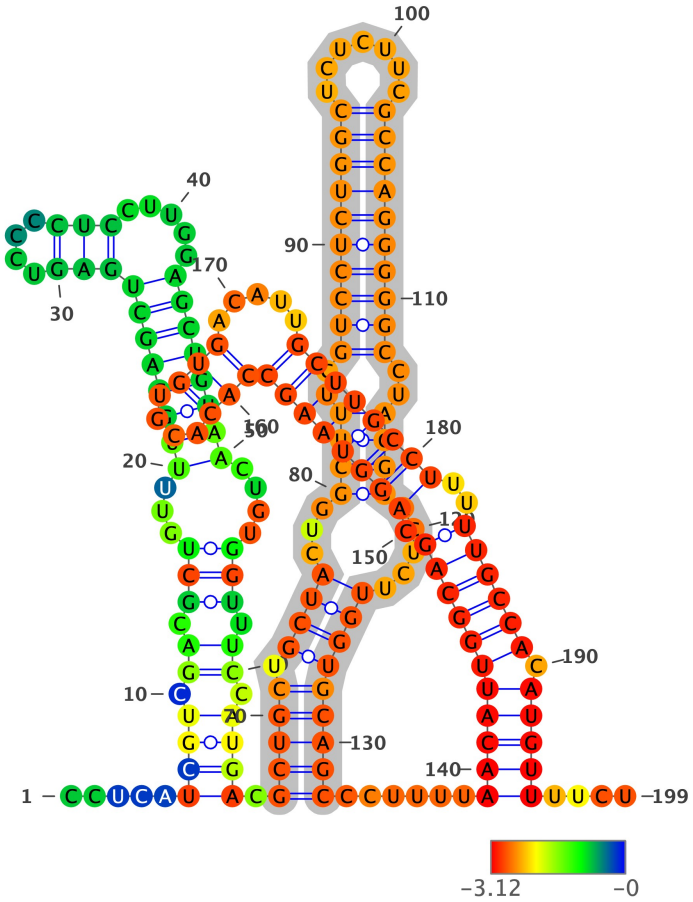
NC_007605.1 (forward strand): Structure number 1 from nt 703 to 768 (nt 67 to 132)

```
5'-GCUGCUGCUACUGGCUUUCGUCCUCUGGCUCUCUUCGCCAGGGGGCCUAGGUACUCUUGGUGCAGC-3'
5'-(((((..((((...(((((..((((((((((.......)))))))))))..))))).....)))))..)))))-3'
Motif MFE = -31.1; z-score = -3.45; ED = 3.84
```



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

Extracted structure model with flanking nucleotides 637 to 835 (motif highlighted in silver):

```
5'-CCUCAUCGUCGACGCUGUUUUGCAGCUGAGUCCCCUCCUUGGAGCUGUAACUGUGGUUUCCAUGACGCUGCUGCUACUGGCUUUCGUCCUCUGGCUCUCUUCGCCAGGGGG
CCUAGGUACUCUUGGUGCAGCCCUUUUAACAUUGGCAGCAGGUAAGCCACACGUGUGACAUUGCUUGCCUUUUUGCCACAUGUUUUCU-3
5'-.....((((.((.((((...((((((((((((....)))).....))))))))....)))).)).)))).(((((.((((...((((..((((((((((.......)))))))))
)..))))).....)))))))))......((((((((((.((((((((((....)))).....)))))))))..)))))))..))))).....-3'
MFE = -69.5; z-score = -3.59; ED = 21.45
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 152--exon, exon-NC_007605.1:58..166458-4, 540-788(+)

Attributes: ['ID=exon-NC_007605.1:58..166458-4', 'Parent=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

3-- nt 1 to 152--CDS, cds-YP_401631.1, 540-788(+)

Attributes: ['ID=cds-YP_401631.1', 'Parent=rna-NC_007605.1:58..166458', 'Dbxref=UniProtKB/TrEMBL:Q777H4,Genbank:YP_401631.1', 'Name=YP_401631.1', 'gbkey=CDS', 'product=membrane protein LMP-2A', 'protein_id=YP_401631.1']

4-- nt 1 to 152--exon, exon-NC_007605.1:58..169448-4, 540-788(+)

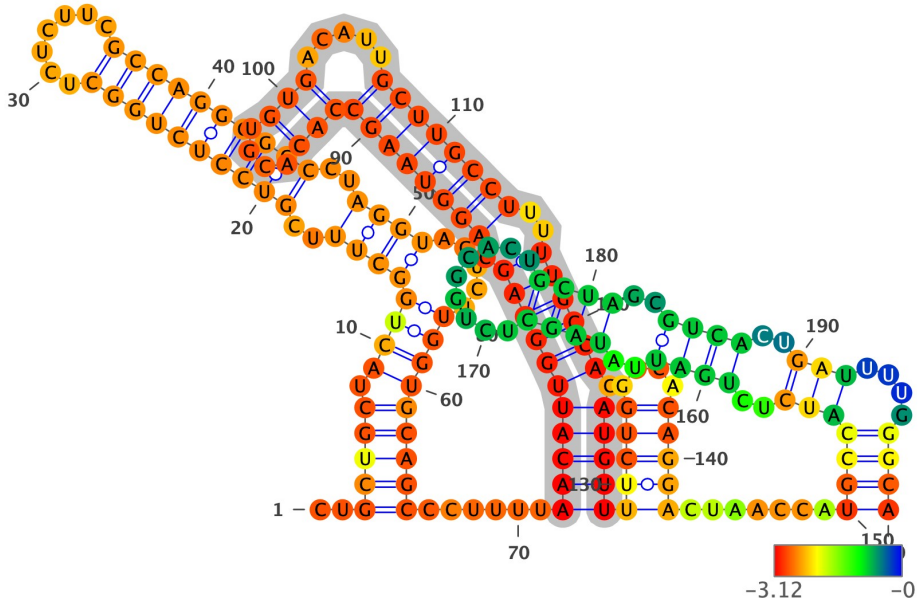
Attributes: ['ID=exon-NC_007605.1:58..169448-4', 'Parent=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 152--CDS, cds-YP_401632.1, 540-788(+)

Attributes: ['ID=cds-YP_401632.1', 'Parent=gene-HHV4_LMP-2B', 'Dbxref=UniProtKB/TrEMBL:Q8AZK9,Genbank:YP_401632.1,GeneID:3783760', 'Name=YP_401632.1', 'gbkey=CDS', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'product=membrane protein LMP-2B', 'protein_id=YP_401632.1']

NC_007605.1 (forward strand): Structure number 2 from nt 775 to 831 (nt 72 to 128)

```
5'-AACAUUGGCAGCAGGUAAGCCACACGUGUGACAUUGCUUGCCUUUUUGCCACAUGUU-3'
5'-(((((((((((.((((((((((((....)))).....)))))))))..)))))))..)))))-3'
Motif MFE = -22.2; z-score = -4.43; ED = 3.21
```



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 704 to 903 (motif highlighted in silver):

```
5'-CUGCUGCUACUGGCUUUCGUCCUCUGGCUCUCUUCGCCAGGGGGCCUAGGUACUCUUGGUGCAGCCCUUUUAACAUUGGCAGCAGGUAAGCCACACGUGUGACAUUGCUUG
CCUUUUUGCCACAUGUUUUCUGGACACAGGACUAACCAUGCCAUCUCUGAUUAUAGCUCUGGCACUGCUAGCGUCACUGAUUUUGGGCA-3
5'-..(((((.(((((((..((((((((((.......)))))))))).)))).....)))))))).....((((((((((.((((((((((....)))).....)))))
)))..)))))).)))))((((....)))).....(((((((..((((..((((.........)))).)))).)))).....)))).....))))-3'
MFE = -70.2; z-score = -3.53; ED = 19.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 85--exon, exon-NC_007605.1:58..166458-4, 540-788(+)

Attributes: ['ID=exon-NC_007605.1:58..166458-4', 'Parent=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

3-- nt 168 to 200--exon, exon-NC_007605.1:58..166458-5, 871-951(+)

Attributes: ['ID=exon-NC_007605.1:58..166458-5', 'Parent=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 85--CDS, cds-YP_401631.1, 540-788(+)

Attributes: ['ID=cds-YP_401631.1', 'Parent=rna-NC_007605.1:58..166458', 'Dbxref=UniProtKB/TrEMBL:Q777H4,Genbank:YP_401631.1', 'Name=YP_401631.1', 'gbkey=CDS', 'product=membrane protein LMP-2A', 'protein_id=YP_401631.1']

5-- nt 168 to 200--CDS, cds-YP_401631.1, 871-951(+)

Attributes: ['ID=cds-YP_401631.1', 'Parent=rna-NC_007605.1:58..166458', 'Dbxref=UniProtKB/TrEMBL:Q777H4,Genbank:YP_401631.1', 'Name=YP_401631.1', 'gbkey=CDS', 'product=membrane protein LMP-2A', 'protein_id=YP_401631.1']

6-- nt 1 to 85--exon, exon-NC_007605.1:58..169448-4, 540-788(+)

Attributes: ['ID=exon-NC_007605.1:58..169448-4', 'Parent=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

7-- nt 168 to 200--exon, exon-NC_007605.1:58..169448-5, 871-951(+)

Attributes: ['ID=exon-NC_007605.1:58..169448-5', 'Parent=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

8-- nt 1 to 85--CDS, cds-YP_401632.1, 540-788(+)

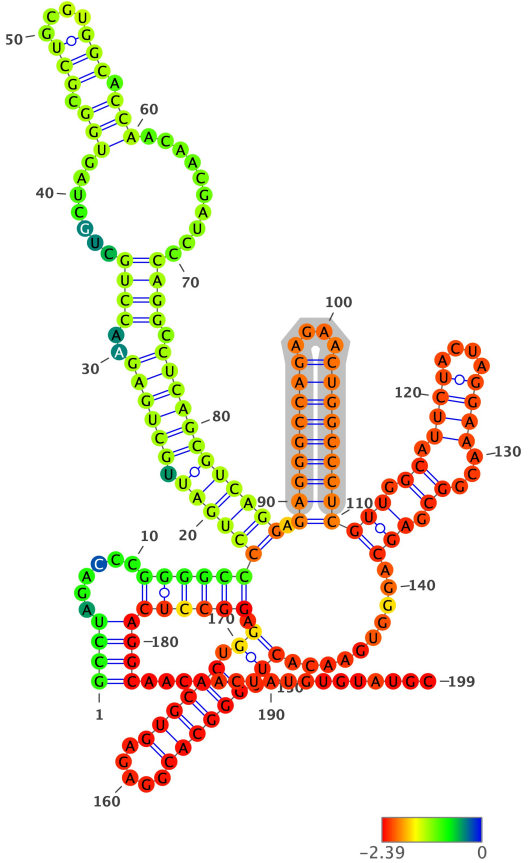
Attributes: ['ID=cds-YP_401632.1', 'Parent=gene-HHV4_LMP-2B', 'Dbxref=UniProtKB/TrEMBL:Q8AZK9,Genbank:YP_401632.1,GeneID:3783760', 'Name=YP_401632.1', 'gbkey=CDS', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'product=membrane protein LMP-2B', 'protein_id=YP_401632.1']

9-- nt 168 to 200--CDS, cds-YP_401632.1, 871-951(+)

Attributes: ['ID=cds-YP_401632.1', 'Parent=gene-HHV4_LMP-2B', 'Dbxref=UniProtKB/TrEMBL:Q8AZK9,Genbank:YP_401632.1,GeneID:3783760', 'Name=YP_401632.1', 'gbkey=CDS', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'product=membrane protein LMP-2B', 'protein_id=YP_401632.1']

NC_007605.1 (forward strand): Structure number 3 from nt 1973 to 1992 (nt 90 to 109)

```
5'-AGGGCCAGAGAACUGGCCCU-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -14.6; z-score = -5.27; 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 1884 to 2082 (motif highlighted in silver):

```
5'-GCCUAGACCCGGGGCCCCUGAUUGCUGAGAACCUGCUGCUAGUGGCGCUGCGUGGCACCAACAACGAUCCCAGGCCUCAGCGUCAGGAGAGGGCCAGAGAACUGGCCCUCG
UUGGCAUUCUACUAGGAAACGGCGAGCAGGGUGAACACUUGGGCACGGAGAGUGCCCUGGAGGCCUCAGGCAACAACUAUGUGUAUGC-3
5'-((((.....((((((((((((.((((((..((((.......(((.((((....)))).))).........))))).))))))))))))).(((((((((....)))))))))(
((.((.((((....))))...)).))).........((.((((((.....)))))).)).))))))))))).................-3'
MFE = -82.9; z-score = -2.42; ED = 18.26
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BNRF1, 1691-5856(+)

