCUUUAAGUUUAGAAUAGACGGUGA-3
5'-.(((((((.............)))))))(((((((((...(((.......))))....)))))))))..(((((.(((((.....(((((((.(((.......)))))))))
))).......))))).)))))..(((((((.....)))))))((..(((((.(((((((.(((.....))).)))))))))))).))...-3'
MFE = -41.1; z-score = -1.95; ED = 37.73
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

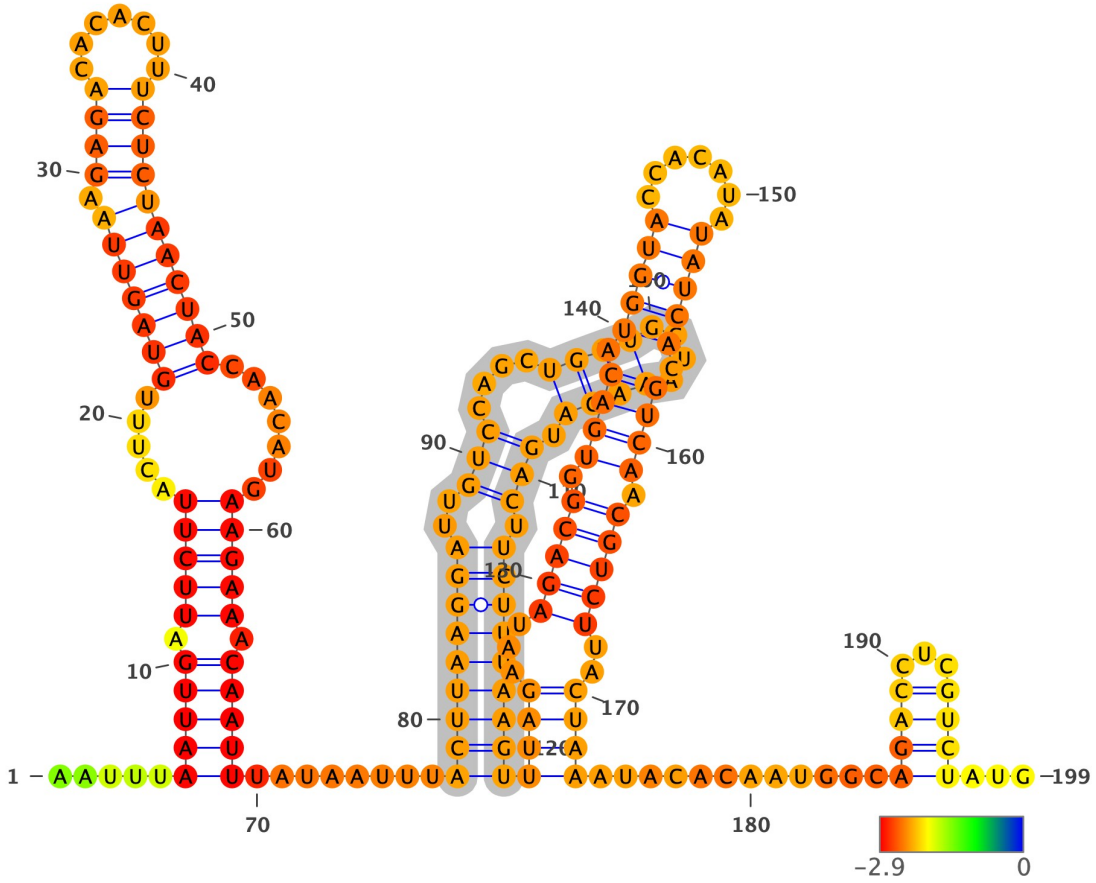
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 234 from nt 13707 to 13750 (nt 78 to 121)

```
5'-ACTTAAGGATTGTCCAGCTGTTGCTAAACATGACTUCUUUAAGU-3'
5'-(((((((((..(((....((((....)))).))).)))))))))-3'
Motif MFE = -11.0; z-score = -2.9; 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 = -3.28; 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(+)

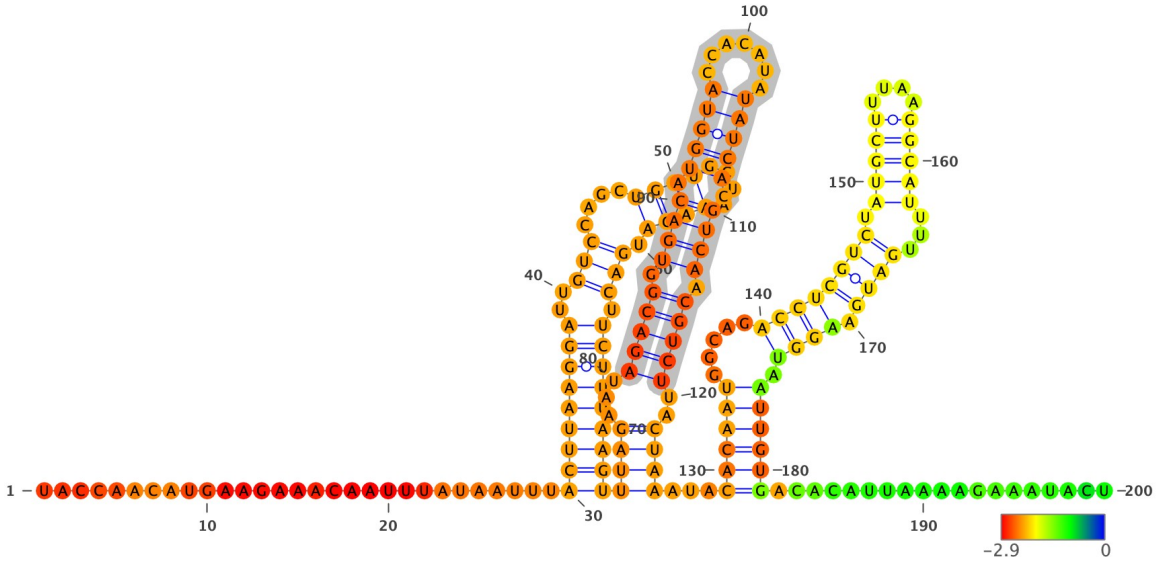
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 235 from nt 13758 to 13796 (nt 81 to 119)

```
5'-AGACGGTGACATGGTACCACATAUAUCACGUCAACGUCU-3'
5'-(((((.((((.(((((.......))))).)))).)))))-3'
Motif MFE = -13.3; z-score = -3.76; 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 = -2.53; 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(+)

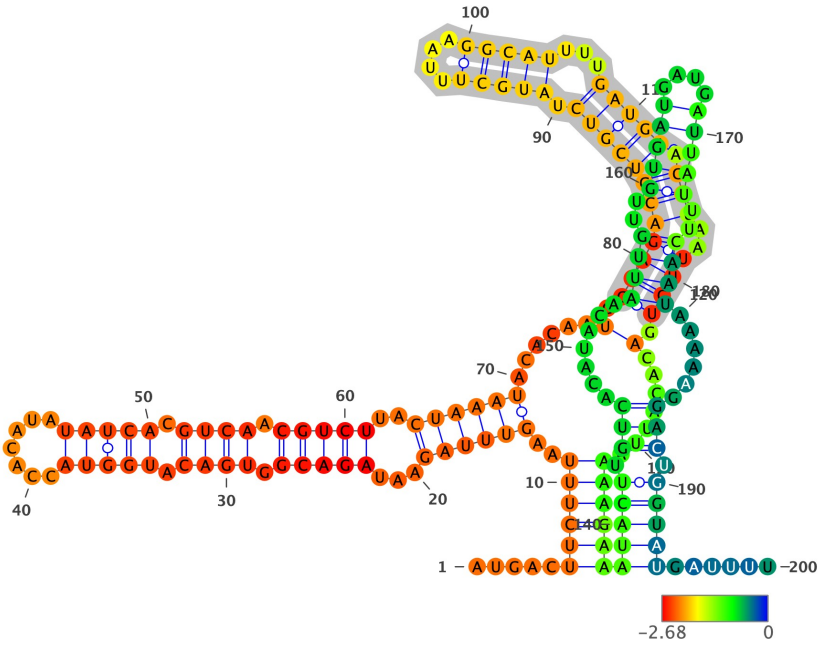
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 236 from nt 13813 to 13857 (nt 78 to 122)

```
5'-GCAGACCTCGTCTATGCTTTAAGGCAUTTTGAUGAAGGTAAUUGU-3'
5'-((((.(((((((.(((((....)))))...)))))).))...))))-3'
Motif MFE = -12.6; z-score = -3.11; 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 13736 to 13935 (motif highlighted in silver):

```
5'-AUGACUUCUUUAAGUUUAGAAUAGACGGUGACAUGGUACCACAUAUAUCACGUCAACGUCUUACUAAAUACACAAUGGCAGACCUCGUCUAUGCUUUAAGGCAUUUUGAUG
AAGGUAAUUGUGACACAUUAAAAGAAAUACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAUUUU-3
5'-.....((((((..((((((...(((((.((((.(((((.......)))))).)))).)))))..))))))......(.((((((((((((.(((((....)))))...))))
).)))..)))).).......))))))(((((.(((.......((((..(((((....)))))..))))......))).)))))......-3'
MFE = -44.6; z-score = -2.27; ED = 36.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

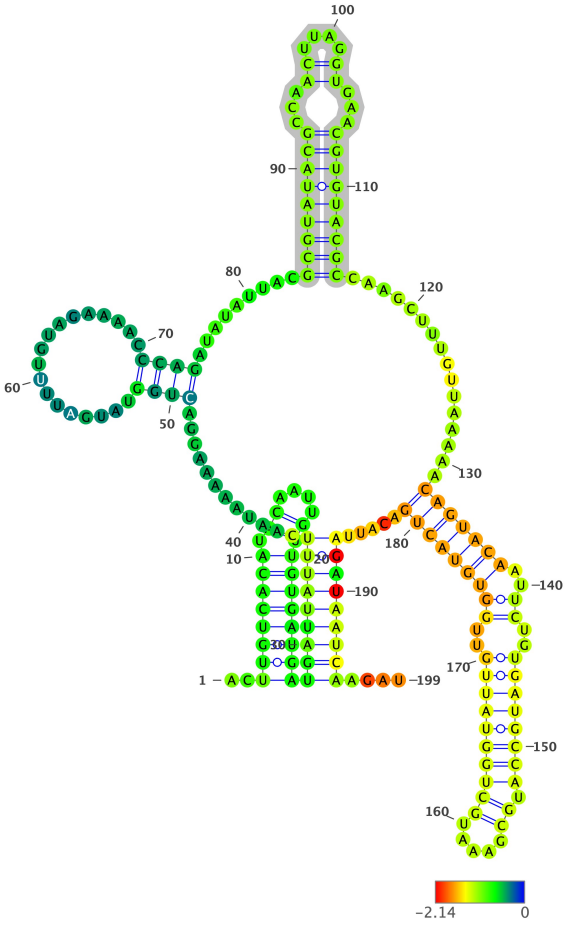
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 237 from nt 13958 to 13989 (nt 84 to 115)

```
5'-GCGTATACGCCAACTTAGGUGAACGUGUACGC-3'
5'-((((((((((...((....))...)))))))))-3'
Motif MFE = -13.3; z-score = -3.65; ED = 1.82
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 13875 to 14073 (motif highlighted in silver):

```
5'-ACUUGUCACAUACAAUUGUUGUGAUGAUGAUUAUUUCAAUAAAAAGGACUGGUAUGAUUUUGUAGAAAACCCAGAUAUAUUACGCGUAUACGCCAACUUAGGUGAACGUGU
ACGCCAAGCUUUGUUAAAAACAGUACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUGACAUUAGAUAAUCAAGAU-3
5'-..((((((((.((....)))))))))((((((((.............((((.................))))..........((((((((...((....))...)))))
))))................(((((((..((..((((((((.((.....)))))))))..)))))))))).....)))))))))....-3'
MFE = -46.8; z-score = -1.94; 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(+)

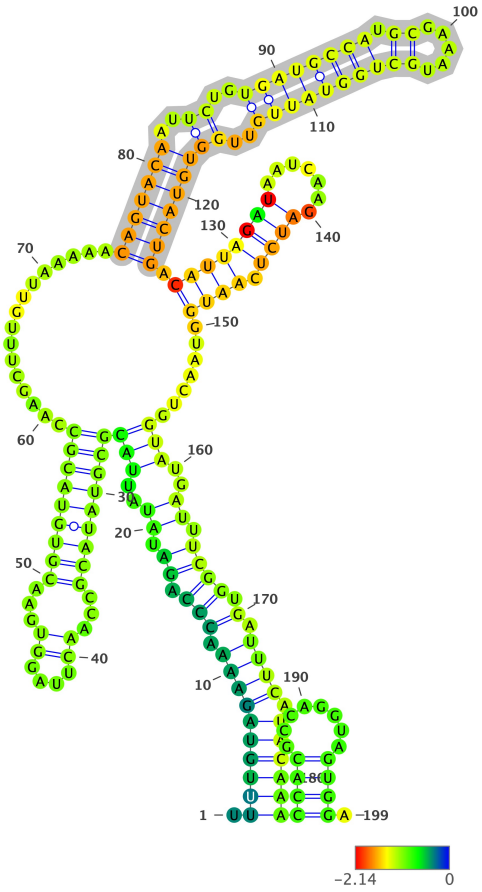
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 238 from nt 14006 to 14055 (nt 75 to 124)

```
5'-CAGTACAATTCTGTGATGCCATGCGAAATGCUGGUAUUGTTGGUGUACUG-3'
5'-(((((((.......(((((((.((.....)))))))))).....)))))))-3'
Motif MFE = -16.7; z-score = -2.69; 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 = -2.42; 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']

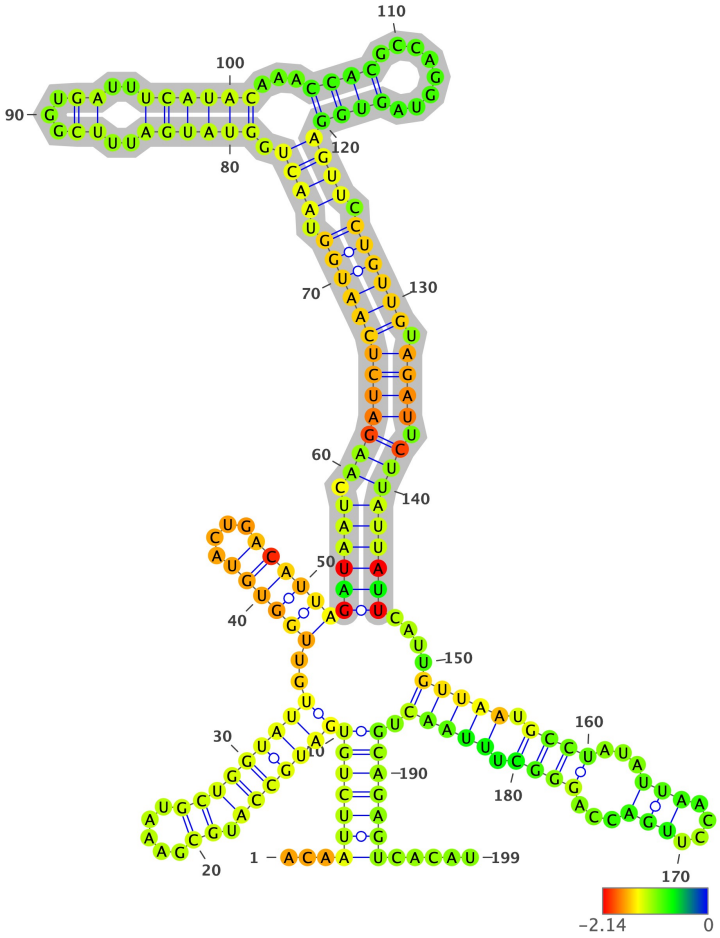
3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

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 239 from nt 14062 to 14155 (nt 53 to 146)

```
5'-GATAATCAAGATCTCAATGGTAACTGGTATGATTTCGGTGATTUCAUACAAACCACGCCAGGTAGUGGAGUUCCUGUUGTAGAUTCTTATTATU-3'

5'-(.(......(((((((((((.((((.((((((..((...))..))))))...................)))).)))))).)))).).....).)-3'
Motif MFE = -25.2; z-score = -2.21; ED = 4.97
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14010 to 14208 (motif highlighted in silver):

```
5'-ACAAUUCUGUGAUGCCAUGCGAAAUGCUGGUAUUGUUGGUGUACUGACAUUAGAUAAUCAAGAUCUCAAUGGUAACUGGUAUGAUUUCGGUGAUUUCAUACAAACCACGCC
AGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAU-3
5'-...(((((((((((((((.((.....)))))))))..((((((....))))))((((((.(((((((((((((.((((.((((((..((...))..))))))...((((...
.....))))))))).)))))).)))).))))))))).....(((((.((((...(((....)))...)))).)))))).)))))))).....-3'
MFE = -52.7; z-score = -2.7; ED = 37.18
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

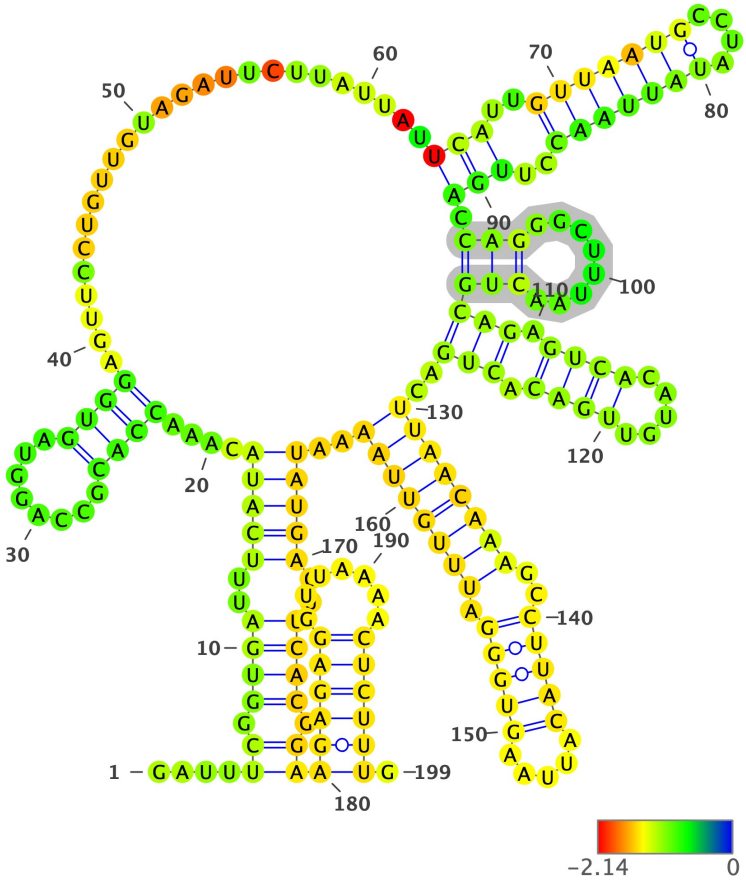
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 240 from nt 14184 to 14197 (nt 93 to 106)

```
5'-CAGGGCTTTAACTG-3'
5'-(............)-3'
Motif MFE = -1.2; z-score = -1.43; 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 14092 to 14290 (motif highlighted in silver):

```
5'-GAUUUCGGUGAUUUCAUACAAACCACGCCAGGUAGUGGAGUUCCUGUUGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAG
UCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUG-3
5'-....((.((((..(((((....((((.........))))........................(((..(((((((....)))))))..))).(((........)))(((.(
(((.....)))).)))..((((((((..(((((.....))))).))))))))..))))).)))).))((((((.......)))))).-3'
MFE = -46.4; z-score = -1.42; ED = 24.39
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

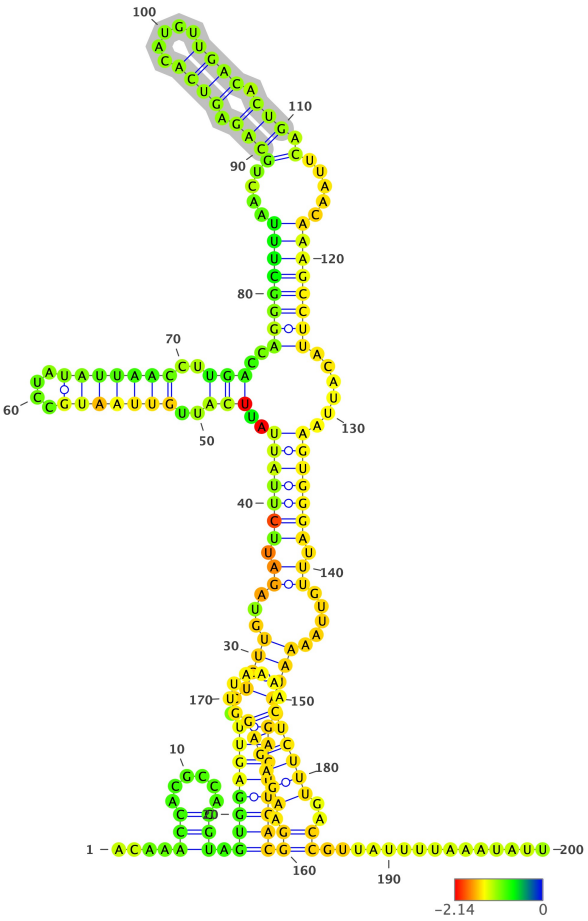
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 241 from nt 14198 to 14218 (nt 90 to 110)

```
5'-CAGAGTCACATGTUGACACUG-3'
5'-(((.((((.....)))).)))-3'
Motif MFE = -4.5; z-score = -1.52; 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 = -1.14; 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(+)

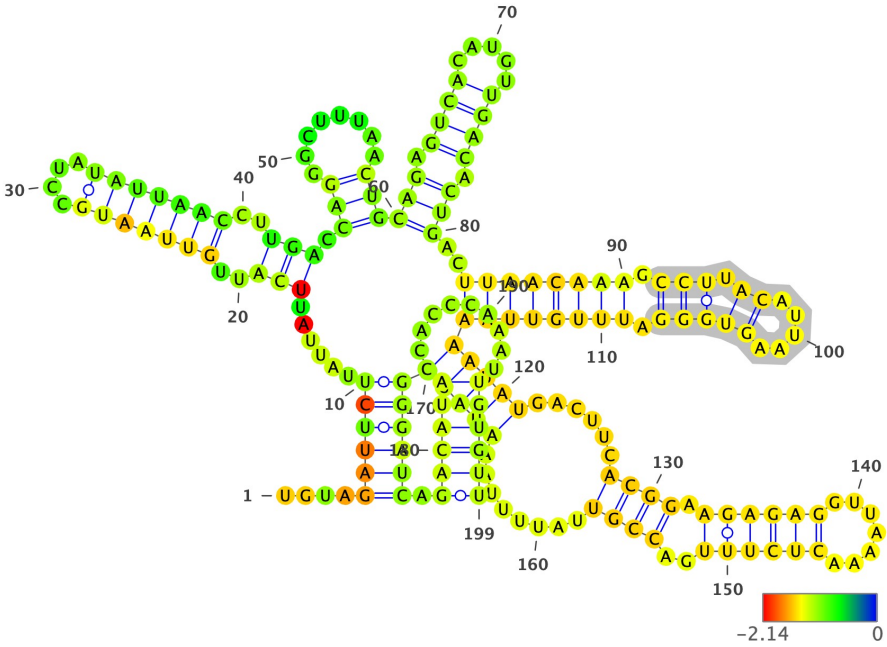
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 242 from nt 14230 to 14245 (nt 92 to 107)

```
5'-CCTTACATTAAGTGGG-3'
5'-(((..........)))-3'
Motif MFE = -1.9; z-score = -0.91; 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 14139 to 14337 (motif highlighted in silver):

```
5'-UGUAGAUUCUUAUUAUUCAUUGUUAAUGCCUAUAUUAACCUUGACCAGGGCUUUAACUGCAGAGUCACAUGUUGACACUGACUUAACAAAGCCUUACAUUAAGUGGGAUUU
GUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUU-3
5'-....((((((......(((..(((((((....)))))))..))).(((........)))(((.((((.....)))).))).((((((((.(((.((.....))))).)))
)))))(((((......((((.((((((.......))))))..))))........))))))))))).((((((..........))))))-3'
MFE = -41.4; z-score = -1.52; ED = 33.15
```

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(+)

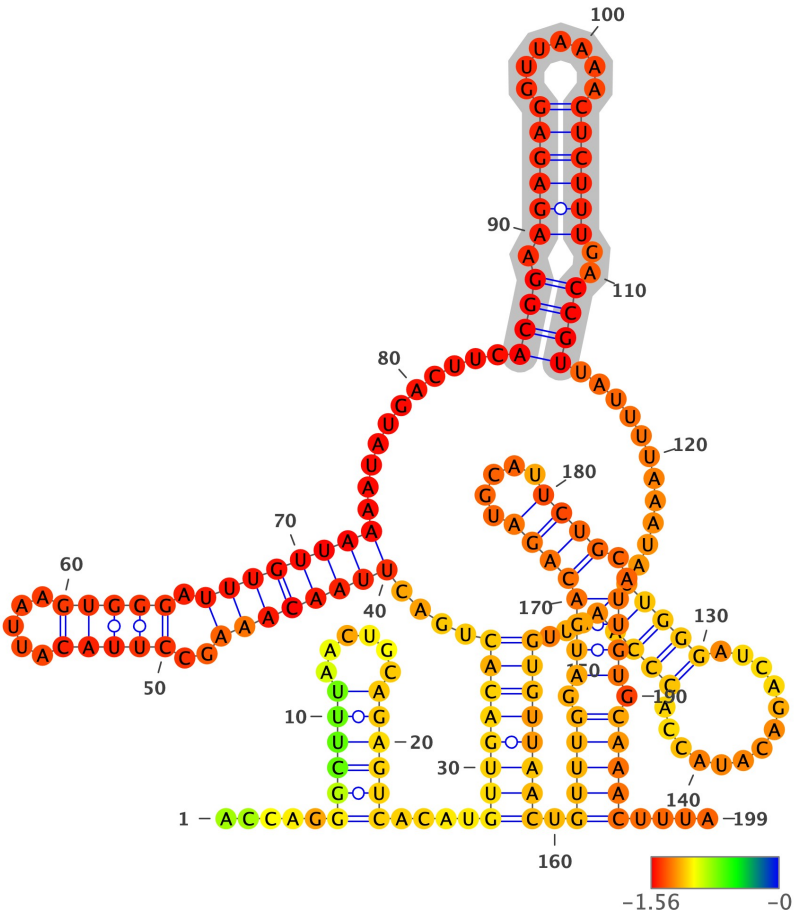
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14266 to 14295 (nt 85 to 114)

```
5'-ACGGAAGAGAGGTTAAAACUCUUUGACCGU-3'
5'-((((.((((((.......))))))..))))-3'
Motif MFE = -10.5; z-score = -3.88; 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 = -1.92; 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(+)

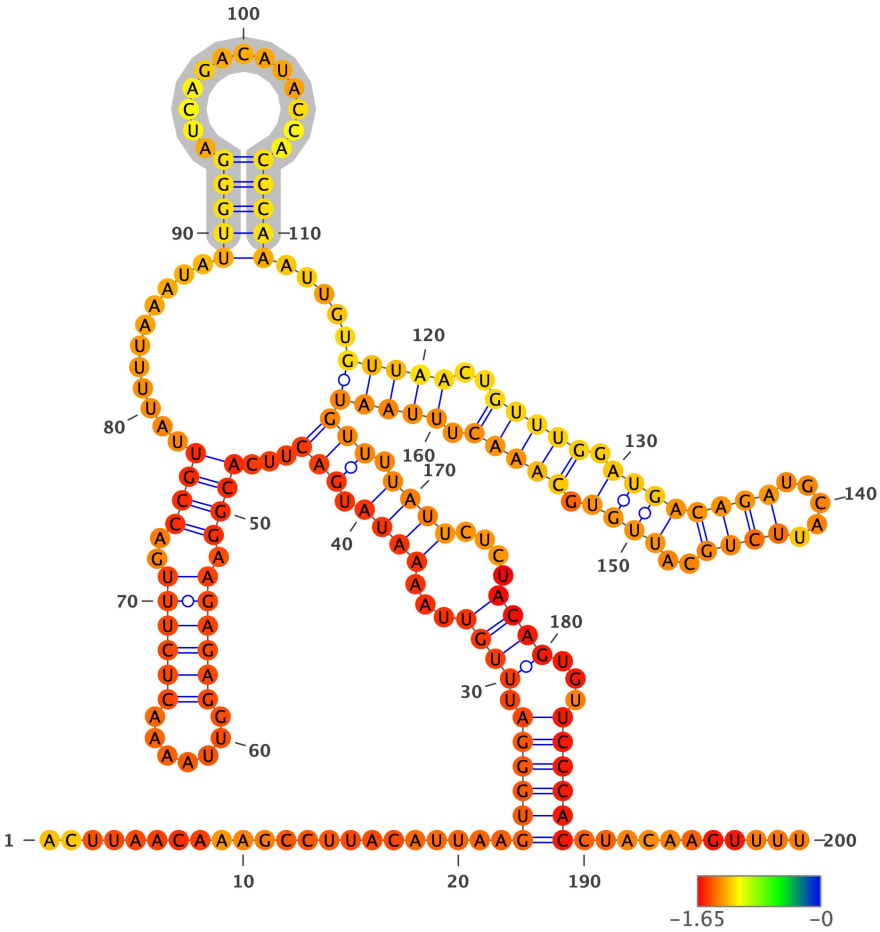
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 244 from nt 14308 to 14328 (nt 90 to 110)

```
5'-TGGGATCAGACATACCACCCA-3'
5'-((((.............))))-3'
Motif MFE = -2.5; z-score = -0.91; 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 14219 to 14418 (motif highlighted in silver):

```
5'-ACUUAACAAAGCCUUACAUUAAGUGGGAUUUGUUAAAAUAUGACUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAA
AUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUU-3
5'-.......................((((((.((((...((((.(((...((((.((((((.......))))))..))))...........(((((.............)))))
.....(((((..(((((.(((((((((.....))))..)))).)))))).))))))))).))))....))))...))))))...........-3'
MFE = -39.3; z-score = -1.6; ED = 60.8
```

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(+)

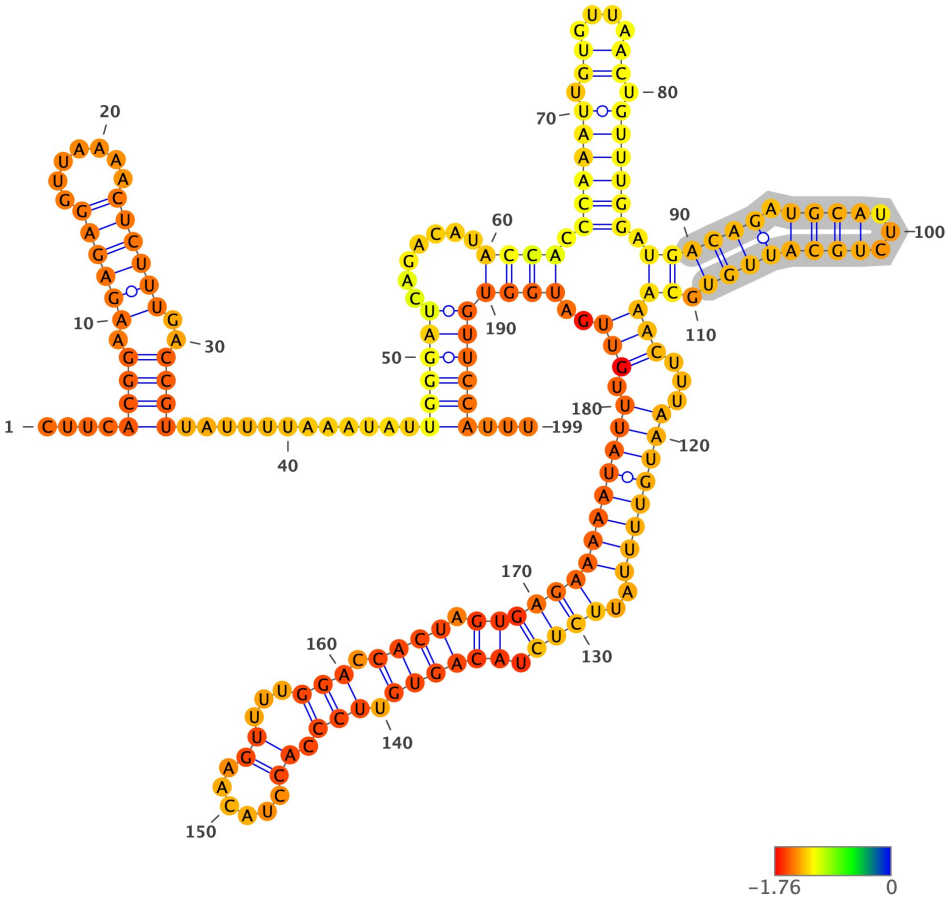
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14351 to 14370 (nt 90 to 109)

```
5'-ACAGATGCATTCUGCAUUGU-3'
5'-((((.((((...))))))))-3'
Motif MFE = -4.1; z-score = -2.24; ED = 3.83
```



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 14262 to 14460 (motif highlighted in silver):

```
5'-CUUCACGGAAGAGAGGUUAAAACUCUUUGACCGUUAUUUUAAAUAUUGGGAUCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGC
AAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUU-3
5'-....((((.((((((.......))))))..))))............((((((.......((((.((((((.((....)).)))))).((((((.((((...)))))))).)
)(((...((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))).)))..)))))))))...-3'
MFE = -45.1; z-score = -1.7; ED = 29.7
```

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_gp01, 266-21555(+)

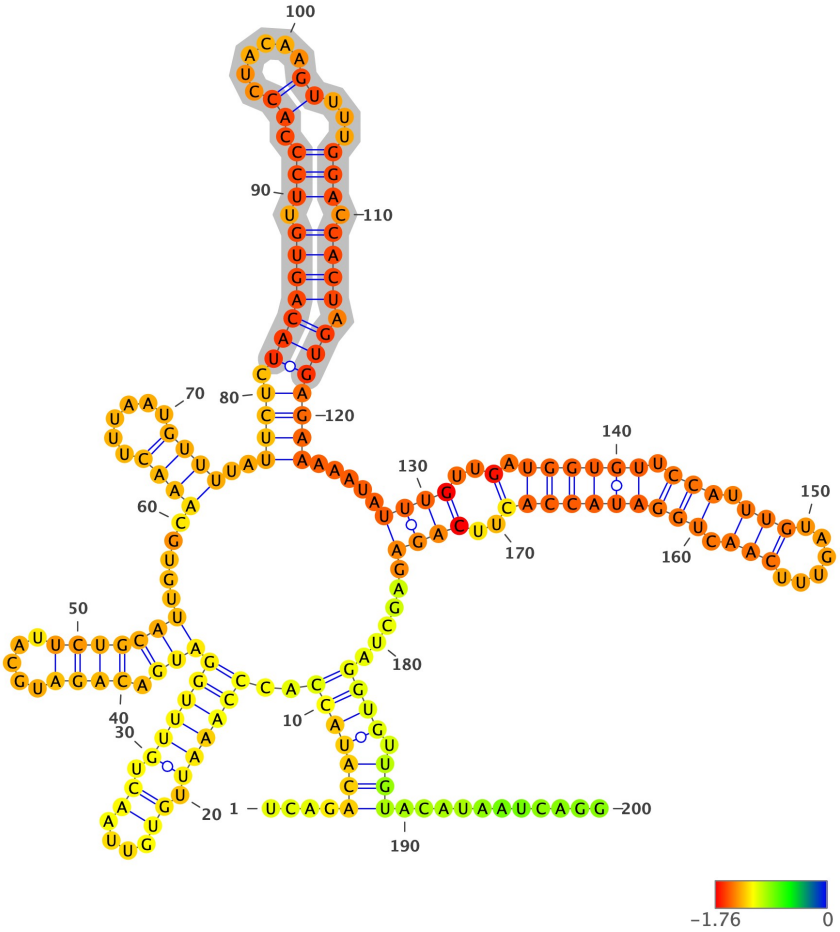
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 14394 to 14430 (nt 82 to 118)

```
5'-TACAGTGTTCCCACCTACAAGUTTTGGACCACUAGUG-3'
5'-(((((((.(((.((......)).)))).)))))).)))-3'
Motif MFE = -6.7; z-score = -1.24; ED = 3.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14313 to 14512 (motif highlighted in silver):

```
5'-UCAGACAUACCACCCAAAUUGUGUUAACUGUUUGGAUGACAGAUGCAUUCUGCAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACC
ACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGG-3
5'-....(((((((..((((((.((....)).)))))))((.((((.....)))))))).....((((......)))))..((((.(((((((.(((.((......)).)))).)
)))).)))))))).....((((..(.((((((.(((.(((......))).))))))))))..))))......)))))).)))...........-3'
MFE = -44.6; z-score = -1.38; ED = 38.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

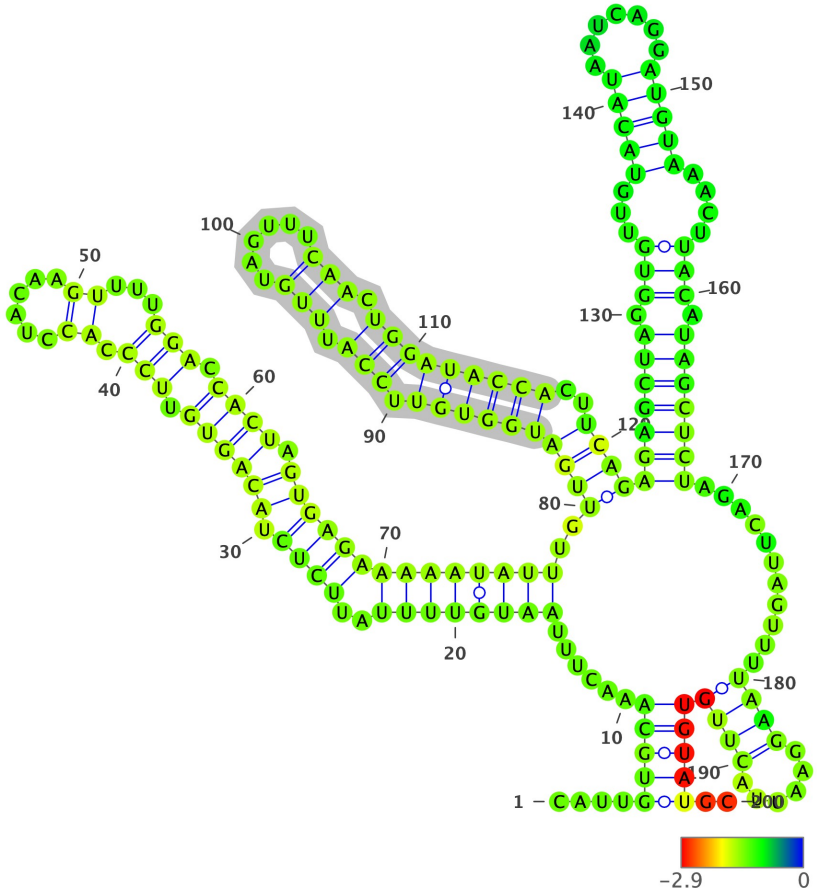
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 247 from nt 14448 to 14480 (nt 84 to 116)

```
5'-TGGTGTTCCATTTGTAGTTTCAACUGGAUACCA-3'
5'-((((((.(((.(((......))).)))))))))-3'
Motif MFE = -10.8; z-score = -3.71; ED = 1.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14365 to 14564 (motif highlighted in silver):

```
5'-CAUUGUGCAAACUUUAAUGUUUUAUUCUCUACAGUGUUCCCACCUACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGA
UACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAACUUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGC-3
5'-....(((((......((((((((..((((.((((((.(((.((......))...))).)))).))))))))))))))..((((((((((.(((.(((......))).))))
))))).)))))(((((((.(((...(((((.......)))))....))).)))))))...........((((......)))))))))..-3'
MFE = -46.1; z-score = -1.56; ED = 27.33
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

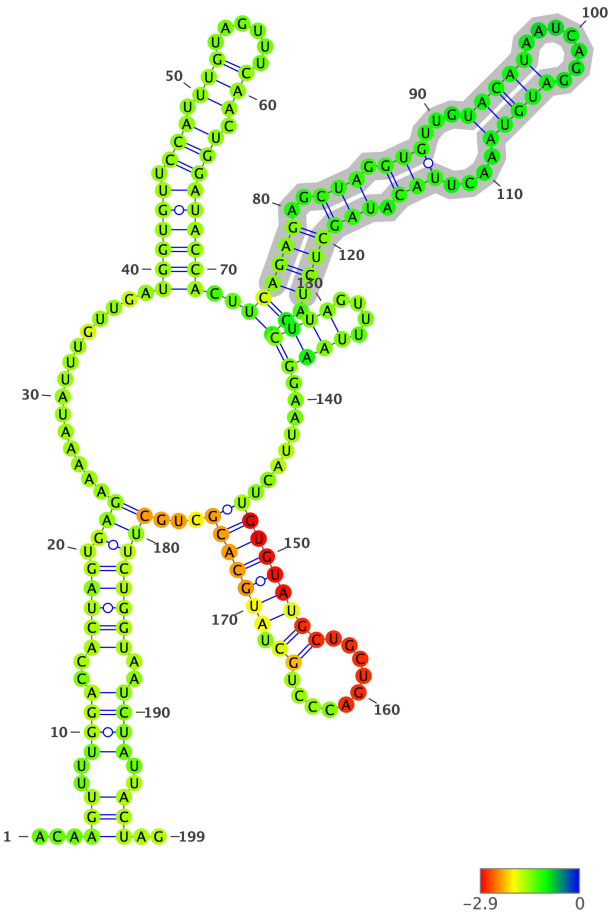
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 248 from nt 14485 to 14532 (nt 76 to 123)

```
5'-AGAGAGCTAGGTGTTGTACATAATCAGGAUGUAAACTUACAUAGCUCU-3'
5'-(((((..(((.(((.......................))).)))))))-3'
Motif MFE = -13.8; z-score = -2.84; ED = 3.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14410 to 14608 (motif highlighted in silver):

```
5'-ACAAGUUUUGGACCACUAGUGAGAAAAAUAUUUGUUGAUGGUGUUCCAUUUGUAGUUUCAACUGGAUACCACUUCAGAGAGCUAGGUGUUGUACAUAAUCAGGAUGUAAAC
UUACAUAGCUCUAGACUUAGUUUUAAGGAAUUACUUGUGUAUGCUGCUGACCCUGCUAUGCACGCUGCUUCUGGUAAUCUAUUACUAG-3
5'-...(((..(((((..(((((.(((.............((((((.(((.(((.....))).)))))))))..((((((..(((.(((...(((((.......)))))...
.))).)))))))).))(((((....)))).........(((((((((.........)).)))))))...)))))))..)))))..)))..-3'
MFE = -40.6; z-score = -1.57; ED = 26.08
```

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(+)

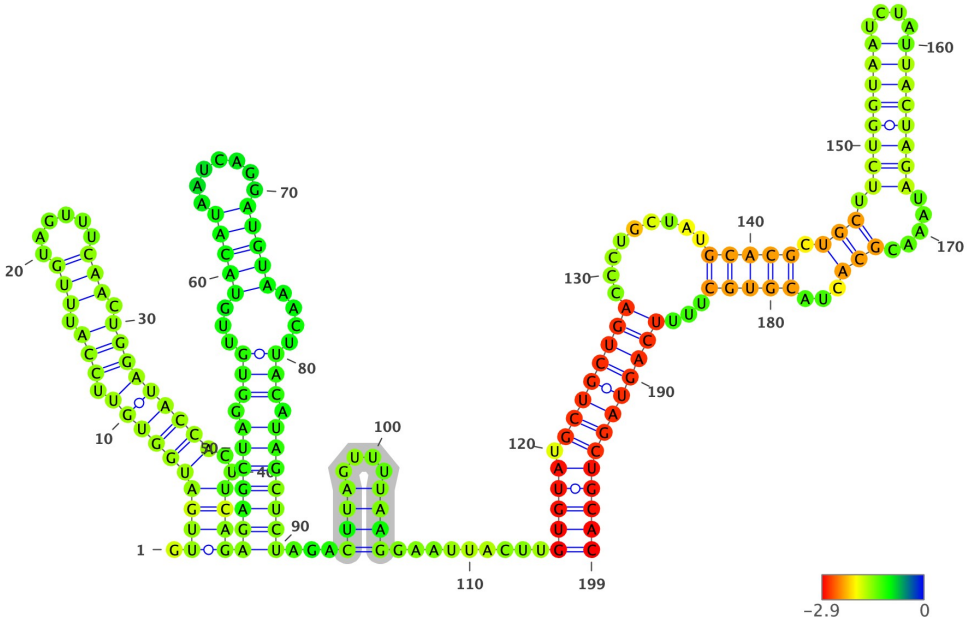
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 249 from nt 14536 to 14547 (nt 94 to 105)

```
5'-CTTAGTTTUAAG-3'
5'-(.((....)).)-3'
Motif MFE = 0.0; z-score = 0.2; 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 = -3.37; 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(+)

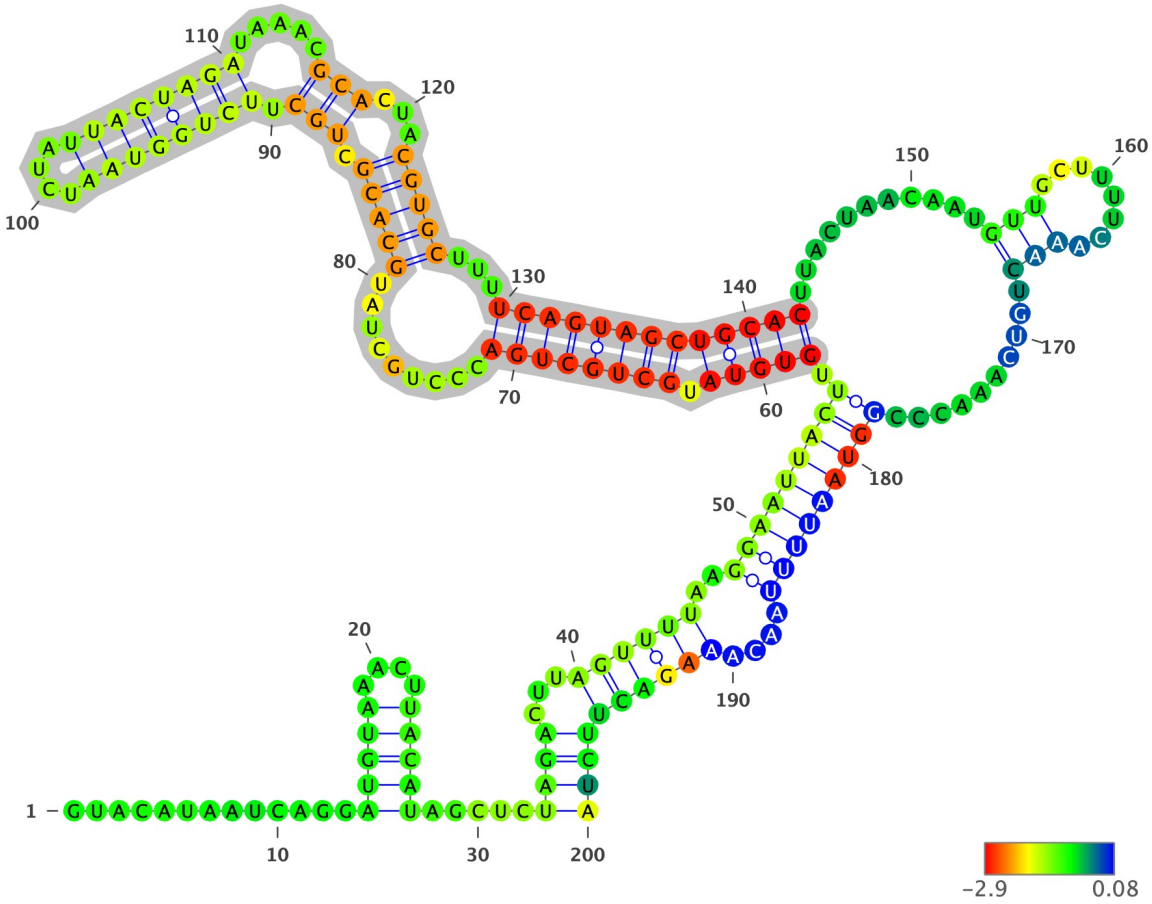
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 250 from nt 14557 to 14641 (nt 58 to 142)

```
5'-GTGTATGCTGCTGACCCTGCTATGCACGCTGCTTCTGGTAATCTATUACUAGATAAACGCACTACGUGCTTTUCAGUAGCUGCAC-3'
5'-(((((.(((((((((.........(((((.(((.(((((((.......)))))))).....)))...)))))...))))))))))))-3'
Motif MFE = -29.9; z-score = -3.5; 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 = -1.22; 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(+)

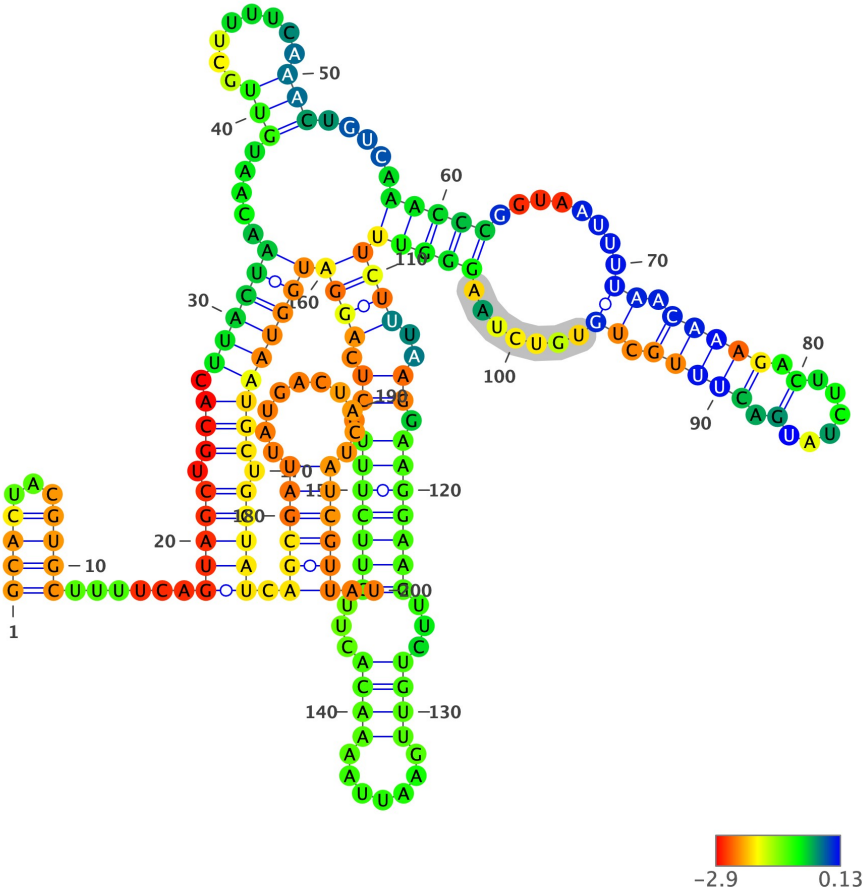
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 251 from nt 14711 to 14717 (nt 97 to 103)

```
5'-TGTCTAA-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 14615 to 14814 (motif highlighted in silver):

```
5'-GCACUACGUGCUUUUCAGUAGCUGCACUUACUAACAAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCU
UUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAU-3
5'-((((...))))......(((((.(((.((((((.....(((........)))).....(((((........((.(((((.(......).))))).)).......)))))(((
(..((.(((((((...((((.......))))...)))))))).)).))))))))))))).))))).((((((..........))))))..-3'
MFE = -42.2; z-score = -0.69; ED = 18.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

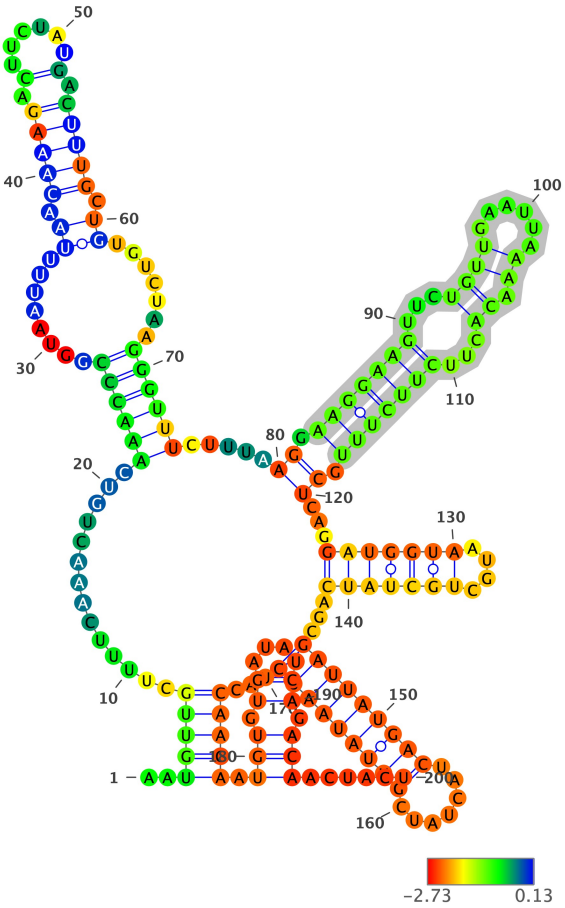
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 252 from nt 14732 to 14766 (nt 83 to 117)

```
5'-AAGGAAGTTCTGTTGAATTAAAACACTTCUUCUUU-3'
5'-(((((((...((((......)).))...)))))))-3'
Motif MFE = -7.1; z-score = -3.18; ED = 3.16
```



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 14650 to 14849 (motif highlighted in silver):

```
5'-AAUGUUGCUUUUCAAACUGUCAAACCCGGUAAUUUUAACAAAGACUUCUAUGACUUUGCUGUGUCUAAGGGUUUCUUUAAGGAAGGAAGUUCUGUUGAAUUAAAACACUUC
UUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACU-3
5'-..(((((.............((((((........((.(((((.(......).)))))).))).......))))))).....((.(((((((...((((......)).))...)
))))))).))...(((((((....)))))))...(((((((((.......)))))))))...)))))).(((.((....)).))).......-3'
MFE = -39.2; z-score = -1.23; ED = 36.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

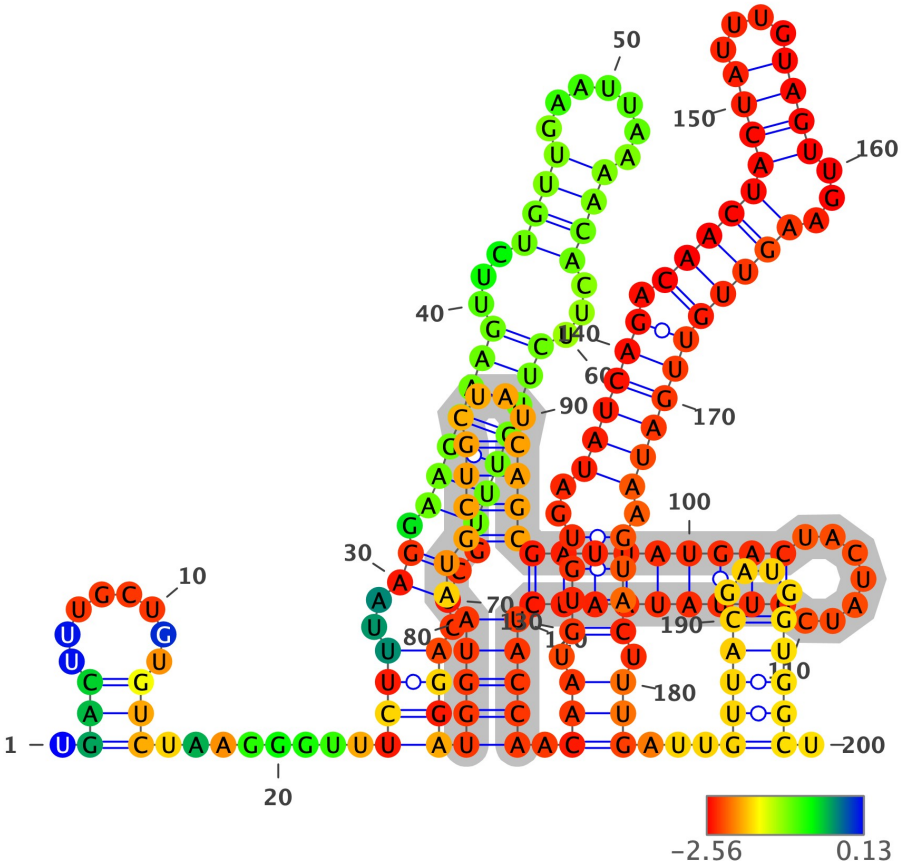
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 253 from nt 14775 to 14823 (nt 76 to 124)

```
5'-TGGTAATGCTGCTATCAGCGATTATGACTACTATCGUUAUAAUCUACCA-3'
5'-((((((..((((....))))((((((((((.......))))))))))))))))-3'
Motif MFE = -14.4; z-score = -3.75; 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 = -2.58; 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(+)

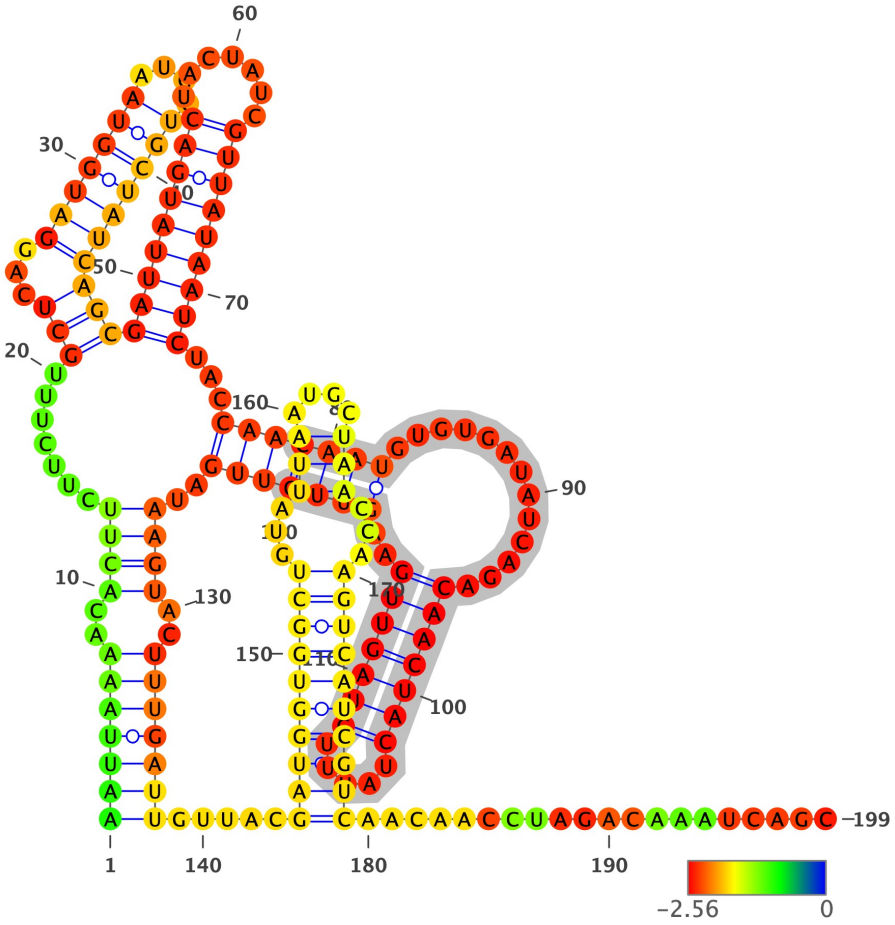
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 254 from nt 14825 to 14866 (nt 79 to 120)

```
5'-CAATGTGTGATATCAGACAACTACTATTTGUAGUUGAAGTTG-3'
5'-(.................(((((((.....)))))))).....)-3'
Motif MFE = -8.3; z-score = -1.72; ED = 4.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14747 to 14945 (motif highlighted in silver):

```
5'-AAUUAAAACACUUCUUCUUUGCUCAGGAUGGUAAUGCUGCUAUCAGCGAUUAUGACUACUAUCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAG
UUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGUCAUCGUCAACAACCUAGACAAAUCAGC-3
5'-(((((((..((((.......(((...(((((((....)))))))))))(((((((((.......)))))))))...(((((((.............(((((((.....))))
)))..)))))))..))))..)))))).....((((((((((...(((....)))...))))))))))...................-3'
MFE = -44.8; z-score = -2.82; 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(+)

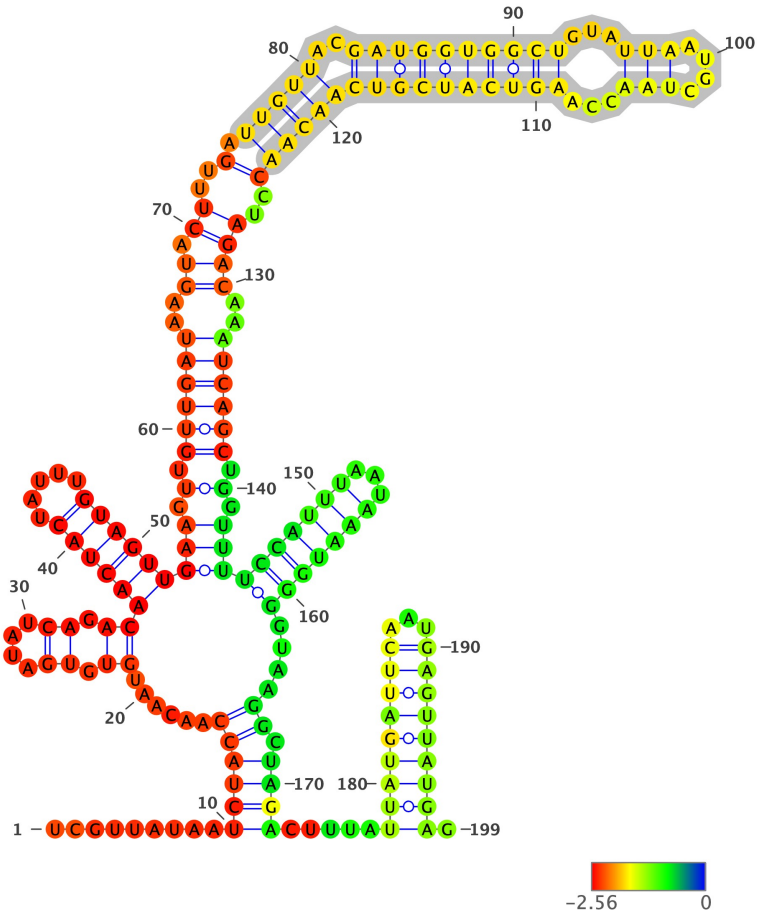
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 14883 to 14930 (nt 76 to 123)

```
5'-TTGTTACGATGGTGGCTGTATTAATGCTAACCAAGUCAUCGUCAACAA-3'
5'-((((((..((((((((((.................))))))))))))))))-3'
Motif MFE = -13.4; z-score = -2.69; ED = 9.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14808 to 15006 (motif highlighted in silver):

```
5'-UCGUUAUAAUCUACCAACAAUGUGUGAUAUCAGACAACUACUAUUUGUAGUUGAAGUUGUUGAUAAGUACUUUGAUUGUUACGAUGGUGGCUGUAUUAAUGCUAACCAAGU
CAUCGUCAACAACCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAG-3
5'-.........((((((......((.((....)).))(((((.....)))))))(((.(.(((((((..((.((..(.((((((..((((((((((...((((....))))...))))
))))))))))))))..)))))..))))))).).)))(((((((...)))))))....)).))))).....(((((((((...)))))))))).-3'
MFE = -43.9; z-score = -1.26; ED = 38.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

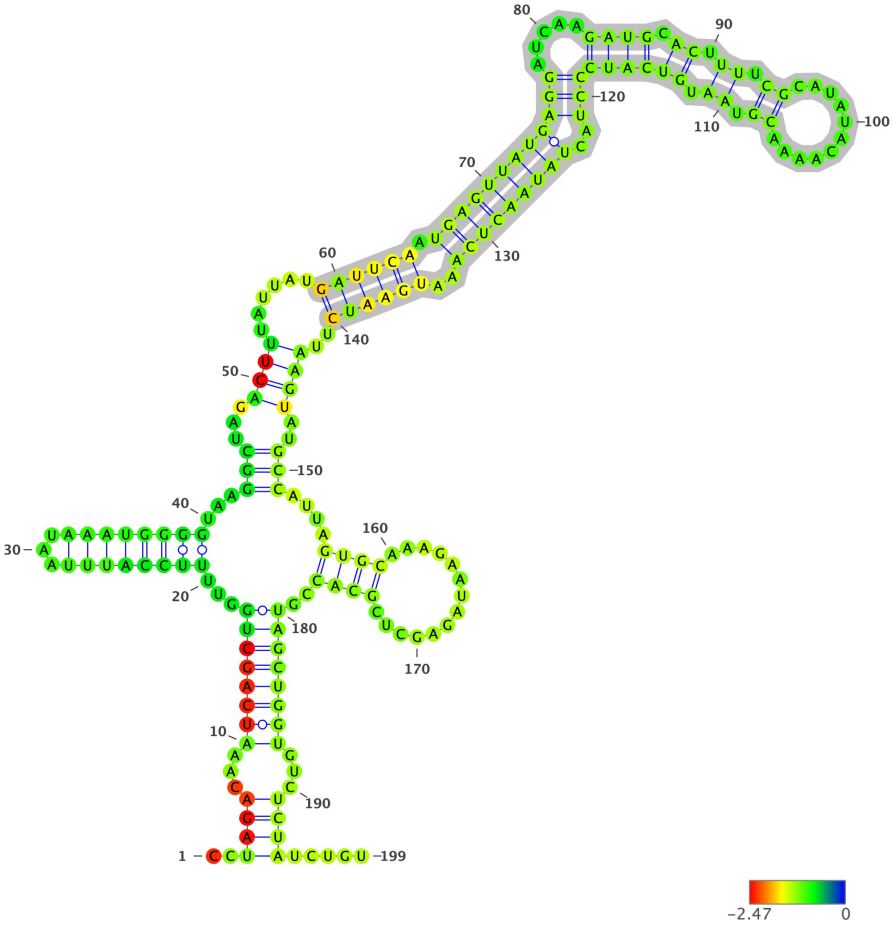
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 256 from nt 14989 to 15070 (nt 59 to 140)

```
5'-GATTCAATGAGTTATGAGGATCAAGATGCACTTTTCGCATATACAAAACGTAATGUCAUCCCUACUAUAACUCAAAUGAATC-3'
5'-(.((((..((...((((((.....((((.((.((.((...........)).)).)))))))))..)))...))...)))).)-3'
Motif MFE = -18.4; z-score = -3.52; ED = 11.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 14931 to 15129 (motif highlighted in silver):

```
5'-CCUAGACAAAUCAGCUGGUUUUCCAUUUAAUAAAUGGGGUAAGGCUAGACUUUAUUAUGAUUCAAUGAGUUAUGAGGAUCAAGAUGCACUUUUCGCAUAUACAAAACGUAA
UGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGU-3
5'-..((((...((((((((...((((((((...))))))))...(((...((((......((((((.(((((((((((((.....((((.((.((.((...........)).))
.)))))))))..)))))))))..))))))..))))..)))....((((..............))))..))))))))...))))).....-3'
MFE = -44.5; z-score = -1.59; ED = 36.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

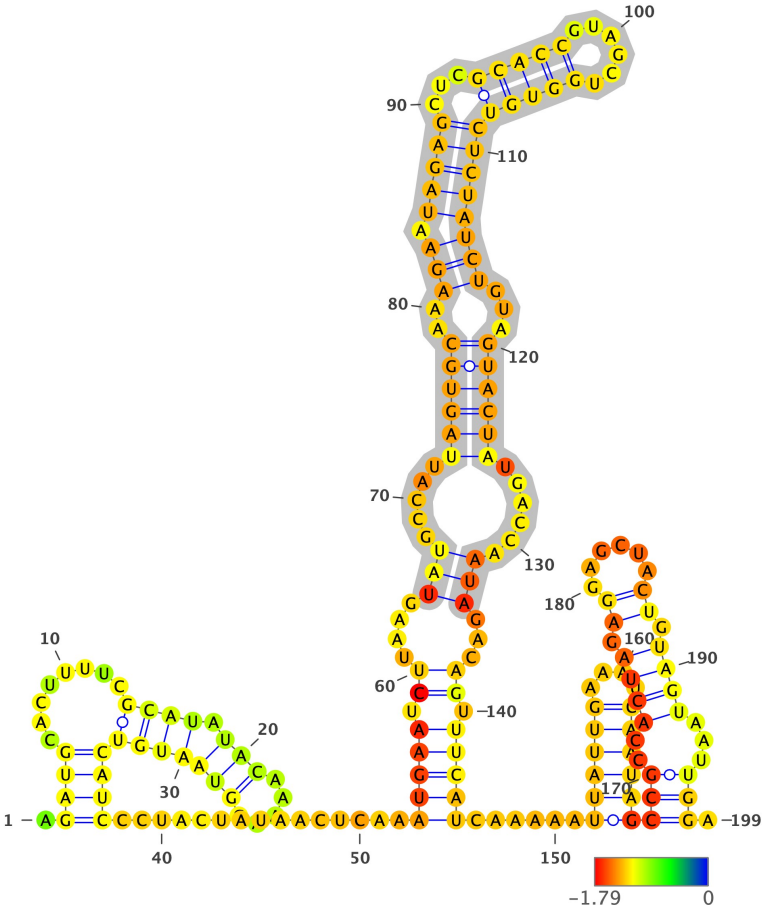
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 257 from nt 15076 to 15145 (nt 65 to 134)

```
5'-TATGCCATTAGTGCAAAGAATAGAGCTCGCACCGTAGCTGGUGUCUCUAUCUGTAGUACUATGACCAATA-3'
5'-(........((((((..(((.((((((...((((((......))))))))))))))...))))))........)-3'
Motif MFE = -20.0; z-score = -2.34; ED = 4.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15012 to 15210 (motif highlighted in silver):

```
5'-AGAUGCACUUUUCGCAUAUACAAAACGUAAUGUCAUCCCUACUAUAACUCAAAUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUC
UAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGA-3
5'-.((((........((((.(((.....)))))))))).............((((((.((....(((.....((((((..(((.((((((...((((((......))))))))))))))...))))))..)))).))))).....((((((....))))))(((..((((.((......)).)))))...))).-3'
MFE = -36.4; z-score = -0.61; ED = 35.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

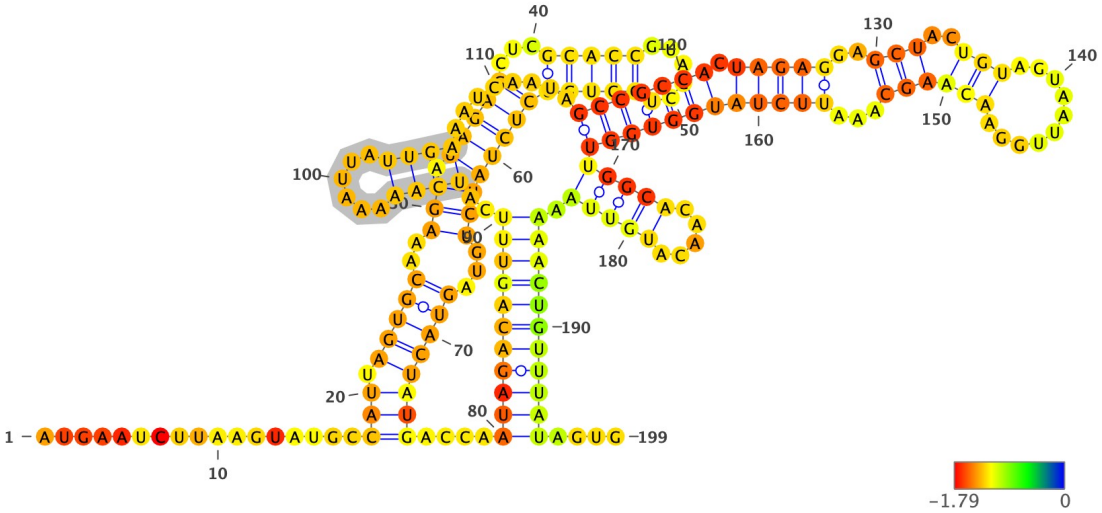
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 258 from nt 15156 to 15169 (nt 93 to 106)

```
5'-TCAAAAATTAUUGA-3'
5'-((((......))))-3'
Motif MFE = 0.0; z-score = 0.2; 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 15064 to 15262 (motif highlighted in silver):

```
5'-AUGAAUCUUAAGUAUGCCAUUAGUGCAAAGAAUAGAGCUCGCACCGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCA
AUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUG-3
5'-.................(((.(((((..(((.(((((...(((((......)))))))))))))...))))))))....((((((((((..((((......))))).....
...(((((((.(((((..(((..(((.........))))))...))))))))))))(((((.....))))).))))))))))....-3'
MFE = -48.1; z-score = -2.38; ED = 29.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

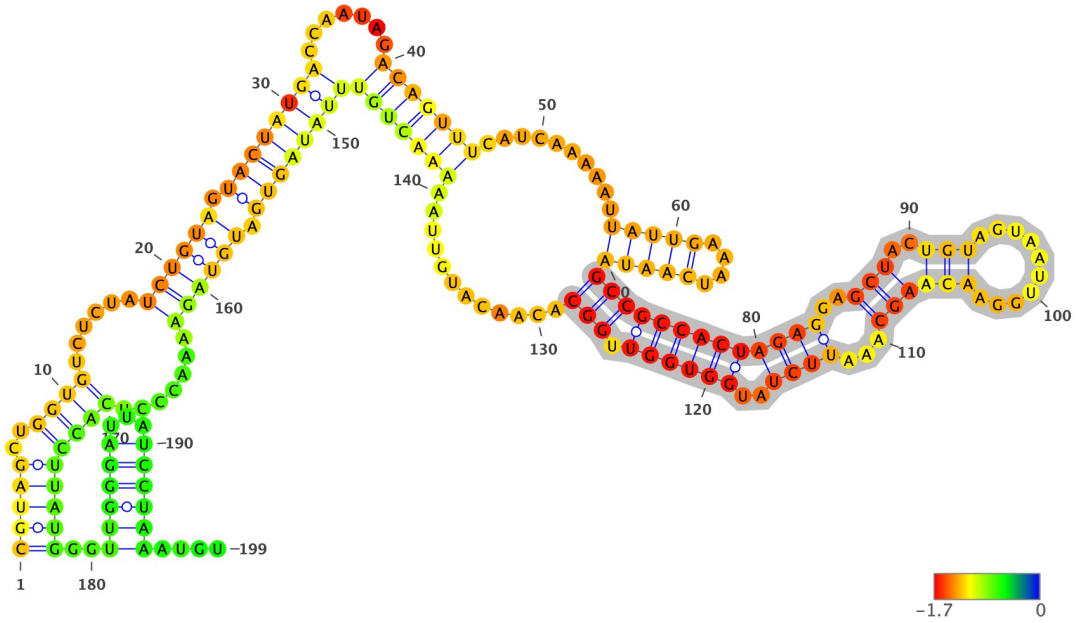
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 259 from nt 15178 to 15235 (nt 71 to 128)

```
5'-GCCGCCACTAGAGGAGCTACTGTAGTAATTGGAACAAGCAAATUCUATGGUGGUTGGC-3'
5'-(((((((((((...(((.................)))....)))..)))))).)))-3'
Motif MFE = -16.8; z-score = -2.2; ED = 13.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15108 to 15306 (motif highlighted in silver):

```
5'-CGUAGCUGGUGUCUCUAUCUGUAGUACUAUGACCAAUAGACAGUUUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAA
AUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUGAUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAUGU-3
5'-(((((..((((......((((((.((((((((.......((((((.........(((((....)))))((((((((((((..(((..(((..........))))))..
.))))..)))))).)))............))))))))))))))).))))))).......)))))))))..((((((...))))))....-3'
MFE = -41.5; z-score = -0.69; ED = 36.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

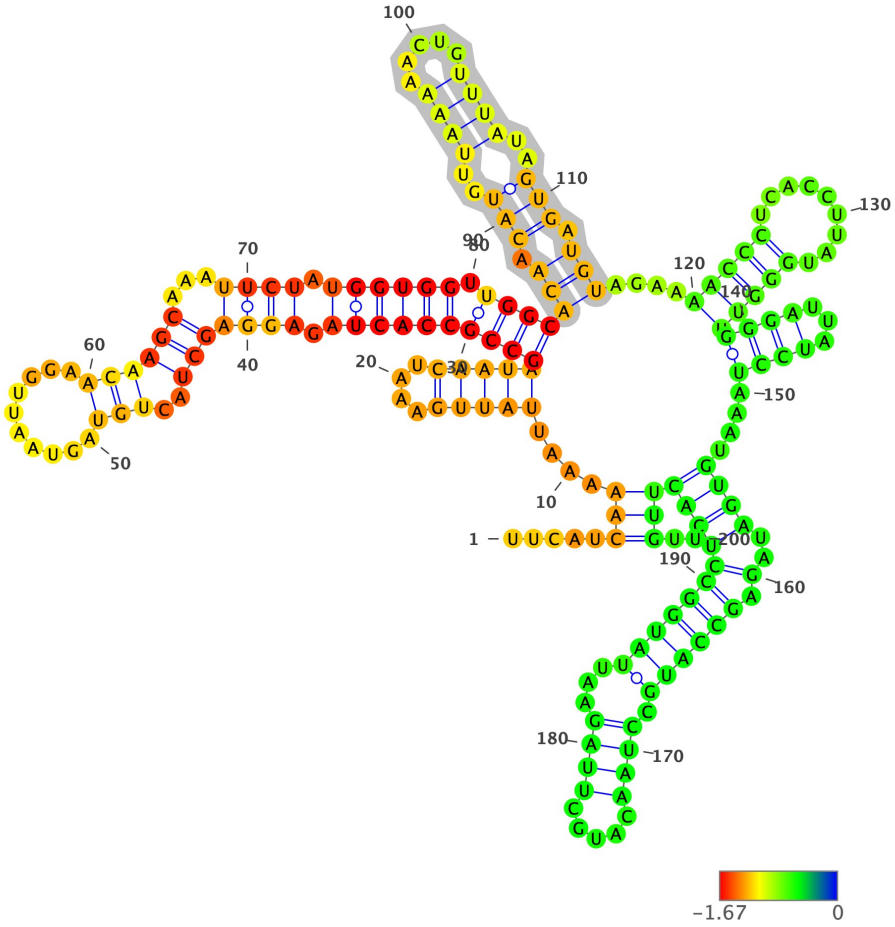
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 260 from nt 15236 to 15266 (nt 85 to 115)

```
5'-ACAACATGTTAAAAACTGTTTATAGUGAUGU-3'
5'-(((.(((.................))).)))-3'
Motif MFE = -3.5; z-score = -1.23; ED = 2.03
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15152 to 15351 (motif highlighted in silver):

```
5'-UUCAUCAAAAAUUAUUGAAAUCAAUAGCCGCCACUAGAGGAGCUACUGUAGUAAUUGGAACAAGCAAAUUCUAUGGUGGUUGGCACAACAUGUUAAAAACUGUUUAUAGUG
AUGUAGAAAACCCUCACCUUAUGGGUUGGGAUUAUCCUAAAUGUGAUAGAGCCAUGCCUAACAUGCUUAGAAUUAUGGCCUCACUUGUU-3
5'-.....(((....(((((....)))))((((((((((.(((((((..(((.........))))))...)))).)))))).))))(((.(((..((((.....))))..)))
.))).....(((((.........)))))((((...)))).....((((..(.((((((.((((.....))))...)))))))))))))..-3'
MFE = -44.6; z-score = -1.63; ED = 33.59
```

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(+)

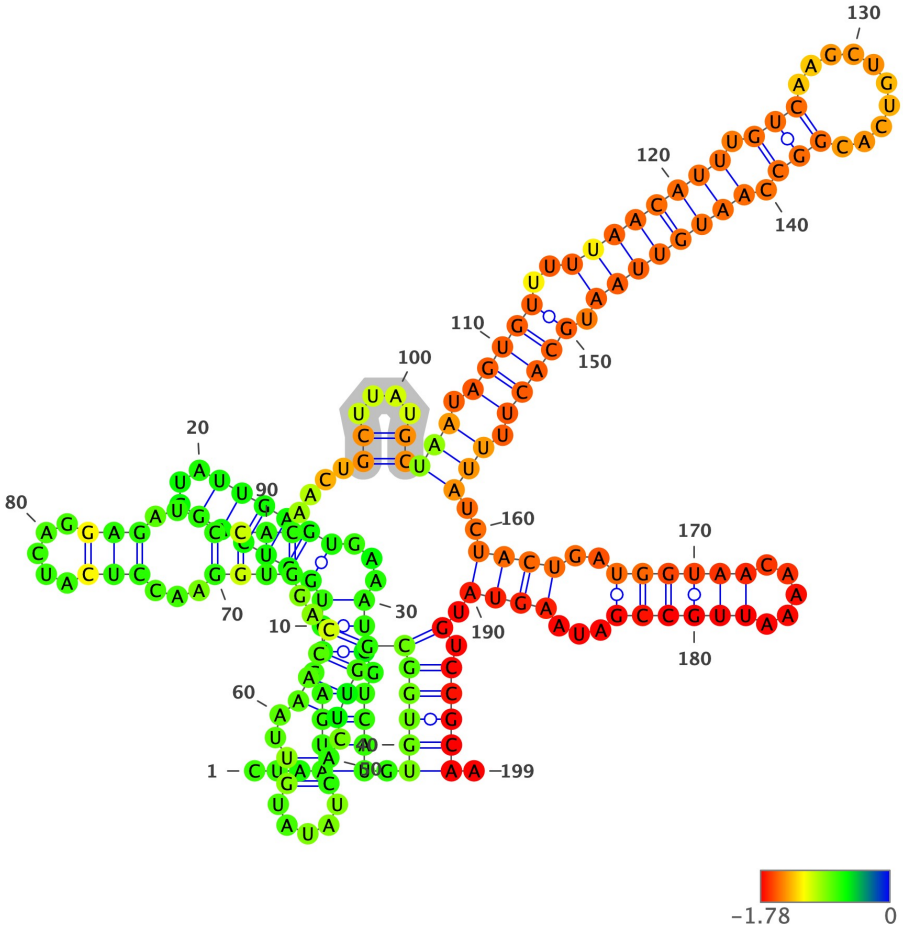
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 261 from nt 15502 to 15509 (nt 96 to 103)

```
5'-GCTTATGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.99
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15407 to 15605 (motif highlighted in silver):

```
5'-CUAAUGAGUGUGCUCAAGUAUUGAGUGAAAUGGUCAUGUGUGGCGGUUCACUAUAUGUUAAACCAGGUGGAACCUCAUCAGGAGAUGCCACAACUGCUUAUGCUAAUAGUG
UUUUUAACAUUUGUCAAGCUGUCACGGCCAAUGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAA-3
5'-...((((.(((((((((...))))))...))).)))).((((((((((.((.....)).)))).((((...(((.....)))...)))).....((....))(((.((((
(..((((((((.(((.........))).)))))))).))))).))).((((..((((((.....))))))...)))).).))))).-3'
MFE = -47.2; z-score = -1.0; 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(+)

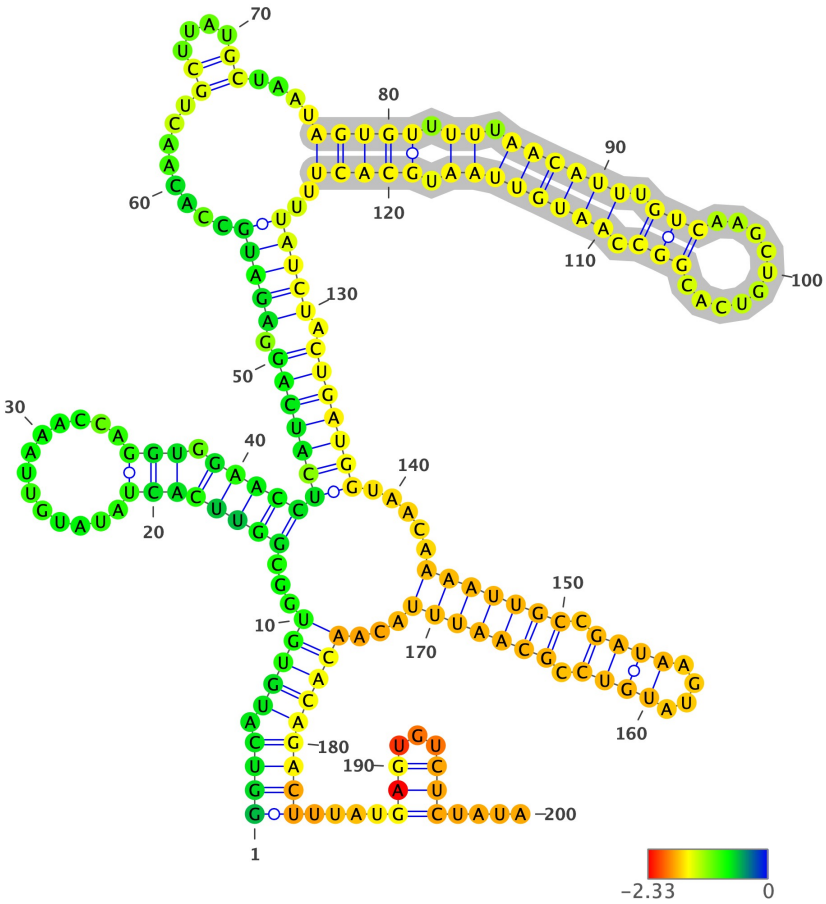
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 262 from nt 15514 to 15560 (nt 77 to 123)

```
5'-AGTGTTTTTAACATTTGTCAAGCTGTCACGGCCAAUGUUAATGCACU-3'
5'-(((((.((.(((((((.(((..........))).))))))))).)))))-3'
Motif MFE = -12.6; z-score = -2.84; ED = 4.37
```



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 15438 to 15637 (motif highlighted in silver):

```
5'-GGUCAUGUGUGGCGGUUCACUAUAUGUUAAACCAGGUGGAACCUCAUCAGGAGAUGCCACAACUGCUUAUGCUAAUAGUGUUUUUAACAUUUGUCAAGCUGUCACGGCCAA
UGUUAAUGCACUUUUAUCUACUGAUGGUAACAAAAUUGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUA-3
5'-((((.(((((...((((((((.............))).)))))(((((((.(((((.........((....)).....(((((.((.(((((((.(((..........))).))
)))))).)))))..)))))).))))))).....(((((((.((((....)))).)))))))...))))))))).....(((...))).....-3'
MFE = -46.1; z-score = -1.89; ED = 18.79
```

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(+)

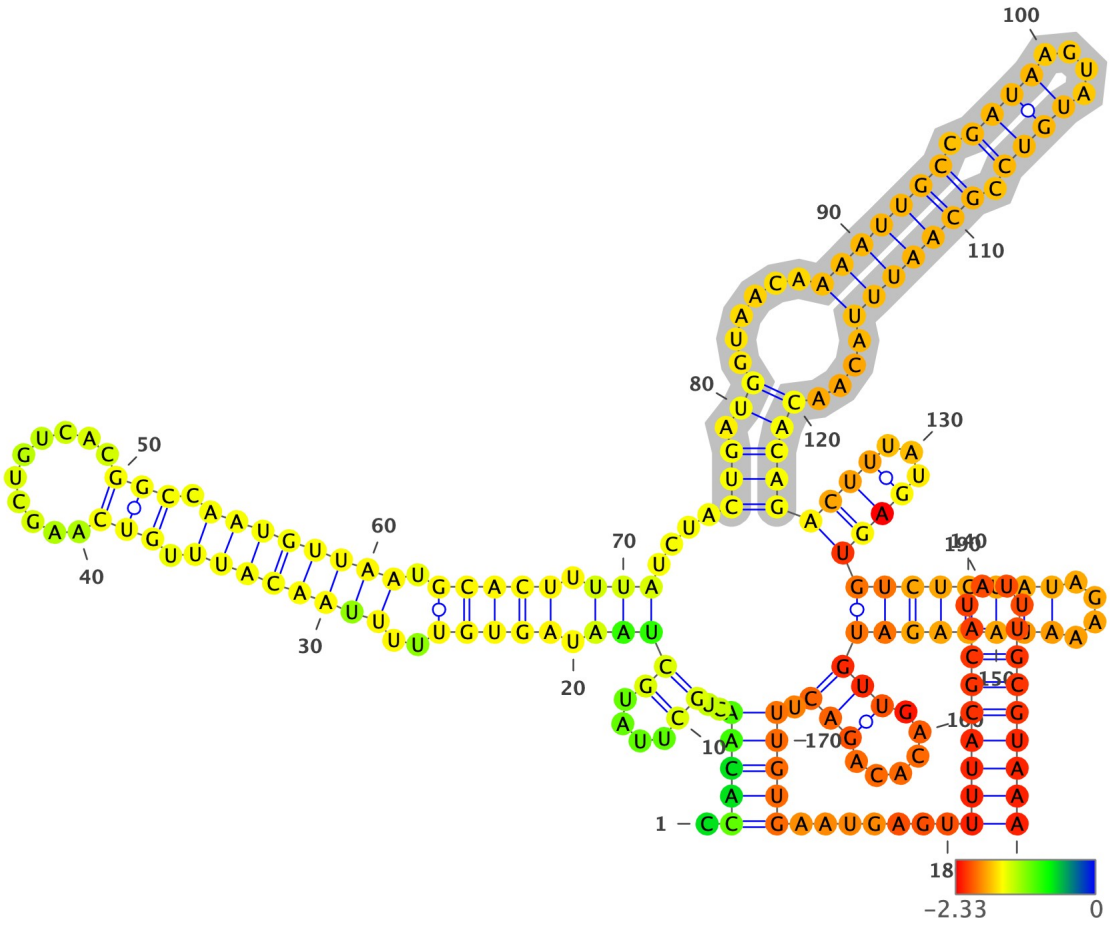
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 263 from nt 15569 to 15617 (nt 76 to 124)

```
5'-CTGATGGTAACAAAATTGCCGATAAGTAUGUCCGCAAUUUACAACACAG-3'
5'-(((.((......(((((((.((((....)))).)))))))....)))))-3'
Motif MFE = -9.6; z-score = -1.89; 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 = -2.59; 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(+)

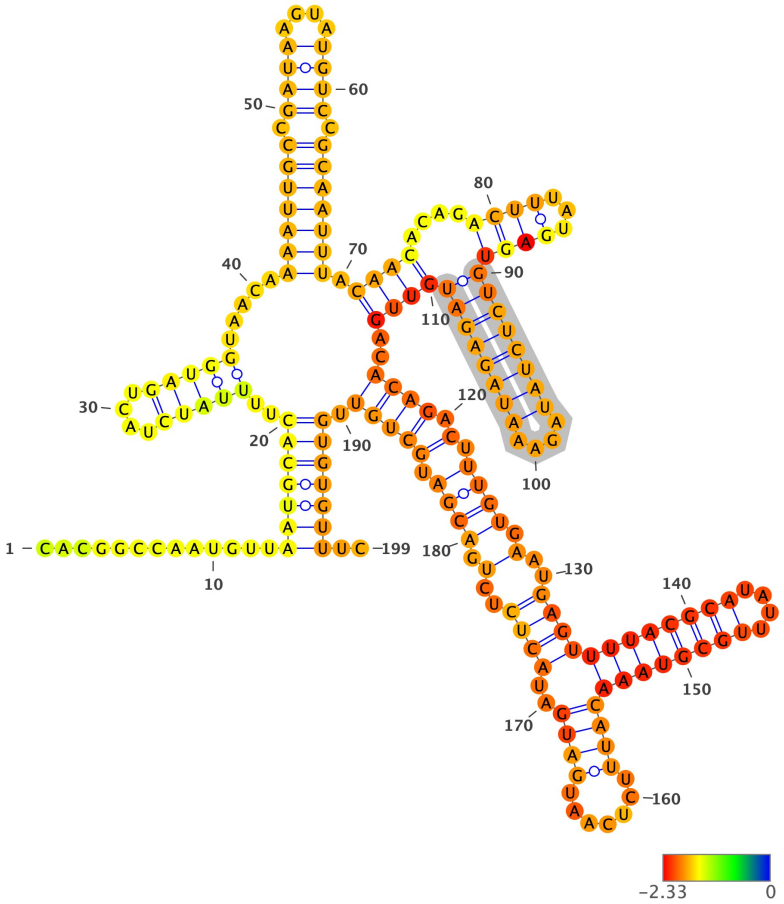
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 264 from nt 15629 to 15648 (nt 90 to 109)

```
5'-GTCTCTATAGAAATAGAGAU-3'
5'-((((((........))))))-3'
Motif MFE = -7.2; z-score = -6.27; 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 = -1.36; ED = 54.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

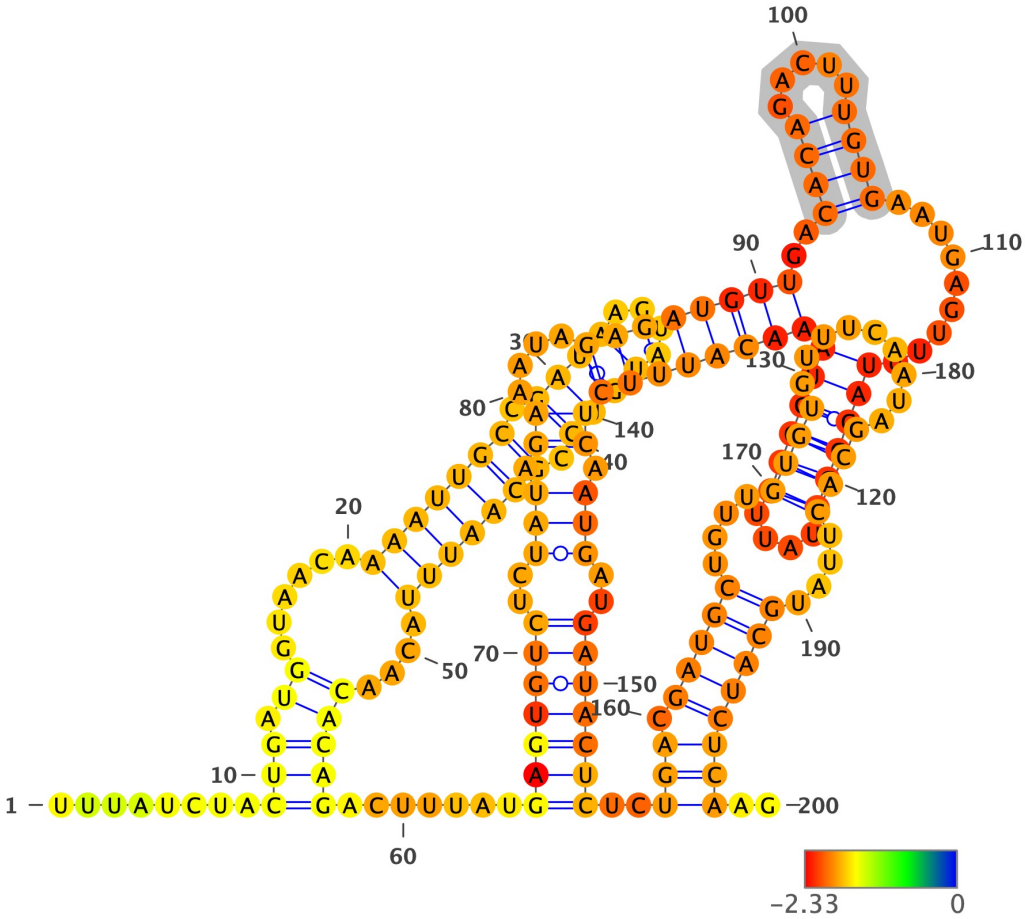
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 265 from nt 15654 to 15666 (nt 94 to 106)

```
5'-CACAGACTTUGUG-3'
5'-((((.....))))-3'
Motif MFE = -1.2; z-score = -3.13; 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 = -2.28; 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(+)

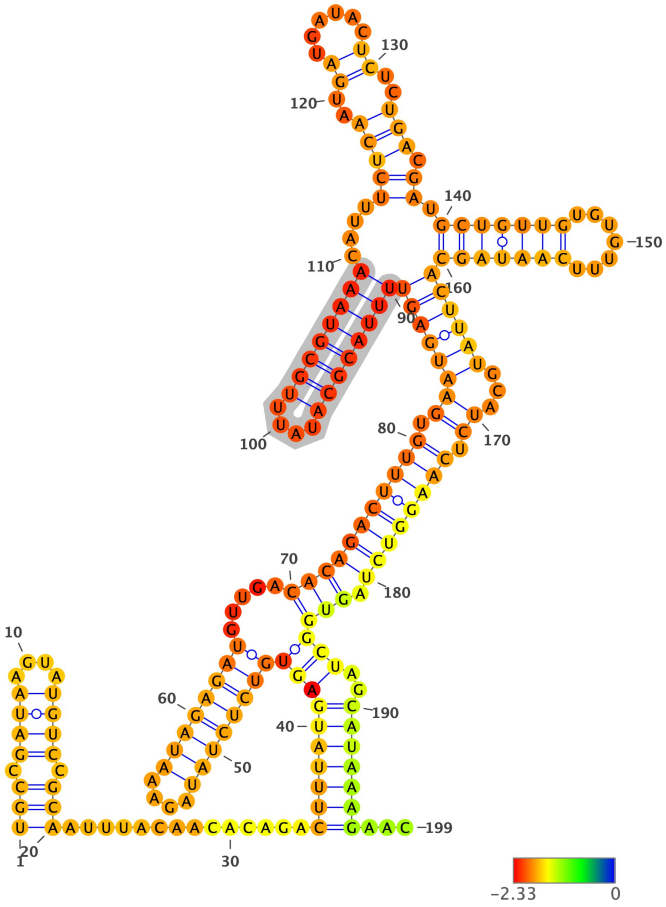
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 266 from nt 15674 to 15693 (nt 90 to 109)

```
5'-TTTACGCATATTTGCGUAAA-3'
5'-(((((((......)))))))-3'
Motif MFE = -8.4; z-score = -7.58; 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 15585 to 15783 (motif highlighted in silver):

```
5'-UGCCGAUAAGUAUGUCCGCAAUUUACAACACAGACUUUAUGAGUGUCUCUAUAGAAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACA
UUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAAC-3
5'-(((.((((....)))).))).............(((((((((((((((((....))))))))).....((((((((((.(((((((((((((((....))))))))..
..(((((..((......))..))).)).(((((((.......)))))))))))))...)).)))))))).))))))..)))))))...-3'
MFE = -53.1; z-score = -2.23; ED = 27.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

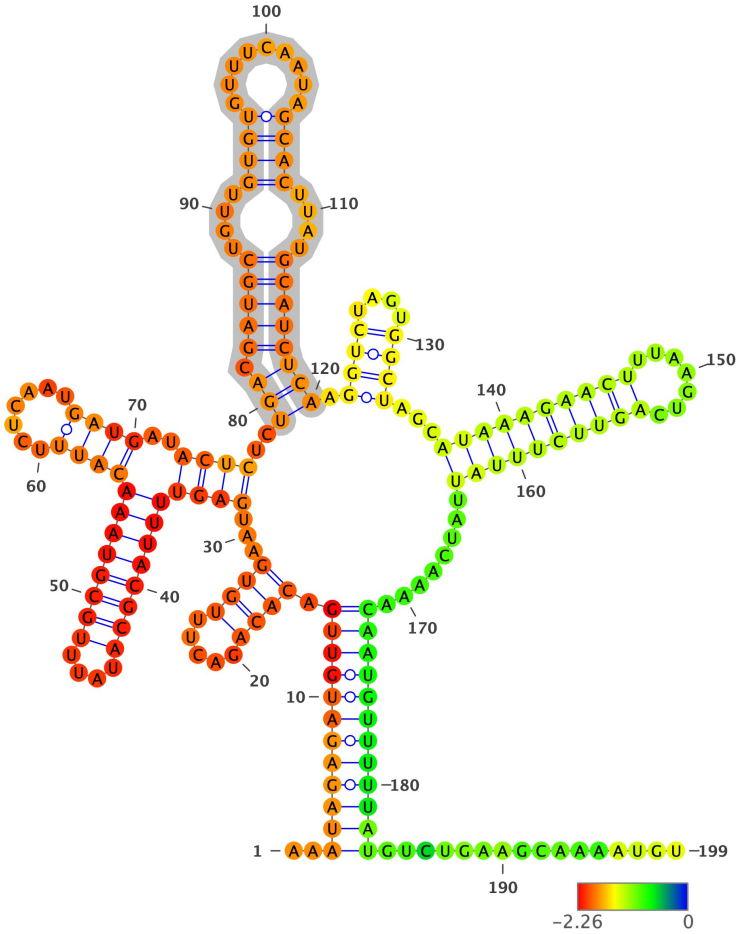
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 267 from nt 15717 to 15758 (nt 79 to 120)

```
5'-TGACGATGCTGTTGTGTGTTTCAATAGCACTTATGCAUCUCA-3'
5'-(((.(((((....((((.........))))....)))))))-3'
Motif MFE = -11.5; z-score = -2.38; ED = 7.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15639 to 15837 (motif highlighted in silver):

```
5'-AAAUAGAGAUGUUGACACAGACUUUGUGAAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUA
UGCAUCUCAAGGUCUAGUGGCUAGCAUAAAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGU-3
5'-..((((((((((((.((((.....)))))...((((((((((((....))))))))))(((.......)))))..)))))..(((.((((((....((((.........))))))...
.))))))))).((((....))))...((((((((((.......))))))))))........))))))))))))).................-3'
MFE = -46.3; z-score = -3.66; ED = 38.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

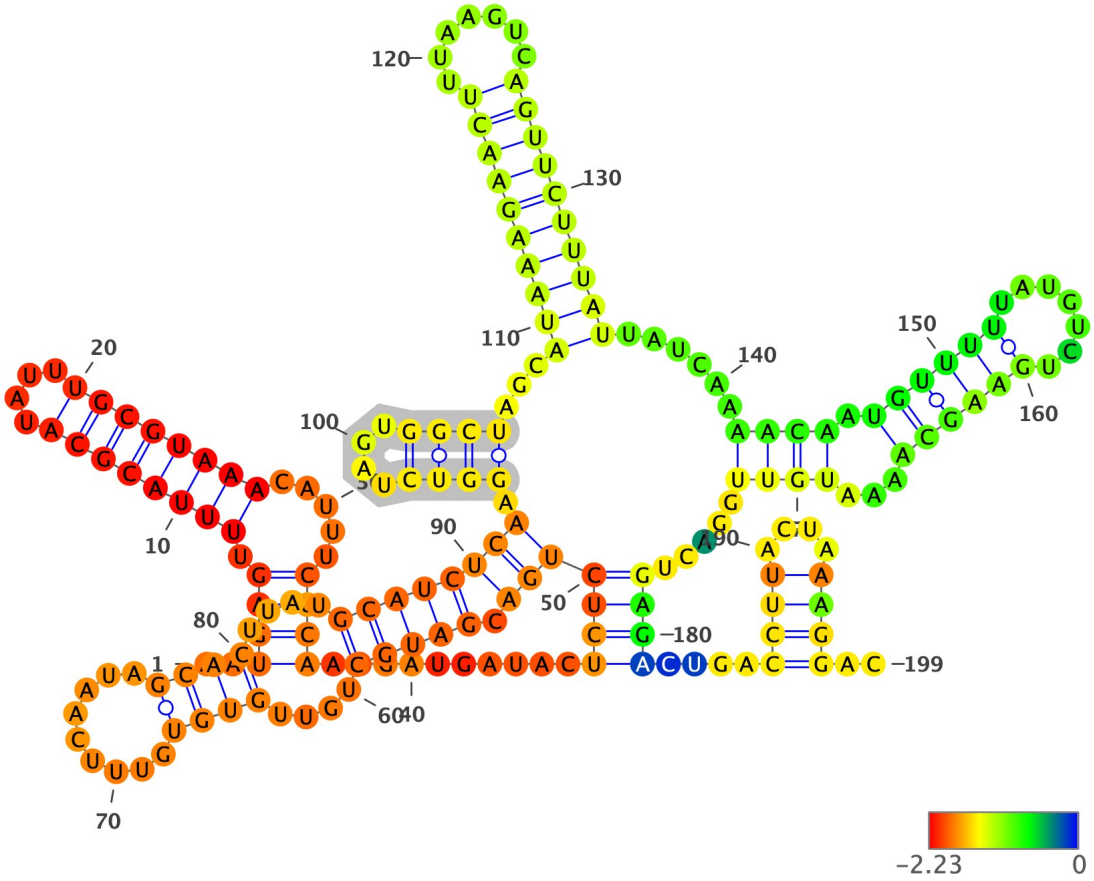
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 268 from nt 15760 to 15771 (nt 94 to 105)

```
5'-GGTCTAGTGGCU-3'
5'-((((....))))-3'
Motif MFE = -2.1; z-score = -4.7; ED = 0.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15667 to 15865 (motif highlighted in silver):