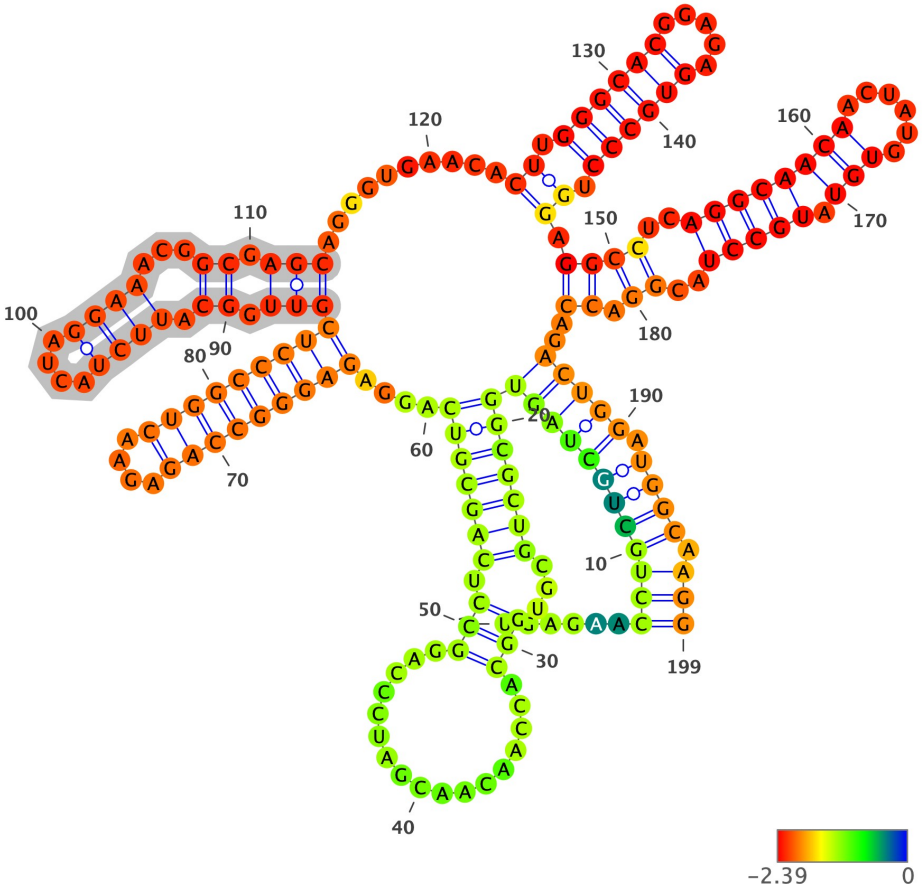
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 199--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 4 from nt 1994 to 2021 (nt 86 to 113)

```
5'-GUUGGCAUUCUACUAGGAAACGGCGAGC-3'
5'-(((.((.((((....))))...)).)))-3'
Motif MFE = -5.2; z-score = -0.33; 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 1909 to 2107 (motif highlighted in silver):

```
5'-UGAGAACCUGCUGCUAGUGGCGCUGCGUGGCACCAACAACGAUCCCAGGCCUCAGCGUCAGGAGAGGGCCAGAGAACUGGCCCUCGUUGGCAUUCUACUAGGAAACGGCGA
GCAGGGUGAACACUUGGGCACGGAGAGUGCCCUGGAGGCCUCAGGCAACAACUAUGUGUAUGCCUACGGACCAGACUGGAUGGCAAGG-3
5'-......((((((((((((((((((...(((.................))).)))))))....(((((((((....)))))))))(((.((.((((....)))).)).)).)).
)).........((.((((((.....)))))).)).((((..(((((((.....))).)))))..)).)).)..)))))).)))).)))-3'
MFE = -77.9; z-score = -2.24; ED = 17.37
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BNRF1, 1691-5856(+)

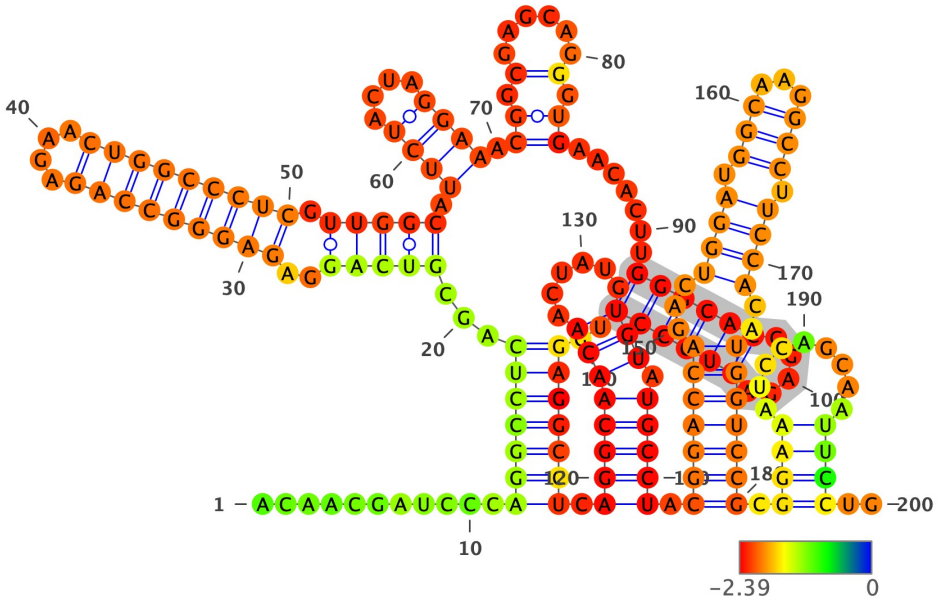
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 199--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 5 from nt 2035 to 2051 (nt 92 to 108)

```
5'-GGGCACGGAGAGUGCCC-3'
5'-((((((.....))))))-3'
Motif MFE = -10.9; z-score = -3.23; 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 1944 to 2143 (motif highlighted in silver):

```
5'-ACAACGAUCCCAGGCCUCAGCGUCAGGAGAGGGCCAGAGAACUGGCCCUCGUUGGCAUUCUACUAGGAAACGGCGAGCAGGGUGAACACUUGGGCACGGAGAGUGCCCUGG
AGGCCUCAGGCAACAACUAUGUGUAUGCCUACGGACCAGACUGGAUGGCAAGGCCUUCCACAUGGUCCGCGGAAAUCCAGCAAUUCCUG-3
5'-...........(((((((...(((((..(((((((((....)))))))))..)))))).((((....)))).((.(......).)).......((((((....)))))))..)
))))))..((((((((.....)))..)))))..(((((((...((((.(((...)))).)))).)).)))))).((((.........)))).)..-3'
MFE = -82.3; z-score = -3.48; ED = 24.73
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BNRF1, 1691-5856(+)

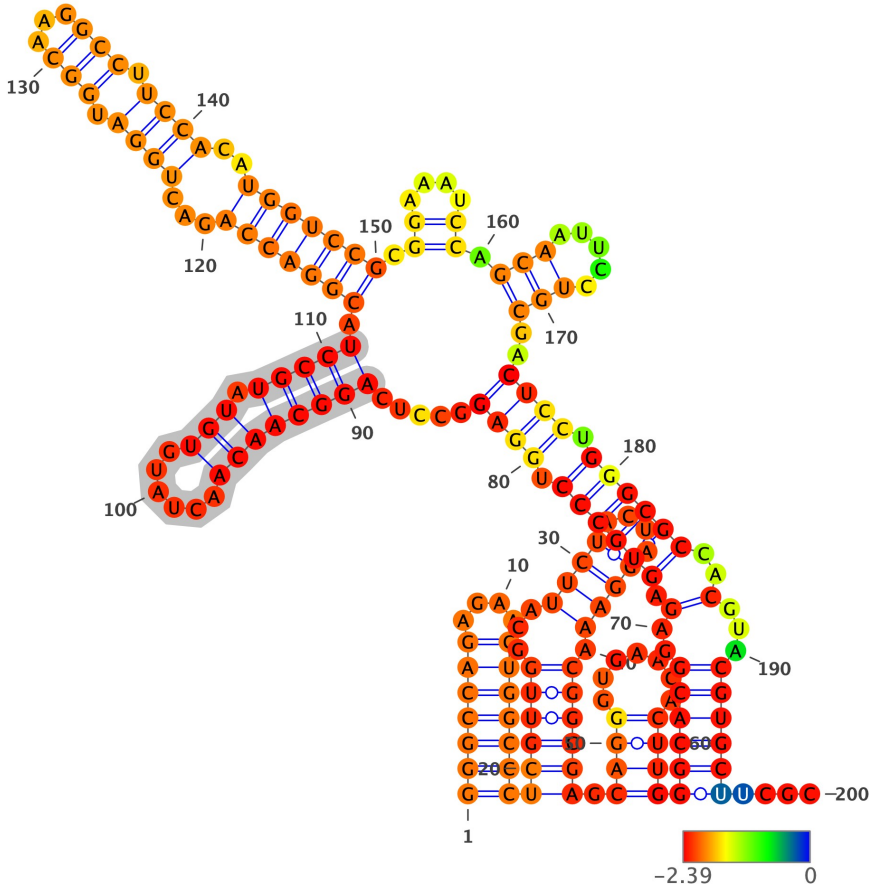
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 200--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 6 from nt 2062 to 2084 (nt 89 to 111)

```
5'-AGGCAACAACUAUGUGUAUGCCU-3'
5'-(((((((.....))).)))))-3'
Motif MFE = -6.7; z-score = -3.01; ED = 2.41
```



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

Extracted structure model with flanking nucleotides 1974 to 2173 (motif highlighted in silver):

```
5'-GGGCCAGAGAACUGGCCCUCGUUGGCAUUCUACUAGGAAACGGCGAGCAGGGUGAACACUUGGGCACGGAGAGUGCCCUGGAGGCCUCAGGCAACAACUAUGUGUAUGCCU
ACGGACCAGACUGGAUGGCAAGGCCUUCCACAUGGUCCGCGGAAAUCCAGCAAUUCCUGCGACUCCUGGGCGCCACGUACGUGCUUCGC-3
5'-(((((((....)))))))((((((...((((....)))).)))))).((((.......)))))((((((..(.((((((.((((.....((((((((.....))).)))))
.(((((((...((((.((((...))).)))).)).))))))).((....)).((.....)))..)))).)))))))..)...)))))))....-3'
MFE = -83.9; z-score = -2.88; ED = 19.14
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BNRF1, 1691-5856(+)

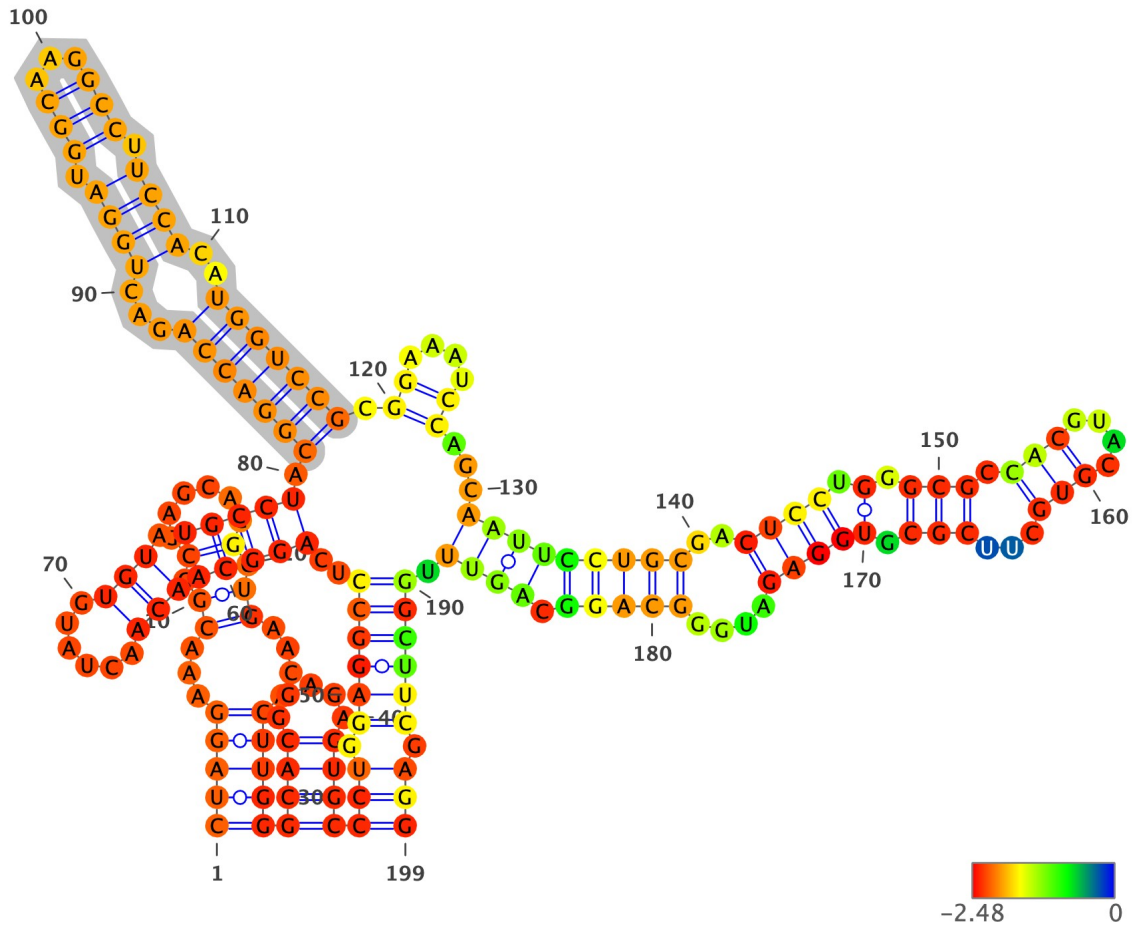
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 200--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 7 from nt 2086 to 2123 (nt 81 to 118)