```
5'-AAUGAGUUUUACGCAUAUUUGCGUAAACAUUUCUCAAUGAUGAUACUCUCUGACGAUGCUGUUGUGUGUUUCAAUAGCACUUAUGCAUCUCAAGGUCUAGUGGCUAGCAUA
AAGAACUUUAAGUCAGUUCUUUAUUAUCAAAACAAUGUUUUUAUGUCUGAAGCAAAAUGUUGGACUGAGACUGACCUUACUAAAGGAC-3
5'-..(((((.(((((((((....)))))))))).....)))).........(((((((.(((((....((((.........))))))....)))))))).((((....)))))...(((
(((((((.......)))))))))).....((((.((((((.......))))))...)))).....)))))....((((....)))))..-3'
MFE = -44.5; z-score = -1.97; ED = 48.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

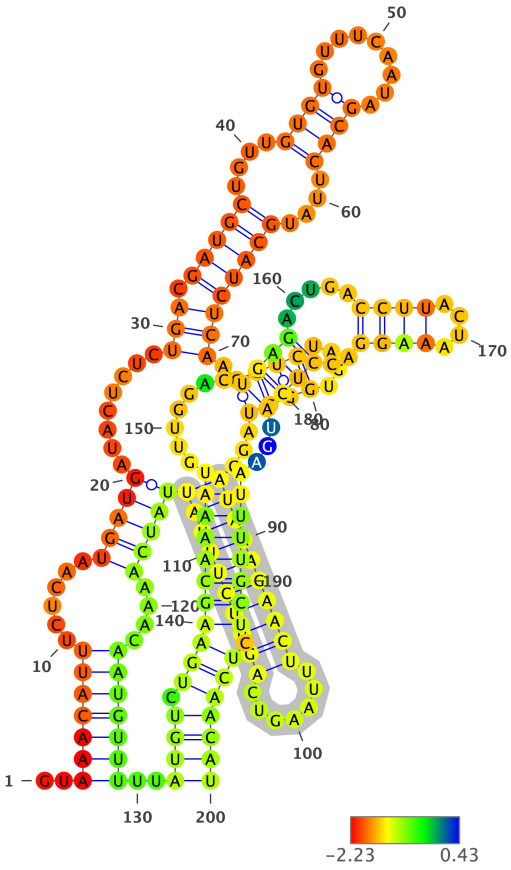
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 269 from nt 15775 to 15801 (nt 87 to 113)

```
5'-ATAAAGAACTTTAAGTCAGUUCUUUAU-3'
5'-((((((((((.......))))))))))-3'
Motif MFE = -7.5; z-score = -3.98; 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 = -1.65; 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(+)

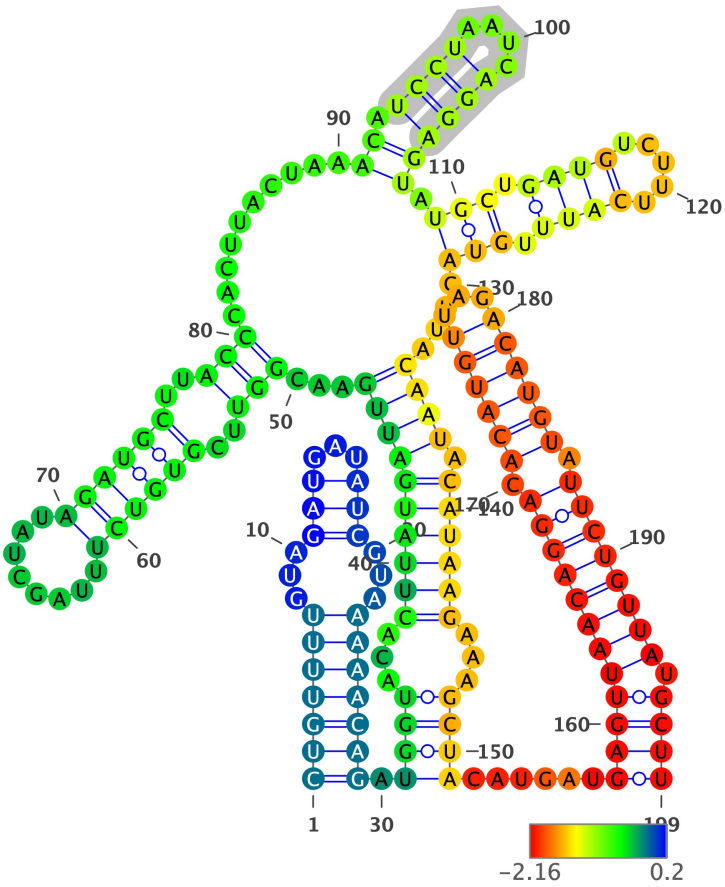
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 270 from nt 16056 to 16067 (nt 94 to 105)

```
5'-TCCTAATCAGGA-3'
5'-((((....))))-3'
Motif MFE = -2.0; z-score = -7.57; ED = 0.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 15963 to 16161 (motif highlighted in silver):

```
5'-CUGUUUUGUAGAUGAUAUCGUAAAAACAGAUGGUACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUGC
UGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUU-3
5'-(((((((...(((...))))...)))))))..((((...((((((((((...(((..((((((........))))))..)))..........((.((((....)))))).(((
.((((.....)))).)))....)))))..)))))))...))))......((((((((((((.((((((...))))))).)))))))).))))-3'
MFE = -46.7; z-score = -2.42; ED = 15.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

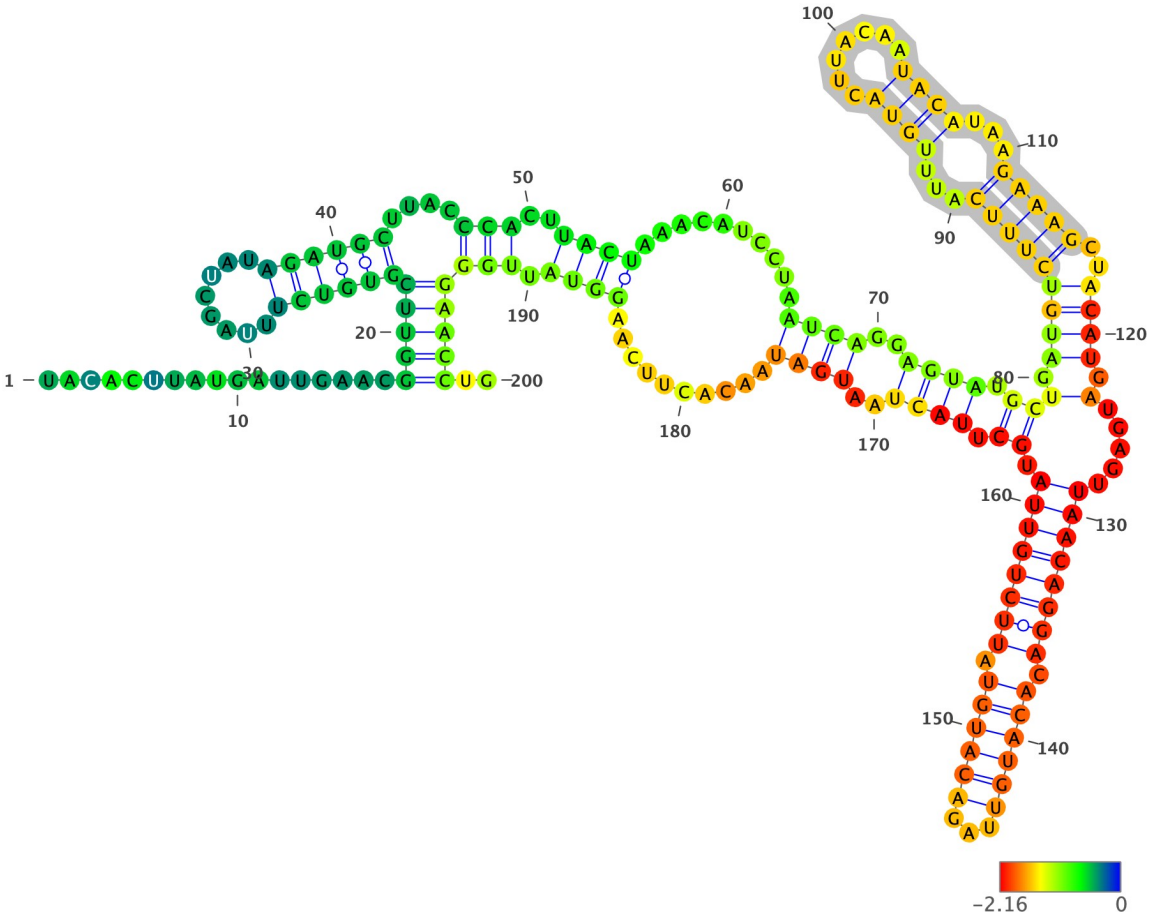
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 271 from nt 16080 to 16110 (nt 85 to 115)

```
5'-CTTTCATTTGTACTTACAAUACATAAGAAAG-3'
5'-(((((....(((.......)))....)))))-3'
Motif MFE = -3.9; z-score = -2.07; 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 15996 to 16195 (motif highlighted in silver):

```
5'-UACACUUAUGAUUGAACGGUUCGUGUCUUUAGCUAUAGAUGCUUACCCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAG
AAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCUGUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUG-3
5'-.................(((((((((((........))))))....(((..((((..........((((..((((.(((.(((((((((...((((.......))))...)
))))..)))).).....((((((((.((((((...)))))).))))))))).)).))))..))))..........)))).))))))))..-3'
MFE = -43.3; z-score = -1.52; ED = 31.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

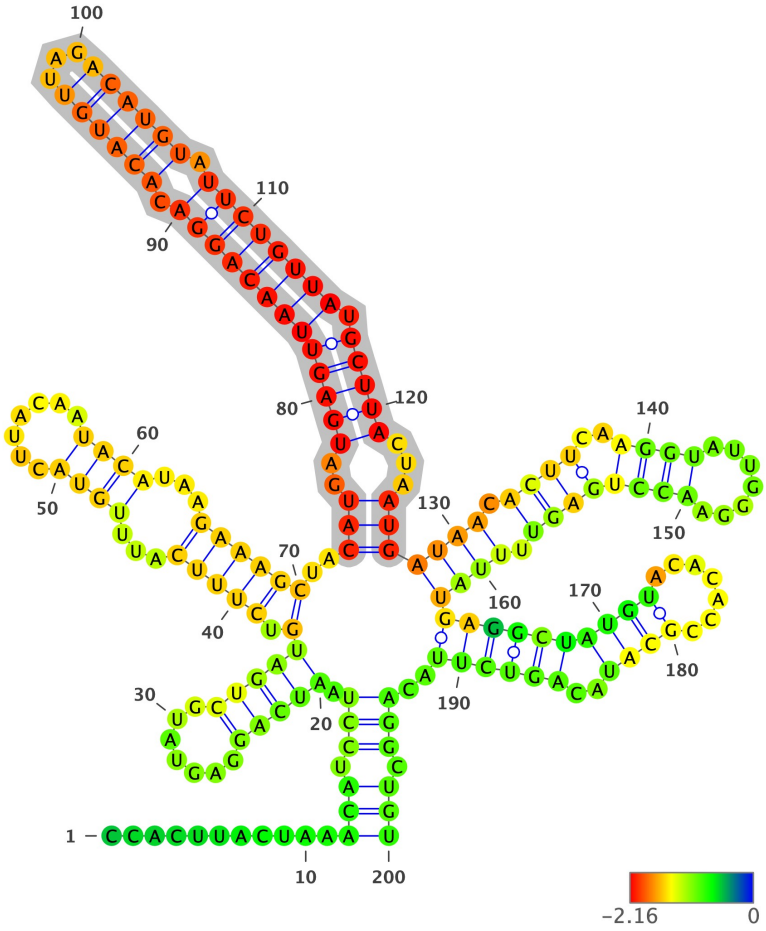
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 272 from nt 16114 to 16168 (nt 73 to 127)

```
5'-CATGATGAGTTAACAGGACACATGTTAGACAUGUAUUCUGUUATGCUUACTAAUG-3'
5'-(((..((((((((((((.(((((.....))))).)))))))).))))))...)))-3'
Motif MFE = -17.3; z-score = -3.66; ED = 3.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16042 to 16241 (motif highlighted in silver):

```
5'-CCACUUACUAAACAUCCUAAUCAGGAGUAUGCUGAUGUCUUUCAUUUGUACUUACAAUACAUAAGAAAGCUACAUGAUGAGUUAACAGGACACAUGUUAGACAUGUAUUCU
GUUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGU-3
5'-...........(((.(((.(((((.......)))))).(((((...((((.......)))).)))))).)))).(((..((((((((((((.(((((((...)))))))))))))))))))))).)))))...)))(((((.(((((..((((.......))))))))).)))).((((((((((.......)))))..)))))..))).)))-3'
MFE = -44.3; z-score = -1.85; ED = 41.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

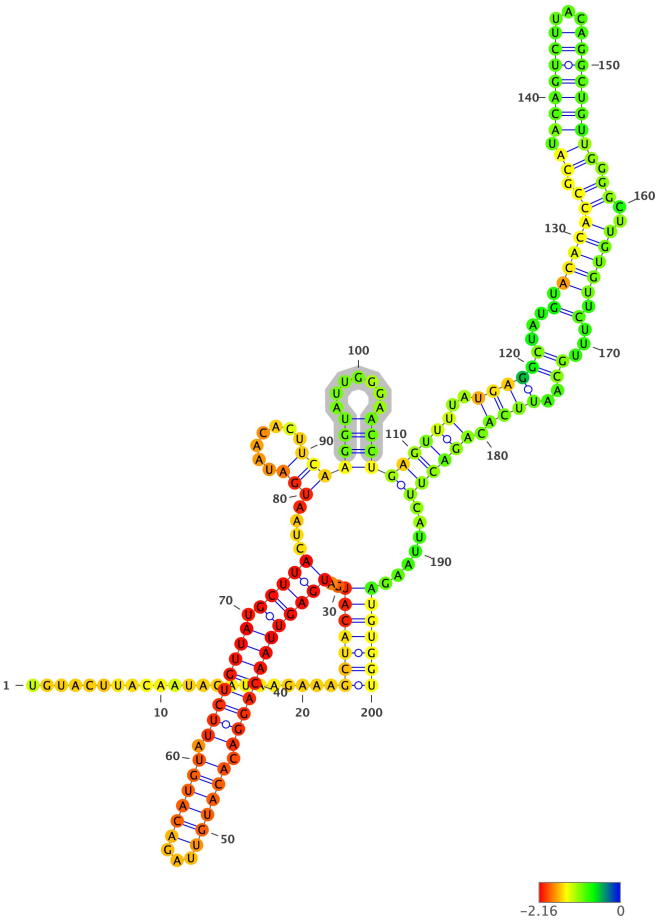
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 273 from nt 16181 to 16193 (nt 94 to 106)

```
5'-GGTATTGGGAACC-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.52; 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 = -2.21; 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(+)

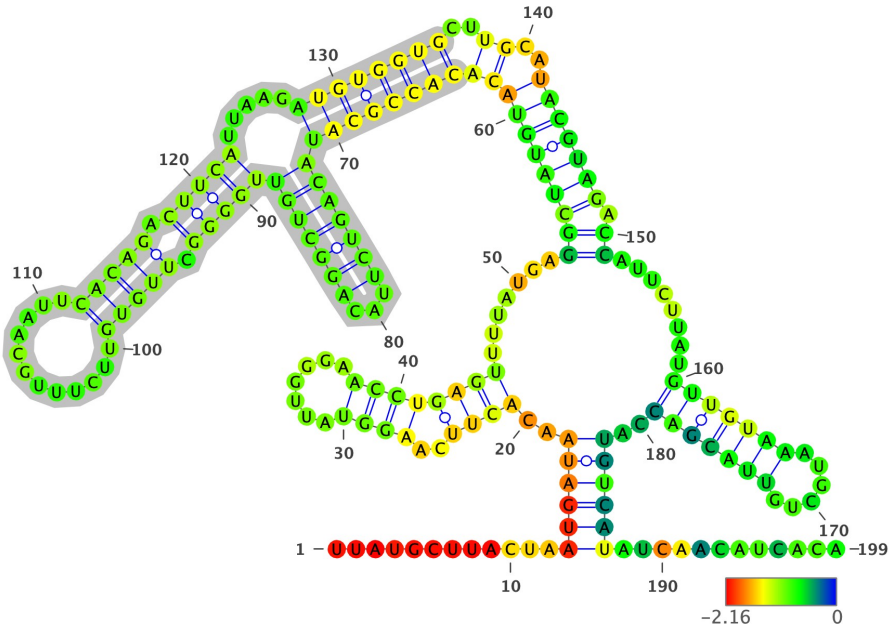
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 274 from nt 16217 to 16288 (nt 64 to 135)

```
5'-CACCGCATACAGTCTTACAGGCUGTTGGGGCTTGTGTTCTTTGCAATTCACAGACUUCATTAAGAUGUGGUG-3'
5'-(((((((.................(((((.(((((............))))).))))).....)))))))-3'
Motif MFE = -22.5; z-score = -2.62; ED = 3.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16154 to 16352 (motif highlighted in silver):

```
5'-UUAUGCUUACUAAUGAUAACACUUCAAGGUAUUGGGAACCUGAGUUUUAUGAGGCUAUGUACACACCGCAUACAGUCUUACAGGCUGUUGGGGCUUGUGUUCUUUGCAAUU
CACAGACUUCAUUAAGAUGUGGUGCUUGCAUACGUAGACCAUUCUUAUGUUGUAAAUGCUGUUACGACCAUGUCAUAUCAACAUCACA-3
5'-............((((((..((((..((((.......))))))))).......(((((((((((((((((((((((...)))))))))))))))))))))))))))(((((.(((((.....
)))))..)))))).....)))))))..))..)))))))..))........(((((((.....)))))))..))))))............-3'
MFE = -44.2; z-score = -0.51; ED = 34.4
```

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(+)

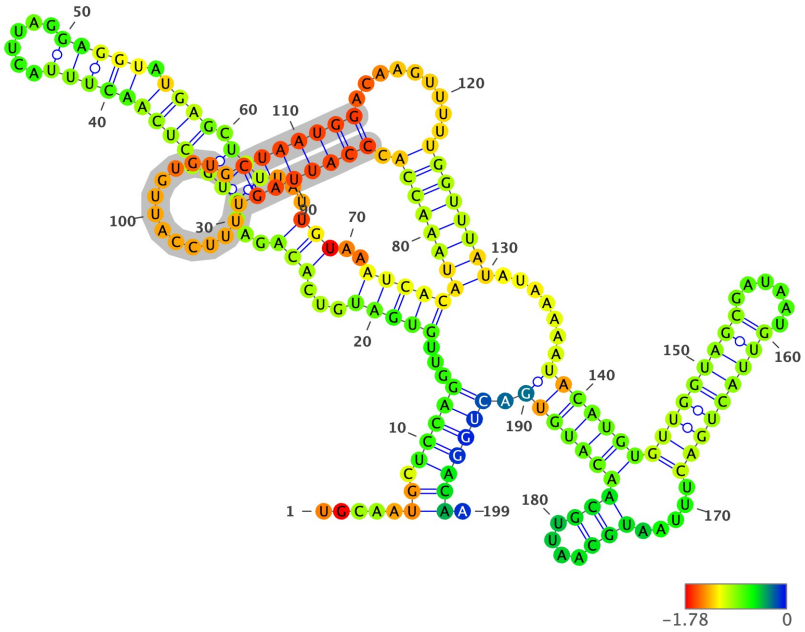
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 275 from nt 16469 to 16496 (nt 86 to 113)

```
5'-CCATTAGTTTTCCATTGTGTGCUAAUGG-3'
5'-(((((((.............)))))))-3'
Motif MFE = -7.5; z-score = -2.74; 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 16384 to 16582 (motif highlighted in silver):

```
5'-UGCAAUGCUCCAGGUUGUGAUGUCACAGAUGUGACUCAACUUUACUUAGGAGGUAUGAGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAU
GGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGACUUUAAUGCAAUUGCAACAUGUGACUGGACAA-3
5'-.....((.(((((...((((((...(((...(((.((((((((((......))))).))))).)))...))))..)))))(((((((.(((((((.............)))))))
)).........)))))))).......((((((((((((((((......))))))))))).....(((....))))))))))).)))))).-3'
MFE = -49.6; z-score = -2.45; ED = 47.92
```

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(+)

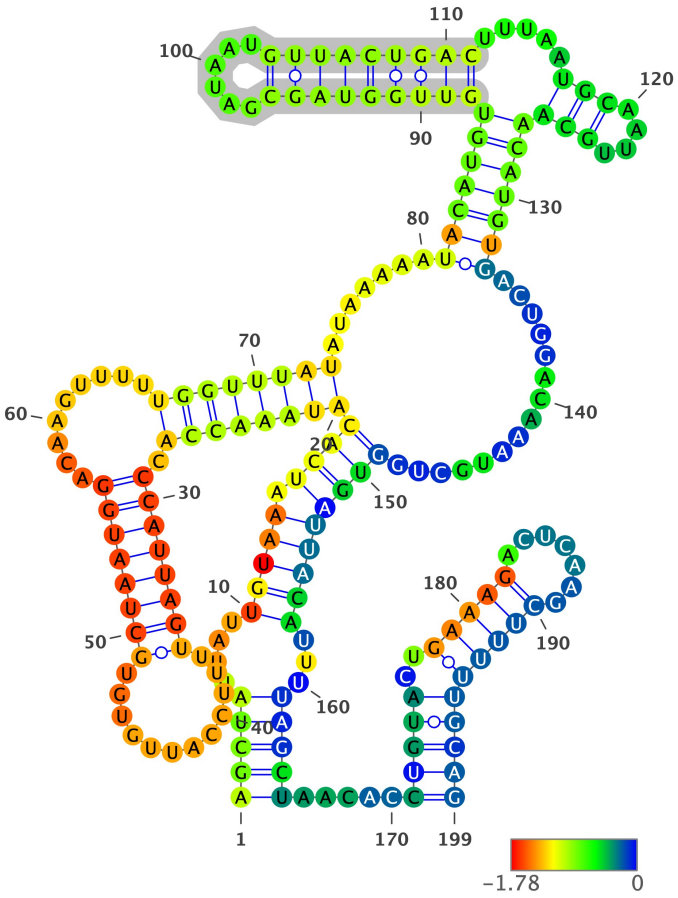
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 276 from nt 16528 to 16551 (nt 88 to 111)

```
5'-GTTGGTAGCGATAATGUUACUGAC-3'
5'-(((.................)))-3'
Motif MFE = -8.0; z-score = -3.21; ED = 0.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16441 to 16639 (motif highlighted in silver):

```
5'-AGCUAUUAUUGUAAAUCACAUAAACCACCCAUUAGUUUUCCAUUGUGUGCUAAUGGACAAGUUUUUGGUUUAUAUAAAAAUACAUGUGUUGGUAGCGAUAAUGUUACUGAC
UUUAAUGCAAUUGCAACAUGUGACUGGACAAAUGCUGGUGAUUACAUUUUAGCUAACACCUGUACUGAAAGACUCAAGCUUUUUGCAG-3
5'-(((((....((((((.(((((((((((.(((((((.............)))))))).........)))))))).......(((((((((((((((.....)))))))))
.....(((....)))))))))).............)))))))...)))))).....(((((..(((((.......)))))))))-3'
MFE = -45.0; z-score = -1.86; 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(+)

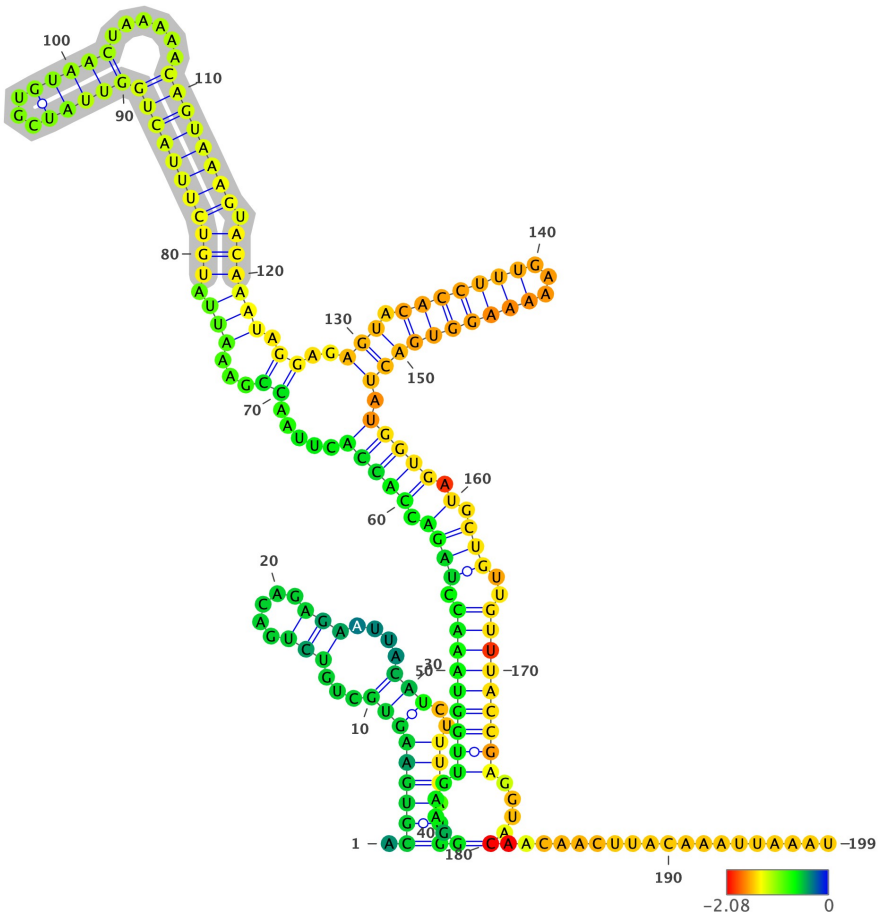
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 277 from nt 16776 to 16817 (nt 79 to 120)

```
5'-TGTCTTTACTGGTTATCGTGTAACTAAAAACAGUAAAGTACA-3'
5'-((((((((((((.....................)))))))).)))-3'
Motif MFE = -9.5; z-score = -2.72; 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 = -1.11; 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(+)

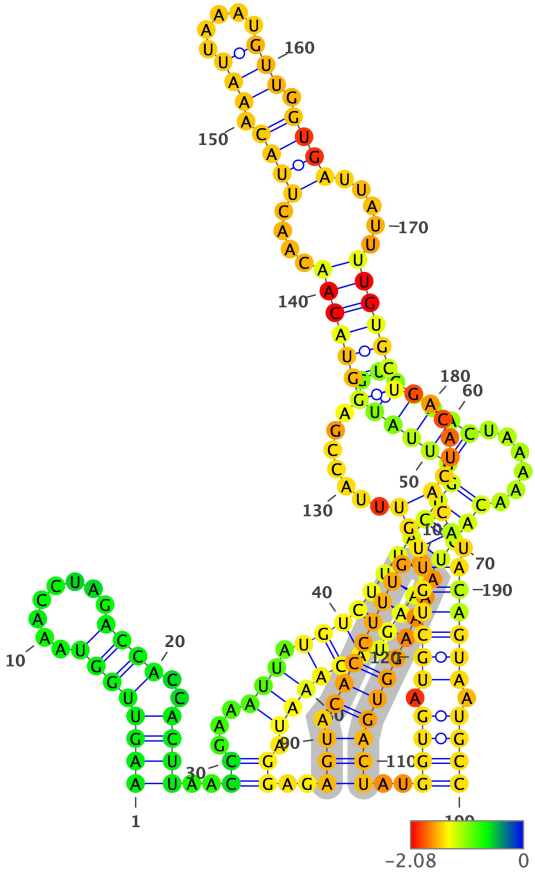
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 278 from nt 16826 to 16849 (nt 88 to 111)

```
5'-AGTACACCTTTGAAAAAGGUGACU-3'
5'-(((.((((.........)))))))-3'
Motif MFE = -8.0; z-score = -4.04; 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 = -1.13; ED = 47.68
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

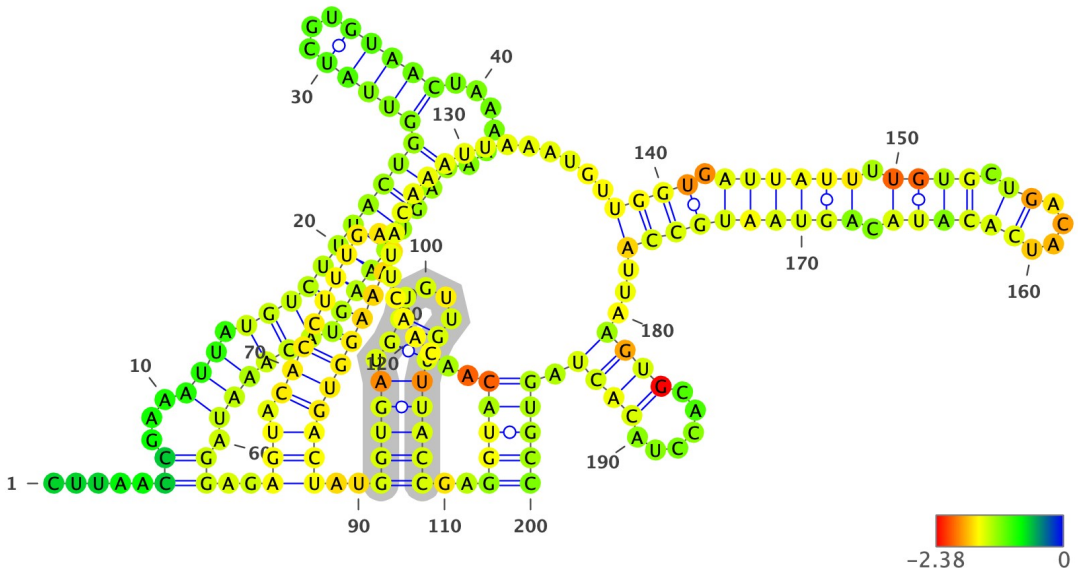
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 279 from nt 16852 to 16870 (nt 91 to 109)

```
5'-GGTGATGCTGTTGUTUACC-3'
5'-((((..((....)).))))-3'
Motif MFE = -3.6; z-score = -1.61; 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 16762 to 16961 (motif highlighted in silver):

```
5'-CUUAACCGAAAUUAUGUCUUUACUGGUUAUCGUGUAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGA
GGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCC-3
5'-.....((...(((.((((((((((((((((...)))))).....)))))))).)))))).))..(((.(((((((...)))))))))..(((((.((....)))))))..
(((((.....................((((.((((((.((((.((....)))))).)))))))))...((((......)))).)))))-3'
MFE = -41.1; z-score = -1.9; ED = 35.21
```

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(+)

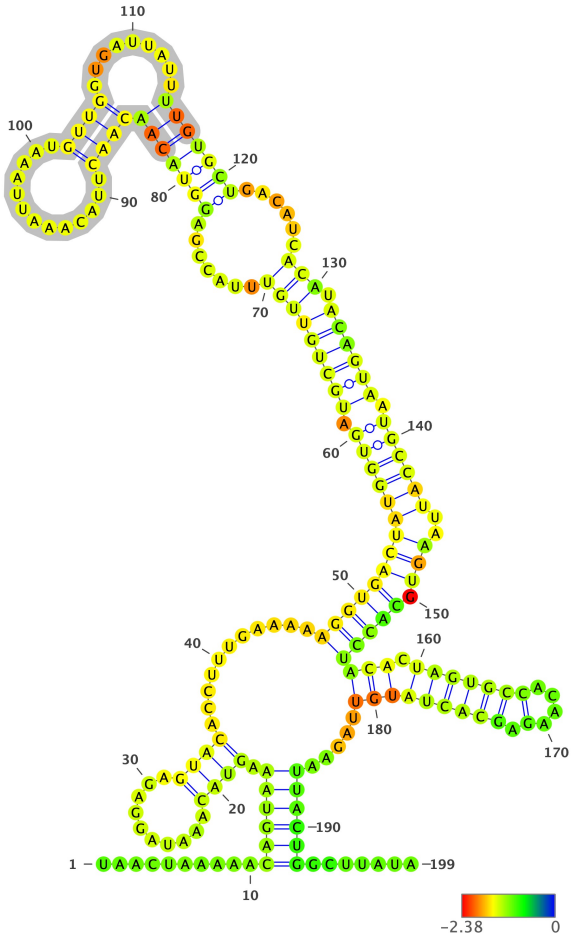
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 280 from nt 16877 to 16912 (nt 82 to 117)

```
5'-CAACAACTTACAAATTAAATGUUGGTGATTATTTUG-3'
5'-((.((((.............)))).........))-3'
Motif MFE = -2.5; z-score = 0.06; ED = 8.06
```



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 16796 to 16994 (motif highlighted in silver):

```
5'-UAACUAAAAACAGUAAAGUACAAAUAGGAGAGUACACCUUUGAAAAAGGUGACUAUGGUGAUGCUGUUGUUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUU
AUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUGUUAGAAUUACUGGCUUAUA-3
5'-..........((((((.((((..........))))...........(((((((((((((.(((((((((.......((((((((((.............))))......
...)))))))......))).))))))).))))))..))).)))))(((.(((((((....).)))))))))).....))))))).......-3'
MFE = -44.7; z-score = -2.52; ED = 25.65
```

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(+)

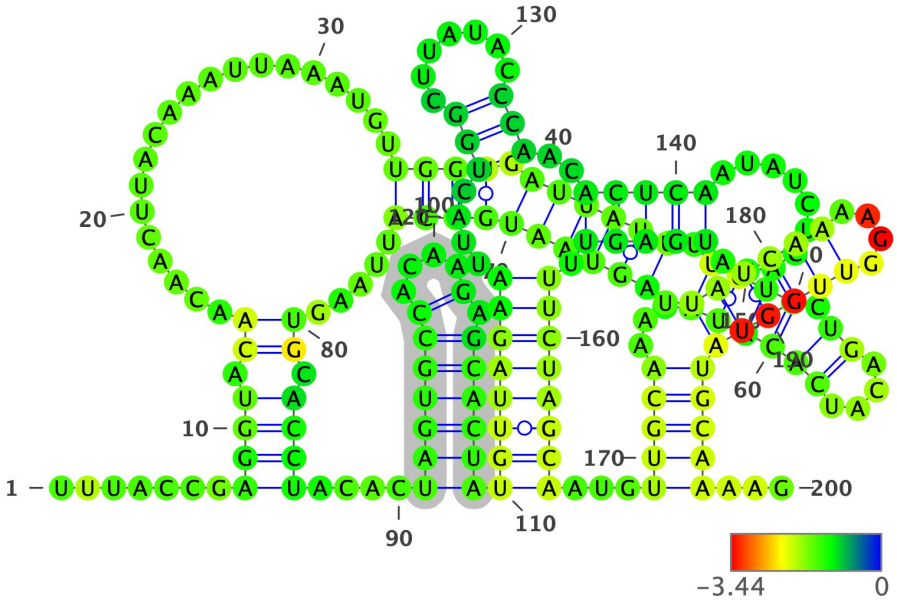
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 281 from nt 16955 to 16973 (nt 91 to 109)

```
5'-TAGTGCCACAAGAGCACUA-3'
5'-(((((.........)))))-3'
Motif MFE = -6.0; z-score = -4.35; 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 16865 to 17064 (motif highlighted in silver):

```
5'-UUUACCGAGGUACAACAACUUACAAAUUAAAUGUUGGUGAUUAUUUUGUGCUGACAUCACAUACAGUAAUGCCAUUAAGUGCACCUACACUAGUGCCACAAGAGCACUAUG
UUAGAAUUACUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAG-3
5'-.......((((.((.....................((((.((((((.((((.((....)))))).))))))))))).....)).))))....(((((((....).))))))((
((((((....(((.......)))..(((((..........)))))).))))))))...(((((...((((((....)))))))))))...-3'
MFE = -34.5; z-score = -0.08; ED = 66.7
```

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(+)

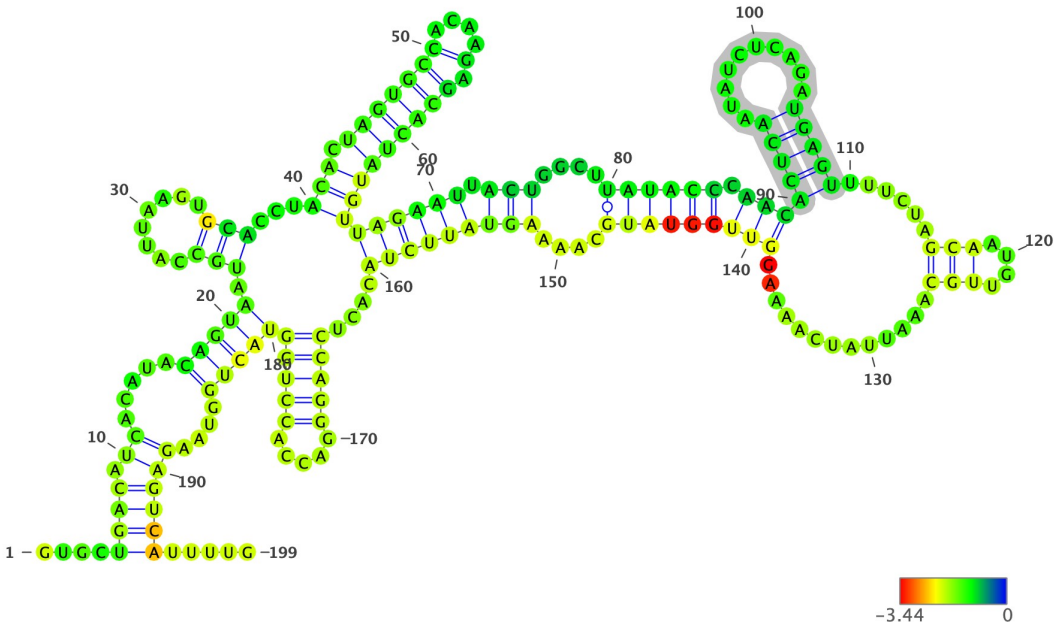
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 282 from nt 17001 to 17020 (nt 90 to 109)

```
5'-ACTCAATATCTCAGAUGAGU-3'
5'-(((((..........)))))-3'
Motif MFE = -2.1; z-score = -1.65; 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 = -1.02; ED = 44.74
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

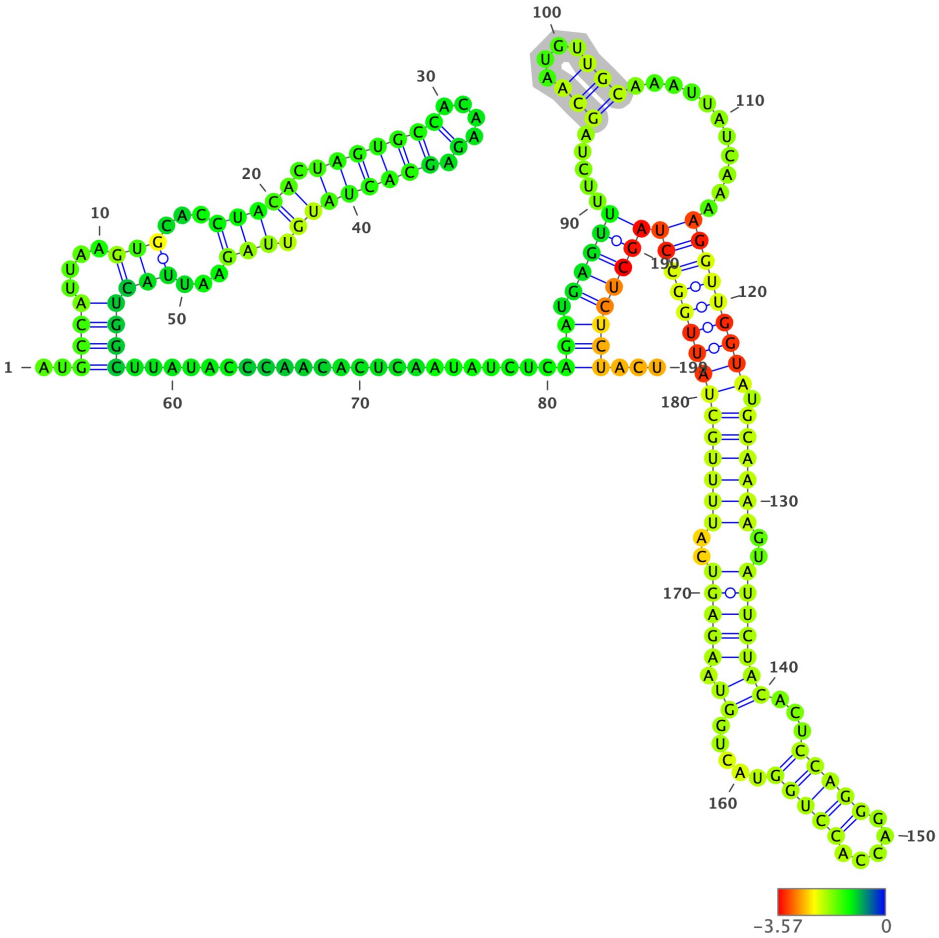
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 283 from nt 17027 to 17036 (nt 95 to 104)

```
5'-GCAATGTUGC-3'
5'-(((....)))-3'
Motif MFE = -0.4; z-score = -3.04; 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 = -2.29; ED = 34.47
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

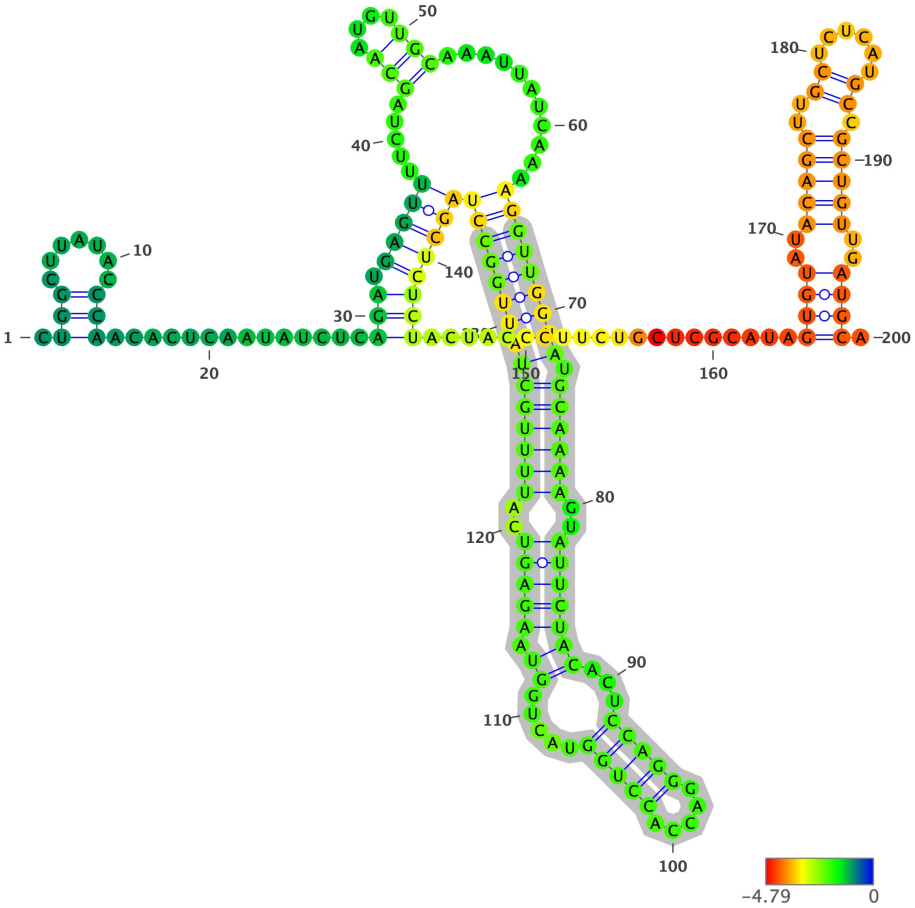
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 284 from nt 17050 to 17118 (nt 66 to 134)

```
5'-GTTGGTATGCAAAAGTATTCTACACTCCAGGGACCACCUGGTACTGGUAAGAGUCAUUUUGCUATTGGC-3'
5'-(((...(.(((((((..(((((((...(((((.....)))))).....)).)))))..)))))))...)))-3'
Motif MFE = -22.3; z-score = -2.85; ED = 4.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 16985 to 17184 (motif highlighted in silver):

```
5'-CUGGCUUAUACCCAACACUCAAUAUCUCAGAUGAGUUUUCUAGCAAUGUUGCAAAUUAUCAAAAGGUUGGUAUGCAAAAGUAUUCUACACUCCAGGGACCACCUGGUACUG
GUAAGAGUCAUUUUGCUAUUGGCCUAGCUCUCUACUACCCUUCUGCUCGCAUAGUGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCA-3
5'-.(((.......)))..............(((.(((((.....(((....))).........((((((((.(((((((..(((((((...(((((.....)))))).....
)).)))))..))))))))))))))))))))))).....................((((..(((((..((......)).)))))..)))).-3'
MFE = -46.5; z-score = -1.34; ED = 28.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

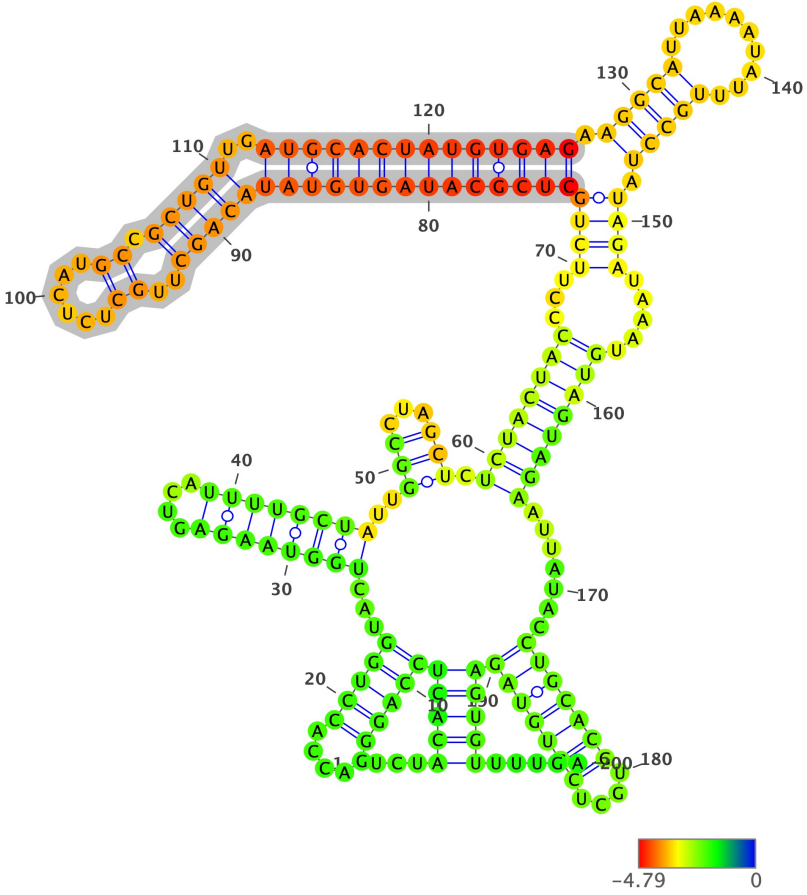
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 285 from nt 17141 to 17193 (nt 74 to 126)

```
5'-CTCGCATAGTGTATACAGCTTGCTCTCATGCCGCUGUTGAUGCACUAUGUGAG-3'
5'-(((((((((((((((((((..((......)).)))))..))))))))))))))-3'
Motif MFE = -27.7; z-score = -5.68; 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 = -4.84; 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(+)

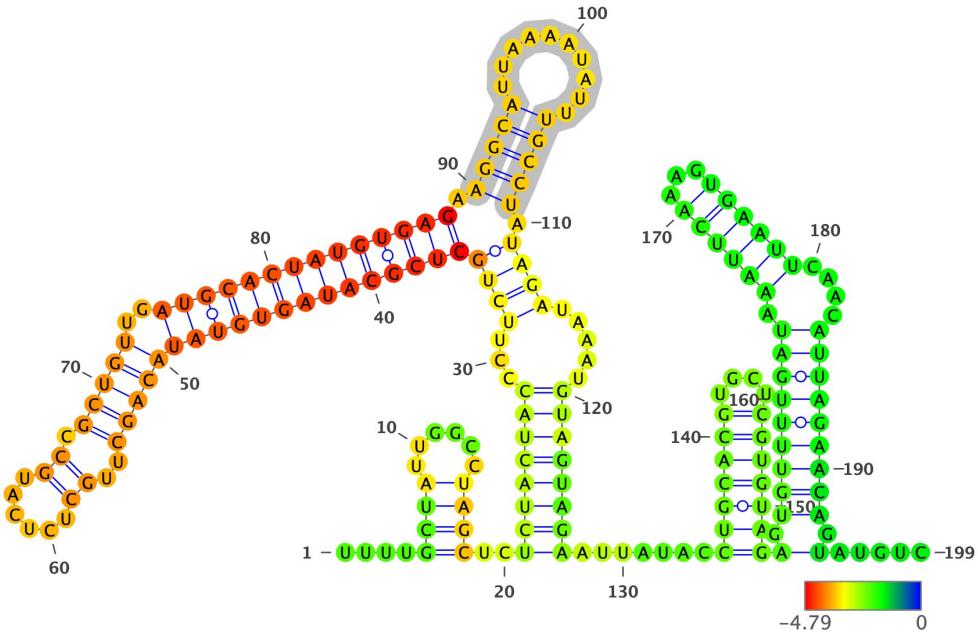
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 286 from nt 17195 to 17214 (nt 90 to 109)

```
5'-AGGCATTAAAATATTUGCCU-3'
5'-(((((..........)))))-3'
Motif MFE = -5.1; z-score = -5.52; 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 = -5.29; 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(+)

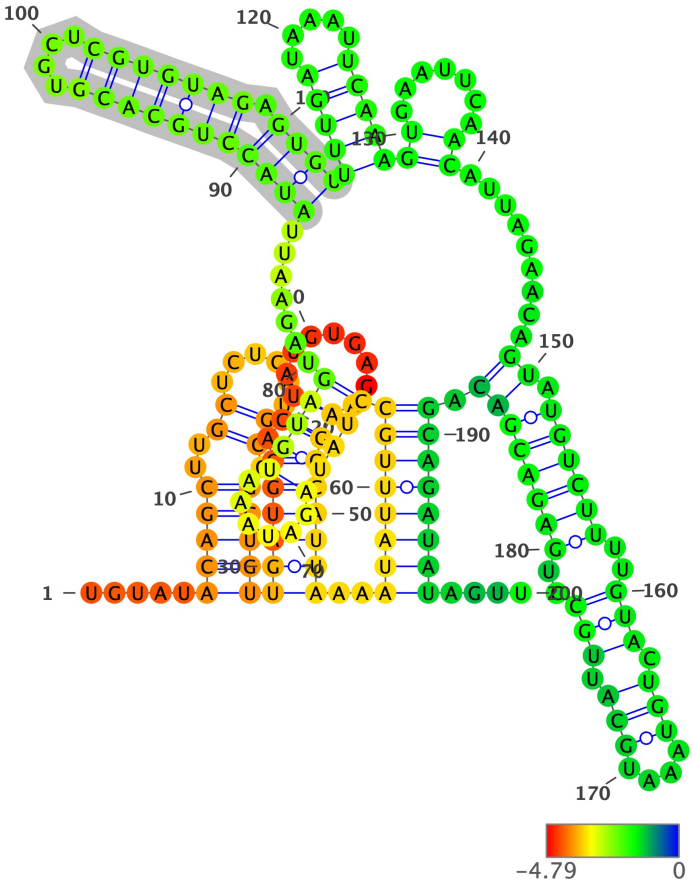
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 287 from nt 17236 to 17262 (nt 87 to 113)

```
5'-ATACCTGCACGTGCTCGUGUAGAGUGU-3'
5'-((((((((((......)))))).))))-3'
Motif MFE = -11.9; z-score = -3.67; 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 17150 to 17349 (motif highlighted in silver):

```
5'-UGUAUACAGCUUGCUCUCAUGCCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGU
GUUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUU-3
5'-.....(((((..((......)).)))))((((((.((........))))))))..((((((((((((.....)))))).......((((((((((....)))))))).))
))(((((.....)))))((.......)).........((.((((((..(((.(((....))).))).)))))))).))))))))....-3'
MFE = -48.0; z-score = -2.24; ED = 60.61
```

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(+)

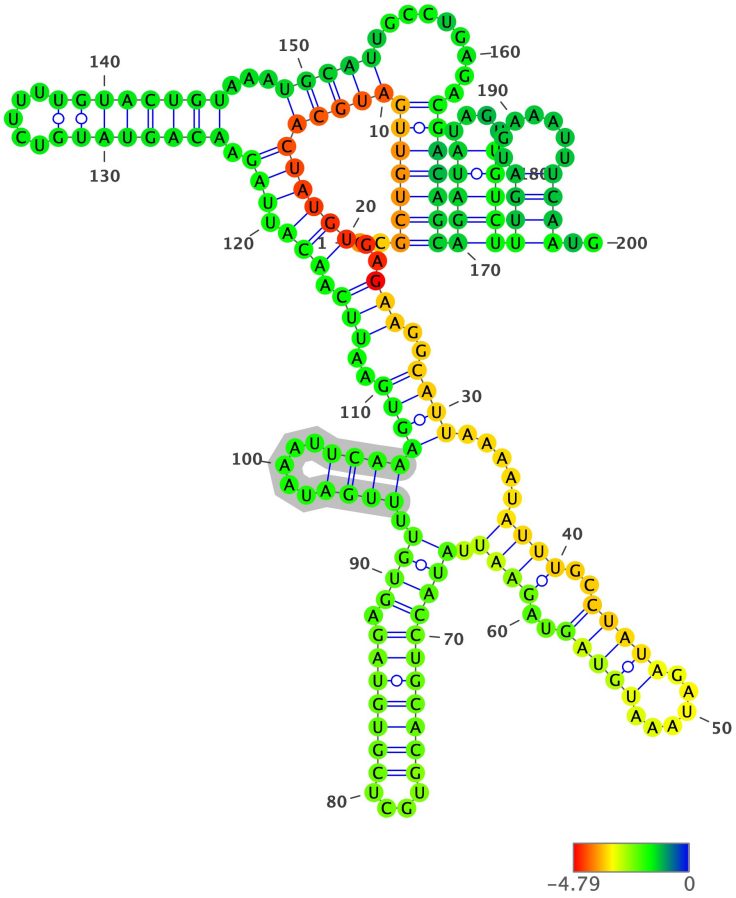
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 288 from nt 17264 to 17276 (nt 94 to 106)

```
5'-TTGATAAATUCAA-3'
5'-((((.....))))-3'
Motif MFE = -0.5; z-score = -5.82; 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 17171 to 17370 (motif highlighted in silver):

```
5'-CCGCUGUUGAUGCACUAUGUGAGAAGGCAUUAAAAUAUUUGCCUAUAGAUAAAUGUAGUAGAAUUAUACCUGCACGUGCUCGUGUAGAGUGUUUUGAUAAAUUCAAAGUGA
AUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUG-3
5'-..(((((((((((((((((..(((..((((.....((((..(((((......)))))..)))).((((((((((....)))))))).)))).((((.....))))))))).
.))).))).))).((((((((.....))))))))...)))))).........)))))))(((((....)))))((((.......))))..-3'
MFE = -45.7; z-score = -1.9; ED = 56.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

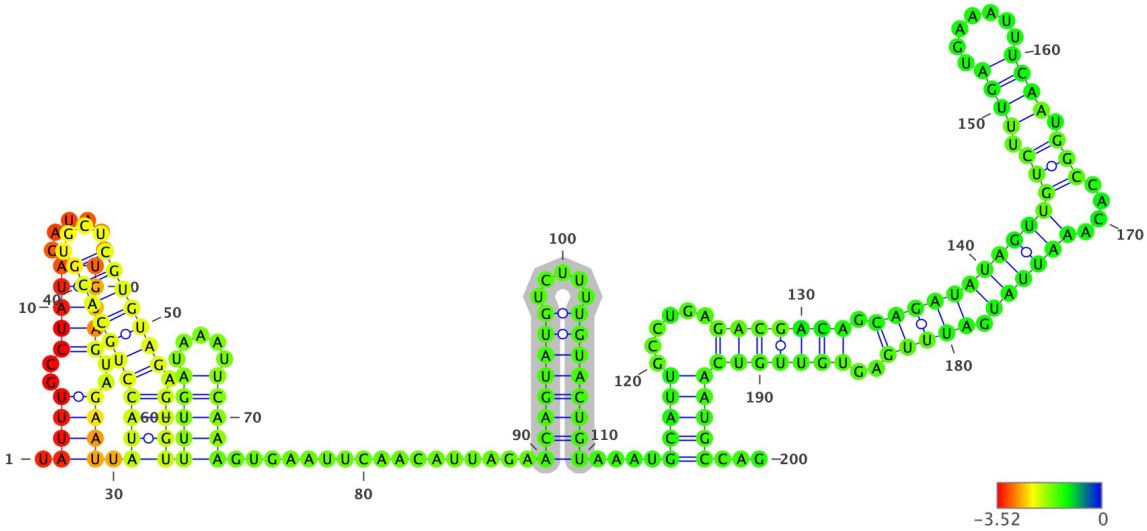
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 289 from nt 17295 to 17315 (nt 90 to 110)

```
5'-ACAGTATGTCTTTTGUACUGU-3'
5'-(((((((.......)))))))-3'
Motif MFE = -5.8; z-score = -4.2; 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 = -1.54; 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(+)

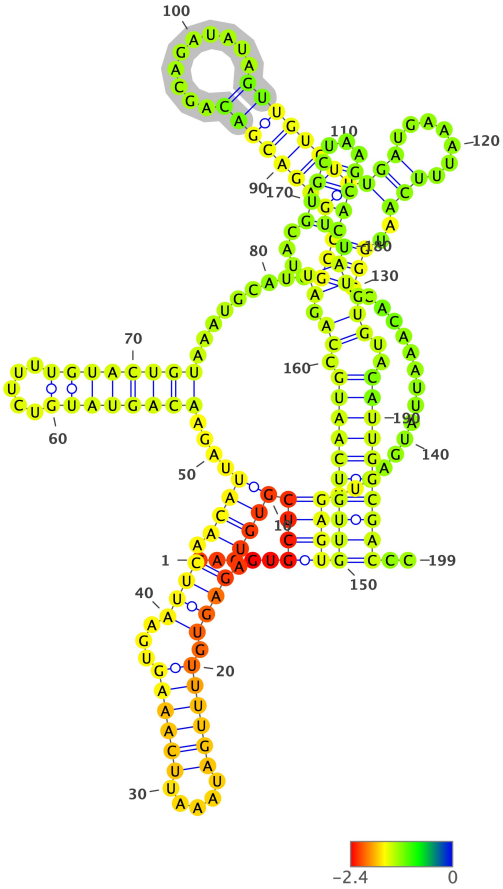
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 290 from nt 17335 to 17348 (nt 93 to 106)

```
5'-ACAGCAGATATAGU-3'
5'-((..........))-3'
Motif MFE = 0.0; z-score = 0.18; 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 17243 to 17441 (motif highlighted in silver):

```
5'-CACGUGCUCGUGUAGAGUGUUUUGAUAAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCU
UUGAUGAAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCC-3
5'-.....(((((((((.((((.((((((.....))))))...)))))..))))....(((((((((.....)))))))))).........(((.(((((((((.........)))))))))
))(((.......)))..)))..............))))((((((((((.((.((...((((...))))..)).)).)..))))))))))..-3'
MFE = -44.6; z-score = -0.76; ED = 41.22
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

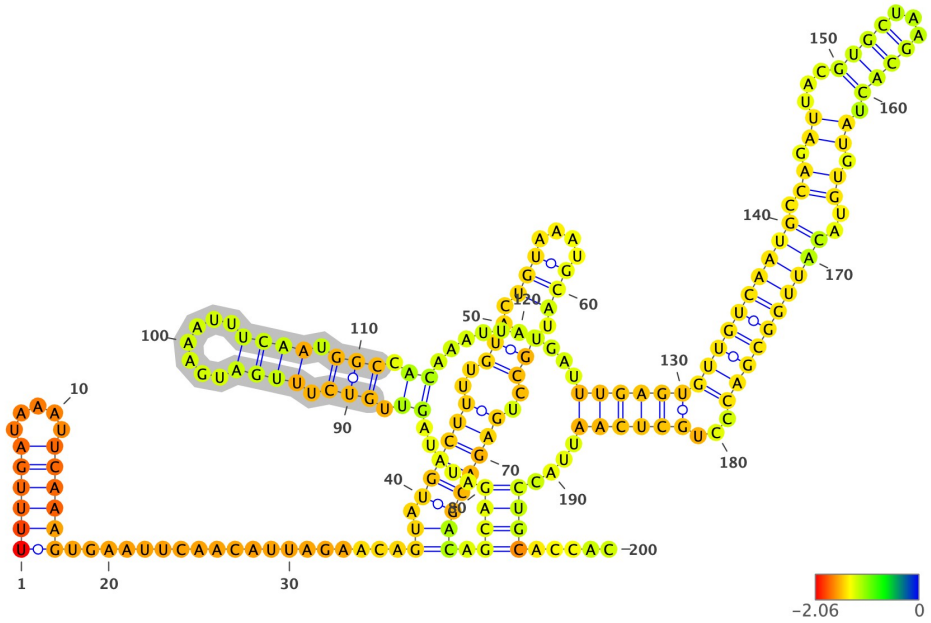
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 291 from nt 17350 to 17372 (nt 89 to 111)

```
5'-GTCTTTGATGAAATTUCAATGGC-3'
5'-(((.((((.......)))).)))-3'
Motif MFE = -3.8; z-score = -2.02; ED = 0.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17262 to 17461 (motif highlighted in silver):

```
5'-UUUUGAUAAAUUCAAAGUGAAUUCAACAUUAGAACAGUAUGUCUUUUGUACUGUAAAUGCAUUGCCUGAGACGACAGCAGAUAUAGUUGUCUUUGAUGAAAUUUCAAUGGC
CACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCAC-3
5'-((((((.....))))))...................((.((((((..(((.(((....))).)))..)))))))).((((.....((.(((.((((.......)))).)))
.)).........((((((((((((((((.((.((...((((...)))).)).)).)..))))))))))...))))))....))))).....-3'
MFE = -44.8; z-score = -1.24; ED = 34.07
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

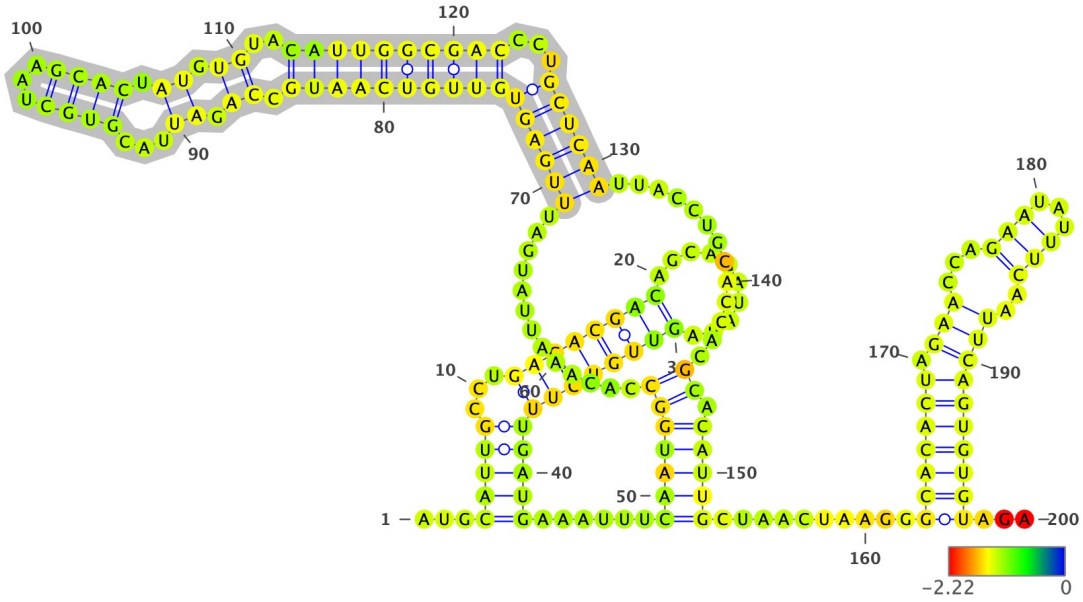
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 292 from nt 17386 to 17448 (nt 69 to 131)

```
5'-TTGAGTGTTGTCAATGCCAGATTACGTGCTAAGCACTAUGUGTACAUUGGCGACCCTGCUCAA-3'
5'-(((((((((((((...((.((...((((...)))).)).)).....)))))))))...)))))-3'
Motif MFE = -21.9; z-score = -3.03; 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 = -1.05; ED = 34.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

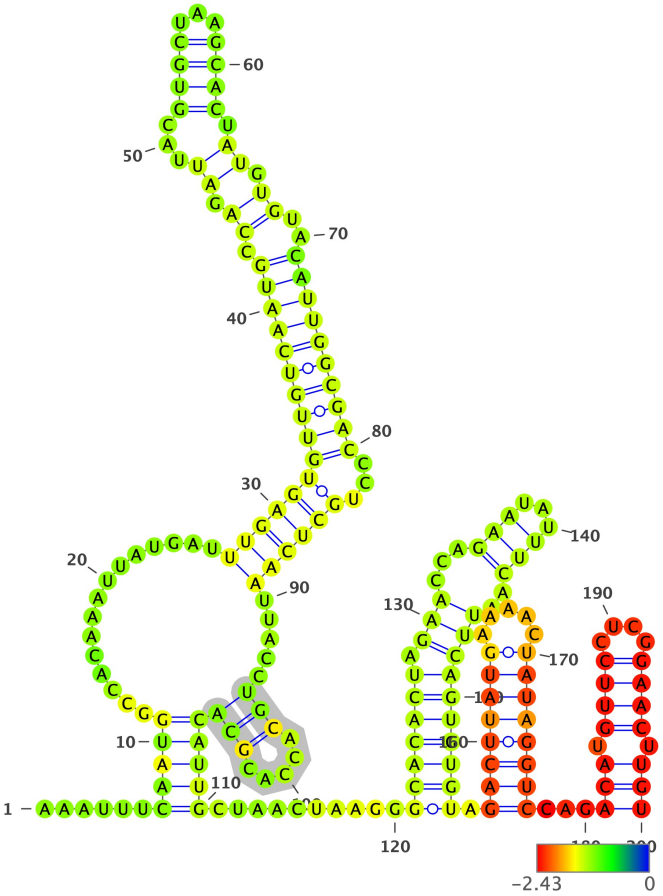
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 293 from nt 17454 to 17464 (nt 95 to 105)

```
5'-TGCACCACGCA-3'
5'-((.......))-3'
Motif MFE = -0.8; z-score = -4.88; 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 17360 to 17559 (motif highlighted in silver):

```
5'-AAAUUUCAAUGGCCACAAAUUAUGAUUUGAGUGUUGUCAAUGCCAGAUUACGUGCUAAGCACUAUGUGUACAUUGGCGACCCUGCUCAAUUACCUGCACCACGCACAUUGC
UAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGU-3
5'-......(((((...............(((((((((((((((.((.((...((((...)))).)).))..))))))))))...))))))).....(((.....)))))))).
.........(((((((.(((...(((...)))..))))))))))).((((((((.....))))))))...(((.((((....)))).)))-3'
MFE = -48.2; z-score = -2.94; ED = 17.61
```

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(+)

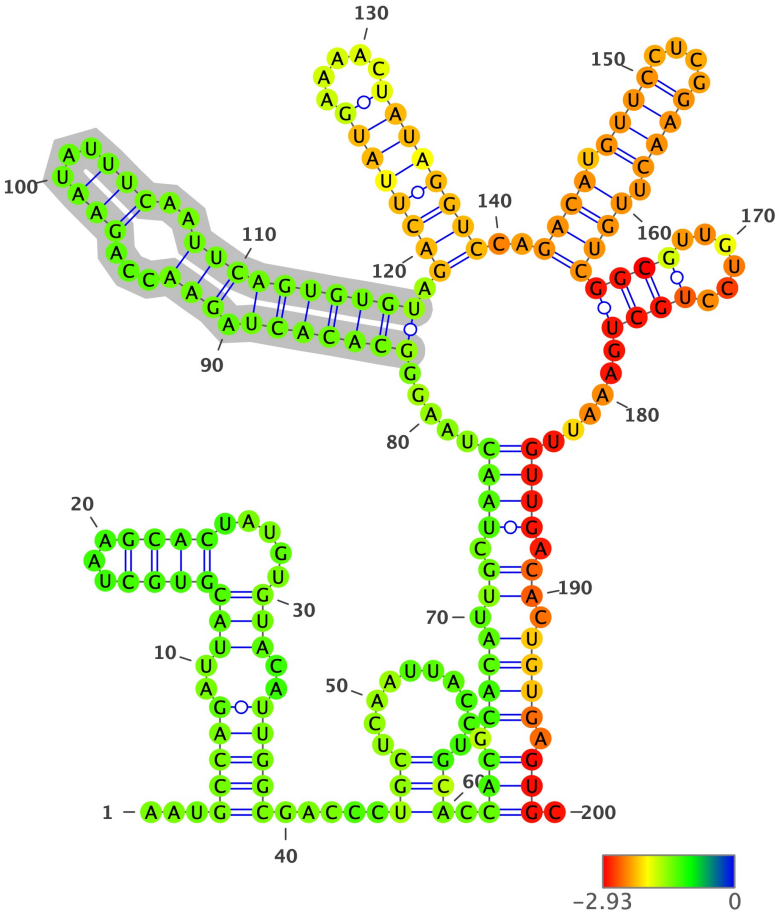
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 294 from nt 17480 to 17514 (nt 83 to 117)

```
5'-GCACACTAGAACCAGAATATTTCAAUUCAGUGUGU-3'
5'-(((((((.(((.............))))))))))-3'
Motif MFE = -8.4; z-score = -2.71; 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 = -1.2; ED = 41.34
```

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(+)

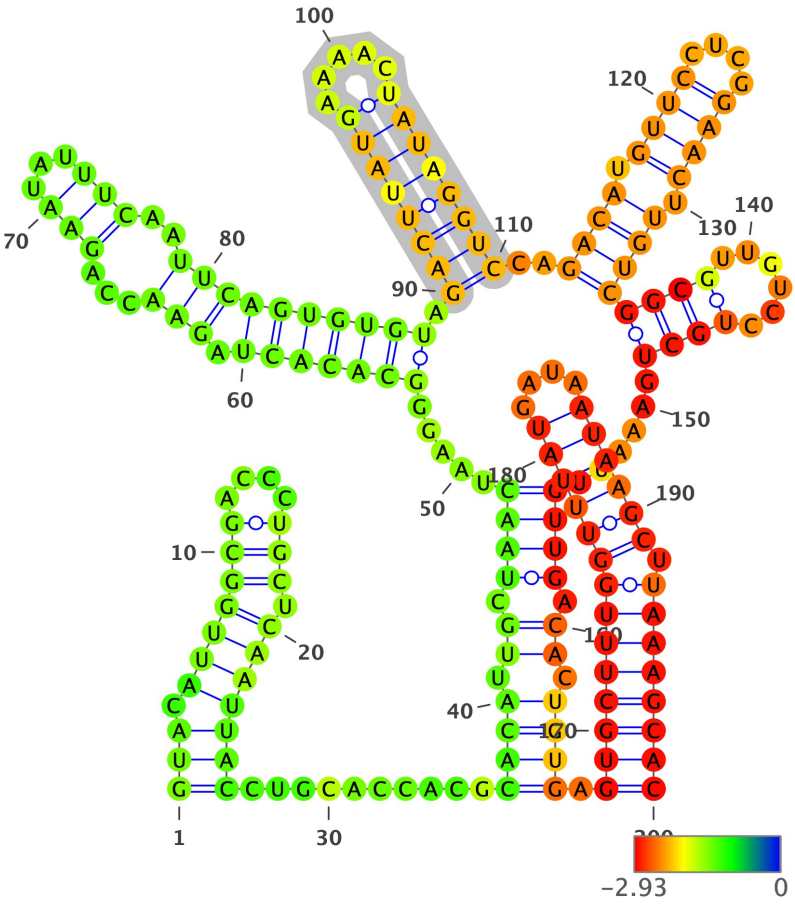
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 295 from nt 17516 to 17536 (nt 90 to 110)

```
5'-GACTTATGAAAACTAUAGGUC-3'
5'-(((((.((.......)).))))-3'
Motif MFE = -5.5; z-score = -3.81; 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 = -2.4; 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(+)

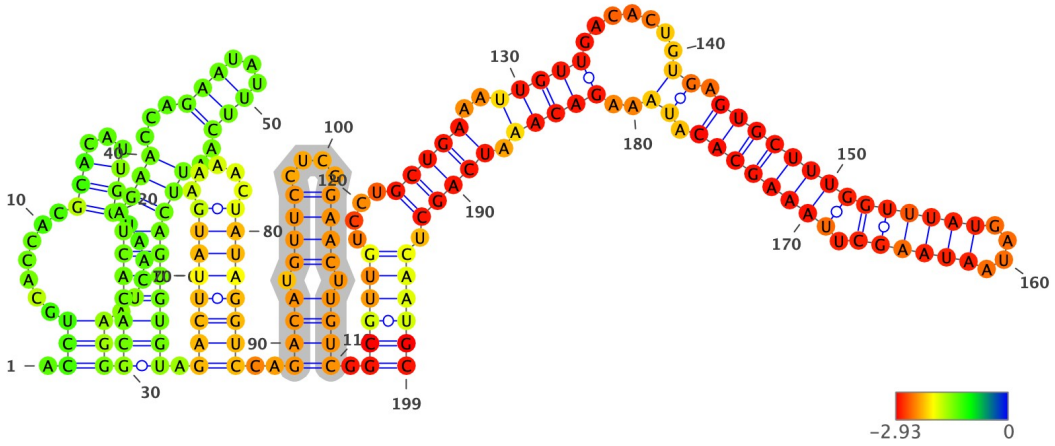
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 296 from nt 17539 to 17560 (nt 89 to 110)

```
5'-GACATGTTCCTCGGAACTUGUC-3'
5'-((((.((((....)))).))))-3'
Motif MFE = -8.9; z-score = -3.58; ED = 0.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17451 to 17649 (motif highlighted in silver):

```
5'-ACCUGCACCACGCACAUUGCUAACUAAGGGCACACUAGAACCAGAAUAUUUCAAUUCAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCG
GCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGC-3
5'-.(((.......(((...))).....)))(((((((.(((...(((...))).))..)))))))))).(((((((.....)))))))..(((((.((((....)))))))))).
((((((....((((((..(((((.......((.(((((((((((((....)))))))))))))))))))))))))..))..))))))))))))))-3'
MFE = -56.6; z-score = -3.69; ED = 16.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

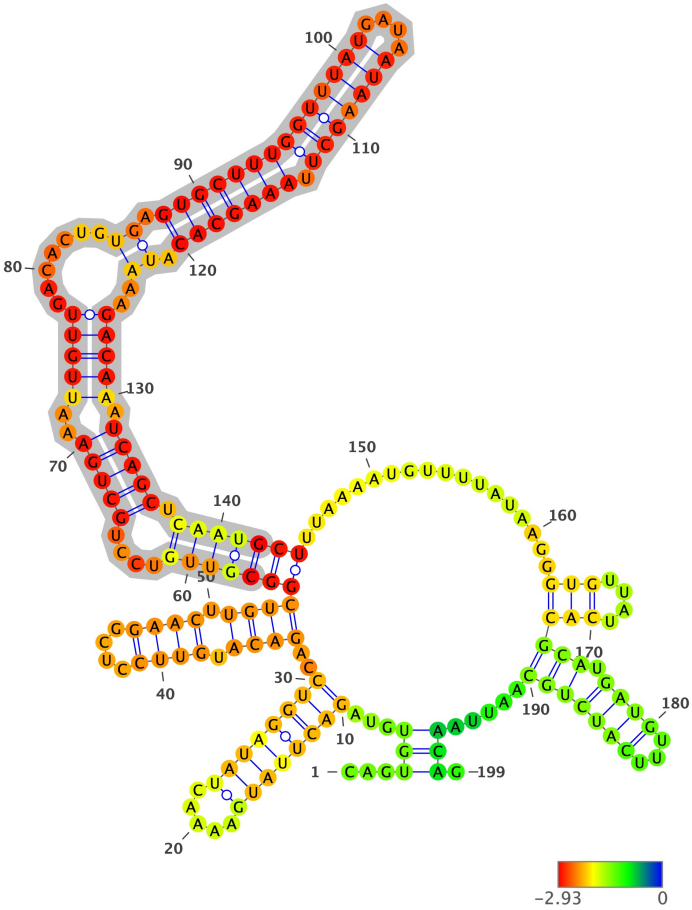
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 297 from nt 17563 to 17648 (nt 57 to 142)

```
5'-CGTTGTCCTGCTGAAATTGTTGACACTGTGAGTGCTTTGGTTTATGATAAUAAGCUTAAAGCACATAAAGACAAAUCAGCTCAATG-3'
5'-(........(((((...((((..........((((((((((.(((....))).))).)))))))).....))))..)))))).....)-3'
Motif MFE = -23.4; z-score = -3.16; ED = 7.93
```



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 17507 to 17705 (motif highlighted in silver):

```
5'-CAGUGUGUAGACUUAUGAAAACUAUAGGUCCAGACAUGUUCCUCGGAACUUGUCGGCGUUGUCCUGCUGAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGC
UUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAUUAACAG-3
5'-...(((...((((((((.....))))))))..((((.((((....)))).))))(((((((....(((((..(((((.......((.(((((((((((((....))))))
).)))))))).))..)))))).)))))).)))))))..................(((....)))(((.((((...)))))))).....))).-3'
MFE = -54.5; z-score = -2.73; ED = 24.02
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

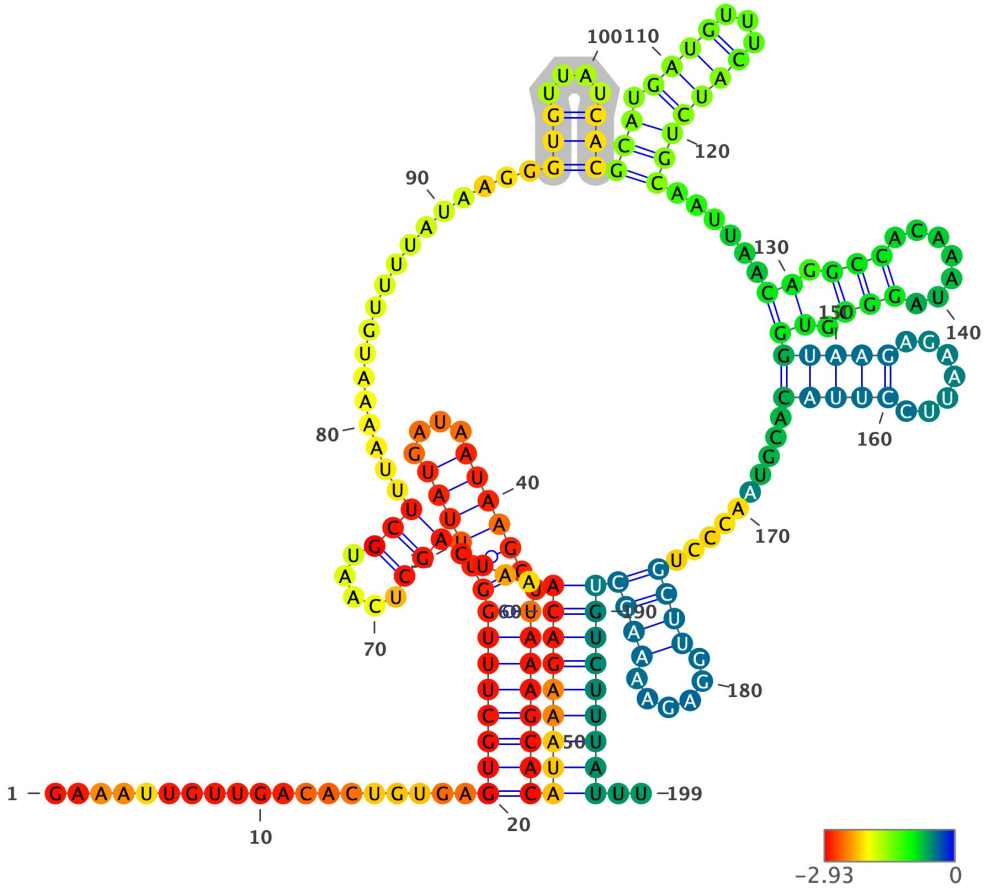
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 17669 to 17678 (nt 95 to 104)

```
5'-GTGTTATCAC-3'
5'-(((....)))-3'
Motif MFE = -0.3; z-score = -2.57; 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 17575 to 17773 (motif highlighted in silver):

```
5'-GAAAUUGUUGACACUGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAU
GUUUCAUCUGCAAUUAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUU-3
5'-...................(((((((((((((((....))))))).)))))))))(((((((((....(((.....)))).................(((....)))))))(.(((
(...)))))))).....((.(((.......))).))((((((.......)))))).........((((.....))))))))))))))..-3'
MFE = -49.1; z-score = -2.74; ED = 22.92
```

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(+)

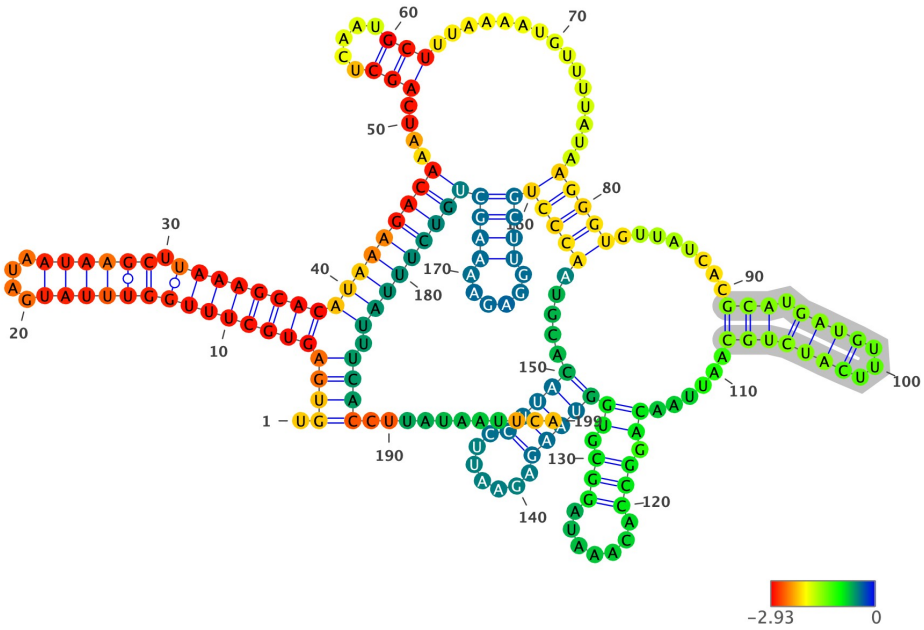
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 299 from nt 17679 to 17696 (nt 91 to 108)

```
5'-GCATGATGTTTCAUCUGC-3'
5'-(((.(((.....))))))-3'
Motif MFE = -4.0; z-score = -2.99; ED = 1.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17589 to 17787 (motif highlighted in silver):

```
5'-UGUGAGUGCUUUGGUUUAUGAUAAUAAGCUUAAAGCACAUAAAGACAAAUCAGCUCAAUGCUUUAAAAUGUUUUAUAAGGGUGUUAUCACGCAUGAUGUUUCAUCUGCAAU
UAACAGGCCACAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCA-3
5'-.(((((((((((((((((....)))))).))))))))(((((((((....(((.....)))...............(((((........(((.((((...)))))))...
...((.(((.......))).))(((((.......)))))).....)))))((((......))))))))))))).))))...........-3'
MFE = -52.3; z-score = -3.4; ED = 18.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

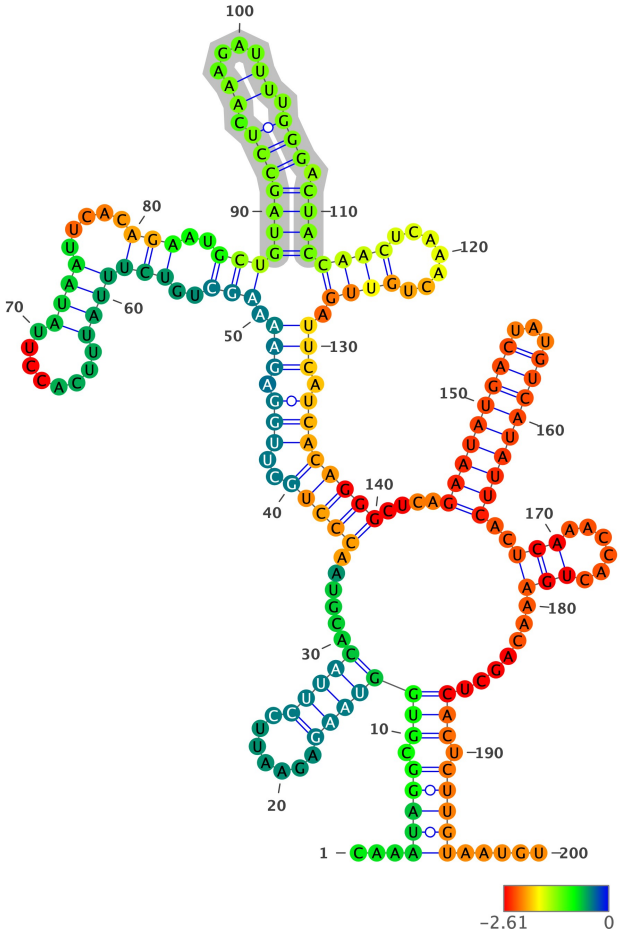
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 300 from nt 17797 to 17821 (nt 88 to 112)

```
5'-GTAGCCTCAAAGATUUTGGGACUAC-3'
5'-(((((((.((....)).))).))))-3'
Motif MFE = -6.7; z-score = -2.39; ED = 2.6
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17710 to 17909 (motif highlighted in silver):

```
5'-CAAAUAGGCGUGGUAAGAGAAUUCCUUACACGUAACCCUGCUUGGAGAAAAGCUGUCUUUAUUUCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUA
CCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACCACUGAAACAGCUCACUCUUGUAAUGU-3
5'-...(((((.(((((((((.......)))))).....(((((..(((.(((.(((..(((((((.........)))).....))).))).(((((((.((....)).))))))))
))))(((.......)))).))).)))))))).....((((((((((...))))))))).((((.....))).......))).)))))).....-3'
MFE = -41.0; z-score = -1.71; 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(+)

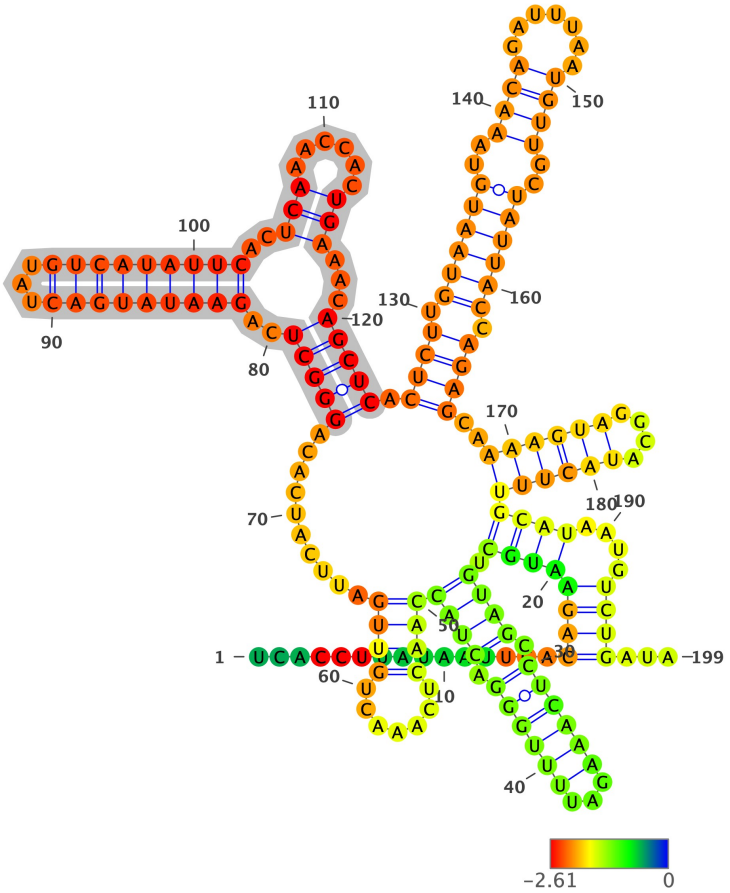
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 301 from nt 17847 to 17896 (nt 75 to 124)

```
5'-GGGCTCAGAATATGACTATGUCAUAUUCACTCAAACCACUGAAACAGCUC-3'
5'-(((((..((((((((((...)))))))))...((......))....)))))-3'
Motif MFE = -12.3; z-score = -3.47; ED = 3.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17773 to 17971 (motif highlighted in silver):

```
5'-UCACCUUAUAAUUCACAGAAUGCUGUAGCCUCAAAGAUUUUGGGACUACCAACUCAAACUGUUGAUUCAUCACAGGGCUCAGAAUAUGACUAUGUCAUAUUCACUCAAACC
ACUGAAACAGCUCACUCUUGUAAUGUAAACAGAUUUAAUGUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUA-3
5'-...............((((((((.((((.((((((...)))))).))))((((.......))))..........(((((..((((((((((...)))))))))..(((....
..)))...)))))).((((.((((((..((((.......))))..))))))).))))..((((((....))))))))))....))))...-3'
MFE = -45.5; z-score = -2.94; 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_gp01, 266-21555(+)

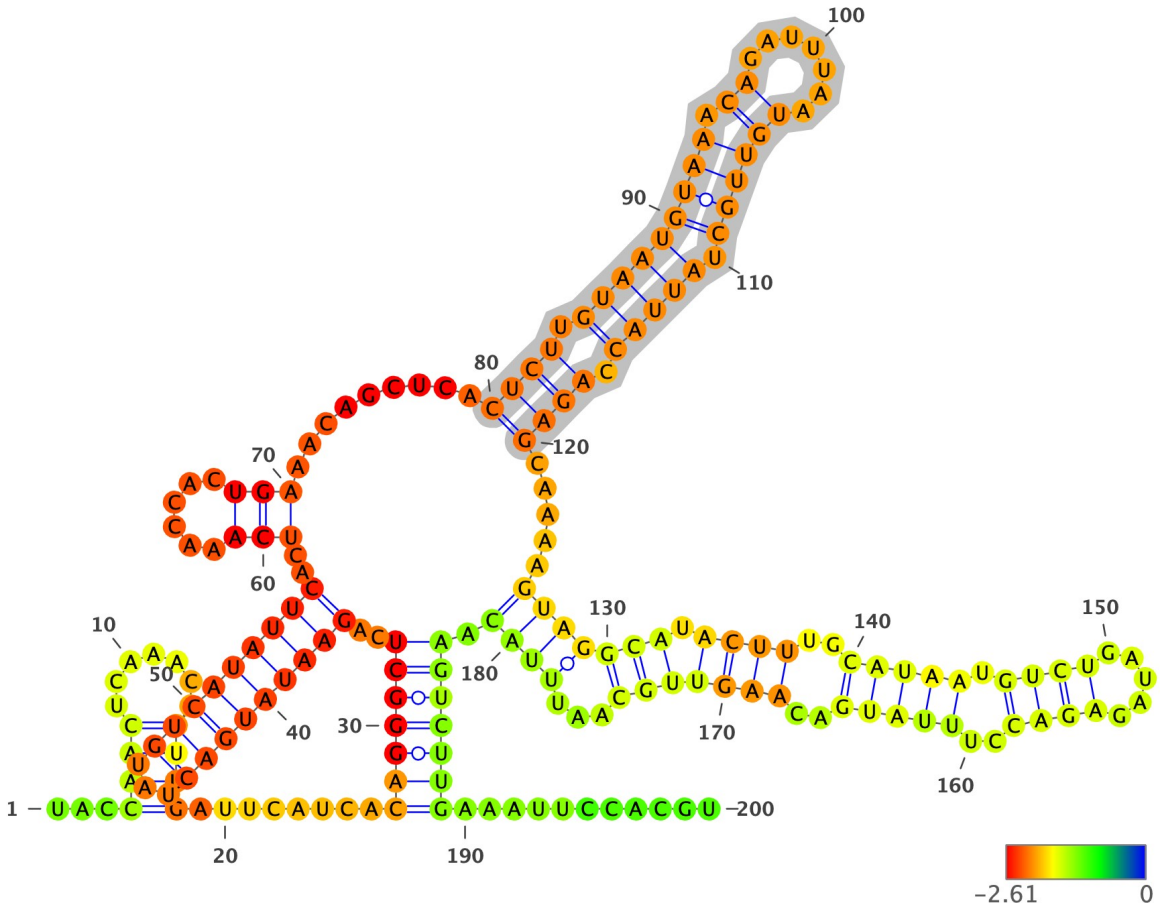
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 17898 to 17938 (nt 80 to 120)

```
5'-CTCTTGTAATGTAAACAGATTTAAUGUUGCTAUUACCAGAG-3'
5'-((((.((((((((((.((.......)))))))..))))))..))))-3'
Motif MFE = -9.7; z-score = -2.74; 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 = -3.23; 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(+)

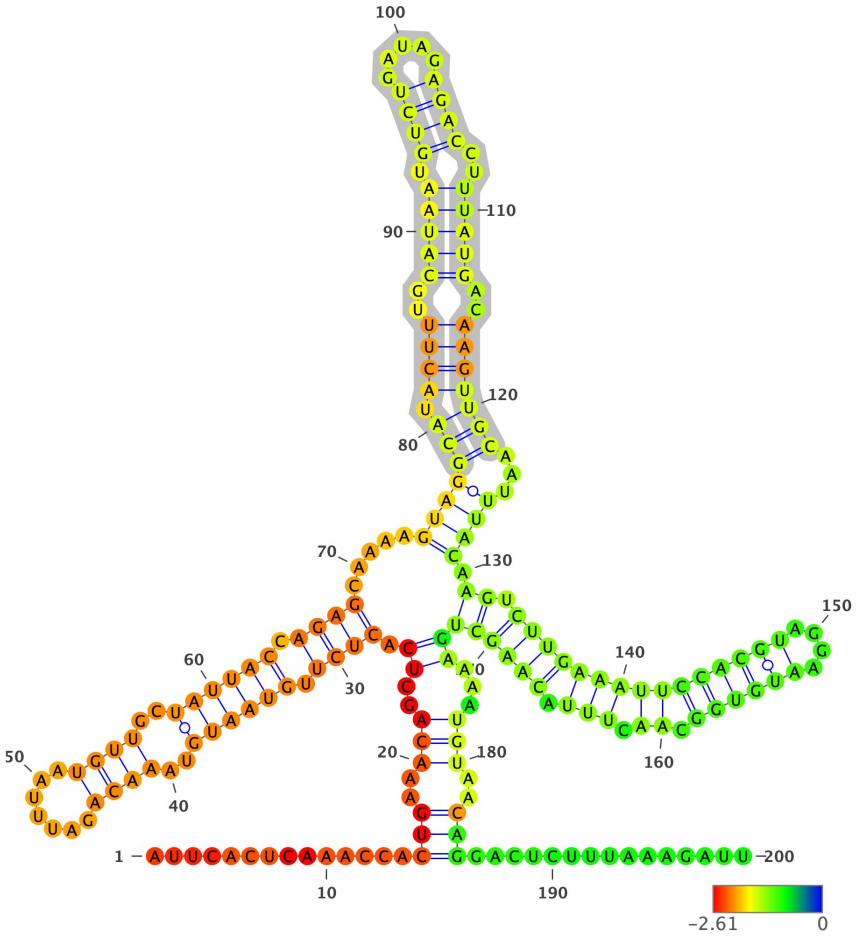
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 303 from nt 17948 to 17992 (nt 78 to 122)

```
5'-GCATACTTTGCATAATGTCTGATAGAGACCTTTAUGACAAGTUGC-3'
5'-(((.......(((...((((.....)))).....)))......)))-3'
Motif MFE = -12.2; z-score = -2.46; 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 = -1.45; ED = 40.99
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

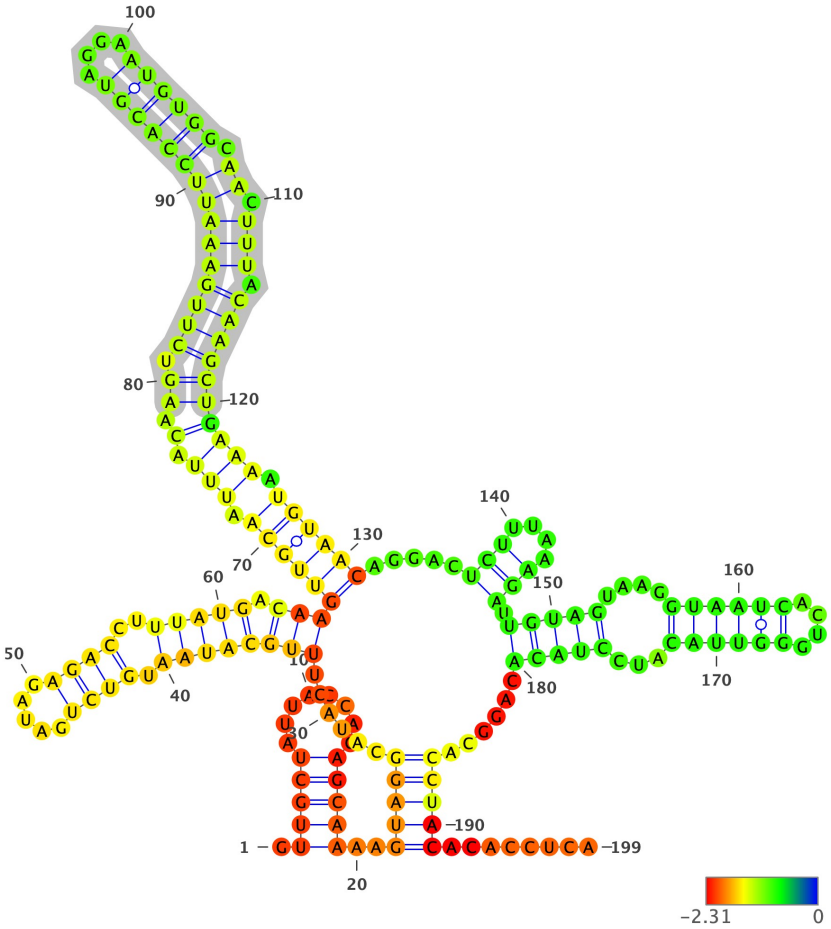
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 304 from nt 18001 to 18042 (nt 79 to 120)

```
5'-AGTCTTGAAATTCCACGTAGGAAUGUGGCAACUUUACAAGCU-3'
5'-((.(((((((((((((((....)))))).)).))).))))))-3'
Motif MFE = -8.8; z-score = -1.52; ED = 4.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 17923 to 18121 (motif highlighted in silver):

```
5'-GUUGCUAUUACCAGAGCAAAAGUAGGCAUACUUUGCAUAAUGUCUGAUAGAGACCUUUAUGACAAGUUGCAAUUUACAAGUCUUGAAAUUCCACGUAGGAAUGUGGCAACU
UUACAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCA-3
5'-.(((((........)))))..(((((......((((((((.((((.....)))).)))))).)))((((((.(((.(.((.((((((((((((((....)))))).)).)
)).))))))))))).))))))).....(((....))).(((((....((((((....))))))...)))))......)))))........-3'
MFE = -44.1; z-score = -1.6; ED = 40.31
```

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(+)

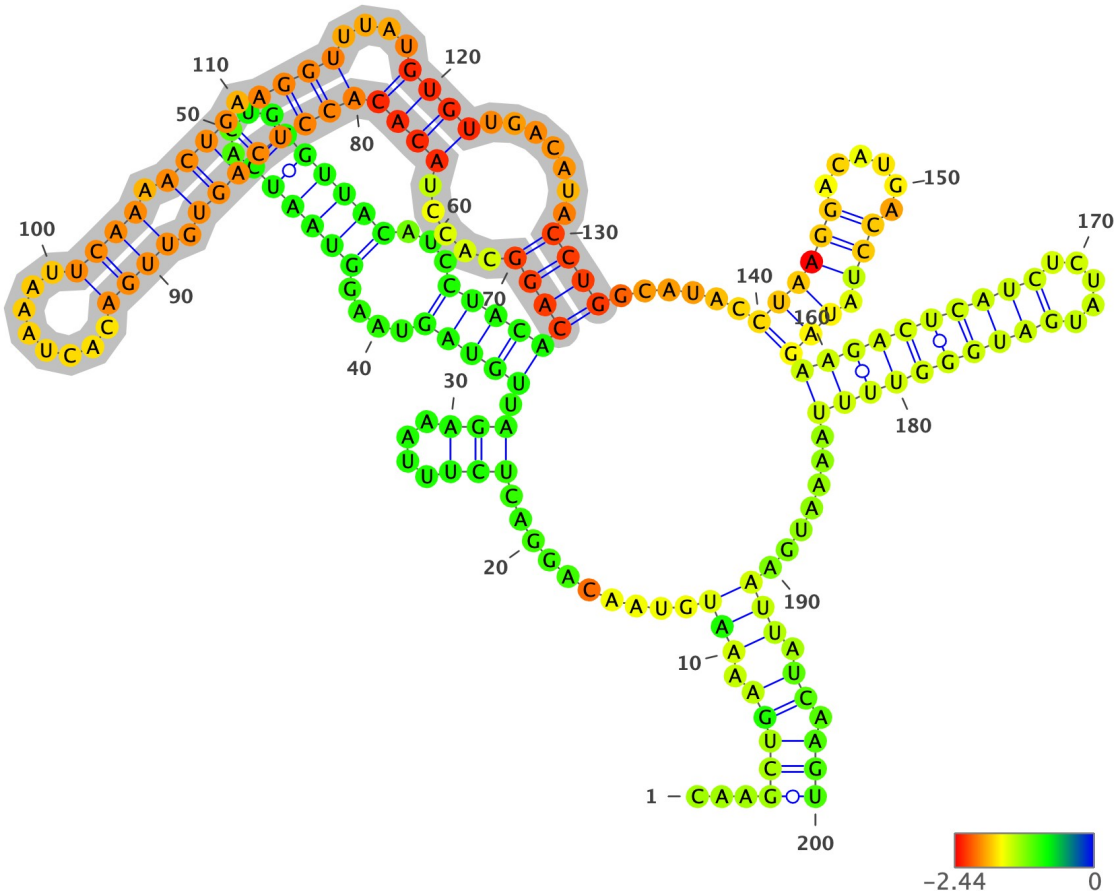
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 18103 to 18169 (nt 67 to 133)

```
5'-CAGGCACCTACACACCTCAGTGTTGACACTAAATUCAAAACUGAAGGUTTATGUGUTGACATACCUG-3'
5'-((((.....(((((((((((.((((........)))).)))).)))).....)))).......))))-3'
Motif MFE = -16.7; z-score = -2.96; ED = 6.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18037 to 18236 (motif highlighted in silver):

```
5'-CAAGCUGAAAAUGUAACAGGACUCUUUAAAGAUUGUAGUAAGGUAAUCACUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAA
GGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGU-3
5'-...(((((.(((..........(((....))).(((((....((((((....))))))...)))))((((.....(((((((((((.((((........)))).)))).)
)))....)))).......)))).....((((((......))).)))((((((((((.....)))))))))).......))).)).)))-3'
MFE = -43.0; z-score = -1.81; ED = 26.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

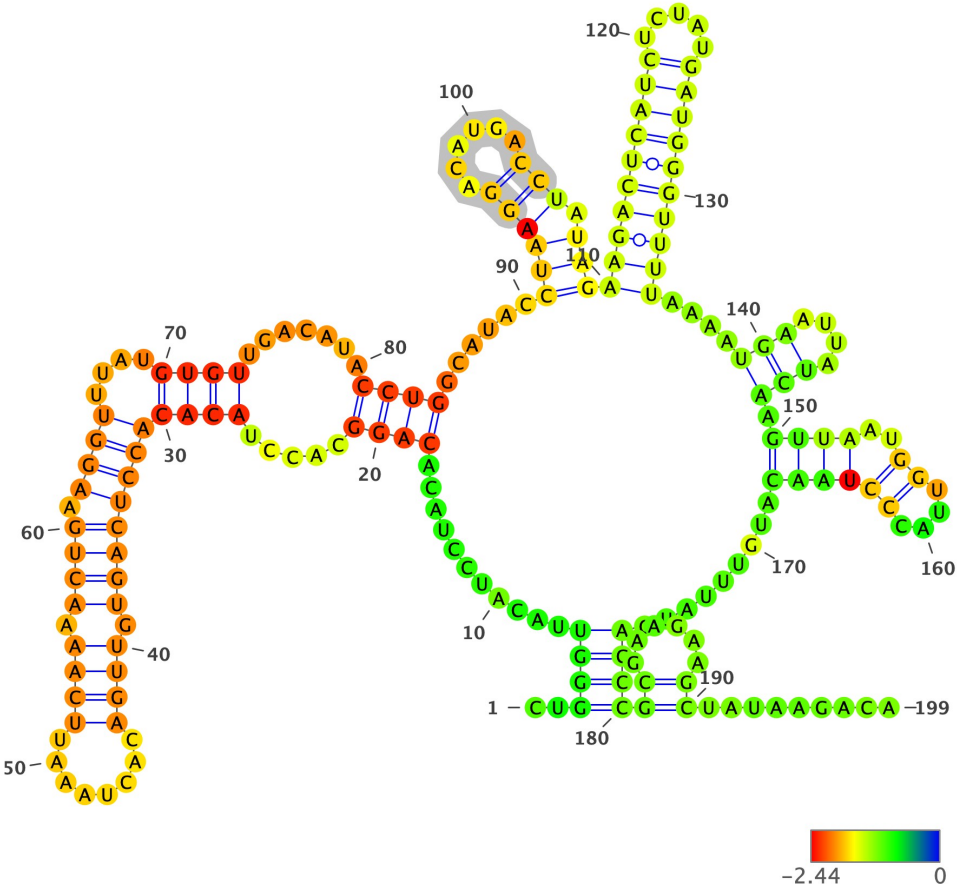
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 306 from nt 18180 to 18189 (nt 95 to 104)

```
5'-GGACATGACC-3'
5'-((......))-3'
Motif MFE = 0.0; z-score = 0.2; 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 18086 to 18284 (motif highlighted in silver):

```
5'-CUGGGUUACAUCCUACACAGGCACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAA
GACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACA-3
5'-..((((...........((((.....(((((((((((.((((........)))).)))).))))....)))).......))))......((((((......))).)))((
((((((((.....))))))))))....(((....))).((((..((....))))))..........))))((......))..........-3'
MFE = -41.6; z-score = -1.98; ED = 30.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

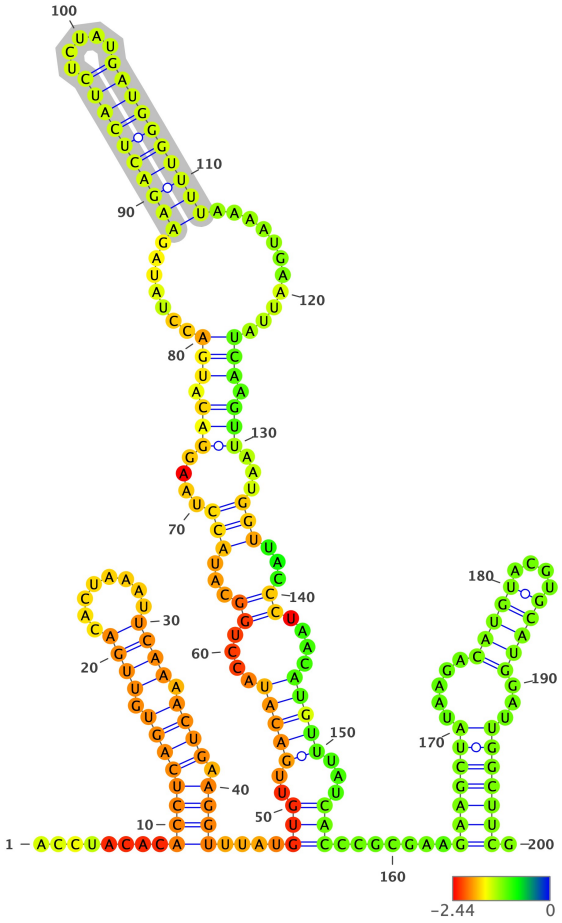
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 307 from nt 18195 to 18219 (nt 88 to 112)

```
5'-AAGACTCATCTCTATGAUGGGUUUU-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -10.1; z-score = -5.01; ED = 0.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18108 to 18307 (motif highlighted in silver):

```
5'-ACCUACACACCUCAGUGUUGACACUAAAUUCAAAACUGAAGGUUUAUGUGUUGACAUACCUGGCAUACCUAAGGACAUGACCUAUAGAAGACUCAUCUCUAUGAUGGGUUU
UAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGGCUUCG-3
5'-........((((((((.((((........)))).)))).)))).....(((..((((((....((...(((....(((.(((.......((((((((((.....)))))))))
).........)))).)))...)))...))....)))))...)))......(((((((.....(((((....)))))...)))))))-3'
MFE = -46.8; z-score = -2.05; 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(+)

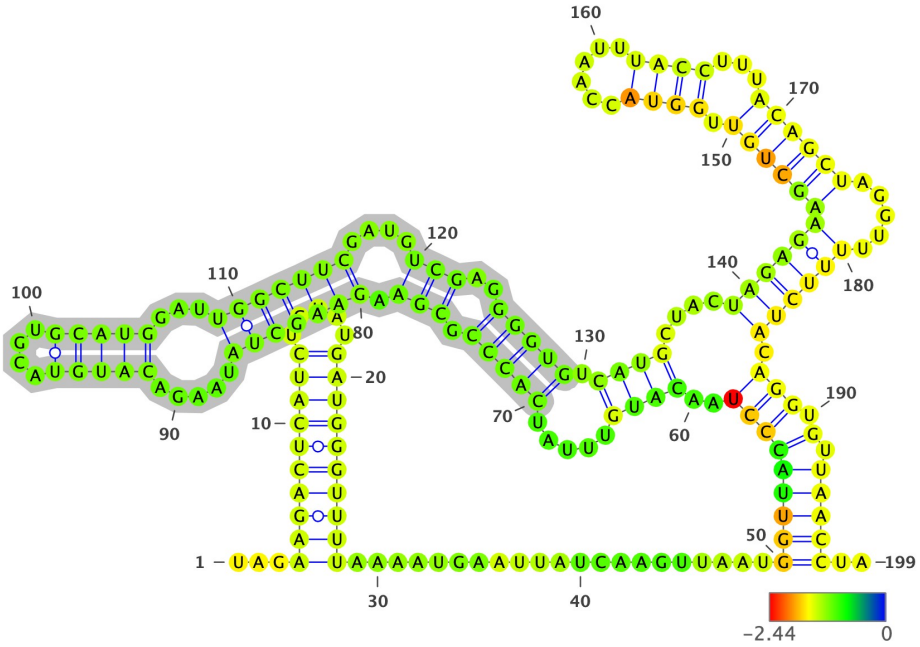
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 308 from nt 18261 to 18320 (nt 70 to 129)

```
5'-CACCCGCGAAGAAGCTATAAGACATGTACGTGCAUGGATUGGCUUCGATGUCGAGGGGUG-3'
5'-(((((.(((.(((((((.....(((((....)))))...)))))))....)))..)))))-3'
Motif MFE = -22.2; z-score = -3.1; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18192 to 18390 (motif highlighted in silver):

```
5'-UAGAAGACUCAUCUCUAUGAUGGGUUUUAAAAUGAAUUAUCAAGUUAAUGGUUACCCUAACAUGUUUAUCACCCGCGAAGAAGCUAUAAGACAUGUACGUGCAUGGAUUGG
CUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUA-3
5'-...((((((((((.....))))))))))....................(((((((((..((((.....(((((.(((.(((((((.....(((((....)))))...)))
))))....)))..)))))).))))....((((((((((((.((((......))))...))))))).....)))))).))).).)))))..-3'
MFE = -54.7; z-score = -2.8; ED = 26.06
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

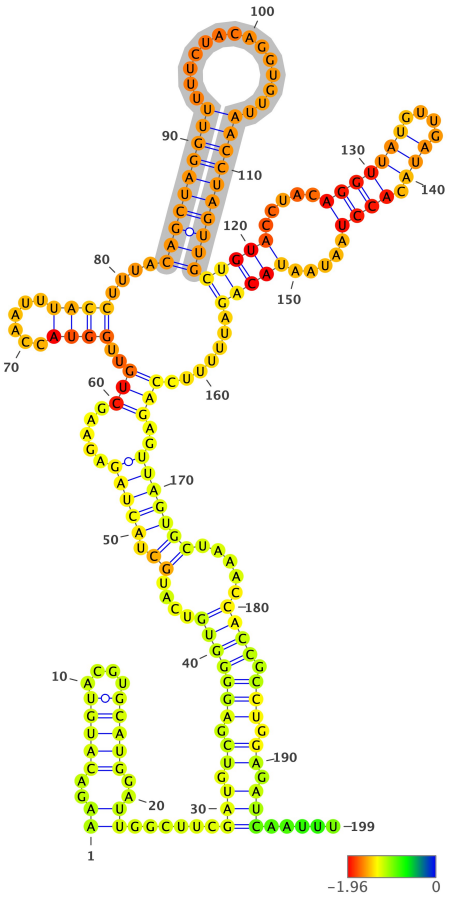
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 309 from nt 18361 to 18394 (nt 83 to 116)

```
5'-CAGCTAGGTTTTTCTACAGGTGTTAACCUAGUUG-3'
5'-((((((((((.............))))))))))-3'
Motif MFE = -11.1; z-score = -3.78; ED = 2.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18279 to 18477 (motif highlighted in silver):

```
5'-AAGACAUGUACGUGCAUGGAUUGGCUUCGAUGUCGAGGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCU
AGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUU-3
5'-((..(((((....)))))..)).....(((.((.(((((((....((.(((((.....(((..((((......))))....((((((((((.............)))))
)))))(((((.....(((((((....))).))))).....)))))).......)))..)))))))).....)))).))).)).)))).....-3'
MFE = -51.8; z-score = -1.48; ED = 54.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

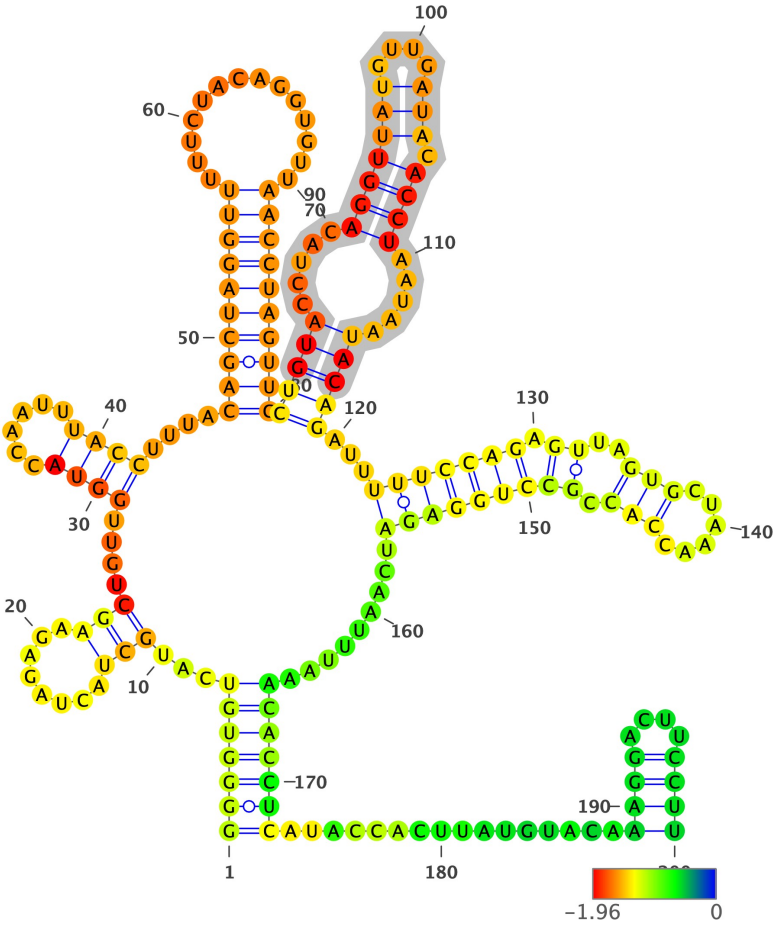
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 310 from nt 18397 to 18431 (nt 83 to 117)

```
5'-GTACCTACAGGTTATGTTGATACACCUAATAATAC-3'
5'-((......((((...........)))).....))-3'
Motif MFE = -3.3; z-score = -0.79; ED = 7.3
```



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 18315 to 18514 (motif highlighted in silver):

```
5'-GGGGUGUCAUGCUACUAGAGAAGCUGUUGGUACCAAUUUACCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAA
UAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCUGGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUU-3
5'-(((((((...(((........)))....((((......))))....((((((((((.............))))))))))(((((.....(((((((....))).)))))..
...)))))...(((((((.((..(((......))).)))))))))........)))))).............((((....))))-3'
MFE = -48.9; z-score = -2.08; ED = 20.08
```

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(+)

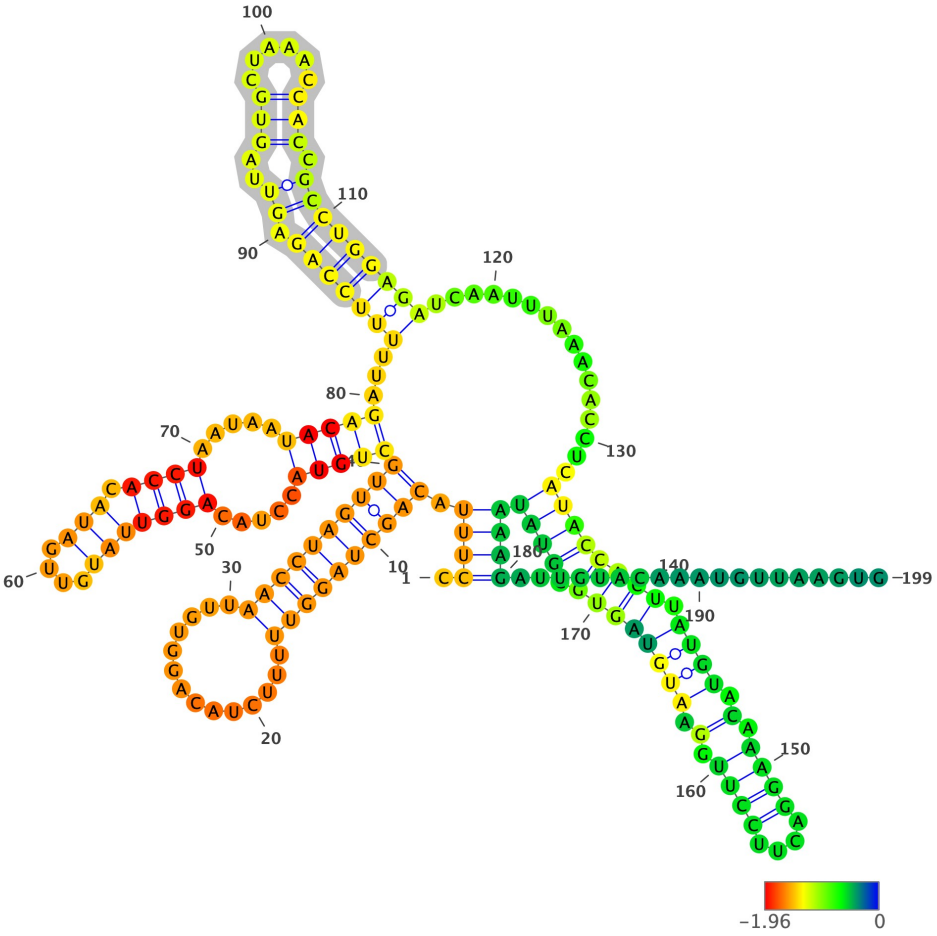
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 311 from nt 18440 to 18467 (nt 86 to 113)

```
5'-CCAGAGTTAGTGCTAAACCACCGCCUGG-3'
5'-((((...................))))-3'
Motif MFE = -6.1; z-score = -1.01; ED = 0.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18355 to 18553 (motif highlighted in silver):

```
5'-CCUUUACAGCUAGGUUUUUCUACAGGUGUUAACCUAGUUGCUGUACCUACAGGUUAUGUUGAUACACCUAAUAAUACAGAUUUUUCCAGAGUUAGUGCUAAACCACCGCCU
GGAGAUCAAUUUAAACACCUCAUACCACUUAUGUACAAAGGACUUCCUUGGAAUGUAGUGCGUAUAAAGAUUGUACAAAUGUUAAGUG-3
5'-.((((.((((((((((.............))))))))))((((.....(((((((....))).))))).....))))))...(((((((.((..(((......))).))))
)))))).................(((((((.((((.(.((((....)))).).)))))))).)))))))...................-3'
MFE = -42.5; z-score = -1.14; ED = 28.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

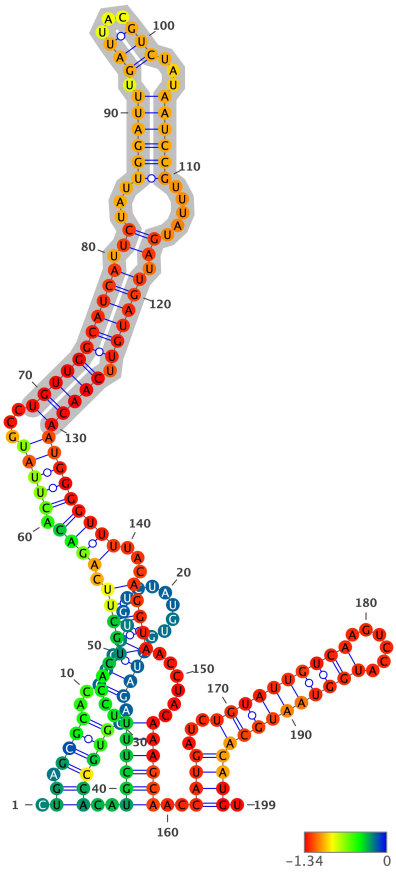
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 312 from nt 18715 to 18776 (nt 69 to 130)

```
5'-TGTTGGCATCATTCTATTGGATTTGATTACGUCTATAAUCCGTTTATGATUGAUGUTCAACA-3'
5'-(((((((((((.((....(((((.(((...)))...)))))......)).))))))).)))))-3'
Motif MFE = -16.9; z-score = -4.03; ED = 5.44
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18647 to 18845 (motif highlighted in silver):

```
5'-CUGAGCGCACCUGUUGUCUAUGUGAUAGACGUGCCACAUGCUUUUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGU
UUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGU-3
5'-.((.((((..(((((.........)))))..))))))..((((((.....(((((.((((.(((((...((((((((((((.((...((((((.(((...)))...)))))).
....)).))))))).))))))))))))))...)))))......))))))..((((...((((((((((.....))))))))))))))).-3'
MFE = -46.7; z-score = -1.01; ED = 51.15
```

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(+)

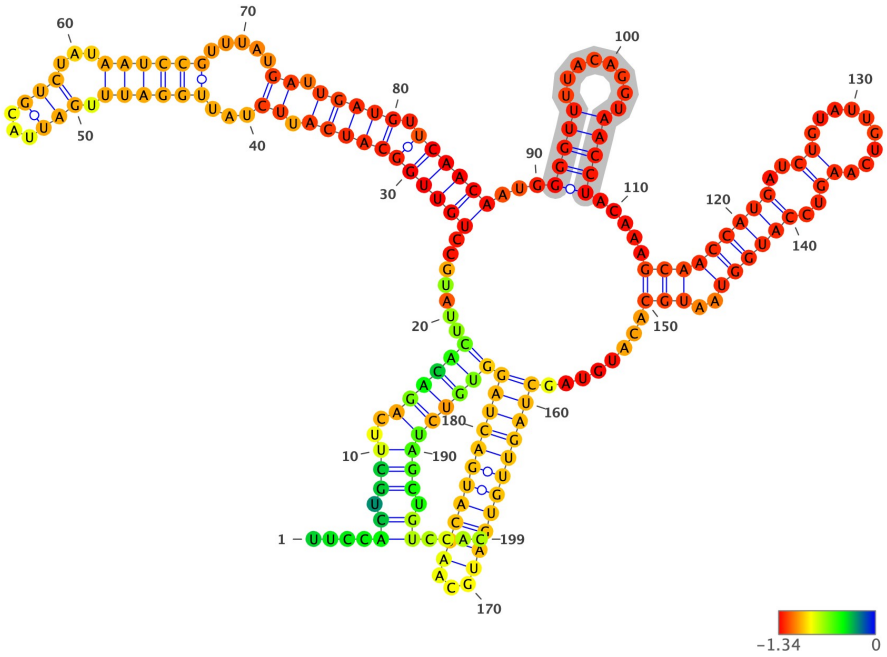
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 18780 to 18797 (nt 91 to 108)

```
5'-GGGTTTTACAGGTAACCU-3'
5'-(((((........)))))-3'
Motif MFE = -3.4; z-score = -1.65; ED = 0.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18690 to 18888 (motif highlighted in silver):

```
5'-UUCCACUGCUUCAGACACUUAUGCCUGUUGGCAUCAUUCUAUUGGAUUUGAUUACGUCUAUAAUCCGUUUAUGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACA
AAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUAGGUGUCUAGCUGUCCAC-3
5'-....((.(((..((((((.......((((((((((.((...((((((.(((...)))...))))))).....)).)))))).))))))...(((((........)))))...
..(((((((((..((.........))..))))))..)))........((((((((((...)))))))))))))))))))).))....-3'
MFE = -55.4; z-score = -3.03; ED = 16.59
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

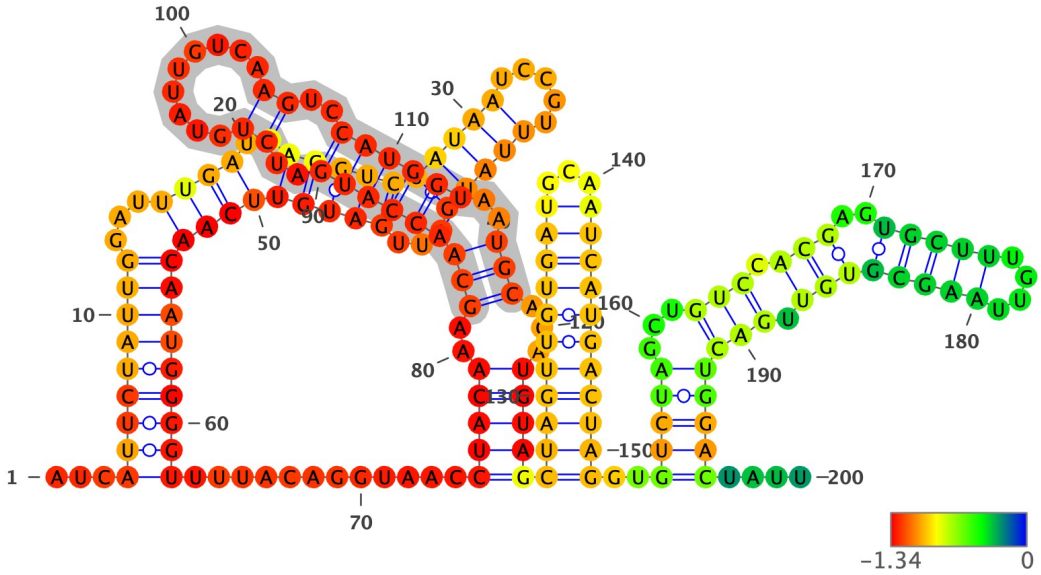
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 314 from nt 18803 to 18839 (nt 82 to 118)

```
5'-GCAACCATGATCTGTATTGTCAAGTCCAUGGUAAUGC-3'
5'-((((((((((..((.........))..))))))..)))-3'
Motif MFE = -9.5; z-score = -2.09; 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 = -1.59; 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(+)

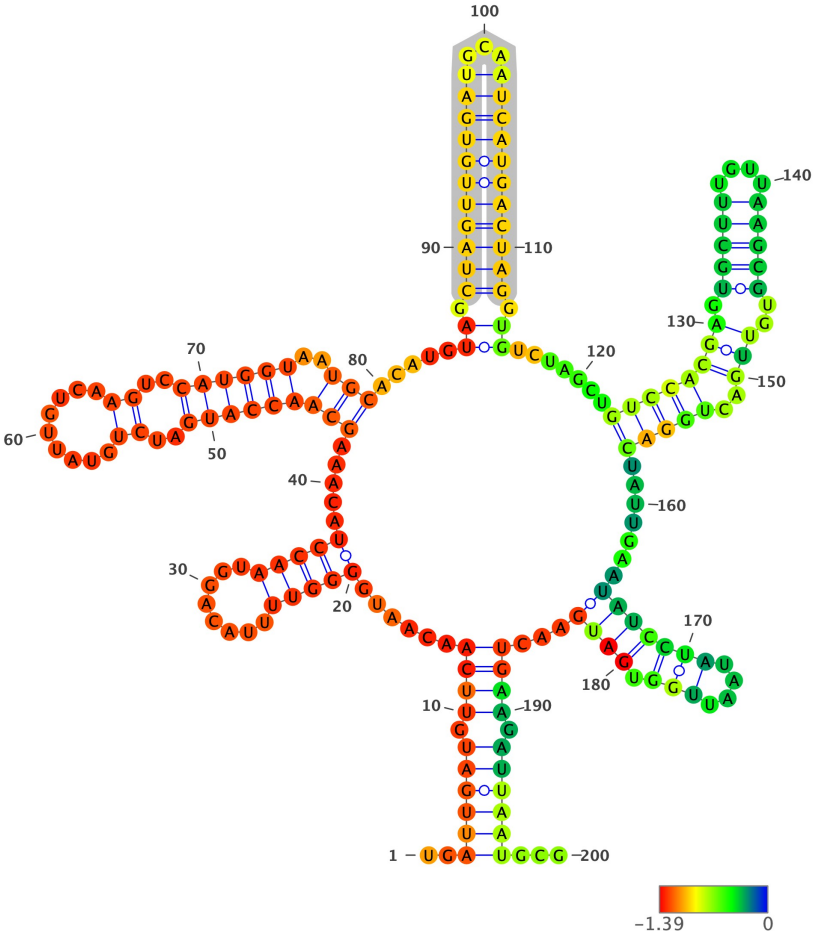
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 315 from nt 18848 to 18872 (nt 88 to 112)

```
5'-CTAGTTGTGATGCAAUCAUGACUAG-3'
5'-(((...................)))-3'
Motif MFE = -9.8; z-score = -4.02; ED = 0.61
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 18761 to 18960 (motif highlighted in silver):

```
5'-UGAUUGAUGUUCAACAAUGGGGUUUUACAGGUAACCUACAAAGCAACCAUGAUCUGUAUUGUCAAGUCCAUGGUAAUGCACAUGUAGCUAGUUGUGAUGCAAUCAUGACUA
GGUGUCUAGCUGUCCACGAGUGCUUUGUUAAGCGUGUUGACUGGACUAUUGAAUAUCCUAUAAUUGGUGAUGAACUGAAGAUUAAUGCG-3
5'-..((((((.((((......(((((........)))))).....(((((((((..((.........))..))))))..)))).....((.(((((((((((...)))))))))))
).))).......((((((((.(((((....)))))..)))..)))))).......(((((((....))).))))...)))).))))))...-3'
MFE = -50.2; z-score = -1.05; ED = 45.14
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

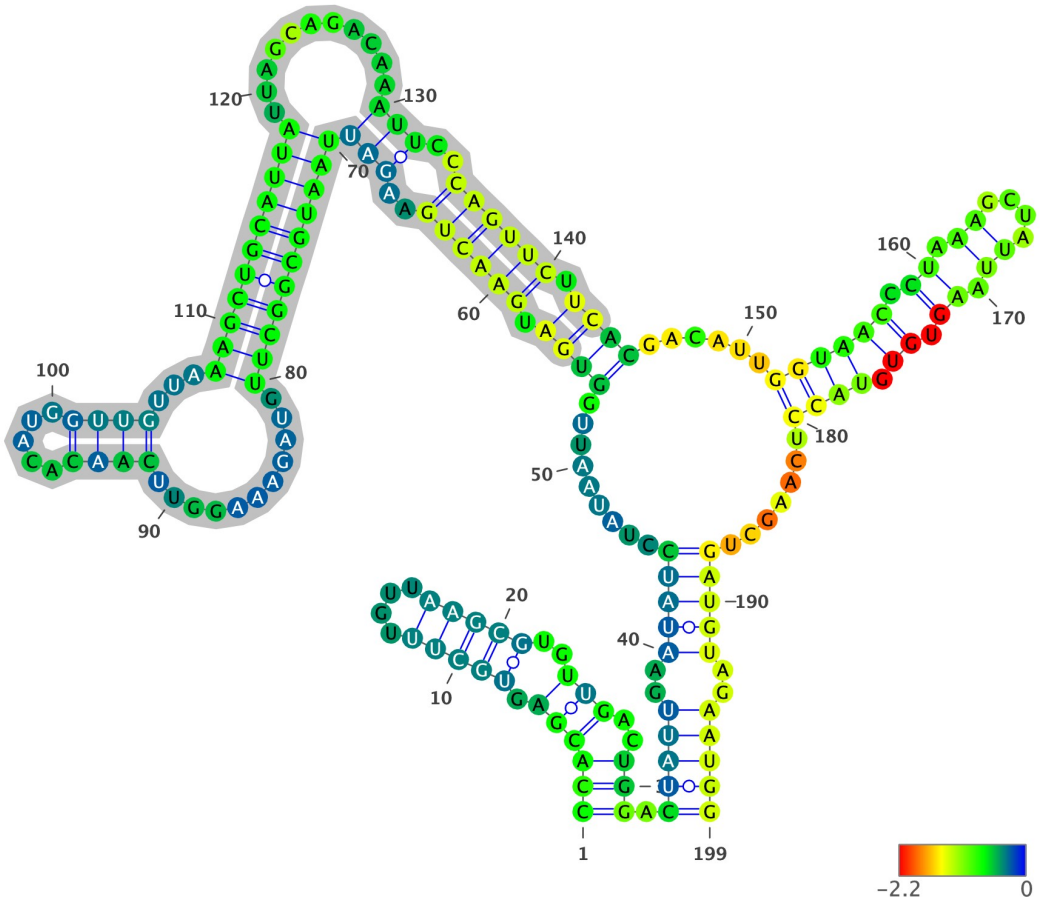
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 316 from nt 18940 to 19027 (nt 56 to 143)

```
5'-GATGAACTGAAGATTAATGCGGCTTGTAGAAAGGTTCAACACATGGTTGTTAAAGCUGCAUUATTAGCAGACAAATTCCCAGUUCTUC-3'
5'-((.((((((.....................................................................))))))).))-3'
Motif MFE = -20.5; z-score = -1.93; 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 = 0.84; 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(+)

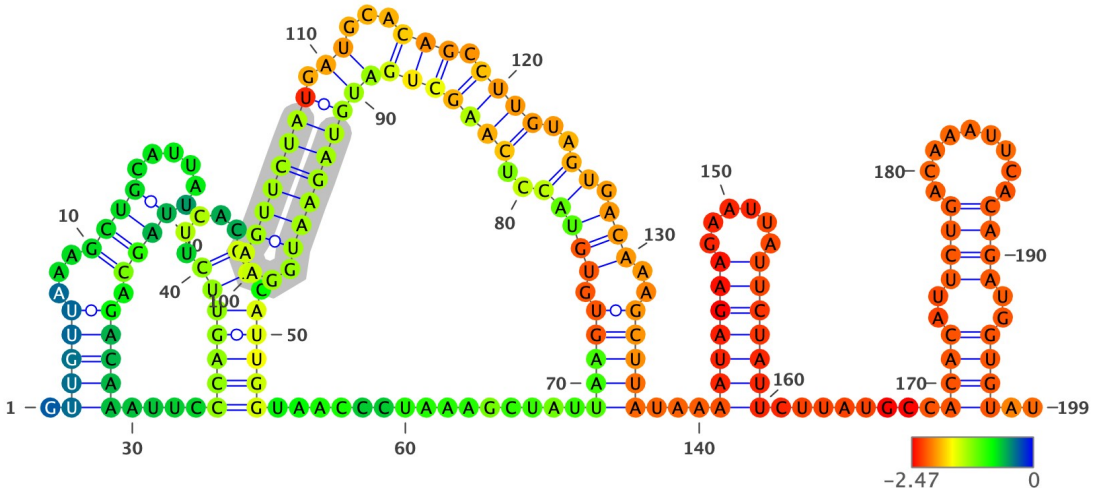
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 317 from nt 19076 to 19091 (nt 92 to 107)

```
5'-TAGAATGGAAGUUCUA-3'
5'-((((((....))))))-3'
Motif MFE = -2.9; z-score = -4.99; 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 18985 to 19183 (motif highlighted in silver):

```
5'-GUUGUUAAAGCUGCAUUAUUAGCAGACAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAU
GCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAU-3
5'-.(((((...((((......)))).)))))....(((((((.....)).)))))...............(((((.(((((..(((((((((((((((....)))))))).))
...))).))))..)).)))..)))))...(((((((......)))))))........((((..((((.........))))..))))..-3'
MFE = -38.5; z-score = -1.56; ED = 45.4
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

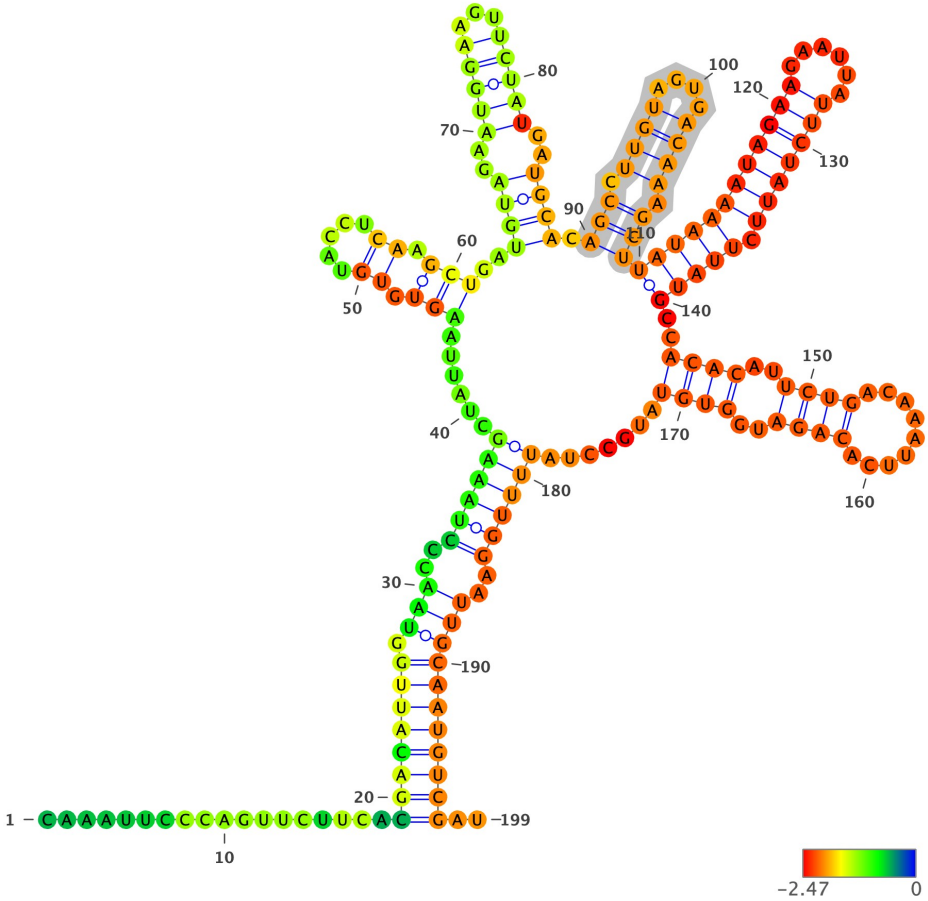
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 19100 to 19119 (nt 90 to 109)

```
5'-AGCCTTGTAGTGACAAAGCU-3'
5'-(((.((((....)))).)))-3'
Motif MFE = -3.9; z-score = -1.35; 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 19011 to 19209 (motif highlighted in silver):

```
5'-CAAAUUCCCAGUUCUUCACGACAUUGGUAACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUA
UAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAU-3
5'-.................(((((((.(((..((((((.....(((.((.....)).))))..((((..((((((...))))))..))))).(((.((((....)))).)))))((
((((((((((.....)))))))).))))))..((((..((((.........))))..))))......))))))..)))))))))))..-3'
MFE = -40.9; z-score = -2.51; ED = 41.06
```

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(+)

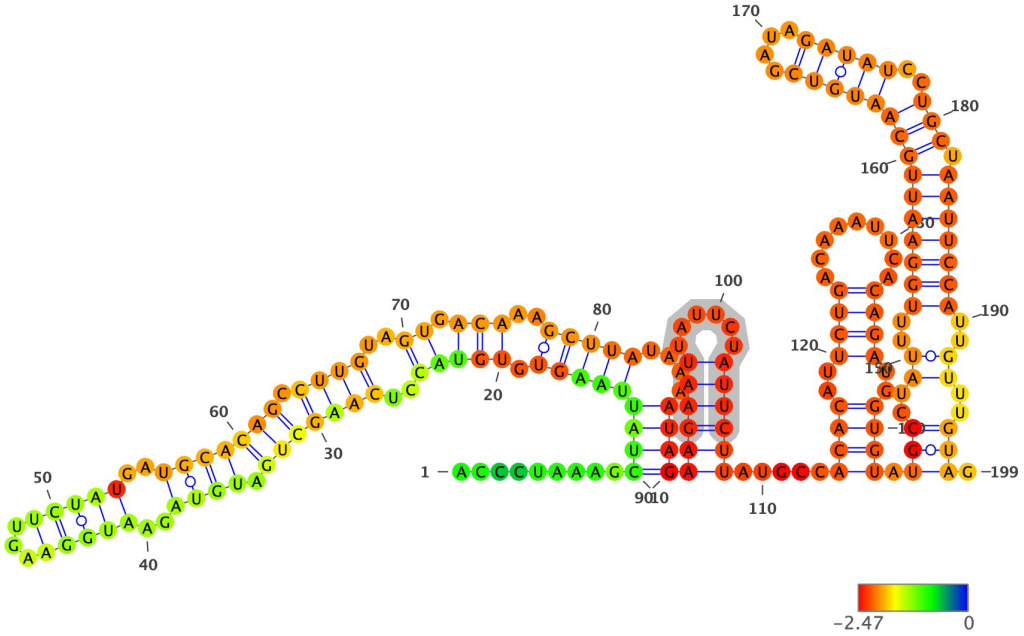
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 319 from nt 19132 to 19145 (nt 93 to 106)

```
5'-GAATTATTCTAUUC-3'
5'-((((.....))))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 2.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19040 to 19238 (motif highlighted in silver):

```
5'-ACCCUAAAGCUAUUAAGUGUGUACCUCAAGCUGAUGUAGAAUGGAAGUUCUAUGAUGCACAGCCUUGUAGUGACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUG
CCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCUAAUUCCAUUGUUUGUAG-3
5'-.........(((((((((.(((((..(((((((.((((..((((((...))))))..)))))))).)))))..)).)))..))))))....))))((((((......)))))).
..((((..((((.........))))..)))).(((..((..((((((((((((((....))))))..)))).)))))))..))..))).-3'
MFE = -49.9; z-score = -2.91; ED = 21.5
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

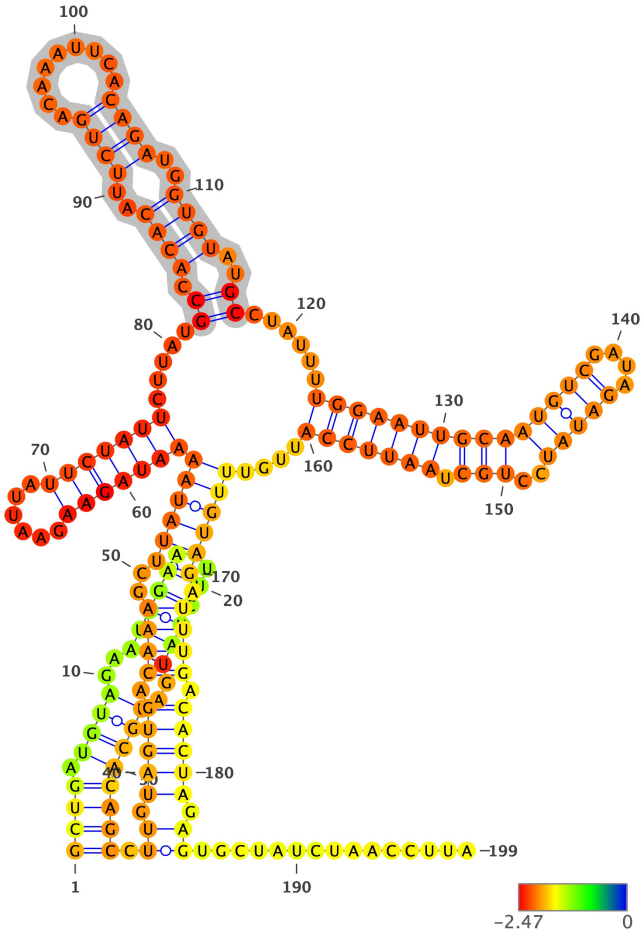
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 320 from nt 19150 to 19185 (nt 82 to 117)

```
5'-GCCACACATTCTGACAAATTCACAGATGGUGUATGC-3'
5'-((.((((..((((.........))))..))))..))-3'
Motif MFE = -8.2; z-score = -1.9; 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 = -3.14; ED = 24.25
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

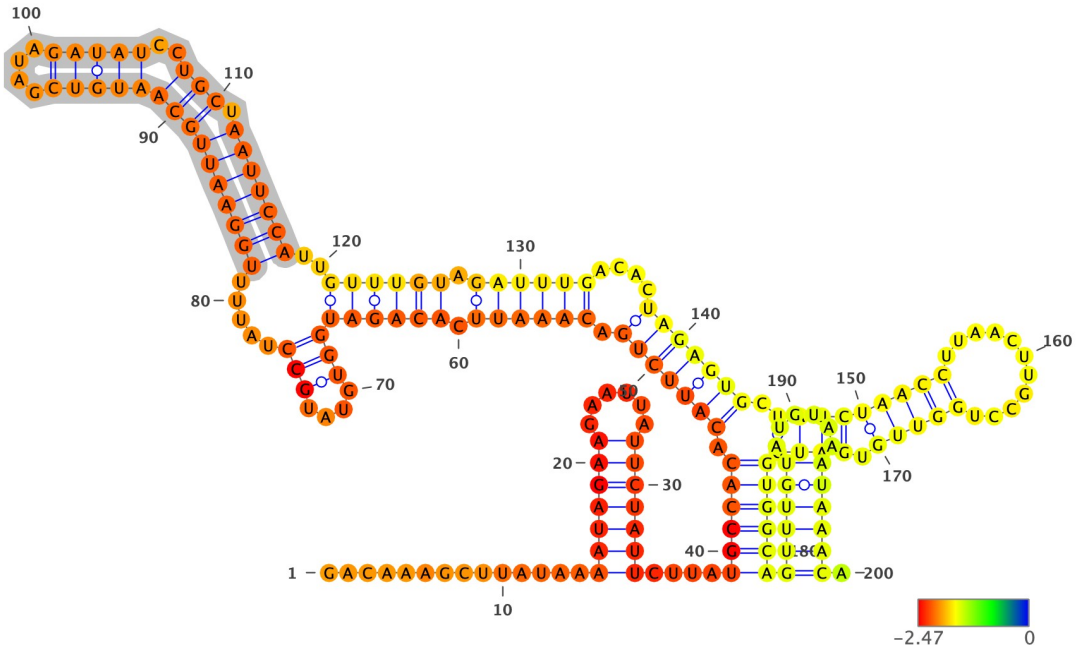
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 321 from nt 19192 to 19228 (nt 82 to 118)

```
5'-TGGAATTGCAATGTCGATAGAUAUCCUGCTAAUUCCA-3'
5'-(((((((((((((((....)))))..))).)))))))-3'
Motif MFE = -12.8; z-score = -3.92; ED = 1.31
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19111 to 19310 (motif highlighted in silver):

```
5'-GACAAAGCUUAUAAAAUAGAAGAAUUAUUCUAUUCUUAUGCCACACAUUCUGACAAAUUCACAGAUGGUGUAUGCCUAUUUUGGAAUUGCAAUGUCGAUAGAUAUCCUGCU
AAUUCCAUUGUUUGUAGAUUUGACACUAGAGUGCUAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACA-3
5'-..............(((((((......)))))))....((((((.(((((((.((((((.(((((((((....)))).....((((((((((((((....)))))..))).
)))))))..)))))).)))))).....)))))))).(((((((((...........))))).))))))))))((((((......)))))).-3'
MFE = -49.3; z-score = -2.78; ED = 27.45
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

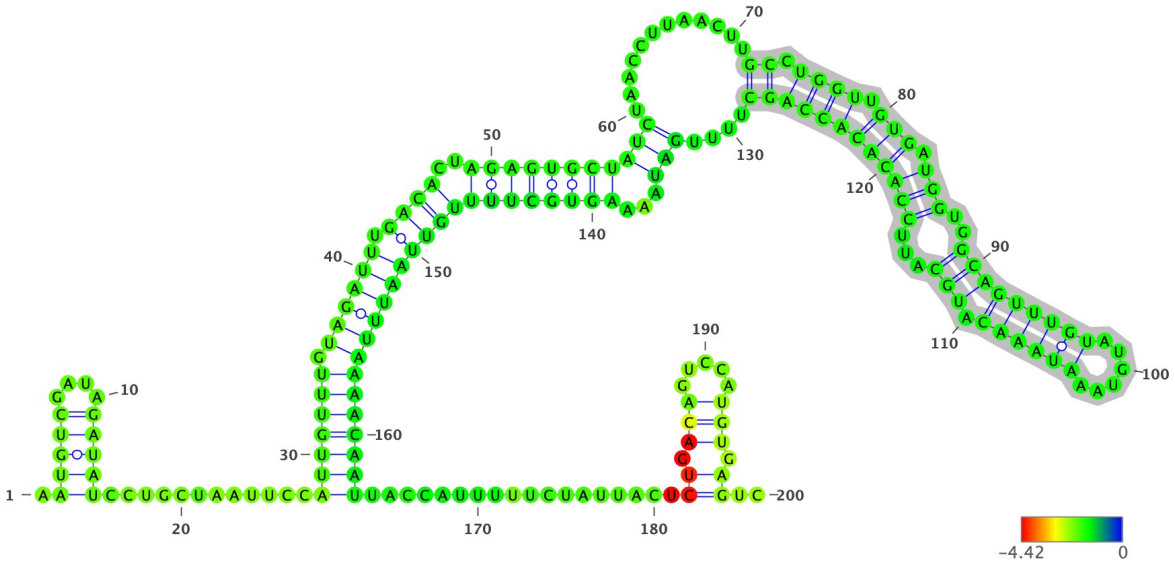
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 322 from nt 19272 to 19328 (nt 72 to 128)

```
5'-GCCTGGTTGTGATGGTGGCAGTTTGTATGTAAATAAACAUGCATTCCACACACCAGC-3'
5'-((.((((.(((.(((..(((((((.........)))).)))...)))))))))))-3'
Motif MFE = -20.3; z-score = -3.21; 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 = -1.06; ED = 27.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

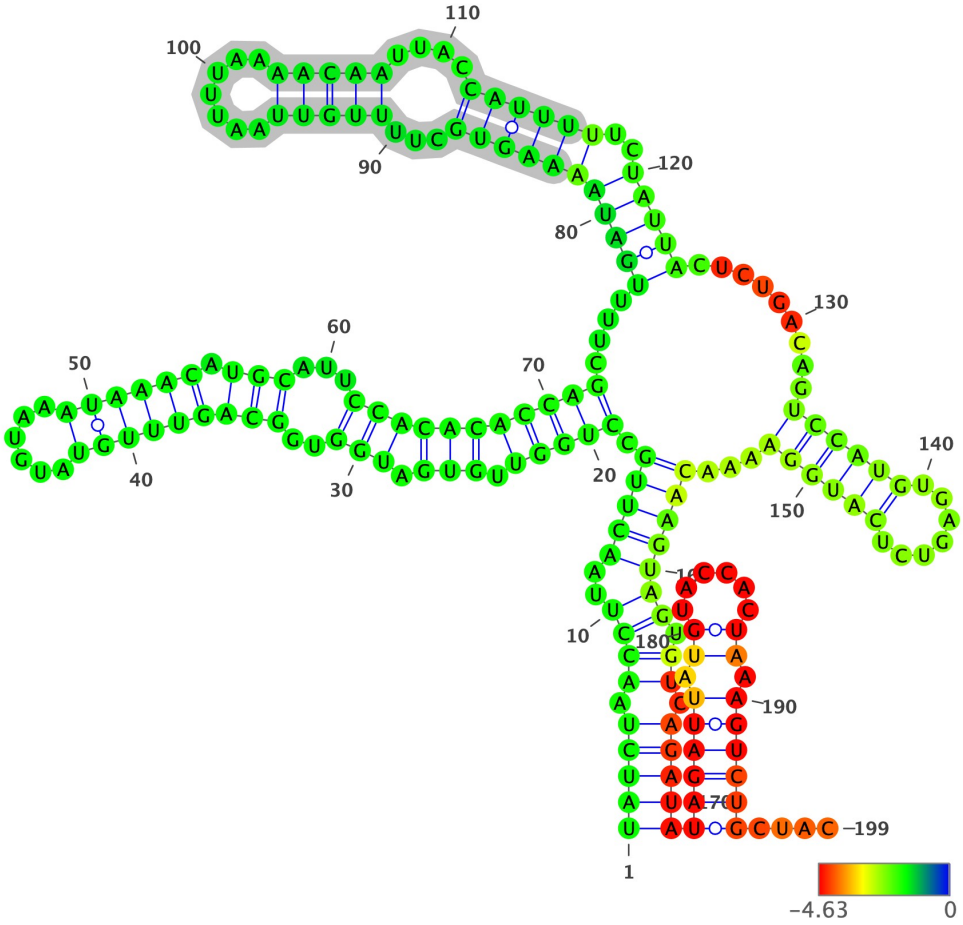
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 323 from nt 19338 to 19371 (nt 83 to 116)

```
5'-AAGTGCTTTTGTTAATTTAAAACAATTACCAUUU-3'
5'-(((((...(((((.......)))))....)))))-3'
Motif MFE = -2.3; z-score = -0.68; ED = 3.99
```



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 19256 to 19454 (motif highlighted in silver):

```
5'-UAUCUAACCUUAACUUGCCUGGUUGUGAUGGUGGCAGUUUGUAUGUAAAUAAACAUGCAUUCCACACACCAGCUUUUGAUAAAAGUGCUUUUGUUAAUUUAAAACAAUUAC
CAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUAC-3
5'-(((((.((((..(((((.(((((.(((.(((..(((((((((.....))))))).)))...)))))))))))....((((((((((...(((((.......)))))....
))))))..)))))........((((((.......))))))...)))))))).)).)))))((((((.((......)).))))))....-3'
MFE = -41.4; z-score = -2.02; ED = 45.98
```

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(+)

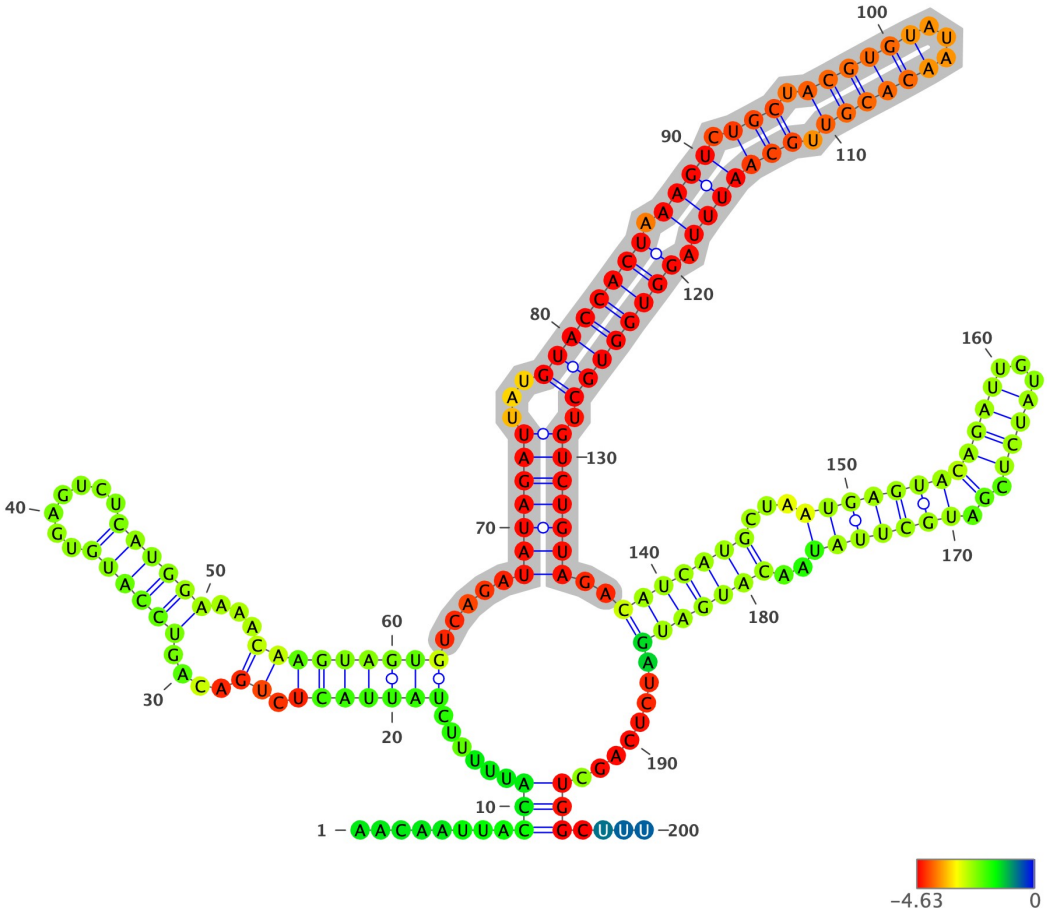
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 324 from nt 19420 to 19494 (nt 63 to 137)

```
5'-TCAGATATAGATTATGTACCACTAAAGTCTGCTACGTGTATAACACGUTGCAAUUUAGGUGGUGCTGUCUGUAGA-3'
5'-((...(((((((...((((((((.((((.(((.(((((.....))))).)))))))).))))))))).)))))))))-3'
Motif MFE = -29.9; z-score = -4.42; ED = 3.22
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19358 to 19557 (motif highlighted in silver):

```
5'-AACAAUUACCAUUUUUCUAUUACUCUGACAGUCCAUGUGAGUCUCAUGGAAAACAAGUAGUGUCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUU
GCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCUUAUAACAUGAUGAUCUCAGCUGGCUUU-3
5'-........(((......(((((((.((....((((((.......))))))...)))))))))).....(((((((...((((((((.((((.(((.((((((...)))))).
)))))))).))))))))).)))))))..(((((((...(((((((((((...)))).).)))))))..)))))))........)))....-3'
MFE = -57.2; z-score = -4.68; ED = 33.46
```

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(+)

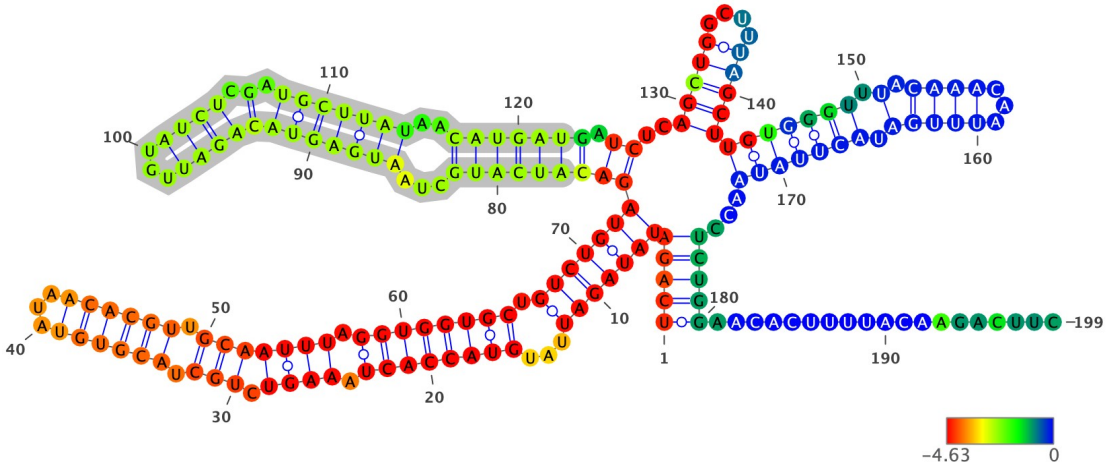
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 325 from nt 19496 to 19541 (nt 77 to 122)

```
5'-ATCATGCTAATGAGTACAGATTGTAUCUCGAUGCUUATAACAUGAU-3'
5'-((((((....((((((.((((...))))...))))))...))))))-3'
Motif MFE = -10.4; z-score = -2.45; ED = 5.06
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19420 to 19618 (motif highlighted in silver):

```
5'-UCAGAUAUAGAUUAUGUACCACUAAAGUCUGCUACGUGUAUAACACGUUGCAAUUUAGGUGGUGCUGUCUGUAGACAUCAUGCUAAUGAGUACAGAUUGUAUCUCGAUGCU
UAUAACAUGAUGAUCUCAGCUGGCUUUAGCUUGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUC-3
5'-(((((((((((...((((((((.((((.((((.((((((...)))))).)))))))).))))))))).)))))))(((((((((...((((((((((((...)))).).))))
)))..)))))))).))..(((((....)))))(((((((.(.((((...)))))).)))))))...)))))).....................-3'
MFE = -56.0; z-score = -3.31; ED = 13.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

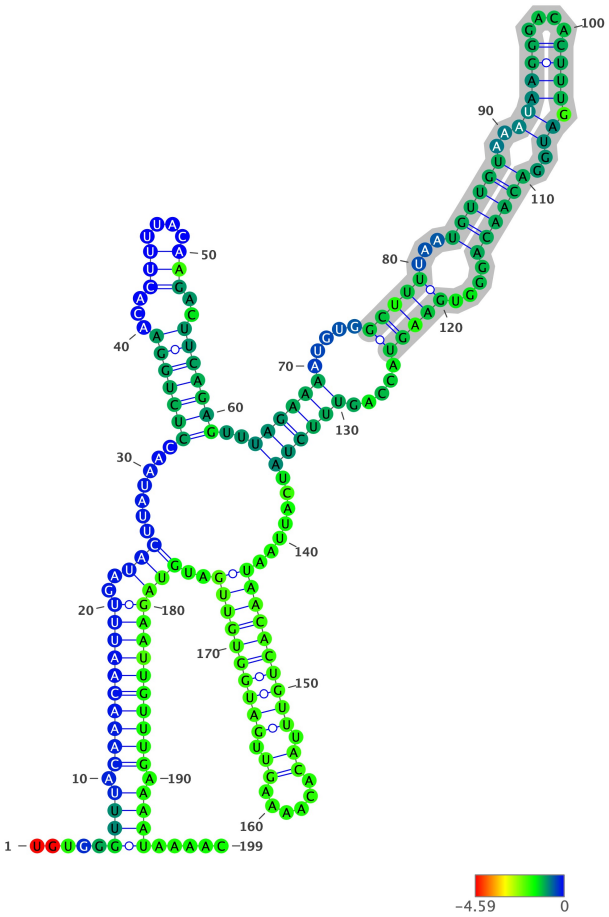
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 326 from nt 19636 to 19685 (nt 75 to 124)

```
5'-GCTTTTAATGTTGTAAATAAGGGACACUTTGATGGACAACAGGGTGAAGU-3'
5'-((.((...((((((......((....))..<....))))))....)).))-3'
Motif MFE = -11.6; z-score = -2.23; ED = 3.23
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19562 to 19760 (motif highlighted in silver):

```
5'-UGUGGGUUUACAAACAAUUUGAUACUUAUAACCUCUGGAACACUUUUACAAGACUUCAGAGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGAC
AACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAAC-3
5'-.....((((.((((((((((..(((.......(((((((...(((....)))..)))))))..((((((.....(((((...((((((..((((((....)))).))..))
))))....)))))).....))))))).......((((((((((.((......)).))))))))))..))))))))))))).))))).....-3'
MFE = -43.7; z-score = -1.9; ED = 17.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

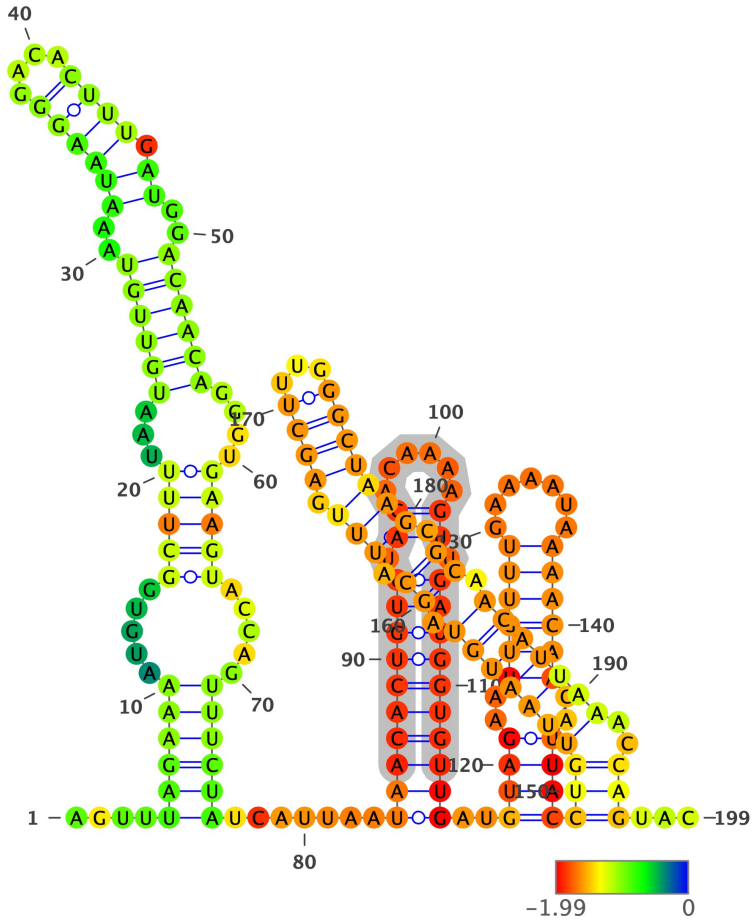
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 327 from nt 19706 to 19733 (nt 86 to 113)

```
5'-ACACTGTTTACACAAAAGUTGAUGGUGU-3'
5'-((((((((.((......)).))))))))-3'
Motif MFE = -6.9; z-score = -2.44; ED = 1.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19621 to 19819 (motif highlighted in silver):

```
5'-AGUUUAGAAAAUGUGGCUUUUAAUGUUGUAAAUAAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGU
GUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUAC-3
5'-....((((((.....(((((...((((((..((((((....)))).))..))))))....)))))).....)))))).......((((((((((.((......)).))))))
))))..((((..((((((.......))))))..))))((((((((((.((.(((.((((...)))))))).)).)))))))..)))...-3'
MFE = -43.8; z-score = -2.19; ED = 49.49
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

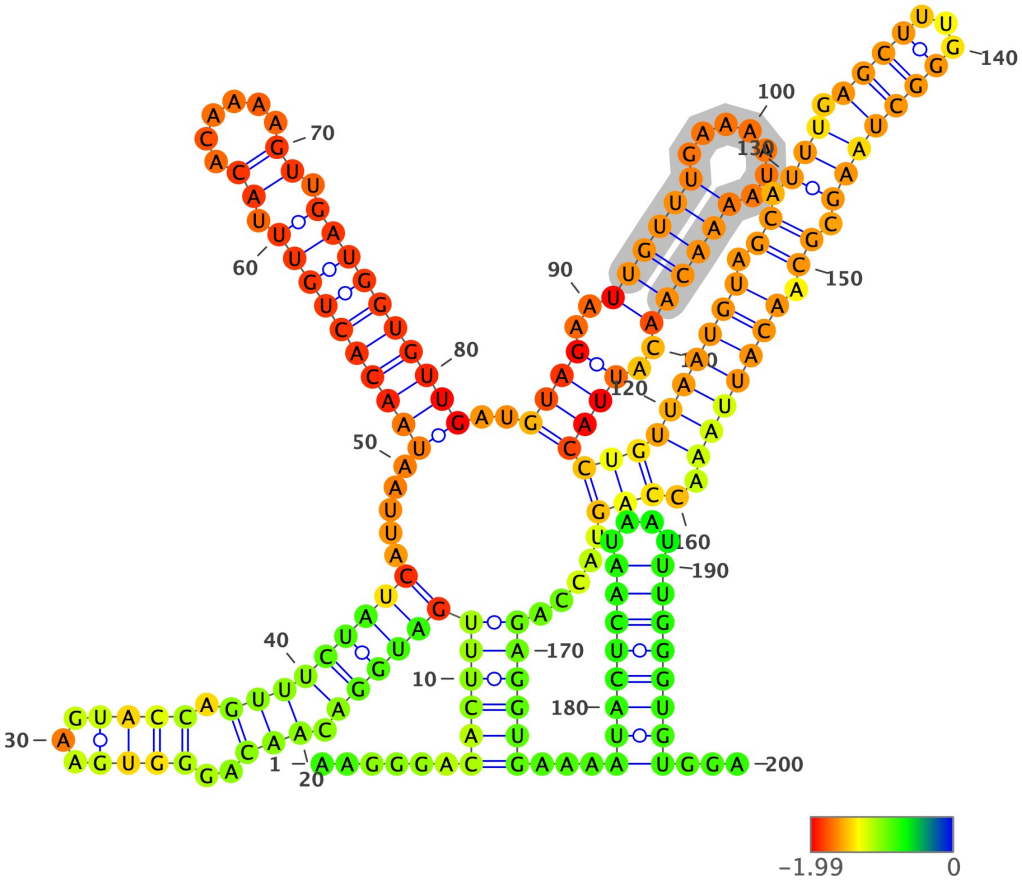
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 328 from nt 19745 to 19761 (nt 92 to 108)

```
5'-TGTTTGAAAATAAAACA-3'
5'-((((.........))))-3'
Motif MFE = -1.1; z-score = -4.17; ED = 1.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19654 to 19853 (motif highlighted in silver):

```
5'-AAGGGACACUUUGAUGGACAACAGGGUGAAGUACCAGUUUCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACA
UUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGCAACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGA-3
5'-......((((((((((((.((((..(((((...)))))..)))))))))).....((((((((((.((......)).)))))))))))..((((..((((((.......))))))..
))))((((((((((.((.(((.(((((...)))))))).)).)))))))..)))).....)))))))...(((((((((....)))))))))...-3'
MFE = -48.3; z-score = -2.4; ED = 35.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

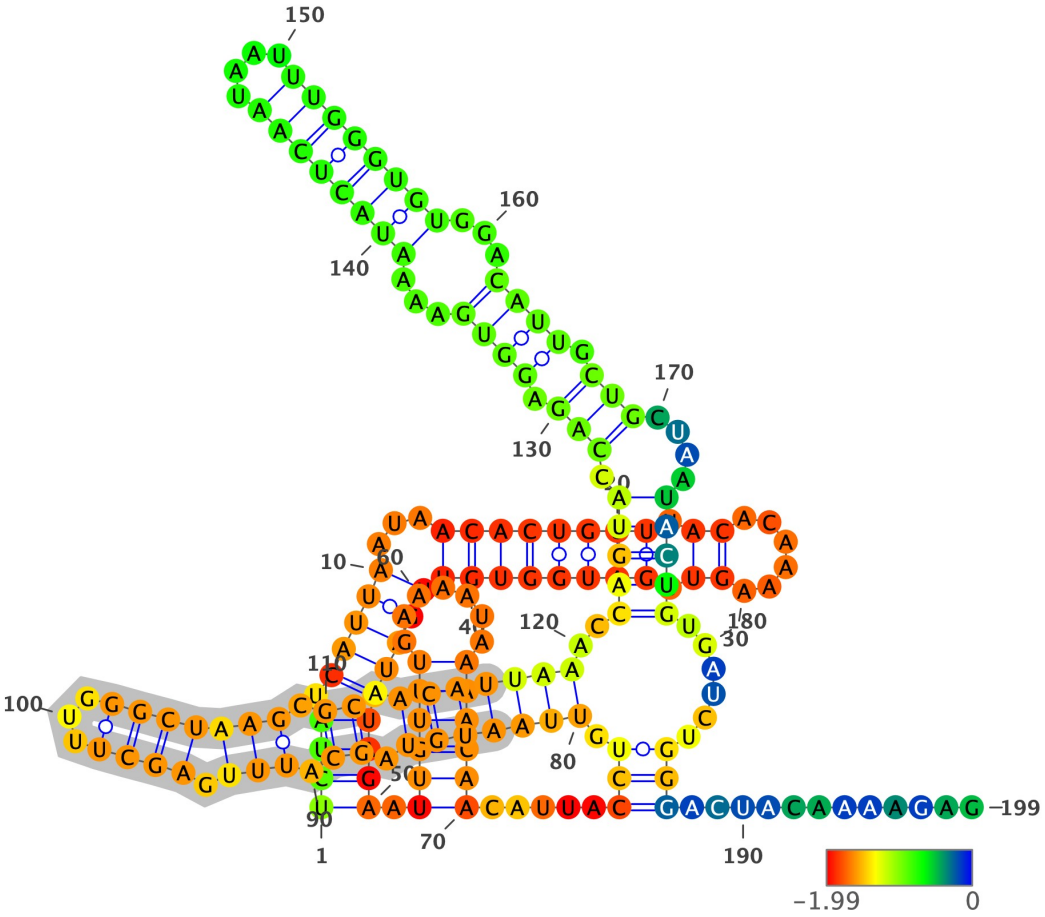
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 329 from nt 19775 to 19808 (nt 83 to 116)

```
5'-ATGTAGCATTTGAGCTTTGGGCUAAGCGCAACAU-3'
5'-((((.((.((..(((((...))))).)).)).))))-3'
Motif MFE = -7.3; z-score = -1.1; ED = 3.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 19693 to 19891 (motif highlighted in silver):

```
5'-UCUAUCAUUAAUAACACUGUUUACACAAAAGUUGAUGGUGUUGAUGUAGAAUUGUUUGAAAAUAAAACAACAUUACCUGUUAAUGUAGCAUUUGAGCUUUGGGCUAAGCGC
AACAUUAAACCAGUACCAGAGGUGAAAAUACUCAAUAAUUUGGGUGUGGACAUUGCUGCUAAUACUGUGAUCUGGGACUACAAAAGAG-3
5'-((((.((((((...(((((((((.((......)).)))))))))))))))))).((((((.......)))))).....(((.(((((((.((.(((.(((((...)))))))).))
.)))))))..((((((.(((.((((((...(((((((((....)))))))))...)))))).))))....)))))......))).............-3'
MFE = -43.7; z-score = -1.44; ED = 26.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

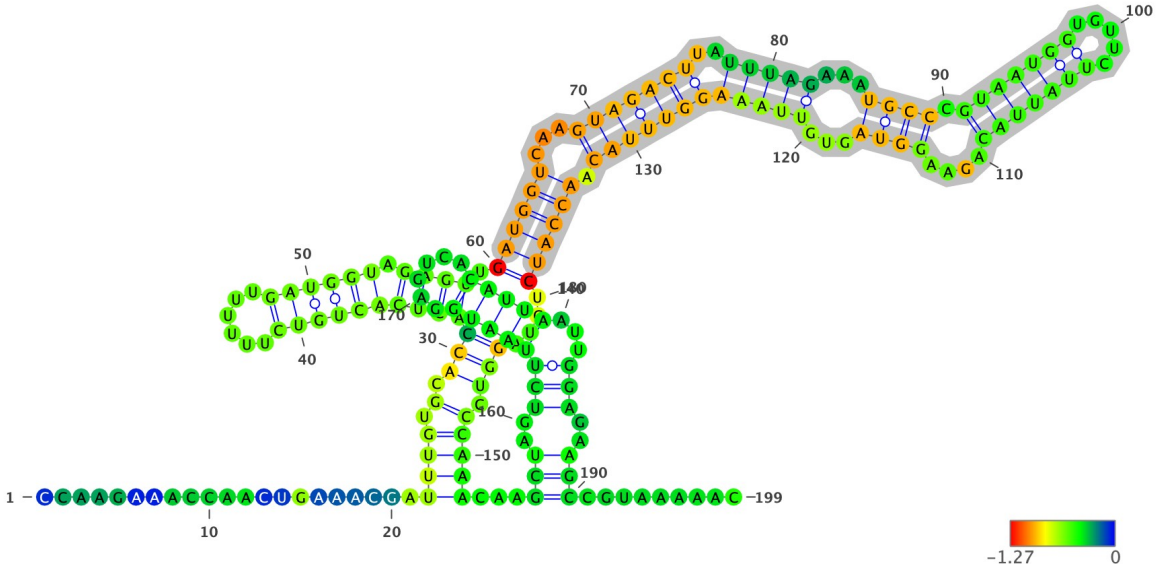
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 330 from nt 20003 to 20080 (nt 61 to 138)

```
5'-ATGGTCAAGTAGACTTATTTAGAAATGCCCGTAATGGTGTTCUUAUUACAGAAGGUAGTGTTAAAGGUUUACAACCAU-3'
5'-(((((...((.............................................................)).)))))-3'
Motif MFE = -17.8; z-score = -2.34; ED = 7.19
```



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 19943 to 20141 (motif highlighted in silver):

```
5'-CCAAGAAACCAACUGAAACGAUUUGUGCACCACUCACUGUCUUUUUUGAUGGUAGAGUUGAUGGUCAAGUAGACUUAUUUAGAAAUGCCCGUAAUGGUGUUCUUAUUACAG
AAGGUAGUGUUAAAGGUUUACAACCAUCUGUAGGUCCCAAACAAGCUAGUCUUAAUGGAGUCACAUUAAUUGGAGAAGCCGUAAAAAC-3
5'-.....................((((.(.(((((((((((((.....)))))).)))).((((((...(((((((..(((((...((((.(((((((.....)))))))..
..))))...))))))))))))).))))))....))).)))))...(((..((((((((.....)))))...)))..))).........-3'
MFE = -42.5; z-score = -0.34; ED = 21.02
```

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(+)

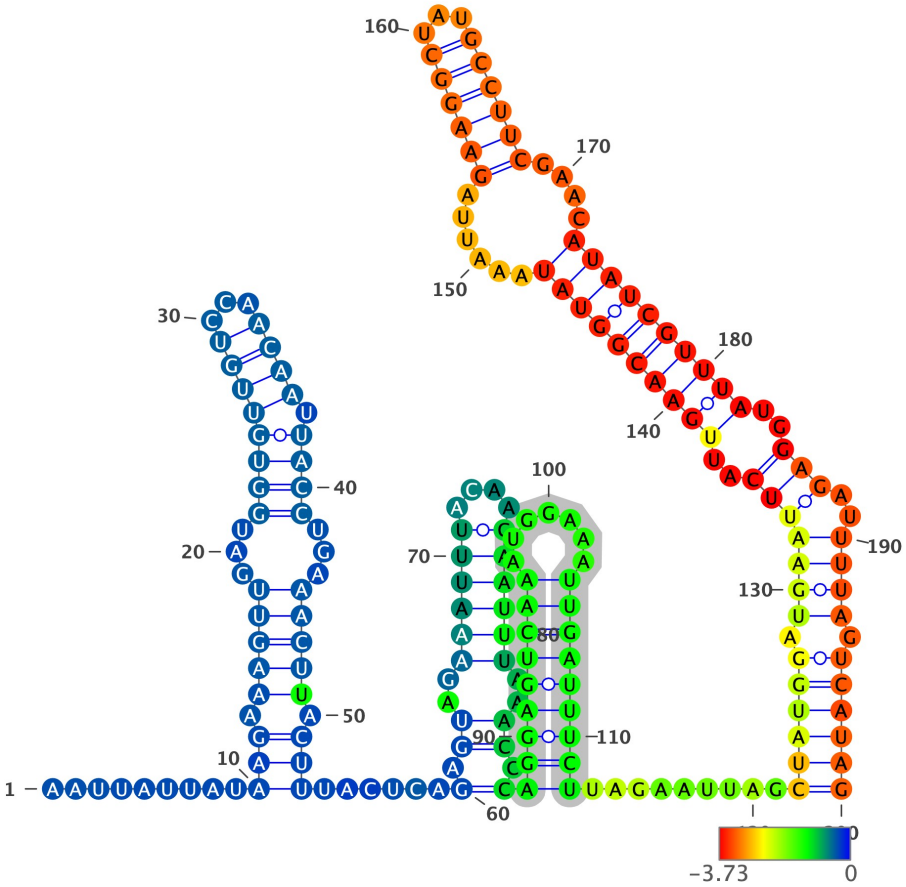
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 20236 to 20260 (nt 88 to 112)

```
5'-AGGAGTCAAATGGAAAUUGAUUUCU-3'
5'-(((((((((.......)))))))))-3'
Motif MFE = -6.1; z-score = -3.6; 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 = -2.08; 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(+)

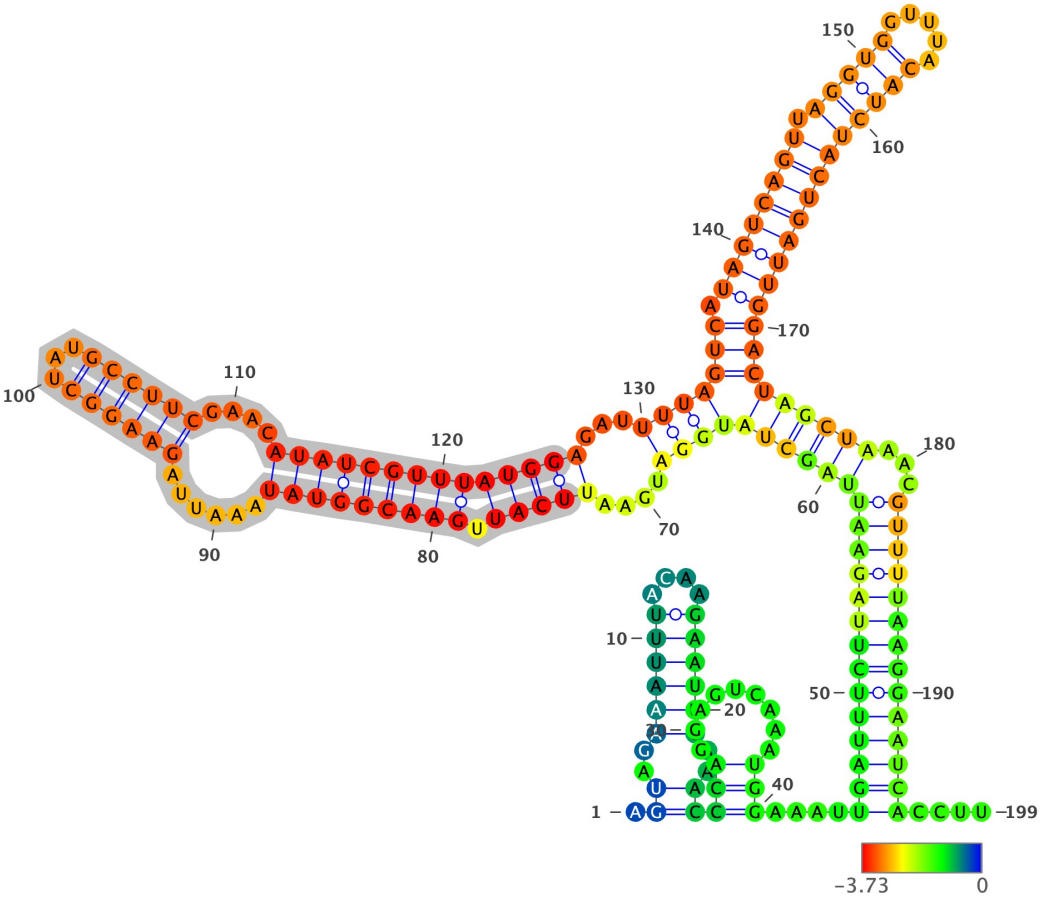
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 332 from nt 20282 to 20333 (nt 74 to 125)

```
5'-TCATTGAACGGTATAAATTAGAAGGCTATGCCUUCGAACAUAUCGUUUAUGG-3'
5'-((((.(((((((((.....((((((...)))))).....))))))))))))-3'
Motif MFE = -17.3; z-score = -3.69; ED = 3.45
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20209 to 20407 (motif highlighted in silver):

```
5'-AGUAGAAAUUUACAAGAAUUUAAACCCAGGAGUCAAAUGGAAAUUGAUUUCUUAGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAA
CAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUU-3
5'-.((..((((((....))))))..))(((.........))).....(((((((((((((((((((((((....(((((.(((((((((.....((((((...))))))...
.)))))))))))))...))))(((.((((((((.(((((.....)))))))))))))))))))))))...)))))))))))))....-3'
MFE = -57.1; z-score = -4.96; ED = 16.29
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

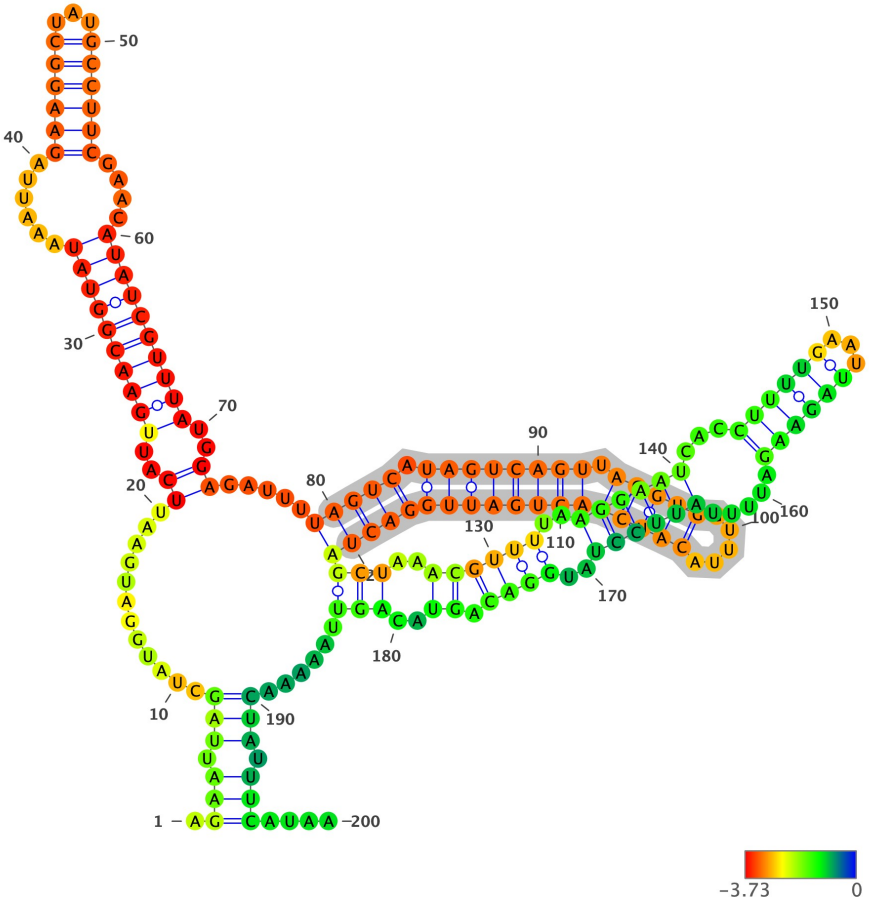
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 333 from nt 20341 to 20381 (nt 80 to 120)

```
5'-AGTCATAGTCAGTTAGGTGGTTTACAUCUACUGAUUGGACU-3'
5'-((((.(((((((((.(((((.....))))))))))))))))))-3'
Motif MFE = -17.7; z-score = -4.07; ED = 1.77
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20262 to 20461 (motif highlighted in silver):

```
5'-AGAAUUAGCUAUGGAUGAAUUCAUUGAACGGUAUAAAUUAGAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACU
GAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAA-3
5'-.(((.(((.............((..((((((((((.....((((((...))))))....))))))))))..)).....(((((.(((((((.(((((.....)))))))
))))))))))))(((..((((((..((((((...((((((...))))))).....))))))..)))))..))..))).....)))..))).....-3'
MFE = -50.7; z-score = -3.47; ED = 31.15
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

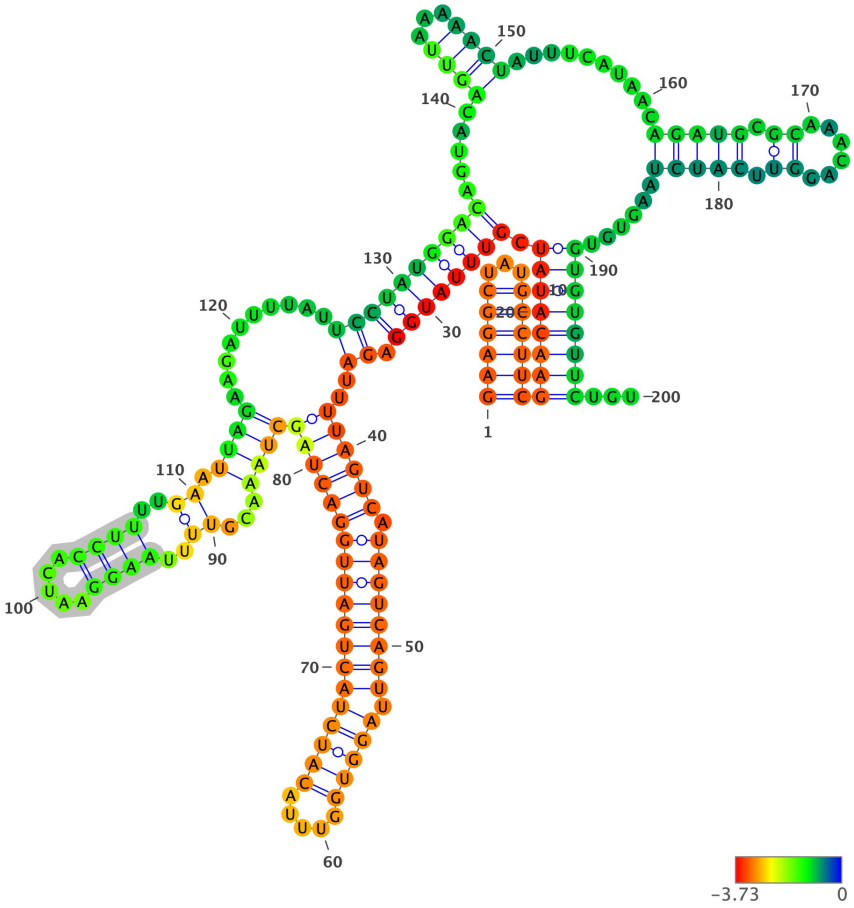
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 334 from nt 20395 to 20407 (nt 94 to 106)

```
5'-AAGGAATCACCUU-3'
5'-((((.....))))-3'
Motif MFE = -1.2; z-score = -3.6; 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 20302 to 20501 (motif highlighted in silver):

```
5'-GAAGGCUAUGCCUUCGAACAUAUCGUUUAUGGAGAUUUUAGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAA
UUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGU-3
5'-((((((...))))))((((((((.((((((((.((..((((((.((((((((.(((((.....)))))))))))))))))))((((...((..((((.....))))..)).
))))..........))))))))))).....((((...))))..........(((((.((......)).)))))......))))))))...-3'
MFE = -50.0; z-score = -2.52; ED = 37.6
```

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(+)

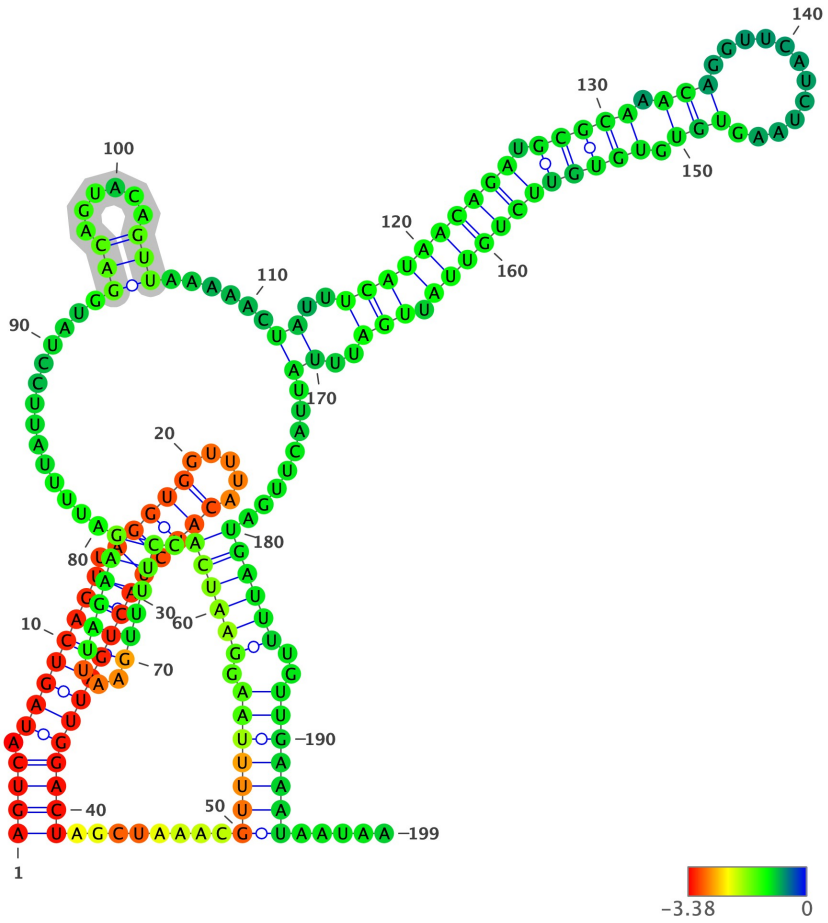
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 20434 to 20445 (nt 94 to 105)

```
5'-GACAGTACAGUU-3'
5'-(((.....)))-3'
Motif MFE = 0.0; z-score = 0.28; ED = 1.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20341 to 20539 (motif highlighted in silver):

```
5'-AGUCAUAGUCAGUUAGGUGGUUUACAUCUACUGAUUGGACUAGCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAAC
UAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAA-3
5'-((((.(((((((((.(((((.....)))))))))))))))))).......(((((((.((((((.((((((...))))))..............(((......))).....
((..((((((((((.(((((.(((............))).)))))))))))).))))..))........)))))))..)))))))).....-3'
MFE = -42.3; z-score = -2.55; ED = 40.96
```

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(+)

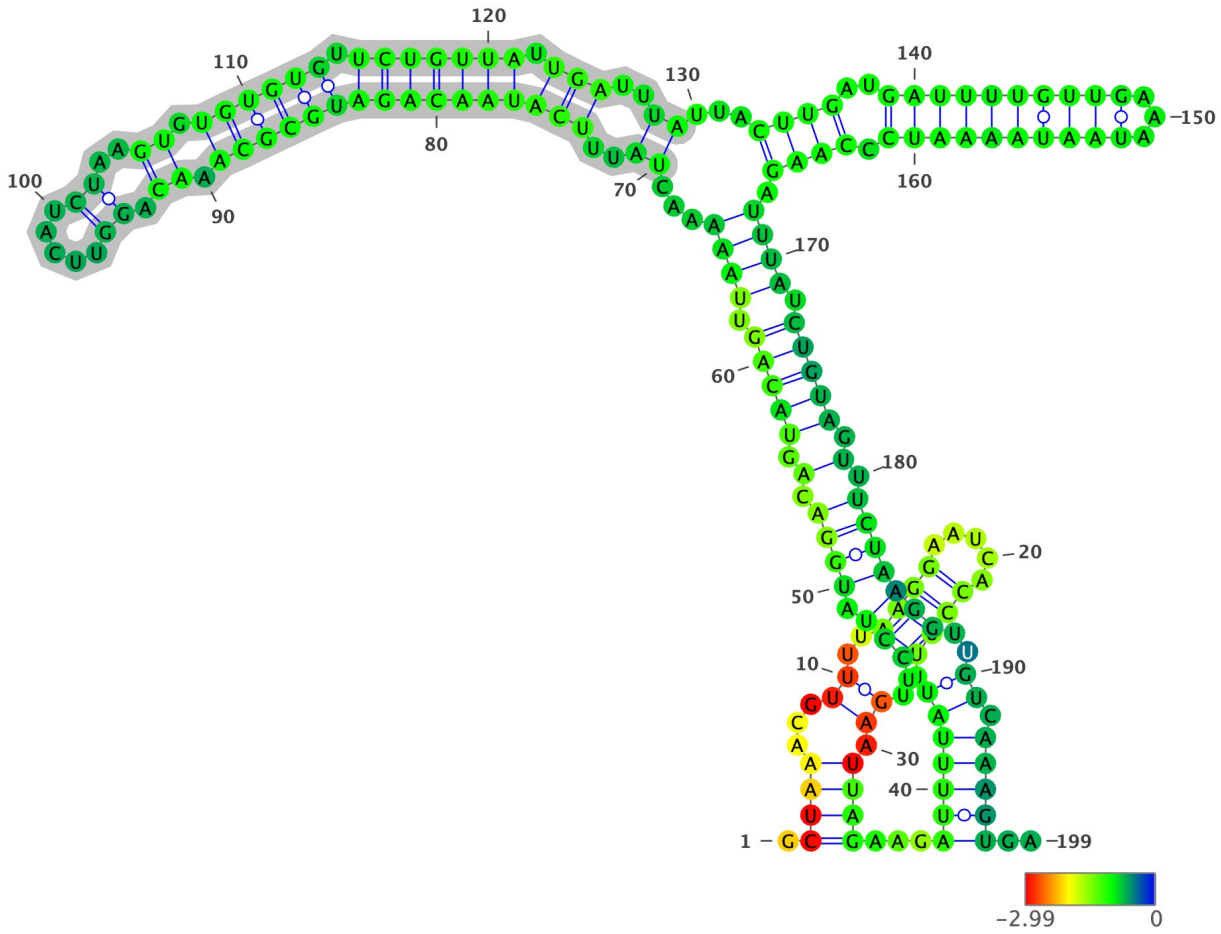
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 336 from nt 20452 to 20511 (nt 70 to 129)

```
5'-TATTTCATAACAGATGCGCAAACAGGTTCATCTAAGUGUGUGUGTUCUGUUATUGATTTA-3'
5'-(...((((((((((.(((((.((............)).)))))..)))))))).)))...)-3'
Motif MFE = -15.2; z-score = -2.61; ED = 13.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20383 to 20581 (motif highlighted in silver):

```
5'-GCUAAACGUUUUAAGGAAUCACCUUUUGAAUUAGAAGAUUUUAUUCCUAUGGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUG
UGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGA-3
5'-.((((...((..((((.....))))..)).))))...(((((((.(((.((((.(.(((((.((((...((..((((((((((((((((.((.((.....)).)).))))
)).)))))))).)))..))...((((..((((((((((...)))))))))).)))).)))).)))))).).)))))))..)).)))))..-3'
MFE = -38.1; z-score = -0.77; ED = 50.8
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

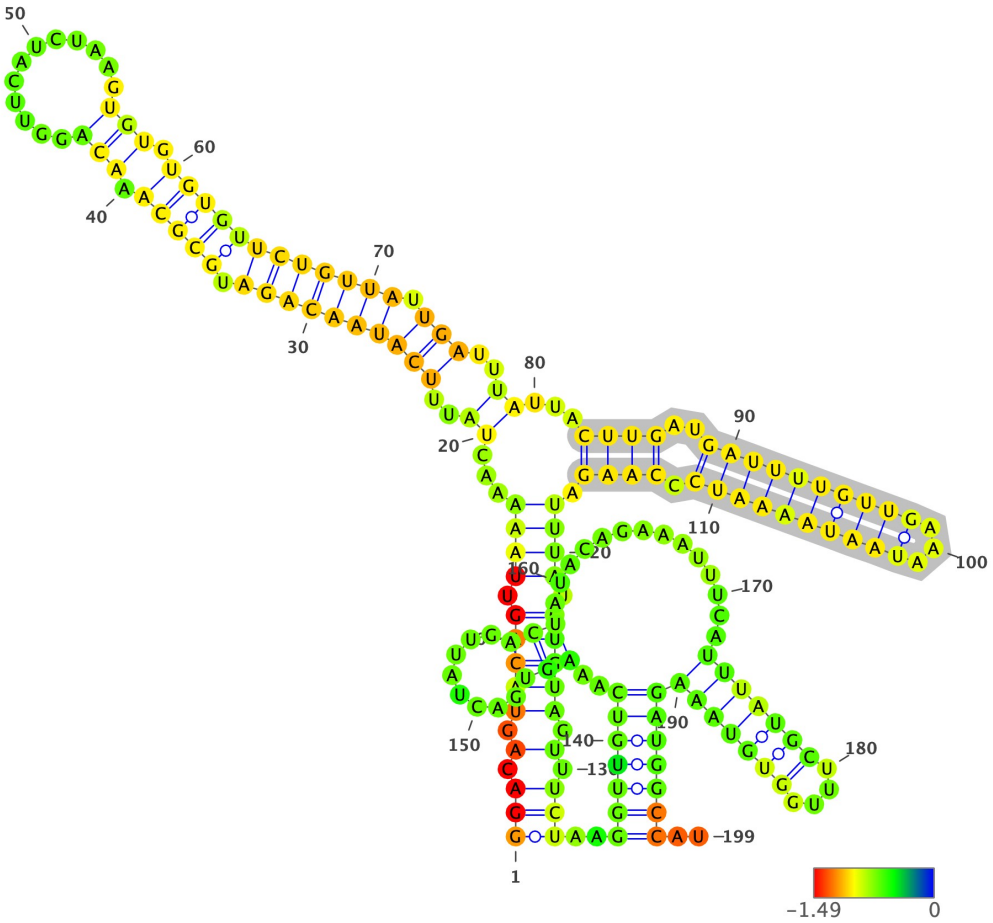
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 337 from nt 20515 to 20548 (nt 83 to 116)

```
5'-CTTGATGATTTTGTTGAAATAAUAAAAUCCCAAG-3'
5'-((((..((((.((((.....)))).)))).))))-3'
Motif MFE = -7.4; z-score = -3.07; ED = 1.08
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20433 to 20631 (motif highlighted in silver):

```
5'-GGACAGUACAGUUAAAAACUAUUUCAUAACAGAUGCGCAAACAGGUUCAUCUAAGUGUGUGUGUUCUGUUAUUGAUUUAUUACUUGAUGAUUUUGUUGAAAUAAUAAAAUC
CCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAU-3
5'-(((.(.(((((.((((...((..((((((((((.(((((.(((............))).))))))))))))).)))..))...((((..((((((((((...))))))))))
.)))).)))).)))))).).)))..(((((((..(((........)))..............(((((((....)))))))))))))..-3'
MFE = -41.9; z-score = -1.39; ED = 46.54
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

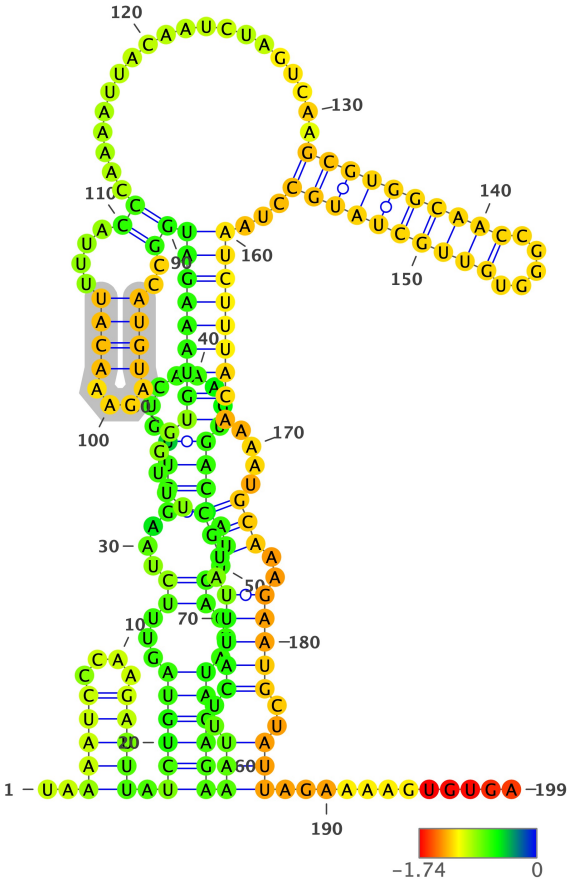
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 338 from nt 20630 to 20641 (nt 94 to 105)

```
5'-ATGTAGAAACAU-3'
5'-((((....))))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 20537 to 20735 (motif highlighted in silver):

```
5'-UAAAAUCCCAAGAUUUAUCUGUAGUUUCUAAGGUUGUCAAAGUGACUAUUGACUAUACAGAAAUUUCAUUUAUGCUUUGGUGUAAAGAUGGCCAUGUAGAAACAUUUUACC
CAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAGAAAAGUGUGA-3
5'-..(((((....))))).(((((((...((...((((........))))...))...)))))))(((..(((((.(((.....((((((((((..((((....))))....))
.....................((((((((((.....))))))))))...))))))))))....)))..))))))..)))............-3'
MFE = -37.7; z-score = -0.78; ED = 52.27
```

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(+)

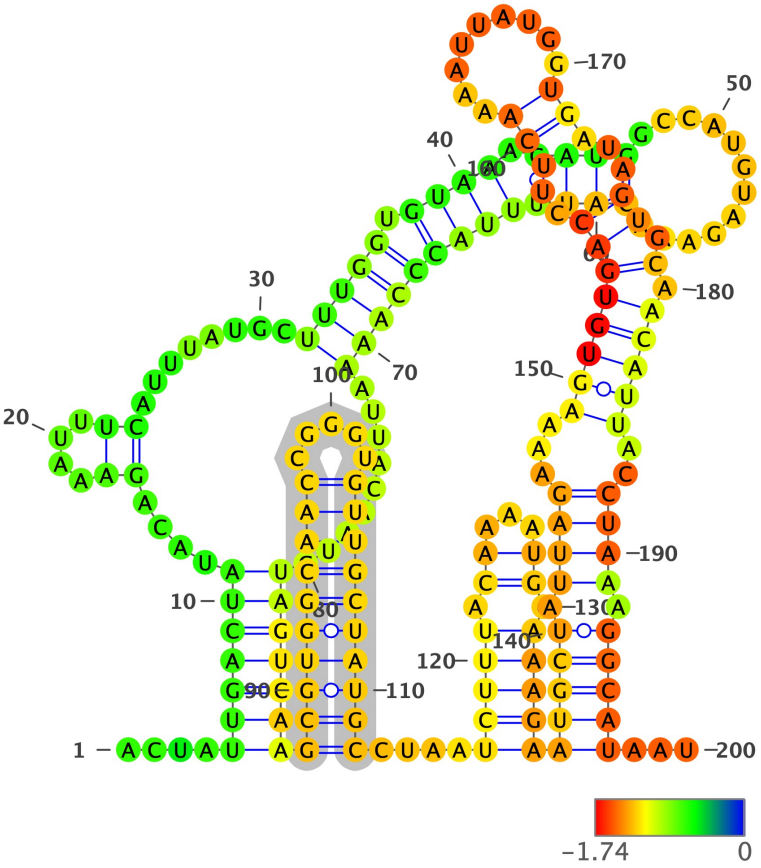
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 339 from nt 20668 to 20692 (nt 88 to 112)

```
5'-GCGTGGCAACCGGGTGUUGCUAUGC-3'
5'-((((((((((.....))))))))))-3'
Motif MFE = -13.0; z-score = -3.18; 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 = -1.11; 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(+)

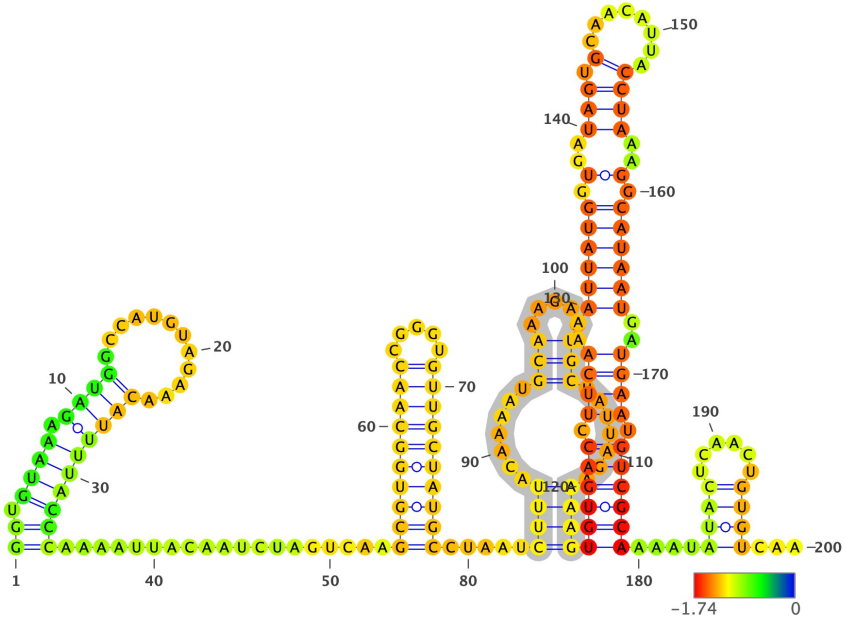
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 340 from nt 20698 to 20730 (nt 84 to 116)

```
5'-CTTTACAAAATGCAAAGAAUGCTATTAGAAAAG-3'
5'-((((.......(((.....))).......))))-3'
Motif MFE = -1.3; z-score = -0.19; ED = 5.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20615 to 20814 (motif highlighted in silver):