```
5'-CGGACCAGACUGGAUGGCAAGGCCUUCCACAUGGUCCG-3'
5'-(((((.............................)))))-3'
Motif MFE = -21.1; z-score = -3.57; 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 2006 to 2204 (motif highlighted in silver):

```
5'-CUAGGAAACGGCGAGCAGGGUGAACACUUGGGCACGGAGAGUGCCCUGGAGGCCUCAGGCAACAACUAUGUGUAUGCCUACGGACCAGACUGGAUGGCAAGGCCUUCCACA
UGGUCCGCGGAAAUCCAGCAAUUCCUGCGACUCCUGGGCGCCACGUACGUGCUUCGCGUGGAGAUGGGCAGGCAGUUUGGCUUCGAGG-3
5'-(((((...((.(......)..)).....)))))((((.....)))))((.(((((((..((((((((.....))).)))))).(((((((...((((.(((...))).)))).)).
)))))))).((....))...(((((((((..((((.(.((((.((((....)))...)))).)))))....)))))).)))).)))))))).)))-3'
MFE = -76.0; z-score = -0.72; ED = 51.44
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BNRF1, 1691-5856(+)

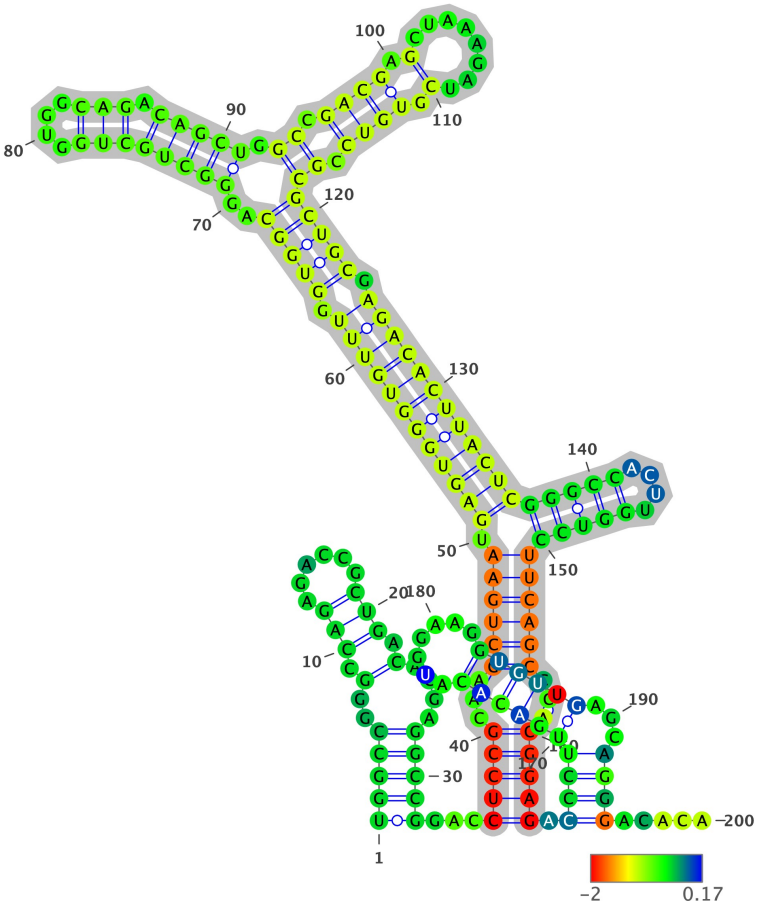
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 199--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 8 from nt 2363 to 2491 (nt 36 to 164)

```
5'-CUCCGCAAGCUGAAUGAGUGGGUGUUUGGUGGCAGGGCUGCUGGUGGCAGACAGCUGGCCGACGAGCUAAAGAUCGUGUCCGCGCUGCGAGACACUUACUCGGGCCACUUG
GUCCUUCAGCCCACGGAG-3'
5'-(.....................................................................................................
.................)-3'
Motif MFE = -61.0; z-score = -2.76; ED = 20.36
```



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 2328 to 2527 (motif highlighted in silver):

```
5'-UGGCCGGGCCAGAGACCGCUGACACGAGGCCGGACCUCCGCAAGCUGAAUGAGUGGGUGUUUGGUGGCAGGGCUGCUGGUGGCAGACAGCUGGCCGACGAGCUAAAGAUCG
UGUCCGCGCUGCGAGACACUUACUCGGGCCACUUGGUCCUUCAGCCCACGGAGACCCUUGACACAUGGAAGGUGUUGAGCAGGGACACA-3
5'-(((((..(.(((......)).)....)))))...((((((...((((((.(((((((((((((.(((((..(((((((((....)))).)))))).((.((((.(........).
))))).)))))))).))))))))))))((((....))))))))))...)))))).((((((((((.......))))))...))))).....-3'
MFE = -80.9; z-score = -0.91; ED = 33.0
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BNRF1, 1691-5856(+)

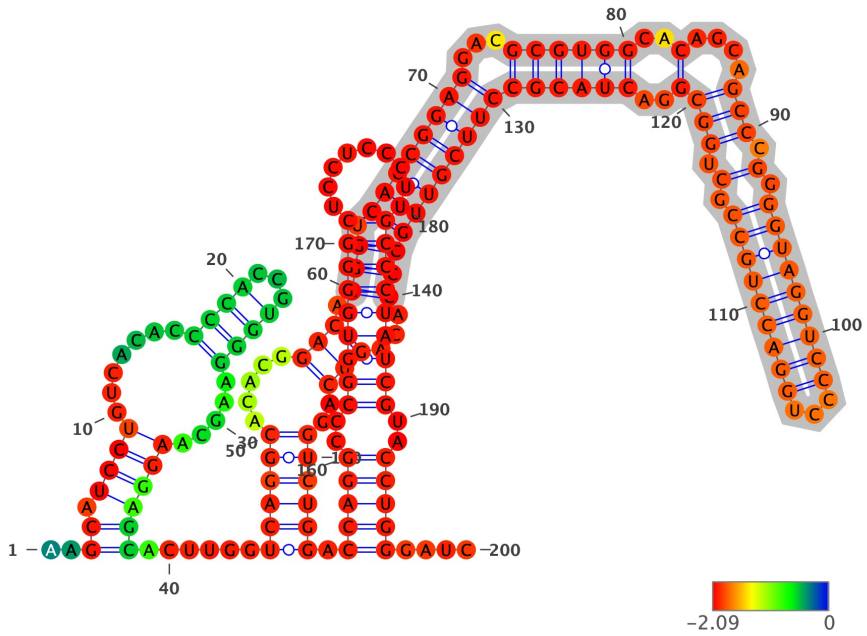
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 200--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 9 from nt 3642 to 3722 (nt 60 to 140)

```
5'-GGGUCAGCGGAGGACGCGUGGCACAGCAGCCCGGGGUAGGUCCCCUGGACCUGCCGCUGGCGGACUACGCCUUCGUUGCCC-3'
5'-(((.(((((((((...((((((..(.....................................)..))))))))))))))))-3'
Motif MFE = -46.9; z-score = -2.85; 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 3583 to 3782 (motif highlighted in silver):

```
5'-AAGCAUCCUGUCACACCCCACCGUGGGAAGCAAGGAGCACUUGGUCAGGCACACGGACAGGGUCAGCGGAGGACGCGUGGCACAGCAGCCCGGGGUAGGUCCCCUGGACCU
GCCGCUGGCGGACUACGCCUUCGUUGCCCACAGUCAGGUCUGGACCAGGCCCGGUGGGGCUCCUCCCUUGCCCUAUCGUACCUGGGAUC-3
5'-..((.((((.......((((...))))).....)))))).....((((((.....(((.(((.(((((((((...((((((..(....(((.(.(((((((((...)))))))
)))).).)))).)).))))))))))))))))...)))..)))))).((((((..(((((((((.........)))))))))..)))))....-3'
MFE = -92.6; z-score = -2.26; ED = 19.52
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BNRF1, 1691-5856(+)

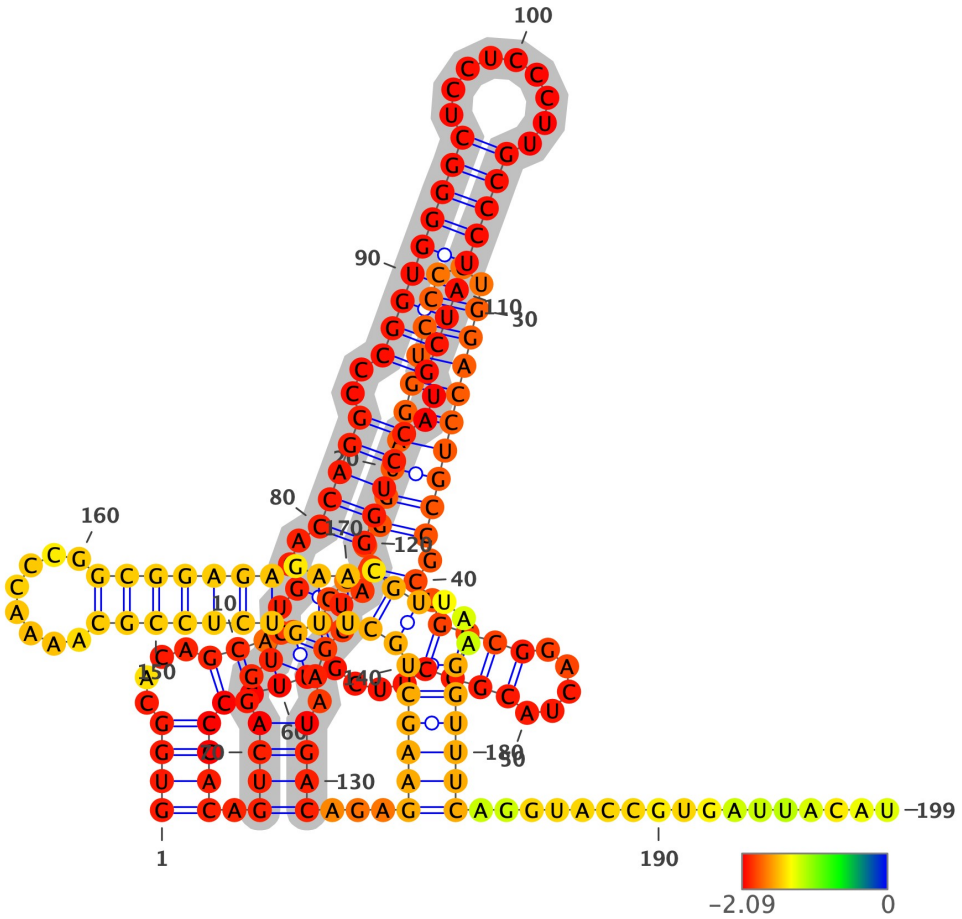
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 200--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 10 from nt 3726 to 3789 (nt 68 to 131)

```
5'-GUCAGGUCUGGACCAGGCCCGGUGGGGCUCCUCCCUUGCCCUAUCGUACCUGGGAUCGAAUGAC-3'
5'-(((...(..(..((((((..(((((((((.........)))))))))..)))))..)..)..)))-3'
Motif MFE = -29.6; z-score = -2.88; 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 3659 to 3857 (motif highlighted in silver):

```
5'-GUGGCACAGCAGCCCGGGGUAGGUCCCCUGGACCUGCCGCUGGCGGACUACGCCUUCGUUGCCCACAGUCAGGUCUGGACCAGGCCCGGUGGGGCUCCUCCCUUGCCCUAU
CGUACCUGGGAUCGAAUGACAGAGAAGCUGCUUGUCUCCGCAAAACCCGGCGGAGAGAACGUUAAGGUUUCAGGUACCGUGAUUACAU-3
5'-((((....((((((..(.(((((((((...)))))))))).).((((.....)))).....)))))))))..((((..((.(..((((((..(((((((((.........)))))))))
))..)))))..).).).))))...((((((((((.(((((((.......)))))))).)).)).....)))))).................-3'
MFE = -85.4; z-score = -2.68; ED = 24.6
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BNRF1, 1691-5856(+)

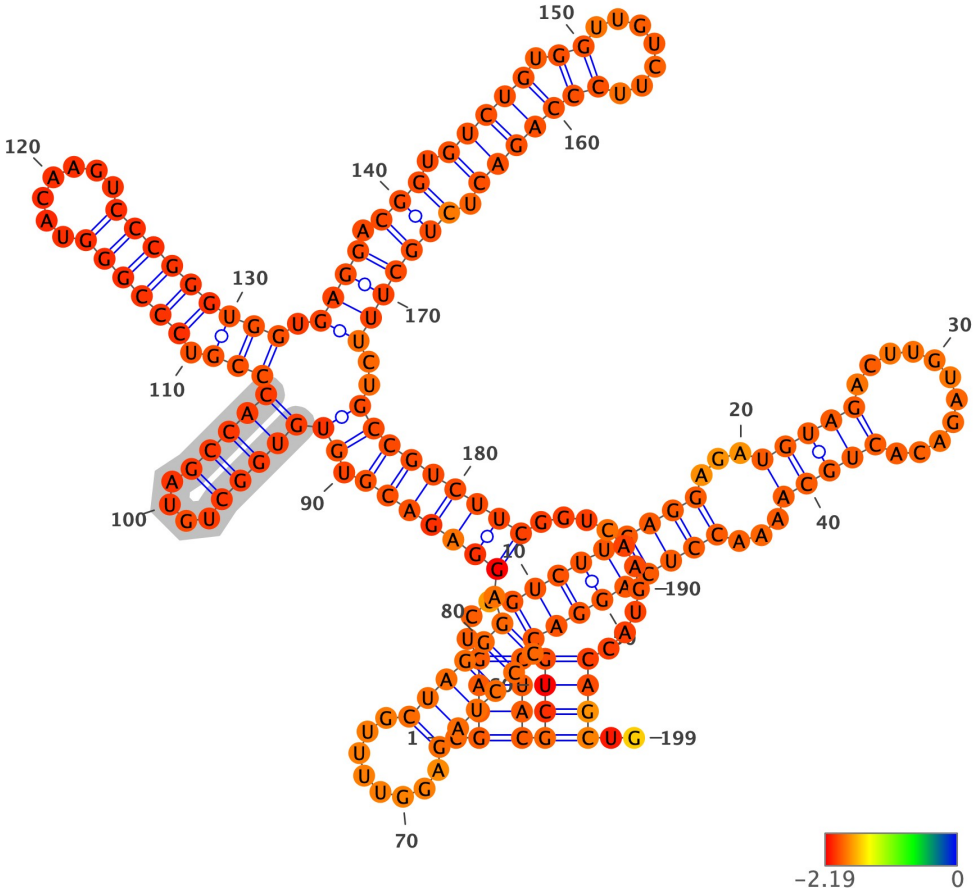
Attributes: ['ID=gene-HHV4_BNRF1', 'Dbxref=GeneID:3783722', 'Name=BNRF1', 'Note=gamma gene%3B FGARAT family', 'gbkey=Gene', 'gene=BNRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BNRF1']

3-- nt 1 to 199--CDS, cds-YP_401633.1, 1736-5692(+)

Attributes: ['ID=cds-YP_401633.1', 'Parent=gene-HHV4_BNRF1', 'Dbxref=UniProtKB/TrEMBL:Q777H3,Genbank:YP_401633.1,GeneID:3783722', 'Name=YP_401633.1', 'gbkey=CDS', 'gene=BNRF1', 'locus_tag=HHV4_BNRF1', 'product=tegument protein G75', 'protein_id=YP_401633.1']

NC_007605.1 (forward strand): Structure number 11 from nt 6673 to 6686 (nt 93 to 106)

```
5'-GUGGCUGUAGCCAC-3'
5'-(((((....)))))-3'
Motif MFE = -6.4; z-score = -3.62; ED = 0.12
```



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

Extracted structure model with flanking nucleotides 6581 to 6779 (motif highlighted in silver):

```
5'-CGUAGUCUGUCUUGAGGAGAUGUAGACUUGUAGACACUGCAAAACCUCAGGACCUACGCUGCCCUAGAGGUUUUGCUAGGGAGGAGACGUGUGUGGCUGUAGCCACCCGUC
CCGGGUACAAGUCCCGGGUGGUGAGGACGGUGUCUGUGGUUGUCUUCCCAGACUCUGCUUUCUGCCGUCUUCGGUCAAGUACCAGCUG-3
5'-.((((...(((((((((...(((((.........)))))...)))))))))))))((((((((((.......))))))).(((((((.(((((((....)))))))((.(
(((((.......)))))))))).((((.(((.(((((.(((.......))))))).))))))..)))))))))..........))))..-3'
MFE = -80.0; z-score = -2.46; ED = 38.55
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 49 to 199--transcript, rna-NC_007605.1:6629..6795, 6629-6795(+)

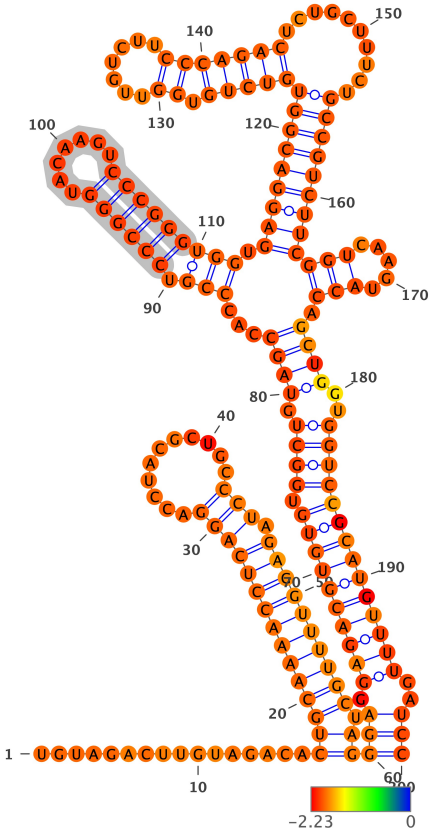
Attributes: ['ID=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

3-- nt 49 to 199--exon, exon-NC_007605.1:6629..6795-1, 6629-6795(+)

Attributes: ['ID=exon-NC_007605.1:6629..6795-1', 'Parent=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

NC_007605.1 (forward strand): Structure number 12 from nt 6691 to 6709 (nt 91 to 109)

```
5'-CCCGGGUACAAGUCCCGGG-3'
5'-((((((.......))))))-3'
Motif MFE = -11.2; z-score = -3.16; 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 6601 to 6800 (motif highlighted in silver):

```
5'-UGUAGACUUGUAGACACUGCAAAACCUCAGGACCUACGCUGCCCUAGAGGUUUUGCUAGGGAGGAGACGUGUGUGGCUGUAGCCACCCGUCCCGGGUACAAGUCCCGGGUG
GUGAGGACGGUGUCUGUGGUUGUCUUCCCAGACUCUGCUUUCUGCCGUCUUCGGUCAAGUACCAGCUGGUGGUCCGCAUGUUUUGAUCC-3
5'-................((((((((((((((((.........)))).)))))))))).))))(.((((((((((.((((.((((...(((.((((((.......)))))))))
).((((((((((((((.((.......)))))))).........))))))))))((.....))).)))))..))))))))))))))..)))-3'
MFE = -79.0; z-score = -1.95; ED = 31.31
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 29 to 195--transcript, rna-NC_007605.1:6629..6795, 6629-6795(+)

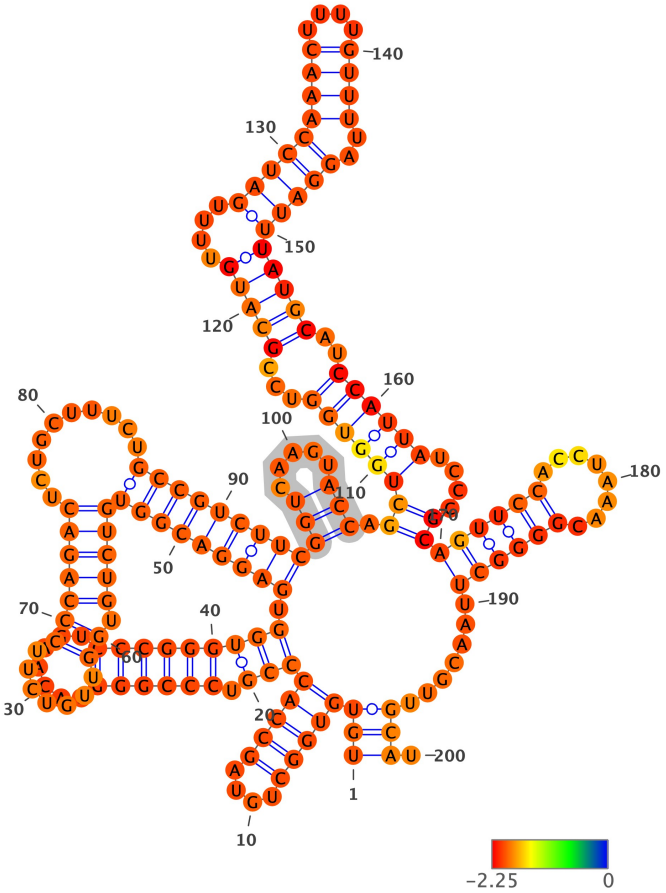
Attributes: ['ID=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

3-- nt 29 to 195--exon, exon-NC_007605.1:6629..6795-1, 6629-6795(+)

Attributes: ['ID=exon-NC_007605.1:6629..6795-1', 'Parent=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

NC_007605.1 (forward strand): Structure number 13 from nt 6764 to 6774 (nt 95 to 105)

```
5'-GGUCAAGUACC-3'
5'-(((.....)))-3'
Motif MFE = 0.0; z-score = 0.27; ED = 1.5
```



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

Extracted structure model with flanking nucleotides 6670 to 6869 (motif highlighted in silver):

```
5'-UGUGUGGCUGUAGCCACCCGUCCCGGGUACAAGUCCCGGGUGGUGAGGACGGUGUCUGUGGUUGUCUUCCCAGACUCUGCUUUCUGCCGUCUUCGGUCAAGUACCAGCUGG
UGGUCCGCAUGUUUUGAUCCAAACUUUUGUUUUAGGAUUUAUGCAUCCAUUAUCCCGCAGUUCCACCUAAACGGGGCUUAACGUUGCAU-3
5'-(((((((((....)))))))((.((((((.......)))))))))).(((((((((((((.((.......)))))))).........)))))))))((.....)).(((((
(((...((((((....((((((((((....))))..))))))))))..)))))).....))((((((........)))))).......))).-3'
MFE = -68.4; z-score = -1.99; ED = 49.22
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 126--transcript, rna-NC_007605.1:6629..6795, 6629-6795(+)

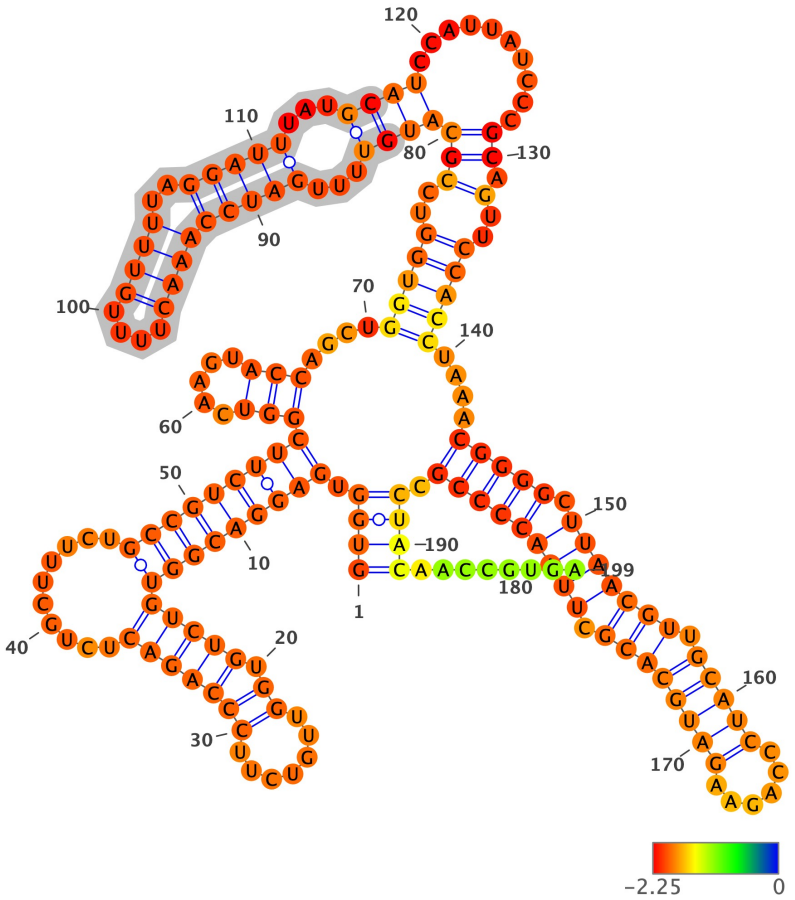
Attributes: ['ID=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