```
5'-GGUGUAAAGAUGGCCAUGUAGAAACAUUUUACCCAAAAUUACAAUCUAGUCAAGCGUGGCAACCGGGUGUUGCUAUGCCUAAUCUUUACAAAAUGCAAAGAAUGCUAUUAG
AAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAA-3
5'-((.(((((.((((.............)))))))))).....................((((((((((.....))))))))))).....((((.......(((.....))).....
.))))(((((((.((((..(((((((.(..(((.(........)))))..).)))))))..)))))..)))))....((((......)))))...-3'
MFE = -41.4; z-score = -1.93; 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(+)

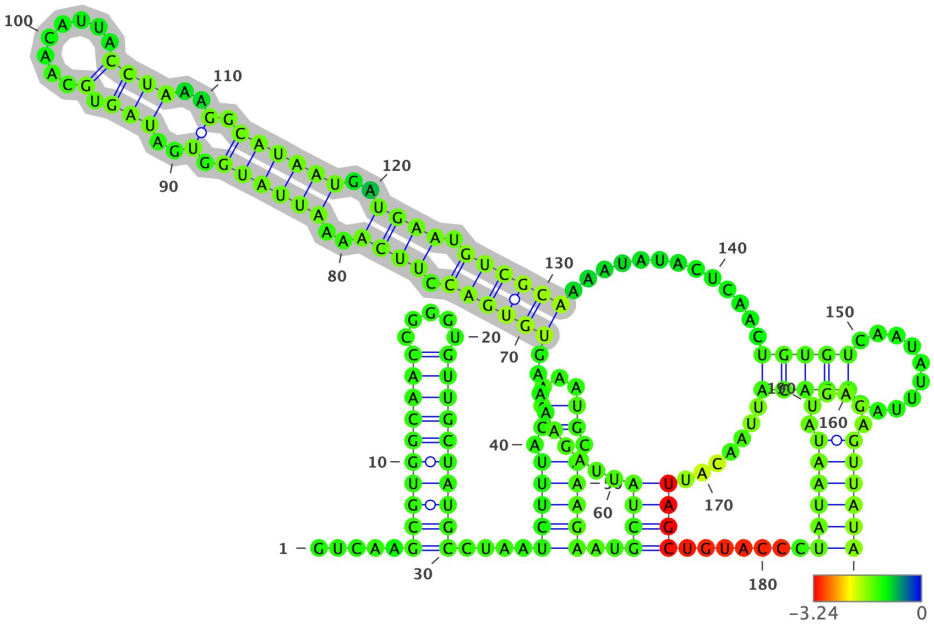
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 341 from nt 20731 to 20793 (nt 69 to 131)

```
5'-TGTGACCTTCAAAATTATGGTGATAGTGCAACATTACCUAAAGGCAUAAUGAUGAATGUCGCA-3'
5'-((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))-3'
Motif MFE = -17.6; z-score = -3.55; 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 = -1.08; 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(+)

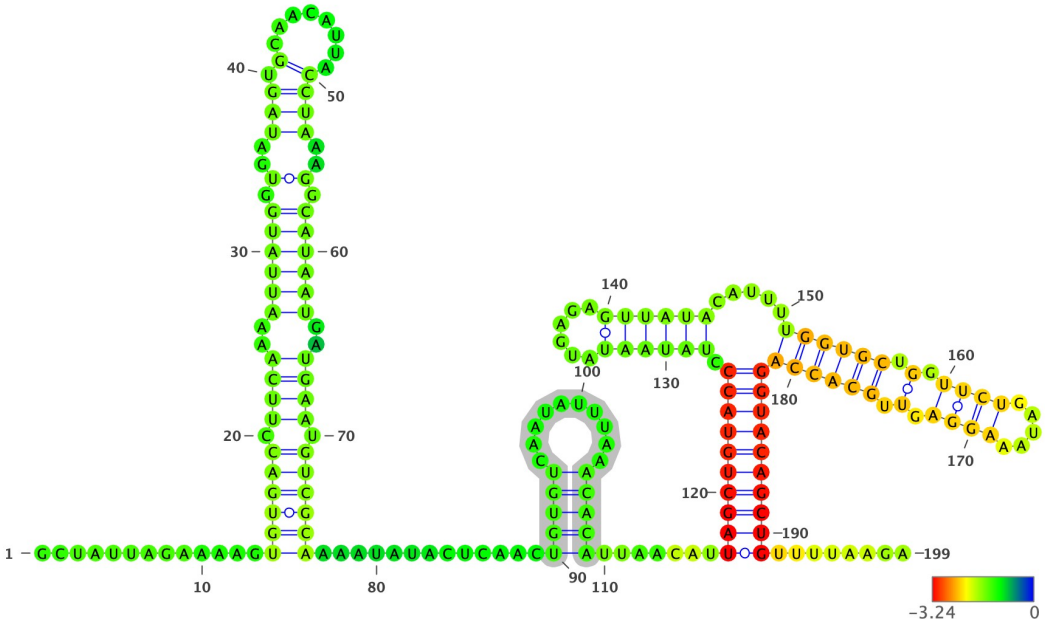
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 342 from nt 20807 to 20826 (nt 90 to 109)

```
5'-TGTGTCAATATTTAAACACA-3'
5'-(((((..........)))))-3'
Motif MFE = -1.8; z-score = -1.95; ED = 1.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20718 to 20916 (motif highlighted in silver):

```
5'-GCUAUUAGAAAAGUGUGACCUUCAAAAUUAUGGUGAUAGUGCAACAUUACCUAAAGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUU
AACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGA-3
5'-.............((((((.((((..((((((.(..(((.(........))))..).))))))..)))).))))))............(((((..........)))))..
.....((((((((((.((((((......))))))).....((((((.(.((((.....)))).).))))))))))))))))........-3'
MFE = -50.4; z-score = -3.05; ED = 15.52
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

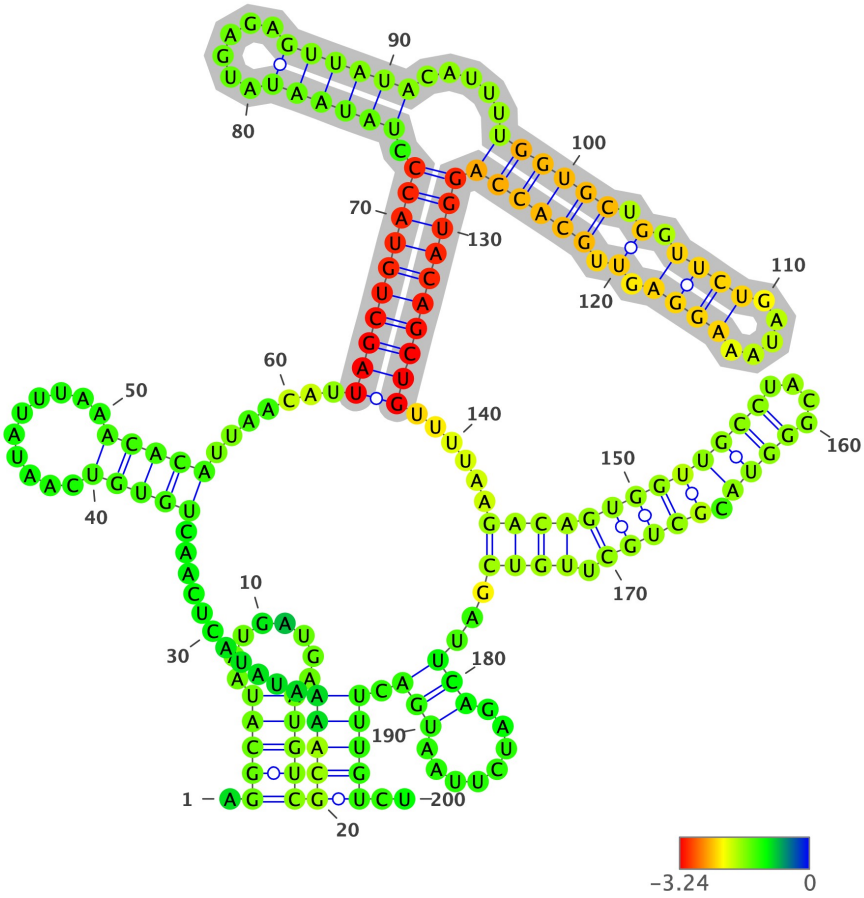
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 343 from nt 20834 to 20908 (nt 63 to 137)

```
5'-TAGCTGTACCCTATAATATGAGAGTTATACATTTTGGTGCTGGTTCTGATAAAGGAGUTGCACCAGGUACAGCUG-3'
5'-((((((((((.........................(((((.(.((((.....)))).).)))))).))))))))))-3'
Motif MFE = -28.8; z-score = -4.6; ED = 3.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20772 to 20971 (motif highlighted in silver):

```
5'-AGGCAUAAUGAUGAAUGUCGCAAAAUAUACUCAACUGUGUCAAUAUUUAAACACAUUAACAUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGA
UAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCU-3
5'-.(((((........)))))(((((...........(((((..........)))))).......((((((((((.((((((......))))))).....((((((.(.((((..
...)))).).))))))))))))))))).....((((((((((((....)))).)))))).))))...(((........))).)))))..-3'
MFE = -52.2; z-score = -2.32; ED = 38.3
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

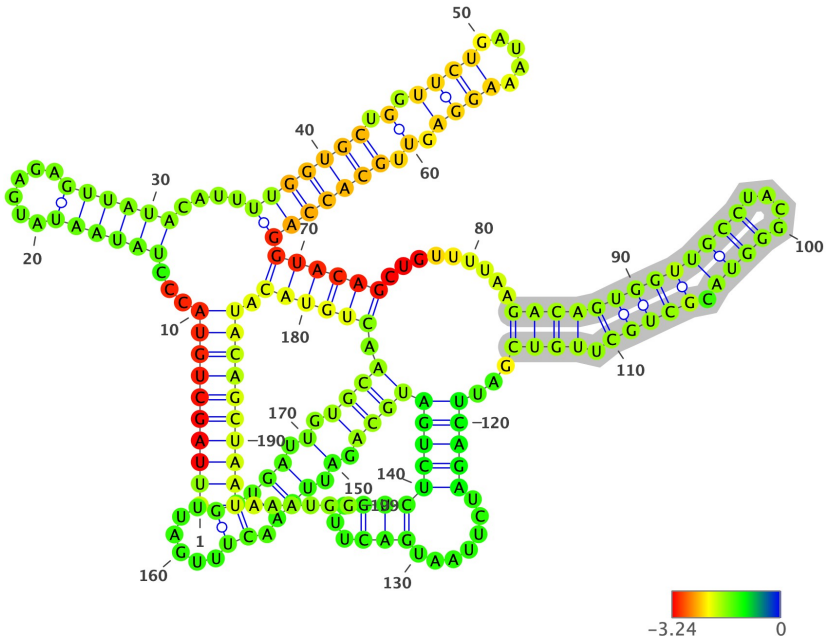
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 344 from nt 20915 to 20946 (nt 84 to 115)

```
5'-GACAGTGGTTGCCTACGGGUACGCUGCTUGUC-3'
5'-((((((((.((((....)))).)))).))))-3'
Motif MFE = -12.6; z-score = -1.91; ED = 1.76
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20832 to 21030 (motif highlighted in silver):

```
5'-AUUAGCUGUACCCUAUAAUAUGAGAGUUAUACAUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCU
UGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGG-3
5'-((((((((((...((((((......))))))....(((((((.(.((((.....)))).).)))))))((((((.........((((((((((((....)))).)))))).
))))...(((((.......(((...))))))))((((.(.(((.((......))))).).)))).)))))).))))))))))......-3'
MFE = -58.9; z-score = -3.17; ED = 32.03
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

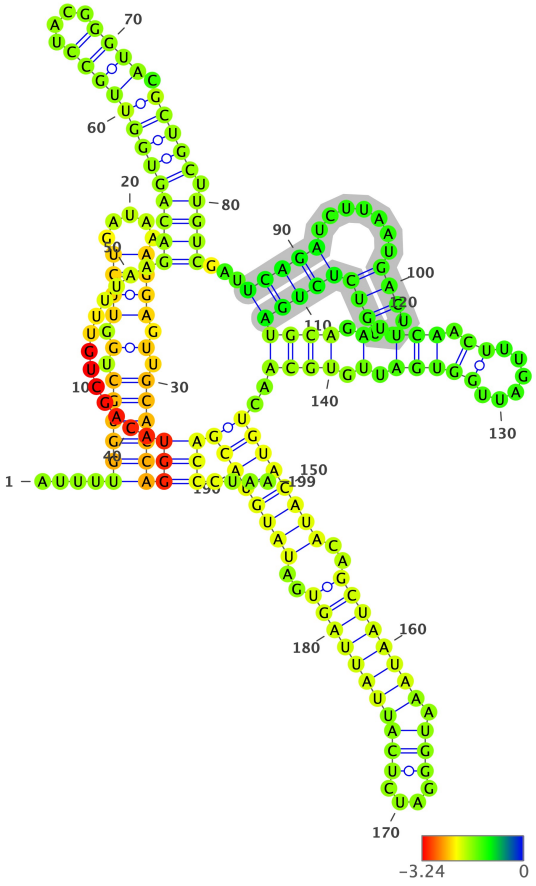
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 345 from nt 20950 to 20975 (nt 87 to 112)

```
5'-TCAGATCTTAATGACTTTGTCUCUGA-3'
5'-(((((.............)))))-3'
Motif MFE = -2.6; z-score = -0.88; ED = 4.31
```



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 20864 to 21062 (motif highlighted in silver):

```
5'-AUUUUGGUGCUGGUUCUGAUAAAGGAGUUGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUG
AUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAA-3
5'-....((((((.(.((((.....)))).).)))))))(((.............((((((((((((....)))).)))))).)))).....(((((.......(((...)))))))
)))))(.(.(((.((......)))))).).)))))..(((((((((..(((((((((.(((....)))))))))))))..)))))))))))....-3'
MFE = -58.3; z-score = -2.54; ED = 31.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp01, 266-21555(+)

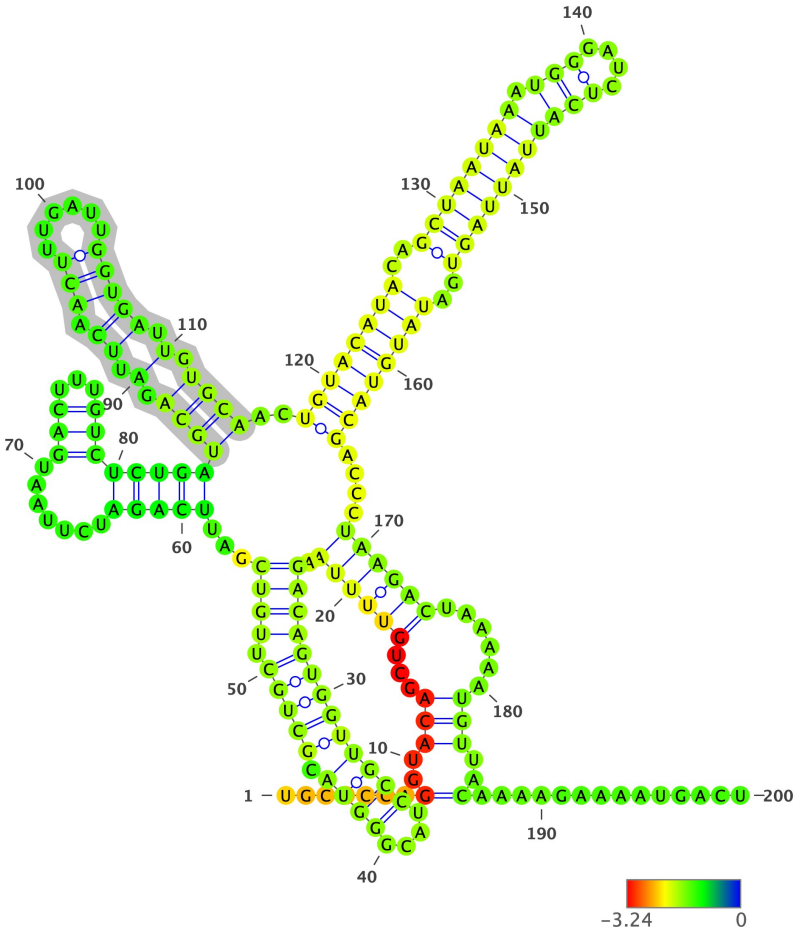
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 346 from nt 20976 to 21006 (nt 85 to 115)

```
5'-TGCAGATTCAACTTTGATTGGUGATTGUGCA-3'
5'-((((......(((......)))).....))))-3'
Motif MFE = -7.1; z-score = -1.88; ED = 2.55
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20892 to 21091 (motif highlighted in silver):

```
5'-UGCACCAGGUACAGCUGUUUUAAGACAGUGGUUGCCUACGGGUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUG
UGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACU-3
5'-.......(..(((...((((((.(((((((((((((....)))).))))).))))...(((((.......(((...))))))))((((.(.((.(((......))))).).
)))).((((((((..((((((((.(((....)))))))))))..))))))))....))))))......)))..)...............-3'
MFE = -47.3; z-score = -1.1; ED = 42.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

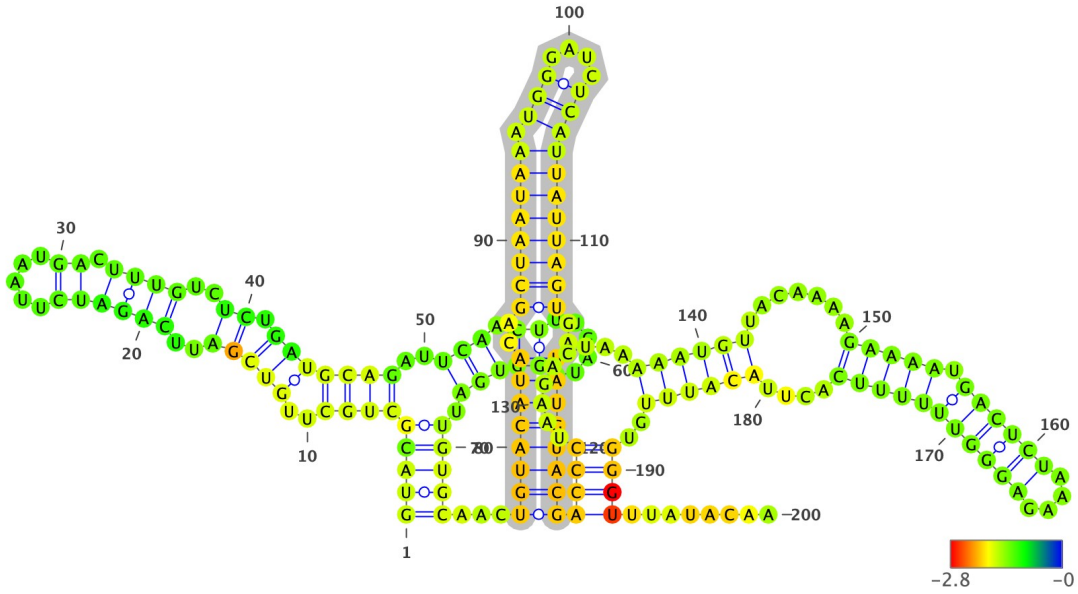
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 347 from nt 21009 to 21055 (nt 77 to 123)

```
5'-TGTACATACAGCTAATAAATGGGATCTCATUAUUAGUGAUAUGUACG-3'
5'-(((((((((..(((((((.............)))))))..)))))))))-3'
Motif MFE = -16.4; z-score = -4.27; ED = 3.09
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20933 to 21132 (motif highlighted in silver):

```
5'-GUACGCUGCUUGUCGAUUCAGAUCUUAAUGACUUUGUCUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUA
GUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAA-3
5'-((((((((((..((((((..((((((.....)).)))))..)).)))))))..(((.((.....)))))).)))))...(((((((((..(((((((((.(((....)))))))))
))..)))))))))(((((.........((((((.......((((((.(((((((....)))))))))))))....)))))))..))))........-3'
MFE = -42.6; z-score = -1.58; ED = 45.23
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

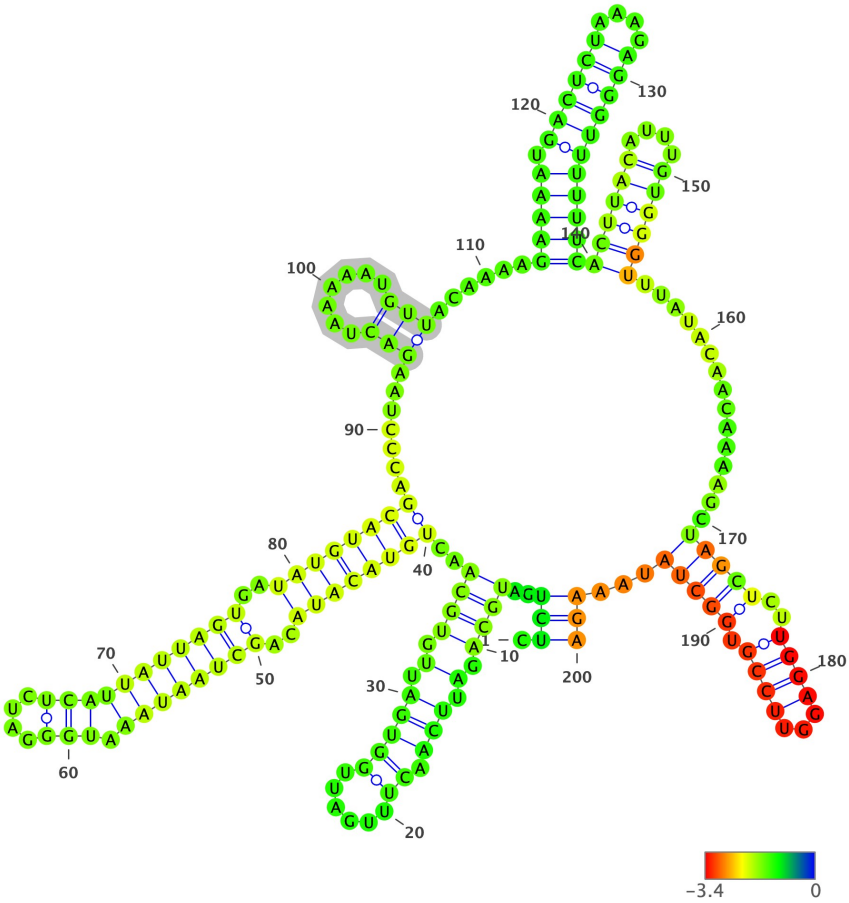
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 348 from nt 21063 to 21075 (nt 94 to 106)

```
5'-GACTAAAAATGUU-3'
5'-(((.......)))-3'
Motif MFE = 0.0; z-score = 0.13; ED = 1.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20970 to 21169 (motif highlighted in silver):

```
5'-CUCUGAUGCAGAUUCAACUUUGAUUGGUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAA
AGAAAAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGA-3
5'-.(((..(((((.(.(((.((......))))).).)))))..(((((((((..(((((((((.(((....)))))))))))..))))))))).......(((.......))).....
.(((((.(((((((....)))))))))))(((((((....)))))))..............(((((..((((...))))).))))))...)))-3'
MFE = -45.4; z-score = -2.17; ED = 21.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

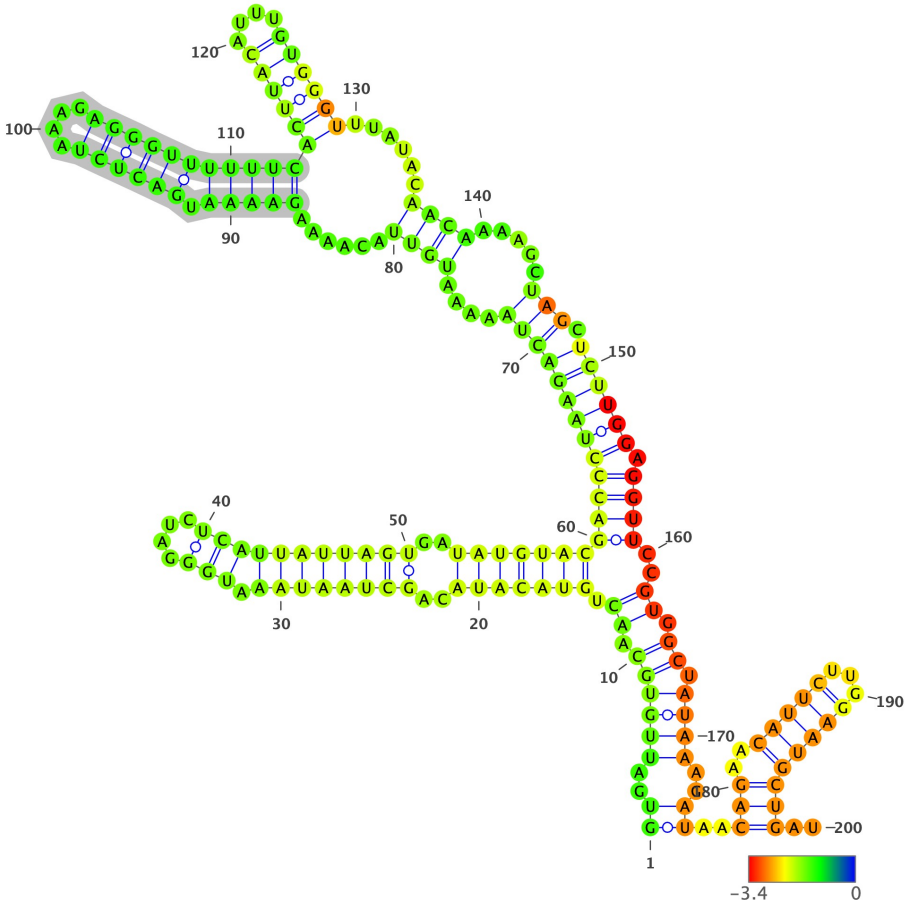
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 349 from nt 21082 to 21108 (nt 87 to 113)

```
5'-GAAAATGACTCTAAAGAGGGUUUUUUC-3'
5'-(((((.((((((....)))))))))))-3'
Motif MFE = -6.0; z-score = -3.27; ED = 2.81
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 20996 to 21195 (motif highlighted in silver):

```
5'-GUGAUUGUGCAACUGUACAUACAGCUAAUAAAUGGGAUCUCAUUAUUAGUGAUAUGUACGACCCUAAGACUAAAAAUGUUACAAAAGAAAAUGACUCUAAAGAGGGUUUUU
UCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU-3
5'-((..((((((.((.(((((((..((((((((.(((....)))))))))))..)))))))((((((((((((....((((......(((((.((((((....)))))))))
))((((((....))))))......))))).....))).)))))).))))..)).)).))))..))..(((..(((((...))))))))..-3'
MFE = -43.9; z-score = -1.6; ED = 49.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

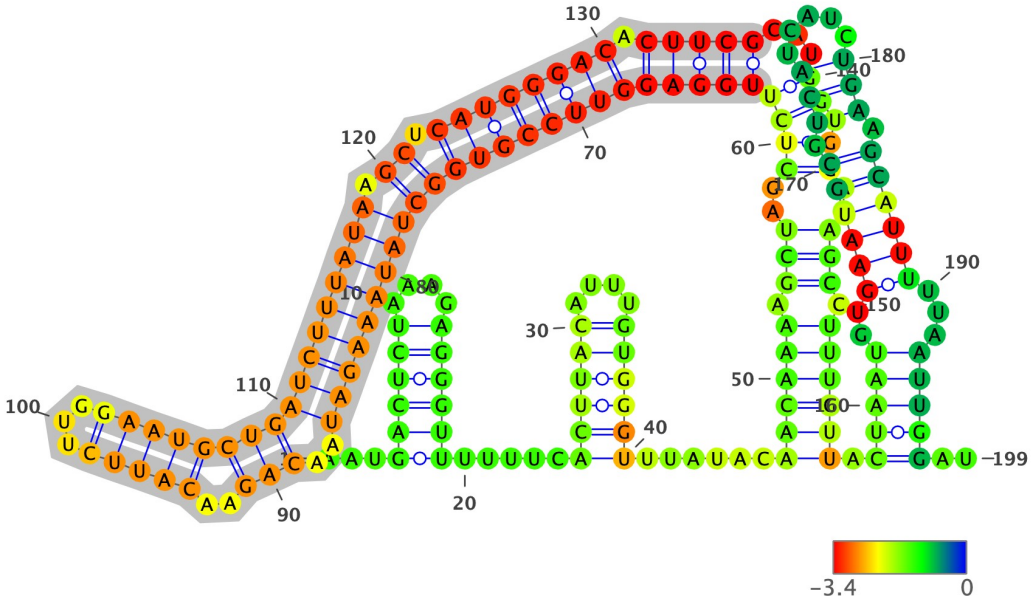
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 350 from nt 21147 to 21220 (nt 63 to 136)

```
5'-TGGAGGTTCCGTGGCTATAAAGATAACAGAACATTCTTGGAAUGCUGAUCUUUAUAAGCTCAUGGGACACUUCG-3'
5'-(((((((((((((((((((((((..(((..((((.....))))))))))))))).)).))))))).)))))-3'
Motif MFE = -30.6; z-score = -5.18; ED = 2.84
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21085 to 21283 (motif highlighted in silver):

```
5'-AAUGACUCUAAAGAGGGUUUUUUCACUUACAUUUGUGGGUUUAUACAACAAAAGCUAGCUCUUGGAGGUUCCGUGGCUAUAAAGAUAACAGAACAUUCUUGGAAUGCUGAU
CUUUAUAAGCUCAUGGGACACUUCGCAUGGUGGACAGCCUUUGUUACUAAUGUGAAUGCGUCAUCAUCUGAAGCAUUUUUAAUUGGAU-3
5'-...((((((....))))))).....((((((....))))))......((((((.(((..(((((((((((((((((((((((((((..(((..(((((...)))))))))))
))))))).)).))))))))).)))))...)).)).)).))).)))))).(((((..((((((.(((.....))).))))))...)))))..-3'
MFE = -57.5; z-score = -3.42; ED = 14.16
```

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(+)

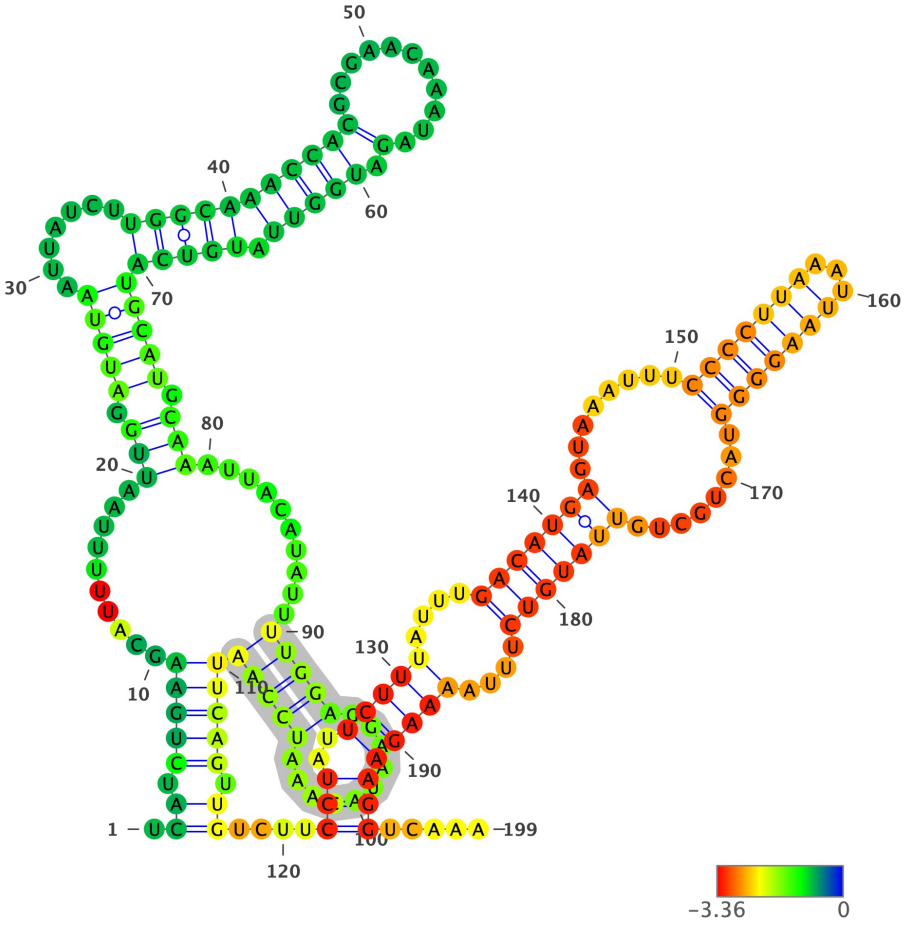
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

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 351 from nt 21348 to 21367 (nt 90 to 109)

```
5'-TTGGAGGAATACAAATCCAA-3'
5'-((((............))))-3'
Motif MFE = -3.0; z-score = -2.35; 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 21259 to 21457 (motif highlighted in silver):

```
5'-UCAUCUGAAGCAUUUUUAAUUGGAUGUAAUUAUCUUGGCAAACCACGCGAACAAAUAGAUGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUU
CAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAA-3
5'-.((.(((((..........(((.(((((.......((((((((((.............).))))).))))))))))).))).........(((((..........)))))))
))).))....(((..(((((....(((((((........(((((((...)))))))........)))))))....)))))))).....-3'
MFE = -43.1; z-score = -1.91; ED = 36.19
```

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(+)

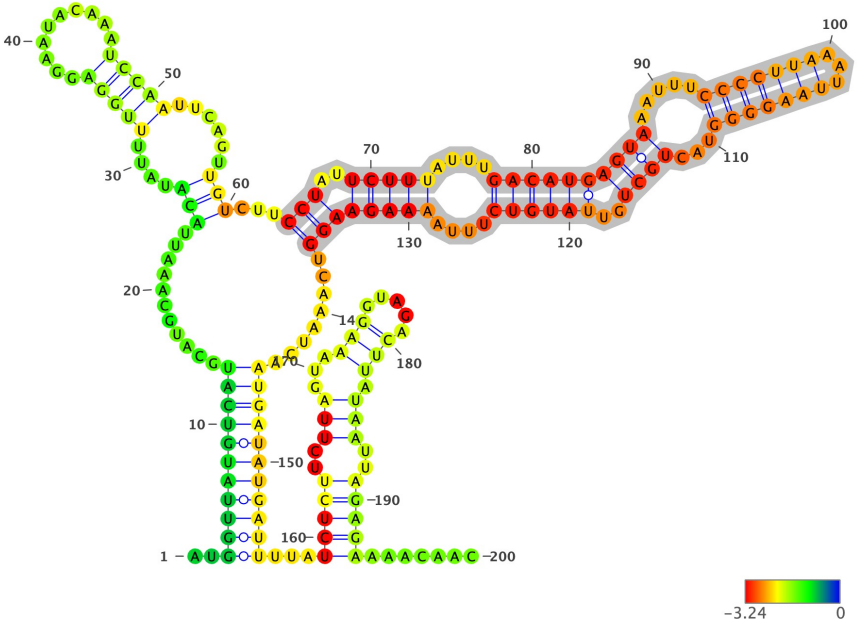
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 199--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal 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 21380 to 21452 (nt 64 to 136)

```
5'-CCTATTCTTTATTTGACATGAGTAAATTTCCCCTTAAATTAAGGGGTACUGCUGTTAUGUCTTTAAAAGAAGG-3'
5'-(((..((((.....(((((.((((.....((((.........))))...))))...)))))).....)))))))-3'
Motif MFE = -21.8; z-score = -3.89; ED = 5.87
```



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 21317 to 21516 (motif highlighted in silver):

```
5'-AUGGUUAUGUCAUGCAUGCAAAUUACAUAUUUUGGAGGAAUACAAAUCCAAUUCAGUUGUCUUCCUAUUCUUUAUUUGACAUGAGUAAAUUUCCCCUUAAAUUAAGGGGUA
CUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAAC-3
5'-..(((((((((((...........(((....(((((..........)))))......)))...(((..(((((....((((((((((.....(((((((...)))))))..
.))))..))))))....))))))))........))))))))))...(((((..(((...(((.....))).)))..)))))........-3'
MFE = -38.5; z-score = -2.49; ED = 32.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp01, 266-21555(+)

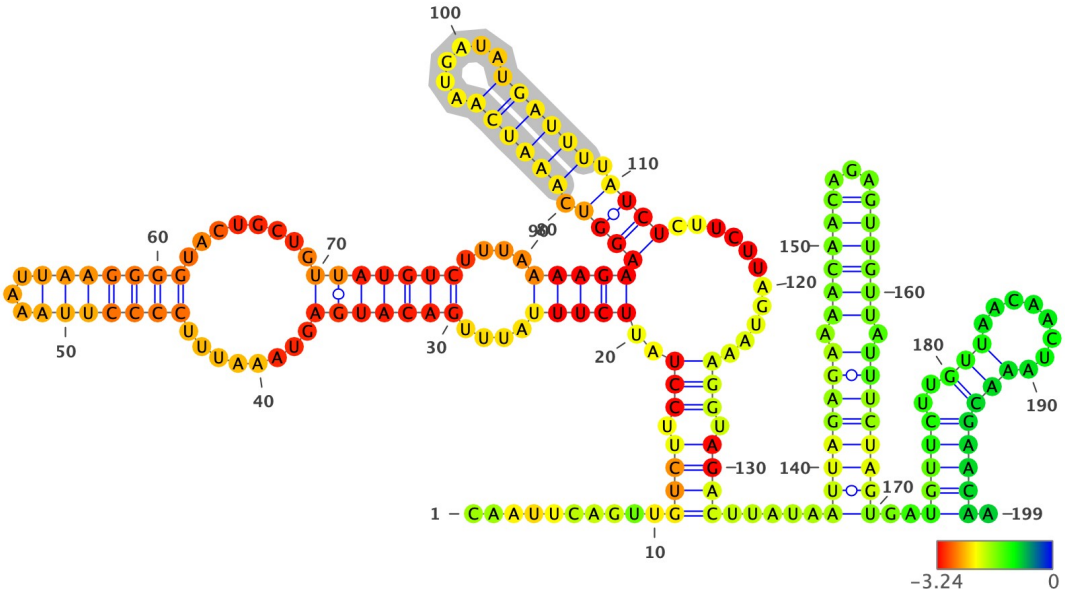
Attributes: ['ID=gene-GU280_gp01', 'Dbxref=GeneID:43740578', 'Name=orf1ab', 'gbkey=Gene', 'gene=orf1ab', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp01']

3-- nt 1 to 200--CDS, cds-YP_009724389.1, 13468-21555(+)

Attributes: ['ID=cds-YP_009724389.1', 'Parent=gene-GU280_gp01', 'Dbxref=Genbank:YP_009724389.1,GeneID:43740578', 'Name=YP_009724389.1', 'Note=pp1ab%3B translated by -1 ribosomal frameshift', 'exception=ribosomal slippage', 'gbkey=CDS', 'gene=orf1ab', 'locus_tag=GU280_gp01', 'product=orf1ab polyprotein', 'protein_id=YP_009724389.1']

NC_045512.2 (forward strand): Structure number 353 from nt 21455 to 21472 (nt 91 to 108)

```
5'-AAATCAATGATATGAUUU-3'
5'-(((((........)))))-3'
Motif MFE = -1.8; z-score = -2.67; 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 = -3.47; 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(+)

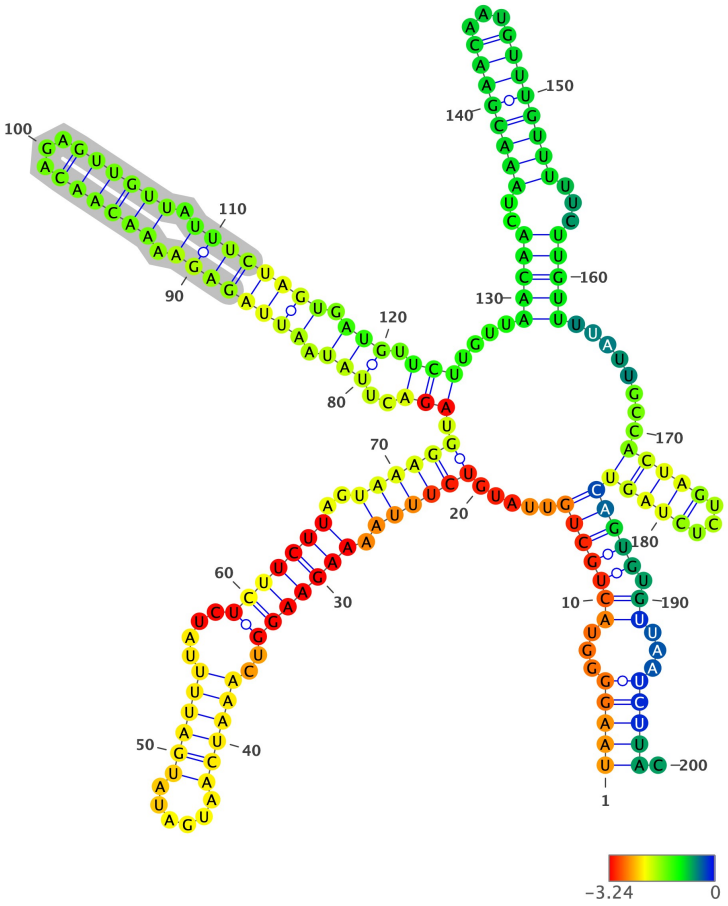
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 354 from nt 21506 to 21530 (nt 88 to 112)

```
5'-GAGAAAACAACAGAGUUGUUATTUC-3'
5'-((...((((((...))))))...))-3'
Motif MFE = -5.3; z-score = -2.37; 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 21419 to 21618 (motif highlighted in silver):

```
5'-UAAGGGGUACUGCUGUUAUGUCUUUAAAAGAAGGUCAAAUCAAUGAUAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUU
CUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUCUUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUAC-3
5'-(((((...(((((((.....((((((.(((((((..((((((......))))))....)))))))..)))))).(((..(((.(((((((((.((((((...))))))).)))
))))).))).)))....(((((..(((((((((...)))))))))...)))))........(((((...)))))))))).))...))))).-3'
MFE = -39.1; z-score = -0.89; ED = 42.08
```

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 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(+)

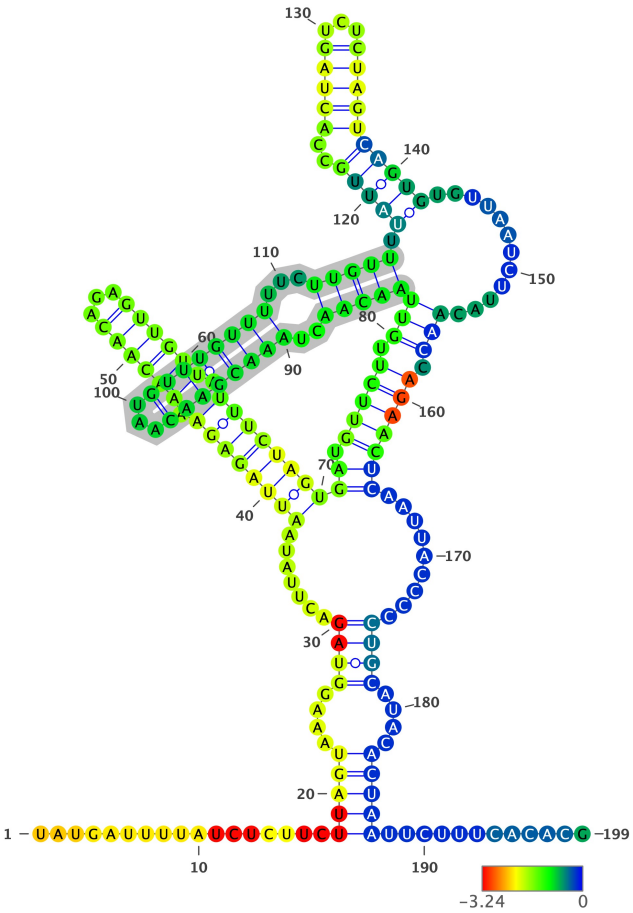
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 355 from nt 21547 to 21580 (nt 83 to 116)

```
5'-AACAACTAAACGAACAATGUUUGUUUTTCUUGUU-3'
5'-(((((.......................)))))-3'
Motif MFE = -6.3; z-score = -2.29; ED = 2.24
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21465 to 21663 (motif highlighted in silver):

```
5'-UAUGAUUUUAUCUCUUCUUAGUAAAGGUAGACUUAUAAUUAGAGAAAACAACAGAGUUGUUAUUUCUAGUGAUGUUCUUGUUAACAACUAAACGAACAAUGUUUGUUUUUC
UUGUUUUAUUGCCACUAGUCUCUAGUCAGUGUGUUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACG-3
5'-.................(((((....((((.......((((((((.((((((...)))))).))))))))((.(((((.((((((((..((((((((...))))))))...
))))).(((((..(((((...)))))))))).............))).)))))))).........))))....)))))............-3'
MFE = -32.8; z-score = -0.86; ED = 31.54
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 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(+)

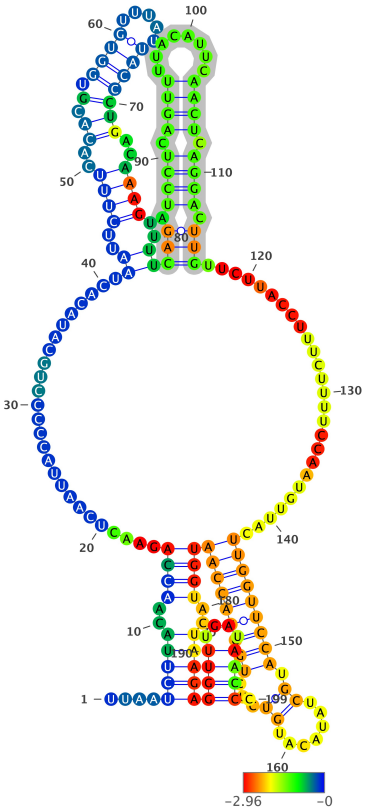
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 356 from nt 21691 to 21724 (nt 83 to 116)

```
5'-CAGATCCTCAGTTTTACATTCAACUCAGGACTTG-3'
5'-(...((((.((((........)))).))))...)-3'
Motif MFE = -6.5; z-score = -2.08; 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 21609 to 21807 (motif highlighted in silver):

```
5'-UUAAUCUUACAACCAGAACUCAAUUACCCCCUGCAUACACUAAUUCUUUCACACGUGGUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGG
ACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCUGGGACCAAUGGUACUAAGAGGUUUGAUAACCC-3
5'-....(((((..((((.........................((..((((..((.(.((((.....)))))))..))))..))(((.((((.((((........)))).)))
).))).........................(((((((((.((.......))...)))))))))))))..)))))((((....)))).-3'
MFE = -32.8; z-score = -1.91; ED = 32.07
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

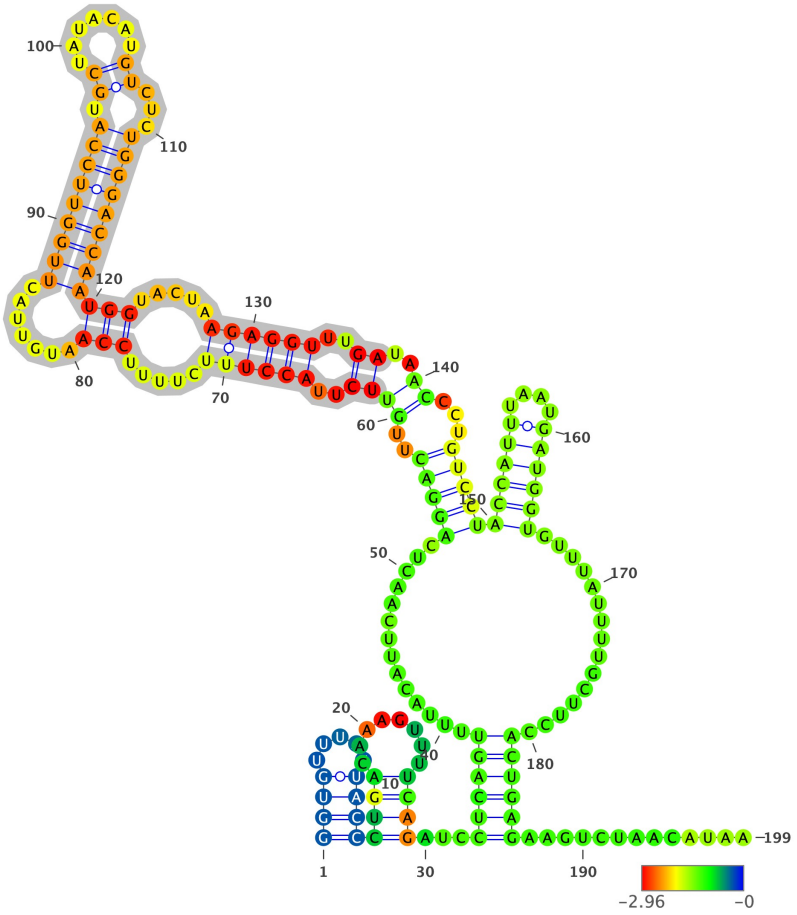
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 357 from nt 21726 to 21801 (nt 62 to 137)

```
5'-TCTTACCTTTCTTTTCCAATGTTACTTGGTTCCATGCTATACATGUCTCUGGGACCAAUGGTACTAAGAGGUTTGA-3'
5'-((..((((.......(((.......((((((((((.((.......))...)))))))))))).......))))..))-3'
Motif MFE = -19.9; z-score = -3.37; ED = 4.34
```



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 21665 to 21863 (motif highlighted in silver):

```
5'-GGUGUUUAUUACCCUGACAAAGUUUUCAGAUCCUCAGUUUUACAUUCAACUCAGGACUUGUUCUUACCUUUCUUUUCCAAUGUUACUUGGUUCCAUGCUAUACAUGUCUCU
GGGACCAAUGGUACUAAGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAA-3
5'-((((.....))))((((........))))...((((((..............(((((..((((..((((((.....(((.......(((((((((.((.......))...)
))))))))))).....))))))..))..))...)))))((((((....))))))...............))))))..............-3'
MFE = -43.7; z-score = -2.33; ED = 26.39
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

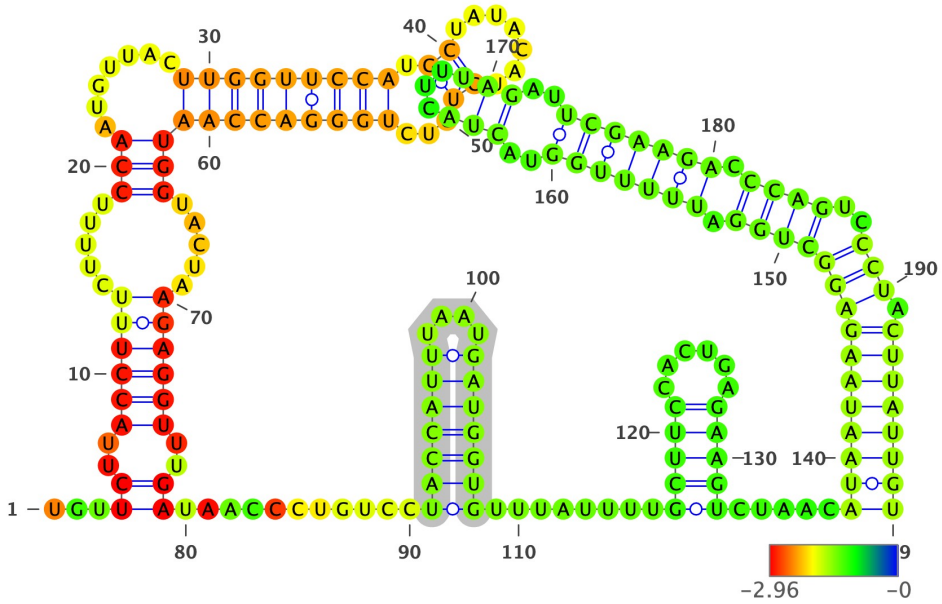
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 358 from nt 21813 to 21830 (nt 91 to 108)

```
5'-TACCATTTAATGAUGGUG-3'
5'-(((((((....)))))))-3'
Motif MFE = -5.8; z-score = -5.91; 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 = -2.36; 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(+)

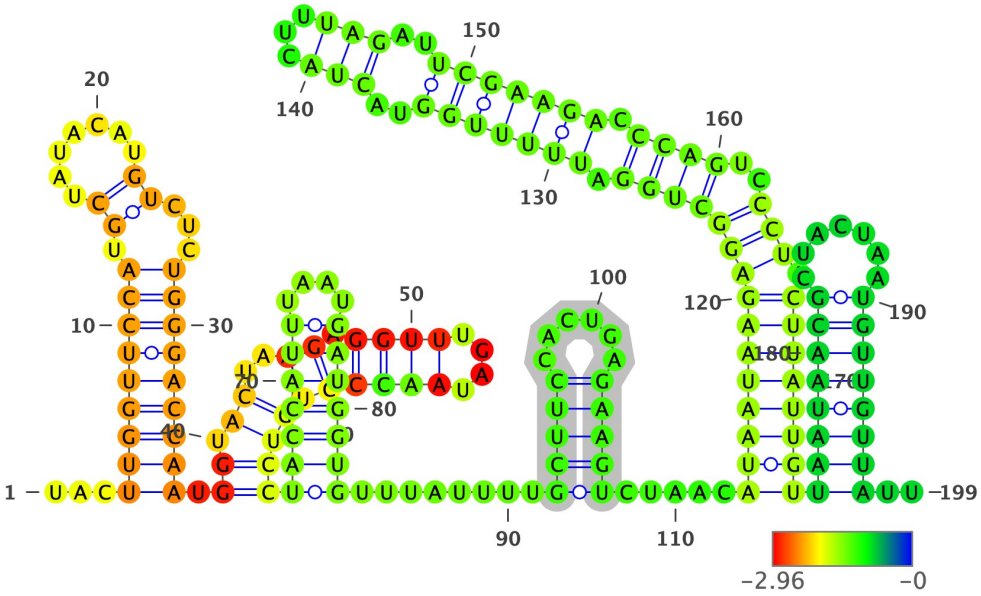
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 359 from nt 21839 to 21854 (nt 92 to 107)

```
5'-GCTTCCACTGAGAAGU-3'
5'-(((((......)))))-3'
Motif MFE = -3.0; z-score = -1.91; 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 = -2.44; 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(+)

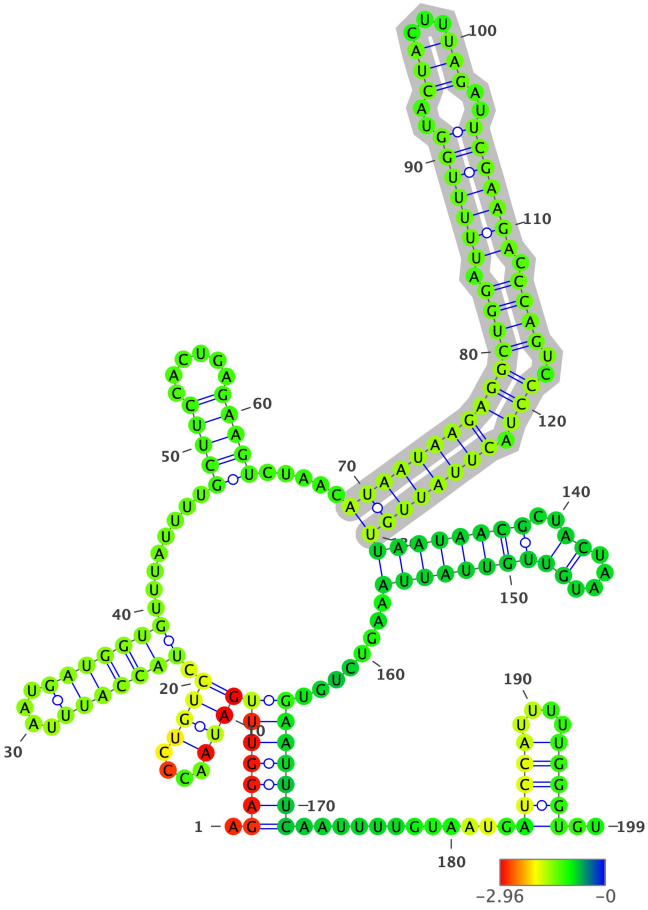
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 360 from nt 21860 to 21921 (nt 69 to 130)

```
5'-ATAATAAGAGGCTGGATTTTTGGTACTACTTUAGATUCGAAGACCCAGTCCCUACUUAUUGU-3'
5'-(((((((((((((((.(((((((..(((...)))..)))))))).))))..))).))))))))-3'
Motif MFE = -17.2; z-score = -2.91; ED = 6.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21792 to 21990 (motif highlighted in silver):

```
5'-AGAGGUUUGAUAACCCUGUCCUACCAUUUAAUGAUGGUGUUUAUUUUGCUUCCACUGAGAAGUCUAACAUAAUAAGAGGCUGGAUUUUUGGUACUACUUUAGAUUCGAAGA
CCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGU-3
5'-.(((((((((((....)))).(((((((....)))))))........(((((......)))))).....(((((((((((((((.(((((((..(((...)))..)))))))
.))))..))).))))))))((((((((..((....)))))))))).........)))))))............(((((....)))))..-3'
MFE = -42.5; z-score = -1.51; ED = 27.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

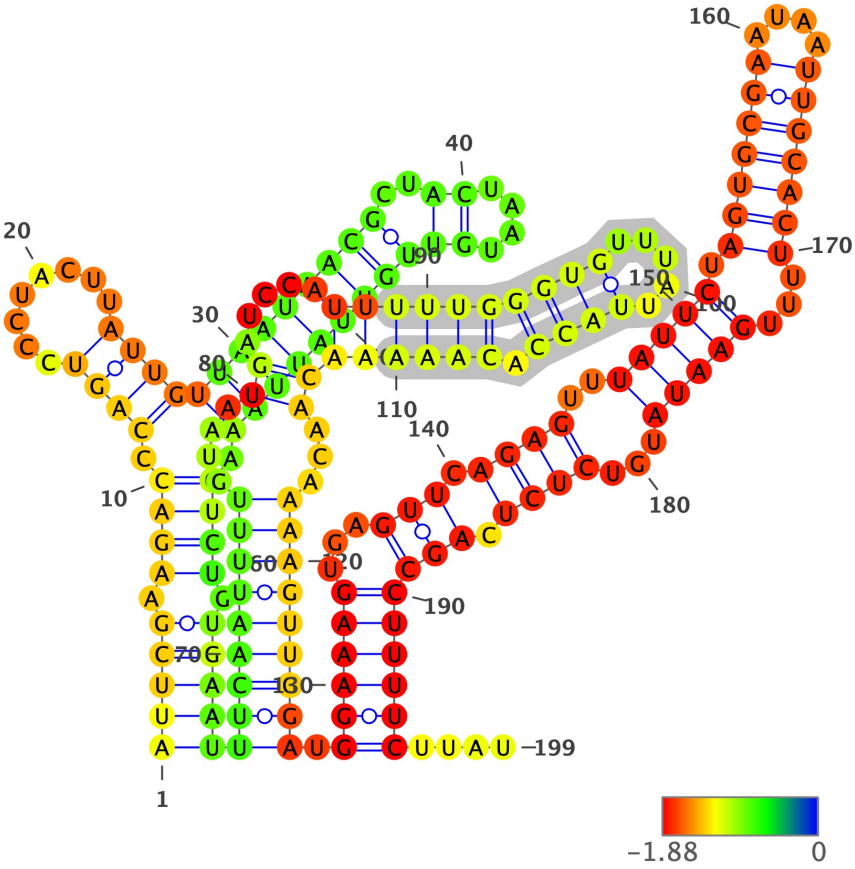
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 361 from nt 21982 to 22003 (nt 89 to 110)

```
5'-TTTGGGTGTTTATUACCACAAA-3'
5'-((((((((.....)))).))))-3'
Motif MFE = -4.8; z-score = -2.86; ED = 1.15
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21894 to 22092 (motif highlighted in silver):

```
5'-AUUCGAAGACCCAGUCCCUACUUAUUGUUAAUAACGCUACUAAUGUUGUUAUUAAAGUCUGUGAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAA
ACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUUGAAUAUGUCUCUCAGCCUUUUCUUAU-3
5'-(((((.((((.((((........))))(((((((((..((....)))))))))))).)))).)))))((((((((....((.....((((((((((.....)))).)))))
)))...))))))))).((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).))))))))....-3'
MFE = -40.5; z-score = -1.88; ED = 32.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

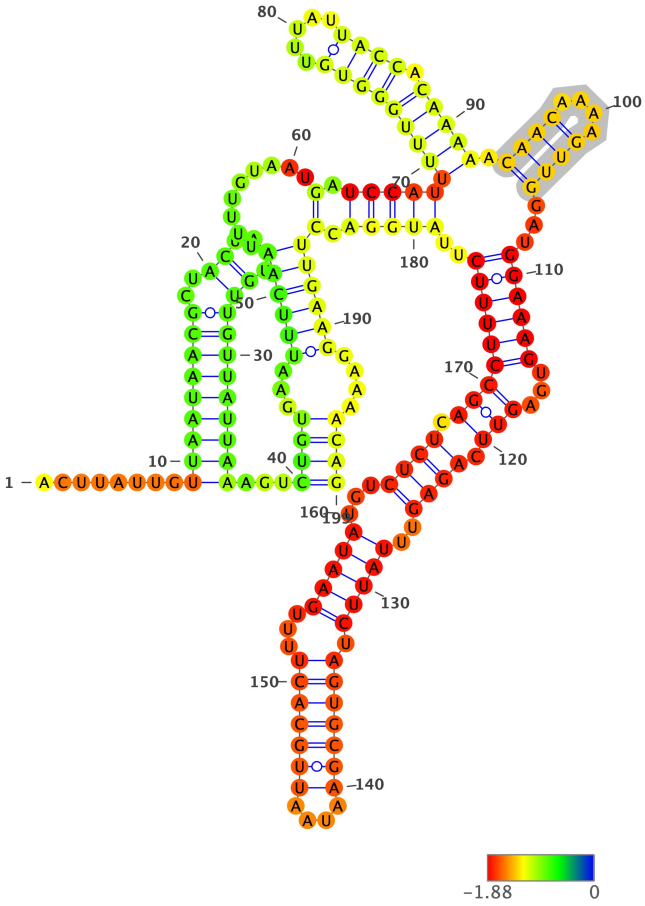
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 362 from nt 22006 to 22017 (nt 94 to 105)

```
5'-CAACAAAAGUUG-3'
5'-((((....))))-3'
Motif MFE = -1.1; z-score = -7.43; 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 = -1.45; 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(+)

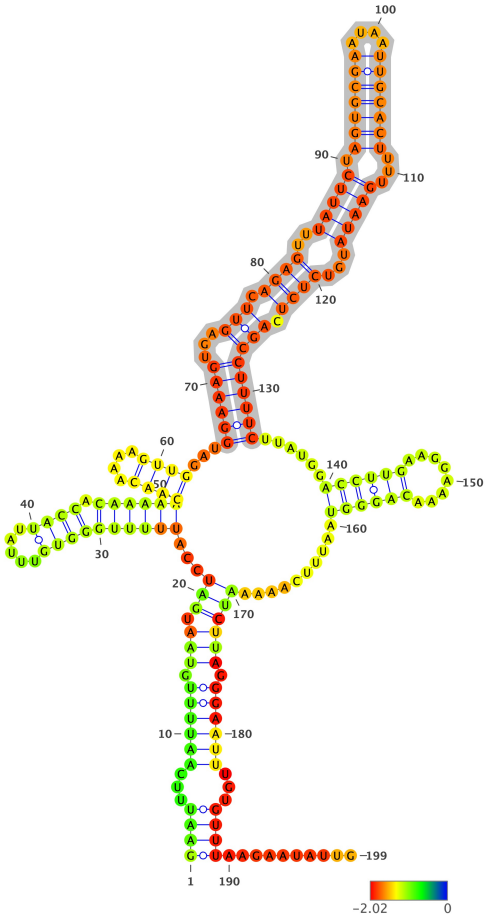
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 363 from nt 22021 to 22088 (nt 66 to 133)

```
5'-GGAAAGTGAGTTCAGAGTTTATTCTAGTGCGAATAAUUGCACUTTTGAAUATGTCUCUCAGCCUUUUC-3'
5'-((((((...(((.((((..(((((.(((((((....)))))))...)))))...)))).)))))))))-3'
Motif MFE = -18.5; z-score = -3.34; ED = 9.7
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 21956 to 22154 (motif highlighted in silver):

```
5'-GAAUUUCAAUUUUGUAAUGAUCCAUUUUUGGGUGUUUAUUACCACAAAAACAACAAAAGUUGGAUGGAAAGUGAGUUCAGAGUUUAUUCUAGUGCGAAUAAUUGCACUUUU
GAAUAUGUCUCUCAGCCUUUUCUUAUGGACCUUGAAGGAAAACAGGGUAAUUUCAAAAAUCUUAGGGAAUUUGUGUUUAAGAAUAUUG-3
5'-((((...((((((.(((.(((...(((((((((((.....)))).))))))((((....))))...((((((...(((.((((..(((((.(((((((....)))))))...
)))))...)))).))))))))).....((((((........))))))..........))))))).))))))...))))..........-3'
MFE = -41.8; z-score = -1.14; ED = 38.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

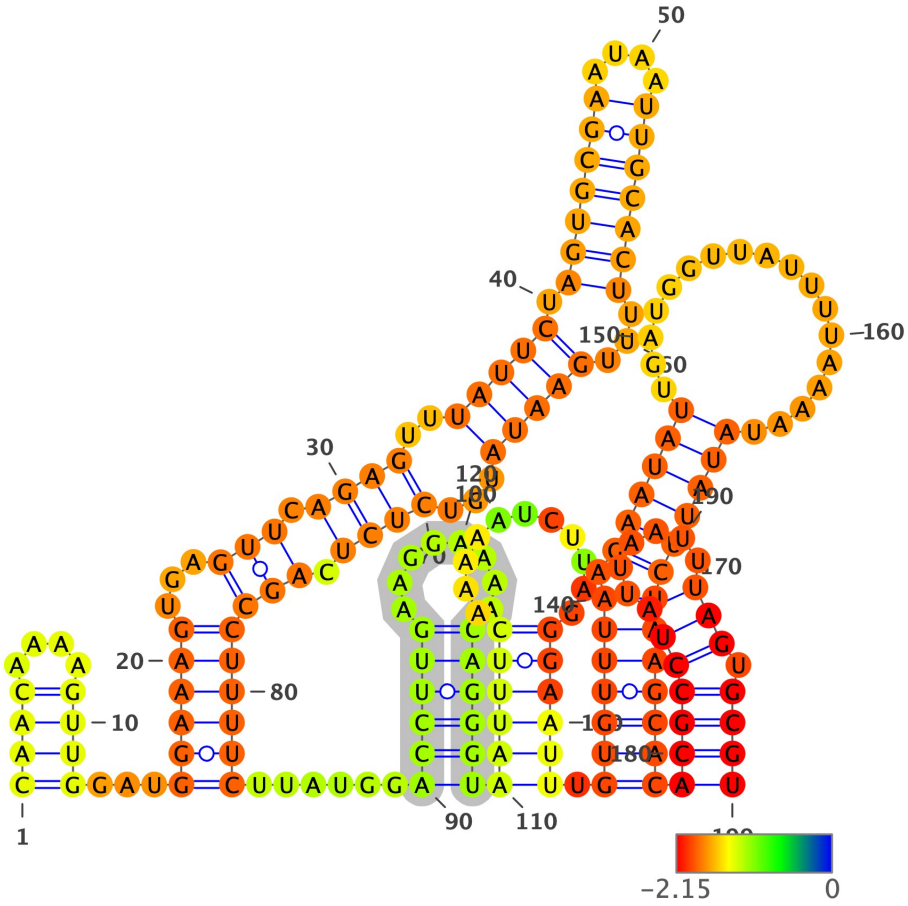
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 364 from nt 22095 to 22114 (nt 90 to 109)

```
5'-ACCTTGAAGGAAAACAGGGU-3'
5'-((((((........))))))-3'
Motif MFE = -5.4; z-score = -3.61; 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 = -2.46; 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(+)

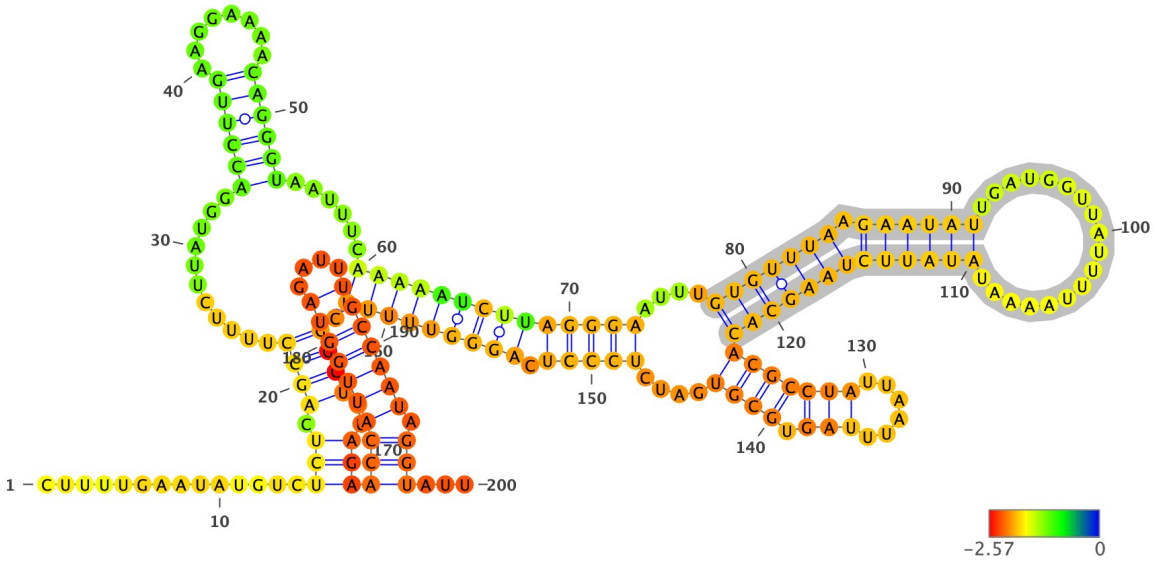
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 365 from nt 22139 to 22183 (nt 78 to 122)

```
5'-GTGTTTAAGAATATTGATGGTTATTTTAAAATAUAUUCUAAGCAC-3'
5'-(((((((.((((((.................)))))))))))))-3'
Motif MFE = -8.5; z-score = -2.67; 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 = -2.64; 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(+)

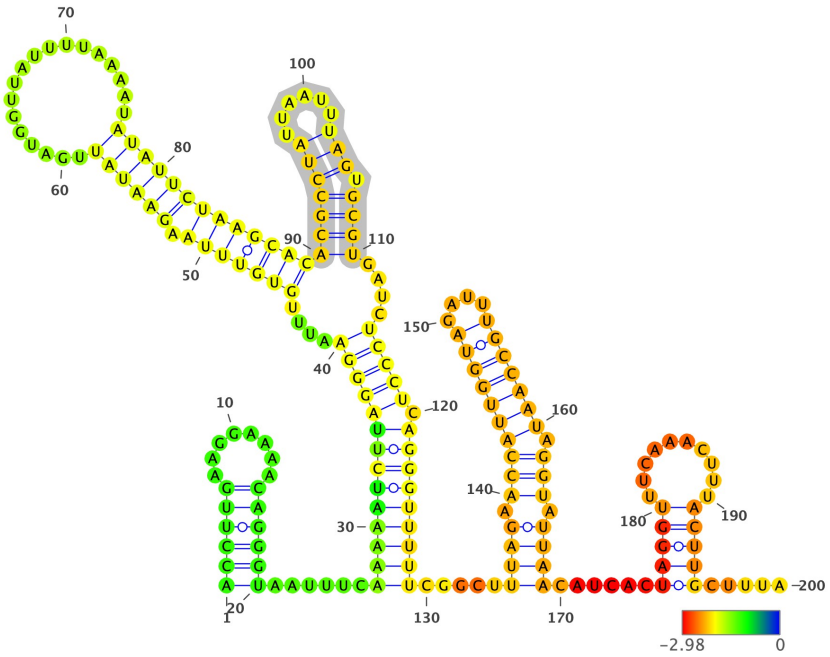
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 366 from nt 22184 to 22204 (nt 90 to 110)

```
5'-ACGCCTATTAATTTAGTGCGU-3'
5'-((((((........)).))))-3'
Motif MFE = -6.2; z-score = -4.59; 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 = -2.78; ED = 22.7
```

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_gp02, 21563-25384(+)

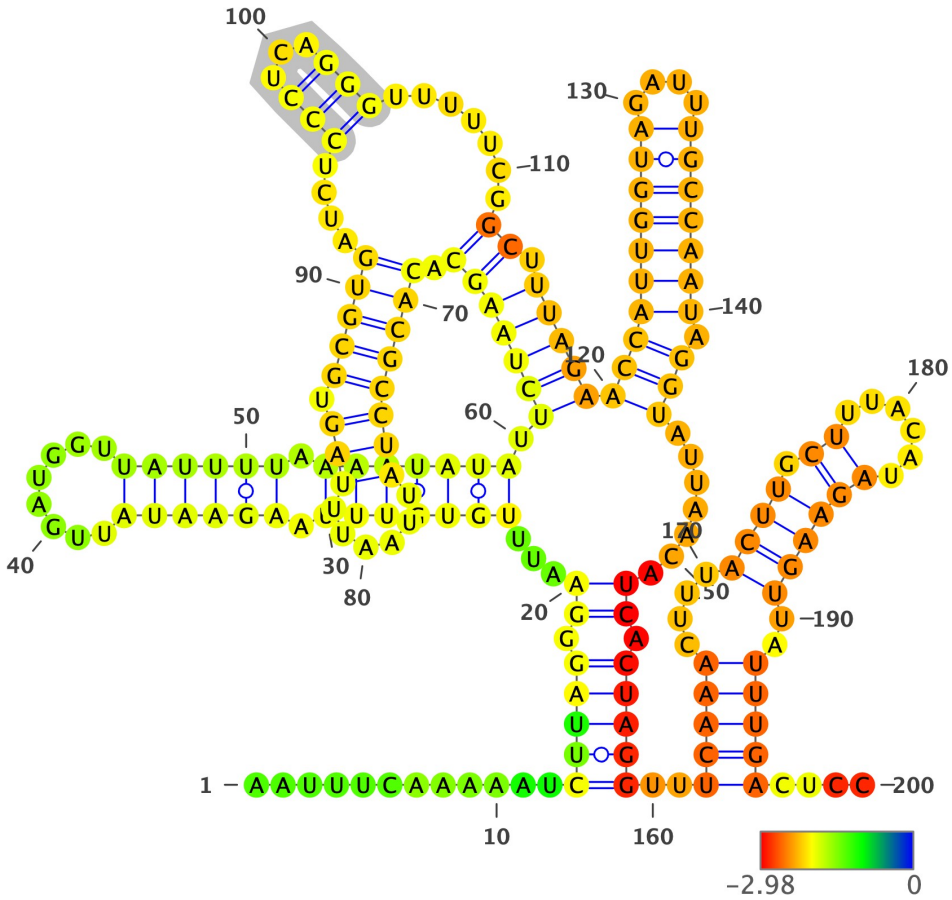
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 367 from nt 22210 to 22218 (nt 96 to 104)

```
5'-CCCTCAGGG-3'
5'-(((...)))-3'
Motif MFE = -1.2; z-score = -6.8; 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 = -2.53; 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(+)

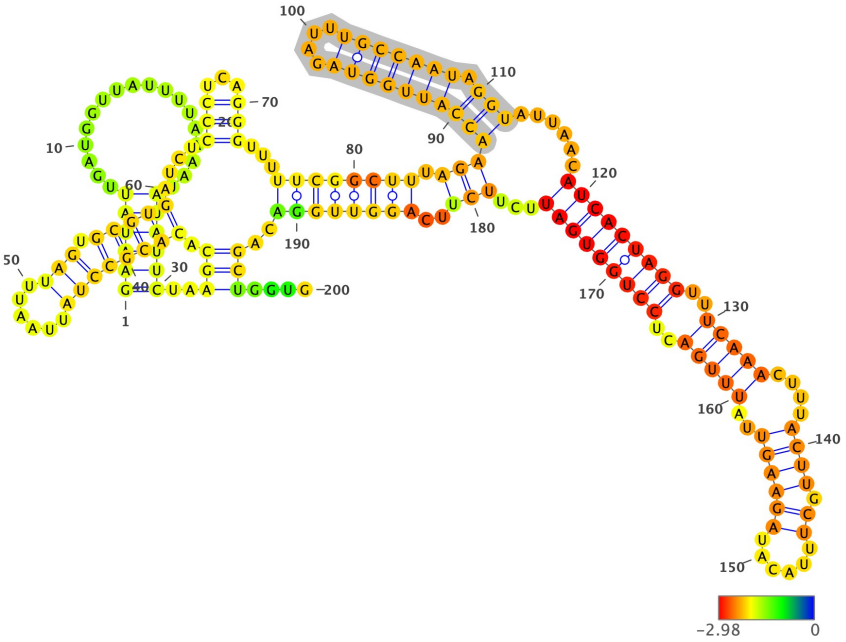
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 368 from nt 22234 to 22258 (nt 88 to 112)

```
5'-ACCATTGGTAGATTTGCCAAUAGGU-3'
5'-(((((((((.....)))))).)))-3'
Motif MFE = -9.1; z-score = -3.78; ED = 0.85
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22147 to 22346 (motif highlighted in silver):

```
5'-GAAUAUUGAUGGUUAUUUUAAAAUAUAUUCUAAGCACACGCCUAUUAAUUUAGUGCGUGAUCUCCCUCAGGGUUUUUCGGCUUUAGAACCAUUGGUAGAUUUGCCAAUAGG
UAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUG-3
5'-((((((..................))))))..(((.(((((((((......))).))))))....(((...))))...(((((((((.(((((((((((((....)))))))))))).))
).....(((((((((..((((((....((((.((......))))))..))))))..))))))))))...))))..)))))))))..))).....-3'
MFE = -50.3; z-score = -2.13; ED = 27.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

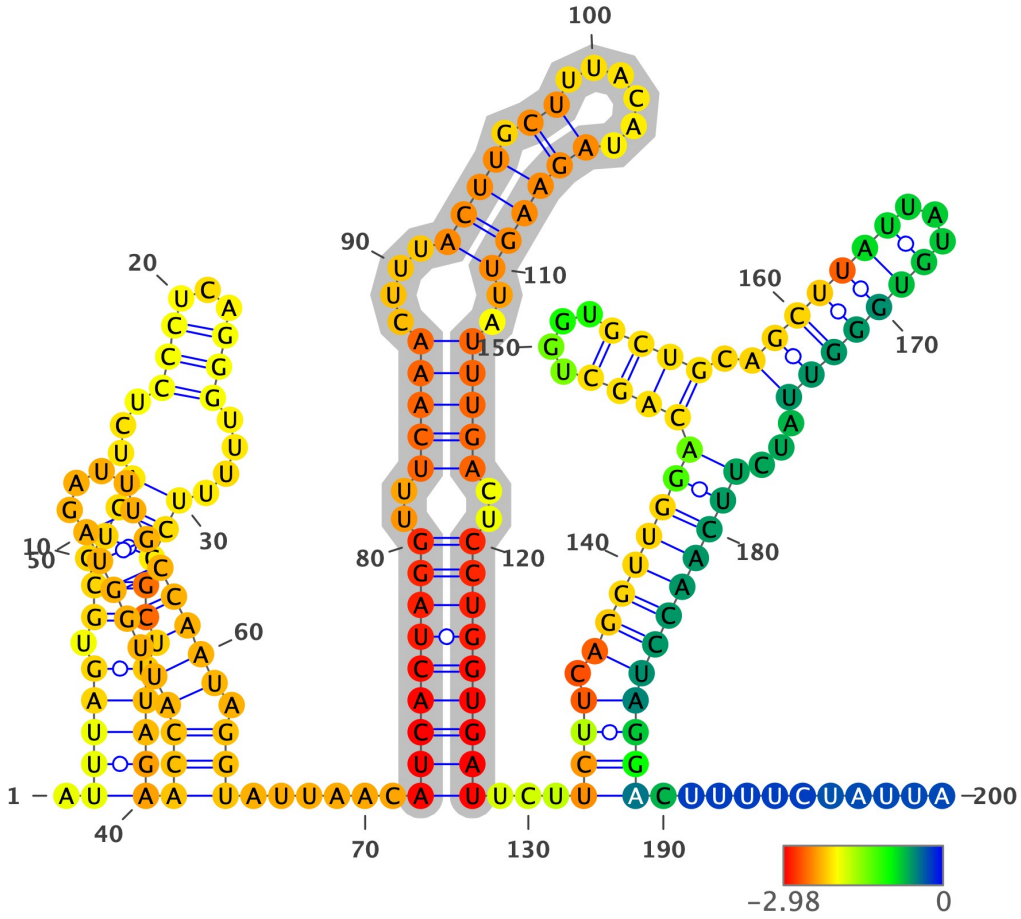
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 369 from nt 22265 to 22321 (nt 72 to 128)

```
5'-ATCACTAGGTTTCAAACTTTACTTGCTTTACATAGAAGUTAUUUGACTCCUGGUGAU-3'
5'-(((((((((..(((((....((((.((......))))))..)))))..)))))))))-3'
Motif MFE = -18.6; z-score = -4.28; 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 = -2.61; ED = 21.88
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

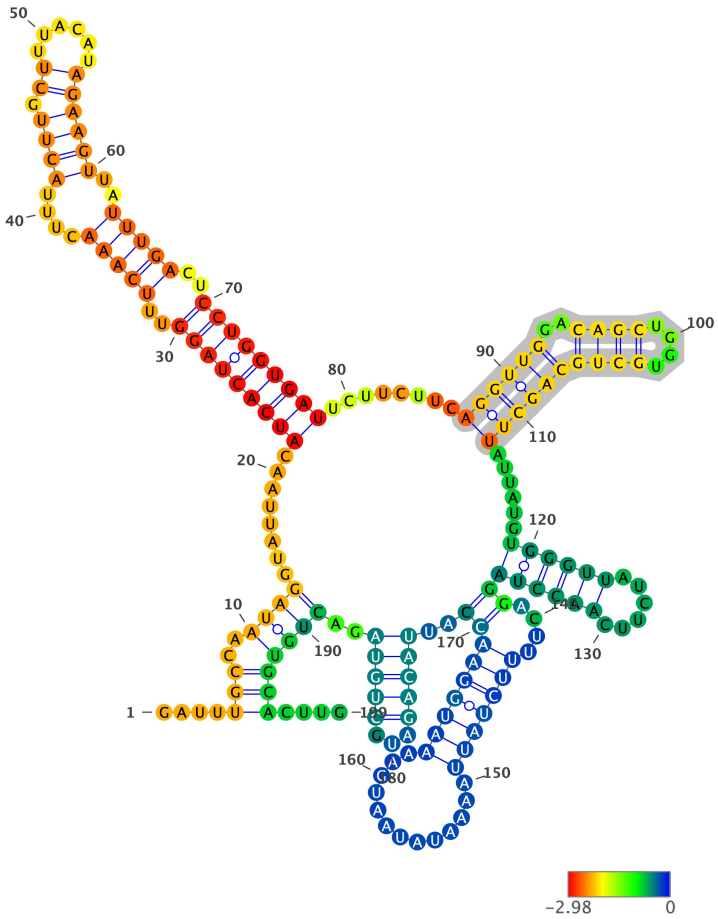
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 370 from nt 22330 to 22355 (nt 87 to 112)

```
5'-AGGTTGGACAGCTGGTGCUGCAGCUU-3'
5'-((((((..((((....))))))))))-3'
Motif MFE = -8.8; z-score = -1.79; ED = 1.62
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22244 to 22442 (motif highlighted in silver):

```
5'-GAUUUGCCAAUAGGUAUUAACAUCACUAGGUUUCAAACUUUACUUGCUUUACAUAGAAGUUAUUUGACUCCUGGUGAUUCUUCUUCAGGUUGGACAGCUGGUGCUGCAGCU
UAUUAUGUGGGUUAUCUUCAACCUAGGACUUUUCUAUUAAAAUAUAAUGAAAAUGGAACCAUUACAGAUGCUGUAGACUGUGCACUUG-3
5'-....(((..((((.........(((((((((..(((((....((((.((......))))))..)))))..)))))))))........((((((..((((....)))))))))
)......((((((......))))))((....(((((((.............)))))))))..(((((...)))))..)))))))....-3'
MFE = -43.6; z-score = -1.74; ED = 28.6
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

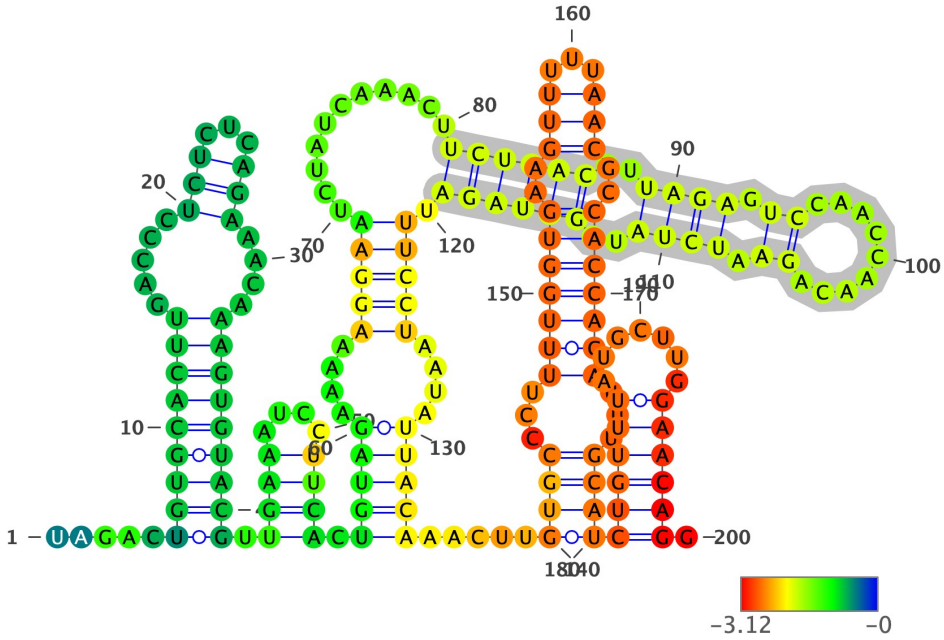
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 371 from nt 22508 to 22546 (nt 81 to 119)

```
5'-TCTAACTTTAGAGTCCAACCAACAGAATCUATTGUUAGA-3'
5'-((((((..(((((.((.........)).)))))..)))))))-3'
Motif MFE = -9.2; z-score = -3.0; 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 = -1.56; ED = 33.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

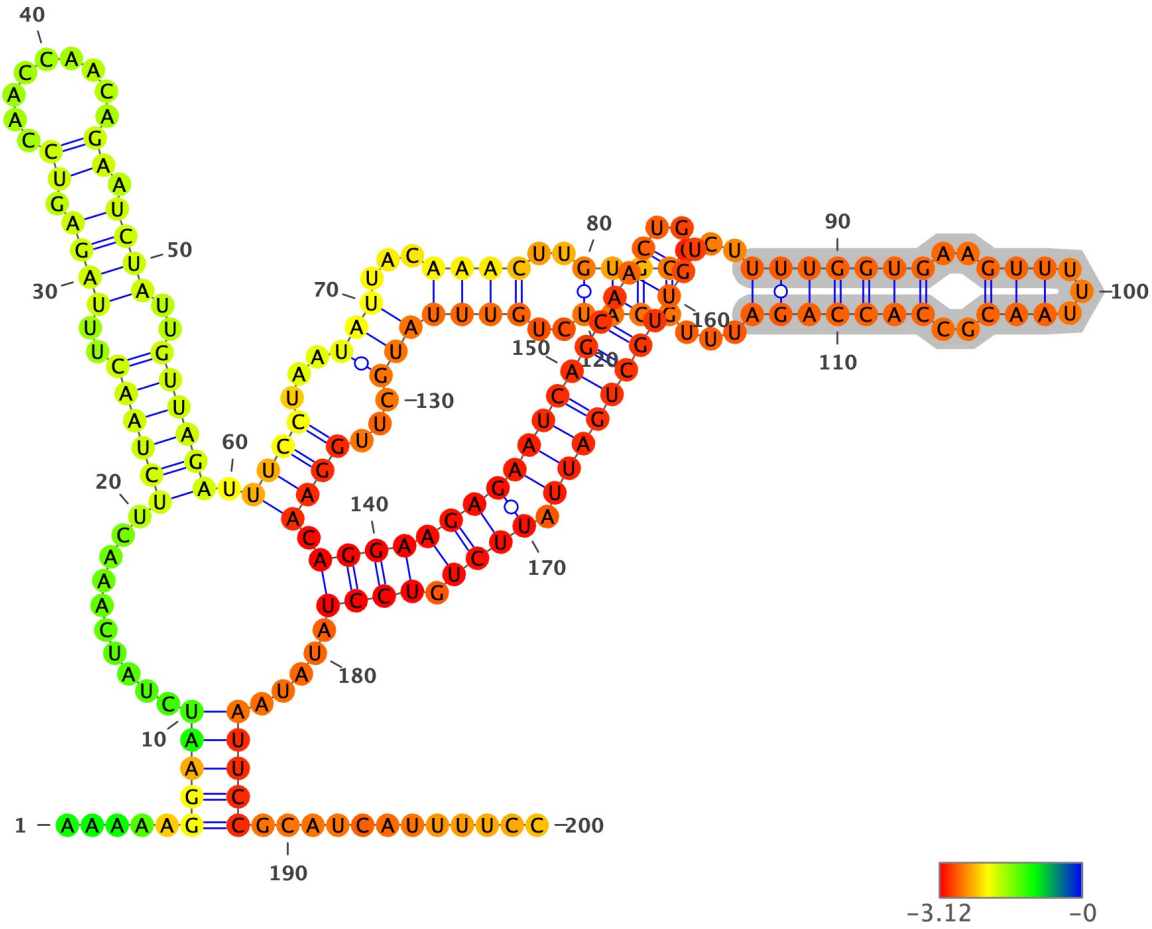
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 372 from nt 22574 to 22600 (nt 87 to 113)

```
5'-TTTGGTGAAGTTTTTAACGCCACCAGA-3'
5'-(((((((..(((...)))..)))))))-3'
Motif MFE = -7.6; z-score = -2.86; ED = 1.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22488 to 22687 (motif highlighted in silver):

```
5'-AAAAAGGAAUCUAUCAAACUUCUAACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCA
GAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCC-3
5'-.....(((((..........((((((..((((.((.........)).))))..)))))).((((...(((...((((..((((...(((((((..(((...)))..)))))
))...))))..)))))))...)))).((((((((((((((((((...)))))))))).)))).))))....)))))............-3'
MFE = -51.5; z-score = -4.45; ED = 21.91
```

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_gp02, 21563-25384(+)

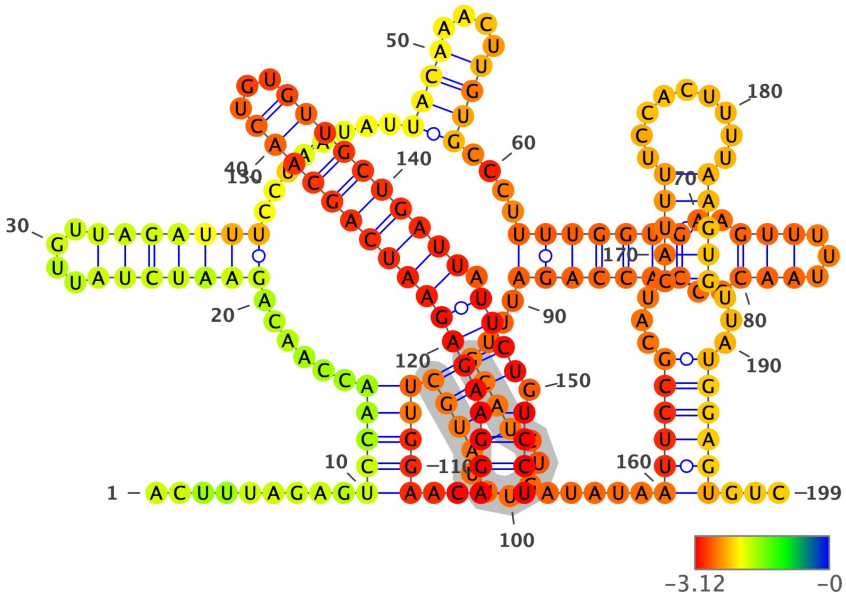
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 22604 to 22617 (nt 93 to 106)

```
5'-GCATCTGTTTAUGC-3'
5'-((((......))))-3'
Motif MFE = -1.2; z-score = -1.7; 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 22512 to 22710 (motif highlighted in silver):

```
5'-ACUUUAGAGUCCAACCAACAGAAUCUAUUGUUAGAUUUCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGA
ACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUC-3
5'-.........(((((......(((((((....)))))))........((((....))))....(((((((..(((...)))..)))))))...((((......)))))))))
..((((((((((((((((((...)))))))))).)))).))))).....((((((...(((((.........)))))...))))))...-3'
MFE = -47.2; z-score = -3.39; ED = 24.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

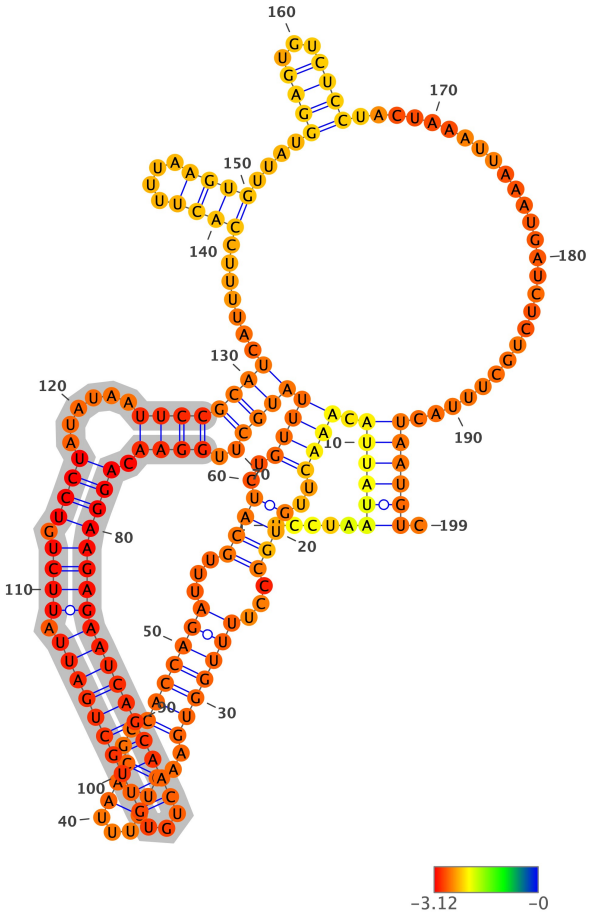
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 374 from nt 22620 to 22675 (nt 72 to 127)

```
5'-GGAACAGGAAGAGAATCAGCAACTGTGTUGCUGAUUAUUCUGUCCUATATAAUUCC-3'
5'-((((.((((((((((((((((.......)))))))).)))).))))......))))-3'
Motif MFE = -19.6; z-score = -3.85; ED = 9.64
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22549 to 22747 (motif highlighted in silver):

```
5'-UCCUAAUAUUACAAACUUGUGCCCUUUUGGUGAAGUUUUUAACGCCACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUC
UGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUC-3
5'-.....((((((.((((..((((...(((((((..(((...)))..)))))))...))))..))))((((..((((.((((((((((((((((...)))))))))).)))
).))))......))))))))).......((((....))))....((((...))))..........................)))))).-3'
MFE = -46.1; z-score = -2.69; ED = 23.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

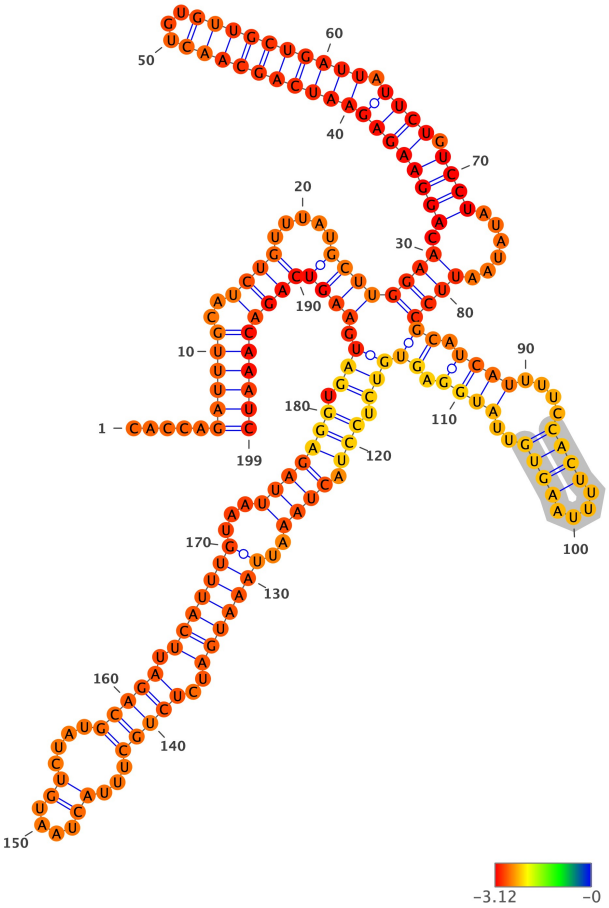
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 375 from nt 22687 to 22698 (nt 94 to 105)

```
5'-CACTTTTAAGUG-3'
5'-(((......)))-3'
Motif MFE = -1.0; z-score = -4.13; ED = 1.19
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22594 to 22792 (motif highlighted in silver):

```
5'-CACCAGAUUUGCAUCUGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGG
AGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUC-3
5'-.....((((((..((((.....((((((((.((((((((((((((((((...)))))))))).)))).))))......))))((.((((....((((....))))..))))
.))(((.(((.((((..(((((((..(((((...((....))....))))).)))))))...)))))))).))).)))))))))))))-3'
MFE = -52.5; z-score = -3.44; ED = 30.91
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

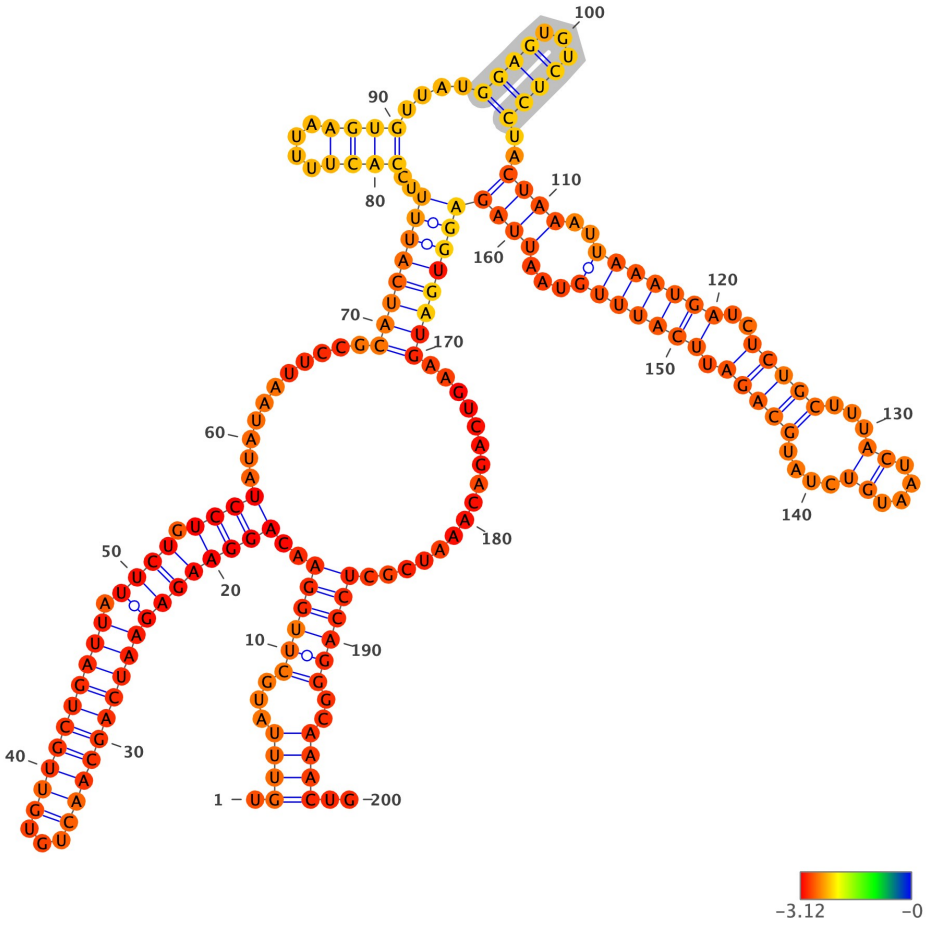
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 376 from nt 22703 to 22713 (nt 95 to 105)

```
5'-GGAGTGTCUCC-3'
5'-((((...))))-3'
Motif MFE = -2.4; z-score = -4.29; 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 22609 to 22808 (motif highlighted in silver):

```
5'-UGUUUAUGCUUGGAACAGGAAGAGAAUCAGCAACUGUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAA
AUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUG-3
5'-.((((...((((((..((((((((((((((((((...)))))))))).)))).))))...........((((((((..((((....))))....((((...))))..((((
..(((((((..(((((...((....))....)))))).)))))))...))))))))))))...............))))))..))))..-3'
MFE = -51.2; z-score = -2.83; ED = 31.19
```

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(+)

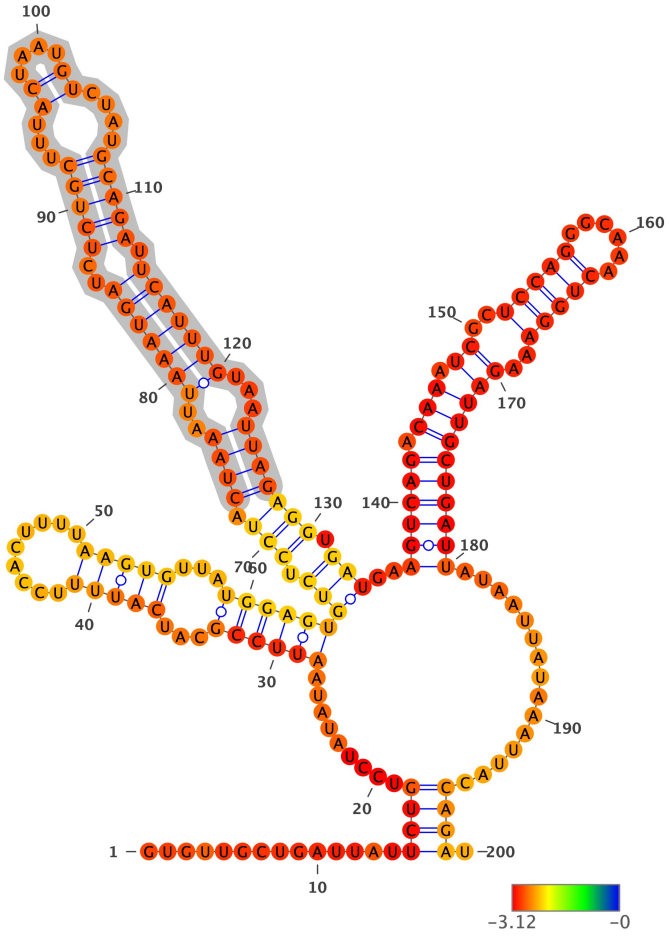
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 377 from nt 22716 to 22770 (nt 73 to 127)

```
5'-CTAAATTAAATGATCTCTGCTTTACTAATGUCTATGCAGATUCAUUUGTAAUUAG-3'
5'-((((...(((((((..((.((...((....)).)).)).)))))).....))))-3'
Motif MFE = -11.9; z-score = -2.94; ED = 4.95
```