3-- nt 1 to 126--exon, exon-NC_007605.1:6629..6795-1, 6629-6795(+)

Attributes: ['ID=exon-NC_007605.1:6629..6795-1', 'Parent=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

NC_007605.1 (forward strand): Structure number 14 from nt 6791 to 6824 (nt 83 to 116)

```
5'-GUUUUGAUCCAAACUUUUGUUUUAGGAUUUAUGC-3'
5'-(....(((((((((....)))))..)))))....)-3'
Motif MFE = -5.6; z-score = -1.99; 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 6709 to 6907 (motif highlighted in silver):

```
5'-GUGGUGAGGACGGUGUCUGUGGUUGUCUUCCCAGACUCUGCUUUCUGCCGUCUUCGGUCAAGUACCAGCUGGUGGUCCGCAUGUUUUGAUCCAAACUUUUGUUUUAGGAUU
UAUGCAUCCAUUAUCCCGCAGUUCCACCUAAACGGGGCUUAACGUUGCAUCCCAGAAGAUGCACGCUUAACCCCGCCUACAACCGUGA-3
5'-((((.(((((((((((((.(((.......)))))))).........))))))))))((.....)))....(((((..(((((((...(((((((((....)))))..))))))
...))))..........)).)..)))))....(((((.(((((((.(((((.....)))))))).)))))))).)))).........-3'
MFE = -63.8; z-score = -2.2; ED = 30.0
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 87--transcript, rna-NC_007605.1:6629..6795, 6629-6795(+)

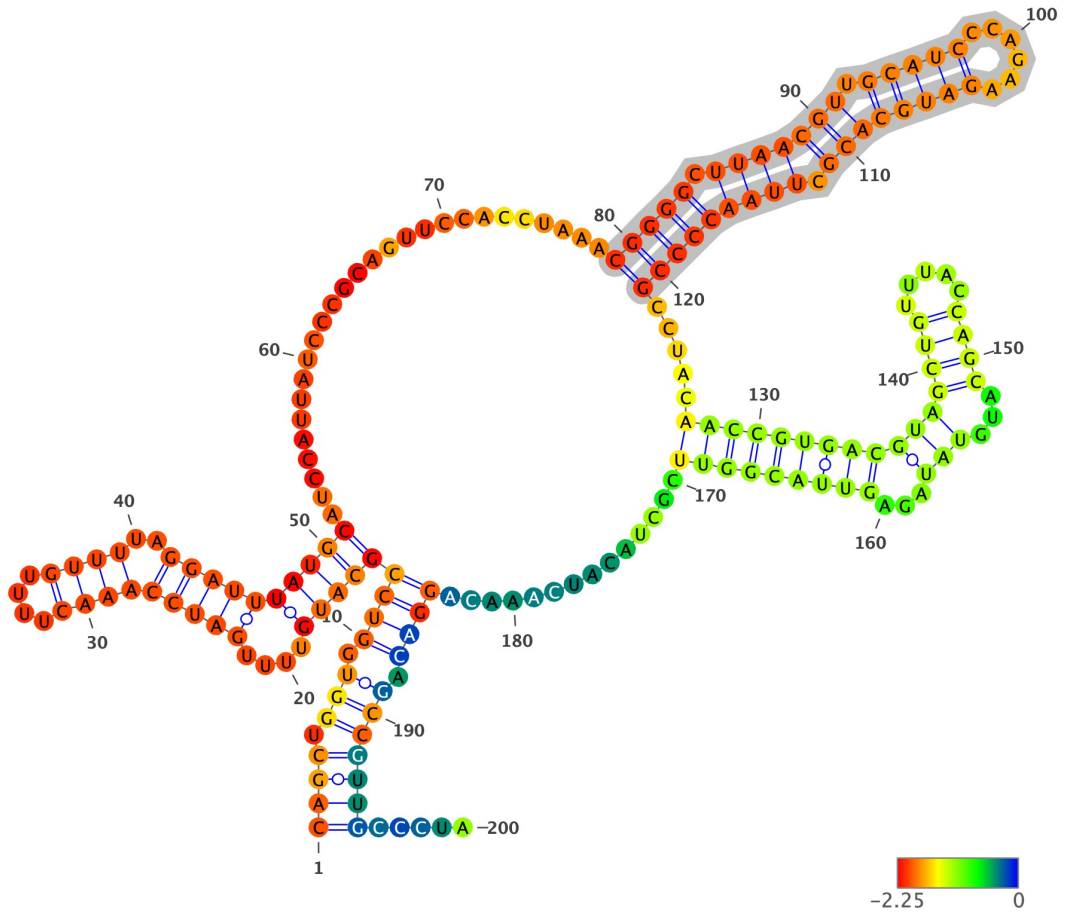
Attributes: ['ID=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

3-- nt 1 to 87--exon, exon-NC_007605.1:6629..6795-1, 6629-6795(+)

Attributes: ['ID=exon-NC_007605.1:6629..6795-1', 'Parent=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

NC_007605.1 (forward strand): Structure number 15 from nt 6852 to 6894 (nt 79 to 121)

```
5'-CGGGGCUUAACGUUGCAUCCCAGAAGAUGCACGCUUAACCCCG-3'
5'-(((((.((((.......................)))))))))-3'
Motif MFE = -19.7; z-score = -4.14; ED = 2.05
```



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 6774 to 6973 (motif highlighted in silver):

```
5'-CAGCUGGUGGUCCGCAUGUUUUGAUCCAAACUUUUGUUUUAGGAUUUAUGCAUCCAUUAUCCCGCAGUUCCACCUAAACGGGGCUUAACGUUGCAUCCCAGAAGAUGCACG
CUUAACCCCGCCUACAACCGUGACGUAGCUGUUUACCAGCAUGUAUAGAGUUACGGUUCGCUACAUCAAACAGGACAGCCGUUGCCCUA-3
5'-((((.(((.(((((((((....((((((((....))))..))))))))))).............................(((((.(((((((.(((((.....)))))))))
.)))))))))).....(((((((((((((((.....)))))...)))).))).))))))))).............))))).))))))).....-3'
MFE = -56.8; z-score = -2.38; ED = 38.09
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 22--transcript, rna-NC_007605.1:6629..6795, 6629-6795(+)

Attributes: ['ID=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

3-- nt 1 to 22--exon, exon-NC_007605.1:6629..6795-1, 6629-6795(+)

Attributes: ['ID=exon-NC_007605.1:6629..6795-1', 'Parent=rna-NC_007605.1:6629..6795', 'gbkey=misc_RNA', 'product=EBER-1 (pol III transcript)']

4-- nt 183 to 200--transcript, rna-NC_007605.1:6956..7128, 6956-7128(+)

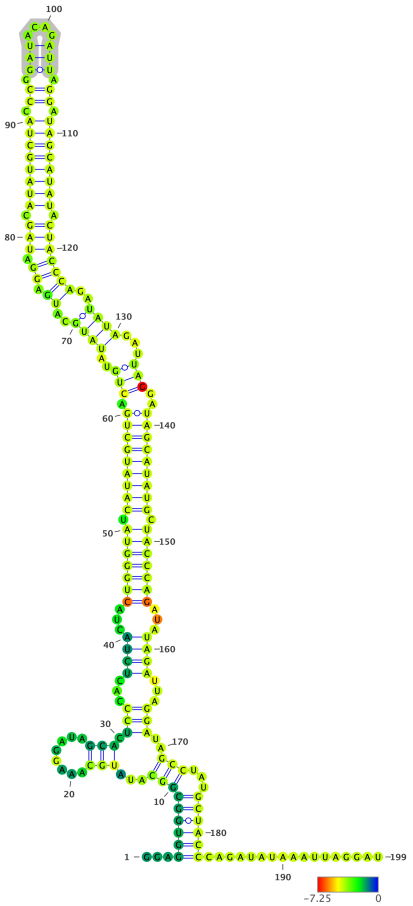
Attributes: ['ID=rna-NC_007605.1:6956..7128', 'gbkey=misc_RNA', 'product=EBER-2 (pol III transcript)']

5-- nt 183 to 200--exon, exon-NC_007605.1:6956..7128-1, 6956-7128(+)

Attributes: ['ID=exon-NC_007605.1:6956..7128-1', 'Parent=rna-NC_007605.1:6956..7128', 'gbkey=misc_RNA', 'product=EBER-2 (pol III transcript)']

NC_007605.1 (forward strand): Structure number 16 from nt 7470 to 7479 (nt 95 to 104)

```
5'-GAUACAGAUU-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 7376 to 7574 (motif highlighted in silver):

```
5'-GGAGGUGGCGGCAUAUGCAAAGGAUAGCACUCCCACUCUACUACUGGGUAUCAUAUGCUGACUGUAUAUGCAUGAGGAUAGCAUAUGCUACCCGGAUACAGAUUAGGAUAG
CAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAU-3
5'-...(((((((((...(((........))).(((...((((...(((((((.(((((((((.((((..((((..((.((.((((.(((((((((.((.((((....)))).)).)))
)))))).)))))))..))))...))))..))))))))).)))))))...))))...))))..))))...))))))).................-3'
MFE = -63.0; z-score = -4.24; ED = 22.57
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

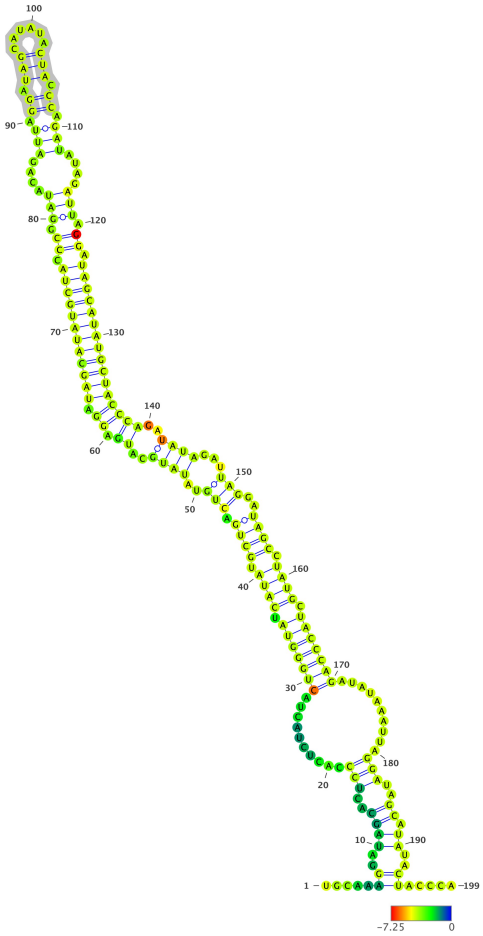
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 46 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 17 from nt 7481 to 7498 (nt 91 to 108)

```
5'-GGAUAGCAUAUACUACCC-3'
5'-((.(((.....))).))-3'
Motif MFE = -1.6; z-score = -0.95; ED = 2.27
```



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

Extracted structure model with flanking nucleotides 7391 to 7589 (motif highlighted in silver):

```
5'-UGCAAAGGAUAGCACUCCCACUCUACUACUGGGUAUCAUAUGCUGACUGUAUAUGCAUGAGGAUAGCAUAUGCUACCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGA
UAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCA-3
5'-.....((..(((((..(((.........(((((((.((((.((((.((((..(((((..((.((.(((((((((((((.((.(((....(((.((.(((......)))).)).))
)....))).)).))))))))))))))))..))))...))))..)))).)))).)))))))).........))))..)).)).)).))).....-3'
MFE = -56.6; z-score = -5.51; ED = 42.0
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

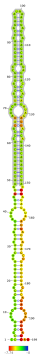
3-- nt 31 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 18 from nt 7514 to 7615 (nt 49 to 150)

5'-UAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUA-3'

5'-(((((((((((.((.....(.(.((.((((..(((((((.((.((((....))).)).)))))))..))).)).).).....)).)))))))))))-3'
Motif MFE = -33.5; z-score = -4.77; ED = 13.06