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 22644 to 22843 (motif highlighted in silver):

```
5'-GUGUUGCUGAUUAUUCUGUCCUAUAUAAUUCCGCAUCAUUUUCCACUUUUAAGUGUUAUGGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAG
AUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAU-3
5'-..............((((.........((((((...(((((.........)))))...))))))))(((.(((.(((((..(((((((..((((((...((....)))....))))
).)))))))...)))))))).)))..((((((.(((.((..(((((......)))))..)))))))))))).............)))).-3'
MFE = -46.9; z-score = -3.22; ED = 31.19
```

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(+)

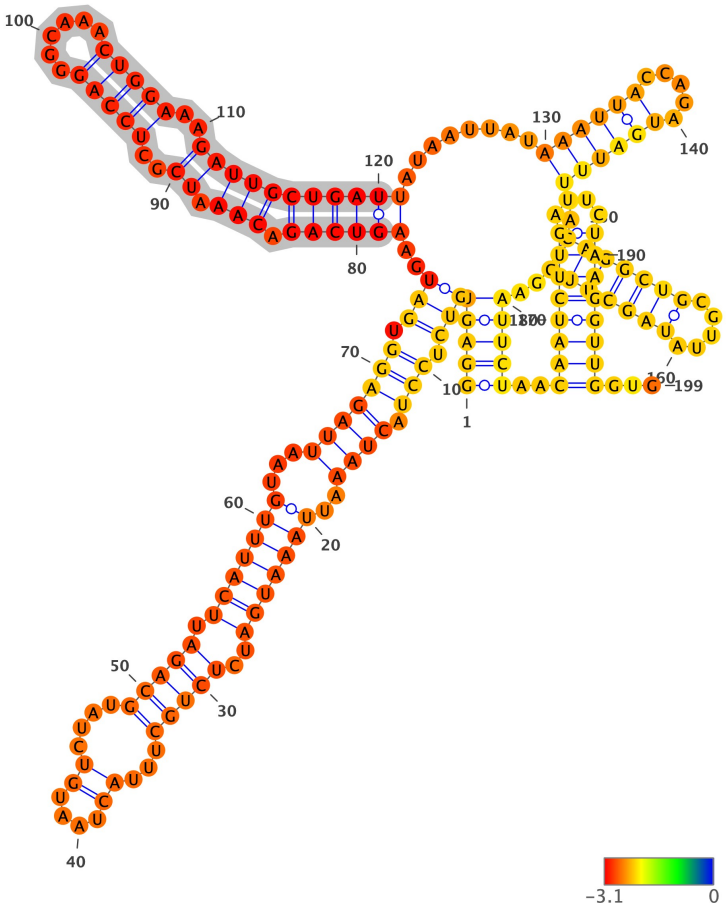
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 378 from nt 22781 to 22822 (nt 79 to 120)

```
5'-GTCAGACAAATCGCTCCAGGGCAAACUGGAAAGAUUGCUGAU-3'
5'-(((((.(((.((..(((((.....)))))..)))))))))-3'
Motif MFE = -15.9; z-score = -4.29; ED = 2.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22703 to 22901 (motif highlighted in silver):

```
5'-GGAGUGUCUCCUACUAAAUUAAAUGAUCUCUGCUUUACUAAUGUCUAUGCAGAUUCAUUUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAG
AUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUG-3
5'-(((((((((.(((.(((((..(((((((..((((((...((....)).....)))))).)))))))...)))))))).)))..((((((.(((.((..(((((.....)))))..)
)))))))))).........((((((.....))))))..(((((((.....)))))))..))))..(((((((((....)))))))))...-3'
MFE = -53.4; z-score = -3.21; ED = 20.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

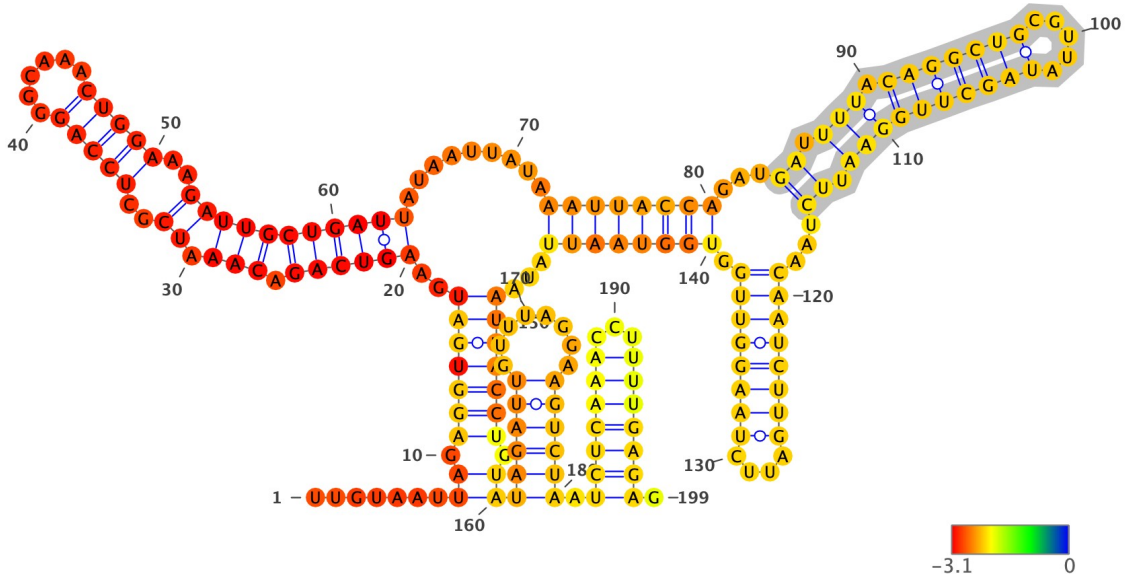
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 379 from nt 22844 to 22875 (nt 84 to 115)

```
5'-GATTTTACAGGCTGCGTTATAGCUUGGAATUC-3'
5'-((.(((.(((((.........))))))))).))-3'
Motif MFE = -7.3; z-score = -1.59; ED = 4.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22761 to 22959 (motif highlighted in silver):

```
5'-UUGUAAUUAGAGGUGAUGAAGUCAGACAAAUCGCUCCAGGGCAAACUGGAAAGAUUGCUGAUUAUAAUUAUAAAUUACCAGAUGAUUUUACAGGCUGCGUUAUAGCUUGGA
AUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAG-3
5'-.......((.(((((((..((((((.(((.((..(((((......)))))..)))))))))))).........((((((((...((.(((.(((((((.....)))))))))
).))...((((((((....))))))))).))))))))...))))))).))((((((........)))))).(((((((...))))))).-3'
MFE = -54.5; z-score = -4.33; ED = 14.45
```

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_gp02, 21563-25384(+)

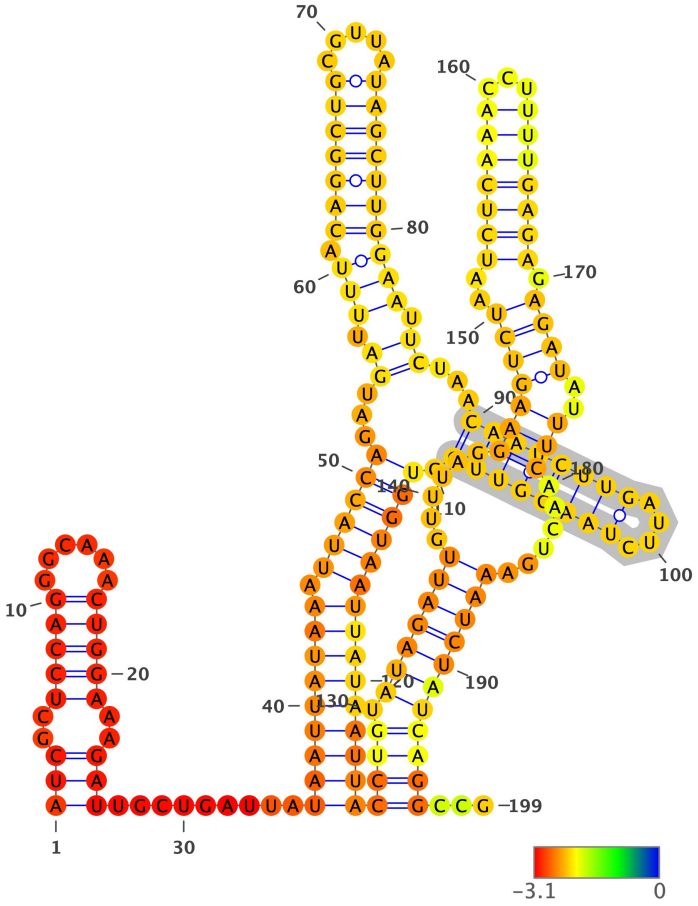
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 380 from nt 22879 to 22898 (nt 90 to 109)

```
5'-CAATCTTGATTCUAAGGUUG-3'
5'-((((((((....))))))))-3'
Motif MFE = -4.8; z-score = -2.7; 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 = -3.98; ED = 20.61
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

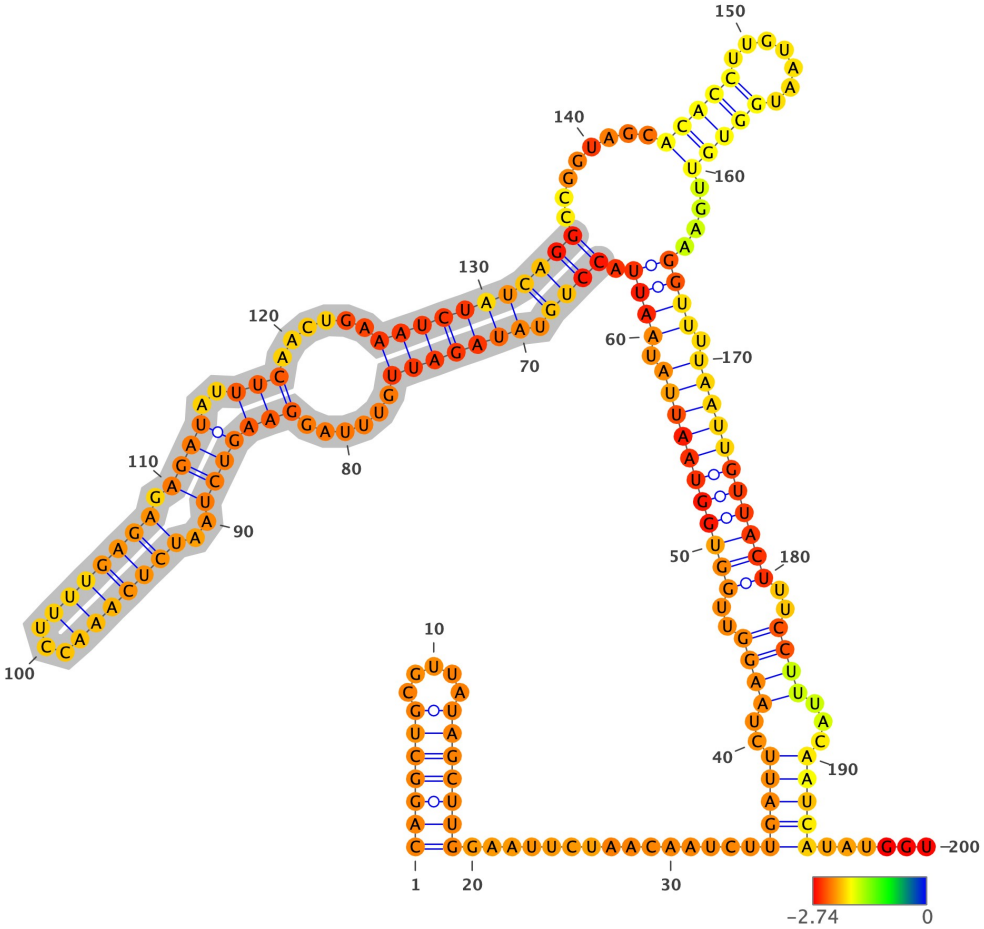
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 381 from nt 22915 to 22985 (nt 65 to 135)

```
5'-CCTGTATAGATTGTTTAGGAAGTCTAATCTCAAACCTTTTGAGAGAGAUATUUCAACTGAAAUCUATCAGG-3'
5'-((.....(((((.....(((((((..((((.........)))).))))..)))......)))))....))-3'
Motif MFE = -21.1; z-score = -3.86; ED = 8.92
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22851 to 23050 (motif highlighted in silver):

```
5'-CAGGCUGCGUUAUAGCUUGGAAUUCUAACAAUCUUGAUUCUAAGGUUGGUGGUAAUUAUAAUUACCUGUAUAGAUUGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAG
AUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGU-3
5'-(((((((.....)))))))...............(((((..((((..(((((((((((.((((.((((.(((((((.....(((((((..(((((((...)))))))).))
))..)))......))))))))))).........(((((.......)))))....)))).))))))))))..))))...)))))......-3'
MFE = -48.4; z-score = -3.13; ED = 32.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

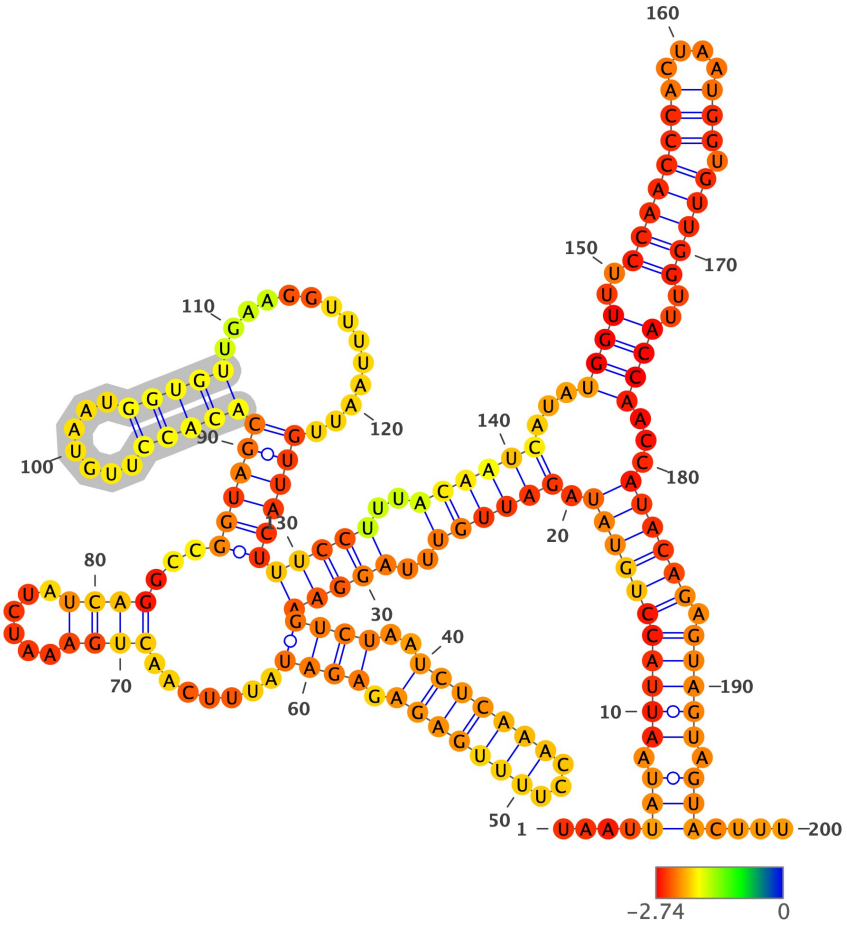
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 382 from nt 22994 to 23010 (nt 92 to 108)

```
5'-ACACCTTGTAATGGUGU-3'
5'-(((((.......)))))-3'
Motif MFE = -5.4; z-score = -5.8; 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 = -4.55; 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(+)

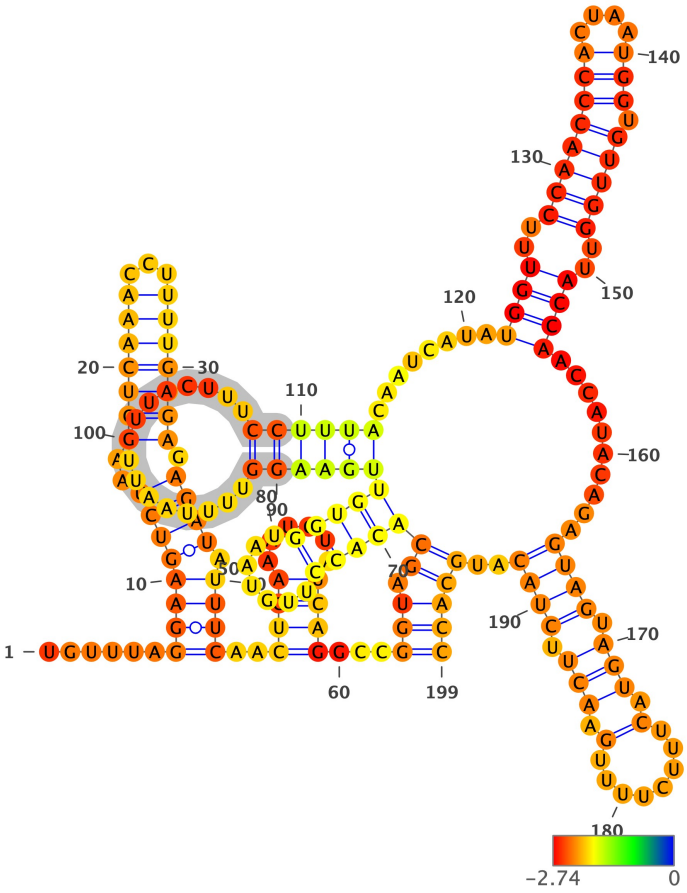
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 383 from nt 23015 to 23034 (nt 90 to 109)

```
5'-GGTTTTAATTGTTACTTTCC-3'
5'-((................))-3'
Motif MFE = 0.0; z-score = 0.46; 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 22926 to 23124 (motif highlighted in silver):

```
5'-UGUUUAGGAAGUCUAAUCUCAAACCUUUUGAGAGAGAUAUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUU
UACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACC-3
5'-......(((((((..(((((((...))))))).)))).))))..((((......))))...(((.(((((((.......)))))))((((((................))))
)).......((((..(((((((....))).)))))..)))).........((((.(((.(........).))).))))..))))))-3'
MFE = -48.0; z-score = -2.76; ED = 45.71
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

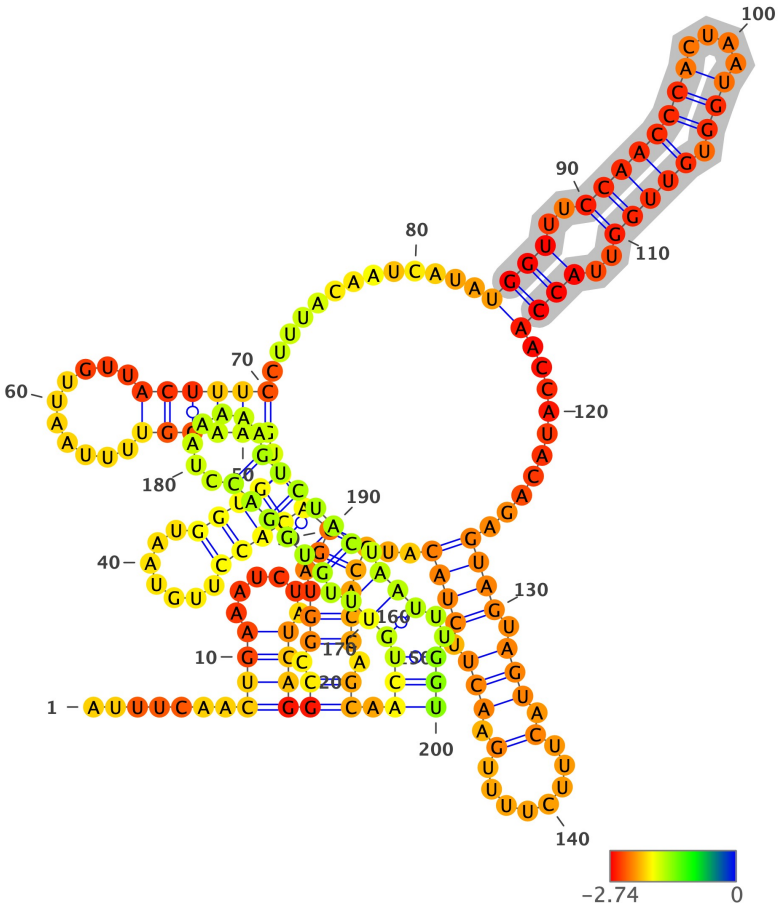
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 384 from nt 23048 to 23078 (nt 85 to 115)

```
5'-GGTTTCCAACCCACTAATGGTGUUGGTTACC-3'
5'-(((..(((((((......)).)))))..)))-3'
Motif MFE = -13.1; z-score = -3.87; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 22964 to 23163 (motif highlighted in silver):

```
5'-AUUUCAACUGAAAUCUAUCAGGCCGGUAGCACACCUUGUAAUGGUGUUGAAGGUUUUAAUUGUUACUUUCCUUUACAAUCAUAUGGUUUCCAACCCACUAAUGGUGUUGGU
UACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGU-3
5'-.......((((......))))((.(((.(((((((.......))))).((((((..........))))))..............((((..((((((((....))).)))))).
.))))..........((((.(((.(........).))).))))..)))))).)).((((((.((((((.......))))))).)))..)))-3'
MFE = -48.1; z-score = -2.66; ED = 55.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

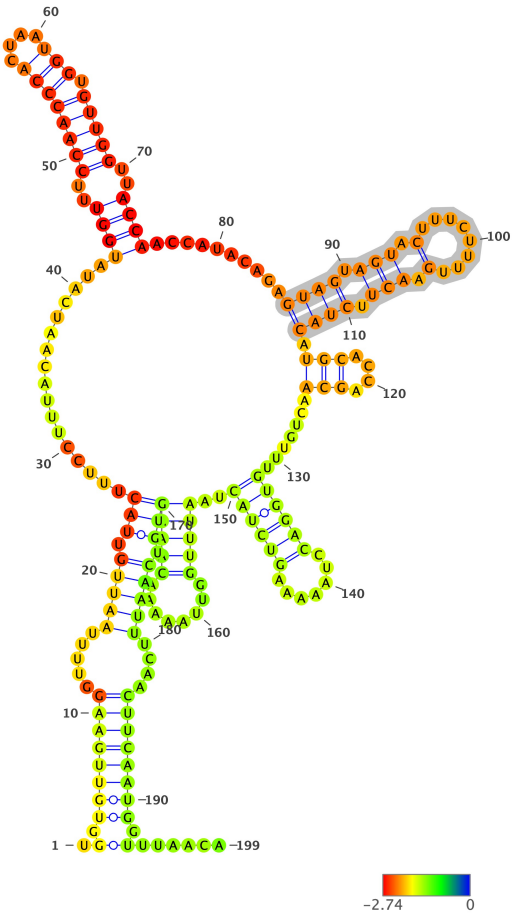
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 385 from nt 23090 to 23117 (nt 86 to 113)

```
5'-GTAGTAGTACTTTCTTTTGAACUTCUAC-3'
5'-((((.(((.(........).))).))))-3'
Motif MFE = -4.1; z-score = -1.96; 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 = -2.41; 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(+)

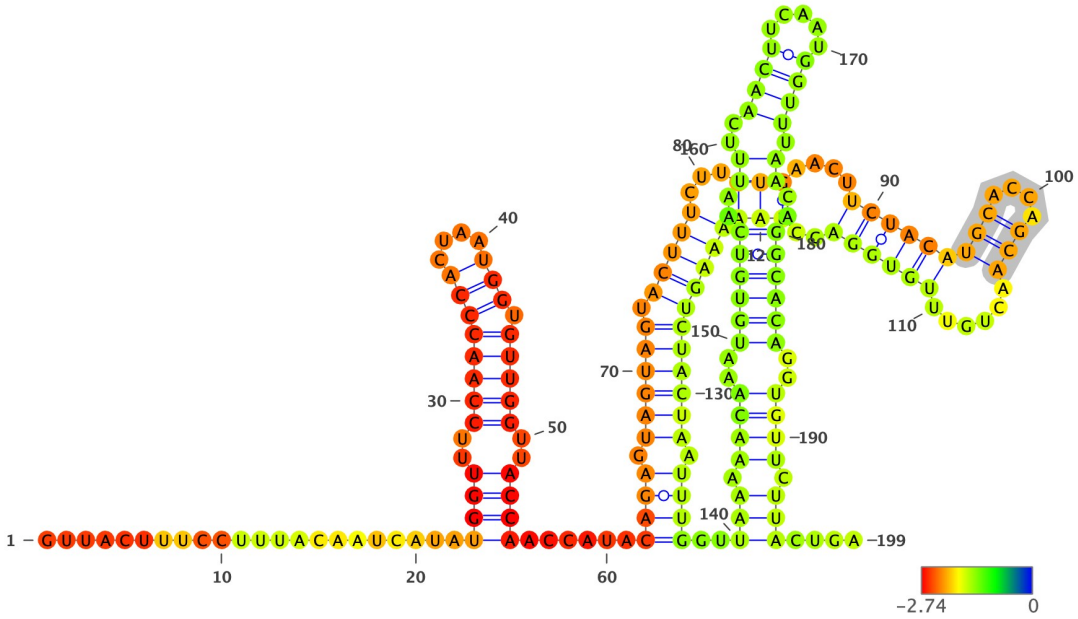
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 386 from nt 23119 to 23128 (nt 95 to 104)

```
5'-TGCACCAGCA-3'
5'-(((....)))-3'
Motif MFE = -0.9; z-score = -8.87; 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 = -2.91; 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(+)

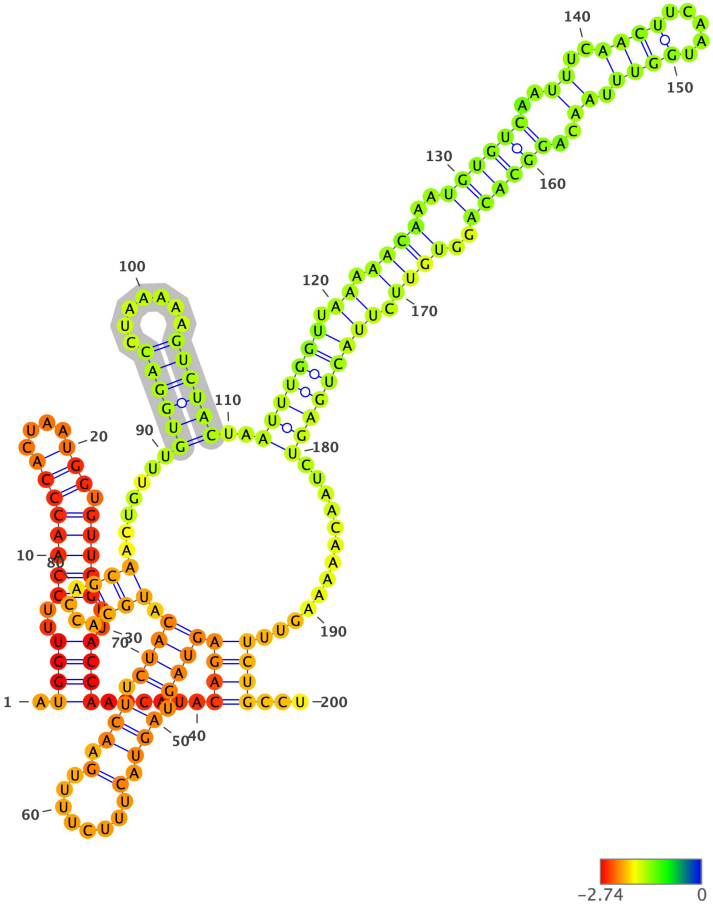
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 387 from nt 23136 to 23154 (nt 91 to 109)

```
5'-GTGGACCTAAAAAGUCUAC-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -2.99; ED = 0.54
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23046 to 23245 (motif highlighted in silver):

```
5'-AUGGUUUCCAACCCACUAAUGGUGUUGGUUACCAACCAUACAGAGUAGUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUA
AUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCU-3
5'-.((((..((((((((....))).)))))..))))......((((((((.(((.(........).))).)))).(((....)))).......((((((.......))))))..
(((((((.((.((((..((((((..((..((((.....)))).))..))))))..)))).))))))))).............))))...-3'
MFE = -47.5; z-score = -2.81; 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(+)

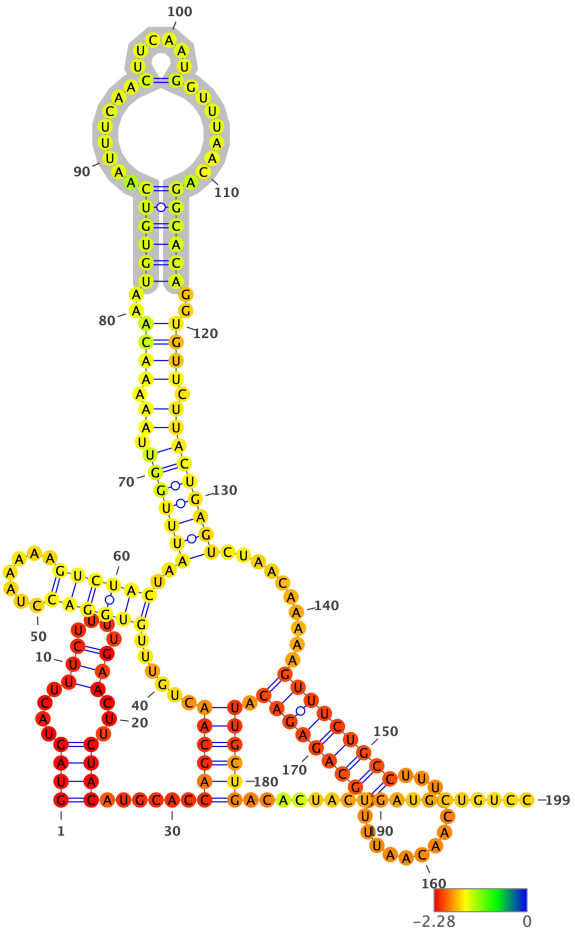
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 388 from nt 23174 to 23209 (nt 82 to 117)

```
5'-TGTGTCAATTTCAACTTCAATGGTTTAACAGGCACA-3'
5'-((((((........(......)........))))))-3'
Motif MFE = -6.5; z-score = -1.29; ED = 2.85
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23093 to 23291 (motif highlighted in silver):

```
5'-GUAGUACUUUCUUUUGAACUUCUACAUGCACCAGCAACUGUUUGUGGACCUAAAAAGUCUACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACA
GGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCC-3
5'-((((....(((....)))...)))).....((((((......((((((.......))))))..(((((((.((.((((..((((((........(......)........
))))))..)))).))))))))).........(((((((((.............)))))))))).))))))..................-3'
MFE = -44.4; z-score = -2.61; ED = 25.86
```

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_gp02, 21563-25384(+)

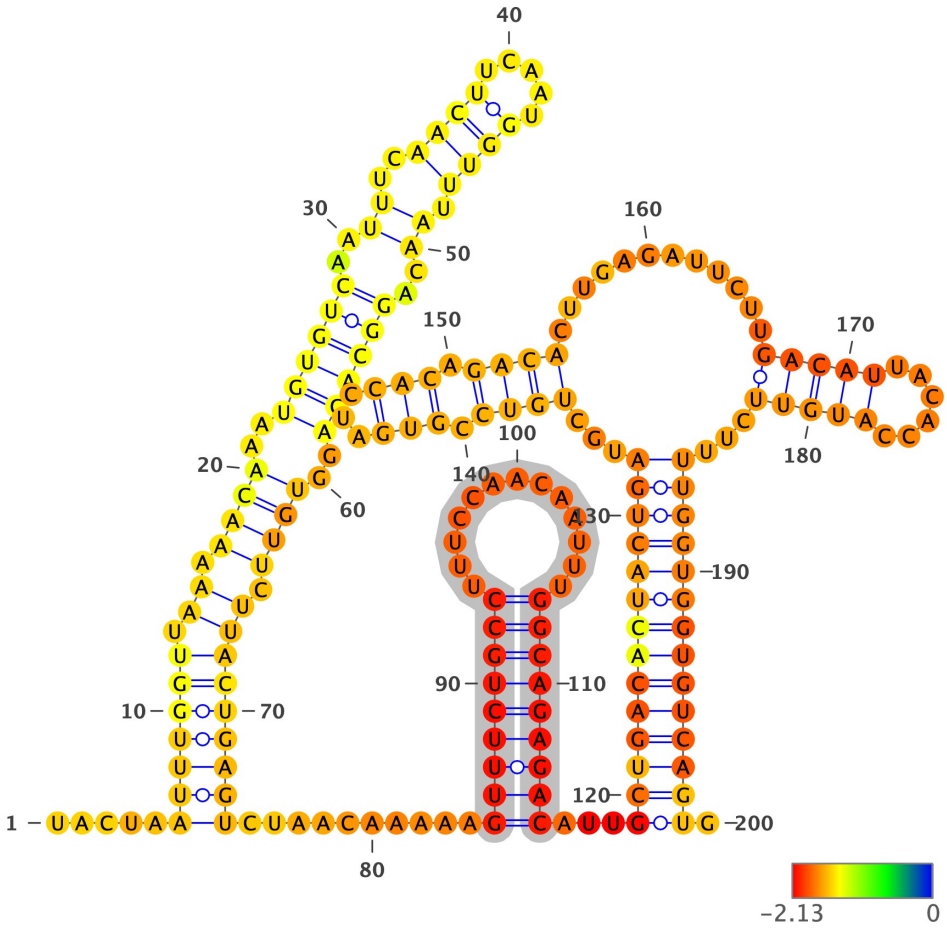
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23236 to 23266 (nt 85 to 115)

```
5'-GTTTCTGCCTTTCCAACAATTTGGCAGAGAC-3'
5'-(((((((((.............)))))))))-3'
Motif MFE = -12.7; z-score = -4.99; ED = 0.2
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23152 to 23351 (motif highlighted in silver):

```
5'-UACUAAUUUGGUUAAAAACAAAUGUGUCAAUUUCAACUUCAAUGGUUUAACAGGCACAGGUGUUCUUACUGAGUCUAACAAAAAGUUUCUGCCUUUCCAACAAUUUGGCAG
AGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUG-3
5'-.....(((((((.((.((((..(((((((..((..((((.....)))).))..))))))..)))).)))))))))..........(((((((((.............)))))
))))...((((((((((((((...((((.(((...))).))))............(((((......)))))...)))))))))))))).-3'
MFE = -54.1; z-score = -3.22; ED = 19.51
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

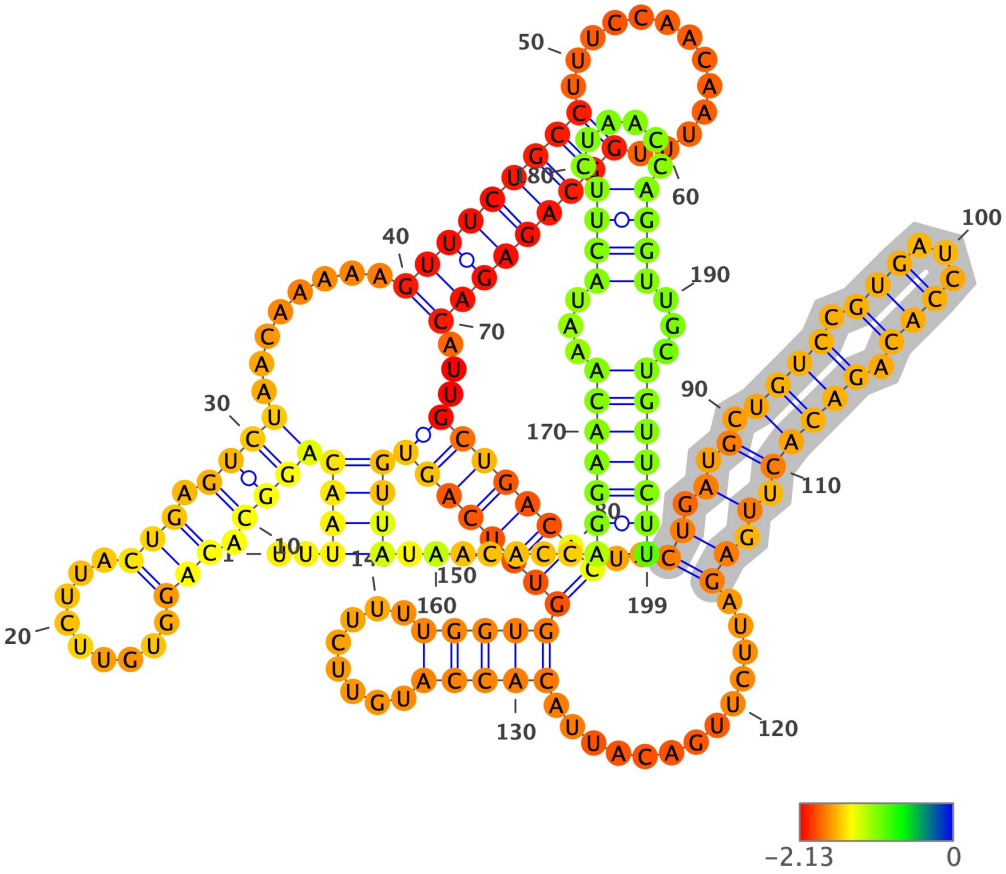
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 390 from nt 23280 to 23311 (nt 84 to 115)

```
5'-CTGATGCTGTCCGTGATCCACAGACACTUGAG-3'
5'-((.(.(.(((((.(((...))))).)))))).).))-3'
Motif MFE = -5.5; z-score = -0.07; 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 = -2.8; ED = 35.09
```

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_gp02, 21563-25384(+)

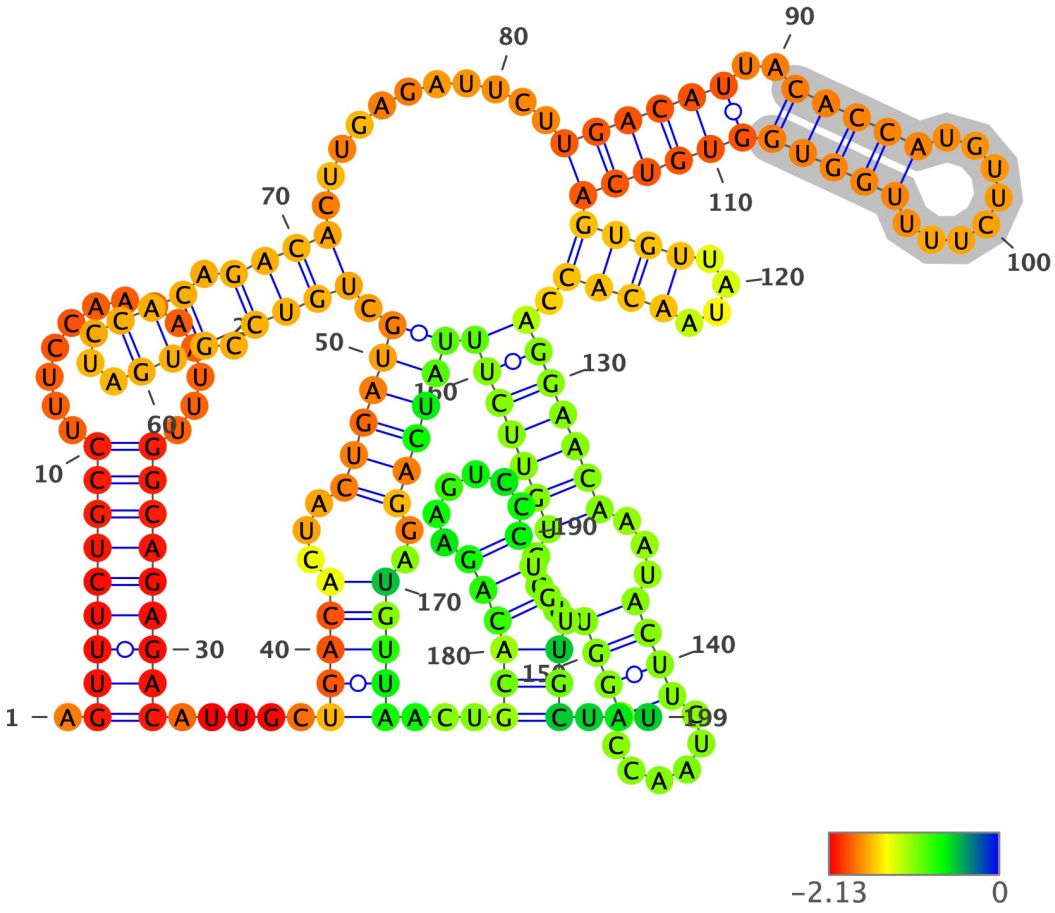
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 391 from nt 23325 to 23342 (nt 91 to 108)

```
5'-CACCATGTTCTTTUGGUG-3'
5'-(((((........)))))-3'
Motif MFE = -5.4; z-score = -3.57; 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(+)

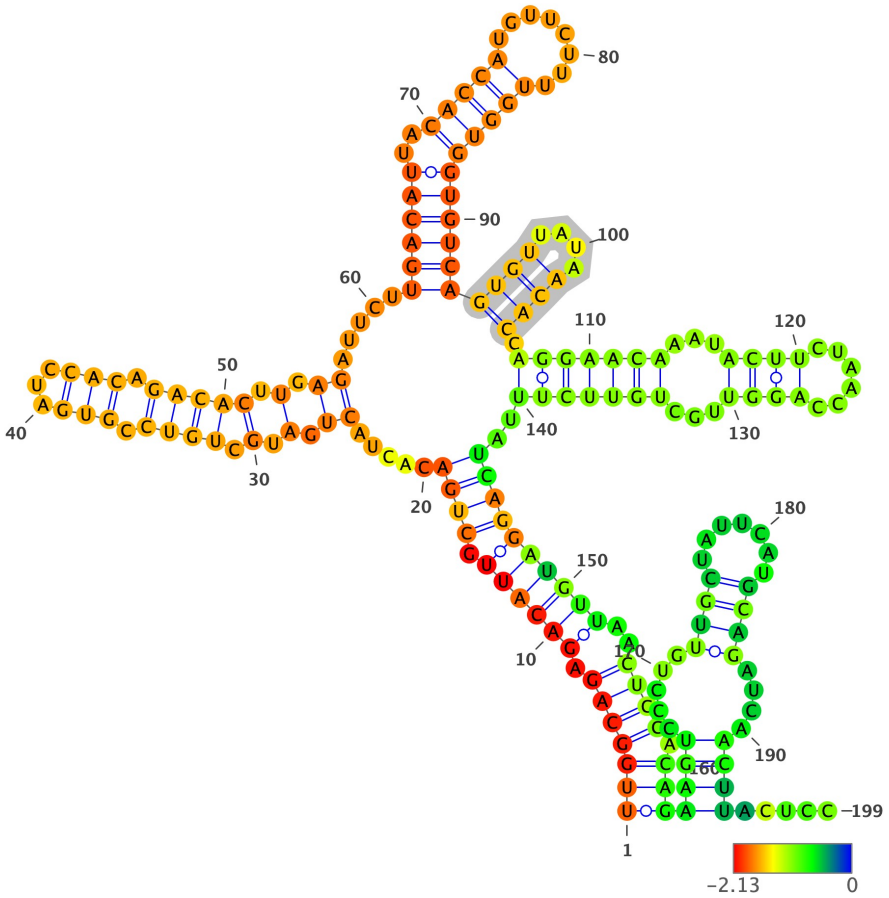
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 392 from nt 23349 to 23360 (nt 94 to 105)

```
5'-GTGTTATAACAC-3'
5'-((((....))))-3'
Motif MFE = -1.1; z-score = -8.41; ED = 1.9
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23256 to 23454 (motif highlighted in silver):

```
5'-UUGGCAGAGACAUUGCUGACACUACUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAA
CAAAUACUUCUAACCAGGUUGCUGUUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCC-3
5'-(((((((.((((((.((((.....((.(.(.((((.(((...))).)))))).).)).....((((((..(((((........)))))))))))))(((....))))).(((((
((...((((......))))...)))))))..))))))))))..)))).)))(((((.....((((.......))))....))))).....-3'
MFE = -48.3; z-score = -1.24; ED = 19.14
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

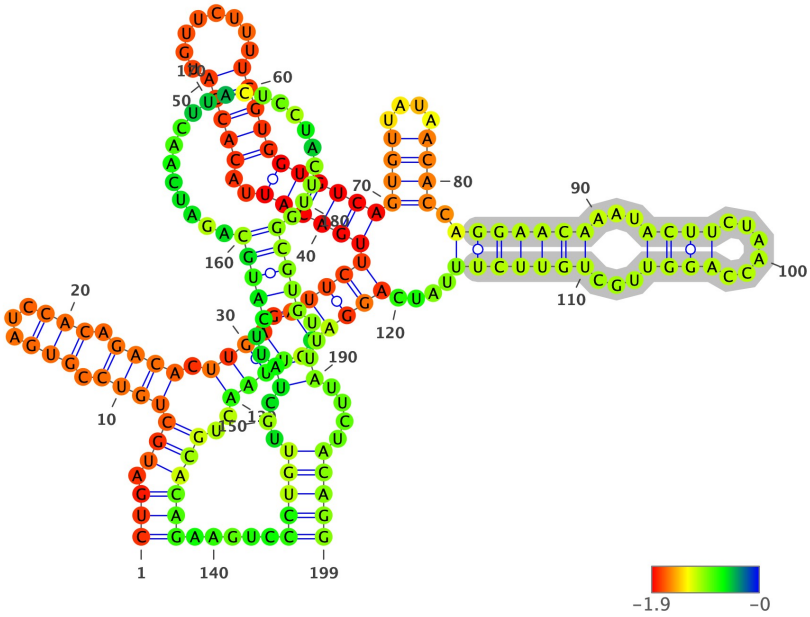
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 393 from nt 23363 to 23394 (nt 84 to 115)

```
5'-GGAACAAATACTTCTAACCAGGUTGCUGUUCU-3'
5'-((((((...((((......))))...))))))-3'
Motif MFE = -6.0; z-score = -1.42; ED = 1.56
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23280 to 23478 (motif highlighted in silver):

```
5'-CUGAUGCUGUCCGUGAUCCACAGACACUUGAGAUUCUUGACAUUACACCAUGUUCUUUUGGUGGUGUCAGUGUUAUAACACCAGGAACAAAUACUUCUAACCAGGUUGCUG
UUCUUUAUCAGGAUGUUAACUGCACAGAAGUCCCUGUUGCUAUUCAUGCAGAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGG-3
5'-(((.(((((((.(((...))).)))).((((.(((((((((((..(((((........)))))))))))((((....)))).(((((((...((((......))))...))
)))))....))))).))))..))))))).....(((((...((..(((((.....................)))))..))....)))))-3'
MFE = -45.9; z-score = -0.96; ED = 45.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

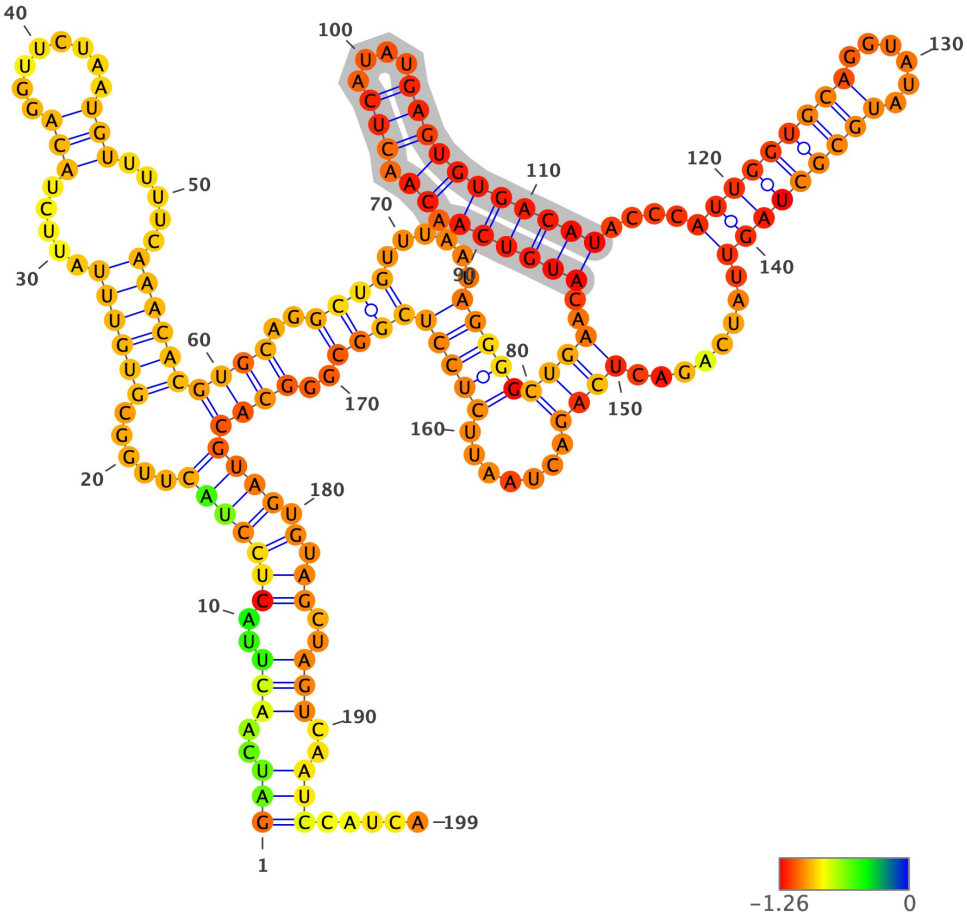
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 394 from nt 23526 to 23553 (nt 86 to 113)

```
5'-ATGTCAACAACTCATATGAGUGUGACAU-3'
5'-((((((.((..((....)).))))))))-3'
Motif MFE = -8.7; z-score = -3.85; ED = 2.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23441 to 23639 (motif highlighted in silver):

```
5'-GAUCAACUUACUCCUACUUGGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGAC
AUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCA-3
5'-(((..(((..(((((((.....((((((.....(((.........))).....))))))((((..((((......(((((((((..((((((.((.(((....)))))))))
))....((((((((.....)))))))))........))))........))))))))).))))))))).).))..)))..)))......-3'
MFE = -48.8; z-score = -0.61; ED = 49.35
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

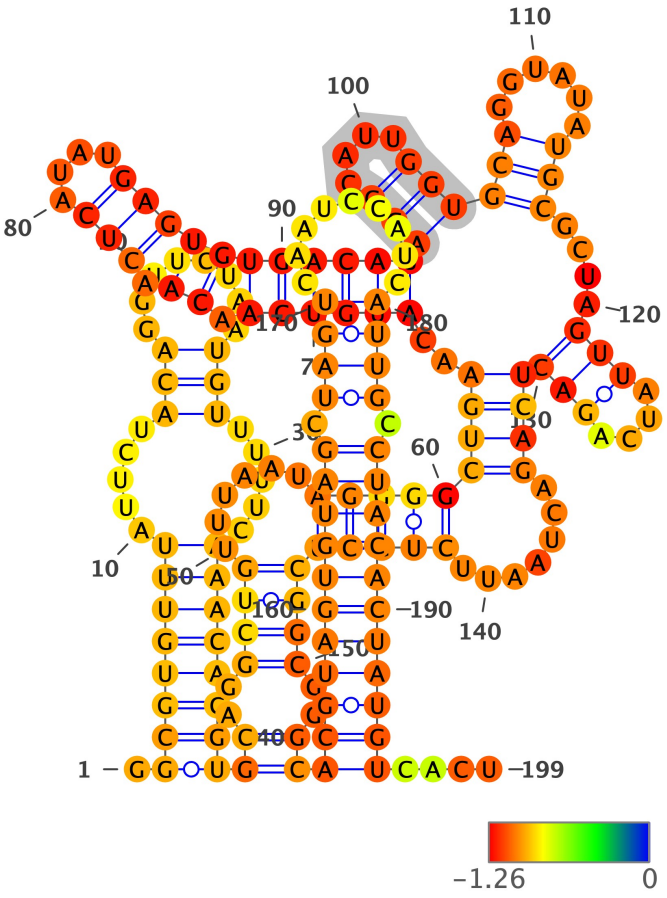
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 395 from nt 23554 to 23563 (nt 95 to 104)

```
5'-ACCCATTGGU-3'
5'-(((....)))-3'
Motif MFE = -0.2; z-score = -1.04; 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 23460 to 23658 (motif highlighted in silver):

```
5'-GGCGUGUUUAUUCUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUA
UAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACU-3
5'-.((((((((.....(((........)))).....))))))))((..((((......((((((((..((((((.((.(((....)))))))))))(((....)))(((....
..)))....(((....)))))))).......)))))))))..))((((((((((.((((.........)))).))))))))))....-3'
MFE = -50.4; z-score = -2.08; ED = 27.36
```

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(+)

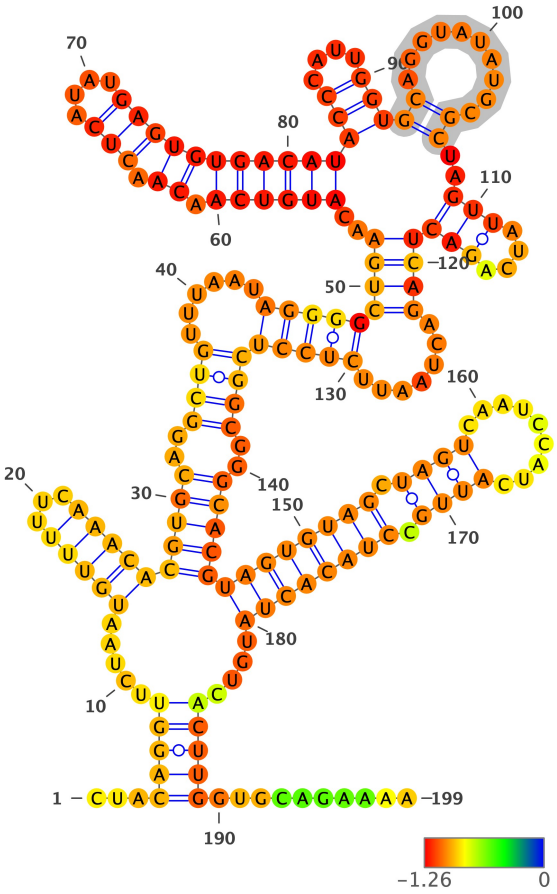
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 396 from nt 23564 to 23577 (nt 93 to 106)

```
5'-GCAGGTATATGCGC-3'
5'-((.........))-3'
Motif MFE = -3.0; z-score = -1.89; ED = 0.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23472 to 23670 (motif highlighted in silver):

```
5'-CUACAGGUUCUAAUGUUUUUCAAACACGUGCAGGCUGUUUAAUAGGGGCUGAACAUGUCAACAACUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUU
AUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUACACUAUGUCACUUGGUGCAGAAAA-3
5'-...(((((.....(((((...)))))((((((..((((......((((((((((..((((((.((.((((....))))))))))))))(((....)))))(..........)).(((
....))))))).......)))))))))..)))))(((((((((.((((.........)))).)))))))))....)))))..........-3'
MFE = -41.6; z-score = -0.71; ED = 51.11
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

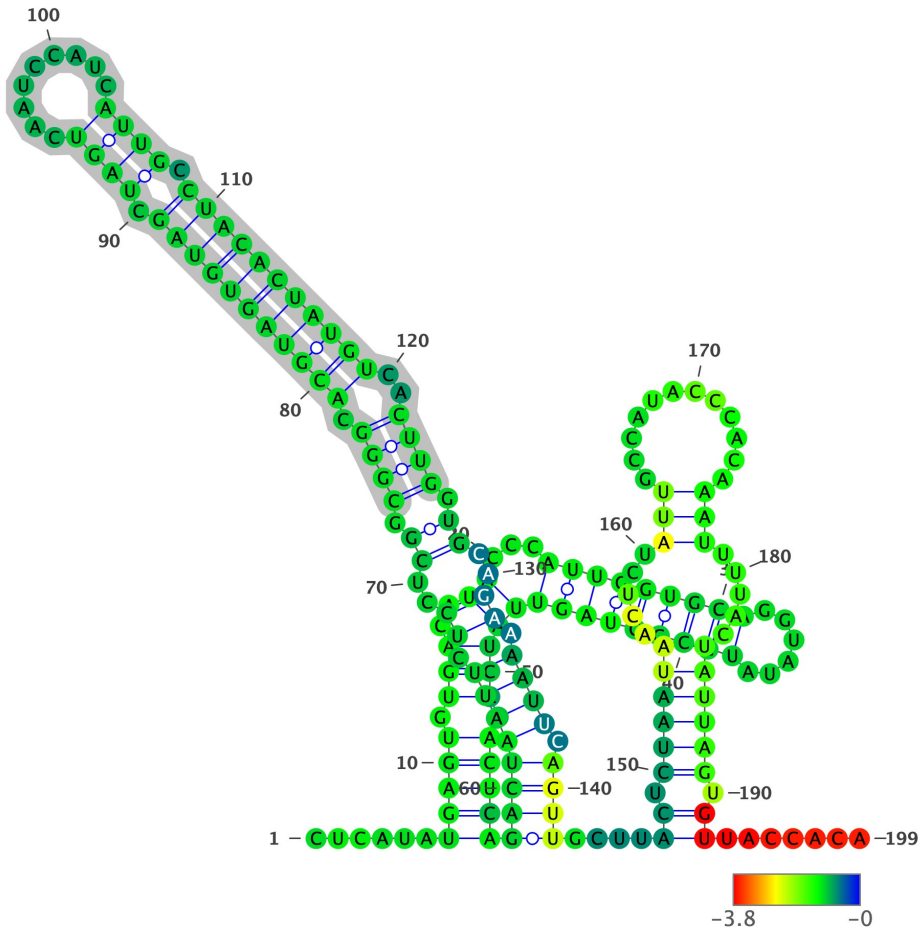
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 397 from nt 23609 to 23660 (nt 74 to 125)

```
5'-CGGGCACGTAGTGTAGCTAGTCAATCCATCAUUGCCUACACUAUGUCACUUG-3'
5'-((((.(((((((((((.((((.........)))).))))))))))..))))-3'
Motif MFE = -15.3; z-score = -2.34; ED = 7.72
```



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 23536 to 23734 (motif highlighted in silver):

```
5'-CUCAUAUGAGUGUGACAUACCCAUUGGUGCAGGUAUAUGCGCUAGUUAUCAGACUCAGACUAAUUCUCCUCGGCGGGCACGUAGUGUAGCUAGUCAAUCCAUCAUUGCCUA
CACUAUGUCACUUGGUGCAGAAAAUUCAGUUGCUUACUCUAAUAACUCUAUUGCCAUACCCACAAAUUUUACUAUUAGUGUUACCACA-3
5'-......(((((.(((..((...(((((((((.....))))))))))))))).)))))((((((((.((..((.((((.(((((((((((.((((.........)))).)))
))))))))..)))).))..)).)))).))))....((.((((((.....(((.............)))).....)))))).)).......-3'
MFE = -43.4; z-score = -1.51; ED = 36.7
```

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(+)

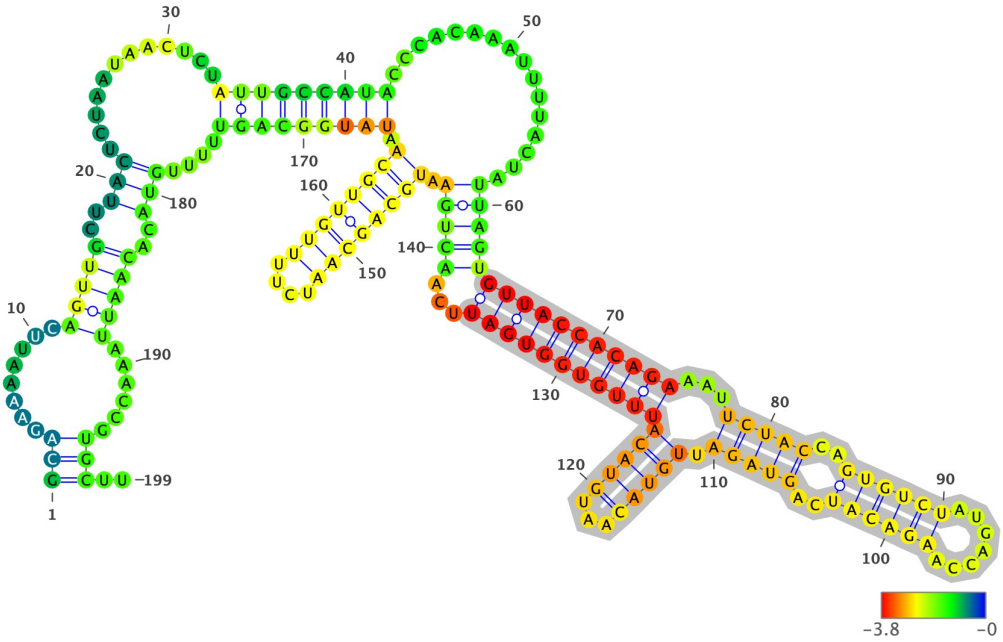
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 398 from nt 23726 to 23797 (nt 64 to 135)

```
5'-GTTACCACAGAAATTCTACCAGTGTCTATGACCAAGACAUCAGUAGATTGTACAATGUACAUUUGUGGUGAU-3'
5'-(((((((((((...(((((..((((((.......))))))..))))).((((.....))))))))))))))-3'
Motif MFE = -24.5; z-score = -4.66; 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 = -3.89; ED = 21.69
```

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_gp02, 21563-25384(+)

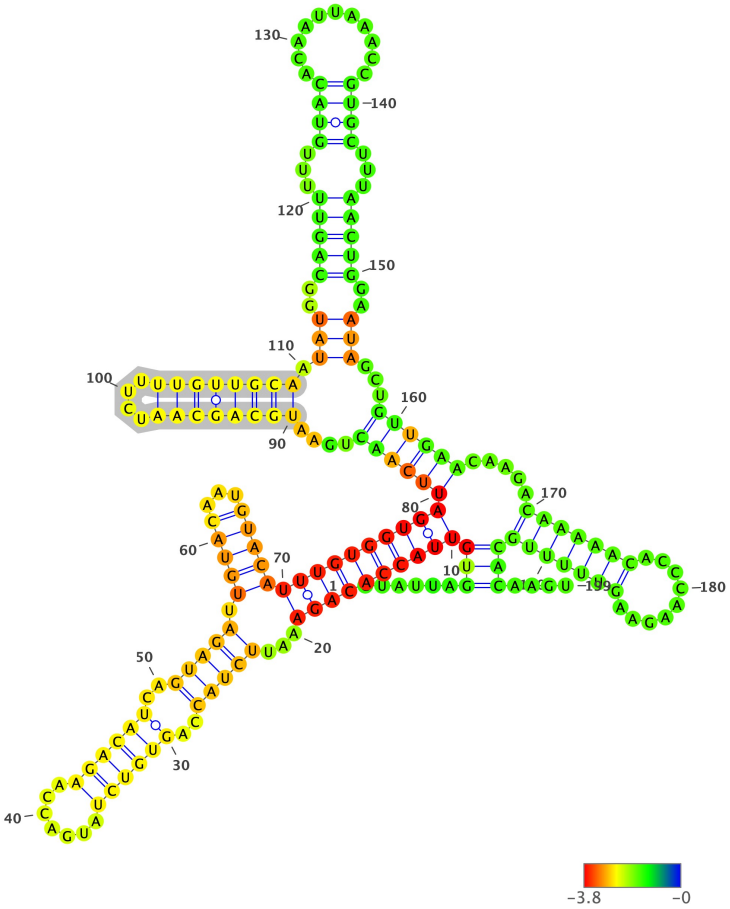
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 23807 to 23826 (nt 90 to 109)

```
5'-TGCAGCAATCTTUUGUUGCA-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.8; z-score = -5.47; ED = 0.73
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23718 to 23916 (motif highlighted in silver):

```
5'-CUAUUAGUGUUACCACAGAAAUUCUACCAGUGUCUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAU
AUGGCAGUUUUUGUACACAAUUAAACCGUGCUUUAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGU-3
5'-......(((((((((((((...(((((..((((((.......))))))..))))).(((((...))))))))))))))))((((((....((((((((....))))))))).(
((..(((((...((((...........))))...)))))..)))...))))))).....(((((((.........))))))))))....-3'
MFE = -50.2; z-score = -3.0; 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(+)

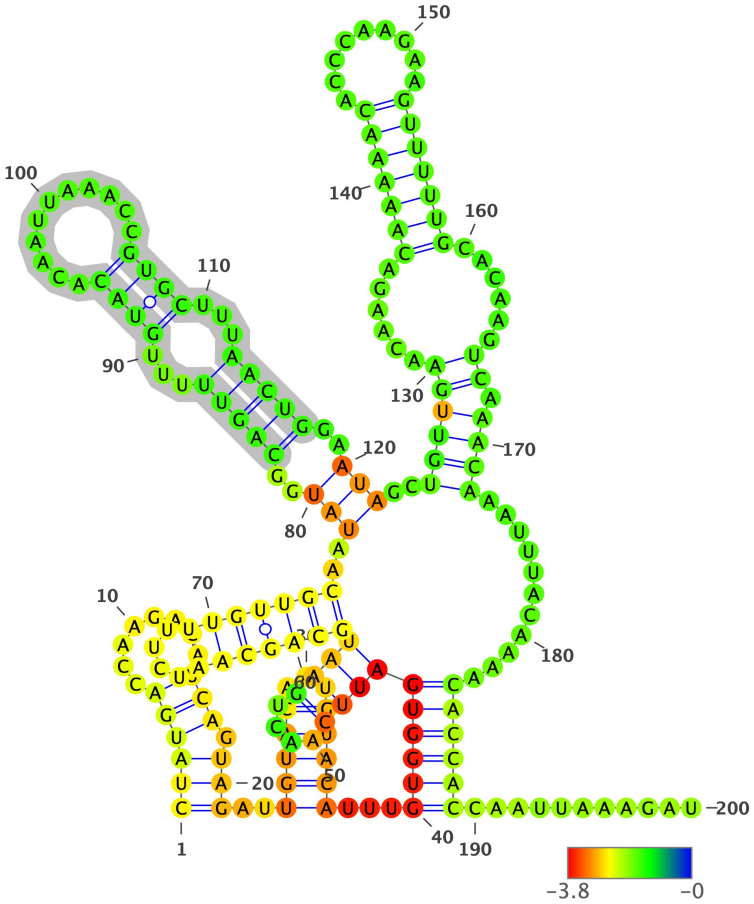
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 400 from nt 23833 to 23867 (nt 83 to 117)

```
5'-CAGTTTTTGTACACAATTAAACCGUGCTTTAACUG-3'
5'-(((((...((((...........))))...)))))-3'
Motif MFE = -6.4; z-score = -1.94; ED = 0.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23751 to 23950 (motif highlighted in silver):

```
5'-CUAUGACCAAGACAUCAGUAGAUUGUACAAUGUACAUUUGUGGUGAUUCAACUGAAUGCAGCAAUCUUUUGUUGCAAUAUGGCAGUUUUUGUACACAAUUAAACCGUGCUU
UAACUGGAAUAGCUGUUGAACAAGACAAAAACACCCAAGAAGUUUUUGCACAAGUCAAACAAAUUUACAAAACACCACCAAUUAAAGAU-3
5'-((((((........))).)))..(((((...)))))...(((((((((((....))))(((((((....)))))))..(((..(((((...((((...........))))..
.)))))..)))..((((((......(((((((.........)))))))......)).))))...........))))))...........-3'
MFE = -37.5; z-score = -2.18; 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(+)

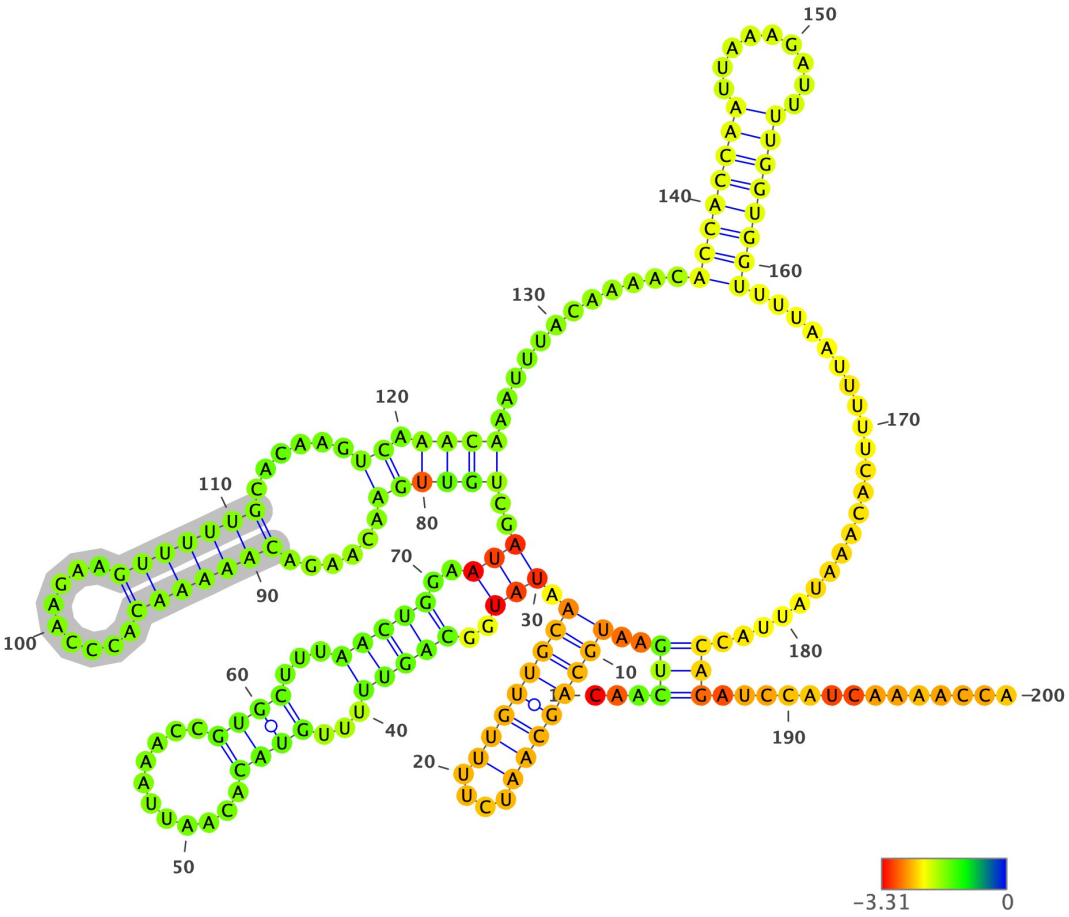
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 401 from nt 23887 to 23909 (nt 89 to 111)

```
5'-CAAAAACACCCAAGAAGUUUUUG-3'
5'-(((((((.........)))))))-3'
Motif MFE = -3.0; z-score = -3.3; 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 = -3.07; 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(+)

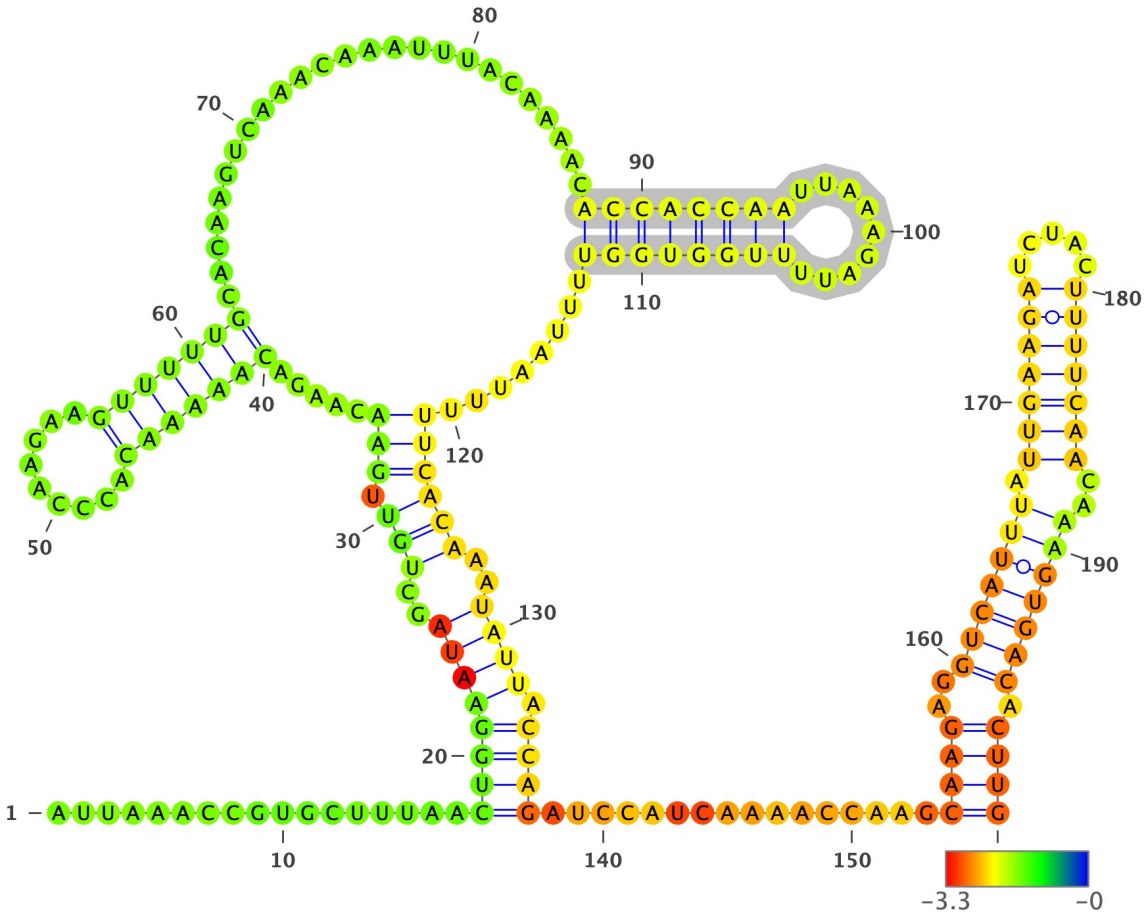
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 402 from nt 23935 to 23959 (nt 88 to 112)

```
5'-ACCACCAATTAAAGATTUUGGUGGU-3'
5'-((((((((.........))))))))-3'
Motif MFE = -10.4; z-score = -5.01; 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 = -2.57; 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(+)

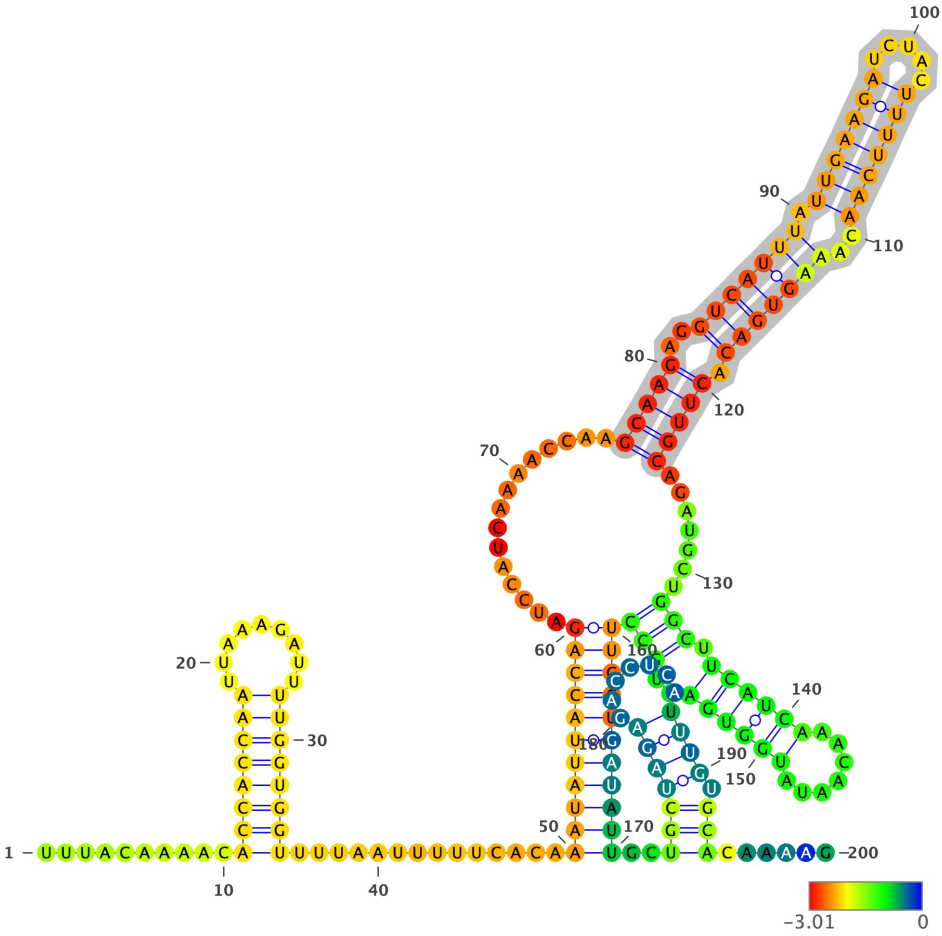
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 403 from nt 24000 to 24048 (nt 76 to 124)

```
5'-GCAAGAGGTCATTTATTGAAGATCTACUUUUCAACAAAGUGACACUUGC-3'
5'-((((((..((((((...(((((((.....)))))))....))))))..))))))-3'
Motif MFE = -16.1; z-score = -4.42; 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 = -3.81; ED = 19.12
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

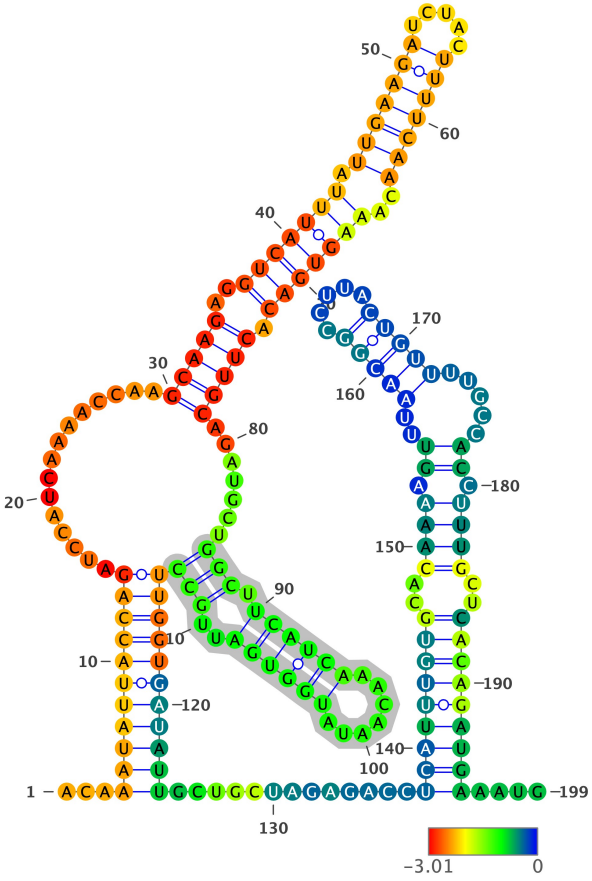
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 404 from nt 24056 to 24083 (nt 86 to 113)

```
5'-GGCTTCATCAAACAATATGGUGATTGCC-3'
5'-(((.(((((.........)))))..)))-3'
Motif MFE = -8.3; z-score = -2.4; ED = 0.42
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 23971 to 24169 (motif highlighted in silver):

```
5'-ACAAAUAUUACCAGAUCCAUCAAAACCAAGCAAGAGGUCAUUUAUUGAAGAUCUACUUUUCAACAAAGUGACACUUGCAGAUGCUGGCUUCAUCAAACAAUAUGGUGAUUG
CCUUGGUGAUAUUGCUGCUAGAGACCUCAUUUGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUG-3
5'-...(((((((((((...............(((((..(((((((.(((((((.....)))))))..)))))))).)))))).......(((.((((((.......))))))..)
))))))))))))).............(((((((((..((((.((..(((((.....)))))).....)).))))..))))))))).....-3'
MFE = -52.1; z-score = -3.2; ED = 12.8
```

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_gp02, 21563-25384(+)

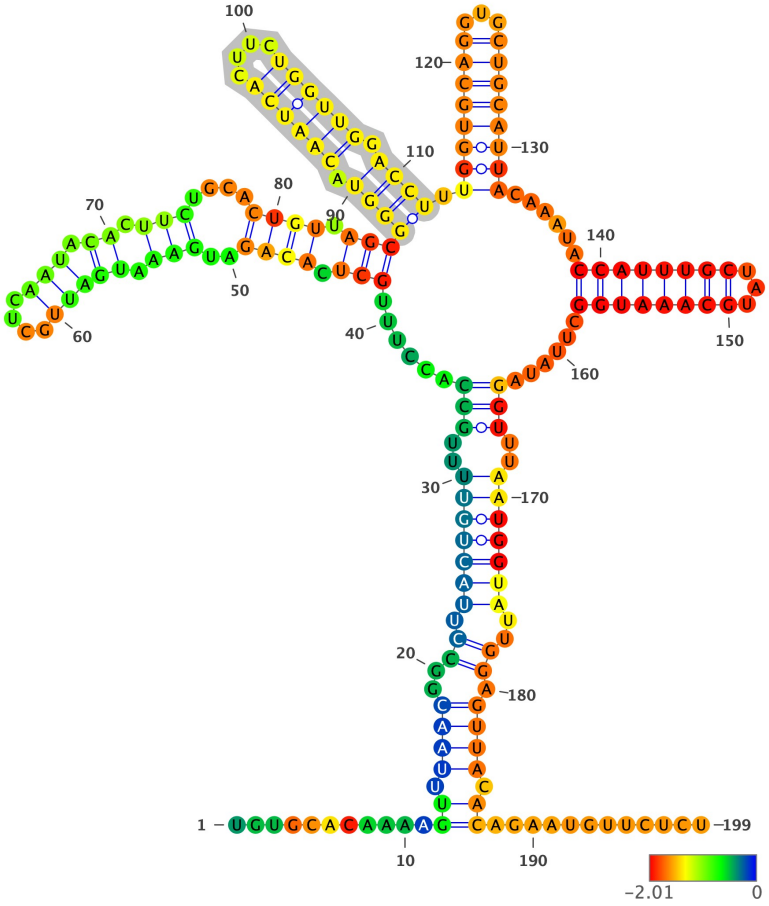
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 405 from nt 24199 to 24224 (nt 87 to 112)

```
5'-GGGTACAATCACTTCUGGUUGGACCU-3'
5'-((((.((((((....)))))).))))-3'
Motif MFE = -8.5; z-score = -2.15; ED = 1.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24113 to 24311 (motif highlighted in silver):

```
5'-UGUGCACAAAAGUUUAACGGCCUUACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACC
UUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCU-3
5'-...........((.((((..((.(((((((..(((......(((.((((..(((.(((((....))).)).)))....)))).)))((((.((((((....)))))).)))
).((((((((...))))))))......((((((((...))))))))......)))..)))))))..)).)))).))............-3'
MFE = -48.1; z-score = -0.98; ED = 36.46
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

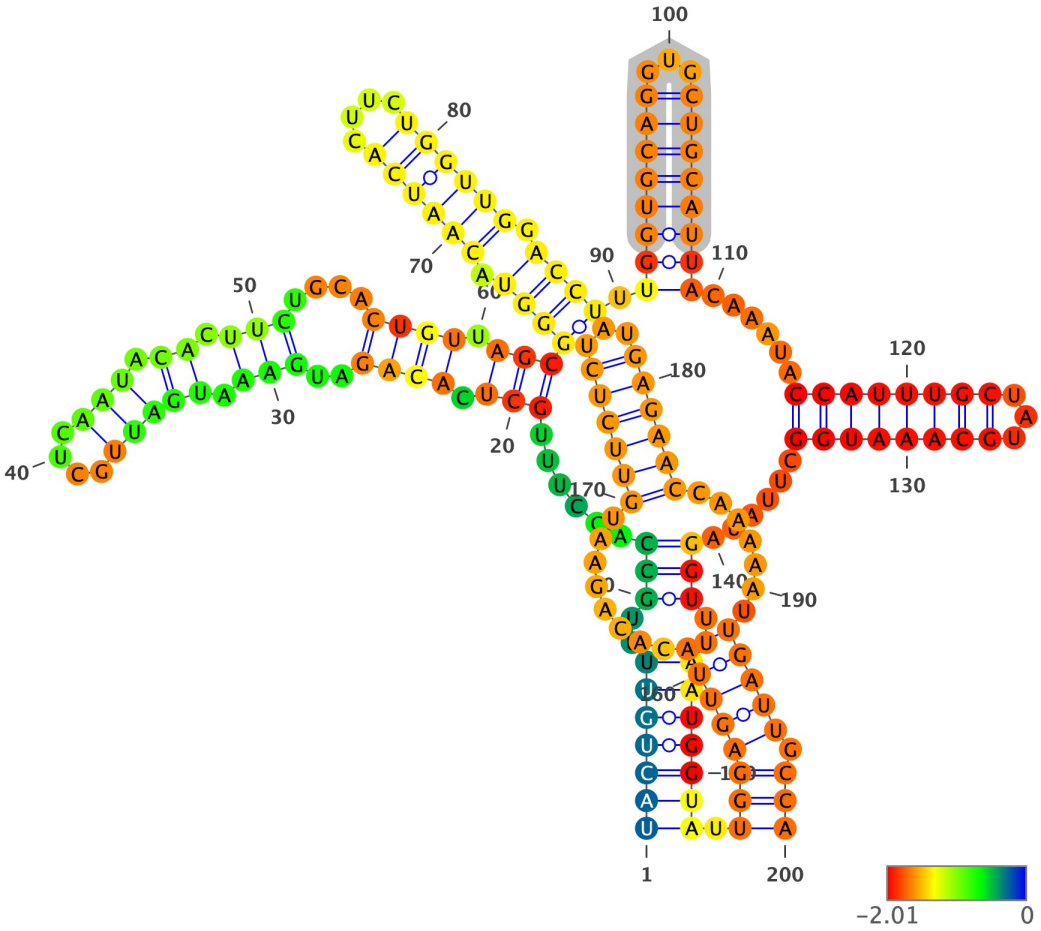
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 406 from nt 24228 to 24242 (nt 93 to 107)

```
5'-GTGCAGGTGCUGCAU-3'
5'-((((((...))))))-3'
Motif MFE = -5.2; z-score = -2.92; 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 24136 to 24335 (motif highlighted in silver):

```
5'-UACUGUUUUGCCACCUUUGCUCACAGAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACA
AAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCA-3
5'-(((((((..(((......(((.((((..(((.(((((....))).)).)))....)))).)))((((.((((((....)))))).)))).((((((((...))))))))..
....((((((((...))))))))......)))..)))))))).((((((((........((((((...))))))).......)))))).)))-3'
MFE = -50.4; z-score = -1.6; ED = 18.07
```

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_gp02, 21563-25384(+)

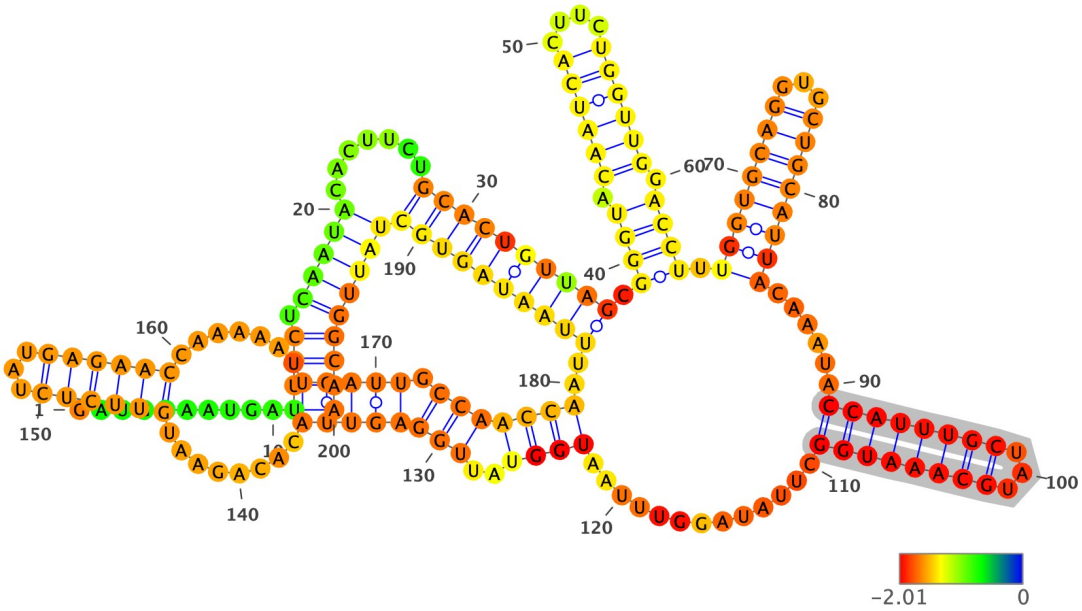
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24251 to 24269 (nt 91 to 109)

```
5'-CCATTTGCTATGCAAAUGG-3'
5'-((((((((...))))))))-3'
Motif MFE = -8.4; z-score = -4.07; ED = 0.14
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24161 to 24360 (motif highlighted in silver):

```
5'-GAUGAAAUGAUUGCUCAAUACACUUCUGCACUGUUAGCGGGUACAAUCACUUCUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCU
UAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAA-3
5'-..........((((.(((((.......((((((((((.((((.((((((....)))))).)))).((((((((...))))))))......((((((((...))))))))..
...........((((..((((((((.........((((((...)))))).......)))))).)))))))..)))))))))))))))))))-3'
MFE = -55.2; z-score = -2.46; 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(+)

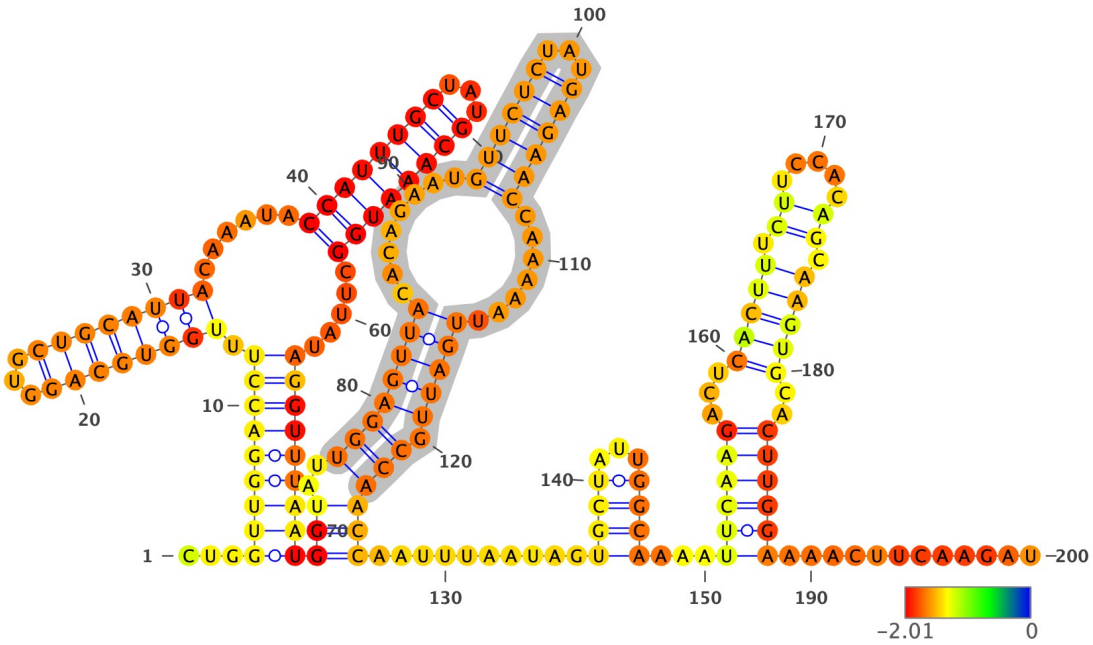
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 408 from nt 24289 to 24335 (nt 77 to 123)

```
5'-TGGAGTTACACAGAATGTTCTCTATGAGAACCAAAAATUGAUUGCCA-3'
5'-(((((((((.......((((((...))))))).......))))).)))-3'
Motif MFE = -8.2; z-score = -1.21; ED = 2.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24213 to 24412 (motif highlighted in silver):

```
5'-CUGGUUGGACCUUUGGUGCAGGUGCUGCAUUACAAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAA
AAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAU-3
5'-...(((((((((.(((((((((...)))))))))......(((((((((...)))))))))).....)))))))))(((..(((((((((.........((((((...)))))))....
...)))))).))))))..........((((...))))...((((((...(((((.((.....)).)))))..))))))............-3'
MFE = -45.4; z-score = -2.5; ED = 37.21
```

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_gp02, 21563-25384(+)

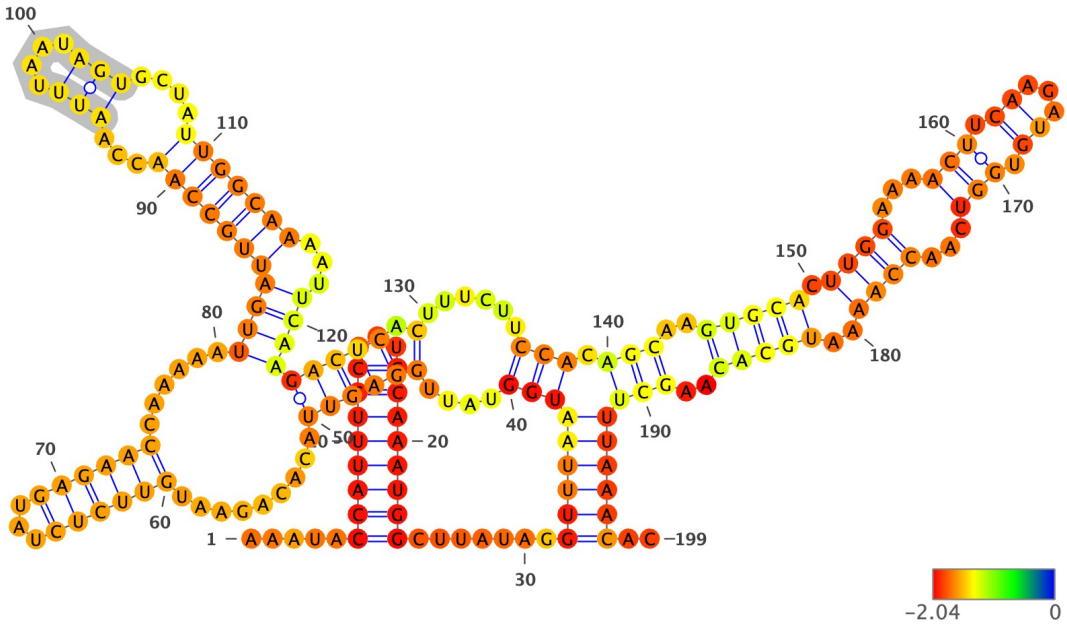
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24340 to 24349 (nt 95 to 104)

```
5'-ATTTAATAGU-3'
5'-(((....)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.05
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24246 to 24444 (motif highlighted in silver):

```
5'-AAAUACCAUUUGCUAUGCAAAUGGCUUAUAGGUUUAAUGGUAUUGGAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUG
GCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACAC-3
5'-.....((((((((...))))))))).......(((((((((....((((((.........((((((...))))))......((((((((((...(((....)))....)))
))))...))))))))).).......))).(((..(((((.((((...(((.((...)).)))...)))))..)))))..))))))))))..-3'
MFE = -42.9; z-score = -2.81; ED = 41.59
```

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_gp02, 21563-25384(+)

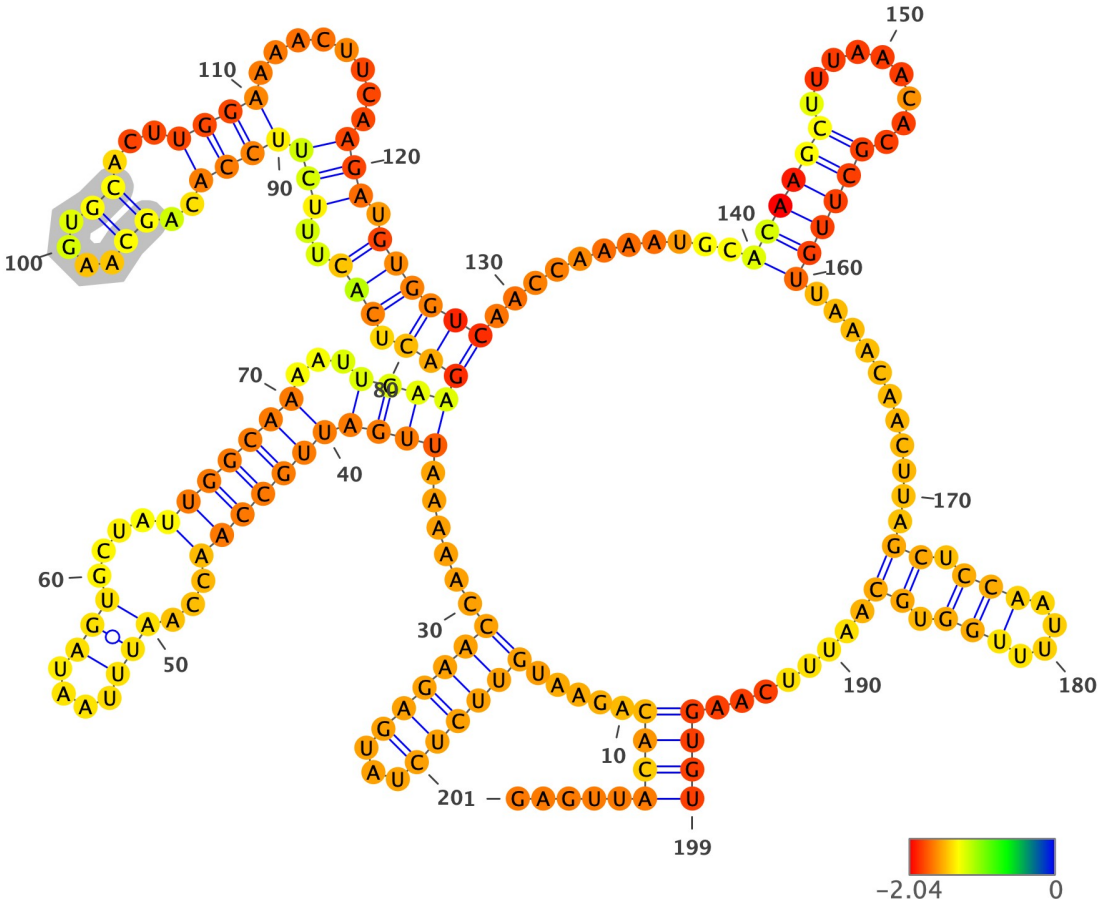
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24386 to 24393 (nt 96 to 103)

```
5'-GCAAGTGC-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.74
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24291 to 24489 (motif highlighted in silver):

```
5'-GAGUUACACAGAAUGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAA
AACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGU-3
5'-.....((((.....((((((...))))))......((((((((((...(((....)))....)))))))...))))))(((.(((..(((((((..((....))...))))).
.......))).))))))..........((((((.........))))))..........((.(((....))).)).........))))-3'
MFE = -39.0; z-score = -2.25; ED = 33.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

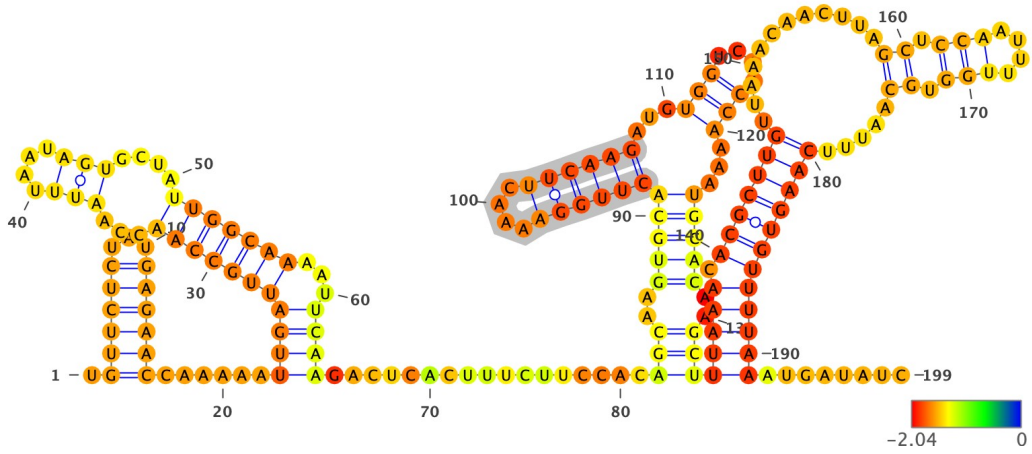
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 411 from nt 24395 to 24410 (nt 92 to 107)

```
5'-CTTGGAAAACTUCAAG-3'
5'-(((((.....)))))-3'
Motif MFE = -2.8; z-score = -6.41; 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 24304 to 24502 (motif highlighted in silver):

```
5'-UGUUCUCUAUGAGAACCAAAAAUUGAUUGCCAACCAAUUUAAUAGUGCUAUUGGCAAAAUUCAAGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGU
GGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUC-3
5'-.((((((...))))))......((((((((((...(((....)))....)))))))...))))..................(((..((((((((((....)))))))...(
((....)))...))))))..)))((((((.(((((((.............((.(((....))))).)).....))))))))))).........-3'
MFE = -37.7; z-score = -1.71; ED = 39.93
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

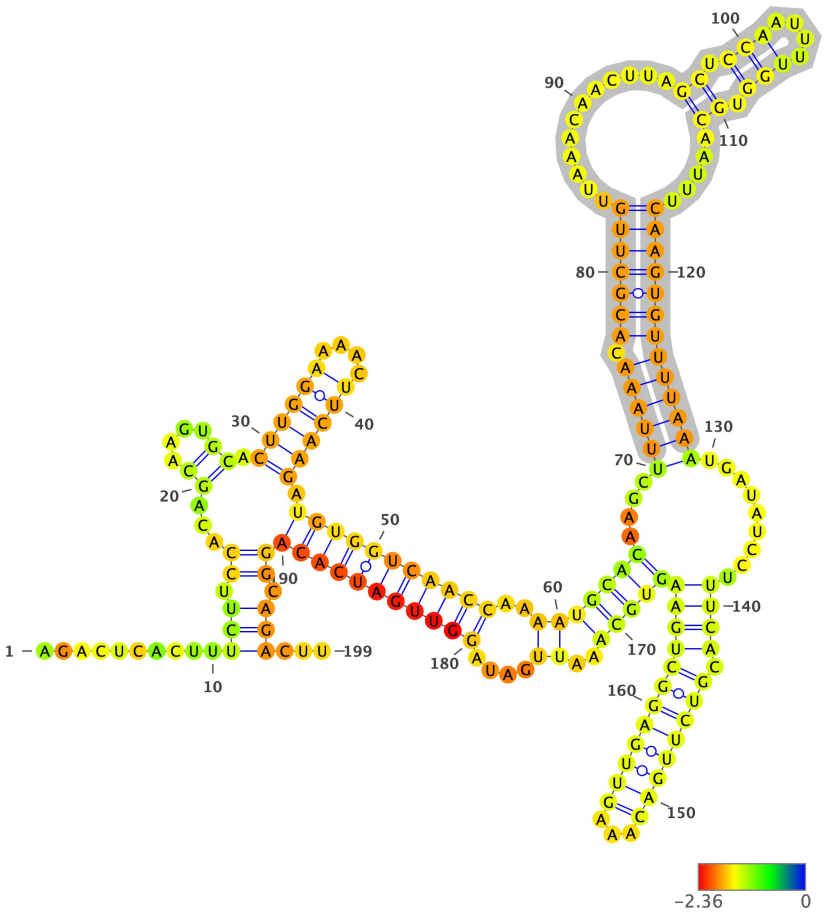
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24437 to 24494 (nt 71 to 128)

```
5'-TTAAACACGCTTGTTAAACAACTTAGCTCCAATTTTGGTGCAATTTCAAGUGUUUUAA-3'
5'-(((((.(((((((.............((.((......)).))).....)))))))))))-3'
Motif MFE = -10.2; z-score = -2.02; ED = 6.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24367 to 24565 (motif highlighted in silver):

```
5'-AGACUCACUUUCUUCCACAGCAAGUGCACUUGGAAAACUUCAAGAUGUGGUCAACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGC
AAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUU-3
5'-..........(((.((...((....)).(((((((....)))))).((((((((((..(((((((....((((((.(((((((.............((.((....)))).)).
.....)))))))))))))).........((((.(((((((((...))))))))))))))))..))....))))))))))))).))...-3'
MFE = -47.9; z-score = -2.36; ED = 18.52
```

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(+)