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 7466 to 7664 (motif highlighted in silver):

5'-CCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAG
CAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAU-3
5'-.((.(((....(((.((.(((((((..(((.((.(((....(((.((.((((((((((((.((.(((....(((.((.((((..(((((((.((.((((....)))).)).)))
))))..)))).)).)))....))).)).))))))))))).)).)))....))).)).))))..)))))))).)).)))....))).)).))..-3'
MFE = -55.7; z-score = -4.5; ED = 19.33

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

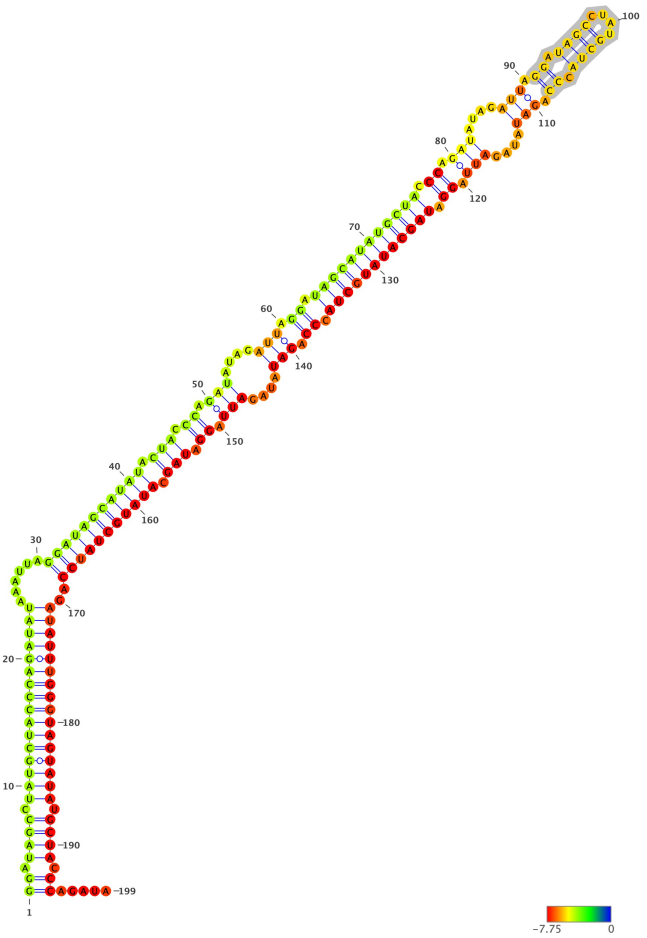
Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 19 from nt 7631 to 7648 (nt 91 to 108)

5'-GGAUAGCCUAUGCUACCC-3'

5'-((.((((....)))).))-3'

Motif MFE = -4.5; z-score = -2.4; 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 7541 to 7739 (motif highlighted in silver):

5'-GGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAGAUA-3

5'-((.((((.(((((((((((((((.....((((((((((.(((.((.(((....(((.((.((((((((((((.((.(((....(((.((.((((....)))).)).)).))).....))).)).)))))))))))))).)).))).....))).)).))).))))))))))..))))))))))))))))).)))))..)).....-3'

MFE = -80.1; z-score = -7.6; ED = 41.14

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

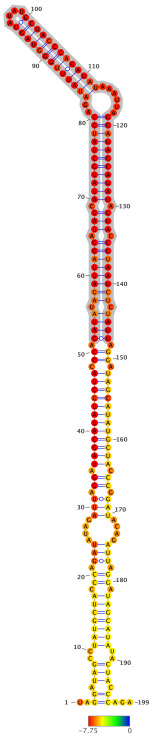
3-- nt 1 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 20 from nt 7680 to 7775 (nt 52 to 147)

5'-GAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCUAAUCUCUAUU-3'

5'-(((....(((.((.(((.(((((((((.((....(((.((.((((....)))).)).)))........)).)))))))).))).)).)))....)))-3'
Motif MFE = -47.0; z-score = -7.9; ED = 2.99



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

Extracted structure model with flanking nucleotides 7629 to 7827 (motif highlighted in silver):

5'-UAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAGAUA
UAAAUUAGGAUAGCAUAUACUACCCUAAUCUCUAUUAGGAUAGCAUAUGCUACCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGA-3
5'-..((.((((..((((((((.((.(((.....(((.((.(((((((((((((.((.((((.((((((((.(((.((((((((((..((((((((((((....)))))))))))))
).....)))))))))))).))).)))))))).)))).)).))))))))))))).)).))).....))).)).))))))).)).))....-3'
MFE = -88.8; z-score = -8.34; ED = 8.75

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 21 from nt 7777 to 7854 (nt 61 to 138)

```
5'-GGAUAGCAUAUGCUACCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCC-3'
5'-((.((((.(((((((((.((.(((....(((.((.(((.....))).)).)))....))).)).)))))))).))).))-3'
Motif MFE = -26.4; z-score = -4.44; ED = 6.18
```

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 7717 to 7915 (motif highlighted in silver):

```
5'-GGGUAGUAUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCUAAUCUCUAUUAGGAUAGCAUAUGCUACCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGA
UAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCA-3
5'-(((((((((((((((.((.((((.((.((((.((.(((((((..(((.((((((((.((((.((.(((((((((((((.((.(((....(((.((.(((.....)))).)).))
)....))).)).))))))))))))).)).)))).)))))))).))..))))))).)).))).)).))).)).))).))))))))))))))).-3'
MFE = -82.5; z-score = -8.09; ED = 10.24
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 22 from nt 7867 to 7914 (nt 76 to 123)

```
5'-GGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCC-3'
5'-((.((((..(((((((.((.(((....))).)).)))))))..))))..))-3'
Motif MFE = -12.7; z-score = -3.77; ED = 4.72
```

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 7792 to 7990 (motif highlighted in silver):

```
5'-CCCGGAUACAGAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAG
CAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAU-3
5'-.((.(((....(((.((.(((((((..(((.((.(((....(((.((.(((((((((((((.((.(((....(((.((.((..(((((((.((.((((....)))).)).)))
))))..)))).)).)))....))).)).))))))))))))).)).)))....))).)).))).)))))))).)).)))....))).)).))..-3'
MFE = -55.7; z-score = -5.08; ED = 23.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

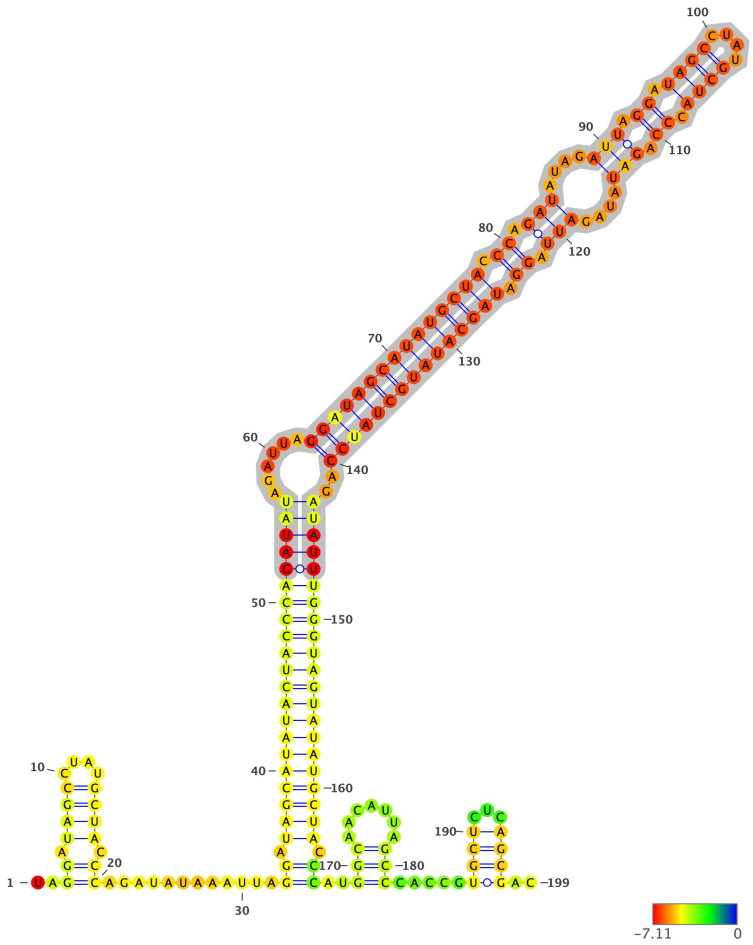
3-- nt 1 to 199--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 23 from nt 7916 to 8011 (nt 52 to 147)

5'-GAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUU-3'

5'-(((.....((.((((((((((((.((.(((....(.(.((.((((....)))).)).).)....))).)).)))))))))))).)).....)))-3'
Motif MFE = -34.1; z-score = -5.85; ED = 12.24



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 7865 to 8063 (motif highlighted in silver):

5'-UAGGAUAGCCUAUGCUACCCAGAUAUAAAUUAGGAUAGCAUAUACUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCA
GAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAUGGCAACAUUAGCCCACCGUGCUCUCAGCGAC-3
5'-..((.((((....)))).))...........((.(((((((((((((((((((.....((((((((((((((.((.(((....(((.((.((((....)))).)).
)))....))).)).))))))))))))))..))))))))))))))))))))).))..(((.......)))).....((((...)))).-3'
MFE = -77.1; z-score = -7.48; ED = 13.07

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

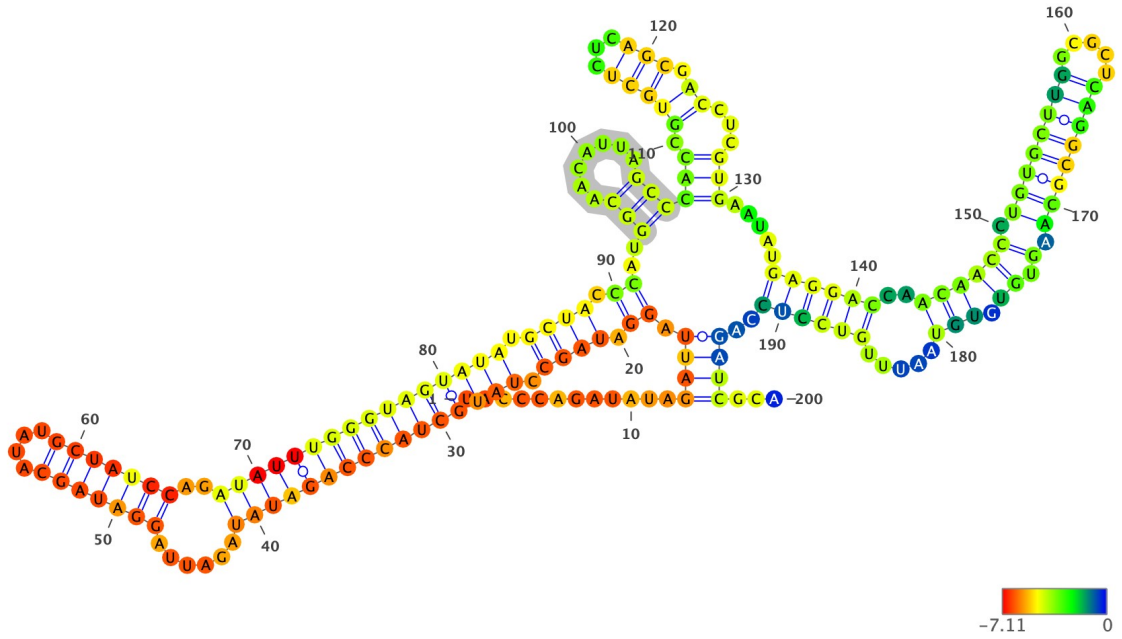
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 178--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 24 from nt 8033 to 8045 (nt 94 to 106)

```
5'-GGCAACAUUAGCC-3'
5'-(((.......)))-3'
Motif MFE = -2.2; z-score = -2.59; 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 7940 to 8139 (motif highlighted in silver):

```
5'-UACCCAGAUAUAGAUUAGGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAUGGCAACAUUAGCCCACCG
UGCUCUCAGCGACCUCGUGAAUAUGAGGACCAACAACCCUGUGCUUGGCGCUCAGGCGCAAGUGUGUGUAAUUUGUCCUCCAGAUCGCA-3
5'-............((((.((.((((.(((((((((((((((.....(((((((....)))))))..))))))))))))))))).)))).)).(((.......)))((((.(
((((...)))).)).....))).....((((((..((((((.(((((((.....)))))))).).)).)))).....)))))).)))).....-3'
MFE = -68.7; z-score = -4.35; ED = 28.39
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