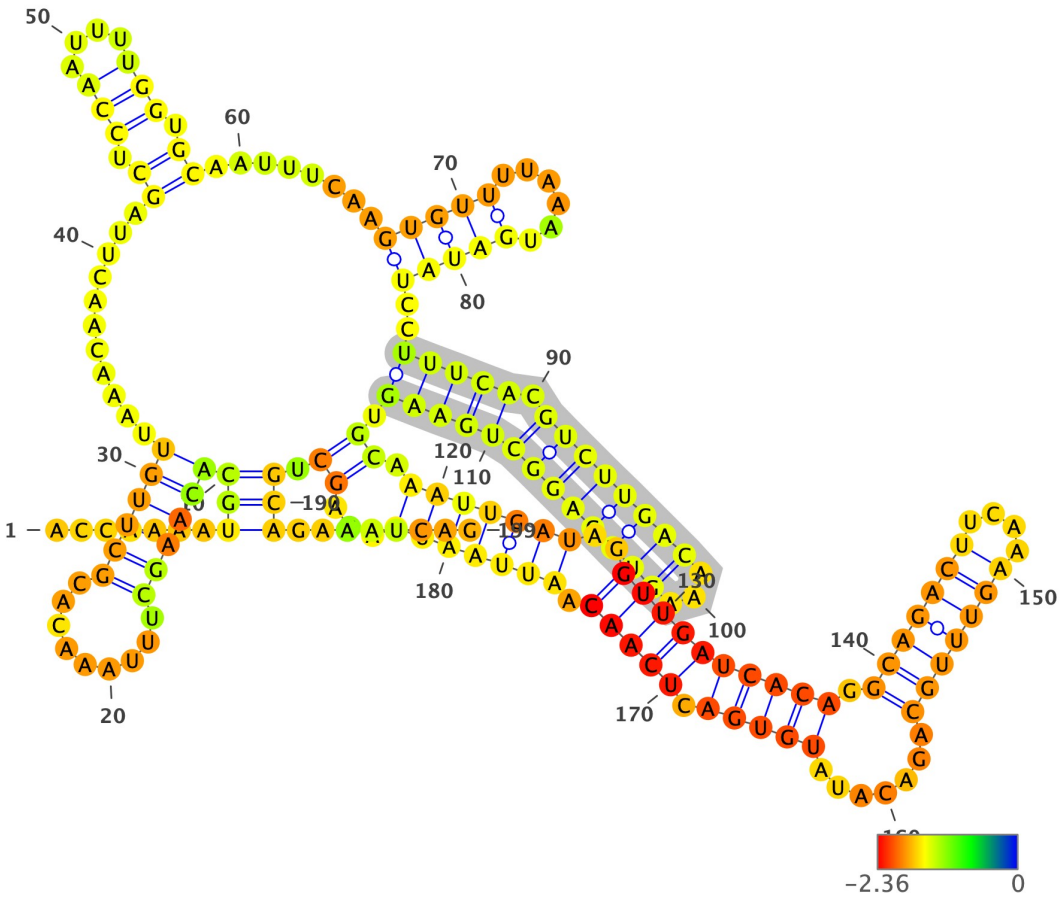
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 413 from nt 24504 to 24533 (nt 85 to 114)

```
5'-TTTCACGTCTTGACAAAGUUGAGGCUGAAG-3'
5'-(((((.(((((((((...))))))))))))))-3'
Motif MFE = -9.4; z-score = -2.93; ED = 0.89
```



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 24420 to 24618 (motif highlighted in silver):

```
5'-ACCAAAAUGCACAAGCUUUAAACACGCUUGUUAAACAACUUAGCUCCAAUUUUGGUGCAAUUUCAAGUGUUUUAAAUGAUAUCCUUUCACGUCUUGACAAAGUUGAGGCUG
AAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAG-3
5'-.......(((((((((.........))))))...........((.(((....))).)).........(((((......)))))..(((((.(((((((((...)))))))))))
))).((.(((((((..((((((((((.(((((((....)))))))).......))))).)))))).)))))))...)).)))........-3'
MFE = -45.1; z-score = -2.13; ED = 27.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

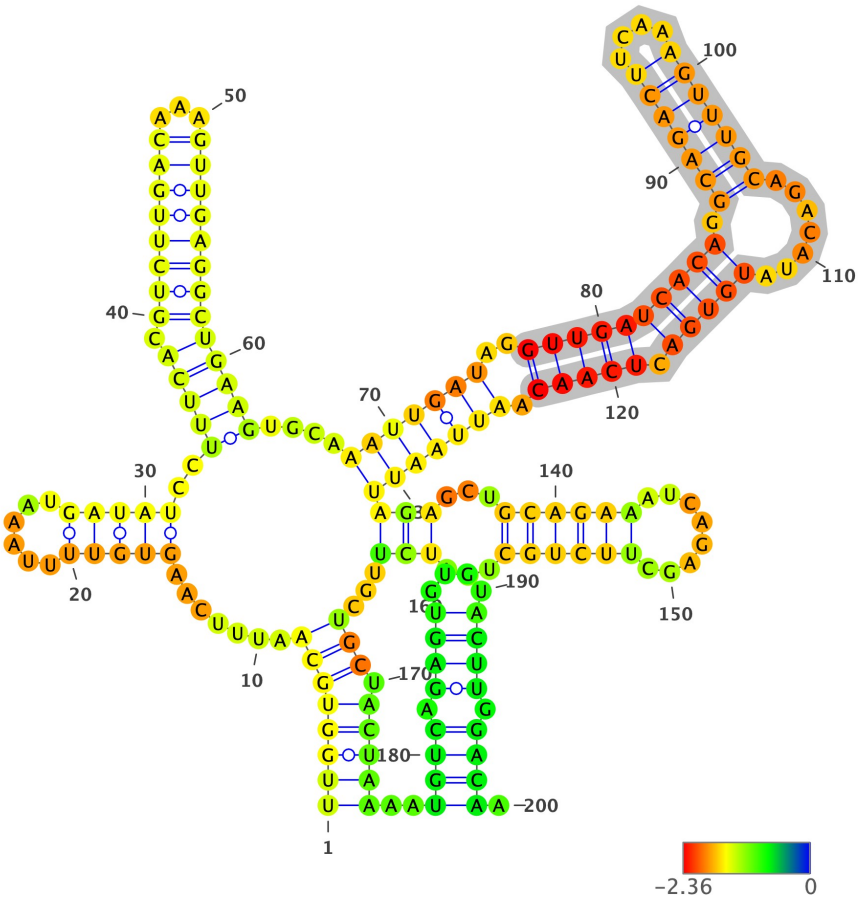
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 414 from nt 24547 to 24593 (nt 77 to 123)

```
5'-GTTGATCACAGGCAGACTTCAAAGUUUGCAGACATAUGUGACUCAAC-3'
5'-((((((((((.((((((......))))))).......))))).)))))-3'
Motif MFE = -14.0; z-score = -2.96; 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 = -2.17; ED = 32.18
```

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_gp02, 21563-25384(+)

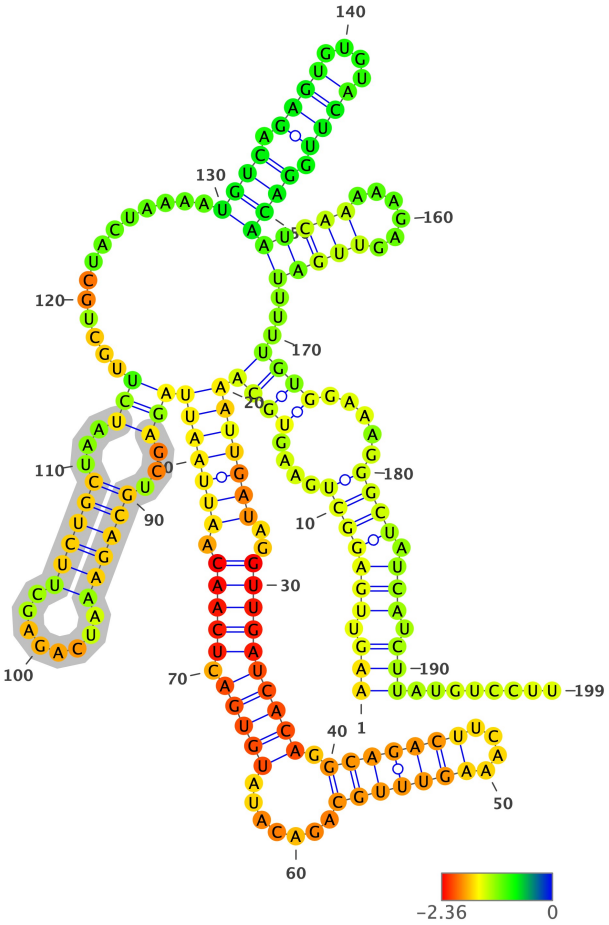
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 415 from nt 24604 to 24631 (nt 86 to 113)

```
5'-AGCTGCAGAAATCAGAGCTUCUGCTAAU-3'
5'-(...(((((..........)))))...)-3'
Motif MFE = -7.1; z-score = -2.51; 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 24519 to 24717 (motif highlighted in silver):

```
5'-AAGUUGAGGCUGAAGUGCAAAUUGAUAGGUUGAUCACAGGCAGACUUCAAAGUUUGCAGACAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUA
AUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU-3
5'-(((.(((((((....((((((((((..((((((((((.(((((((....)))))))).......))))).))))).)))))))(((...((((((........))))))..
.))).............((((.((((....)))).))))(((((......)))))...))))).....)))).))).))).........-3'
MFE = -44.8; z-score = -1.37; ED = 37.92
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

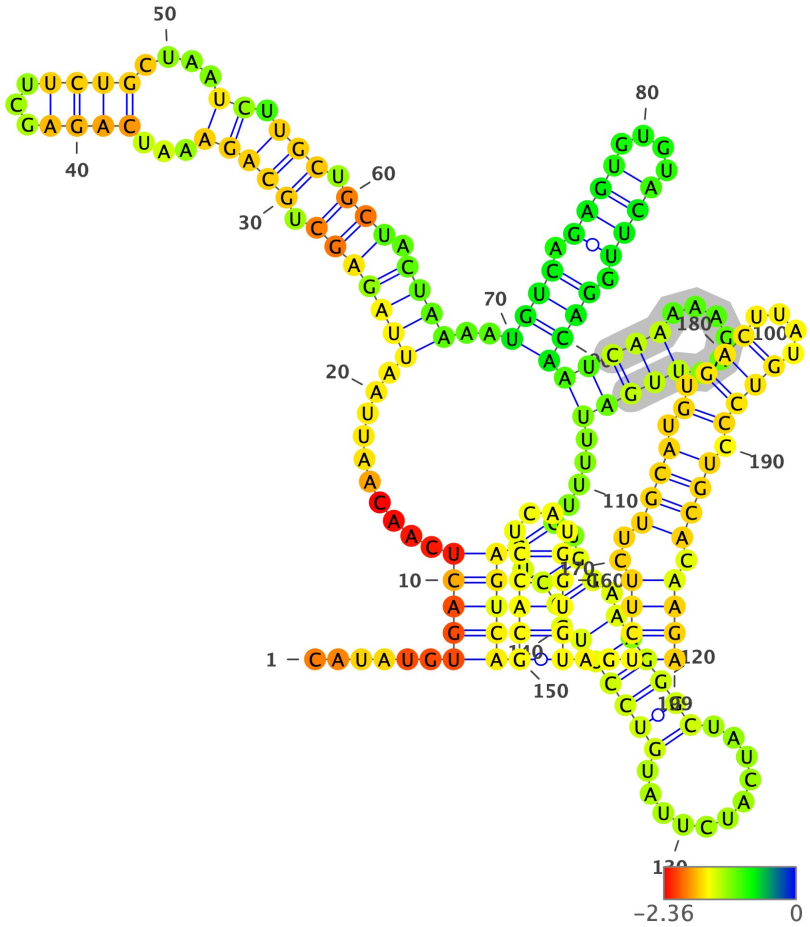
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 416 from nt 24672 to 24683 (nt 94 to 105)

```
5'-CAAAAAGAGUUG-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = 0.1; ED = 0.26
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24579 to 24777 (motif highlighted in silver):

```
5'-CAUAUGUGACUCAACAAUUAAUUAGAGCUGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUU
GUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGA-3
5'-......(((((..........(((((((.(((((...((((...))))....)).))).))).))))..((((.((((....)))).))))(((((......)))))....
(.((.((((((...........)))))).)).))))))(((((....)))))..((((..((((.(.(((....)))).)))).))))-3'
MFE = -48.9; z-score = -1.46; ED = 37.78
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

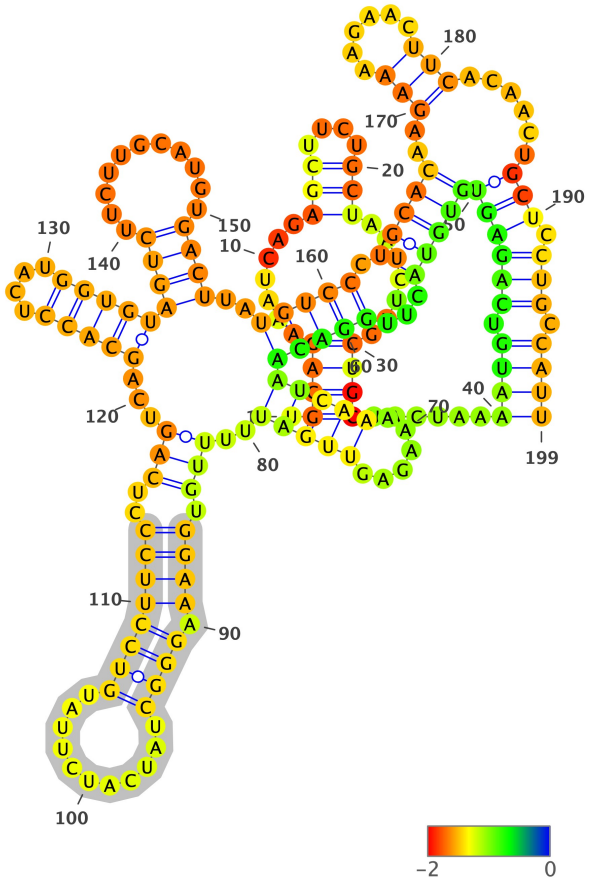
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 417 from nt 24692 to 24719 (nt 86 to 113)

```
5'-GGAAAGGGCTATCATCTTATGUCCUUCC-3'
5'-((((.((((...........))))))))-3'
Motif MFE = -7.7; z-score = -2.22; ED = 3.13
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24607 to 24805 (motif highlighted in silver):

```
5'-UGCAGAAAUCAGAGCUUCUGCUAAUCUUGCUGCUACUAAAAUGUCAGAGUGUGUACUUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUU
CCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCACAAGAAAAGAACUUCACAACUGCUCCUGCCAUU-3
5'-.((((.......(((....)))........))))......((((.(((((((((((...((((((((((......)))))..(((.((((.((((...........))))))
))..)))...(((((....)))))((((...........))))..)))))).)))))..(((......)))......))).))).))))-3'
MFE = -44.9; z-score = -0.89; ED = 53.13
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

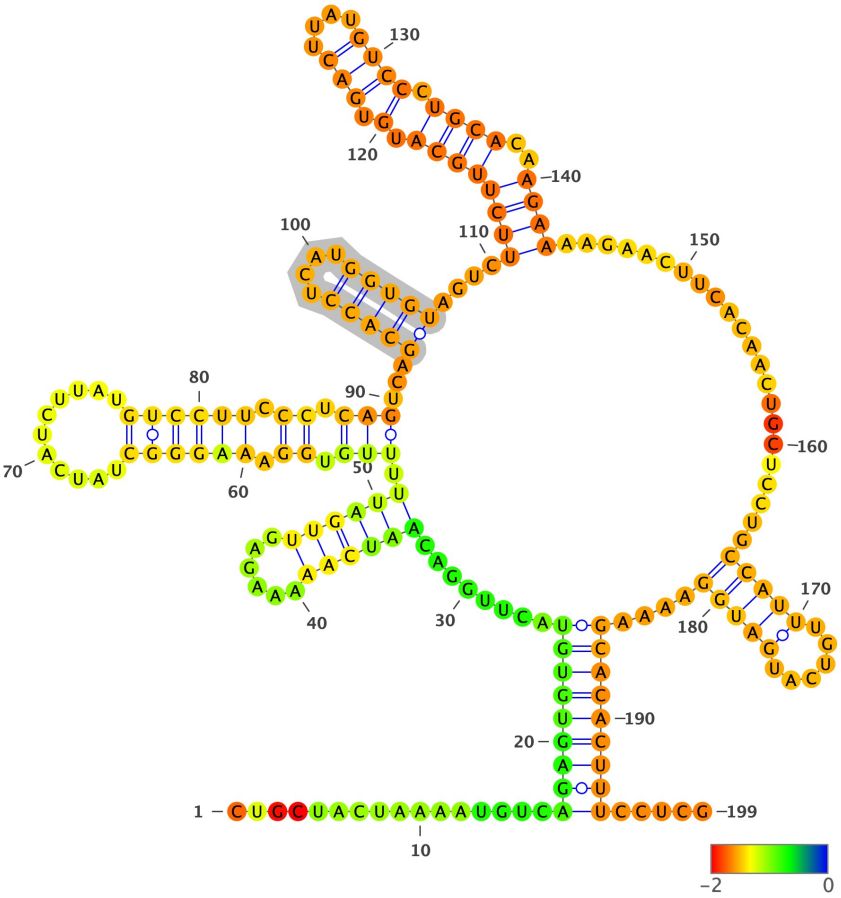
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 418 from nt 24728 to 24741 (nt 93 to 106)

```
5'-GCACCTCATGGUGU-3'
5'-(((((....)))))-3'
Motif MFE = -6.1; z-score = -6.57; 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 = -1.09; 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(+)

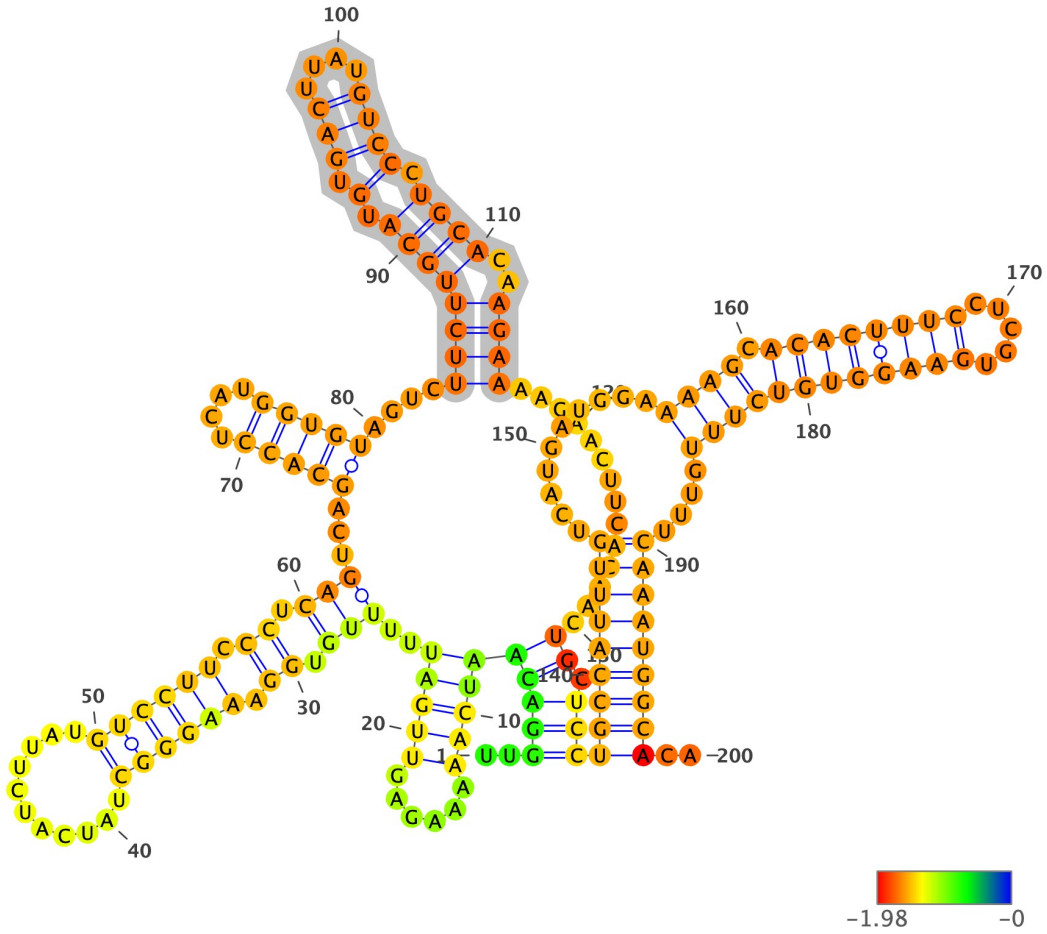
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 419 from nt 24746 to 24778 (nt 84 to 116)

```
5'-TTCTTGCATGTGACTTATGUCCCUGCACAAGAA-3'
5'-((((((((.(.(((....)))).))))..))))-3'
Motif MFE = -8.2; z-score = -2.38; ED = 3.79
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24663 to 24862 (motif highlighted in silver):

```
5'-UUGGACAAUCAAAAAGAGUUGAUUUUUGUGGAAAGGGCUAUCAUCUUAUGUCCUUCCCUCAGUCAGCACCUCAUGGUGUAGUCUUCUUGCAUGUGACUUAUGUCCCUGCAC
AAGAAAAGAACUUCACAACUGCUCCUGCCAUUUGUCAUGAUGGAAAAGCACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACA-3
5'-..(((((((((.....)))))..(((.((.((((((...........))))))).)).)))...(((((....)))))....((((((((.(.(((....)))).)))).
.))))..............)).)))((((((((.........((((.((((((((.....))))))))))))....)))))))))..-3'
MFE = -52.9; z-score = -2.38; ED = 34.44
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

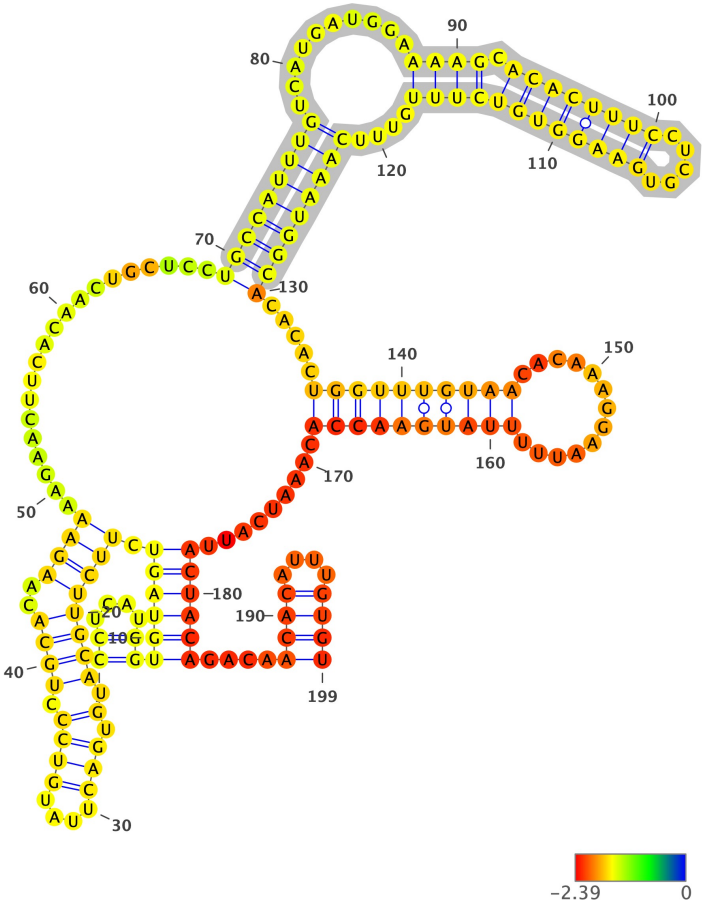
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 420 from nt 24800 to 24859 (nt 70 to 129)

```
5'-GCCATTTGTCATGATGGAAAAGCACACTTTCCTCGTGAAGGUGUCUUUGTTTCAAAUGGC-3'
5'-((((((((..........((((.(((((((.......)))))))))))....))))))))-3'
Motif MFE = -18.9; z-score = -2.78; 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 = -1.97; ED = 32.87
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp02, 21563-25384(+)

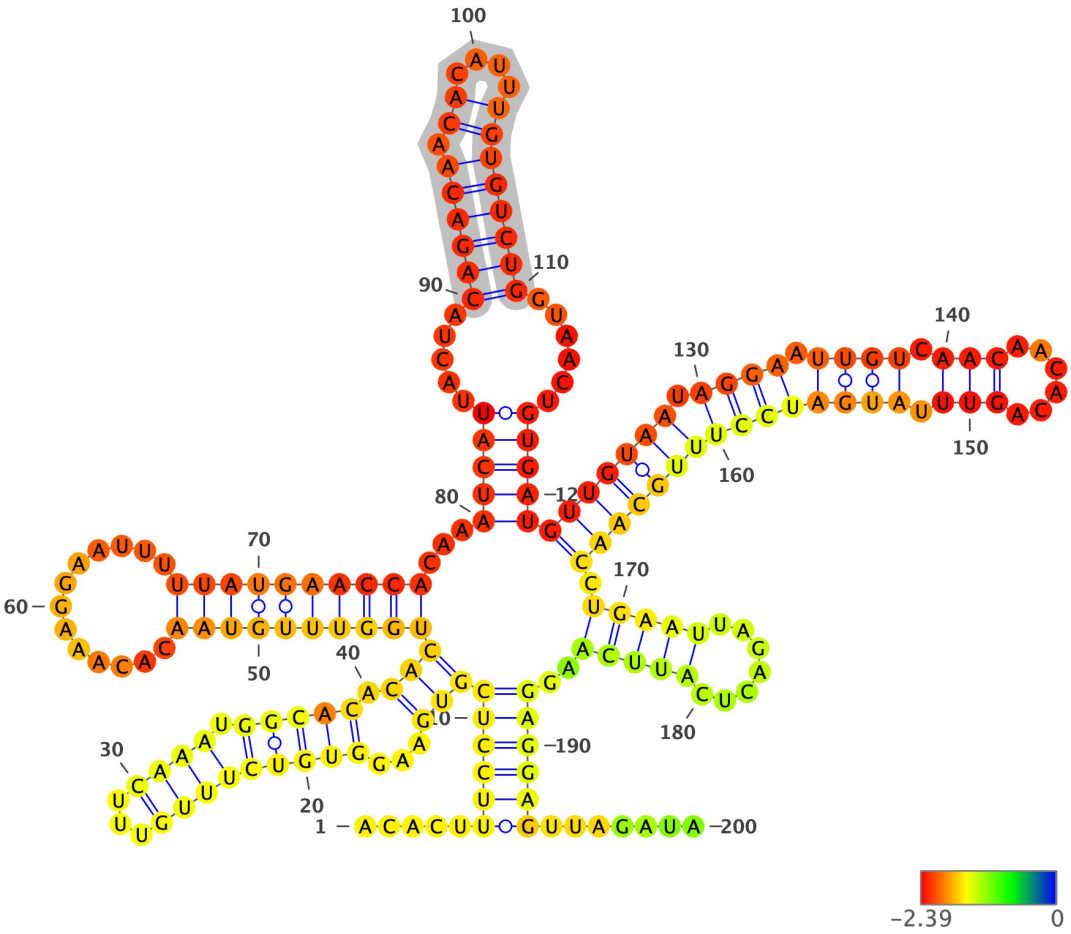
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 421 from nt 24912 to 24932 (nt 90 to 110)

```
5'-CAGACAACACATTTGTGUCUG-3'
5'-(((((...........)))))-3'
Motif MFE = -6.0; z-score = -3.47; ED = 1.82
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24823 to 25022 (motif highlighted in silver):

```
5'-ACACUUUCCUCGUGAAGGUGUCUUUGUUUCAAAUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGG
UAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUA-3
5'-.....(((((((((...((((((((((...)))).))))).)))((((((((((.............)))))))))...(((((.....((((((.((....)))))))).
.....)))))(((((((.((((.((((.(((......))).))))))))))))))).(((((.......)))))..))))))........-3'
MFE = -48.5; z-score = -2.62; ED = 59.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

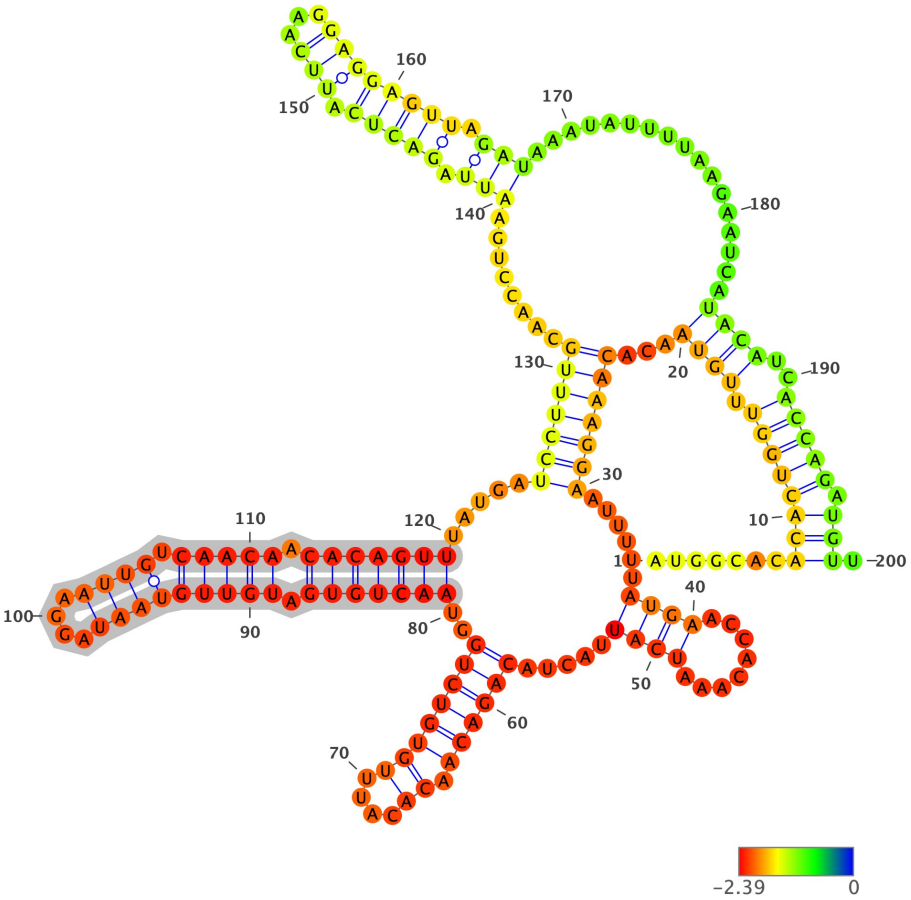
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 24935 to 24973 (nt 81 to 119)

```
5'-AACTGTGATGTTGTAATAGGAATTGTCAACAACACAGUU-3'
5'-(((((((.(((((.............))))).)))))))-3'
Motif MFE = -13.8; z-score = -4.41; ED = 2.1
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24855 to 25054 (motif highlighted in silver):

```
5'-AUGGCACACACUGGUUUGUAACACAAAGGAAUUUUUAUGAACCACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACA
ACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUU-3
5'-.......((((((((.((((...(((((((.......((((........))))).....((((((.((....))))))))..(((((((.((((((((((....)))).)))))
.)))))))).....)))))))........(((.(((((.(((...))))))))).)))................))))..)))))).))).-3'
MFE = -43.4; z-score = -2.22; 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_gp02, 21563-25384(+)

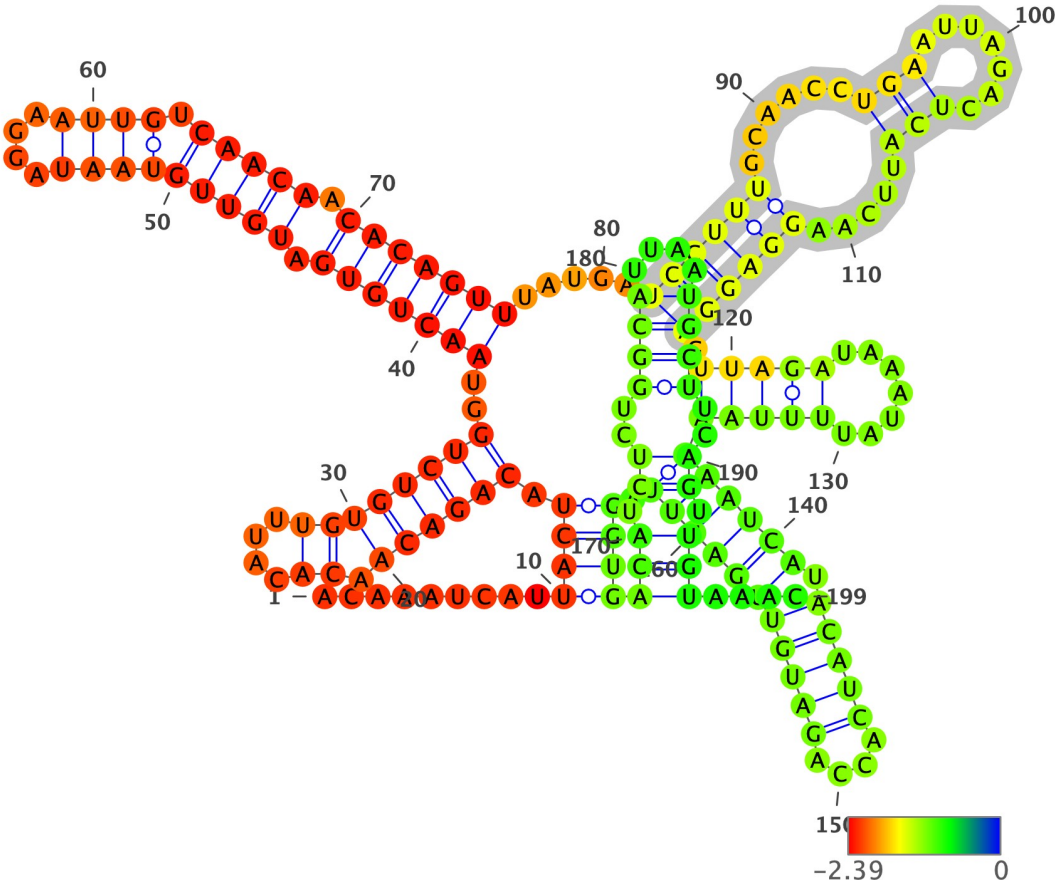
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 423 from nt 24979 to 25014 (nt 82 to 117)

```
5'-TCCTTTGCAACCTGAATTAGACTCATTCAAGGAGGA-3'
5'-((((((.......................))))))-3'
Motif MFE = -4.6; z-score = -0.23; ED = 8.05
```



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 24898 to 25096 (motif highlighted in silver):

```
5'-ACAAAUCAUUACUACAGACAACACAUUUGUGUCUGGUAACUGUGAUGUUGUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAA
GGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAUUUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAAC-3
5'-.........((((.((((((.((....))))))))..(((((((.(((((((((....)))).))))).)))))))).....((((((......(((.......)))).....
)))))).(((((.......)))))((((((.(((((....)))))))))))).))))(((.((..((((....))))..)).)))....-3'
MFE = -43.8; z-score = -2.5; ED = 25.77
```

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_gp02, 21563-25384(+)

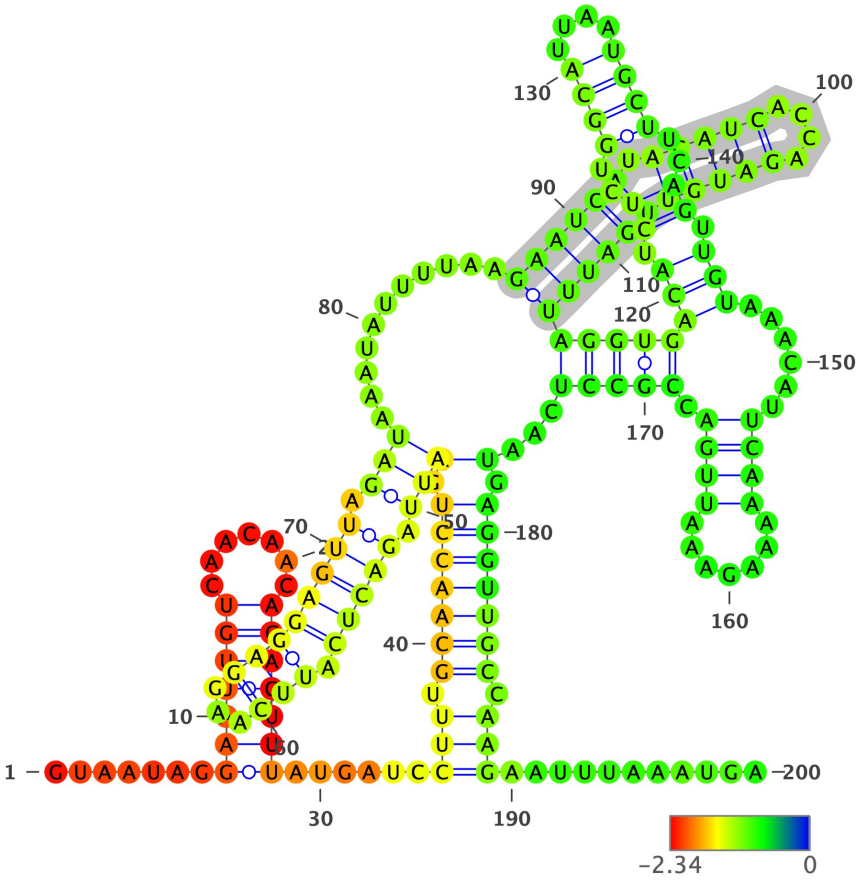
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 199--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 424 from nt 25033 to 25059 (nt 87 to 113)

```
5'-GAATCATACATCACCAGAUGTUGAUUU-3'
5'-((((((..((((....)))).))))))-3'
Motif MFE = -8.1; z-score = -3.84; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 24947 to 25146 (motif highlighted in silver):

```
5'-GUAAUAGGAAUUGUCAACAACACAGUUUAUGAUCCUUUGCAACCUGAAUUAGACUCAUUCAAGGAGGAGUUAGAUAAAUAUUUUAAGAAUCAUACAUCACCAGAUGUUGAU
UUAGGUGACAUCUCUGGCAUUAAUGCUUCAGUUGUAAACAUUCAAAAAGAAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGA-3
5'-.......(((((((.......)))))))......(((.(((((((.((((.(((((.(((...)))))))).))).........((((((.(((((....)))))))))
))((((((((.((..((((....))))..)).))).....((((.......)))).)))))...).)))))))).))).........-3'
MFE = -39.4; z-score = -1.29; ED = 40.83
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

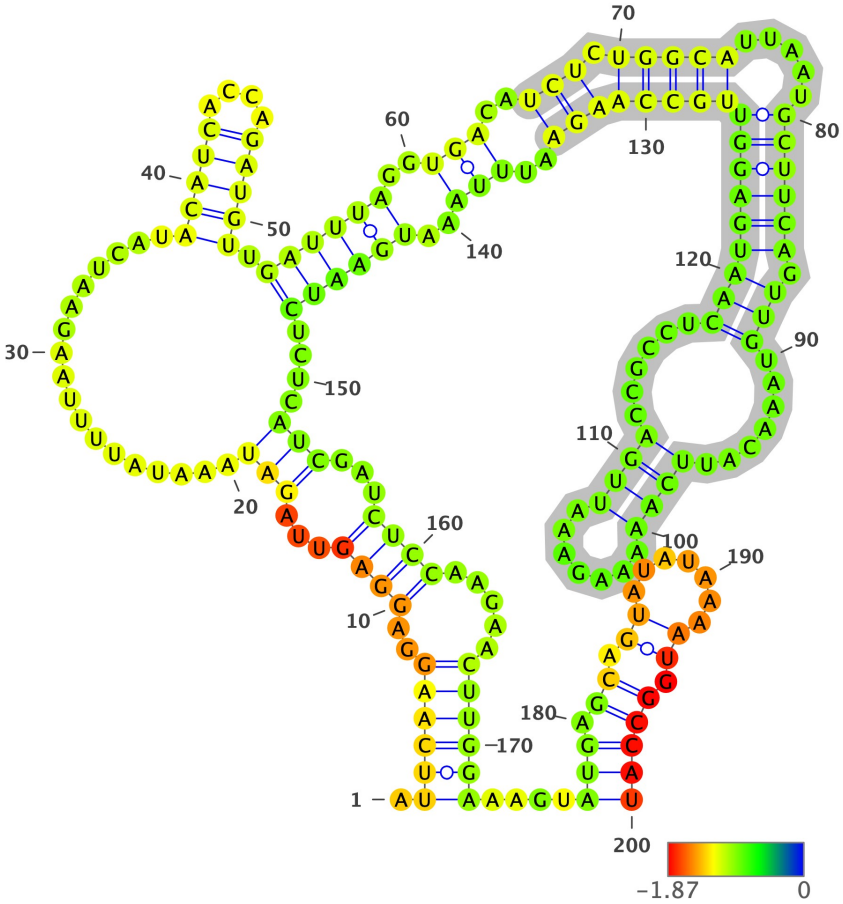
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 425 from nt 25068 to 25136 (nt 66 to 134)

```
5'-TCTCTGGCATTAATGCTTCAGTTGTAAACATTCAAAAAGAAAUUGACCGCCTCAATGAGGUUGCCAAGA-3'
5'-(((.(((((.....................................................))))))))-3'
Motif MFE = -13.2; z-score = -1.31; 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 = -0.12; 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(+)

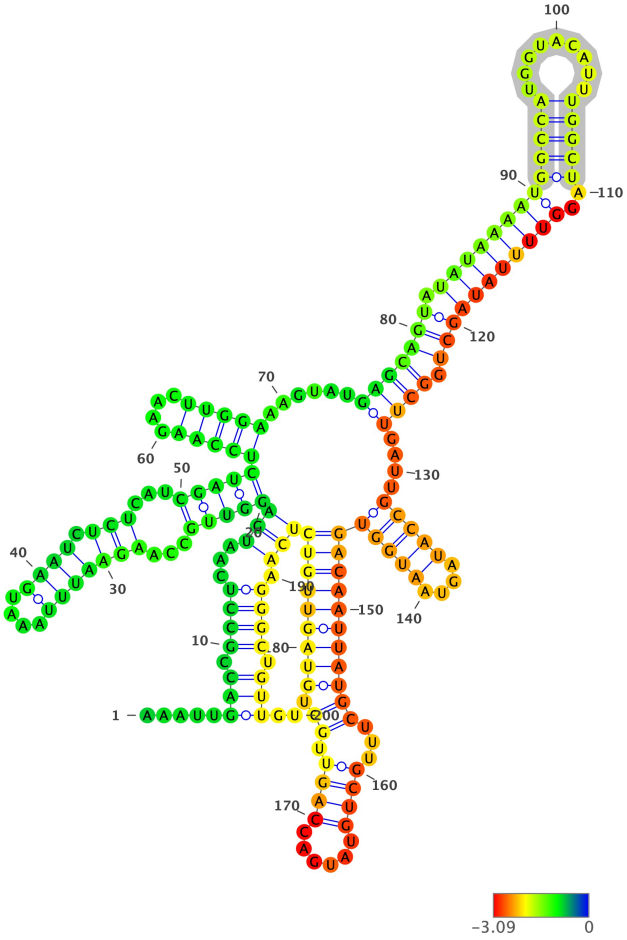
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 426 from nt 25197 to 25215 (nt 91 to 109)

```
5'-GGCCATGGTACATTUGGCU-3'
5'-(((((.........)))))-3'
Motif MFE = -5.2; z-score = -1.97; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25107 to 25306 (motif highlighted in silver):

```
5'-AAAUUGACCGCCUCAAUGAGGUUGCCAAGAAUUUAAAUGAAUCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAG
GUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGU-3
5'-.....(((.((((...((((((((...(((((((....)))).)))...)))))(((((....)))))......(((((((.((((((((((((.........)))))..
)))))))))))).))))....(((((....)))))((((((((((...((((......)))).)).))))))))))))).)))).)))..-3'
MFE = -51.6; z-score = -1.55; ED = 62.32
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp02, 21563-25384(+)

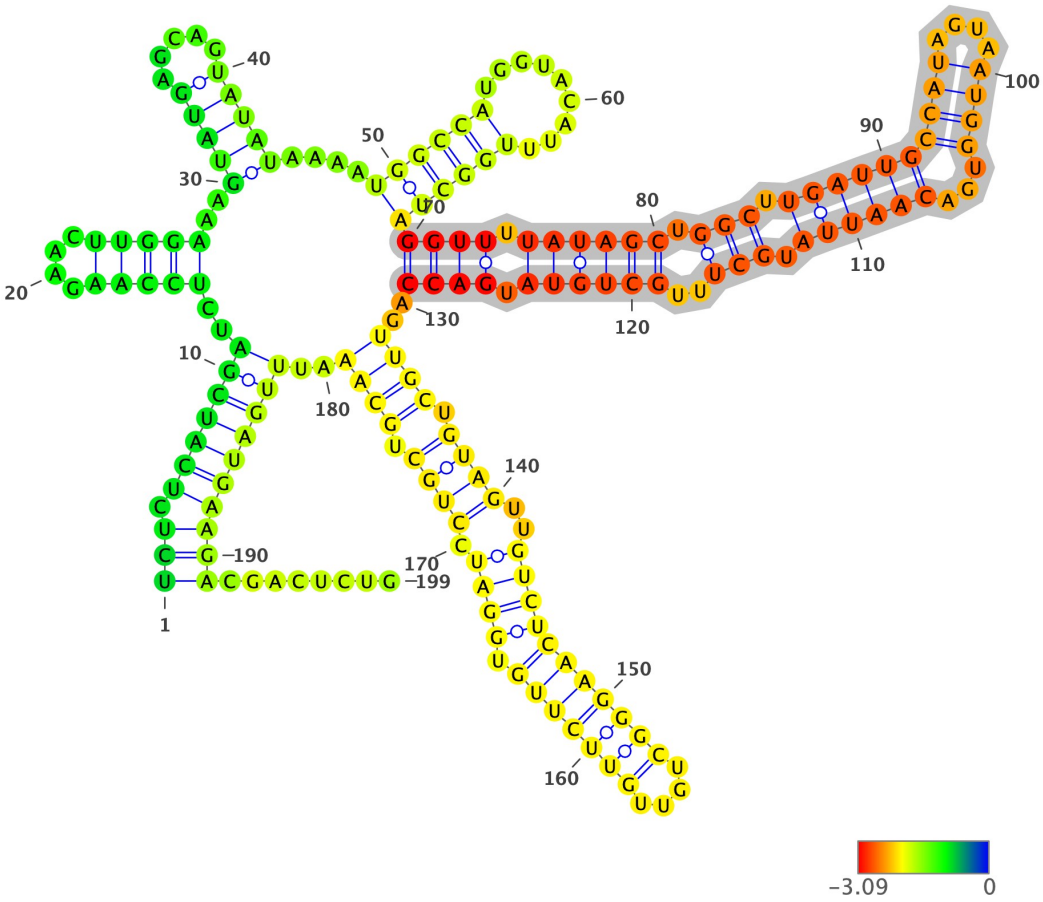
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 200--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

NC_045512.2 (forward strand): Structure number 427 from nt 25217 to 25276 (nt 70 to 129)

```
5'-GGTTTTATAGCTGGCTTGATTGCCATAGTAAUGGTGACAAUUATGCUTTGCUGUATGACC-3'
5'-((((.((((((.(((.((((((((((....))))...)))))).))).)))))).))))-3'
Motif MFE = -21.5; z-score = -3.74; ED = 5.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25148 to 25346 (motif highlighted in silver):

```
5'-UCUCUCAUCGAUCUCCAAGAACUUGGAAAGUAUGAGCAGUAUAUAAAAUGGCCAUGGUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUU
AUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUG-3
5'-(((.(((((((..(((((....))))).(((((.....))))).....((((((.........))))))((((.((((((.(((.((((((((((....))))...)))))
).)))..)))))).)))).((((.((((..((((((((((((....)))))))).)))).)))).)))).))))))))))........-3'
MFE = -61.3; z-score = -2.94; 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(+)

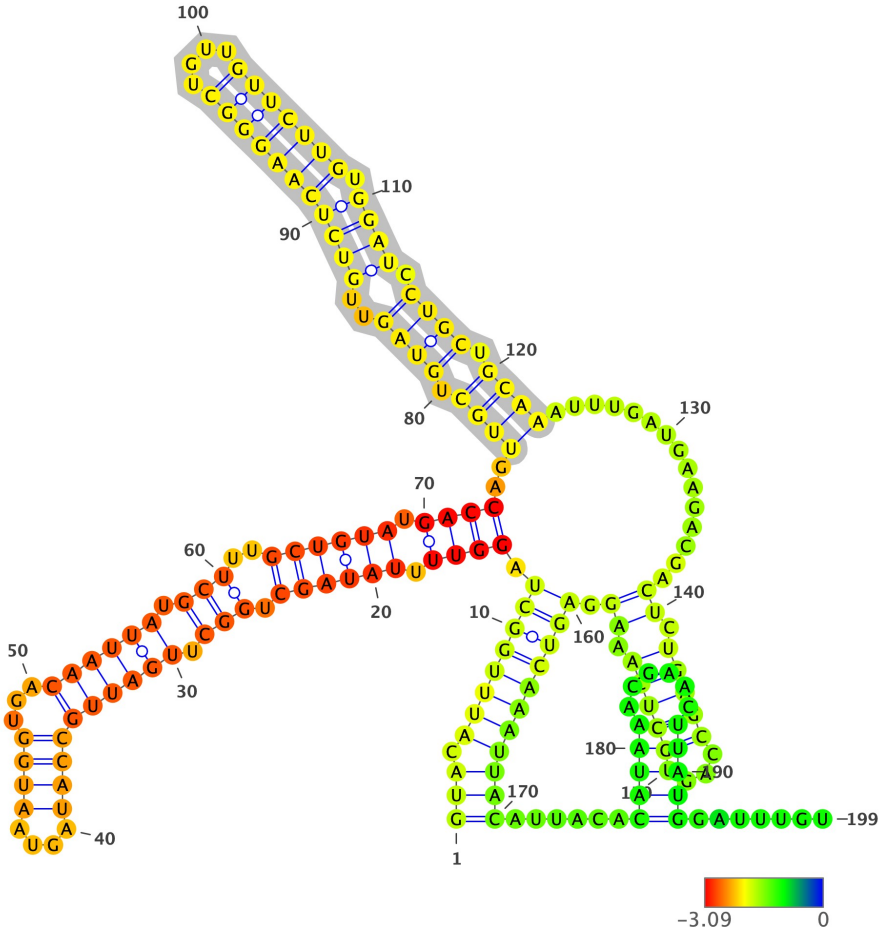
Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

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 428 from nt 25279 to 25326 (nt 76 to 123)

```
5'-TTGCTGTAGTTGTCTCAAGGGCTGTTGUUCUUGTGGAUCCUGCTGCAA-3'
5'-((((.((((..(((((((((((....)))))))).)))).)))).))))-3'
Motif MFE = -17.9; z-score = -3.19; ED = 4.27
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25204 to 25402 (motif highlighted in silver):

```
5'-GUACAUUUGGCUAGGUUUUAUAGCUGGCUUGAUUGCCAUAGUAAUGGUGACAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGG
AUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGU-3
5'-(((.((((((((.((((.((((((.(((.(((((((((((....))))...))))))).)))..))))))).))))..((((.((((..(((((((((((....)))))))).))
)).)))).))))...............((.(((((....))))).)).))))))))))).....(((((......)))))........-3'
MFE = -59.0; z-score = -2.71; ED = 26.86
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 181--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 181--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 190 to 199--gene, gene-GU280_gp03, 25393-26220(+)

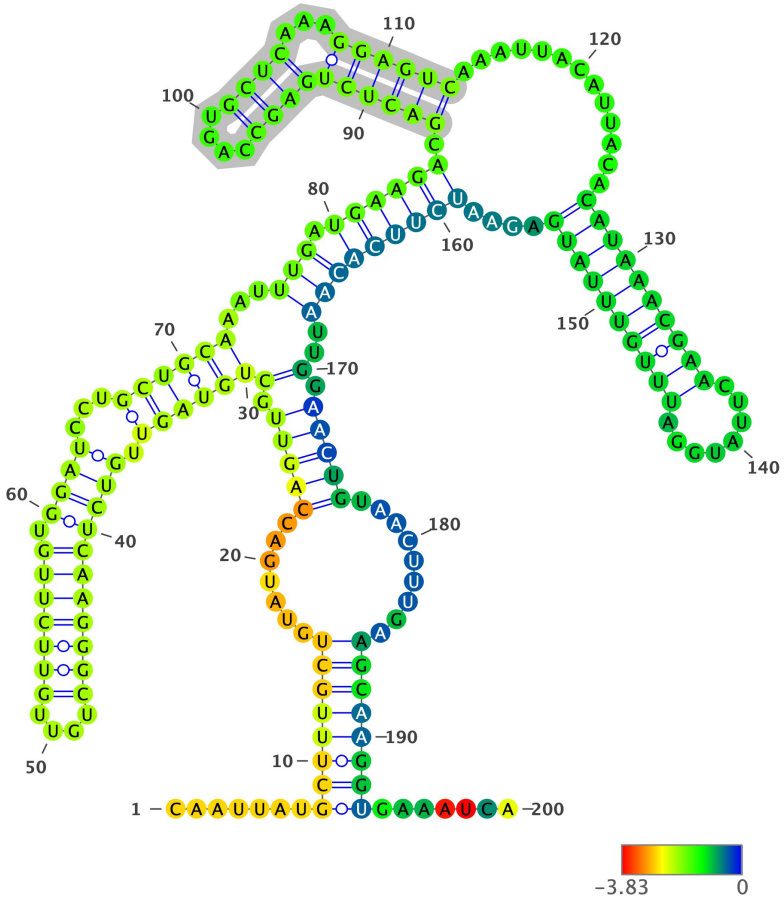
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 190 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 429 from nt 25340 to 25366 (nt 87 to 113)

```
5'-GACTCTGAGCCAGTGCUCAAAGGAGUC-3'
5'-((((((((((....))))...)))))))-3'
Motif MFE = -10.6; z-score = -3.0; ED = 1.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25254 to 25453 (motif highlighted in silver):

```
5'-CAAUUAUGCUUUGCUGUAUGACCAGUUGCUGUAGUUGUCUCAAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAG
UCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUAUGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCA-3
5'-.......(((((((((.......(((((.(((((((.((((((((((....)))))))..)))))...)))))))...(((.((((((.((((((((((....)))))...))))
)).............((((((((((........))))))))))....))))))))..).)))))........)))))))).......-3'
MFE = -55.1; z-score = -2.74; ED = 19.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 131--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 131--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 140 to 200--gene, gene-GU280_gp03, 25393-26220(+)

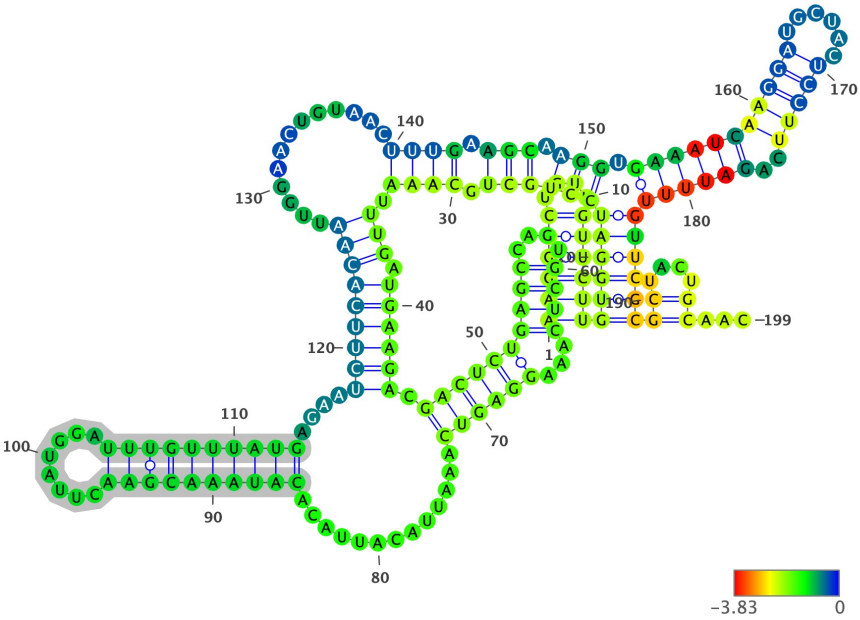
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

5-- nt 140 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 430 from nt 25380 to 25407 (nt 86 to 113)

```
5'-CATAAACGAACTTATGGAUUUGUUUAUG-3'
5'-((((((((((........))))))))))-3'
Motif MFE = -6.7; z-score = -2.67; ED = 1.52
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25295 to 25493 (motif highlighted in silver):

```
5'-AAGGGCUGUUGUUCUUGUGGAUCCUGCUGCAAAUUUGAUGAAGACGACUCUGAGCCAGUGCUCAAAGGAGUCAAAUUACAUUACACAUAAACGAACUUAUGGAUUUGUUUA
UGAGAAUCUUCACAAUUGGAACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAAC-3
5'-((((((....))))))((((((((((((.((((.(((.((((((.((((((((((....)))))...))))))).............((((((((((........))))))))))
))....))))))))).............))))).))).))).(((((((((((.....))))))..)))))))))))((....))...-3'
MFE = -45.8; z-score = -0.67; ED = 48.79
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 90--gene, gene-GU280_gp02, 21563-25384(+)

Attributes: ['ID=gene-GU280_gp02', 'Dbxref=GeneID:43740568', 'Name=S', 'gbkey=Gene', 'gene=S', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp02']

3-- nt 1 to 90--CDS, cds-YP_009724390.1, 21563-25384(+)

Attributes: ['ID=cds-YP_009724390.1', 'Parent=gene-GU280_gp02', 'Dbxref=Genbank:YP_009724390.1,GeneID:43740568', 'Name=YP_009724390.1', 'Note=structural protein%3B spike protein', 'gbkey=CDS', 'gene=S', 'locus_tag=GU280_gp02', 'product=surface glycoprotein', 'protein_id=YP_009724390.1']

4-- nt 99 to 199--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

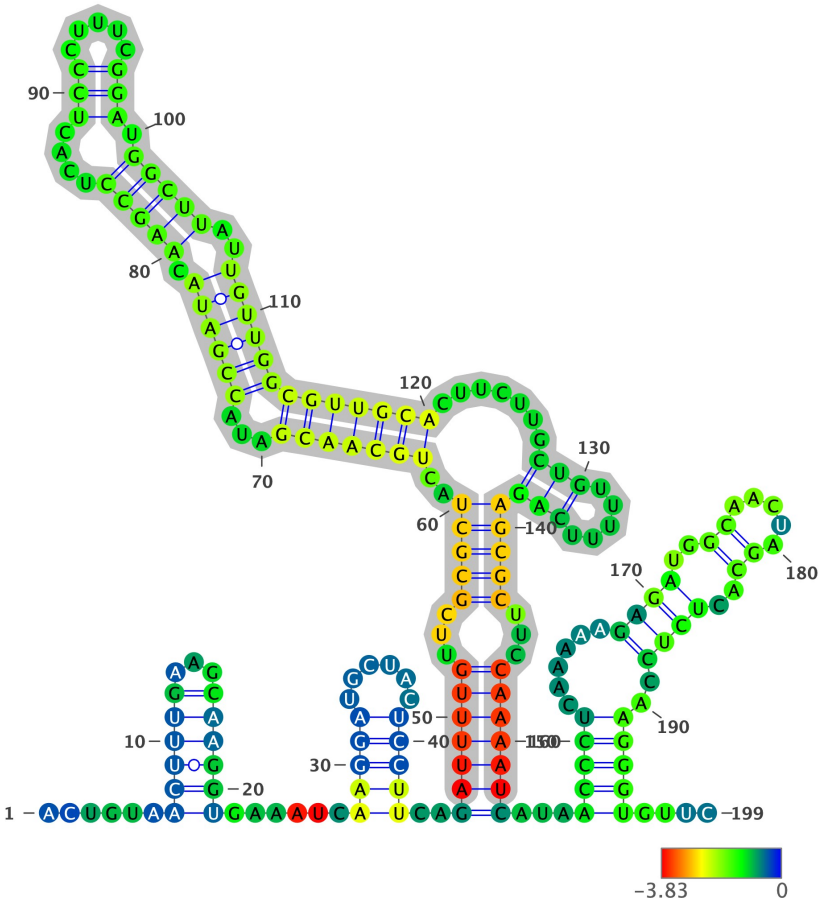
5-- nt 99 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 431 from nt 25472 to 25577 (nt 47 to 152)

```
5'-ATTTTGTTCGCGCTACTGCAACGATACCGATACAAGCCTCACTCCCTTTCGGATGGCUUATUGUUGGCGUUGCACTTCTTGCTGTTTTTCAGAGCGCTTCCAAAAU-3'

5'-((((((...(((((..(((((((...((((((.(((((....(((.....))).)))))..))))))))))))).................)))))...))))))-3'
Motif MFE = -31.2; z-score = -3.49; ED = 7.16
```



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 25426 to 25624 (motif highlighted in silver):

```
5'-ACUGUAACUUUGAAGCAAGGUGAAAUCAAGGAUGCUACUCCUUCAGAUUUUGUUCGCGCUACUGCAACGAUACCGAUACAAGCCUCACUCCCUUUCGGAUGGCUUAUUGUU
GGCGUUGCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUC-3
5'-......((((((...))))))......(((((......)))))..(((((((...(((((..(((((((...((((((.(((((....(((.....))).)))))..))))
))))))))).......(((.....))))))))...)))))))...(((((......((((..((.....))..))))..)))))....-3'
MFE = -53.2; z-score = -2.37; ED = 26.05
```

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_gp03, 25393-26220(+)

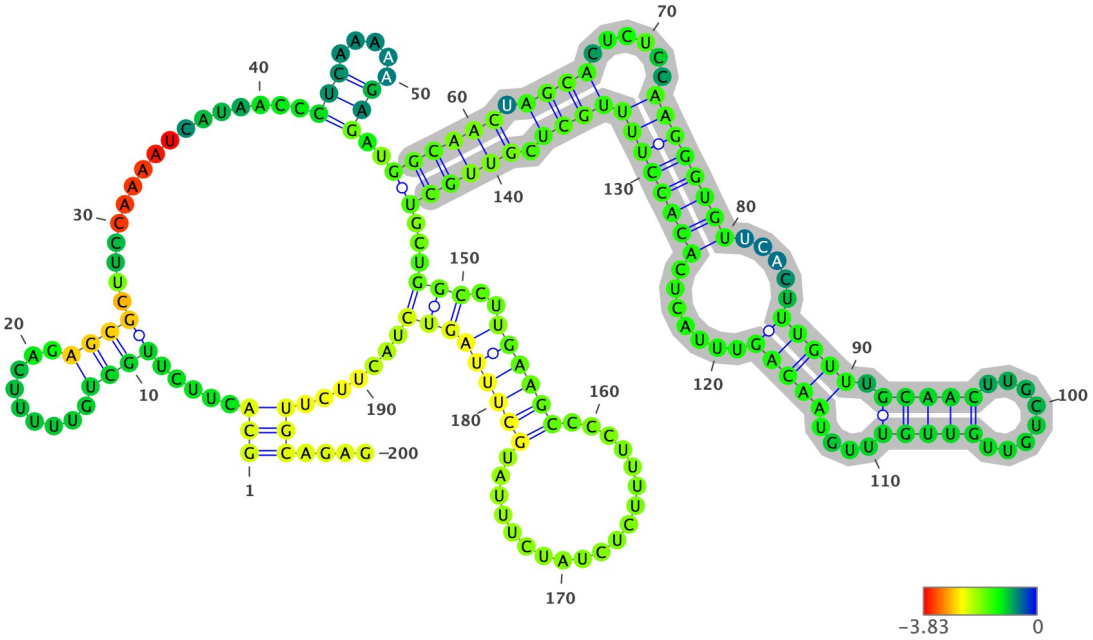
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 25599 to 25685 (nt 57 to 143)

```
5'-GCAACTAGCACTCTCCAAGGGTGTTCACTTTGTTTGCAACTTGCTGTTGUUGUTTGTAACAGTTTACTCACACCTTTTGCTCGTTGC-3'
5'-((.....((..........(.(((.....(((((.(((((........)))))....)))))).......))).)....)).....))-3'
Motif MFE = -23.2; z-score = -2.97; ED = 11.11
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25543 to 25742 (motif highlighted in silver):

```
5'-GCACUUCUUGCUGUUUUUCAGAGCGCUUCCAAAAUCAUAACCCUCAAAAAGAGAUGGCAACUAGCACUCUCCAAGGGUGUUCACUUUGUUUGCAACUUGCUGUUGUUGUUU
GUAACAGUUUACUCACACCUUUUGCUCGUUGCUGCUGGCCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAG-3
5'-(((.....((((.........))))..................(((.....)))..((((((.((((......((((((((.....(((((.(((((........)))))..
..)))))).......))))))))))))).))))))...(((..((((((...................))))))))).......))).....-3'
MFE = -36.4; z-score = 0.36; ED = 33.67
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

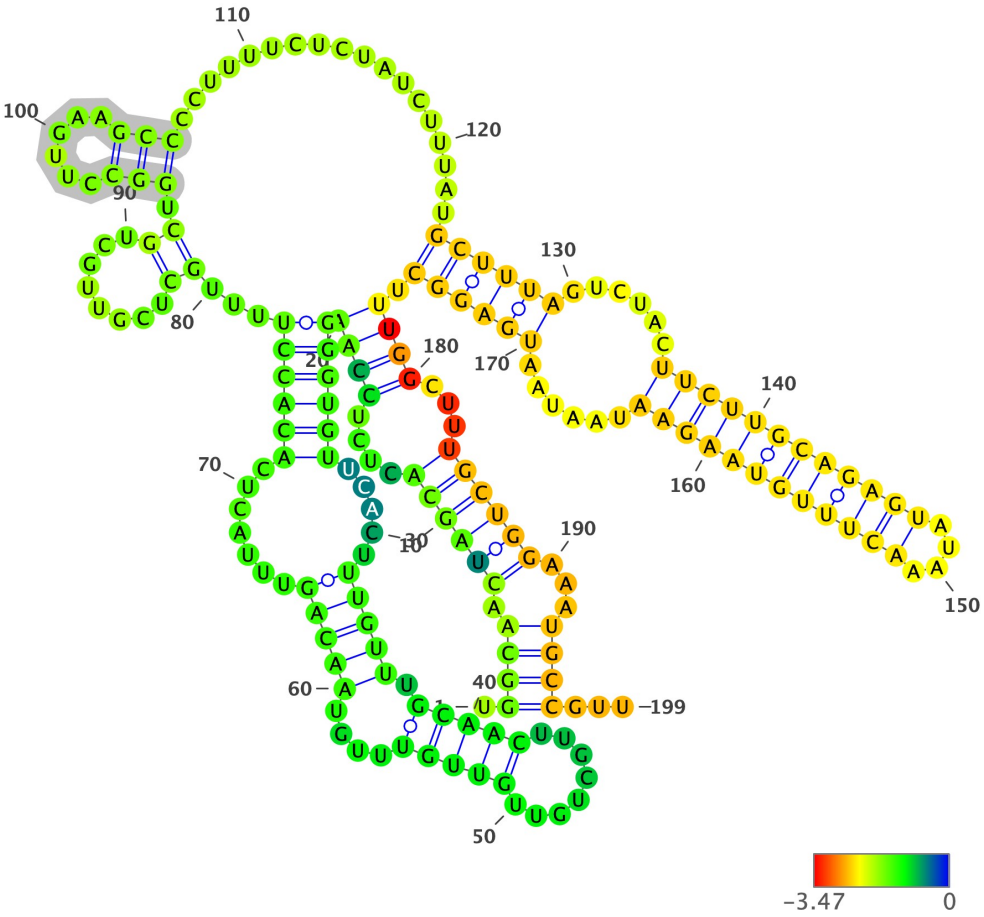
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 433 from nt 25690 to 25701 (nt 94 to 105)

```
5'-GGCCTTGAAGCC-3'
5'-(((......)))-3'
Motif MFE = -2.3; z-score = -2.01; 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 = -3.18; 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(+)

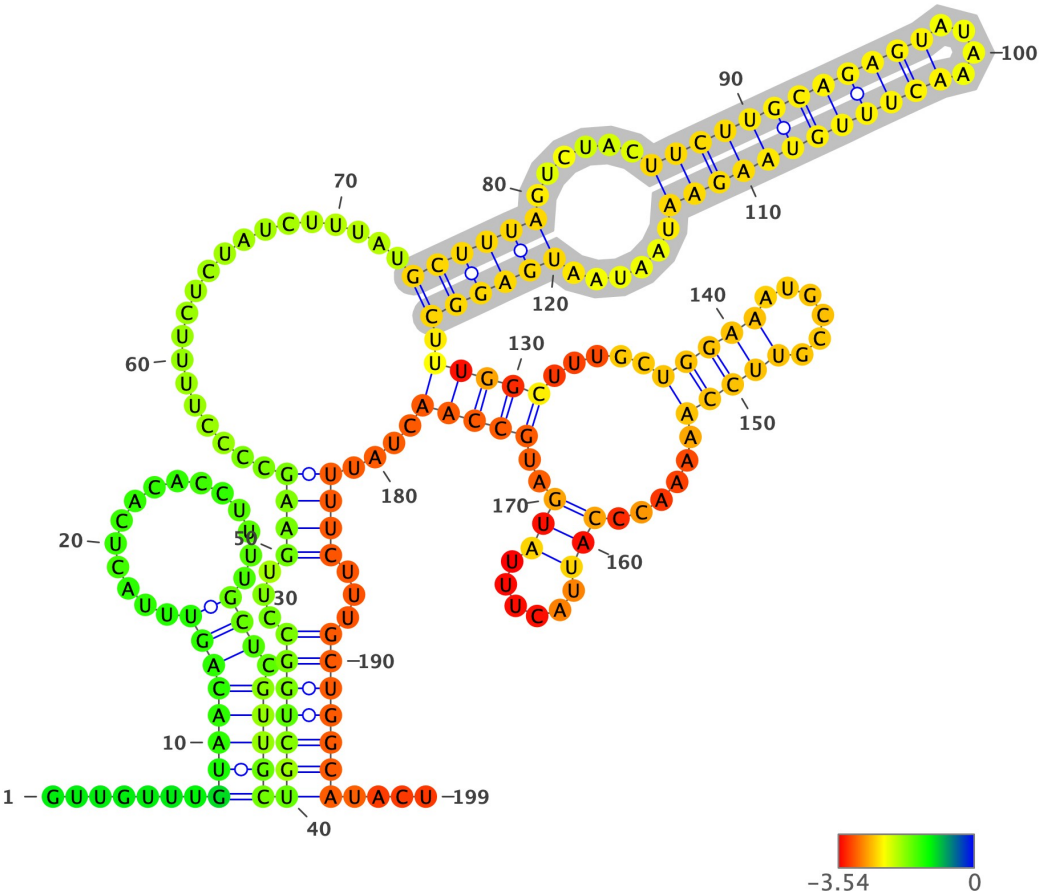
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 434 from nt 25720 to 25771 (nt 74 to 125)

```
5'-GCTTTAGTCTACTTCTTGCAGAGTATAAACUUUGUAAGAATAATAAUGAGGC-3'
5'-((((((......((((((((((((....))))))))))))......))))))-3'
Motif MFE = -18.3; z-score = -4.21; 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 = -1.7; ED = 39.26
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

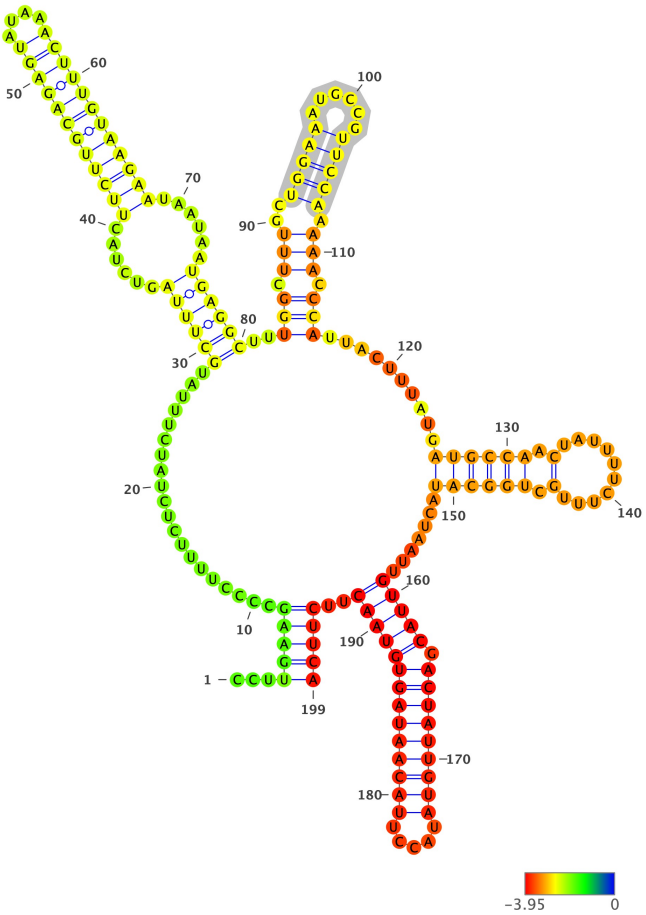
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 435 from nt 25783 to 25798 (nt 92 to 107)

```
5'-TGGAAATGCCGUUCCA-3'
5'-(((((......)))))-3'
Motif MFE = -3.1; z-score = -1.95; ED = 1.07
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25692 to 25890 (motif highlighted in silver):

```
5'-CCUUGAAGCCCCUUUUCUCUAUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAA
CCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCA-3
5'-...(((((.....................((((((......(((((((((((((....)))))))))))))).....))))))..(((.(((..(((((......)))))).)))
.)))..........((((((.(..........).))))))).......(((((.(((((((((.....)))))))))))))))..)))))-3'
MFE = -51.5; z-score = -4.95; ED = 15.64
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

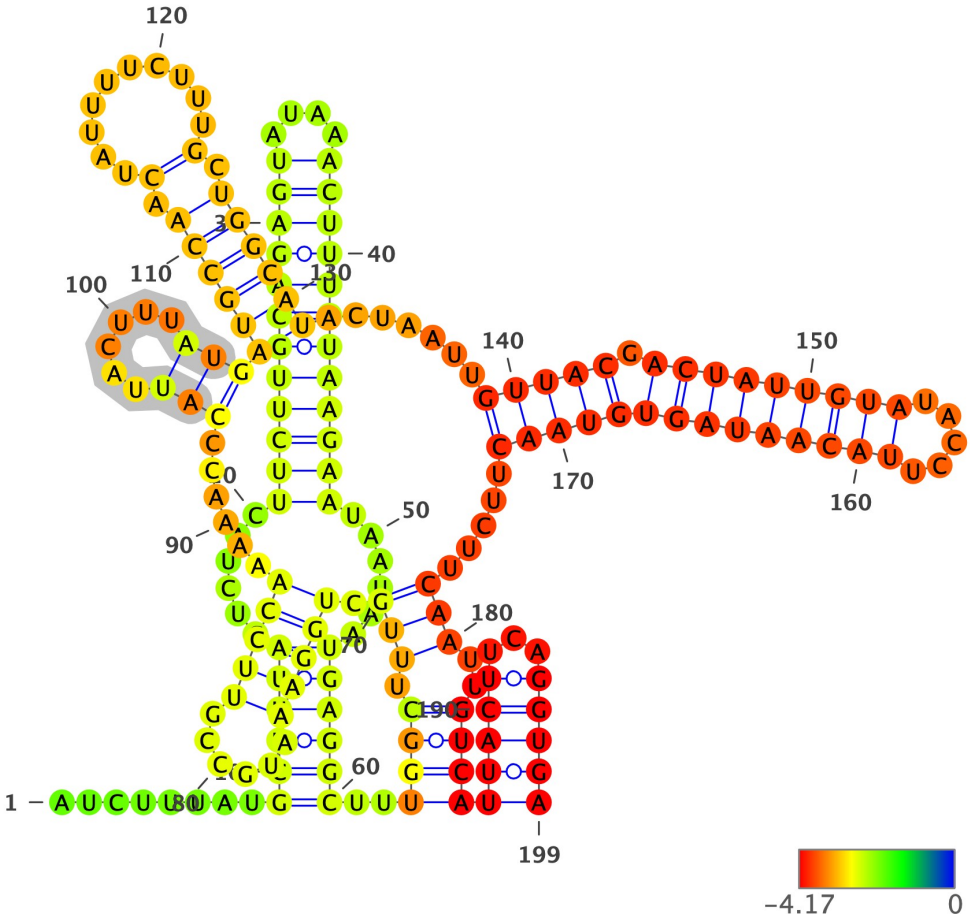
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 436 from nt 25806 to 25815 (nt 95 to 104)

```
5'-ATTACTTTAU-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.02
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25712 to 25910 (motif highlighted in silver):

```
5'-AUCUUUAUGCUUUAGUCUACUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCA
ACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGA-3
5'-........((((((......(((((((((((....)))))))))))).....))))))..((((.(((.(((((......)))))......(((......)))((((((
.(..........).))))))).......(((((.((((((((.....)))))))))))))).....)))..))))(((((...)))))-3'
MFE = -49.0; z-score = -3.91; ED = 25.81
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

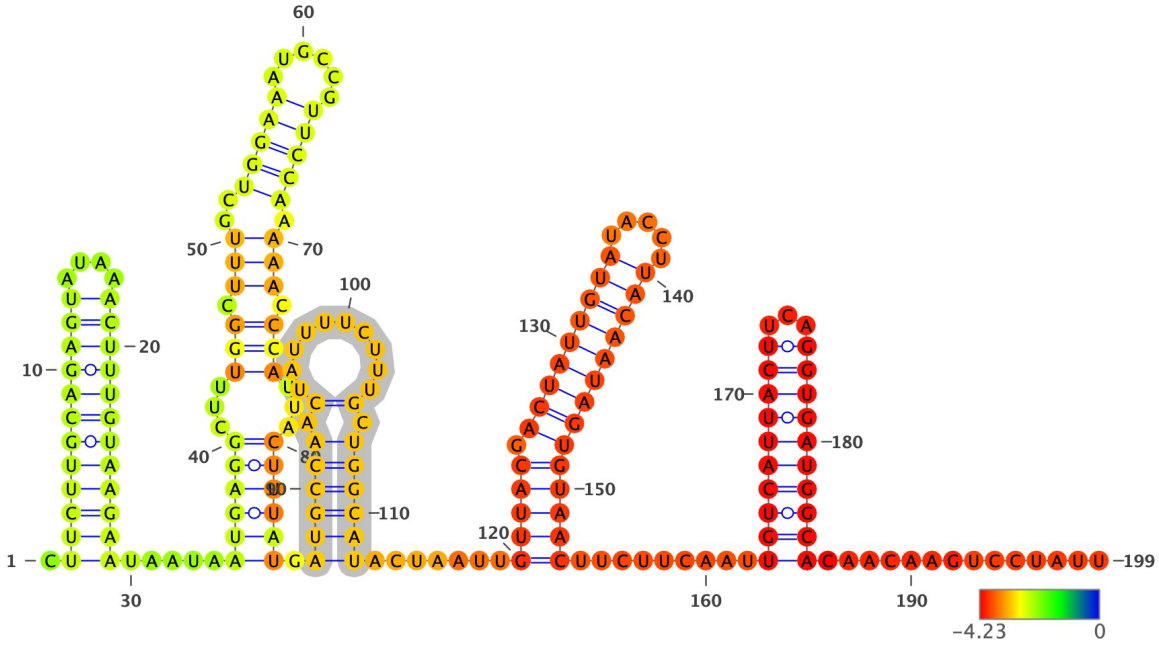
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 437 from nt 25817 to 25842 (nt 87 to 112)

```
5'-ATGCCAACTATTTTCTTTGCUGGCAU-3'
5'-((((((.(.........).)))))))-3'
Motif MFE = -5.9; z-score = -3.44; ED = 1.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25731 to 25929 (motif highlighted in silver):

```
5'-CUUCUUGCAGAGUAUAAACUUUGUAAGAAUAAUAAUGAGGCUUUGGCUUUGCUGGAAAUGCCGUUCCAAAAACCCAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCA
UACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCACAACAAGUCCUAUU-3
5'-.(((((((((((....)))))))))))).....((((((...(((.(((..(((((.....)))))).))).)))...))))))).((((((.(.........).))))))
).......(((((.(((((((((.....)))))))))))))).........((((((((((...))))))))))..............-3'
MFE = -56.9; z-score = -4.83; ED = 21.94
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp03, 25393-26220(+)

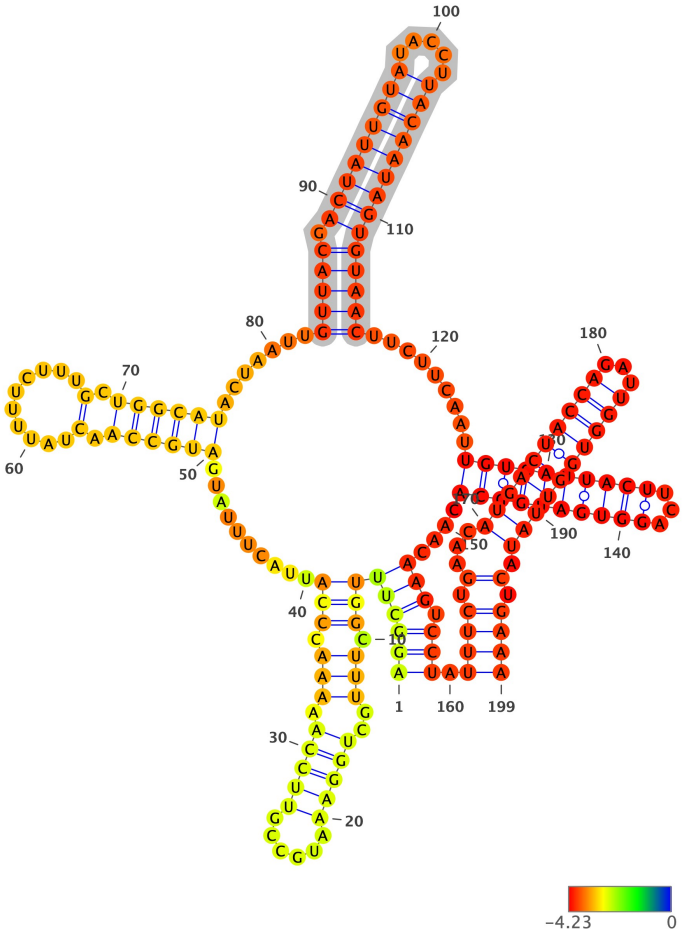
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 438 from nt 25850 to 25883 (nt 83 to 116)

```
5'-GTTACGACTATTGTATACCTUACAAUAGUGUAAC-3'
5'-(((((.((((((((((.....))))))))))))))-3'
Motif MFE = -13.6; z-score = -5.59; 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 = -4.0; 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(+)

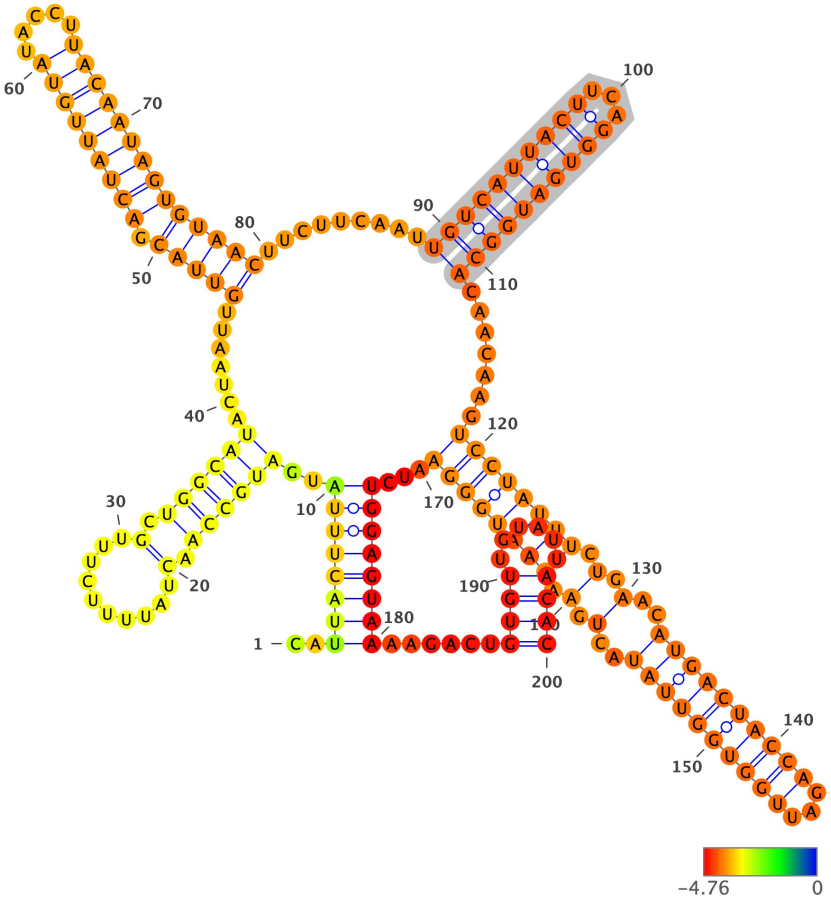
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 439 from nt 25893 to 25915 (nt 89 to 111)

```
5'-TGTCATTACTTCAGGUGAUGGCA-3'
5'-((((((((((...))))))))))-3'
Motif MFE = -9.5; z-score = -4.3; ED = 0.82
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 25805 to 26004 (motif highlighted in silver):

```
5'-CAUUACUUUAUGAUGCCAACUAUUUUCUUUGCUGGCAUACUAAUUGUUACGACUAUUGUAUACCUUACAAUAGUGUAACUUCUUCAAUUGUCAUUACUUCAGGUGAUGGCA
CAACAAGUCCUAUUUCUGAACAUGACUACCAGAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACAC-3
5'-..(((((((((..((((((.(..........).))))))).......(((((.(((((((((.....)))))))))))))))).........((((((((((...))))))))))
.......(((((((((.(.(..((((((((((...))))))))))..).).)))))))))...)))))))).....((((......))))-3'
MFE = -57.7; z-score = -4.55; ED = 14.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp03, 25393-26220(+)

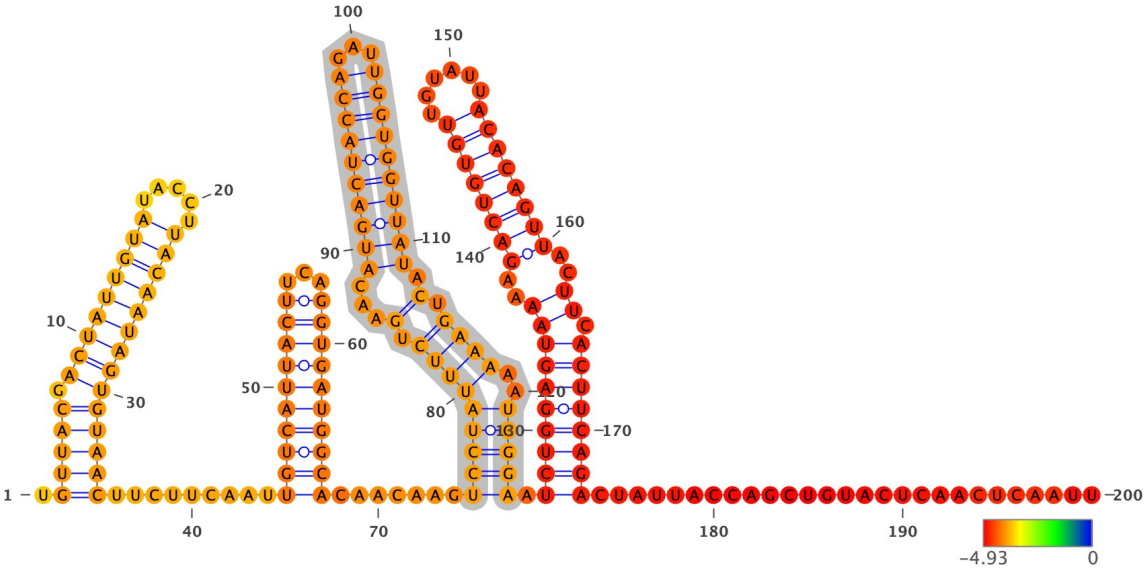
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 200--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 440 from nt 25923 to 25973 (nt 75 to 125)

```
5'-TCCTATTTCTGAACATGACTACCAGATUGGUGGUUAUACTGAAAAAUGGGA-3'
5'-((((((((((.(...((((((((((...))))))))))).).)))))..))))))-3'
Motif MFE = -17.8; z-score = -4.54; 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 = -61.1; z-score = -5.75; ED = 16.93
```

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_gp03, 25393-26220(+)

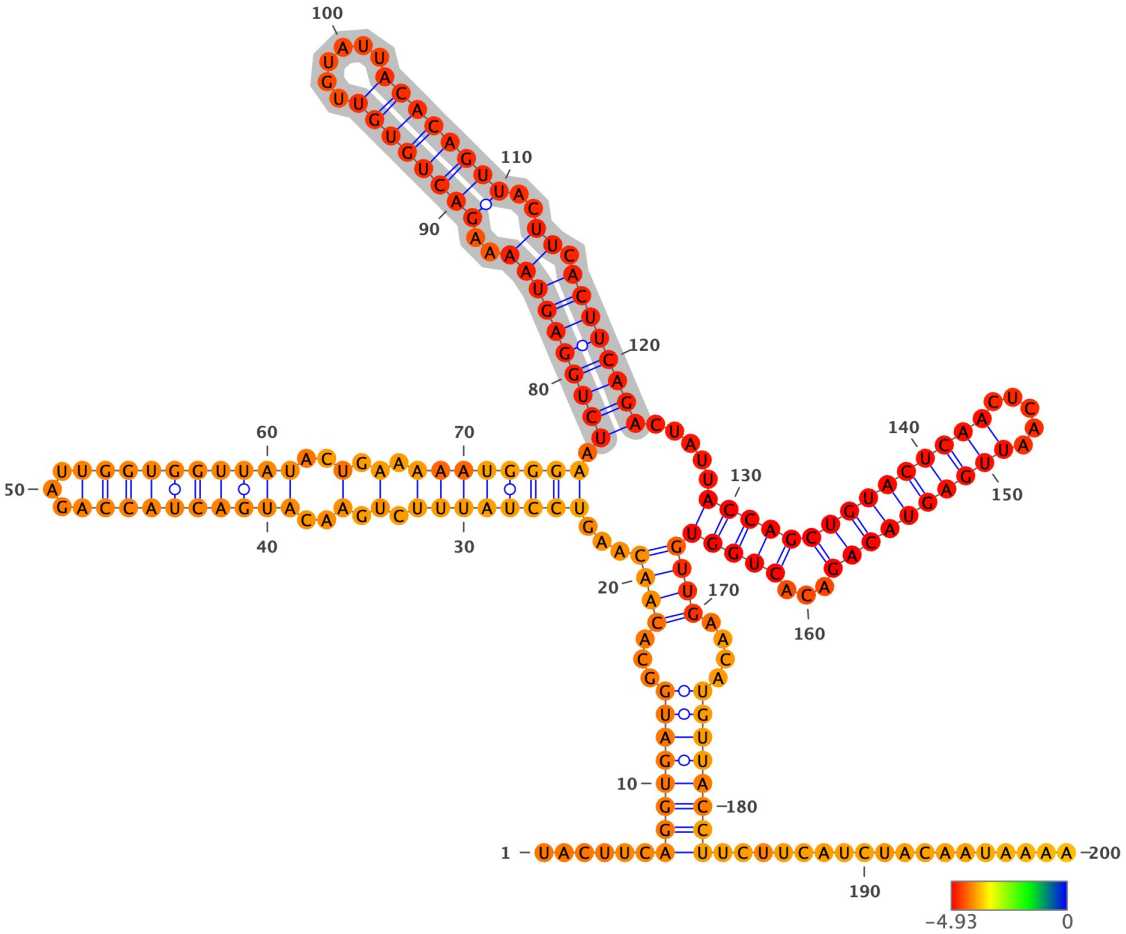
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 441 from nt 25975 to 26021 (nt 77 to 123)

```
5'-TCTGGAGTAAAAGACTGTGTTGTATTACACAGUUACUUCACUUCAGA-3'
5'-((((((((((..(((((((((.....)))))))))..)).)))))))))-3'
Motif MFE = -19.0; z-score = -5.01; 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 = -5.76; 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(+)

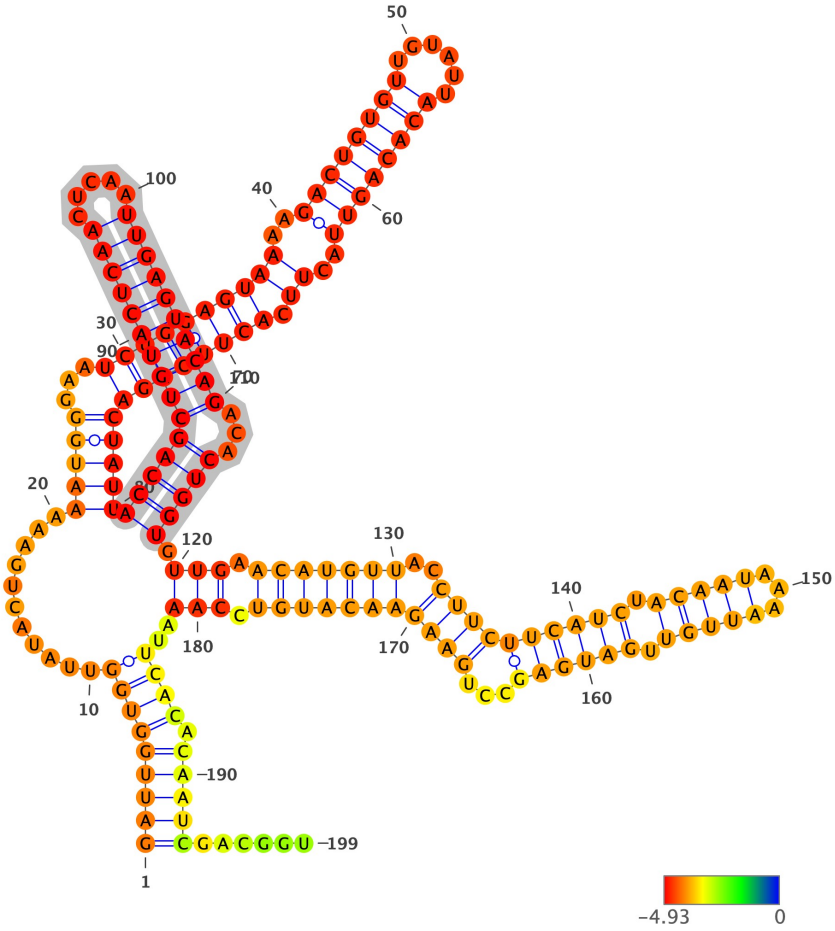
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 442 from nt 26027 to 26064 (nt 81 to 118)

```
5'-ACCAGCTGTACTCAACTCAAUUGAGUACAGACACUGGU-3'
5'-(((((((((((((((.....)))))))))...)))))-3'
Motif MFE = -17.8; z-score = -5.83; 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 25947 to 26145 (motif highlighted in silver):

```
5'-GAUUGGUGGUUAUACUGAAAAAUGGGAAUCUGGAGUAAAAGACUGUGUUGUAUUACACAGUUACUUCACUUCAGACUAUUACCAGCUGUACUCAACUCAAUUGAGUACAGA
CACUGGUGUUGAACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGU-3
5'-(((((((((...........(((((...((((((((((..((((((((.....))))))))..)).))))))))))))((((((((((((((.....)))))))))).
..))))).(((.(((((((..((((((((((.(((((...))))).))))))...))))))))))).)))..)))).)))))......-3'
MFE = -66.8; z-score = -6.19; ED = 11.95
```

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_gp03, 25393-26220(+)

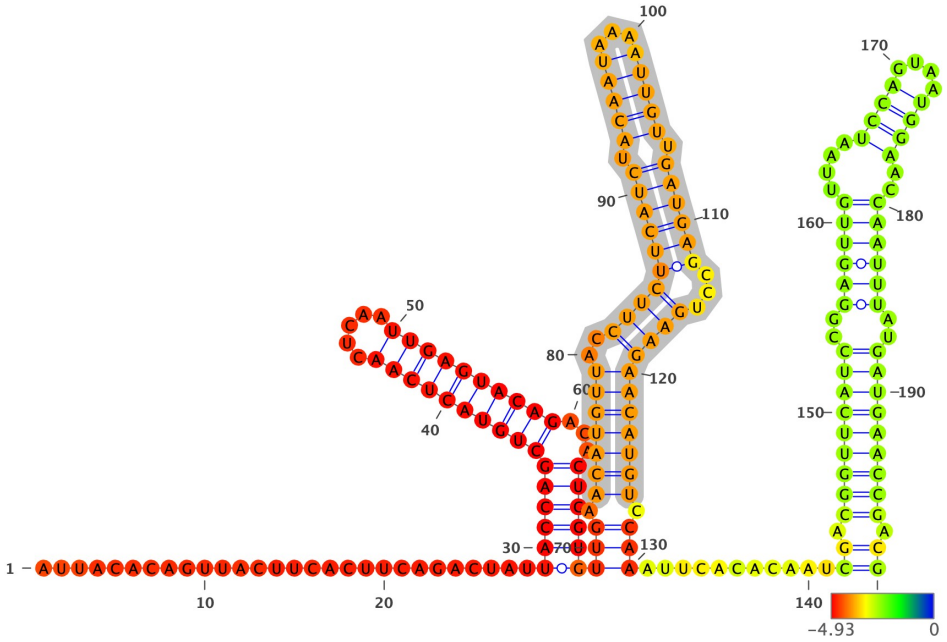
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

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 443 from nt 26070 to 26123 (nt 73 to 126)

```
5'-ACATGTTACCTTCTTCATCTACAATAAAAUUGUTGAUGAGCCTGAAGAACAUGU-3'
5'-(((((((..((((.((((((.((((.....)))).)))))).....)))))))))))-3'
Motif MFE = -16.3; z-score = -5.2; 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 = -5.45; ED = 10.45
```

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_gp03, 25393-26220(+)

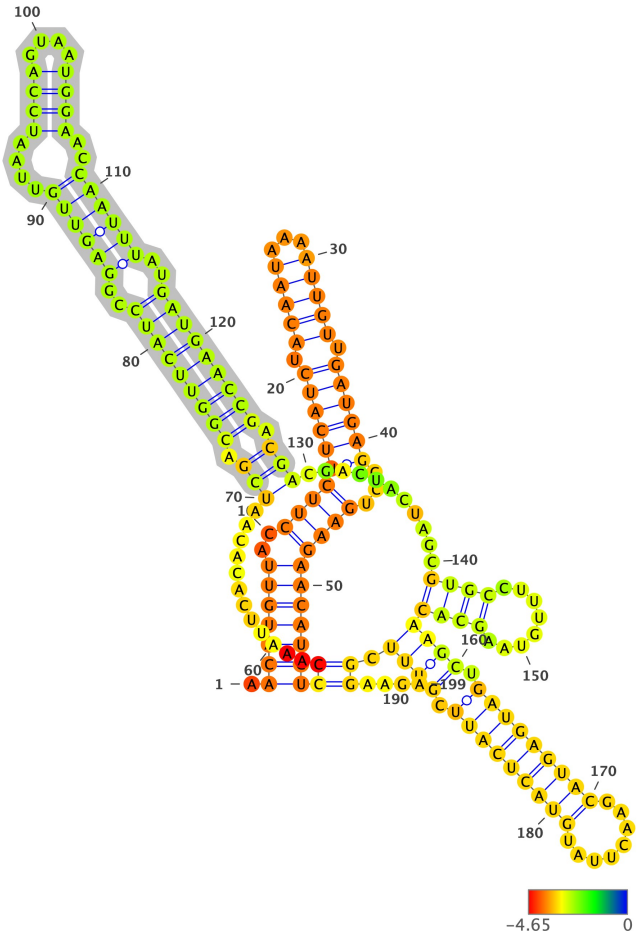
Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 199--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

NC_045512.2 (forward strand): Structure number 444 from nt 26139 to 26196 (nt 71 to 128)

```
5'-CGACGGTTCATCCGGAGTTGTTAATCCAGTAAUGGAACCAAUUUATGAUGAACCGACG-3'
5'-(..(((((((((..((((((....((((....))))..))))))..))))))))))..)-3'
Motif MFE = -21.2; z-score = -3.65; ED = 2.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26069 to 26267 (motif highlighted in silver):

```
5'-AACAUGUUACCUUCUUCAUCUACAAUAAAAUUGUUGAUGAGCCUGAAGAACAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAA
UUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGA-3
5'-.(((((((..(((((((((((.(((((...))))).))))))...))))))))))))((.............(((.(((((((((..((((((....((((....))))..)))
)))..)))))))))).))).........((((........))))((((.(((((((((........))))))))).)))).))....-3'
MFE = -59.6; z-score = -4.22; ED = 14.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 152--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 152--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 177 to 199--gene, gene-GU280_gp04, 26245-26472(+)

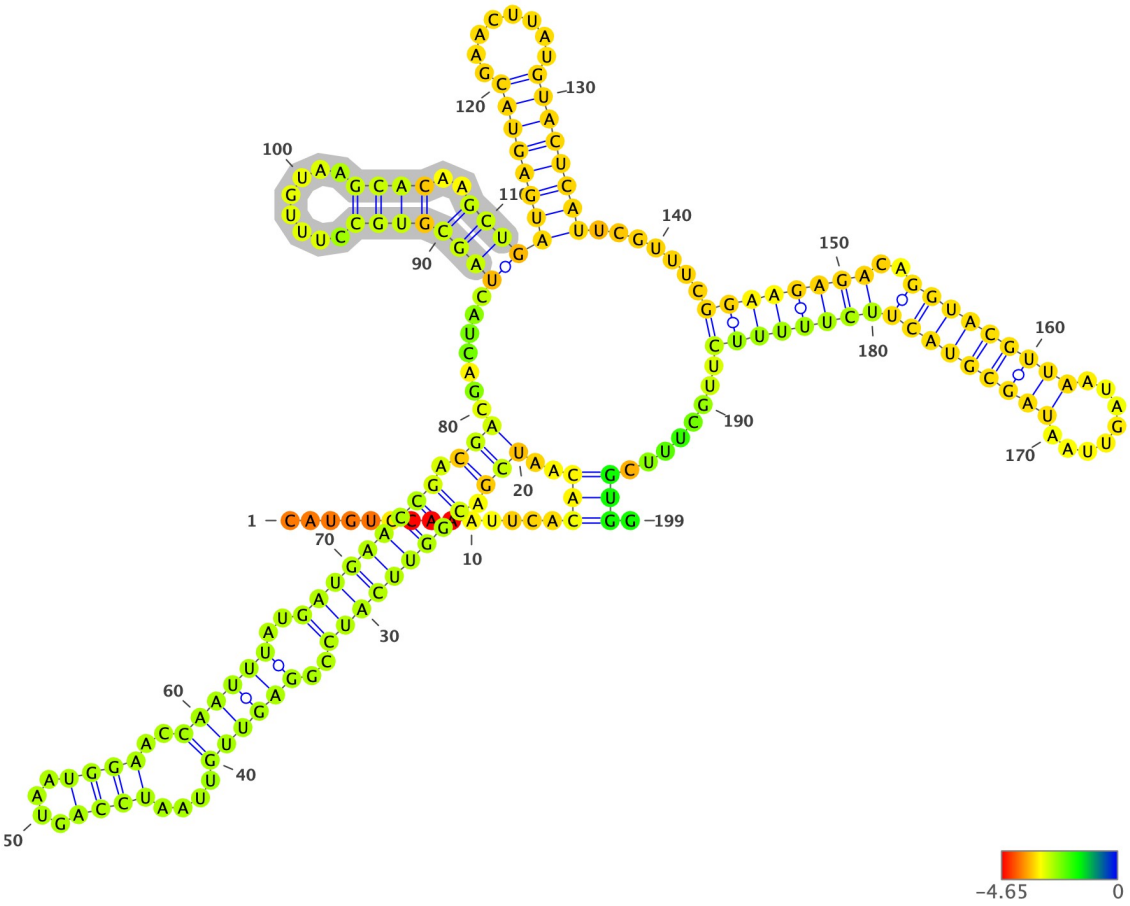
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 177 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 445 from nt 26206 to 26229 (nt 88 to 111)

```
5'-AGCGTGCCTTTGTAAGCACAAGCU-3'
5'-(((.(((........))))...)))-3'
Motif MFE = -5.4; z-score = -1.74; ED = 1.83
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26119 to 26317 (motif highlighted in silver):

```
5'-CAUGUCCAAAUUCACACAAUCGACGGUUCAUCCGGAGUUGUUAAUCCAGUAAUGGAACCAAUUUAUGAUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCU
GAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGG-3
5'-..............(((..((((.((((((((((..((((((....((((....))))..))))))..))))))))).))).......(((((((........)))))..)))
)(((((((((........)))))))).......(((((((..(((((((((........)))))))))))))))))........))).-3'
MFE = -60.4; z-score = -4.08; ED = 20.01
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 102--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 102--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 127 to 199--gene, gene-GU280_gp04, 26245-26472(+)

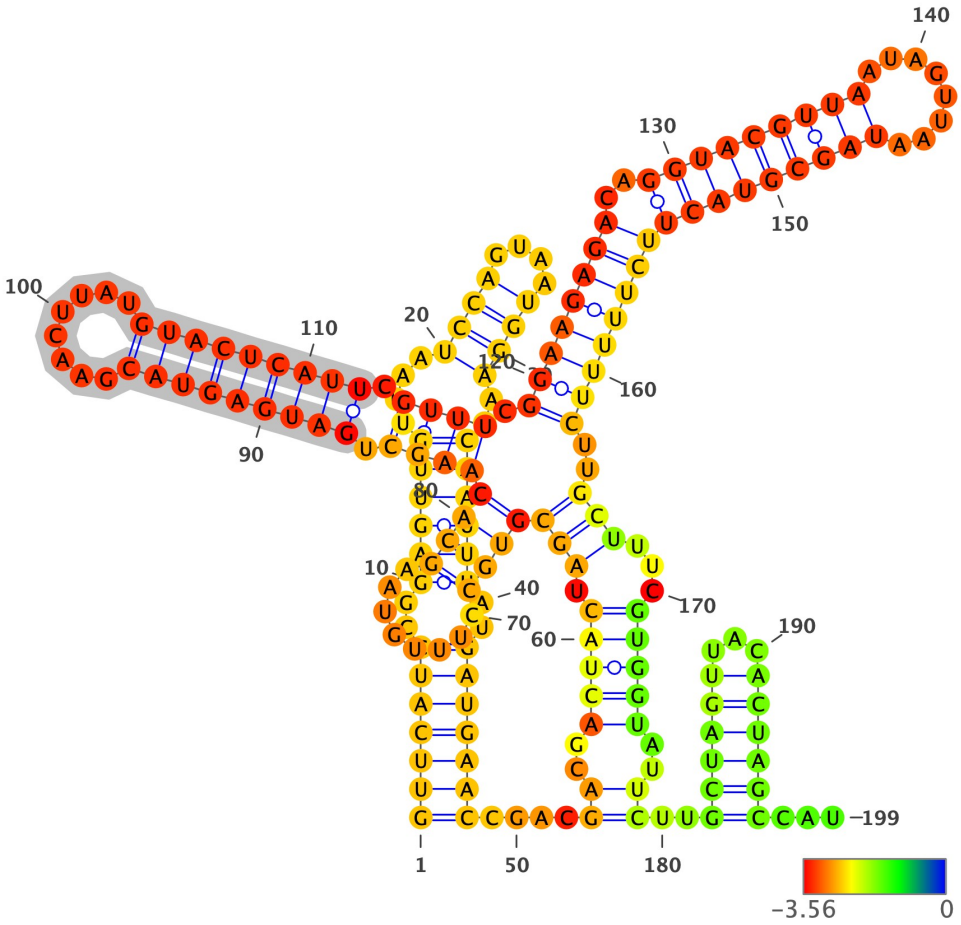
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 127 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 446 from nt 26230 to 26255 (nt 87 to 112)

```
5'-GATGAGTACGAACTTATGUACUCAUU-3'
5'-(((((((((.........)))))))))-3'
Motif MFE = -10.2; z-score = -4.39; 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 = -4.53; 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(+)

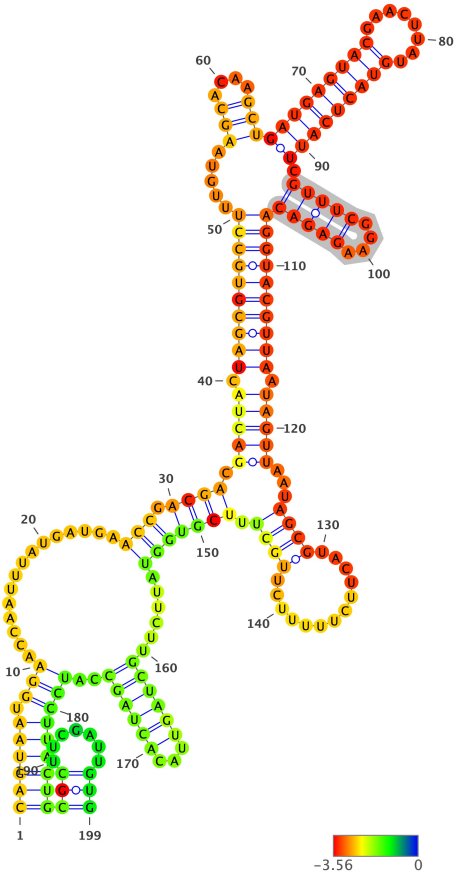
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 447 from nt 26257 to 26270 (nt 93 to 106)

```
5'-GTTTCGGAAGAGAC-3'
5'-(((((....)))))-3'
Motif MFE = -3.2; z-score = -3.88; 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 = -2.84; 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(+)

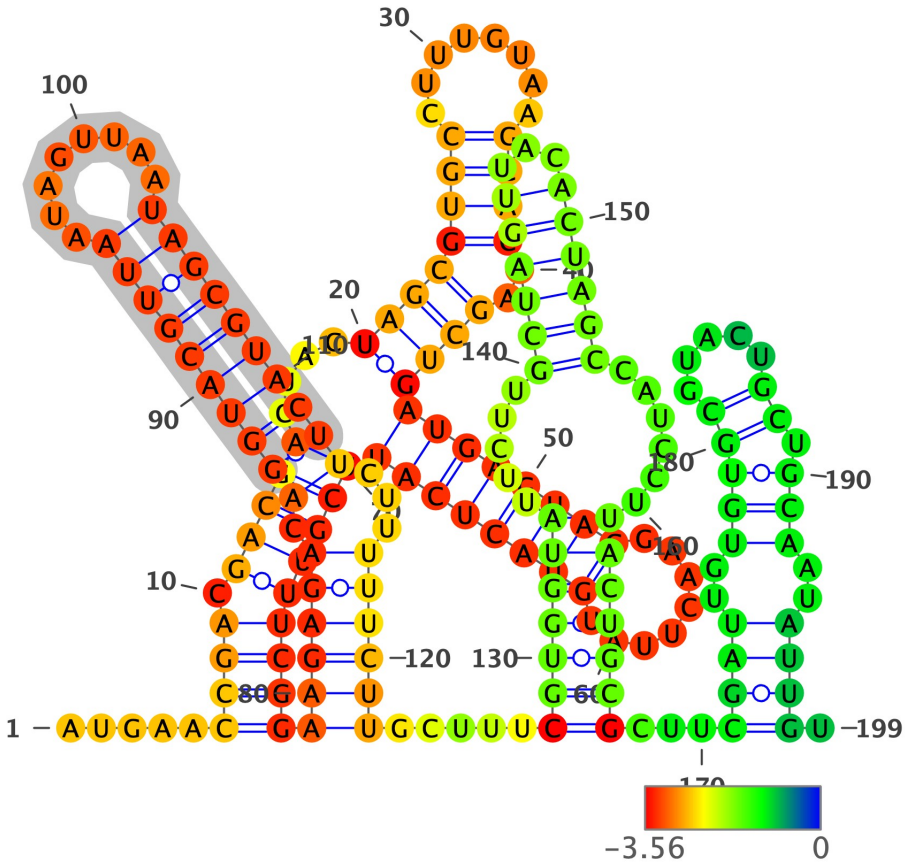
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 448 from nt 26272 to 26297 (nt 87 to 112)

```
5'-GGTACGTTAATAGTTAAUAGCGUACU-3'
5'-(((((((((........)))))))))-3'
Motif MFE = -8.9; z-score = -3.58; ED = 0.69
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26186 to 26384 (motif highlighted in silver):

```
5'-AUGAACCGACGACGACUACUAGCGUGCCUUUGUAAGCACAAGCUGAUGAGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUAC
UUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGU-3
5'-.....((((.(((((....((((((((........))))..))))((((((((........)))))))))))))))))((((((.((((((((((........))))))))
))...))))))).....((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..)))).-3'
MFE = -56.3; z-score = -2.4; ED = 36.63
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 35--gene, gene-GU280_gp03, 25393-26220(+)

Attributes: ['ID=gene-GU280_gp03', 'Dbxref=GeneID:43740569', 'Name=ORF3a', 'gbkey=Gene', 'gene=ORF3a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp03']

3-- nt 1 to 35--CDS, cds-YP_009724391.1, 25393-26220(+)

Attributes: ['ID=cds-YP_009724391.1', 'Parent=gene-GU280_gp03', 'Dbxref=Genbank:YP_009724391.1,GeneID:43740569', 'Name=YP_009724391.1', 'gbkey=CDS', 'gene=ORF3a', 'locus_tag=GU280_gp03', 'product=ORF3a protein', 'protein_id=YP_009724391.1']

4-- nt 60 to 199--gene, gene-GU280_gp04, 26245-26472(+)

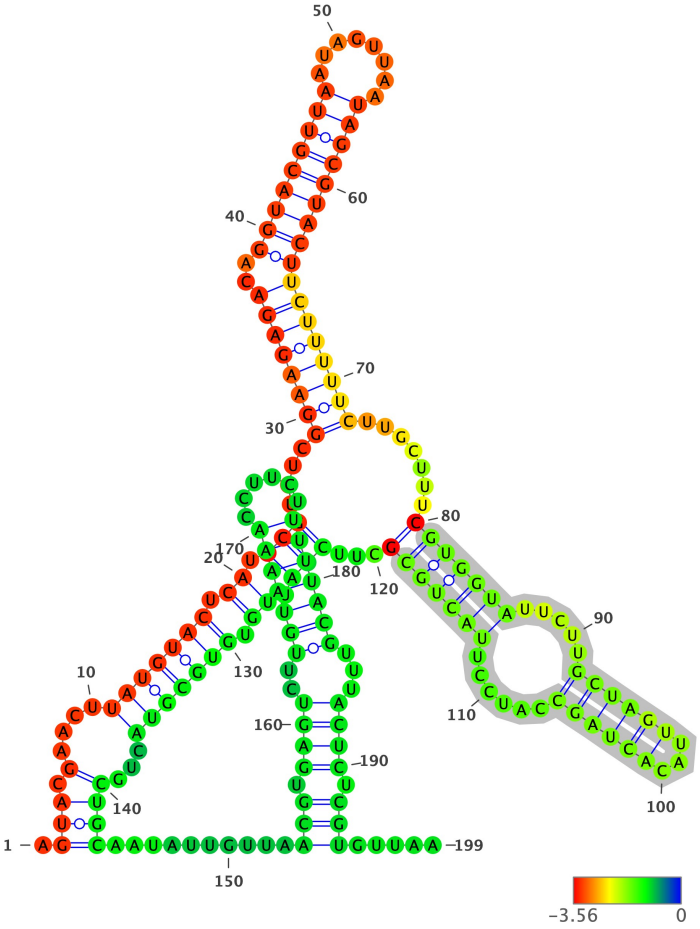
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

5-- nt 60 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 449 from nt 26314 to 26351 (nt 81 to 118)

```
5'-GTGGTATTCTTGCTAGTTACACUAGCCATCCTUACUGC-3'
5'-((((((.....((((.......))))).....))))))-3'
Motif MFE = -9.7; z-score = -2.82; ED = 1.75
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26234 to 26432 (motif highlighted in silver):

```
5'-AGUACGAACUUAUGUACUCAUUCGUUUCGGAAGAGACAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCC
UUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAA-3
5'-.(((.(....(((((((.((.(((....(((((((..(((((((((........)))))))))))))))))).......(((((((.....((((((...)))))).....
.)))))))...))).)).)))))))...)))).........(((.((((..(((((((.....)))))))...)))).))).....-3'
MFE = -50.8; z-score = -2.84; ED = 27.05
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 12 to 199--gene, gene-GU280_gp04, 26245-26472(+)

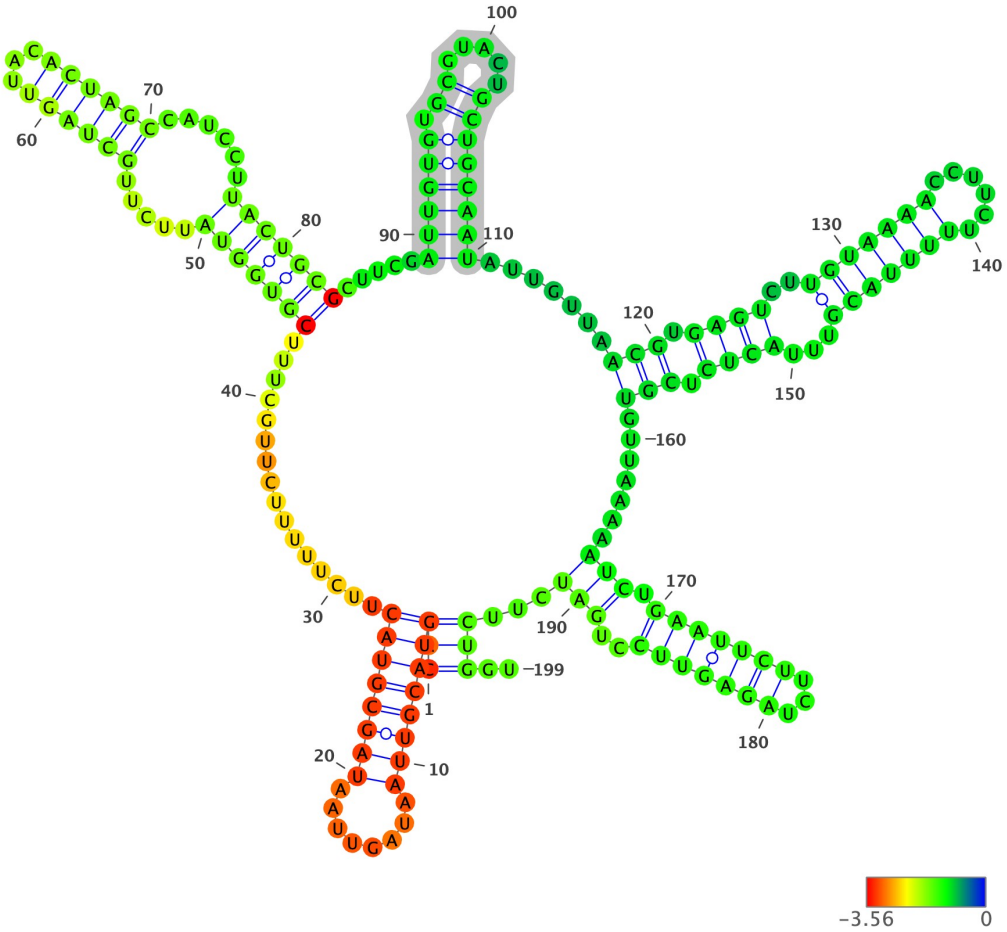
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 12 to 199--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 450 from nt 26358 to 26379 (nt 89 to 110)

```
5'-ATTGTGTGCGTACTGCUGCAAU-3'
5'-((((((.(.....))))))))-3'
Motif MFE = -3.3; z-score = -0.73; ED = 3.34
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26270 to 26468 (motif highlighted in silver):

```
5'-CAGGUACGUUAAUAGUUAAUAGCGUACUUCUUUUUCUUGCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUA
UUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGU-3
5'-((((((((((((........))))))))).................(((((((.....((((((...))))))......)))))))).....((((((.((.....)))))))).
......(((.(((((..(((((((.....)))))))...))))).))).......(((.(((((((...)))))))..)))...))))..-3'
MFE = -45.2; z-score = -2.29; ED = 19.1
```

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_gp04, 26245-26472(+)

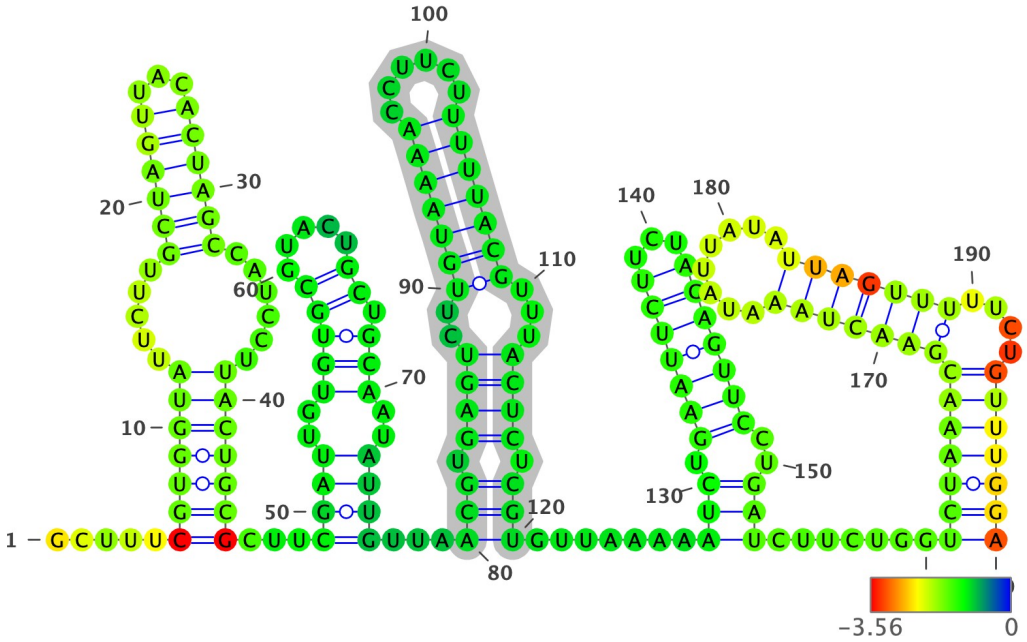
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

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 451 from nt 26387 to 26427 (nt 80 to 120)

```
5'-ACGTGAGTCTTGTAAAACCTTCTUUUUACGTTTACUCTCGU-3'
5'-(((.((((..(((((((.....)))))))...)))).)))-3'
Motif MFE = -9.6; z-score = -3.53; ED = 1.39
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26308 to 26507 (motif highlighted in silver):

```
5'-GCUUUCGUGGUAUUCUUGCUAGUUACACUAGCCAUCCUUACUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUU
UACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGA-3
5'-.....(((((((.....((((((...))))))......)))))))...((((..(((((.....)).)))..))))...(((.((((..(((((((.....)))))))..
.)))).)))......(((.(((((((...)))))))..)))......((((((((((((((.......))))))).....)))))))-3'
MFE = -42.5; z-score = -1.64; ED = 20.96
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 165--gene, gene-GU280_gp04, 26245-26472(+)

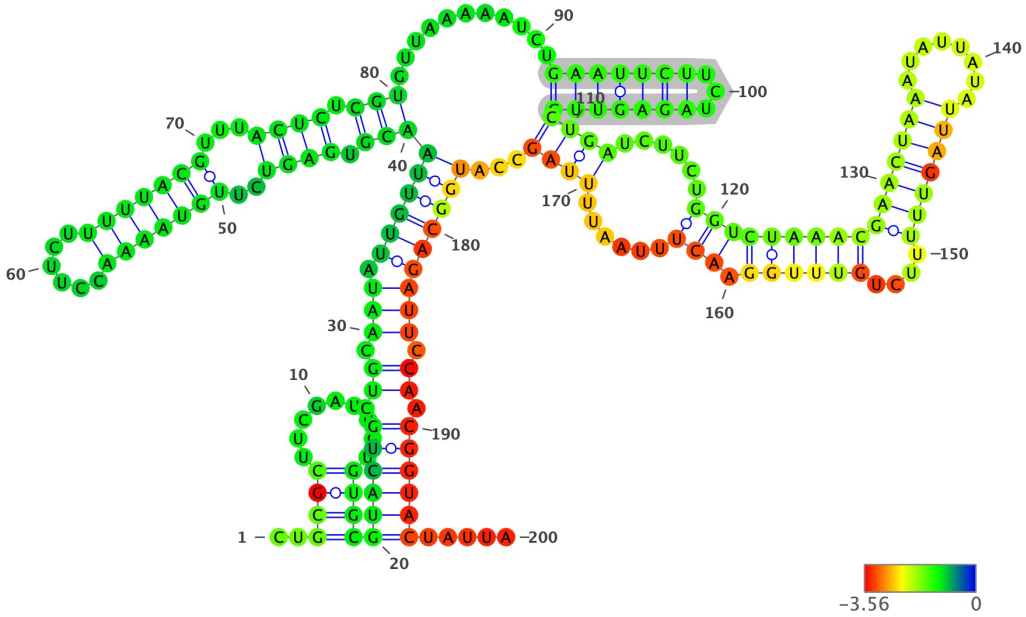
Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 165--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

NC_045512.2 (forward strand): Structure number 452 from nt 26439 to 26455 (nt 92 to 108)

```
5'-GAATTCTTCTAGAGUUC-3'
5'-(((((((...)))))))-3'
Motif MFE = -3.9; z-score = -3.7; ED = 0.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26348 to 26547 (motif highlighted in silver):

```
5'-CUGCGCUUCGAUUGUGUGCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUG
AUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUA-3
5'-..((((.........))))((((((.((.(((.(((((((((.((((..(((((((.......)))))))...)))).))).........(((((((...)))))))(((
(......((((((((((((((((.........)))))))....)))))).)))......))))...)))))))))).)).))))))).....-3'
MFE = -42.6; z-score = -1.98; 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(+)

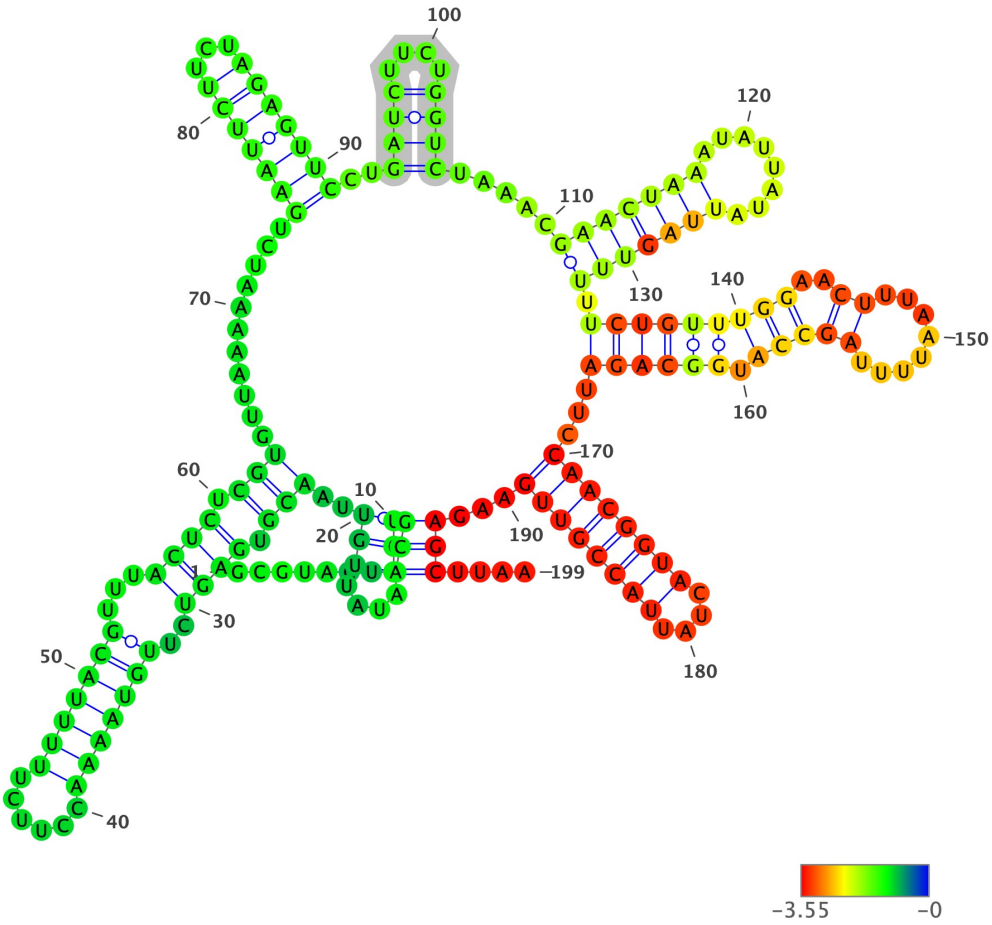
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 453 from nt 26458 to 26469 (nt 94 to 105)

```
5'-GATCTTCTGGUC-3'
5'-((((....))))-3'
Motif MFE = -1.8; z-score = -3.85; ED = 0.48
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26365 to 26563 (motif highlighted in silver):

```
5'-GCGUACUGCUGCAAUAUUGUUAACGUGAGUCUUGUAAAACCUUCUUUUUACGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACG
AACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAA-3
5'-.......((((((....)))..(((.((((..(((((((.....)))))))...)))))..)))..........(((((((...)))))))..((((....)))).....(
((((((........)))))))..(((((((((..((........))))).)))))))...(((((((((....)))))))))...)))....-3'
MFE = -44.1; z-score = -2.39; ED = 38.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 108--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 108--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 159 to 199--gene, gene-GU280_gp05, 26523-27191(+)

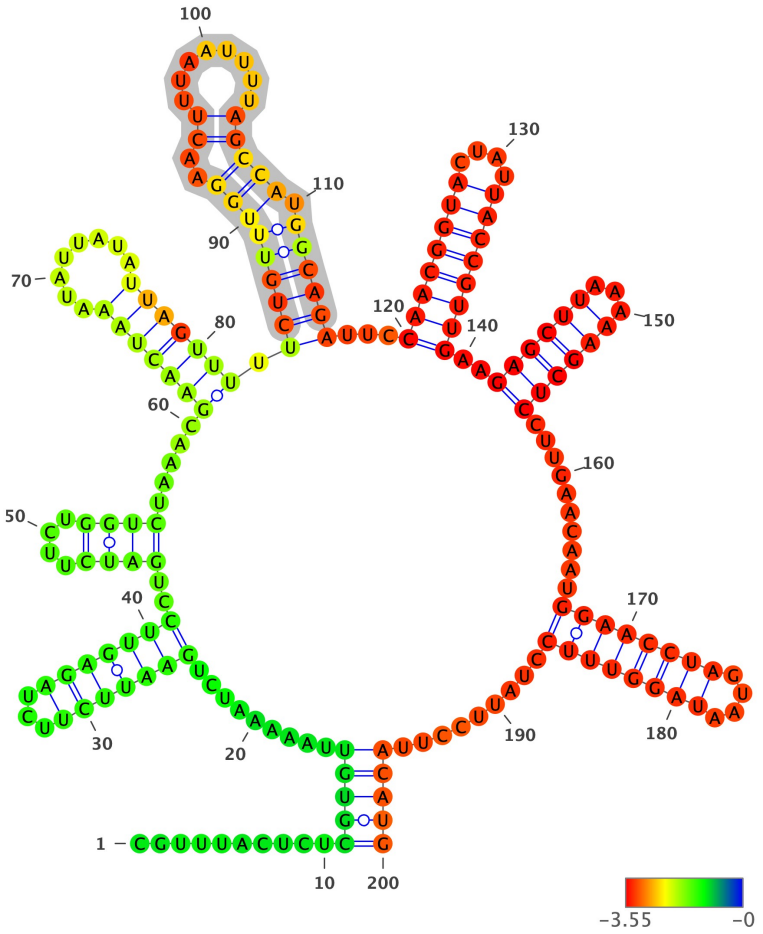
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 159 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 454 from nt 26499 to 26529 (nt 85 to 115)

```
5'-CTGTTTGGAACTTTAATTTTAGCCATGGCAG-3'
5'-(.(.......((........)).....).)-3'
Motif MFE = -4.1; z-score = -0.42; ED = 2.35
```



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 26415 to 26614 (motif highlighted in silver):

```
5'-CGUUUACUCUCGUGUUAAAAAUCUGAAUUCUUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUG
GCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUG-3
5'-.........(((((.........(((((((...)))))))..((((....)))).....(((((((........)))))))..(((((((((..((........)))))).)
)))))...(((((((((....)))))))))..(((((((...)))))).........(((((((((....)))))))))........)))))-3'
MFE = -48.7; z-score = -3.62; ED = 18.59
```

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 58--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 58--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 109 to 200--gene, gene-GU280_gp05, 26523-27191(+)

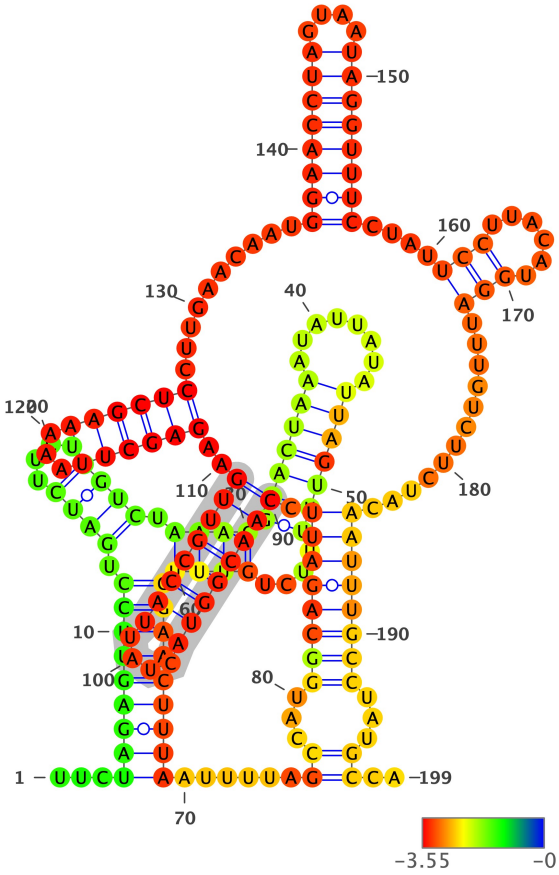
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 109 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 455 from nt 26534 to 26553 (nt 90 to 109)

```
5'-CAACGGTACTATUACCGUUG-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -9.0; z-score = -5.62; ED = 0.47
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26445 to 26643 (motif highlighted in silver):

```
5'-UUCUAGAGUUCCUGAUCUUCUGGUCUAAACGAACUAAAUAUUAUAUUAGUUUUUCUGUUUGGAACUUUAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAA
GAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCA-3
5'-...(((((((((.((((....)))))).(((((((((((........)))))))....)))))))))))).....((...(((((((.(((((((((....)))))))))..
((((((...)))))).........(((((((((....)))))))))....(((......))).............)))))))...))..-3'
MFE = -55.1; z-score = -5.05; 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(+)

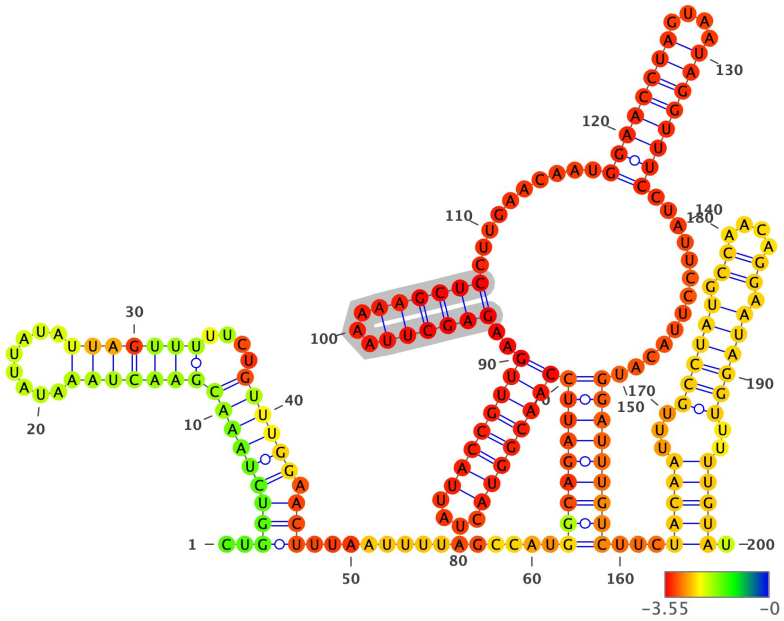
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 456 from nt 26556 to 26570 (nt 93 to 107)

```
5'-GAGCTTAAAAAGCUC-3'
5'-((((.......))))-3'
Motif MFE = -5.0; z-score = -5.82; 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 = -4.03; ED = 22.95
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 9--gene, gene-GU280_gp04, 26245-26472(+)

Attributes: ['ID=gene-GU280_gp04', 'Dbxref=GeneID:43740570', 'Name=E', 'gbkey=Gene', 'gene=E', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp04']

3-- nt 1 to 9--CDS, cds-YP_009724392.1, 26245-26472(+)

Attributes: ['ID=cds-YP_009724392.1', 'Parent=gene-GU280_gp04', 'Dbxref=Genbank:YP_009724392.1,GeneID:43740570', 'Name=YP_009724392.1', 'Note=ORF4%3B structural protein%3B E protein', 'gbkey=CDS', 'gene=E', 'locus_tag=GU280_gp04', 'product=envelope protein', 'protein_id=YP_009724392.1']

4-- nt 60 to 200--gene, gene-GU280_gp05, 26523-27191(+)

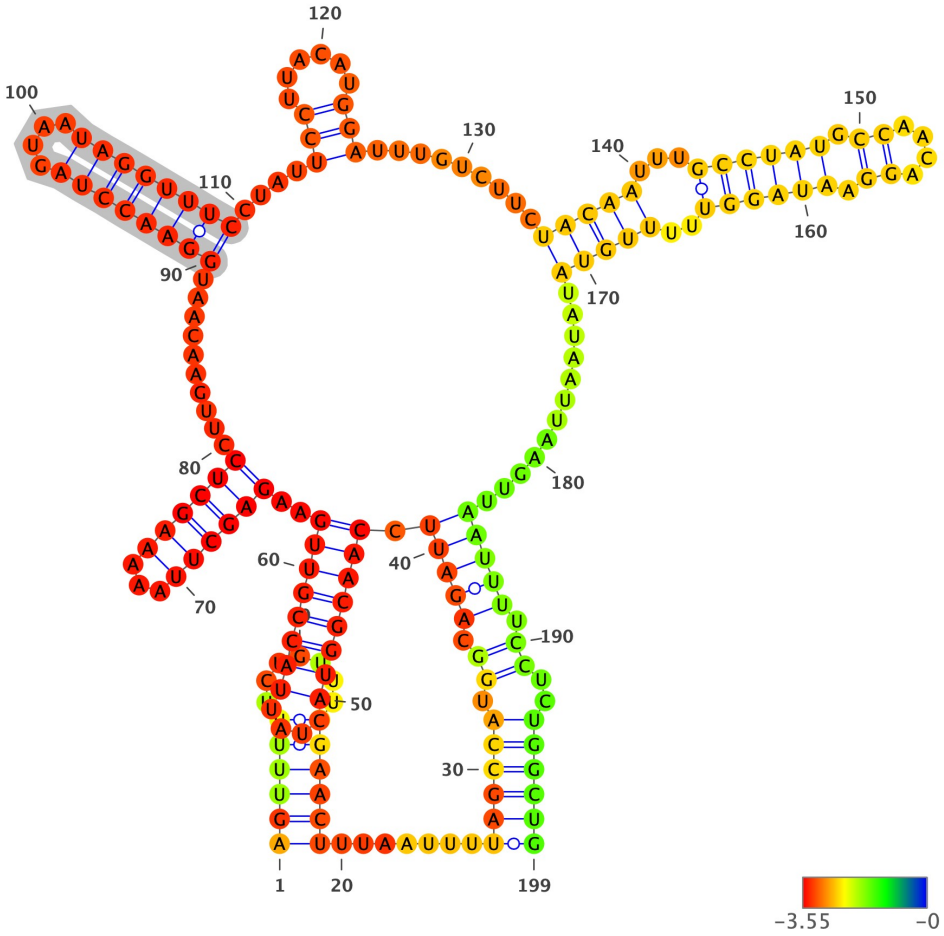
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

5-- nt 60 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 457 from nt 26581 to 26600 (nt 90 to 109)

```
5'-GGAACCTAGTAAUAGGUUUC-3'
5'-((((((((....))))))))-3'
Motif MFE = -8.2; z-score = -5.08; 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 = -3.36; 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(+)

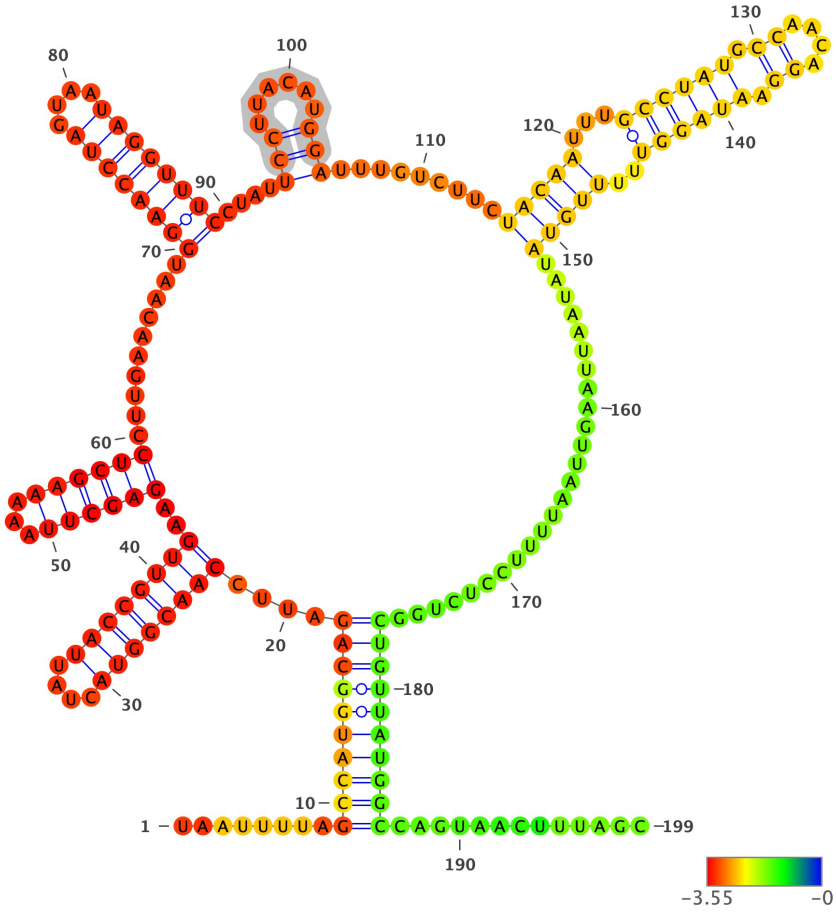
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 458 from nt 26606 to 26615 (nt 95 to 104)

```
5'-CCTTACATGG-3'
5'-((......))-3'
Motif MFE = 0.0; z-score = 0.19; ED = 1.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26512 to 26710 (motif highlighted in silver):

```
5'-UAAUUUUAGCCAUGGCAGAUUCCAACGGUACUAUUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUC
UUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGC-3
5'-........((((((((((....(((((((((....)))))))))..((((((...))))))..........(((((((((....)))))))))....(((......)))).....
...(((((...(((((((.((....)).)))))))..)))))).........................)))))))))............-3'
MFE = -56.4; z-score = -4.26; ED = 20.33
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 12 to 199--gene, gene-GU280_gp05, 26523-27191(+)

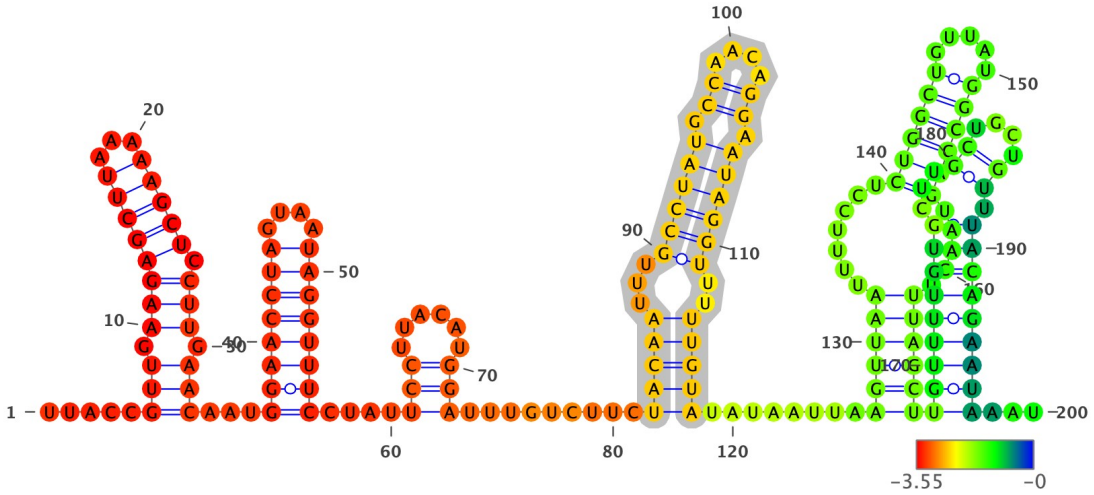
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 12 to 199--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 459 from nt 26626 to 26662 (nt 82 to 118)

```
5'-TACAATTTGCCTATGCCAACAGGAAUAGGUTTUUGUA-3'
5'-(((((...((((((.((....)).))))))..)))))-3'
Motif MFE = -10.9; z-score = -3.13; ED = 1.5
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26545 to 26744 (motif highlighted in silver):

```
5'-UUACCGUUGAAGAGCUUAAAAAGCUCCUUGAACAAUGGAACCUAGUAAUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGU
UUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAU-3
5'-.....(((.((((((((...))))).))).)))...((((((((....))))))))....(((......)))........(((((...((((((.((....)).))))))
..)))))........((((((.......((((((.....))))))).....))))))((((((((...((....)).)))))))))...-3'
MFE = -51.0; z-score = -3.29; 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(+)

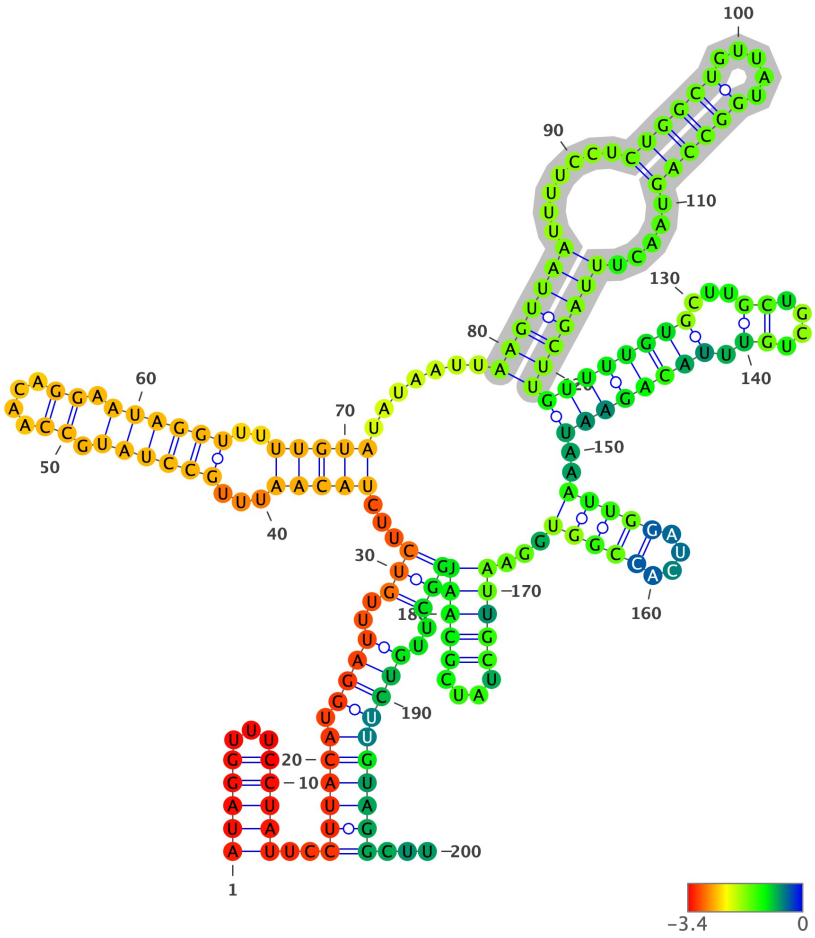
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 460 from nt 26670 to 26712 (nt 79 to 121)

```
5'-AAGTTAATTTTCCTCTGGCTGTTATGGCCAGTAACTUUAGCUU-3'
5'-(((((((.......((((((.....))))))).....)))))))-3'
Motif MFE = -12.0; z-score = -2.77; 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 26592 to 26791 (motif highlighted in silver):

```
5'-AUAGGUUUCCUAUUCCUUACAUGGAUUUGUCUUCUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUA
ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUU-3
5'-(((((...)))))..((((((.((((..(((...((((((...((((((.((....)).))))))..)))))).......(((((((.......((((((.....)))))))..
...)))))))((((((((...((....)).))))))))..(((((....)))))...(((((....)))))))).))))))))))...-3'
MFE = -50.0; z-score = -1.97; ED = 43.48
```

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_gp05, 26523-27191(+)

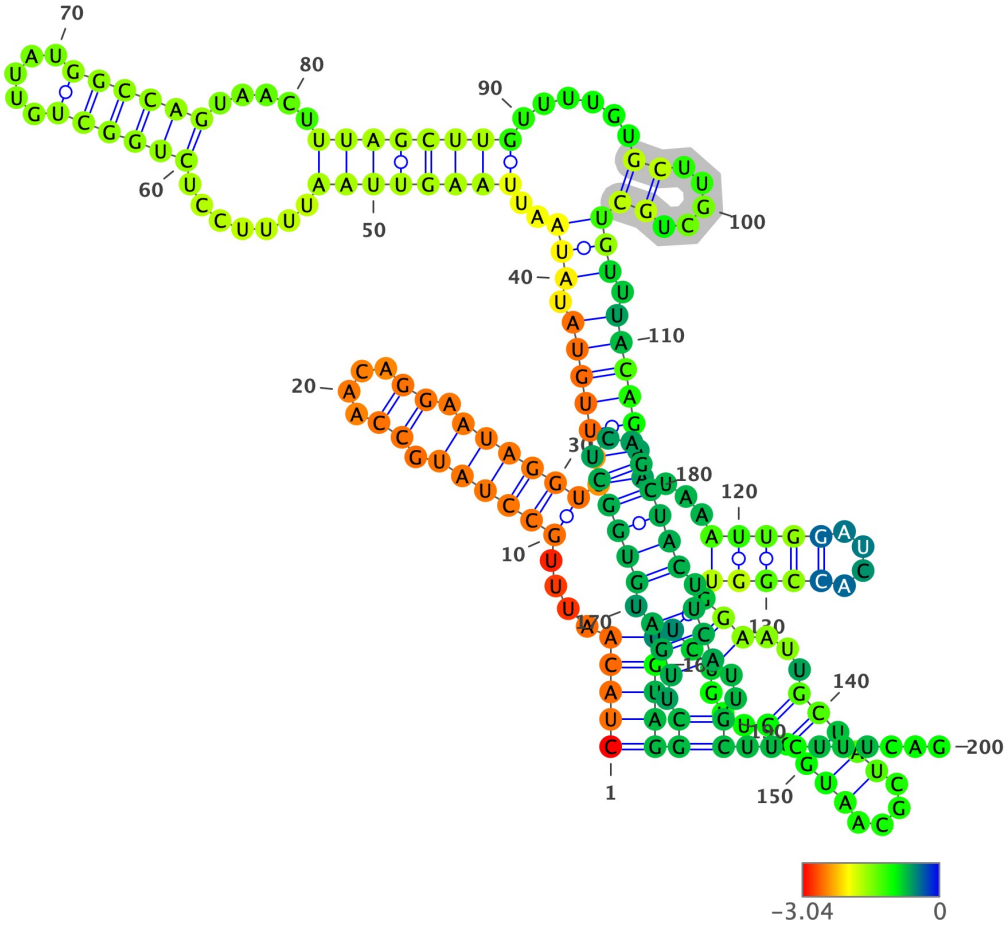
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 461 from nt 26720 to 26728 (nt 96 to 104)

```
5'-GCTTGCTGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.17; ED = 0.98
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26625 to 26824 (motif highlighted in silver):

```
5'-CUACAAUUUGCCUAUGCCAACAGGAAUAGGUUUUUGUAUAUAAUUAAGUUAAUUUUCCUCUGGCUGUUAUGGCCAGUAACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUAC
AGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUUGCUUCUUUCAG-3
5'-(((((....((((((.((....)).))))))(((((((.(((..(((((((((.......((((((.....))))))).....))))))))).....((.....)))))).)))
))))...((((((....))))))(((...((((((....))))))...)))))))))(.(((.(((((...))))))..))).)..)).........-3'
MFE = -48.4; z-score = -1.75; ED = 43.77
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

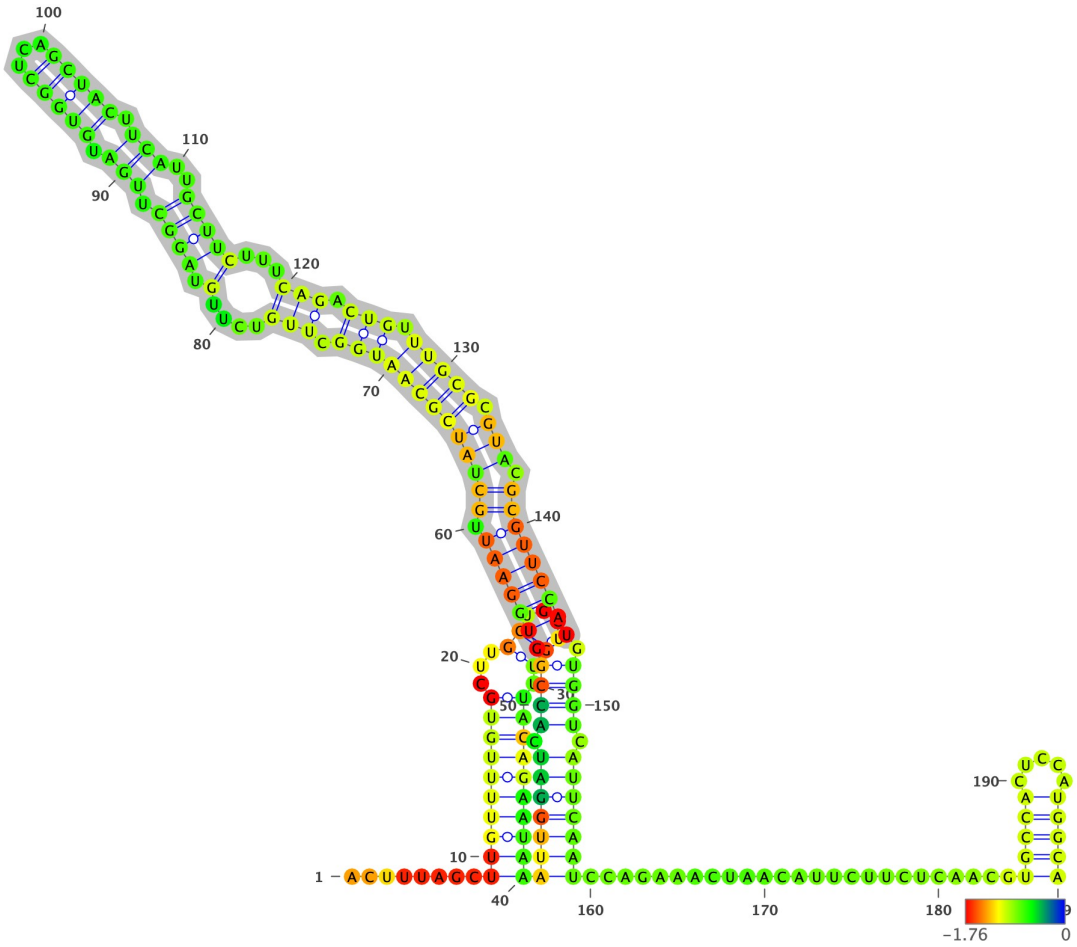
3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 462 from nt 26755 to 26848 (nt 53 to 146)

```
5'-GTGGAATTGCTATCGCAATGGCTTGTCTTGTAGGCTTGATGTGGCTCAGCUACTUCATTGCUUCTTTCAGACUGTUUGCGCGUACGCGUUCCAU-3'

5'-((.((((.((.(((((((((((.(((....(.............................)...))))..))))..))))))..))..)))))))..))-3'
Motif MFE = -29.4; z-score = -2.29; ED = 11.16
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26703 to 26901 (motif highlighted in silver):

```
5'-ACUUUAGCUUGUUUUGUGCUUGCUGCUGUUUACAGAAUAAAUUGGAUCACCGGUGGAAUUGCUAUCGCAAUGGCUUGUCUUGUAGGCUUGAUGUGGCUCAGCUACUUCAUU
GCUUCUUUCAGACUGUUUGCGCGUACGCGUUCCAUGUGGUCAUUCAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCA-3
5'-........((((((((((...((....)).)))))))))).(((((((.((((((((((.(((((((((((.(((....(.((((.(((.((((((...)))))).))))..
))))))...))).))).))))))..))).))))))))).))))).....................(((((.....)))))-3'
MFE = -51.0; z-score = -1.45; ED = 16.82
```

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_gp05, 26523-27191(+)

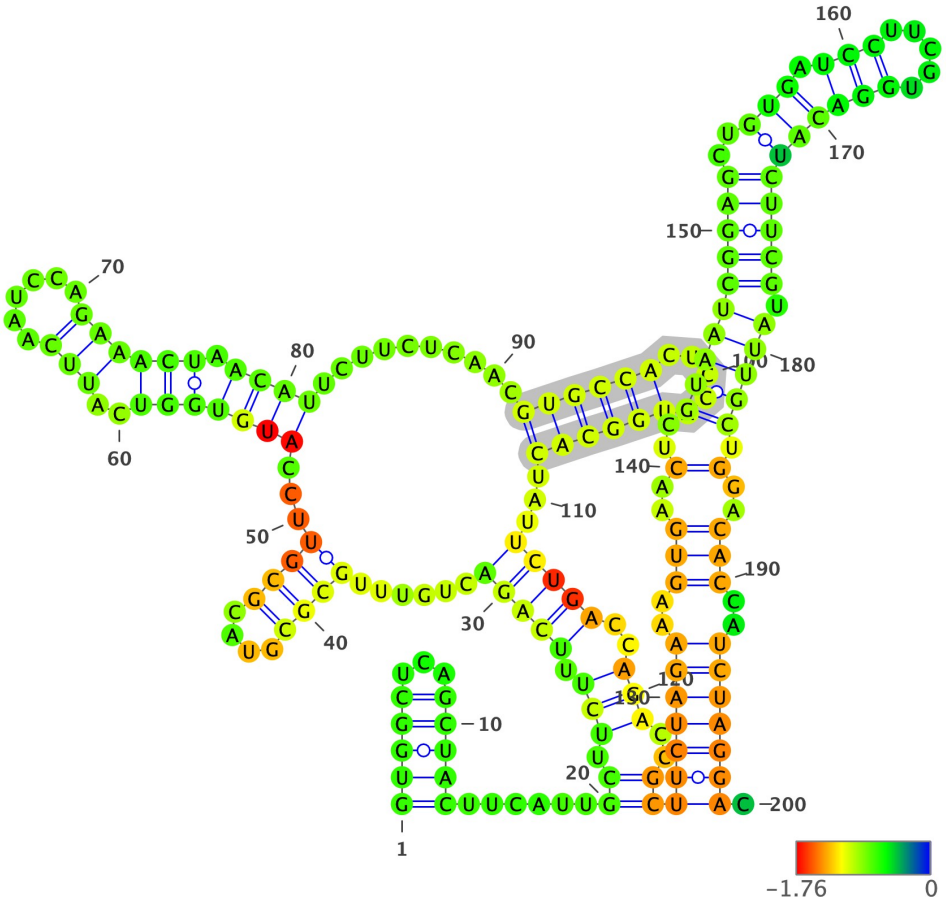
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 463 from nt 26886 to 26902 (nt 92 to 108)

```
5'-GTGCCACTCCAUGGCAC-3'
5'-((((((.....))))))-3'
Motif MFE = -7.5; z-score = -4.39; 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 = -1.21; 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(+)

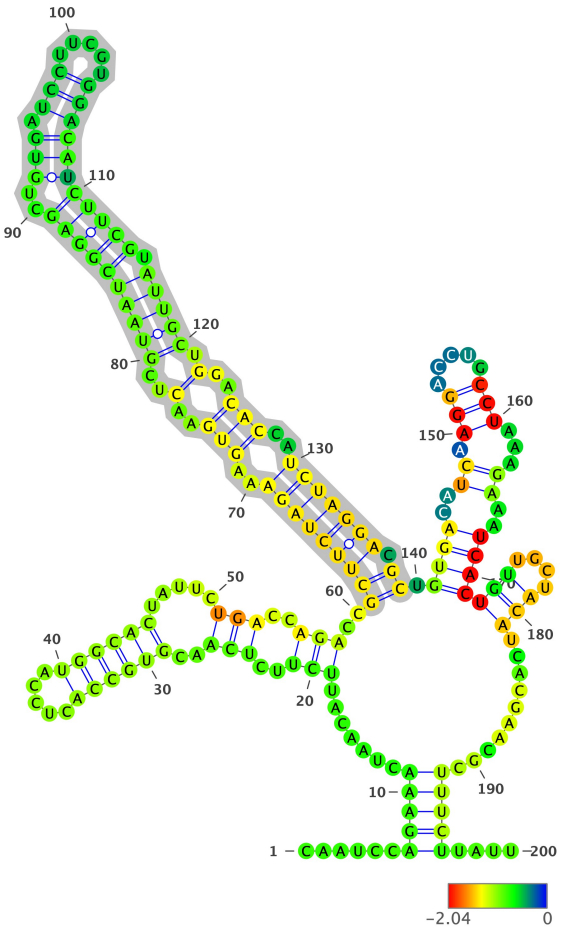
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 464 from nt 26918 to 26996 (nt 61 to 139)

```
5'-GCTTCTAGAAAGTGAACTCGTAATCGGAGCTGTGATCCTTCGTGGACATCUUCGTAUUGCTGGACACCAUCUAGGACGC-3'
5'-(((((((((..(((..(.........................................)..)))..)))))))).))-3'
Motif MFE = -25.9; z-score = -2.26; ED = 4.38
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 26858 to 27057 (motif highlighted in silver):

```
5'-CAAUCCAGAAACUAACAUUCUUCUCAACGUGCCACUCCAUGGCACUAUUCUGACCAGACCGCUUCUAGAAAGUGAACUCGUAAUCGGAGCUGUGAUCCUUCGUGGACAUCU
UCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUU-3
5'-......(((((.......(((..(((..((((((.....))))))).....)))..)))..(((((((((..(((..(..(((((((((((..(((.(((.....))))))))
))).))))).)..)))..)))))))).)).((((..((.(((.....)))...))..))))(((....)))..........)))))....-3'
MFE = -44.3; z-score = -0.94; ED = 23.27
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp05, 26523-27191(+)

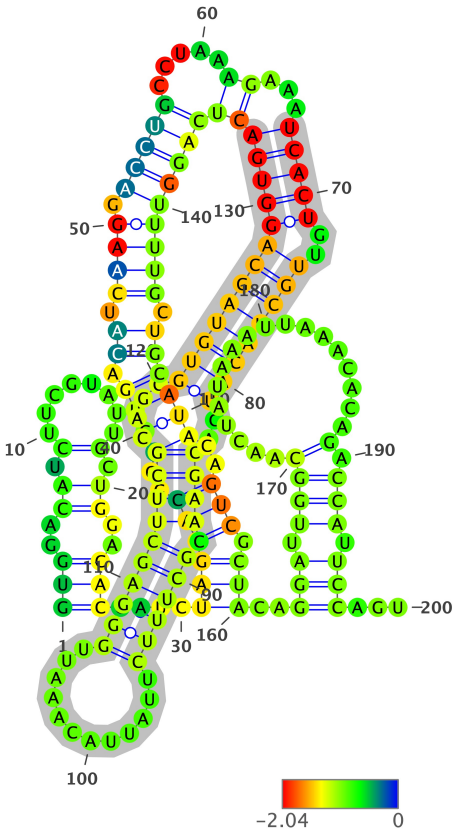
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 200--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

NC_045512.2 (forward strand): Structure number 465 from nt 27025 to 27091 (nt 67 to 133)

```
5'-TCACTGTTGCTACATCACGAACGCTTTCTTATTACAAATTGGGAGCUUCGCAGCGUGUAGCAGGUGA-3'
5'-(((((..(((((((((..((((.((((((............)))))))))....)))))))))))))-3'
Motif MFE = -23.4; z-score = -3.32; 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 26959 to 27158 (motif highlighted in silver):

```
5'-GUGGACAUCUUCGUAUUGCUGGACACCAUCUAGGACGCUGUGACAUCAAGGACCUGCCUAAAGAAAUCACUGUUGCUACAUCACGAACGCUUUCUUAUUACAAAUUGGGAG
CUUCGCAGCGUGUAGCAGGUGACUCAGGUUUUGCUGCAUACAGUCGCUACAGGAUUGGCAACUAUAAAUUAAACACAGACCAUUCCAGU-3
5'-(((..((.(........).))..)))....((((((..((((.((.((((.(((((.....((...(((((..(((((((((..((((.((((((............)))))
)))))....))))))))))))))))))))))).))))))..))).)))..(((.((((.................).))).)))...-3'
MFE = -50.5; z-score = -0.97; ED = 24.46
```

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_gp05, 26523-27191(+)

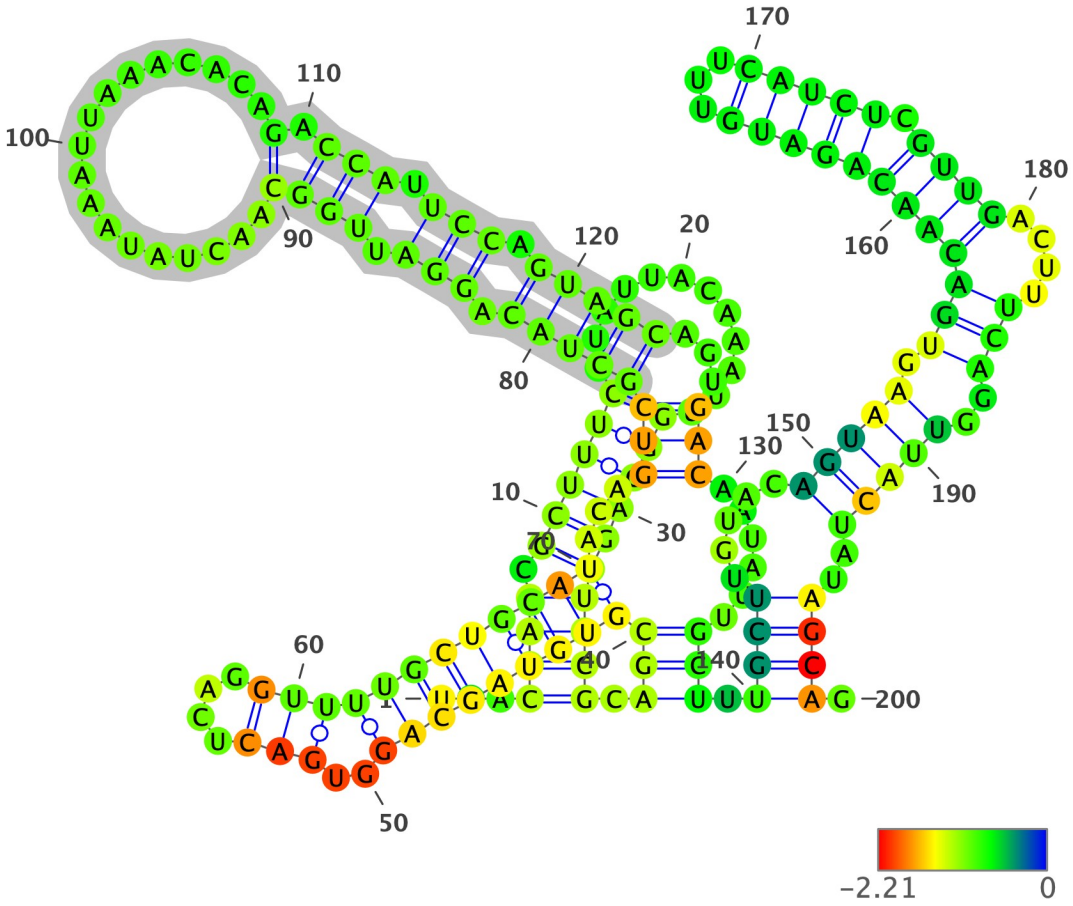
Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

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 466 from nt 27115 to 27161 (nt 77 to 123)

```
5'-GCTACAGGATTGGCAACTATAAATTAAACACAGACCATUCCAGUAGC-3'
5'-(((((.(((.(((.....................))).))).)))))-3'
Motif MFE = -12.0; z-score = -3.42; 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 = -0.98; ED = 29.43
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 153--gene, gene-GU280_gp05, 26523-27191(+)

Attributes: ['ID=gene-GU280_gp05', 'Dbxref=GeneID:43740571', 'Name=M', 'gbkey=Gene', 'gene=M', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp05']

3-- nt 1 to 153--CDS, cds-YP_009724393.1, 26523-27191(+)

Attributes: ['ID=cds-YP_009724393.1', 'Parent=gene-GU280_gp05', 'Dbxref=Genbank:YP_009724393.1,GeneID:43740571', 'Name=YP_009724393.1', 'Note=ORF5%3B structural protein', 'gbkey=CDS', 'gene=M', 'locus_tag=GU280_gp05', 'product=membrane glycoprotein', 'protein_id=YP_009724393.1']

4-- nt 164 to 200--gene, gene-GU280_gp06, 27202-27387(+)

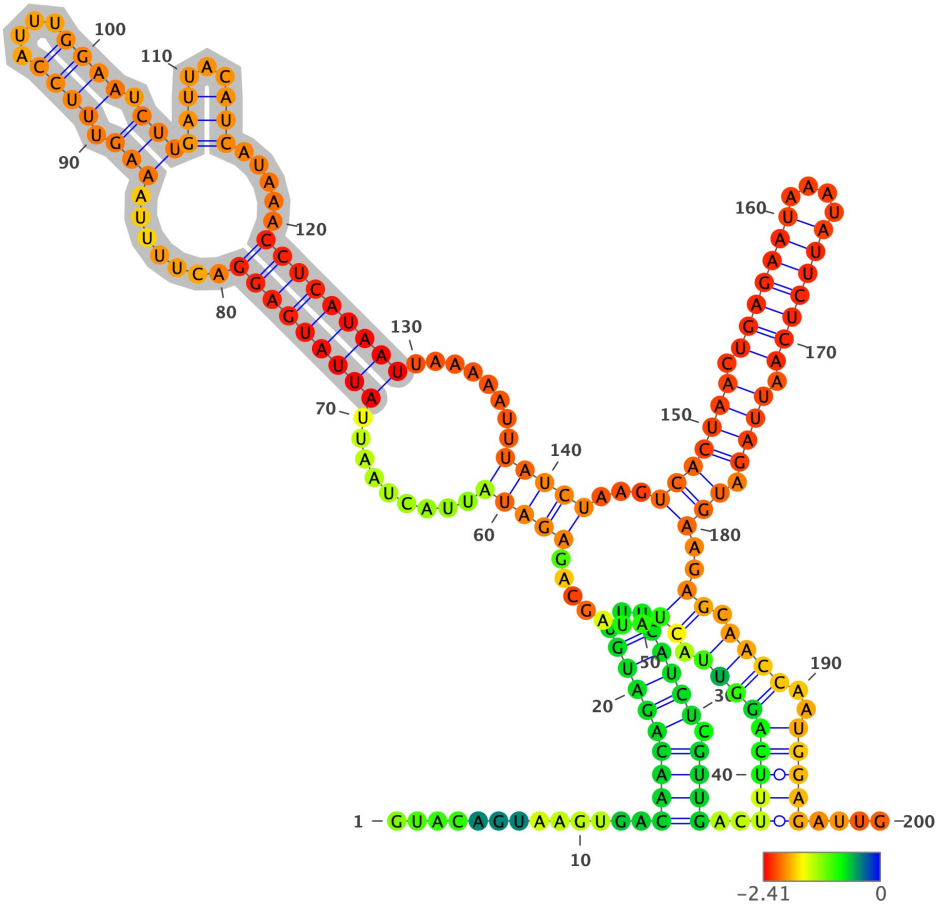
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

5-- nt 164 to 200--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

NC_045512.2 (forward strand): Structure number 467 from nt 27253 to 27311 (nt 71 to 129)

```
5'-ATTATGAGGACTTTTAAAGTTTCCATTTGGAATCUUGATTACATCATAAACCUCAUAAU-3'
5'-(((((((((.......(((.((((....)))).)))..............)))))))))-3'
Motif MFE = -12.7; z-score = -3.5; ED = 6.58
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27183 to 27382 (motif highlighted in silver):

```
5'-GUACAGUAAGUGACAACAGAUGUUUCAUCUCGUUGACUUUCAGGUUACUAUAGCAGAGAUAUUACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUA
CAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUG-3
5'-.............(((((((((...))))).))))..(((((((((.((.......(((((.........(((((((((.......(((.((((....)))).)))(((..
.)))).....))))))))).......))))).....(((((((.(((((((....)))))))).)))).)))..)).))))..)))))....-3'
MFE = -39.0; z-score = -2.07; 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(+)

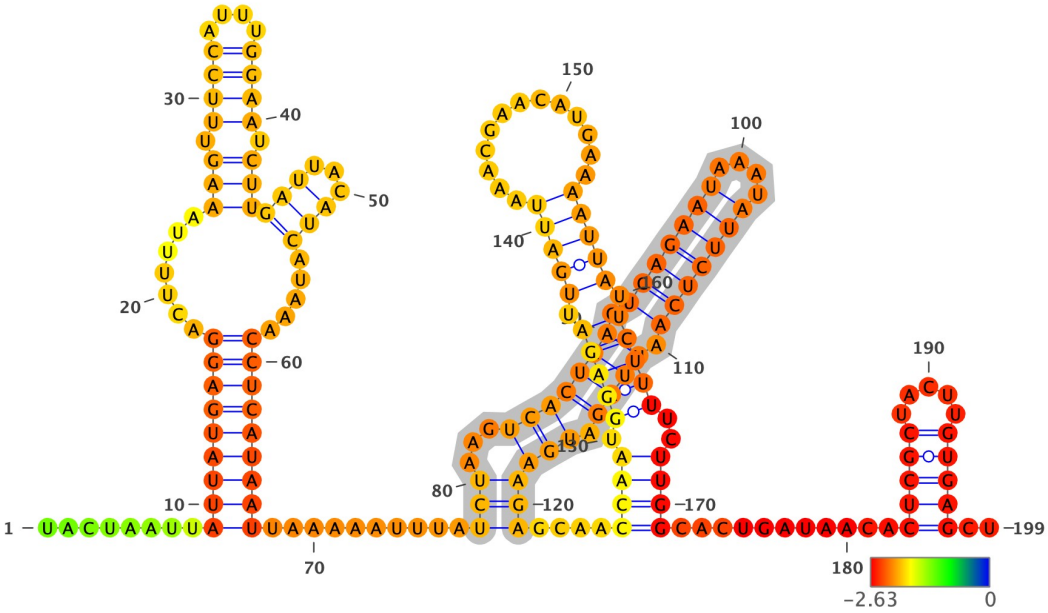
Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

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 468 from nt 27322 to 27365 (nt 78 to 121)

```
5'-TCTAAGTCACTAACTGAGAATAAATAUUCUCAAUUAGAUGAAGA-3'
5'-(((...(((((((.((((((.....)))))).)))))).)))))-3'
Motif MFE = -11.3; z-score = -3.8; 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 27245 to 27443 (motif highlighted in silver):

```
5'-UACUAAUUAUUAUGAGGACUUUUAAAGUUUCCAUUUGGAAUCUUGAUUACAUCAUAAACCUCAUAAUUAAAAAUUUAUCUAAGUCACUAACUGAGAAUAAAUAUUCUCAAU
UAGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCU-3
5'-.........(((((((((.......(((.((((....)))).)))(((...))).....)))))))))..........(((...(((((((.(((((((....)))))))))))))))))).....((((.(((((.(((((.............)))))).)))))..))))..........(((((.....)))))..-3'
MFE = -38.2; z-score = -2.83; ED = 15.61
```

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 143--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 143--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 150 to 199--gene, gene-GU280_gp07, 27394-27759(+)

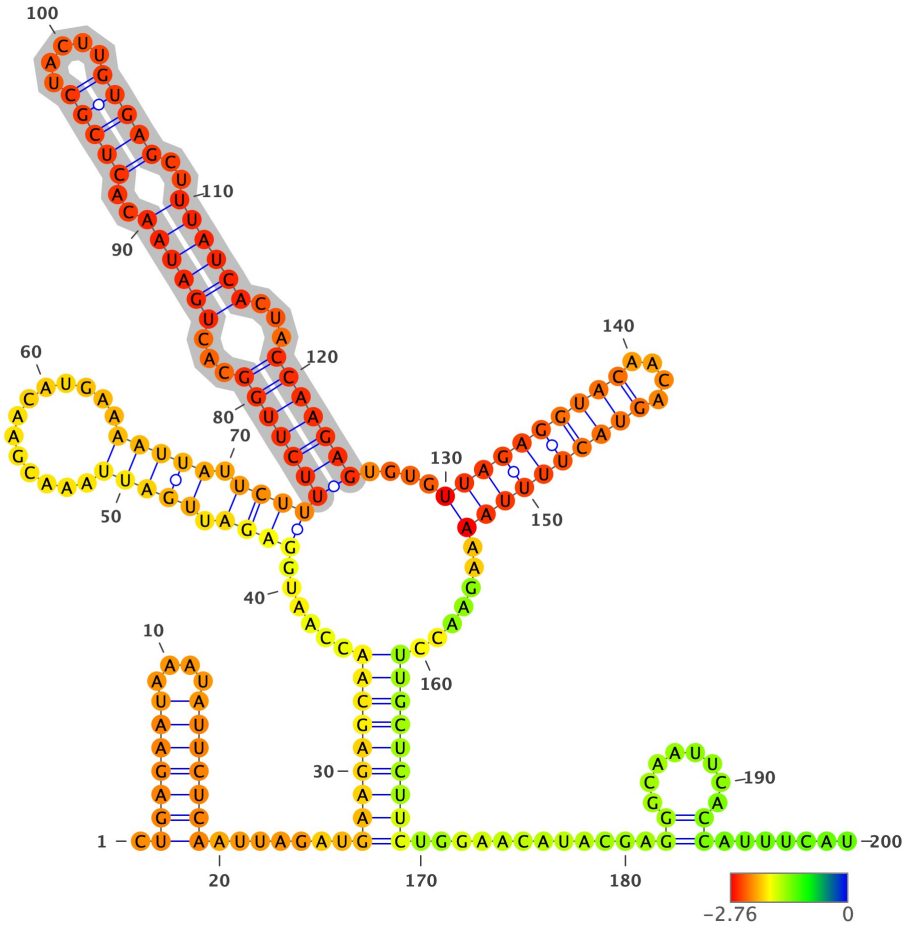
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 150 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 469 from nt 27409 to 27459 (nt 75 to 125)

```
5'-TTCTTGGCACTGATAACACTCGCTACTTGTGAGCTTUAUCACTACCAAGAG-3'
5'-(((((((...(((((((..(((((.....)))))..)))))))...)))))))-3'
Motif MFE = -19.5; z-score = -5.03; ED = 1.25
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27335 to 27534 (motif highlighted in silver):

```
5'-CUGAGAAUAAAUAUUCUCAAUUAGAUGAAGAGCAACCAAUGGAGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUU
AUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAAAAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAU-3
5'-.(((((((....)))))))......(((((((((.....((((.(((((.............))))).))))(((((((...((((((..(((((.....)))))..))
))))...)))))))....((((((((((....))))))))))).....)))))))).............((........)).......-3'
MFE = -51.2; z-score = -3.97; ED = 21.04
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 53--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 53--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 60 to 200--gene, gene-GU280_gp07, 27394-27759(+)

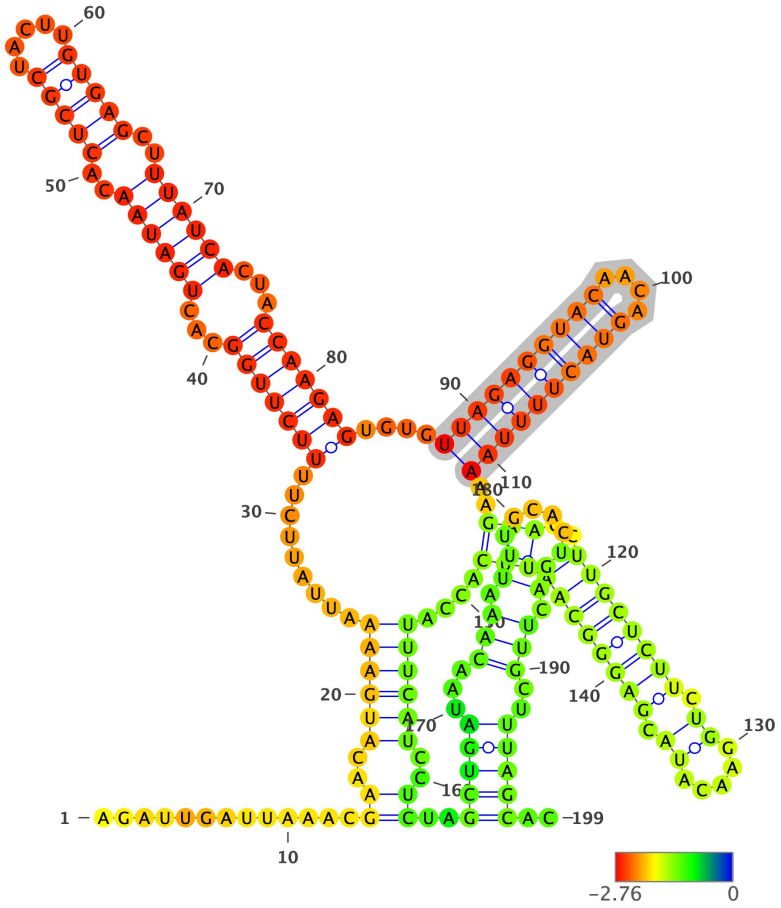
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 60 to 200--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 470 from nt 27464 to 27487 (nt 88 to 111)

```
5'-TTAGAGGTACAACAGUACUUUUAA-3'
5'-((((((((((....))))))))))-3'
Motif MFE = -8.0; z-score = -5.51; ED = 0.68
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27377 to 27575 (motif highlighted in silver):

```
5'-AGAUUGAUUAAACGAACAUGAAAAUUAUUCUUUUCUUGGCACUGAUAACACUCGCUACUUGUGAGCUUUAUCACUACCAAGAGUGUGUUAGAGGUACAACAGUACUUUUAA
AAGAACCUUGCUCUUCUGGAACAUACGAGGGCAAUUCACCAUUUCAUCCUCUAGCUGAUAACAAAUUUGCACUGACUUGCUUUAGCAC-3
5'-............((..((((((.........(((((((...((((((..(((((.....)))))..))))))...)))))))....((((((((((....))))))))))
..(((..(((((((((.((.....)).)))))))))))....))))))..))..((((((...(((.((......)).))))..))))))..-3'
MFE = -44.6; z-score = -2.48; ED = 21.66
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 11--gene, gene-GU280_gp06, 27202-27387(+)

Attributes: ['ID=gene-GU280_gp06', 'Dbxref=GeneID:43740572', 'Name=ORF6', 'gbkey=Gene', 'gene=ORF6', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp06']

3-- nt 1 to 11--CDS, cds-YP_009724394.1, 27202-27387(+)

Attributes: ['ID=cds-YP_009724394.1', 'Parent=gene-GU280_gp06', 'Dbxref=Genbank:YP_009724394.1,GeneID:43740572', 'Name=YP_009724394.1', 'gbkey=CDS', 'gene=ORF6', 'locus_tag=GU280_gp06', 'product=ORF6 protein', 'protein_id=YP_009724394.1']

4-- nt 18 to 199--gene, gene-GU280_gp07, 27394-27759(+)

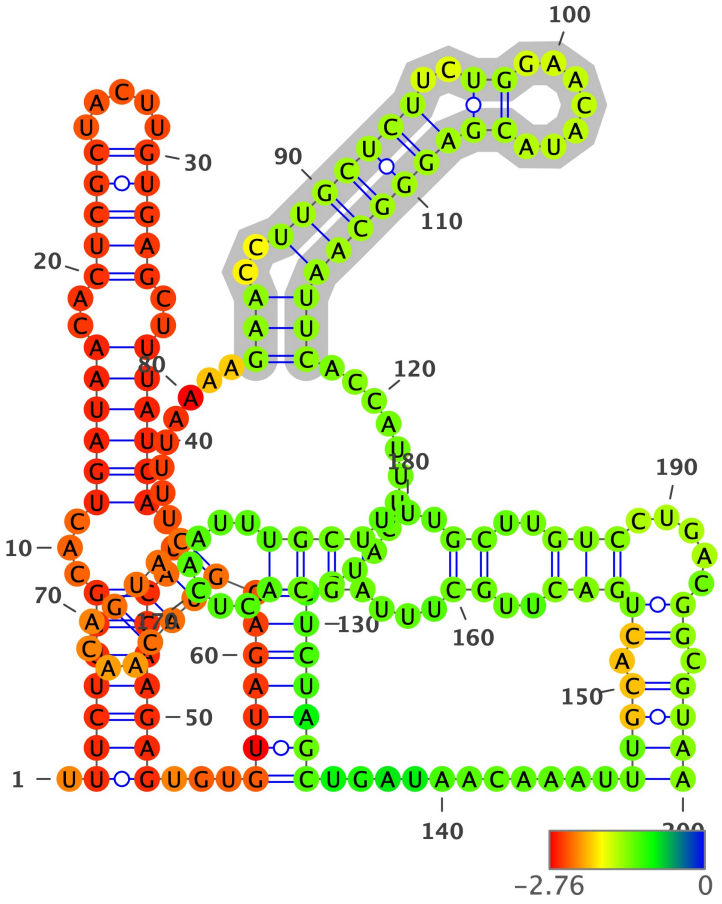
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

5-- nt 18 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 471 from nt 27490 to 27524 (nt 83 to 117)

```
5'-GAACCTTGCTCTTCTGGAACATACGAGGGCAAUUC-3'
5'-(((..(((((((..((.......)))))))))))))-3'
Motif MFE = -8.1; z-score = -1.18; 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 = -47.4; z-score = -2.64; ED = 27.18
```

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_gp07, 27394-27759(+)

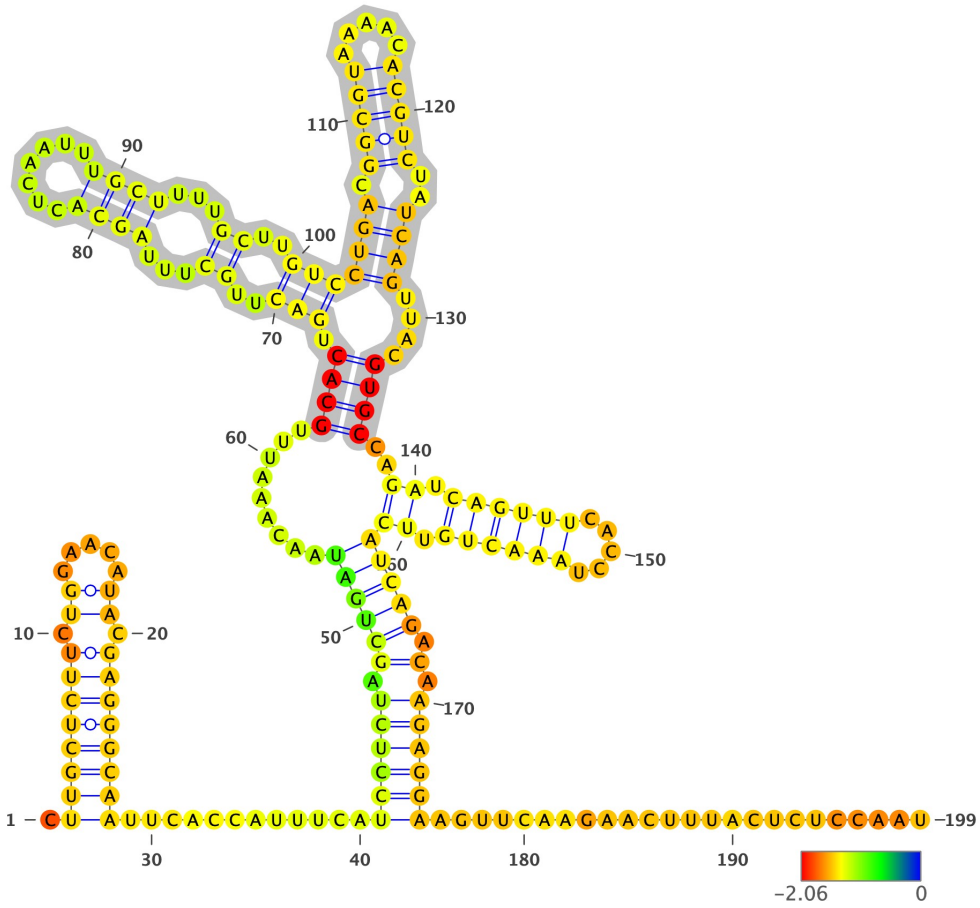
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 472 from nt 27556 to 27629 (nt 63 to 136)

```
5'-GCACTGACTTGCTTTAGCACTCAATTTGCUTTTGCTTGUCCTGACGGCGTAAAACACGUCTAUCAGTTACGUGC-3'
5'-((((.(((..((...(((.........)))...))..)))((((.(((((.....)))))..))))....))))-3'
Motif MFE = -19.8; z-score = -2.32; 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 = -2.79; ED = 13.62
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp07, 27394-27759(+)

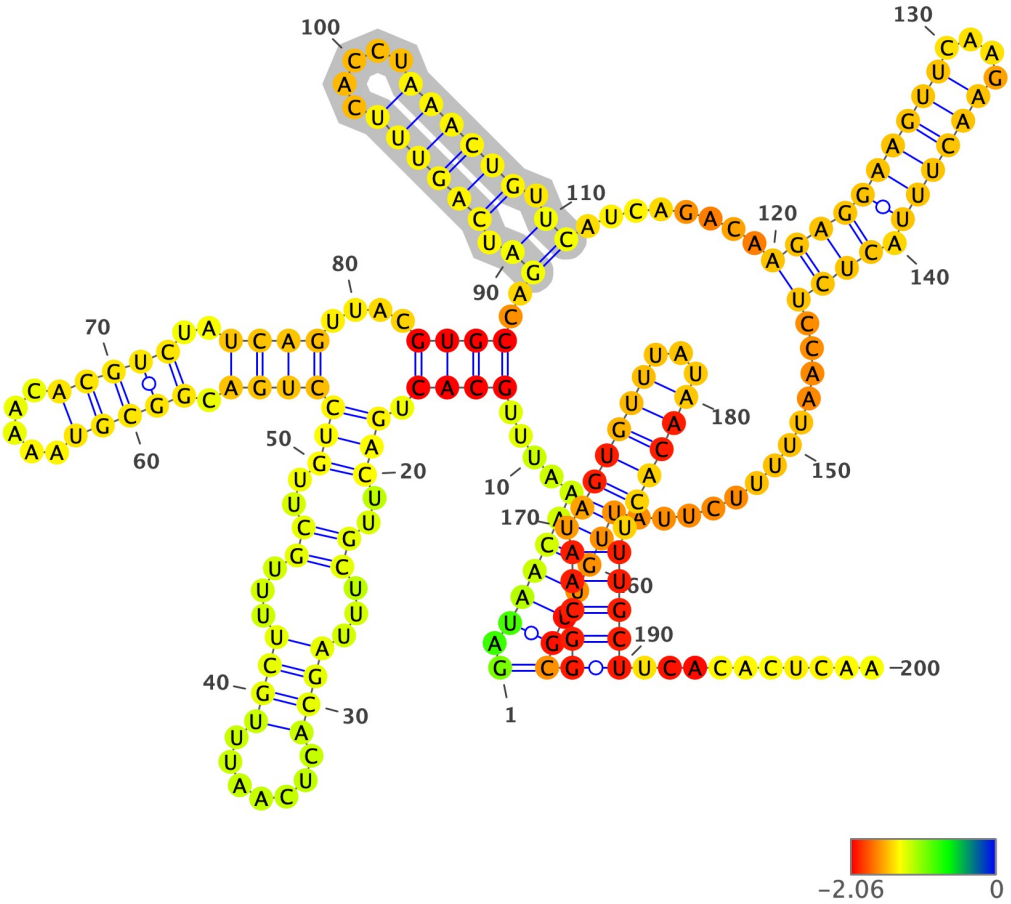
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 199--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

NC_045512.2 (forward strand): Structure number 473 from nt 27632 to 27654 (nt 89 to 111)

```
5'-GATCAGTTTCACCTAAACUGTUC-3'
5'-((.(((((((.....)))))))).))-3'
Motif MFE = -4.1; z-score = -3.07; 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 = -2.46; 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(+)

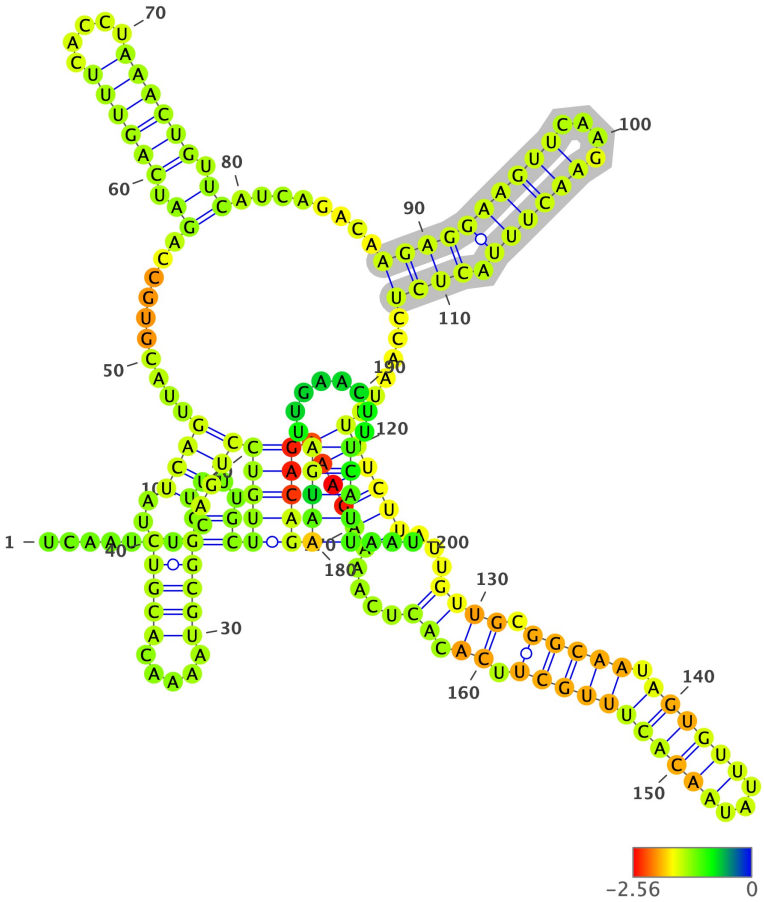
Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

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 474 from nt 27663 to 27687 (nt 88 to 112)

```
5'-AGAGGAAGTTCAAGAACUUUACUCU-3'
5'-((((((((((....)))))).))))-3'
Motif MFE = -5.8; z-score = -2.8; 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 = -2.69; 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(+)

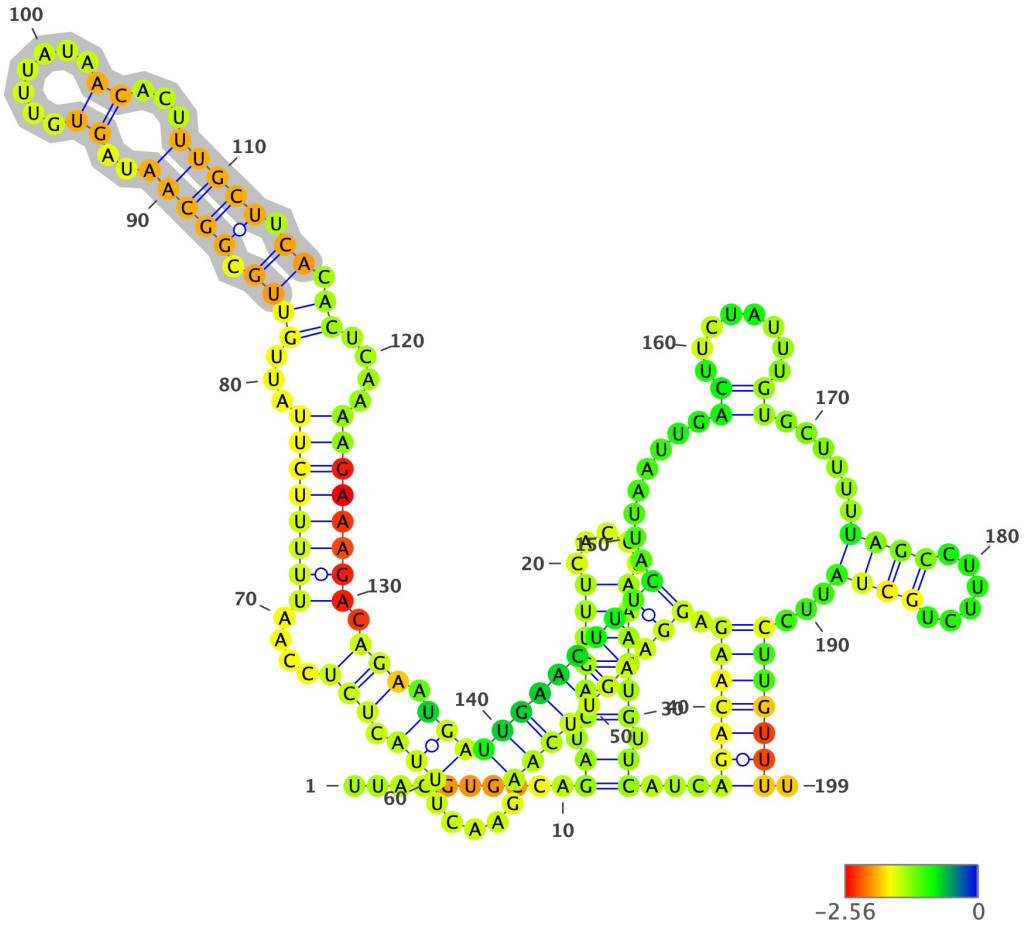
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

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 475 from nt 27705 to 27736 (nt 84 to 115)

```
5'-TGCGGCAATAGTGTTTATAACACTUUGCUTCA-3'
5'-((.(((((..((.......))...))))).))-3'
Motif MFE = -9.6; z-score = -3.68; ED = 1.95
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27622 to 27820 (motif highlighted in silver):

```
5'-UUACGUGCCAGAUCAGUUUCACCUAAACUGUUCAUCAGACAAGAGGAAGUUCAAGAACUUUACUCUCCAAUUUUUCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGC
UUCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUU-3
5'-..........((.((((((.....)))))).))...(((((((.((((((((((.....(((.(((....((((((((...((((.(((((..((.......))...))))
).)).))....)))))))).))).))))))))))))).........((........)).....((((......))))...))))))).-3'
MFE = -32.9; z-score = -2.36; ED = 33.05
```

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 138--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 138--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 135 to 199--gene, gene-GU280_gp08, 27756-27887(+)

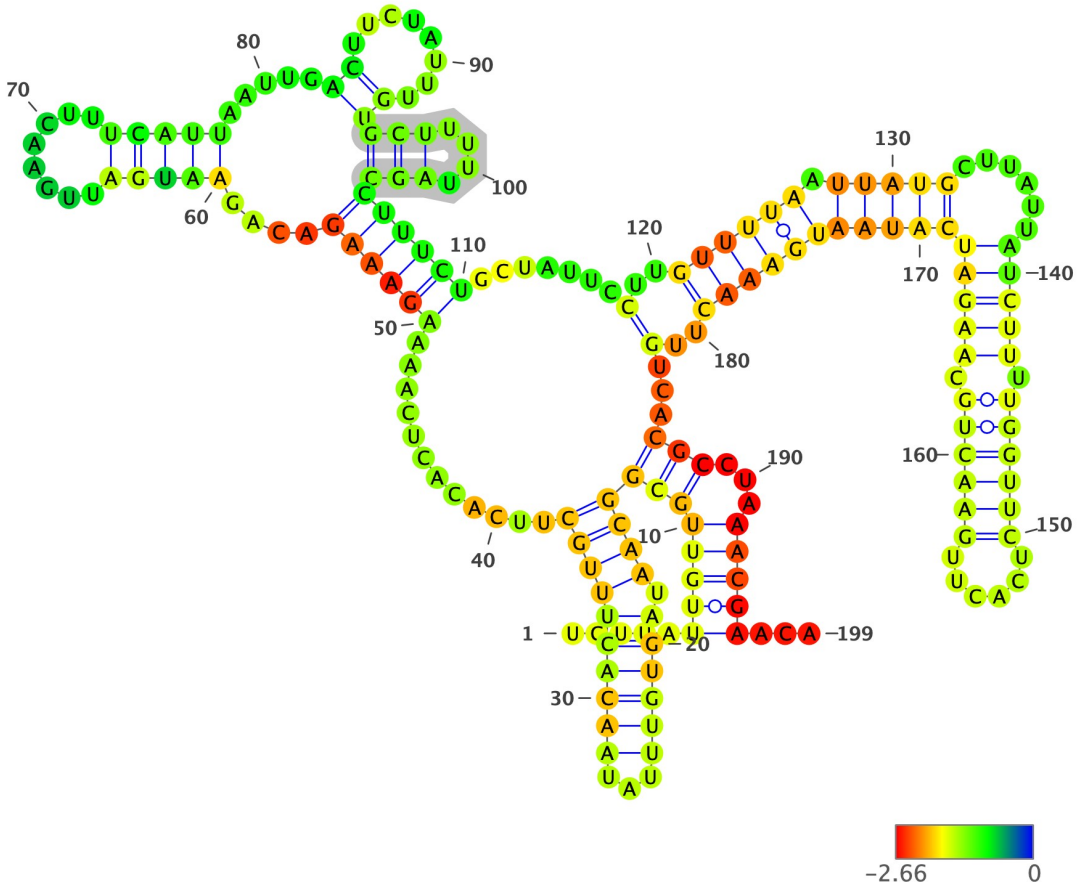
Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 135 to 199--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

NC_045512.2 (forward strand): Structure number 476 from nt 27790 to 27799 (nt 95 to 104)

```
5'-GCTTTTTAGC-3'
5'-(((....)))-3'
Motif MFE = -0.8; z-score = -4.96; ED = 1.04
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27696 to 27894 (motif highlighted in silver):

```
5'-UCUUAUUGUUGCGGCAAUAGUGUUUAUAACACUUUGCUUCACACUCAAAAGAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUG
CUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACA-3
5'-.....(((((((((((.((((((...)))))))))).............((((((....(((((........)))))).....((........))(((....))))))))).
......(..((((((.(((((......(((((.((((((......))))))).))))))))))))))))..)...)))...)))))...-3'
MFE = -35.0; z-score = -1.4; ED = 34.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 64--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 64--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 61 to 192--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 61 to 192--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 199 to 199--gene, gene-GU280_gp09, 27894-28259(+)

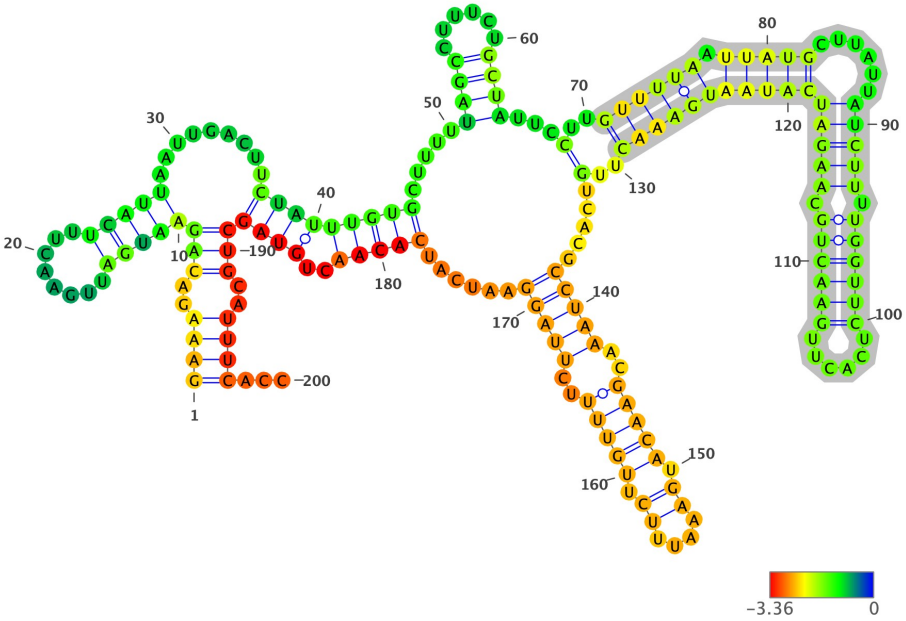
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 199 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 27816 to 27874 (nt 71 to 129)

```
5'-GTTTTAATTATGCTTATTATCTTTTGGTTCTCACTTGAACUGCAAGATCATAAUGAAAC-3'
5'-(..(((....((........(((.((((((.....))))))).)))..))...))))..)-3'
Motif MFE = -12.7; z-score = -3.03; ED = 3.59
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27746 to 27945 (motif highlighted in silver):

```
5'-GAAAGACAGAAUGAUUGAACUUUCAUUAAUUGACUUCUAUUUGUGCUUUUUAGCCUUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACU
GCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACC-3
5'-((((..(((((((((........)))))).........(((((((((.....((((......)))))...(..((((((.(((((.......(((((.(((((((.....)))))
).)))))))))))))))..).....(((((..((((((.((....)).)))))..)))))).....)))))..)))))))..)))).--3'
MFE = -36.5; z-score = -2.06; ED = 17.08
```

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 14--gene, gene-GU280_gp07, 27394-27759(+)

Attributes: ['ID=gene-GU280_gp07', 'Dbxref=GeneID:43740573', 'Name=ORF7a', 'gbkey=Gene', 'gene=ORF7a', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp07']

3-- nt 1 to 14--CDS, cds-YP_009724395.1, 27394-27759(+)

Attributes: ['ID=cds-YP_009724395.1', 'Parent=gene-GU280_gp07', 'Dbxref=Genbank:YP_009724395.1,GeneID:43740573', 'Name=YP_009724395.1', 'gbkey=CDS', 'gene=ORF7a', 'locus_tag=GU280_gp07', 'product=ORF7a protein', 'protein_id=YP_009724395.1']

4-- nt 11 to 142--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

5-- nt 11 to 142--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

6-- nt 149 to 200--gene, gene-GU280_gp09, 27894-28259(+)

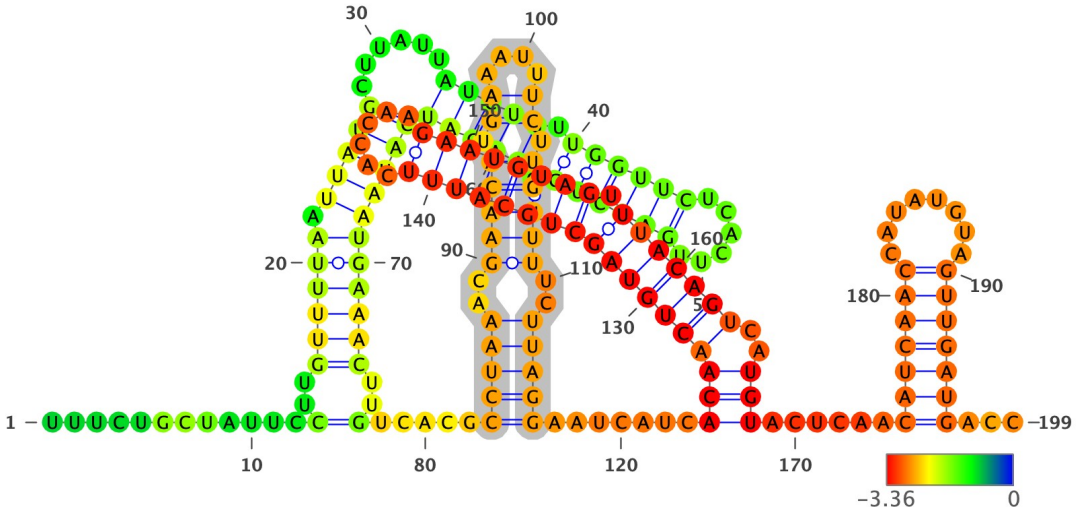
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

7-- nt 149 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 478 from nt 27883 to 27916 (nt 83 to 116)