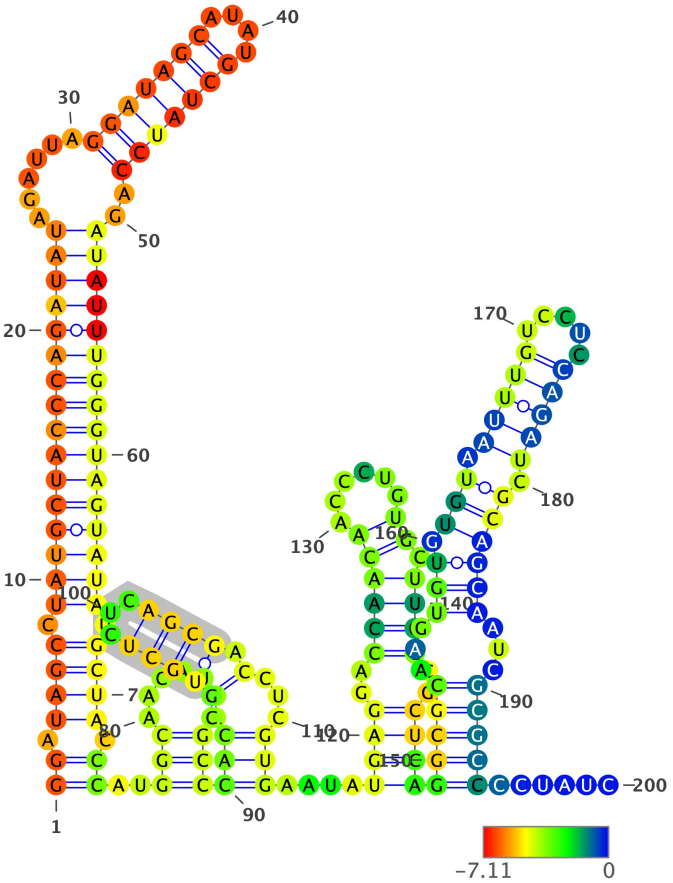
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 103--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 25 from nt 8051 to 8061 (nt 95 to 105)

```
5'-UGCUCUCAGCG-3'
5'-(((((...)))))-3'
Motif MFE = -1.1; z-score = -2.93; 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 7957 to 8156 (motif highlighted in silver):

```
5'-GGAUAGCCUAUGCUACCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAUGGCAACAUUAGCCCACCGUGCUCUCAGCGACCUCG
UGAAUAUGAGGACCAACAACCCUGUGCUUGGCGCUCAGGCGCAAGUGUGUGUAAUUUGUCCUCCAGAUCGCAGCAAUCGCGCCCCUAUC-3
5'-((.((((.(((((((((((((((.....(((((((....)))))))..))))))))))))))).)))).))..(((.......)))(((.(((((...))))).)...)
))....((((..((((((.....)).)))).))))))))...(((.(((.(((((.....)))))).)))))).....-3'
MFE = -71.2; z-score = -4.45; ED = 41.29
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

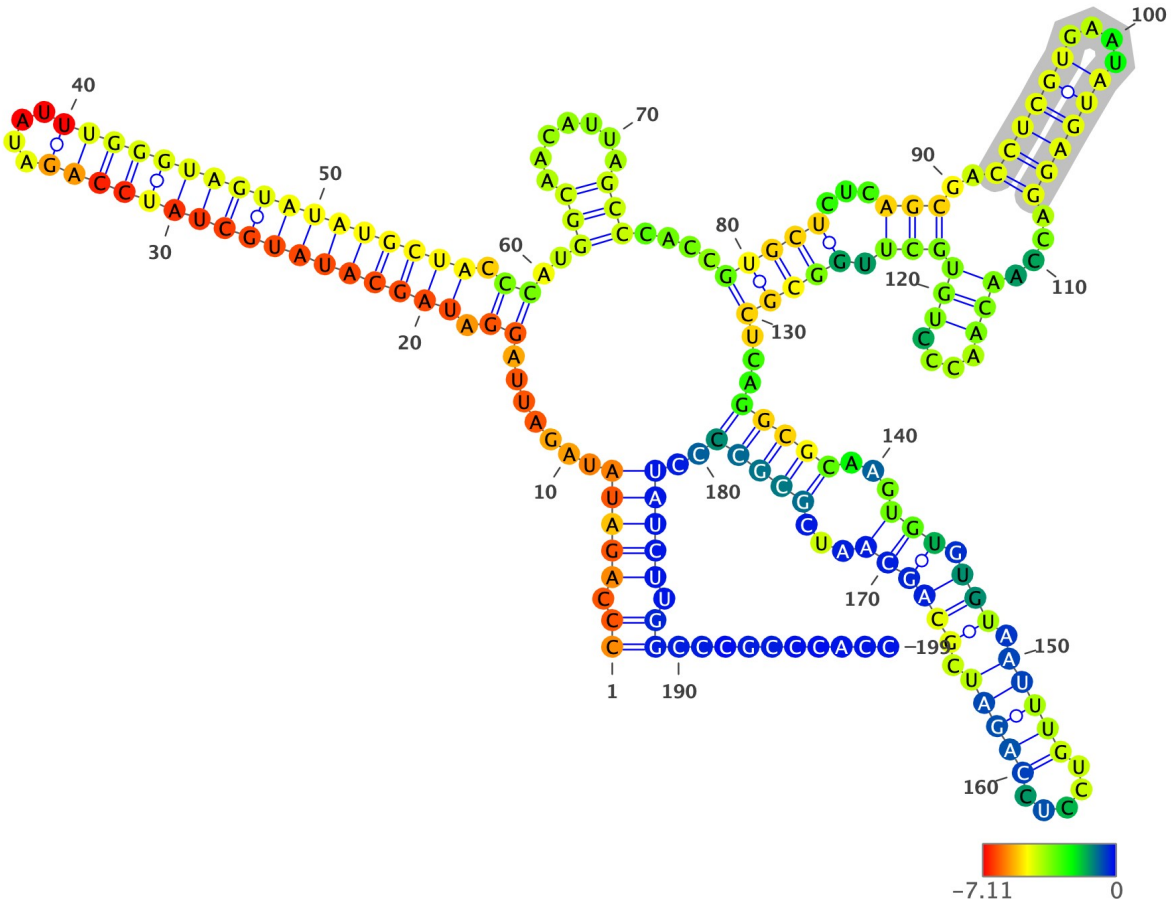
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 86--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 26 from nt 8063 to 8078 (nt 92 to 107)

```
5'-CCUCGUGAAUAUGAGG-3'
5'-((((((....)))))))-3'
Motif MFE = -5.3; z-score = -3.57; 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 7972 to 8170 (motif highlighted in silver):

```
5'-CCCAGAUAUAGAUUAGGAUAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAUGGCAACAUUAGCCCACCGUGCUCUCAGCGACCUCGUGAAUAUGAGGACCA
ACAACCCUGUGCUUGGCGCUCAGGCGCAAGUGUGUGUAAUUUGUCCUCCAGAUCGCAGCAAUCGCGCCCCUAUCUUGGCCCGCCCACC-3
5'-((.(((((.......((.((((((((((((((((((....)))))))))))))))))))).)).(((.......)))....(((((...(((..((((((....)))))))....
(((....)))))).)))))...(((((...(((.(((.(((((....)))))).)))))))...)))))..)))))).)).........-3'
MFE = -64.4; z-score = -2.84; ED = 35.09
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

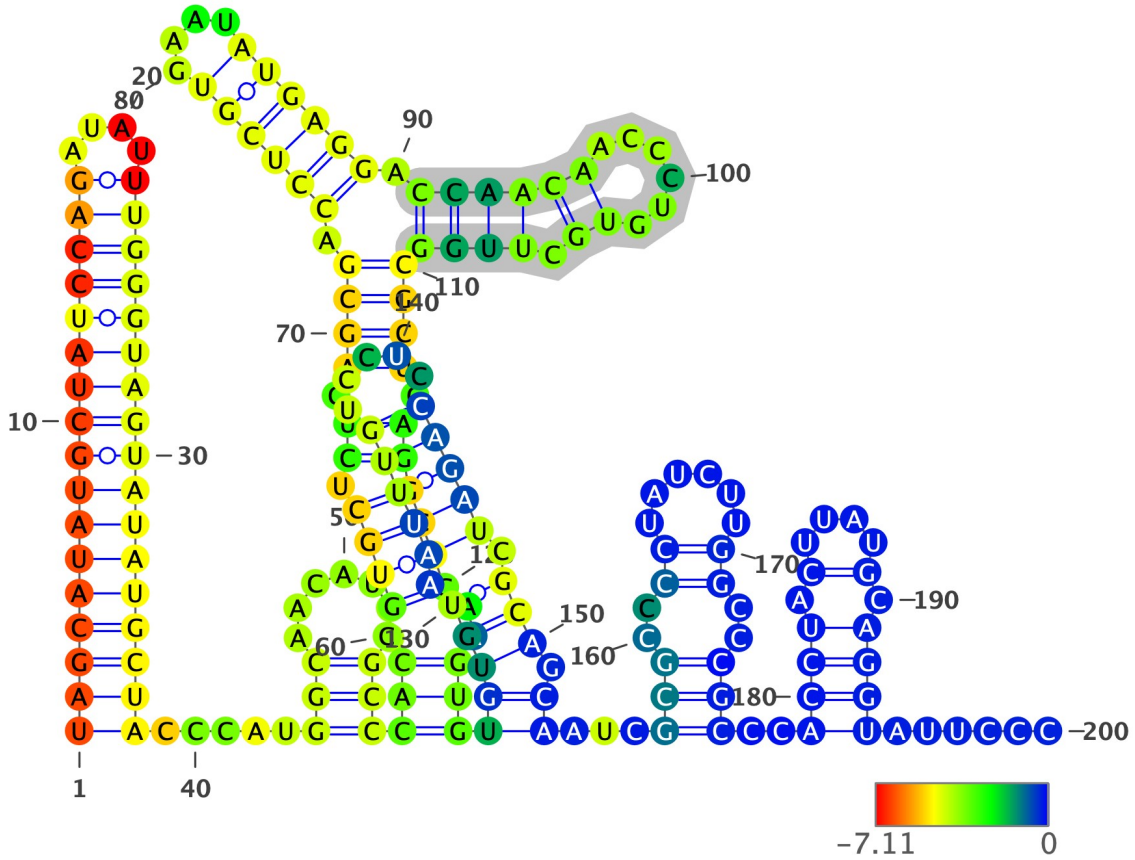
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 71--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 27 from nt 8080 to 8098 (nt 91 to 109)

```
5'-CCAACAACCCUGUGCUUGG-3'
5'-(..(((......)).)..)-3'
Motif MFE = -1.7; z-score = -0.32; ED = 3.37
```



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

Extracted structure model with flanking nucleotides 7990 to 8189 (motif highlighted in silver):

```
5'-UAGCAUAUGCUAUCCAGAUAUUUGGGUAGUAUAUGCUACCCAUGGCAACAUUAGCCCACCGUGCUCUCAGCGACCUCGUGAAUAUGAGGACCAACAACCCUGUGCUUGGCG
CUCAGGCGCAAGUGUGUGUAAUUUGUCCUCCAGAUCGCAGCAAUCGCGCCCCUAUCUUGGCCCGCCCACCUACUUAUGCAGGUAUUCCC-3
5'-(((((((((((((((((....)))))))))))))))))).....(((.......)))((((.((((.((.((((.(((((((....)))))))).((((((.....)).))))))
)).)))))))..)))((((.(((((.....)))))).))).))...(((..((.....))..)))..((((.(....).))))......-3'
MFE = -60.9; z-score = -3.03; ED = 45.8
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

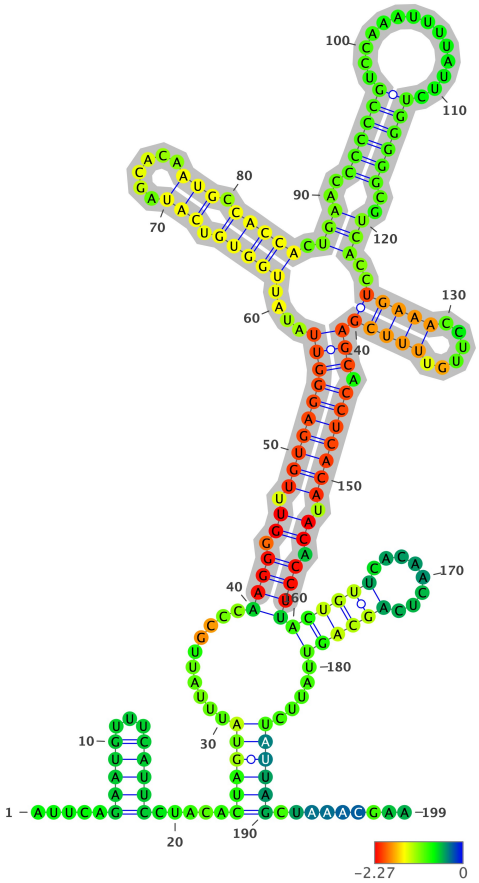
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 1 to 53--direct_repeat, id-NC_007605.1:7421..8042, 7421-8042(+)

Attributes: ['ID=id-NC_007605.1:7421..8042', 'Note=binding sites for EBNA-1 (site I%2C family of repeats%2C FR)%3B also functions as a cell type-specific enhancer', 'gbkey=repeat_region', 'rpt_type=direct', 'rpt_unit_range=7421..7450']

NC_007605.1 (forward strand): Structure number 28 from nt 8686 to 8803 (nt 41 to 158)