```
5'-CCTAAACGAACATGAAATTUCTUGUUUTCUUAGG-3'
5'-(((((..(((((.((....)).)))))..)))))-3'
Motif MFE = -8.0; z-score = -3.41; ED = 0.86
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27801 to 27999 (motif highlighted in silver):

```
5'-UUUCUGCUAUUCCUUGUUUUAAUUAUGCUUAUUAUCUUUUGGUUCUCACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUC
UUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUUUACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACC-3
5'-............(..((((((.(((((......(((((.((((((......))))))).))))))))))))))))..).....(((((..(((((.((....)).)))))..
)))))).......((((((((((((((((((.....)))))))).)))))))..))).....(((((((........)))))))...-3'
MFE = -46.6; z-score = -3.51; ED = 12.85
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 87--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 87--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 94 to 199--gene, gene-GU280_gp09, 27894-28259(+)

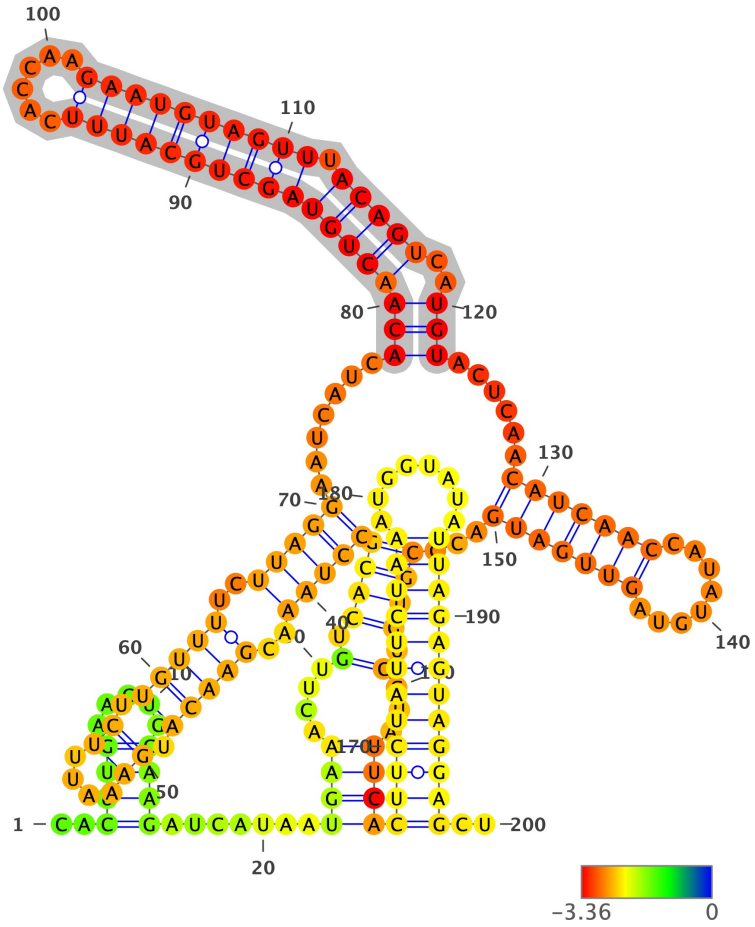
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 94 to 199--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 479 from nt 27924 to 27968 (nt 78 to 122)

```
5'-ACAACTGTAGCTGCATTTCACCAAGAAUGUAGUUTACAGTCAUGU-3'
5'-(((.((((((((((((.....))))))))))).)))))...)))-3'
Motif MFE = -15.2; z-score = -4.08; ED = 4.71
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 27847 to 28046 (motif highlighted in silver):

```
5'-CACUUGAACUGCAAGAUCAUAAUGAAACUUGUCACGCCUAAACGAACAUGAAAUUUCUUGUUUUCUUAGGAAUCAUCACAACUGUAGCUGCAUUUCACCAAGAAUGUAGUU
UACAGUCAUGUACUCAACAUCAACCAUAUGUAGUUGAUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCU-3
5'-..((((.....))))........((((....(.((((((((..(((((.((....)).)))))..)))))).......((((((((((((((((.....))))))))))
.)))))..)))......(((((((.........)))))))...)))))...)...))))((((((((((((.........))))))))))))..--3'
MFE = -51.6; z-score = -4.3; ED = 15.97
```

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 41--gene, gene-GU280_gp08, 27756-27887(+)

Attributes: ['ID=gene-GU280_gp08', 'Dbxref=GeneID:43740574', 'Name=ORF7b', 'gbkey=Gene', 'gene=ORF7b', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp08']

3-- nt 1 to 41--CDS, cds-YP_009725296.1, 27756-27887(+)

Attributes: ['ID=cds-YP_009725296.1', 'Parent=gene-GU280_gp08', 'Dbxref=Genbank:YP_009725296.1,GeneID:43740574', 'Name=YP_009725296.1', 'gbkey=CDS', 'gene=ORF7b', 'locus_tag=GU280_gp08', 'product=ORF7b', 'protein_id=YP_009725296.1']

4-- nt 48 to 200--gene, gene-GU280_gp09, 27894-28259(+)

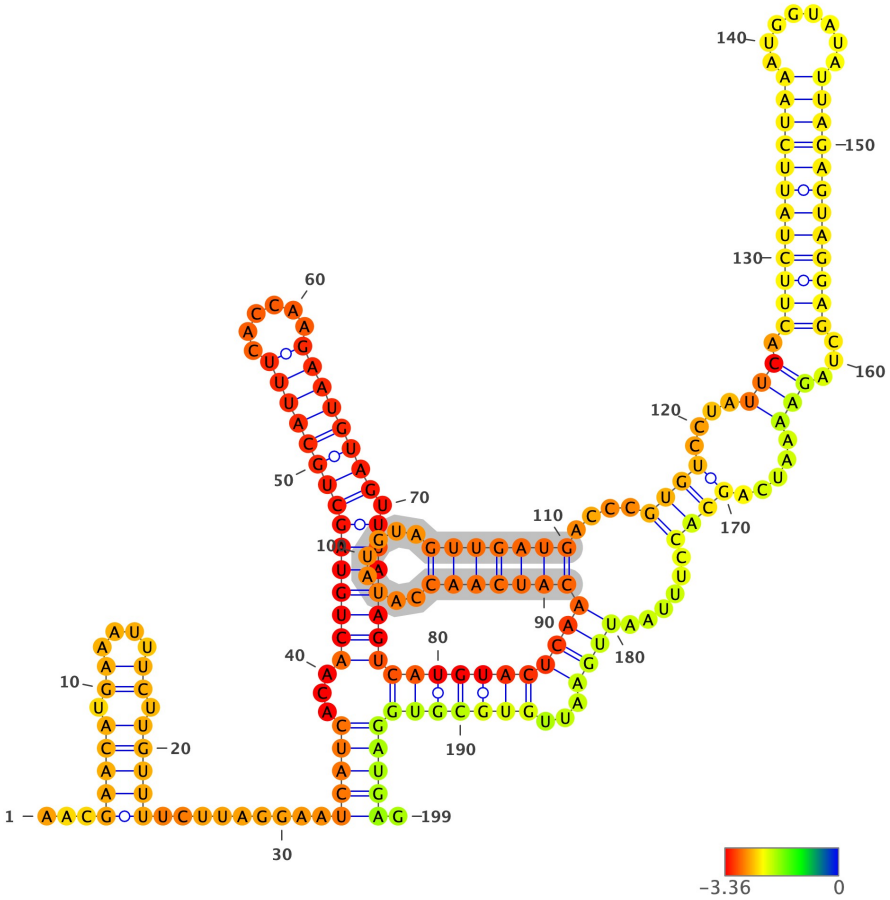
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

5-- nt 48 to 200--CDS, cds-YP_009724396.1, 27894-28259(+)

Attributes: ['ID=cds-YP_009724396.1', 'Parent=gene-GU280_gp09', 'Dbxref=Genbank:YP_009724396.1,GeneID:43740577', 'Name=YP_009724396.1', 'gbkey=CDS', 'gene=ORF8', 'locus_tag=GU280_gp09', 'product=ORF8 protein', 'protein_id=YP_009724396.1']

NC_045512.2 (forward strand): Structure number 480 from nt 27975 to 27996 (nt 89 to 110)

```
5'-CATCAACCATATGTAGUUGAUG-3'
5'-(((((((........)))))))-3'
Motif MFE = -6.3; z-score = -3.87; 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 = -3.35; 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(+)

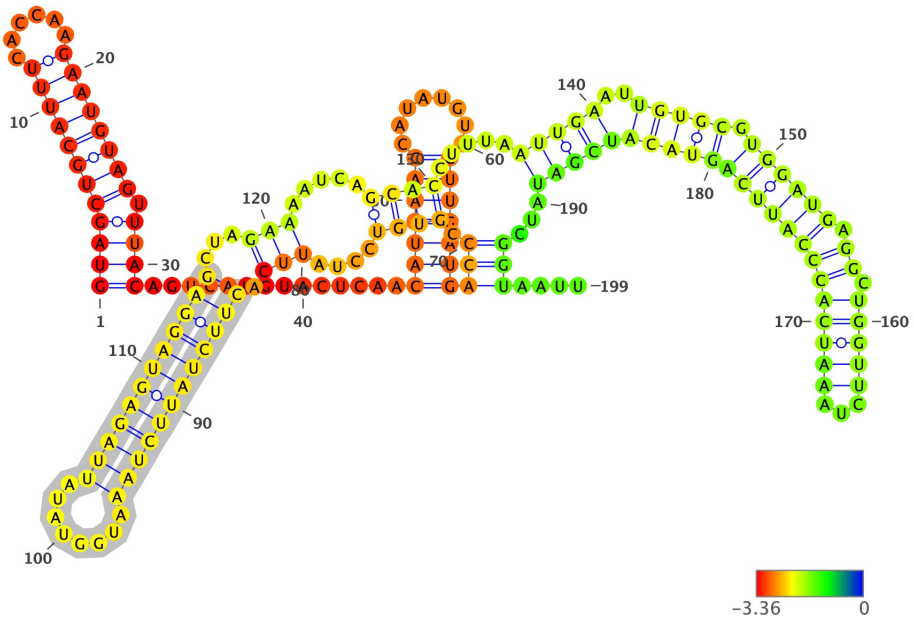
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 481 from nt 28013 to 28044 (nt 84 to 115)

```
5'-CTTCTATTCTAAATGGTATATUAGAGUAGGAG-3'
5'-(((((((((((.........))))))))))))-3'
Motif MFE = -11.8; z-score = -4.25; 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 = -3.28; ED = 31.87
```

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_gp09, 27894-28259(+)

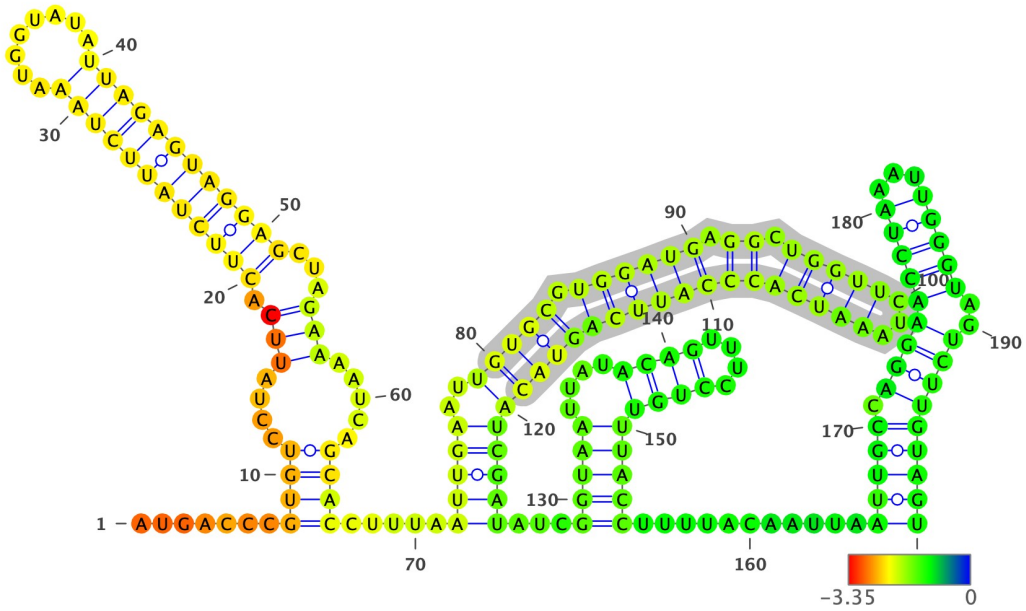
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 482 from nt 28073 to 28112 (nt 80 to 119)

```
5'-GTGCGTGGATGAGGCTGGTTCTAAAUCACCCAUUCAGUAC-3'
5'-(((...(((((.((.(((.......)))))))))..)))-3'
Motif MFE = -13.3; z-score = -2.53; 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 27994 to 28192 (motif highlighted in silver):

```
5'-AUGACCCGUGUCCUAUUCACUUCUAUUCUAAAUGGUAUAUUAGAGUAGGAGCUAGAAAAUCAGCACCUUUAAUUGAAUUGUGCGUGGAUGAGGCUGGUUCUAAAUCACCCA
UUCAGUACAUCGAUAUCGGUAAUUAUACAGUUUCCUGUUUACCUUUUACAAUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGU-3
5'-.......((((....(((.((((((((((((.........)))))))))))...)))).....)))).....(((((..(((((.((((((.((.(((((...)))))))))
))))))))))))))...(((((....((((....)))))))))...........(((((.(((((((((...)))))..)))))))))-3'
MFE = -48.5; z-score = -2.1; ED = 29.61
```

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_gp09, 27894-28259(+)

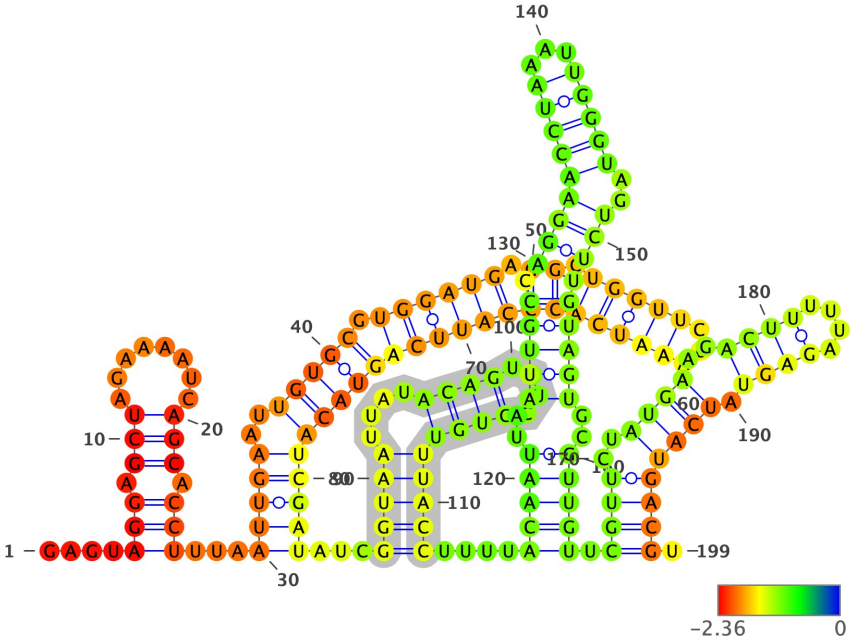
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 483 from nt 28122 to 28147 (nt 87 to 112)

```
5'-GGTAATTATACAGTTTCCUGUUUACC-3'
5'-(((((....((((....)))))))))-3'
Motif MFE = -4.9; z-score = -2.22; 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 = -1.12; 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(+)

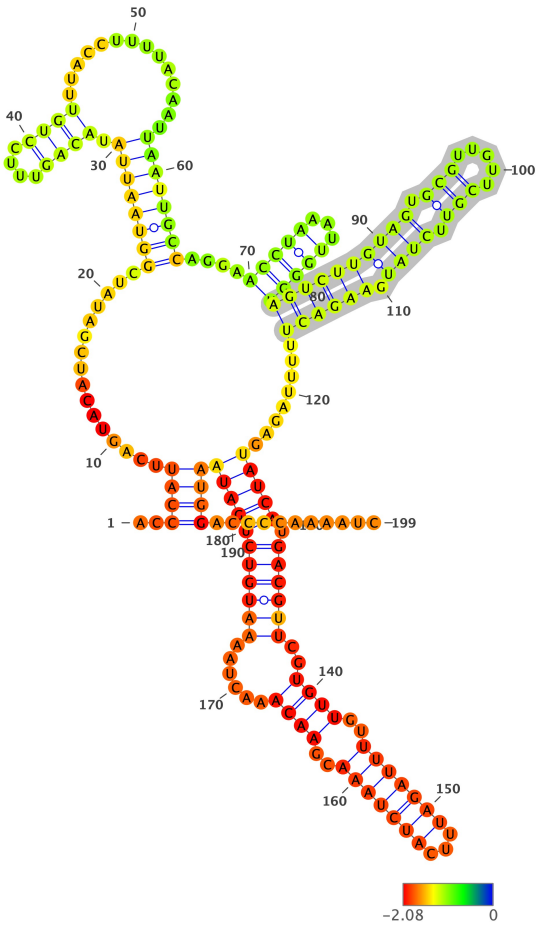
Attributes: ['ID=gene-GU280_gp09', 'Dbxref=GeneID:43740577', 'Name=ORF8', 'gbkey=Gene', 'gene=ORF8', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp09']

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 484 from nt 28182 to 28215 (nt 83 to 116)

```
5'-AGTCTTGTAGTGCGTTGTTCGUTCUAUGAAGACU-3'
5'-((((((((((.(((.....))).)))))..)))))-3'
Motif MFE = -11.3; z-score = -3.22; 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 = -1.75; 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(+)

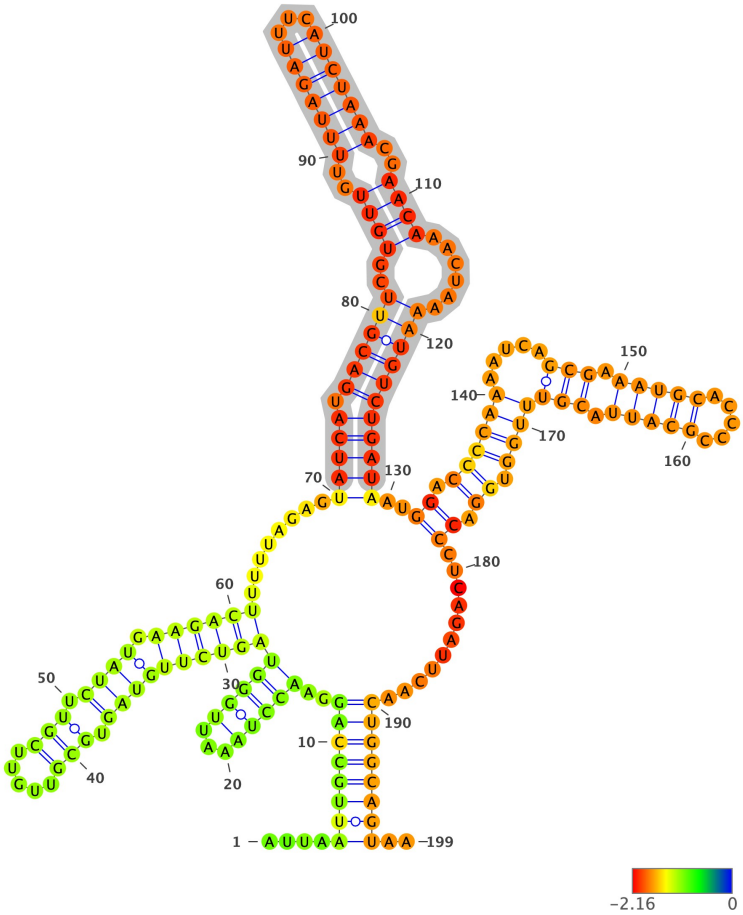
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 485 from nt 28225 to 28282 (nt 71 to 128)

```
5'-ATCATGACGTTCGTGTTGTTTTAGATTTCAUCUAAACGAACAAACTAAAAUGUCUGAU-3'
5'-((((.((((....((((..(((((((...)))))))..))))........))))))))-3'
Motif MFE = -13.4; z-score = -2.78; ED = 9.4
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28155 to 28353 (motif highlighted in silver):

```
5'-AUUAAUUGCCAGGAACCUAAAUUGGGUAGUCUUGUAGUGCGUUGUUCGUUCUAUGAAGACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAAC
AAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAA-3
5'-....(((((((((..((((((...))))))((((((((((.(((.....))).)))))..))))))).......(((((.((((((..((((..(((((((...)))))))..)))
).....))))))))))))..((.((((((.....(((.(((((.....)))))).)))))))..)).))..........))))))))..-3'
MFE = -57.2; z-score = -3.38; ED = 16.2
```

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 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(+)

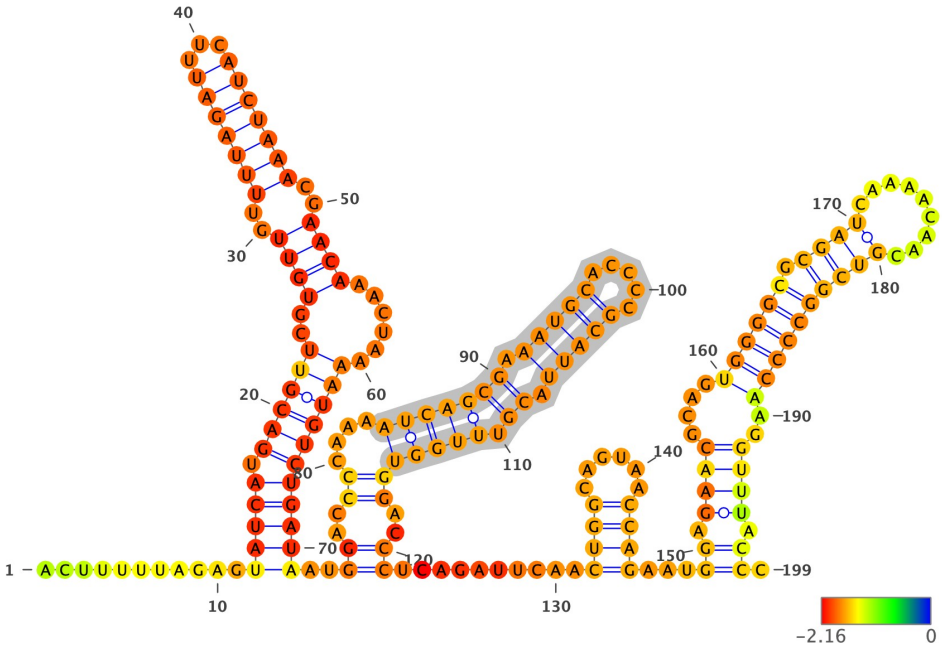
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 486 from nt 28296 to 28327 (nt 84 to 115)

```
5'-ATCAGCGAAATGCACCCCGCAUUACGTUUGGU-3'
5'-(((((((.(((((.....))))))..)).))))-3'
Motif MFE = -8.3; z-score = -1.92; 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 28213 to 28411 (motif highlighted in silver):

```
5'-ACUUUUUAGAGUAUCAUGACGUUCGUGUUGUUUUAGAUUUCAUCUAAACGAACAAACUAAAAUGUCUGAUAAUGGACCCCAAAAUCAGCGAAAUGCACCCCGCAUUACGUU
UGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUUUACCC-3
5'-...........(((((.((((((..((((..(((((((...)))))))..))))......))))))))))..((..((....(((((((.(((((.....))))))..)).)
))))))..))..........((((......))))...((.((((....((((((.((((.........))))))))))..))))).)).-3'
MFE = -51.0; z-score = -2.19; ED = 33.75
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 47--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 47--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 62 to 199--gene, gene-GU280_gp10, 28274-29533(+)

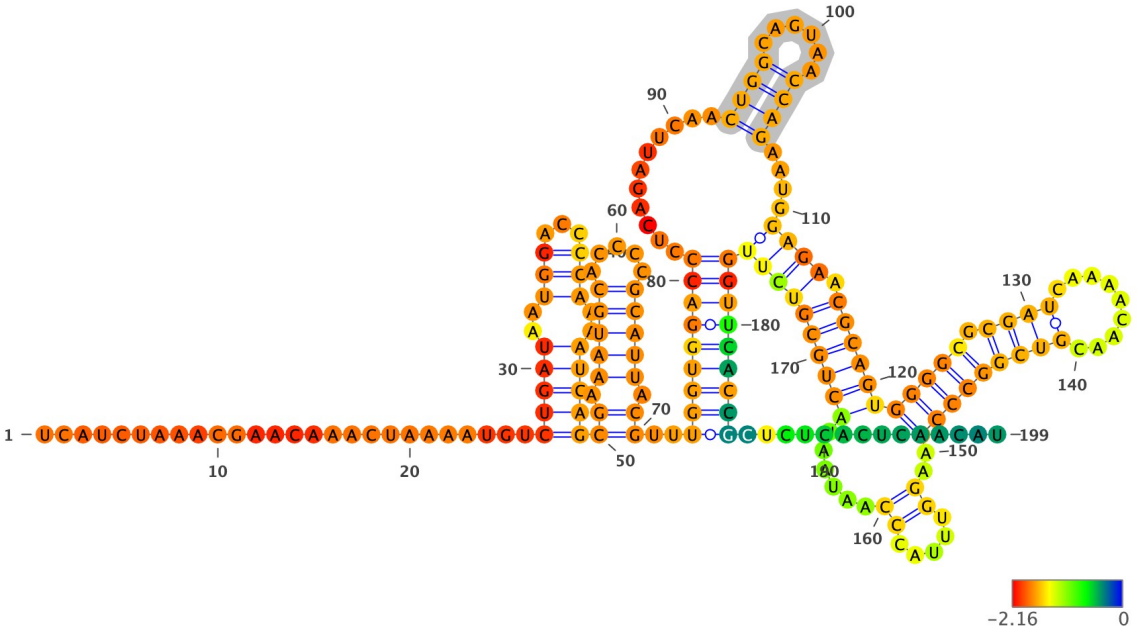
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

5-- nt 62 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 28344 to 28357 (nt 93 to 106)

```
5'-CTGGCAGTAACCAG-3'
5'-((((......))))-3'
Motif MFE = -3.2; z-score = -2.92; 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 = -2.54; 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(+)

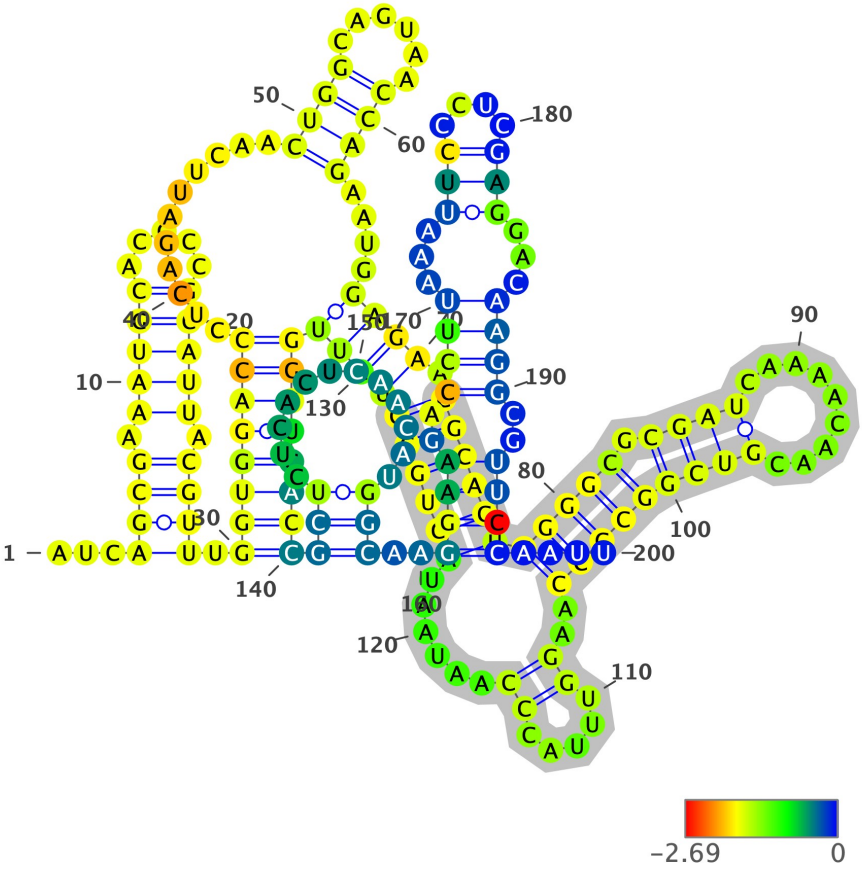
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 488 from nt 28367 to 28423 (nt 72 to 128)

```
5'-CGCAGTGGGGCGCGATCAAAACAACGUCGGCCCCAAGGTTTACCCAATAATACUGCG-3'
5'-(((((.(((((..((((.........)))).)))))..((.....)).......)))))-3'
Motif MFE = -20.2; z-score = -2.7; ED = 4.36
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28296 to 28495 (motif highlighted in silver):

```
5'-AUCAGCGAAAUGCACCCCGCAUUACGUUUGGUGGACCCUCAGAUUCAACUGGCAGUAACCAGAAUGGAGAACGCAGUGGGGCGCGAUCAAAACAACGUCGGCCCCAAGGUU
UACCCAAUAAUACUGCGUCUUGGUUCACCGCUCUCACUCAACAUGGCAAGGAAGACCUUAAAUUCCCUCGAGGACAAGGCGUUCCAAUU-3
5'-...((((.(((((.....))))).)))).(((((((.(((((.....))))).....((((.....)))).....(((((.(((((((((((.(((((.........)))))))))))..((..
...))......))))))))))))))))))((((.............)))).((((..((((...(((....)))...))))..))))....-3'
MFE = -59.0; z-score = -2.16; ED = 16.62
```

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_gp10, 28274-29533(+)

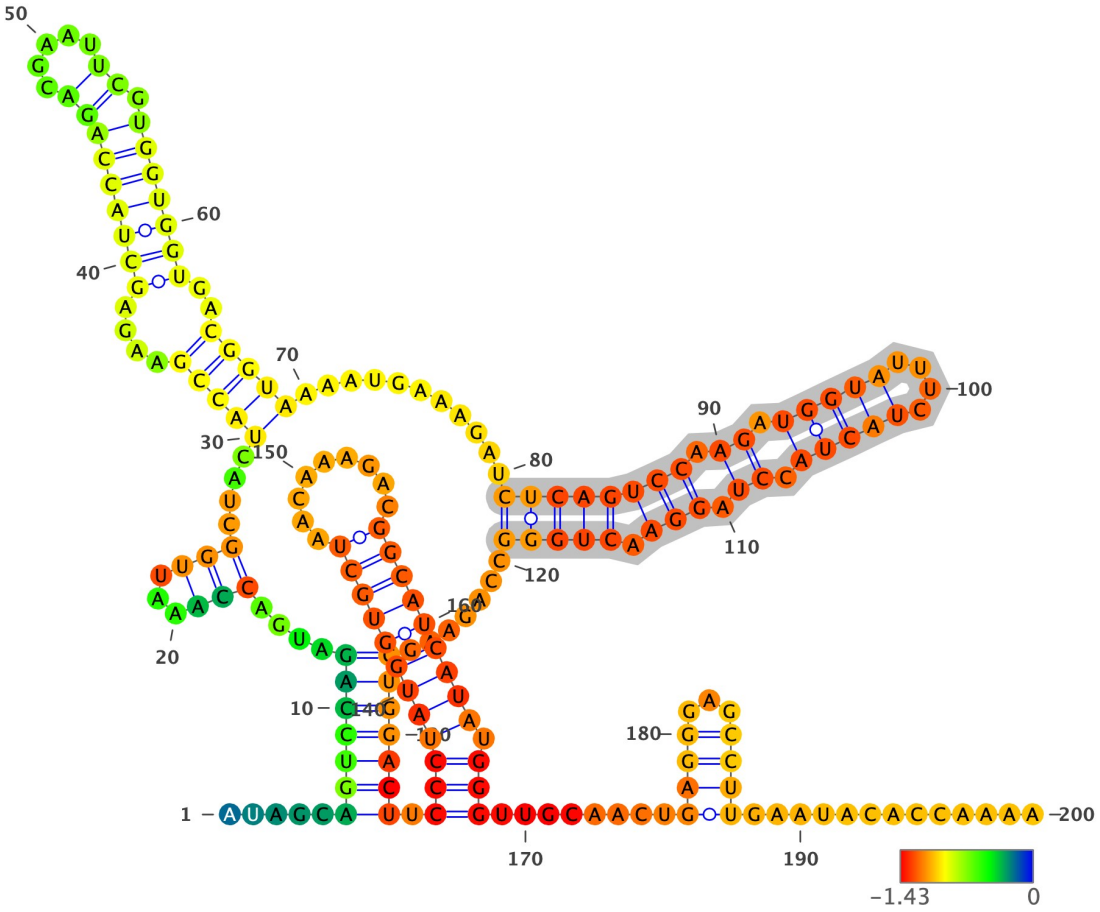
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 489 from nt 28583 to 28621 (nt 81 to 119)

```
5'-CTCAGTCCAAGATGGTATTTCTACUACCUAGGAACUGGG-3'
5'-(((((((((.((.(((........))).)).))).))))))-3'
Motif MFE = -12.9; z-score = -3.45; ED = 2.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28503 to 28702 (motif highlighted in silver):

```
5'-AUAGCAGUCCAGAUGACCAAAUUGGCUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAG
GAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAA-3
5'-.....(((((((....(((...))))....(((((....(((((((((.....)).)))))))..)))))..........(((((((.((.(((((....)))))).)).)
)).)))))......)))))).((((((((((((.........)))))))))).)))........((((...))))............-3'
MFE = -55.2; z-score = -1.83; ED = 20.17
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

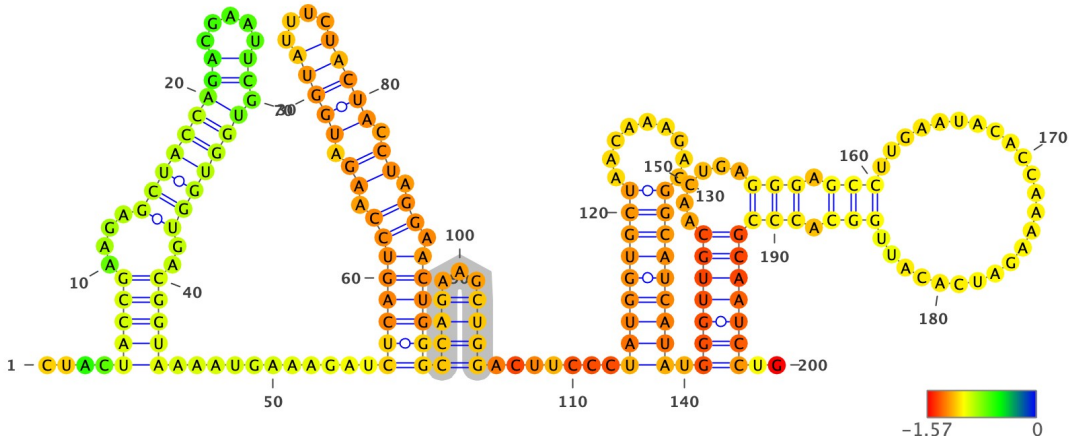
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 490 from nt 28622 to 28632 (nt 95 to 105)

```
5'-CCAGAAGCUGG-3'
5'-(((((...)))))-3'
Motif MFE = -2.1; z-score = -4.07; ED = 0.41
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28528 to 28727 (motif highlighted in silver):

```
5'-CUACUACCGAAGAGCUACCAGACGAAUUCGUGGUGGUGACGGUAAAAUGAAAGAUCUCAGUCCAAGAUGGUAUUUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCC
CUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUUGGCACCCGCAAUCCUG-3
5'-....(((((....((((((((((.....)).)))))))..)))))..........(((((((((.((.(((((....)))))).)).)).)))))))(((...))))......
.(((((((((.........)))))))).(((((((.....(((.(((.........................))).))))))))))..-3'
MFE = -57.7; z-score = -2.11; ED = 16.68
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

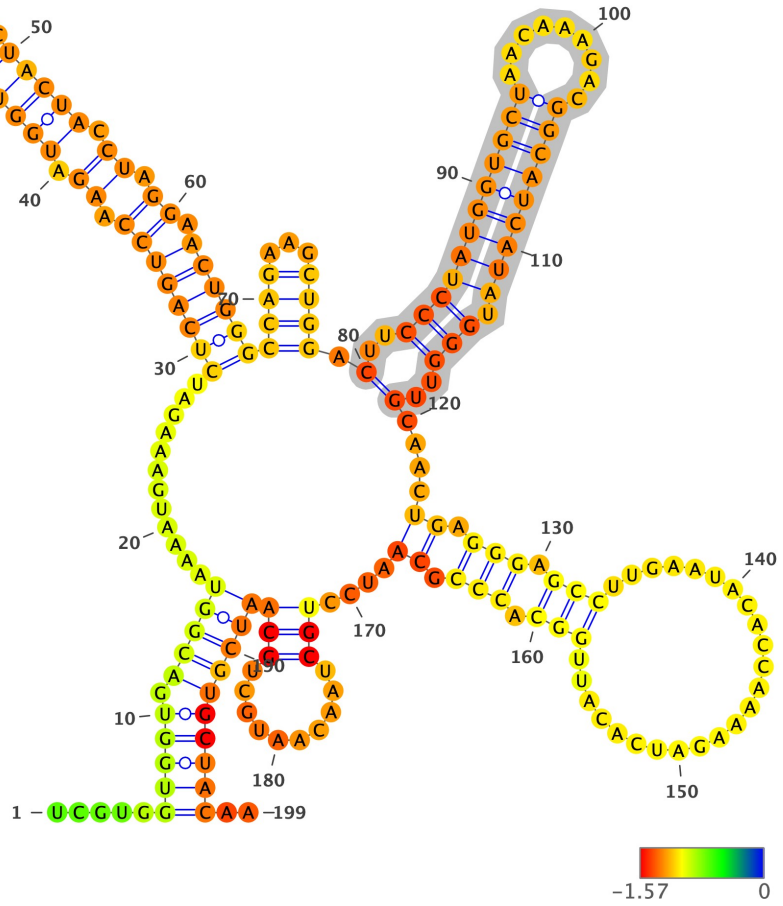
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 491 from nt 28634 to 28673 (nt 80 to 119)

```
5'-CTTCCCTATGGTGCTAACAAAGACGGCAUCAUATGGGTTG-3'
5'-(..(((.((((((((.........))))))))..)))..)-3'
Motif MFE = -14.5; z-score = -3.09; 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 = -1.5; 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(+)

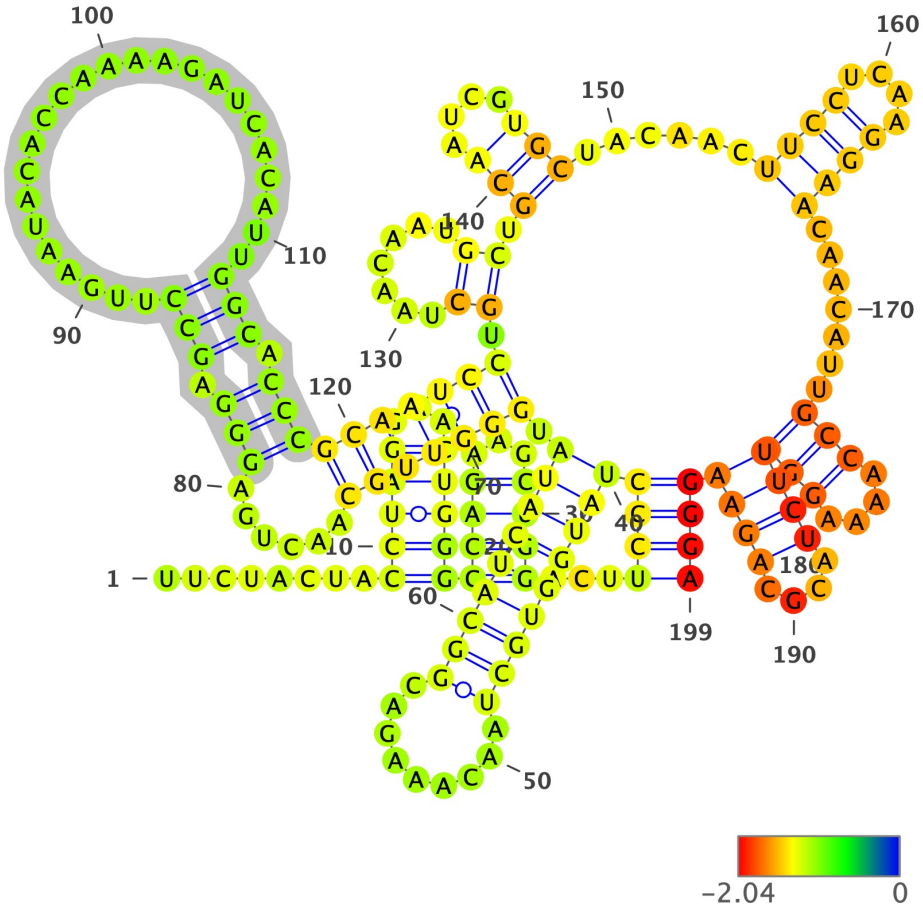
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 492 from nt 28681 to 28718 (nt 81 to 118)

```
5'-GGGAGCCTTGAATACACCAAAAGATCACATTGGCACCC-3'
5'-(((.(((.....................))).)))-3'
Motif MFE = -7.1; z-score = -1.27; ED = 2.46
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28601 to 28799 (motif highlighted in silver):

```
5'-UUCUACUACCUAGGAACUGGGCCAGAAGCUGGACUUCCCUAUGGUGCUAACAAAGACGGCAUCAUAUGGGUUGCAACUGAGGGAGCCUUGAAUACACCAAAAGAUCACAUU
GGCACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAGGGA-3
5'-........(((((...)))))(((((...))))).((((((((((((.........)))))))))).(((((((.....(((.(((.....................
))).)))))))))).((.......)).(((....))).....((((....)))).....(((....)))(((((....)))))))-3'
MFE = -49.6; z-score = -1.18; ED = 27.65
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

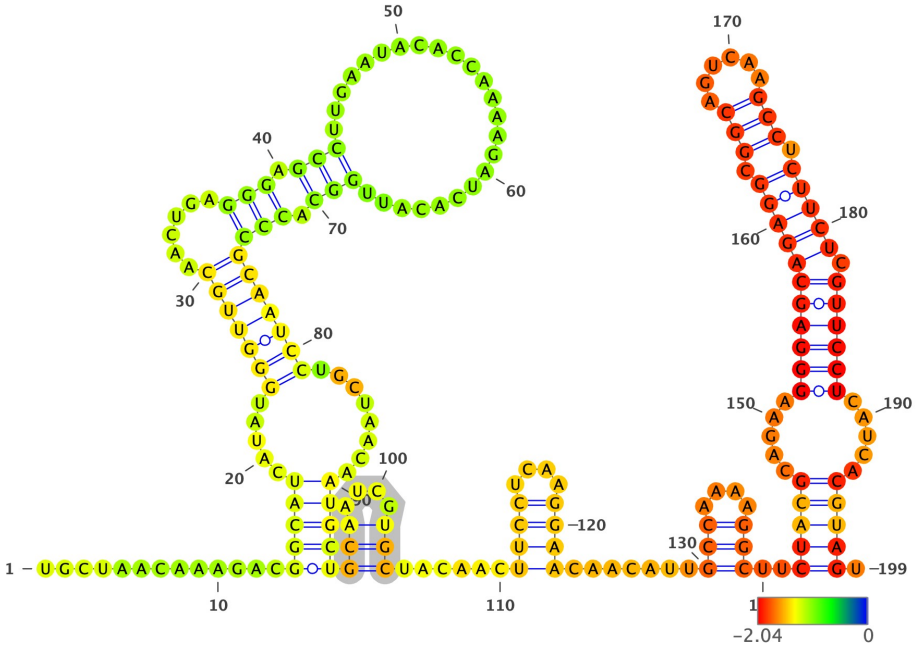
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 493 from nt 28739 to 28748 (nt 95 to 104)

```
5'-GCAATCGTGC-3'
5'-((......))-3'
Motif MFE = -0.2; z-score = -0.52; 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 = -1.55; 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(+)

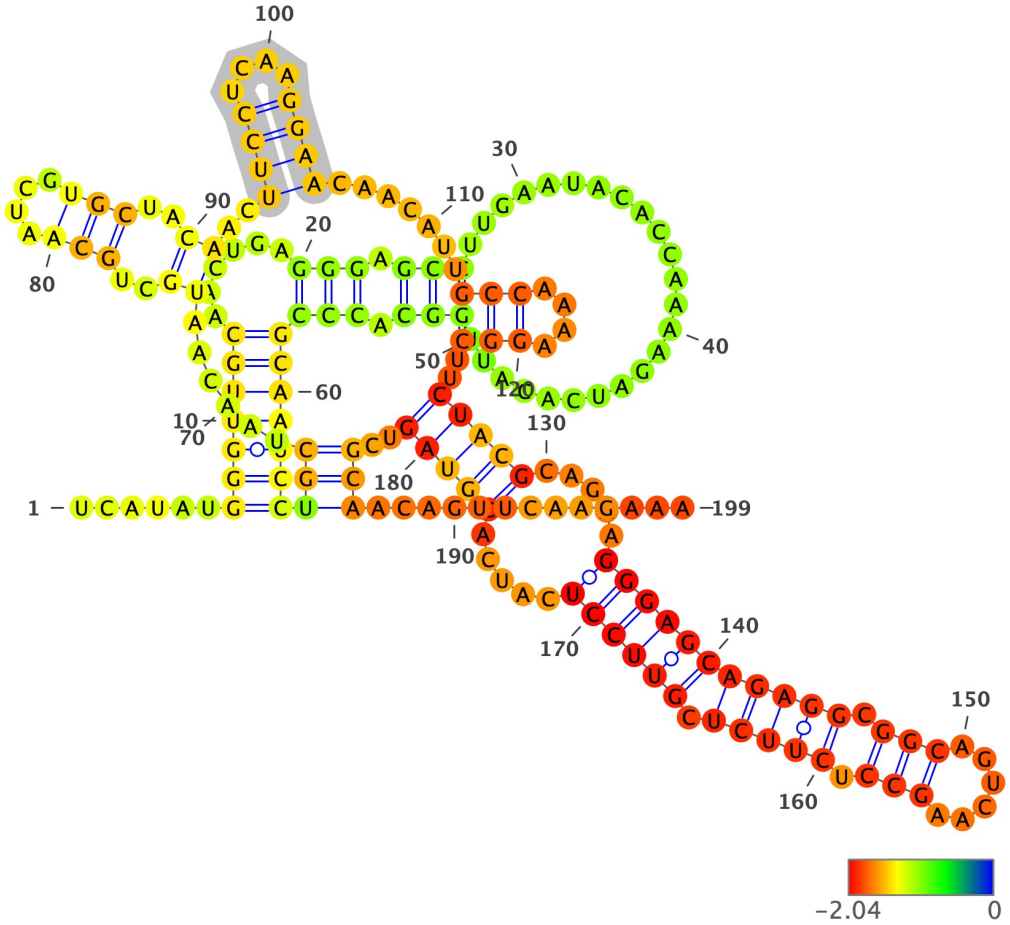
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 494 from nt 28755 to 28766 (nt 94 to 105)

```
5'-TTCCTCAAGGAA-3'
5'-((((....))))-3'
Motif MFE = -1.6; z-score = -5.99; 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 = -1.74; 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(+)

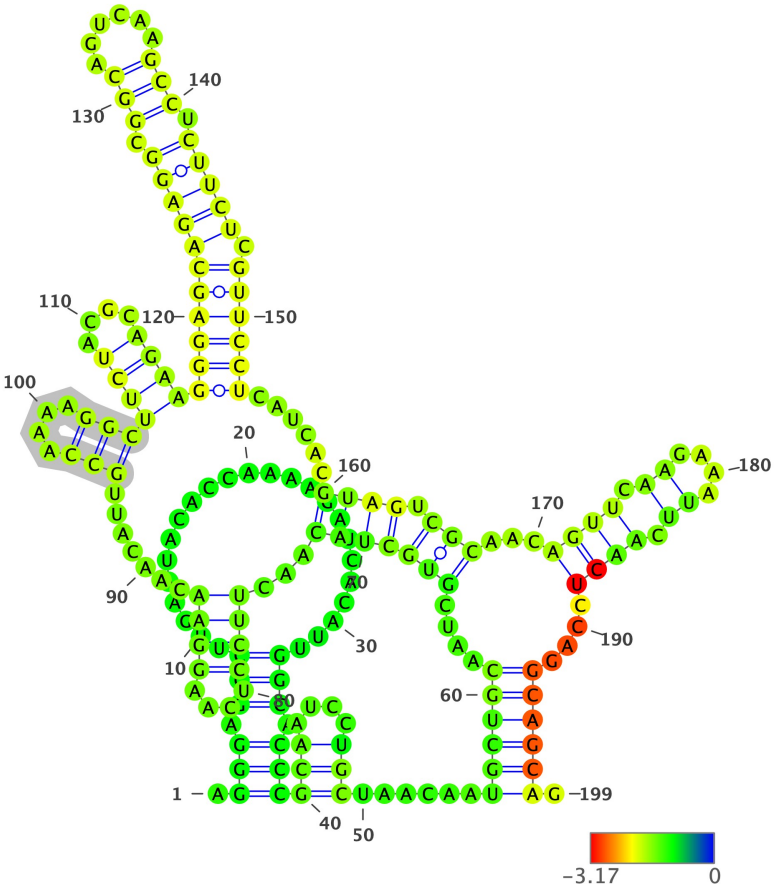
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 495 from nt 28774 to 28783 (nt 95 to 104)

```
5'-GCCAAAAGGC-3'
5'-(((....)))-3'
Motif MFE = -2.6; z-score = -9.77; 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 = -2.24; 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(+)

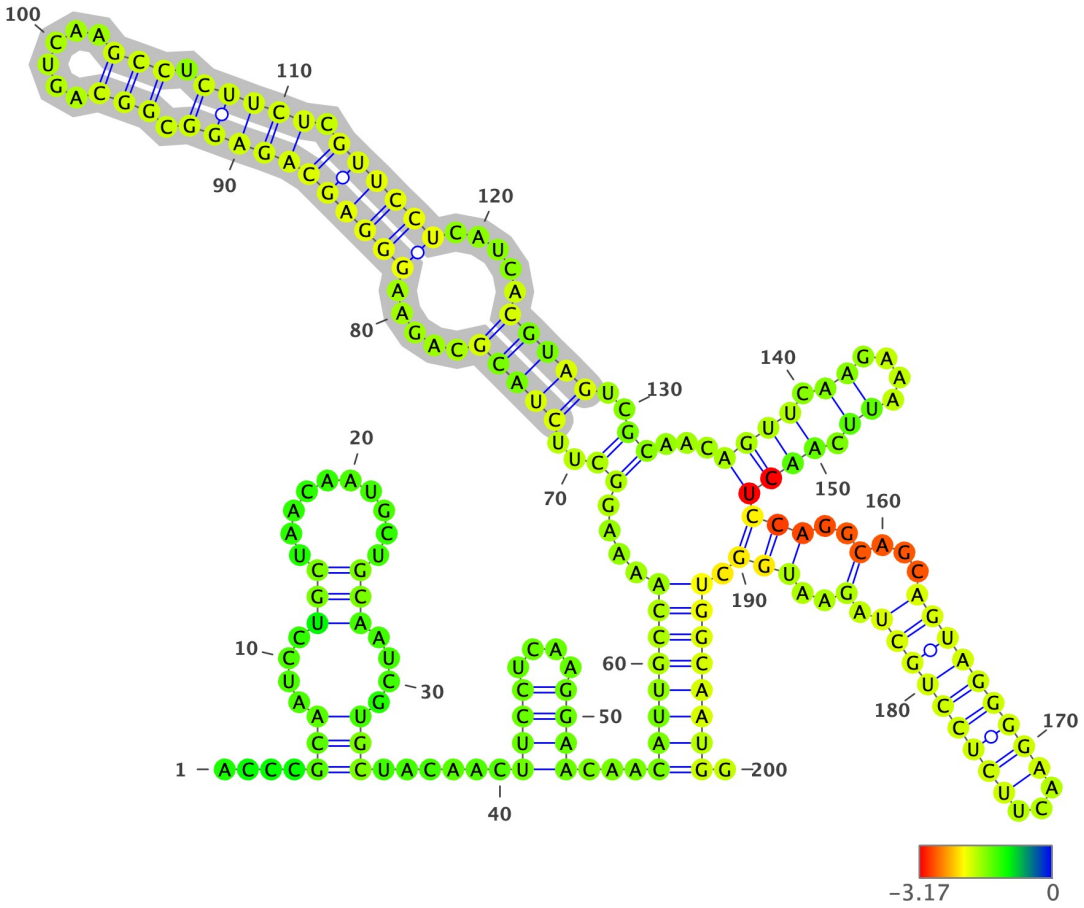
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 496 from nt 28786 to 28842 (nt 72 to 128)

```
5'-CTACGCAGAAGGGAGCAGAGGCGGCAGTCAAGCCTCUUCUCGUUCCUCATCACGTAG-3'
5'-((..(.....(((((((((((.(((......))).))))).))))))).....)..))-3'
Motif MFE = -24.0; z-score = -3.1; ED = 2.89
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28715 to 28914 (motif highlighted in silver):

```
5'-ACCCGCAAUCCUGCUAACAAUGCUGCAAUCGUGCUACAACUUCCUCAAGGAACAACAUUGCCAAAAGGCUUCUACGCAGAAGGGAGCAGAGGCGGCAGUCAAGCCUCUUCU
CGUUCCUCAUCACGUAGUCGCAACAGUUCAAGAAAUUCAACUCCAGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGG-3
5'-....(((....(((..........)))....)))......((((....))))...((((((((....((..(((((.....(((((((((((.(((......))).)))))
.))))))).....)))))..))...((((.((....)).))))(((..(...((((((((((...)))))))))).)..))).)))))))).-3'
MFE = -61.5; z-score = -3.18; 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(+)

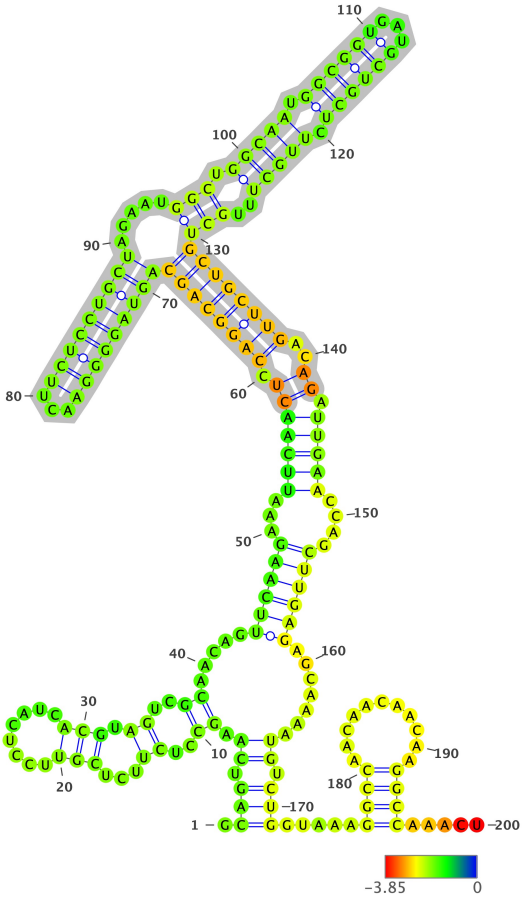
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 497 from nt 28866 to 28950 (nt 58 to 142)

```
5'-CTCCAGGCAGCAGTAGGGGAACTUCUCCUGCUAGAATGGCTGGCAATGGCGGTGATGCUGCUCUUGCUTTGCUGCUGCUUGACAG-3'
5'-((.(((((((((((((((((...)))))))))).....(((.(((((.(((((.....))))).))))).))))))))))))..))-3'
Motif MFE = -39.4; z-score = -3.73; 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 = -2.01; 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(+)

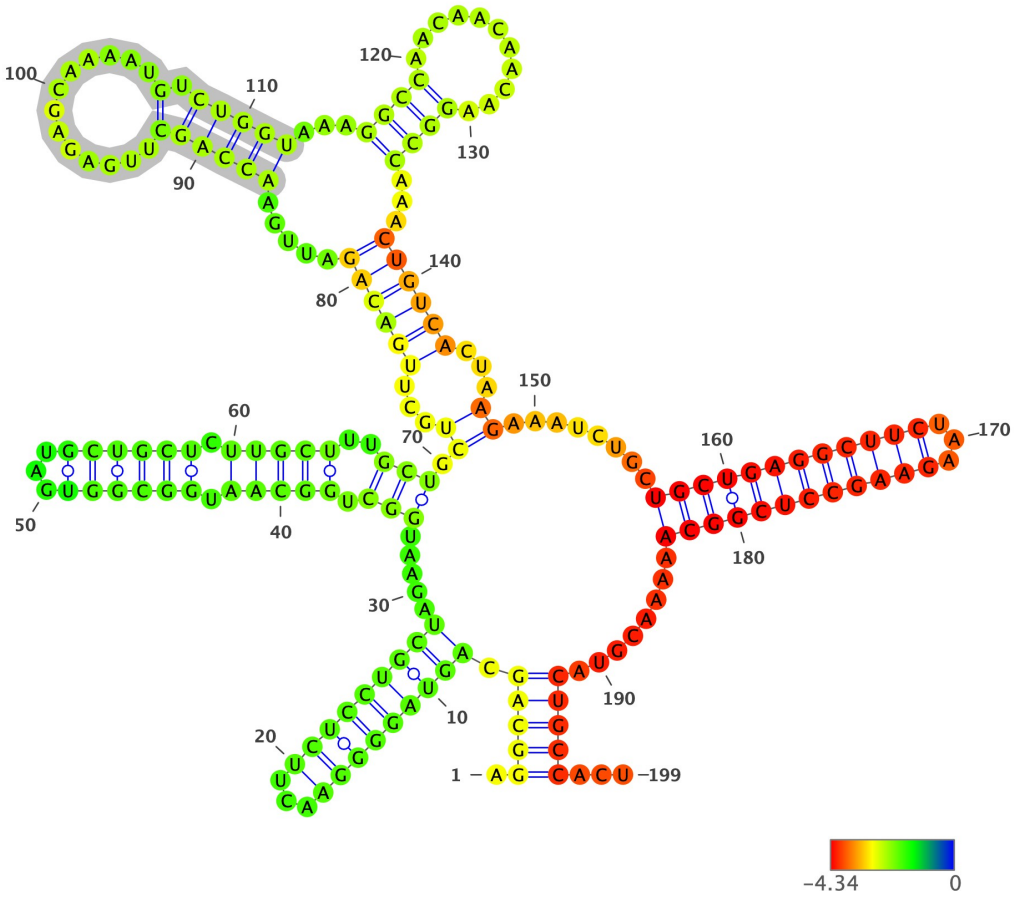
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 498 from nt 28956 to 28981 (nt 87 to 112)

```
5'-ACCAGCTTGAGAGCAAAATGTCUGGU-3'
5'-(((((.(((....))).....))))))-3'
Motif MFE = -4.1; z-score = -1.02; ED = 3.67
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 28870 to 29068 (motif highlighted in silver):

```
5'-AGGCAGCAGUAGGGGAACUUCUCCUGCUAGAAUGGCUGGCAAUGGCGGUGAUGCUGCUCUUGCUUUGCUGCUGCUUGACAGAUUGAACCAGCUUGAGAGCAAAAUGUCUGG
UAAAGGCCAACAACAACAAGGCCAAACUGUCACUAAGAAAUCUGCUGCUGAGGCUUCUAAGAAGCCUCGGCAAAAACGUACUGCCACU-3
5'-.(((((.((((((((((...)))))))))).....(((.(((((.((((((...)))))).)))))..))).((...((((((.....((((((.............).))))
)...((((...........))))...)))))))...)).......((((((((((((...))))))))))))........))))))...-3'
MFE = -74.5; z-score = -4.12; ED = 15.25
```

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(+)

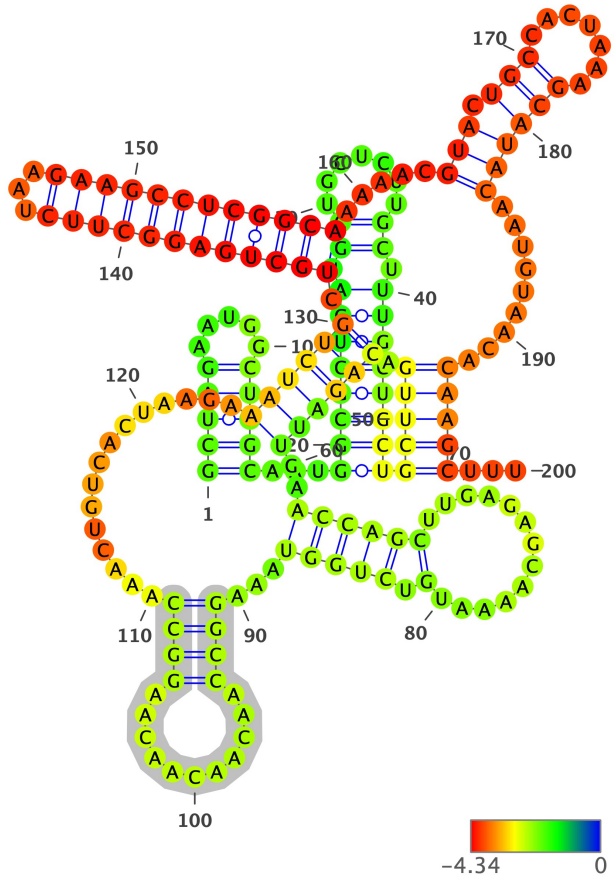
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 28985 to 29003 (nt 91 to 109)

```
5'-GGCCAACAACAACAAGGCC-3'
5'-((((...........))))-3'
Motif MFE = -4.9; z-score = -4.35; 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 = -3.11; 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(+)

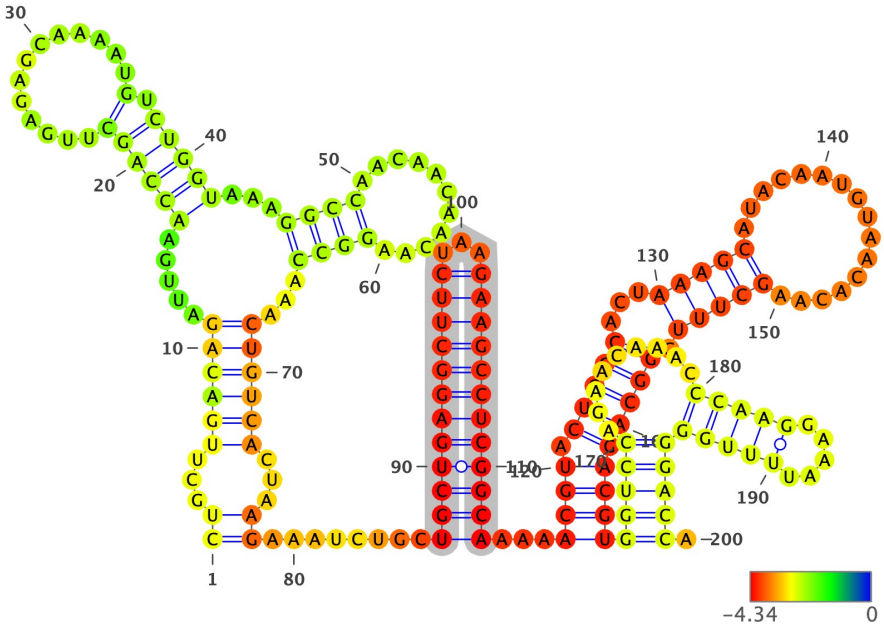
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 500 from nt 29026 to 29052 (nt 87 to 113)

```
5'-TGCTGAGGCTTCTAAGAAGCCUCGGCA-3'
5'-(((((((((((...)))))))))))-3'
Motif MFE = -19.7; z-score = -6.1; 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 = -4.53; 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(+)

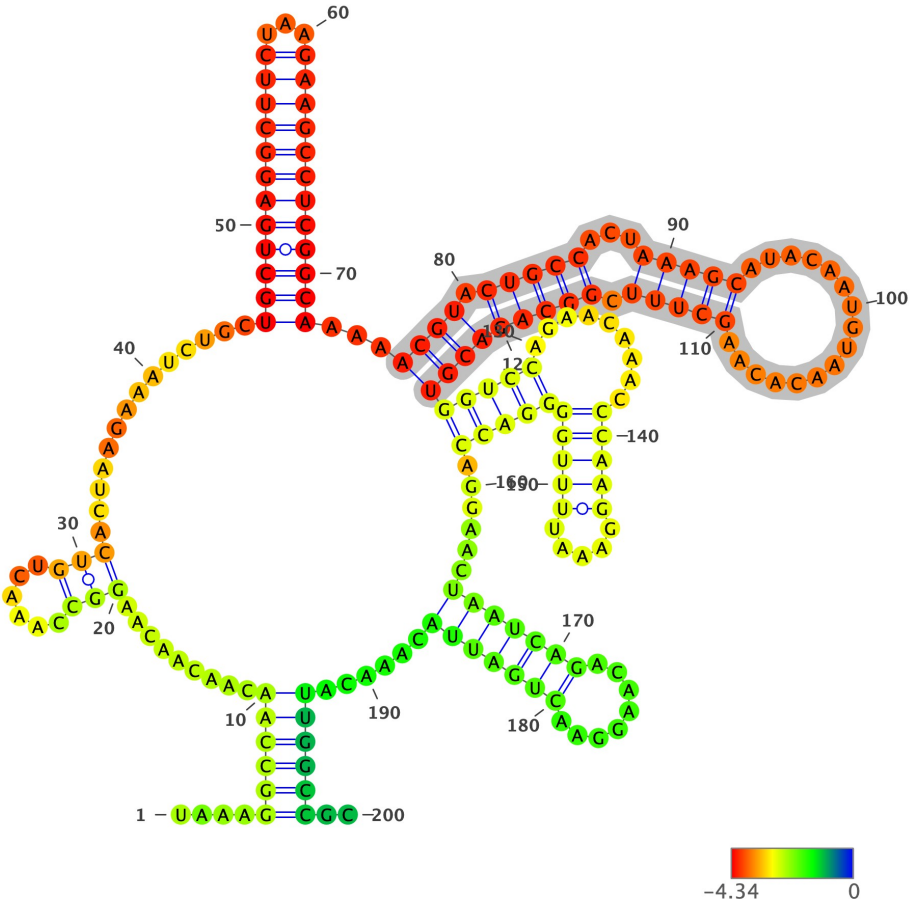
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 501 from nt 29056 to 29104 (nt 76 to 124)

```
5'-ACGTACTGCCACTAAAGCATACAATGTAACACAAGCUUUCGGCAGACGU-3'
5'-((((.(((((...(((((.................))))).)))))))))-3'
Motif MFE = -14.6; z-score = -3.4; 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 = -5.29; 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(+)

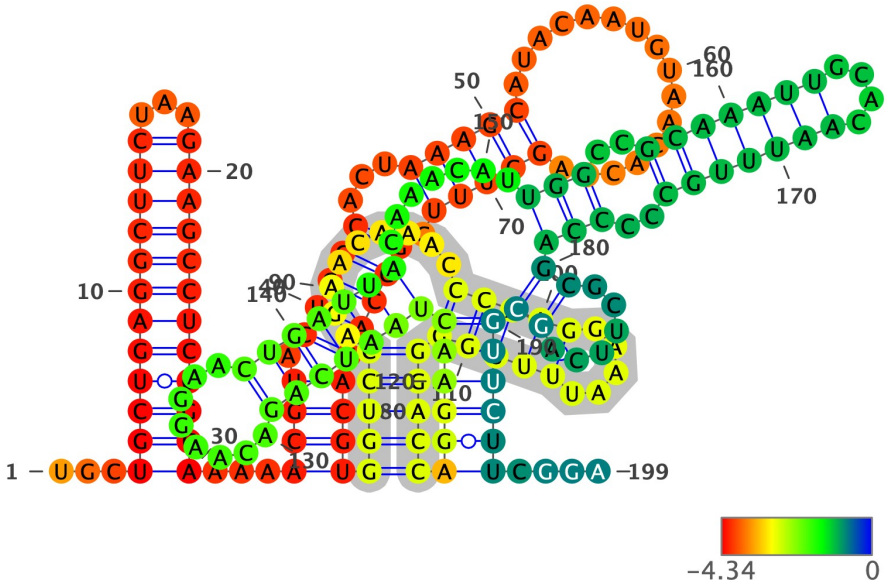
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 502 from nt 29105 to 29138 (nt 83 to 116)

```
5'-GGTCCAGAACAAACCCAAGGAAATUUUGGGGACC-3'
5'-(((((.........(((((.....)))))))))))-3'
Motif MFE = -8.1; z-score = -1.78; 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 = -4.64; ED = 11.58
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

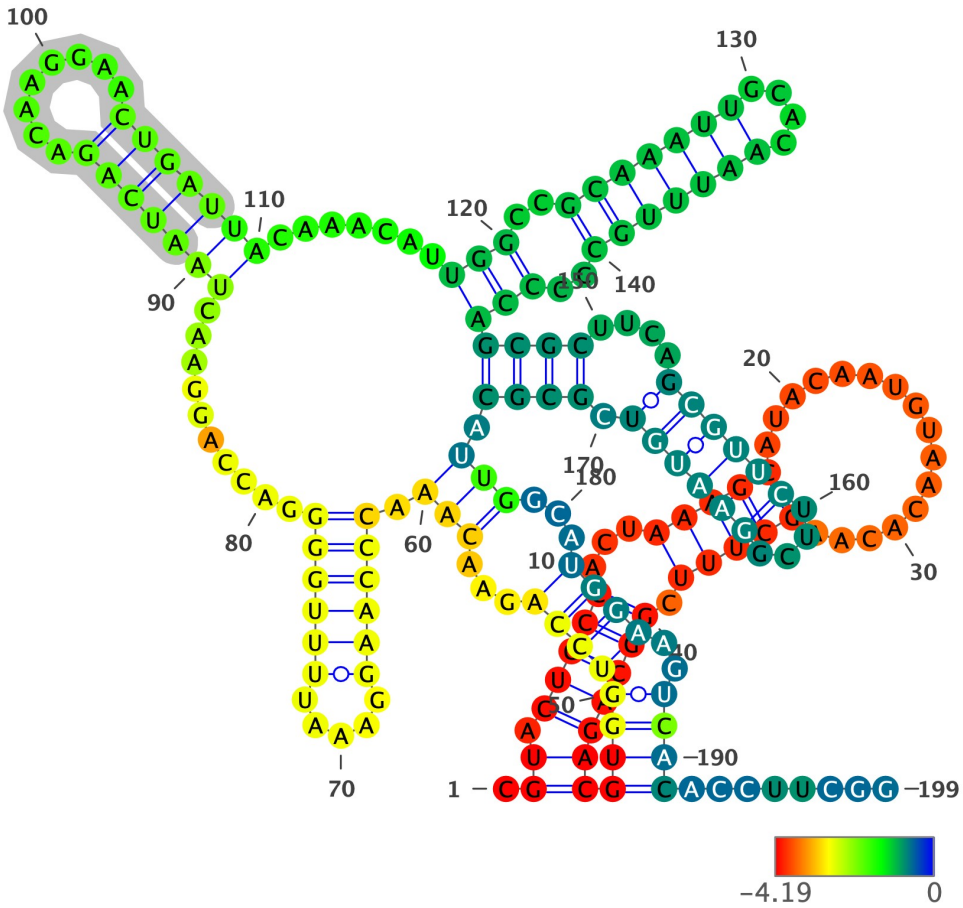
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 503 from nt 29147 to 29164 (nt 91 to 108)

```
5'-ATCAGACAAGGAACUGAU-3'
5'-(((((........)))))-3'
Motif MFE = -2.8; z-score = -2.56; 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 29057 to 29255 (motif highlighted in silver):

```
5'-CGUACUGCCACUAAAGCAUACAAUGUAACACAAGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUAC
AAACAUUGGCCGCAAAUUGCACAAUUUGCCCCCAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGG-3
5'-.((.((((((...(((((.................)))))).)))))))(((((((((...(((.((((((.....))))))..........(((((((........)))))))..
......(((..(((((((....)))))))..)))((((....((((((....))))))..))))..)))...)))))..))))........-3'
MFE = -53.1; z-score = -1.34; ED = 28.24
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

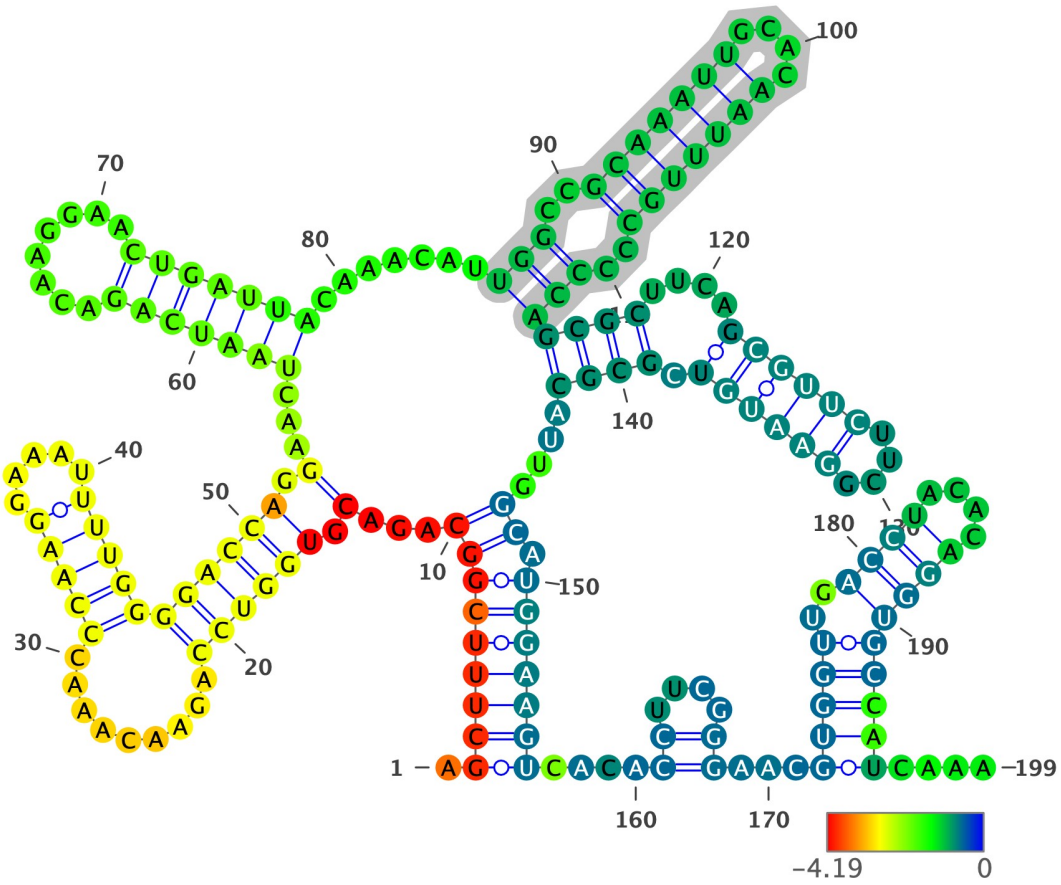
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 29174 to 29201 (nt 86 to 113)

```
5'-TGGCCGCAAATTGCACAATUUUGCCCCCA-3'
5'-(((..(((((((....)))))))..)))-3'
Motif MFE = -7.6; z-score = -2.44; 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 29089 to 29287 (motif highlighted in silver):

```
5'-AGCUUUCGGCAGACGUGGUCCAGAACAAACCCAAGGAAAUUUUGGGGACCAGGAACUAAUCAGACAAGGAACUGAUUACAAACAUUGGCCGCAAAUUGCACAAUUUGCCCC
CAGCGCUUCAGCGUUCUUCGGAAUGUCGCGCAUUGGCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAUCAAA-3
5'-.((((((((((...(.((((((.........(((((.....)))))))))))).)...(((((((........)))))))).......(((..(((((((....)))))))..)
))))((....((((((....)))))).))))....)).)))))))....((....))...((((((..((((....))))))))))....-3'
MFE = -54.9; z-score = -1.17; ED = 35.38
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 199--gene, gene-GU280_gp10, 28274-29533(+)

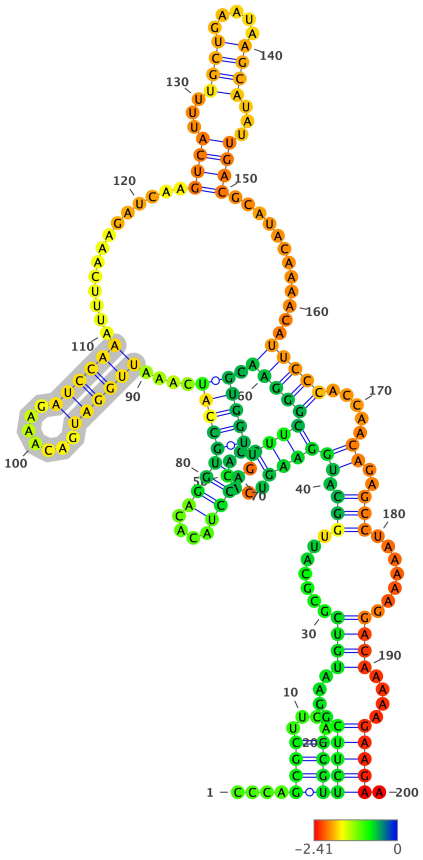
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 199--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 505 from nt 29288 to 29306 (nt 91 to 109)

```
5'-TTGGATGACAAAGAUCCAA-3'
5'-((((((.......))))))-3'
Motif MFE = -4.9; z-score = -4.02; 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 = -2.18; 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(+)

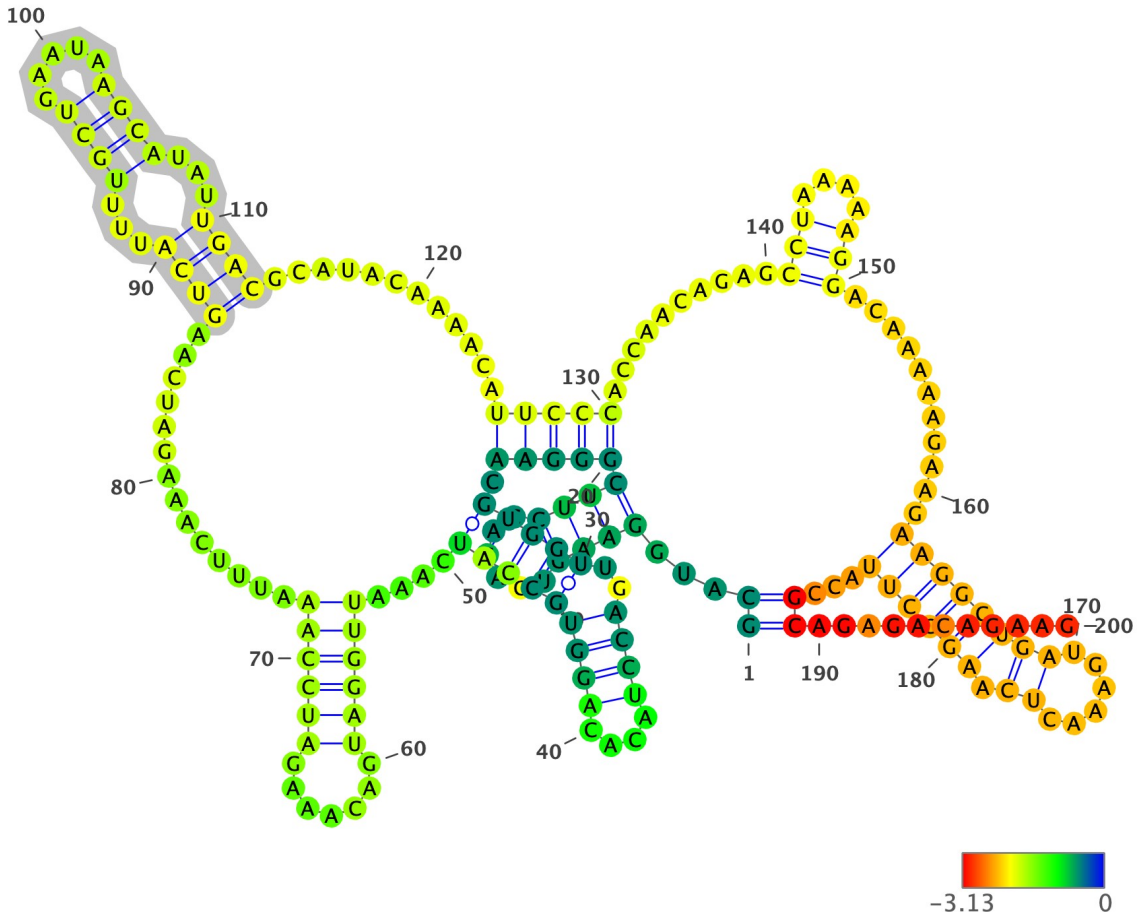
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 506 from nt 29321 to 29347 (nt 87 to 113)

```
5'-GTCATTTTGCTGAATAAGCATATUGAC-3'
5'-((((....(((.....)))....))))-3'
Motif MFE = -7.9; z-score = -4.11; ED = 0.66
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29235 to 29434 (motif highlighted in silver):

```
5'-GCAUGGAAGUCACACCUUCGGGAACGUGGUUGACCUACACAGGUGCCAUCAAAUUGGAUGACAAAGAUCCAAAUUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUG
ACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAG-3
5'-((...((((......))))(((((.(((((..((((....)))))))))....((((((.......))))))..............((((...((((.....))))...))
))............)))))..........(((....)))...........(((((((.....)).))))))...))...........-3'
MFE = -42.6; z-score = -2.09; ED = 18.55
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 200--gene, gene-GU280_gp10, 28274-29533(+)

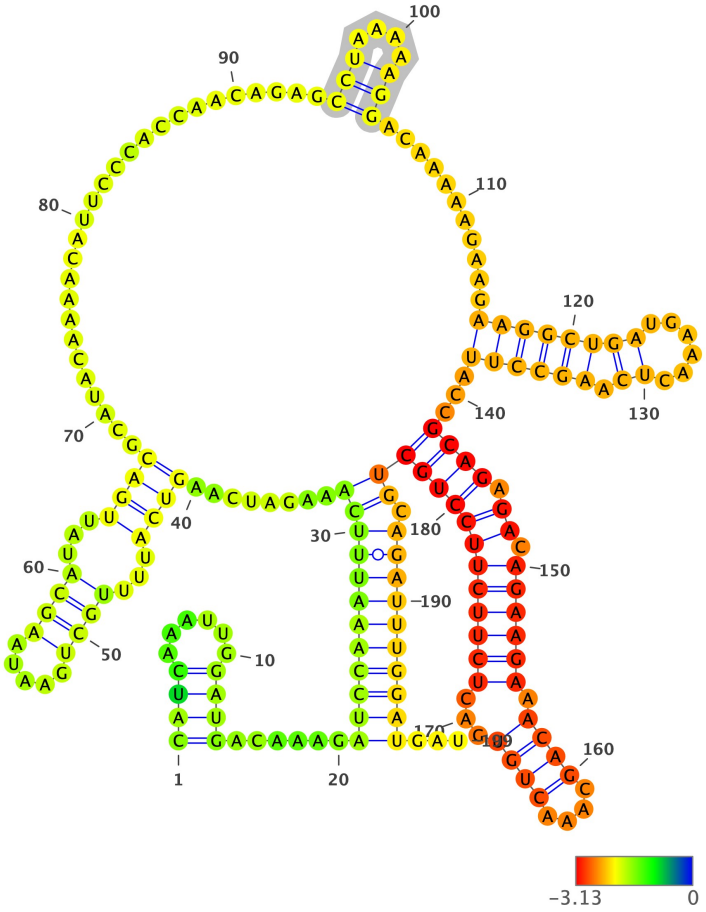
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 200--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

NC_045512.2 (forward strand): Structure number 507 from nt 29375 to 29384 (nt 95 to 104)

```
5'-CCTAAAAAGG-3'
5'-((......))-3'
Motif MFE = -0.3; z-score = -10.1; ED = 1.43
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29281 to 29479 (motif highlighted in silver):

```
5'-CAUCAAAUUGGAUGACAAAGAUCCAAAUUUCAAAGAUCAAGUCAUUUUGCUGAAUAAGCAUAUUGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAA
GAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAU-3
5'-((((......))))......((((((((((((........((((...((((.....))))...))))).........................(((....))).......
....(((((((((......)).))))))...((((.((.(((((((.(((((....)))))...))))))))))))).))))))))))...-3'
MFE = -48.5; z-score = -4.91; 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(+)

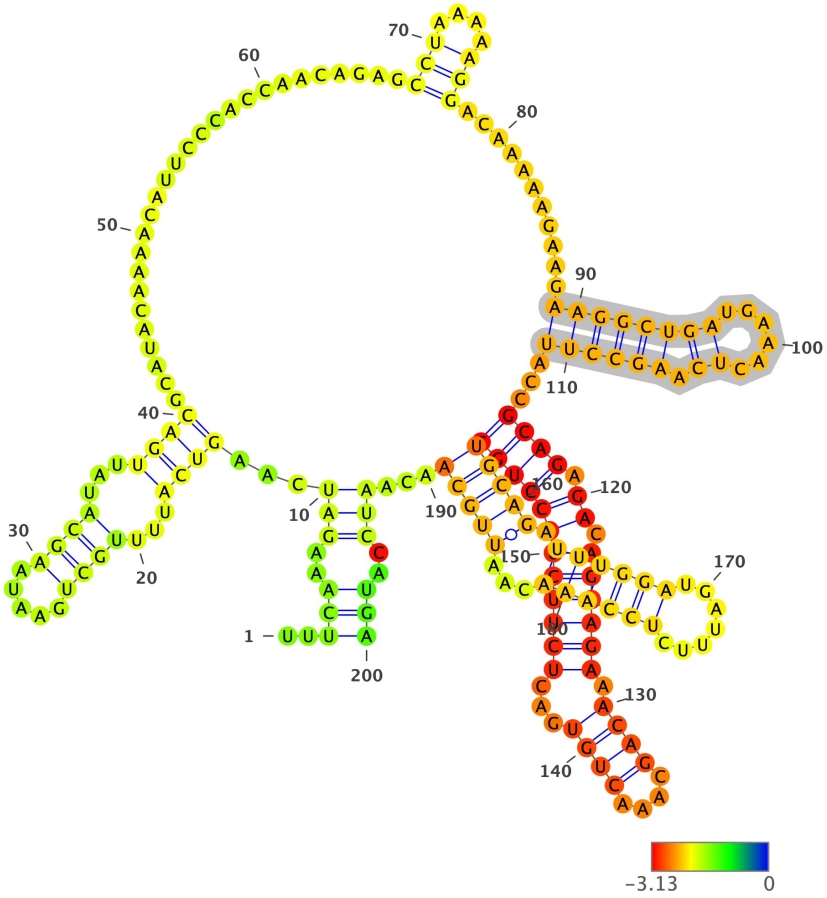
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 508 from nt 29396 to 29418 (nt 89 to 111)

```
5'-AAGGCTGATGAAACUCAAGCCUU-3'
5'-((((((((......)).))))))-3'
Motif MFE = -6.9; z-score = -3.83; 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 = -3.96; 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(+)

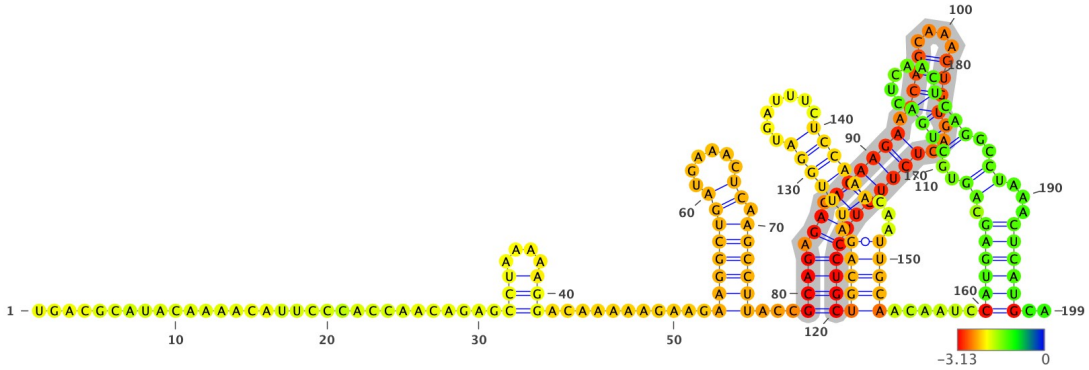
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 509 from nt 29422 to 29463 (nt 79 to 120)

```
5'-GCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGC-3'
5'-((((.((.(((((((.((((....))))...))))))))))))-3'
Motif MFE = -14.7; z-score = -3.7; ED = 1.01
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29344 to 29542 (motif highlighted in silver):

```
5'-UGACGCAUACAAAACAUUCCCACCAACAGAGCCUAAAAAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCU
UCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCA-3
5'-...............................(((....)))...........((((((((......)).))))))...((((.((.(((((((.((((....))))...)))
))))))))))(((((.(((((((.......))))))...)))))......((((((.((..((((......))))..))...))))))..-3'
MFE = -46.0; z-score = -3.32; 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(+)

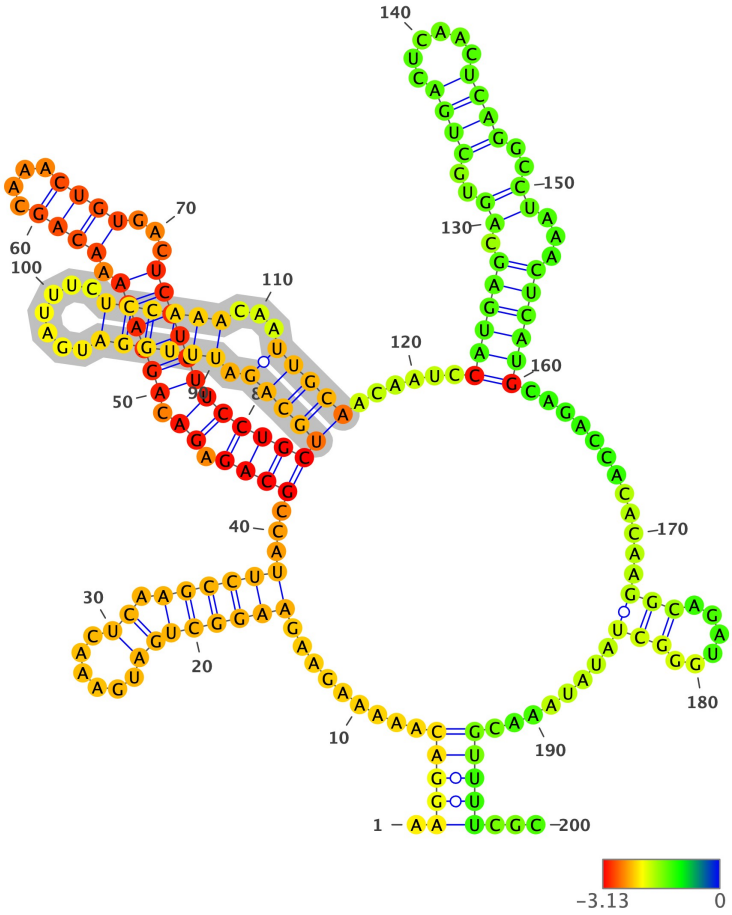
Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

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 510 from nt 29464 to 29496 (nt 84 to 116)

```
5'-TGCAGATTTGGATGATTTCUCCAAACAAUUGCA-3'
5'-(((((.((((((.......))))))...)))))-3'
Motif MFE = -7.9; z-score = -2.65; ED = 1.78
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29381 to 29580 (motif highlighted in silver):

```
5'-AAGGACAAAAAGAAGAAGGCUGAUGAAACUCAAGCCUUACCGCAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAA
UUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGC-3
5'-.(((((.........((((((((......)).))))))...((((.((.((((((.((((....))))...)))))))))))))(((((.((((((.......))))))...
)))))......((((((.((..((((......))))..))...))))))............(((......)))........)))))...-3'
MFE = -48.8; z-score = -2.69; ED = 28.94
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 153--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 153--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 178 to 200--gene, gene-GU280_gp11, 29558-29674(+)

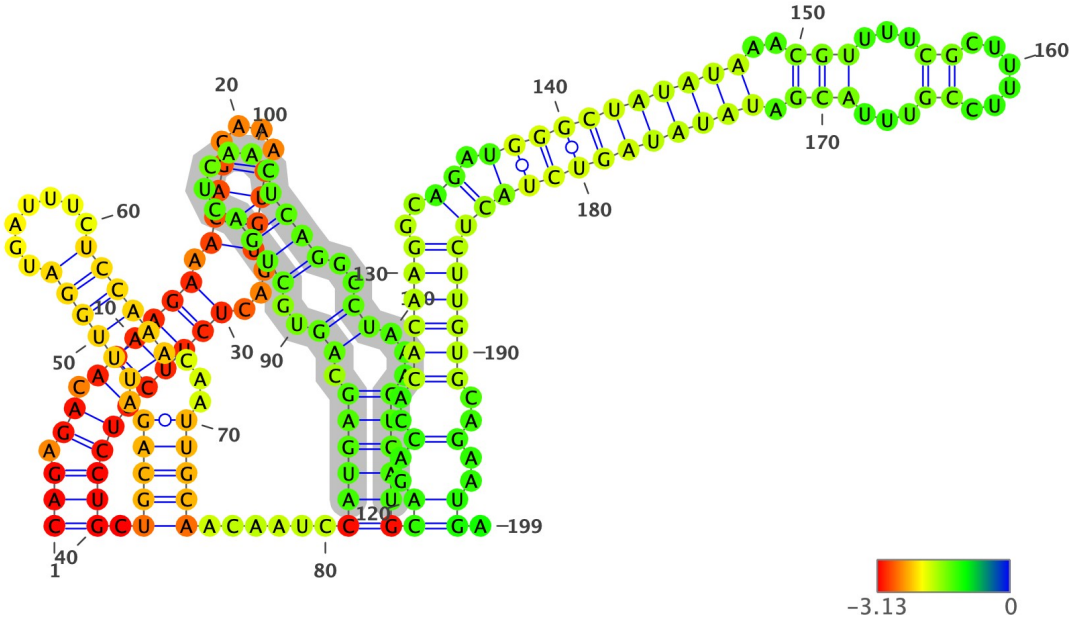
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 178 to 200--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

NC_045512.2 (forward strand): Structure number 511 from nt 29504 to 29539 (nt 82 to 117)

```
5'-ATGAGCAGTGCTGACTCAACUCAGGCCUAAACUCAU-3'
5'-(((((.((..((((......))))..))...)))))-3'
Motif MFE = -8.1; z-score = -2.15; ED = 2.21
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29423 to 29621 (motif highlighted in silver):

```
5'-CAGAGACAGAAGAAACAGCAAACUGUGACUCUUCUUCCUGCUGCAGAUUUGGAUGAUUUCUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAA
ACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGA-3
5'-(((.((.((((((.((((....))))...))))))))))).(((((.((((((.......))))))...)))))......((((((.((..((((......))))..))..
.))))))((..(..((((((..((.(((((((((((..(((...((......))...))).))))))))))))))))))..)..)).-3'
MFE = -53.2; z-score = -3.1; ED = 12.16
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 111--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 111--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 136 to 199--gene, gene-GU280_gp11, 29558-29674(+)

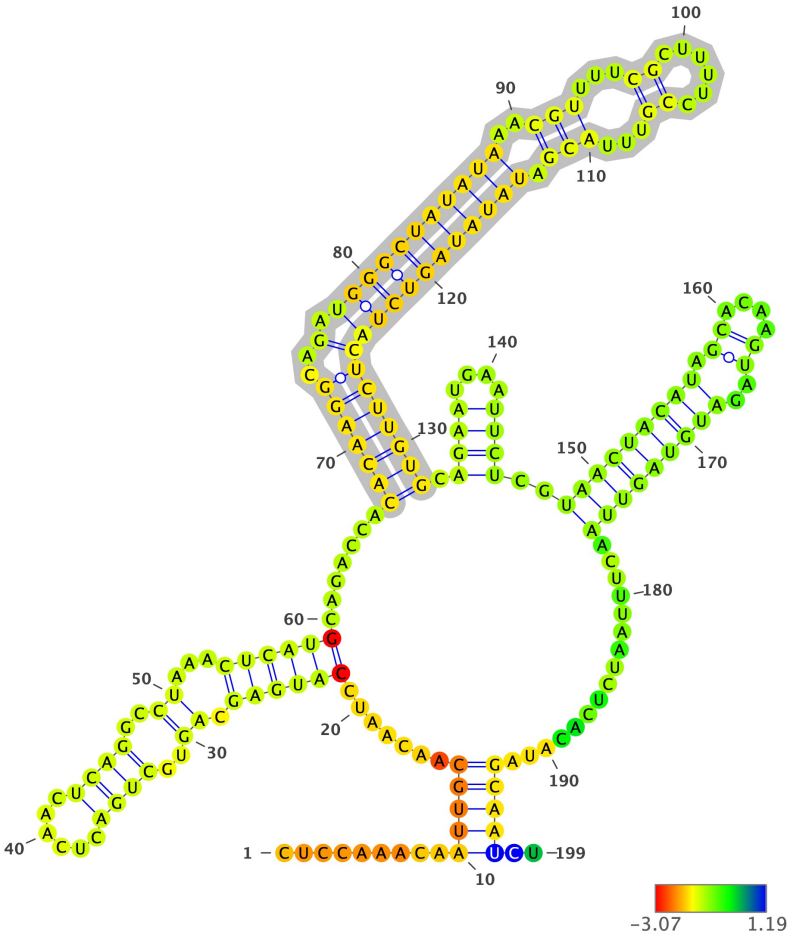
Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 136 to 199--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

NC_045512.2 (forward strand): Structure number 512 from nt 29548 to 29613 (nt 67 to 132)

```
5'-CACAAGGCAGATGGGCTATATAAACGTTTTCGCTTTTCCGTTTACGAUAUAUAGUCUACUCUUGUG-3'
5'-(((((((.....((((((((((..(((...((......)).)))).)))))))))))..)))))))-3'
Motif MFE = -19.7; z-score = -3.18; ED = 3.3
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29482 to 29680 (motif highlighted in silver):

```
5'-CUCCAAACAAUUGCAACAAUCCAUGAGCAGUGCUGACUCAACUCAGGCCUAAACUCAUGCAGACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUAC
GAUAUAUAGUCUACUCUUGUGCAGAAUGAAUUCUCGUAACUACAUAGCACAAGUAGAUGUAGUUAACUUUAAUCUCACAUAGCAAUCU-3
5'-.........(((((.......((((((.((..((((.....))))).))...))))))).......(((((((..(.((((((((((..(((...((......)).)))
).)))))))))))))))))).((((....)))).((((((((((.((....)).))))))))).................))))))..-3'
MFE = -45.3; z-score = -2.87; ED = 11.57
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 1 to 52--gene, gene-GU280_gp10, 28274-29533(+)

Attributes: ['ID=gene-GU280_gp10', 'Dbxref=GeneID:43740575', 'Name=N', 'gbkey=Gene', 'gene=N', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp10']

3-- nt 1 to 52--CDS, cds-YP_009724397.2, 28274-29533(+)

Attributes: ['ID=cds-YP_009724397.2', 'Parent=gene-GU280_gp10', 'Dbxref=Genbank:YP_009724397.2,GeneID:43740575', 'Name=YP_009724397.2', 'Note=ORF9%3B structural protein', 'gbkey=CDS', 'gene=N', 'locus_tag=GU280_gp10', 'product=nucleocapsid phosphoprotein', 'protein_id=YP_009724397.2']

4-- nt 77 to 193--gene, gene-GU280_gp11, 29558-29674(+)

Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

5-- nt 77 to 193--CDS, cds-YP_009725255.1, 29558-29674(+)

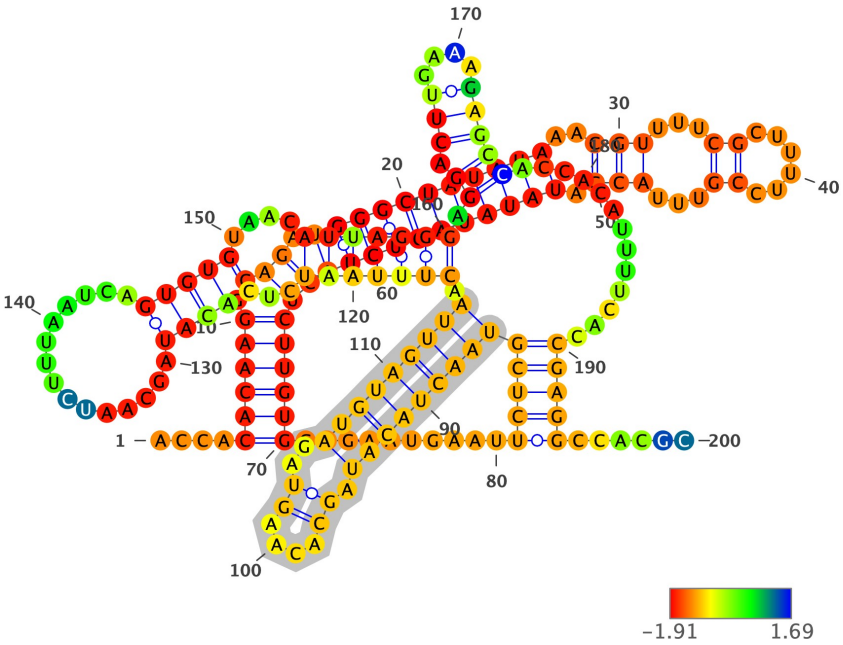
Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

6-- nt 194 to 199--three_prime_UTR, id-NC_045512.2:29675..29903, 29675-29903(+)

Attributes: ['ID=id-NC_045512.2:29675..29903', "gbkey=3'UTR"]

NC_045512.2 (forward strand): Structure number 513 from nt 29629 to 29657 (nt 86 to 114)

```
5'-TAACTACATAGCACAAGUAGAUGUAGUUA-3'
5'-(((((...................)))))-3'
Motif MFE = -8.5; z-score = -4.69; ED = 0.93
```



Structure has been colored based on the Zavg value for the nucleotide arrangment (color scale shown below). ViennaRNA's RNAfold (2.4.14) has been used to fold all structures at 37C, z-scores have been calculated using 100 mono-nucleotide shuffled sequences.

Extracted structure model with flanking nucleotides 29544 to 29743 (motif highlighted in silver):

```
5'-ACCACACAAGGCAGAUGGGCUAUAUAAACGUUUUCGCUUUUCCGUUUACGAUAUAUAGUCUACUCUUGUGCAGAAUGAAUUCUCGUAACUACAUAGCACAAGUAGAUGUAG
UUAACUUUAAUCUCACAUAGCAAUCUUUAAUCAGUGUGUAACAUUAGGGAGGACUUGAAAGAGCCACCACAUUUUCACCGAGGCCACGC-3
5'-....((((((..((.((((((((((..(((...((......))...))).))))))))))))))))))).........((((((((((((((.((....))..))))))
))).(((((((..(((((...............))))).....))))))).((.(((....)))))..............)))))......-3'
MFE = -42.8; z-score = -1.1; ED = 35.69
```

Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_045512.2:1..29903, 1-29903(+)

Attributes: ['ID=NC_045512.2:1..29903', 'Dbxref=taxon:2697049', 'collection-date=Dec-2019', 'country=China', 'gbkey=Src', 'genome=genomic', 'isolate=Wuhan-Hu-1', 'mol_type=genomic RNA', 'nat-host=Homo sapiens']

2-- nt 15 to 131--gene, gene-GU280_gp11, 29558-29674(+)

Attributes: ['ID=gene-GU280_gp11', 'Dbxref=GeneID:43740576', 'Name=ORF10', 'gbkey=Gene', 'gene=ORF10', 'gene_biotype=protein_coding', 'locus_tag=GU280_gp11']

3-- nt 15 to 131--CDS, cds-YP_009725255.1, 29558-29674(+)

Attributes: ['ID=cds-YP_009725255.1', 'Parent=gene-GU280_gp11', 'Dbxref=Genbank:YP_009725255.1,GeneID:43740576', 'Name=YP_009725255.1', 'gbkey=CDS', 'gene=ORF10', 'locus_tag=GU280_gp11', 'product=ORF10 protein', 'protein_id=YP_009725255.1']

4-- nt 132 to 200--three_prime_UTR, id-NC_045512.2:29675..29903, 29675-29903(+)

Attributes: ['ID=id-NC_045512.2:29675..29903', "gbkey=3'UTR"]