```
5'-AGGGGUUUGUGAGGGUUAUAUUGGUGUCAUAGCACAAUGCCACCACUGAACCCCCCGUCCAAAUUUUAUUCUGGGGGCGUCACCUGAAACCUUGUUUUCGAGCACCUCACA
UACACCU-3'
5'-(((.((.(((((((((((.....................................................................(.............)))))..)))))))
.)).)))-3'
Motif MFE = -36.5; z-score = -2.93; ED = 14.71
```



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 8646 to 8844 (motif highlighted in silver):

```
5'-AUUCAGAAUGUUUCAUUCCUACACUAGUAUUUAUUGCCCAAGGGGUUUGUGAGGGUUAUAUUGGUGUCAUAGCACAAUGCCACCACUGAACCCCCCGUCCAAAUUUUAUUC
UGGGGGCGUCACCUGAAACCUUGUUUUCGAGCACCUCACAUACACCUUACUGUUCACAACUCAGCAGUUAUUCUAUUAGCUAAACGAA-3
5'-.....(((((...))))).....((((((..........((((.((.(((((((((((....(((((.(((......))).)))))).(((..((((((.............
))))))..)))..(((((......)))))))).)))))))..)).))))((((((........)))))).....)))))).........-3'
MFE = -45.6; z-score = -1.91; ED = 23.97
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

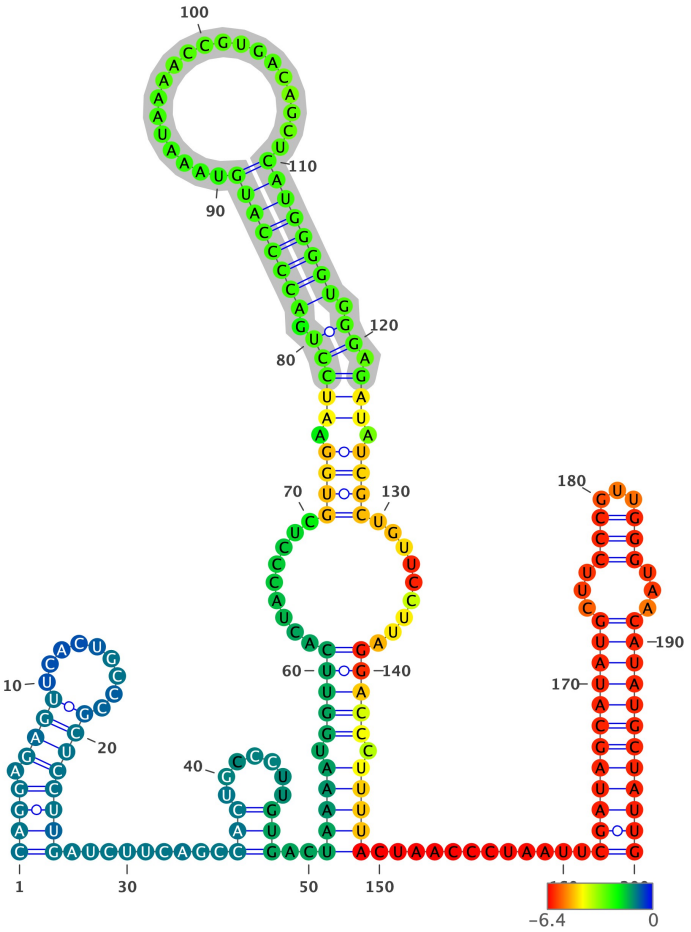
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

NC_007605.1 (forward strand): Structure number 29 from nt 8948 to 8992 (nt 78 to 122)

```
5'-CCUGACCCCAUGUAAAUAAAACCGUGACAGCUCAUGGGGUGGGAG-3'
5'-(((.(((((((((.....................)))))))))).)).)-3'
Motif MFE = -16.1; z-score = -2.86; ED = 3.12
```



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

Extracted structure model with flanking nucleotides 8871 to 9070 (motif highlighted in silver):

```
5'-CAGGAGAGUUCACUGCCCGCUCCUUGAUCUUCAGCCACUGCCCUUGUGACUAAAAUGGUUCACUACCCUCGUGGAAUCCUGACCCCAUGUAAAUAAAACCGUGACAGCUCA
UGGGGUGGGAGAUAUCGCUGUUCCUUAGGACCCUUUUACUAACCCUAAUUCGAUAGCAUAUGCUUCCCGUUGGGUAACAUAUGCUAUUG-3
5'-((((.((((.........)))))))).........((.......)))..(((((.(((((.........((((.(((((.(((((((((.....................))
))))))).)).))).)))).........)))))).)))))............((((((((((((...(((...))).....)))))))))))-3'
MFE = -55.5; z-score = -1.87; ED = 32.78
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

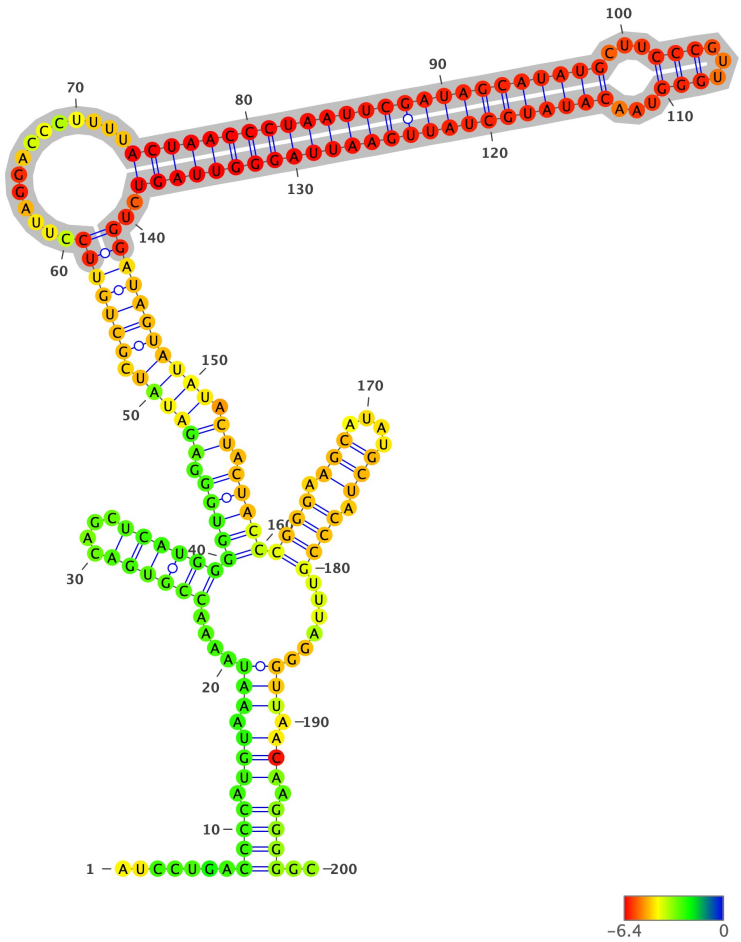
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 151 to 200--inverted_repeat, id-NC_007605.1:9021..9135, 9021-9135(+)

Attributes: ['ID=id-NC_007605.1:9021..9135', 'Note=dyad symmetry%2C binding site for EBNA-1 (site II)', 'gbkey=repeat_region', 'rpt_type=inverted']

NC_007605.1 (forward strand): Structure number 30 from nt 9003 to 9087 (nt 58 to 142)

```
5'-UCCUUAGGACCCUUUUACUAACCCUAAUUCGAUAGCAUAUGCUUCCCGUUGGGUAACAUAUGCUAUUGAAUUAGGGUUAGUCUGG-3'
5'-((.............((((((((((((((((((((((...(((...)))...)))))))))))))))))))))))))..))-3'
Motif MFE = -42.7; z-score = -7.17; 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 8946 to 9145 (motif highlighted in silver):

```
5'-AUCCUGACCCCAUGUAAAUAAAACCGUGACAGCUCAUGGGGUGGGAGAUAUCGCUGUUCCUUAGGACCCUUUUACUAACCCUAAUUCGAUAGCAUAUGCUUCCCGUUGGGU
AACAUAUGCUAUUGAAUUAGGGUUAGUCUGGAUAGUAUAUACUACUACCCGGGAAGCAUAUGCUACCCGUUUAGGGUUAACAAGGGGGC-3
5'-.......((((.((((.((((....((((((....)))))))(((((.((((((.(((((((.............((((((((((((((((((((((...(((...))).
..))))))))))))))))))))))))..)))))))))))).)).))))))((((.(((....))).)))).....))).))).)))))..-3'
MFE = -81.9; z-score = -6.62; ED = 15.22
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

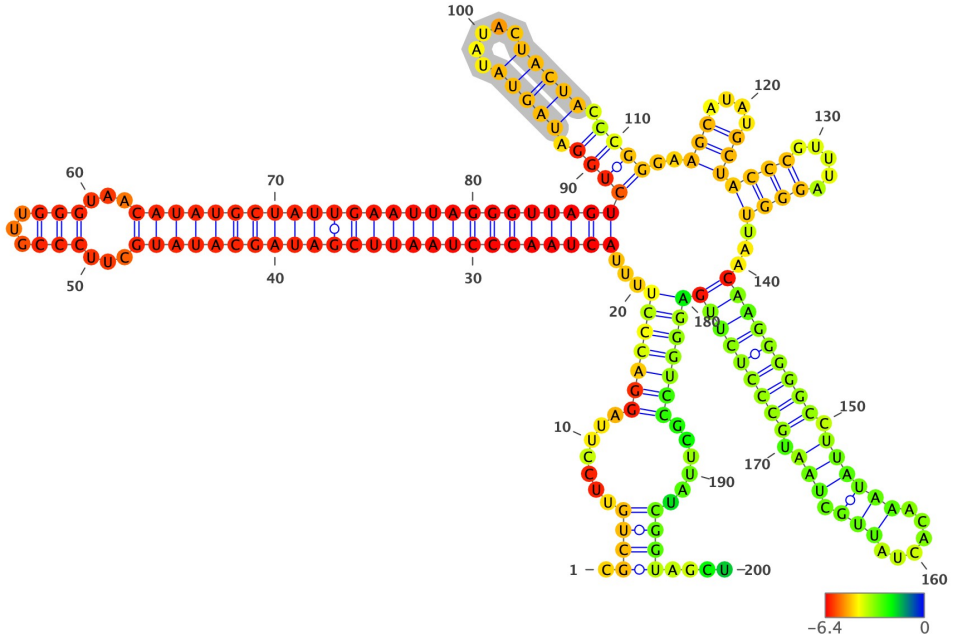
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 76 to 190--inverted_repeat, id-NC_007605.1:9021..9135, 9021-9135(+)

Attributes: ['ID=id-NC_007605.1:9021..9135', 'Note=dyad symmetry%2C binding site for EBNA-1 (site II)', 'gbkey=repeat_region', 'rpt_type=inverted']

NC_007605.1 (forward strand): Structure number 31 from nt 9089 to 9103 (nt 93 to 107)

```
5'-UAGUAUAUACUACUA-3'
5'-(((((.....)))))-3'
Motif MFE = -1.0; z-score = -7.63; ED = 3.39
```



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 8997 to 9196 (motif highlighted in silver):

```
5'-CGCUGUUCCUUAGGACCCUUUUACUAACCCUAAUUCGAUAGCAUAUGCUUCCCGUUGGGUAACAUAUGCUAUUGAAUUAGGGUUAGUCUGGAUAGUAUAUACUACUACCCG
GGAAGCAUAUGCUACCCGUUUAGGGUUAACAAGGGGGCCUUAUAAACACUAUUGCUAAUGCCCUCUUGAGGGUCCGCUUAUCGGUAGCU-3
5'-.((((.......(((((((...((((((((((((((((((((((((...(((...)))...))))))))))))))))))))))))))))))))((((.(((((.....)))))).)))
)..(((....)))((((.....))))...(((((((((.(((((.......))).))).))))))))))))))))).....)))).....-3'
MFE = -90.6; z-score = -7.23; ED = 12.62
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

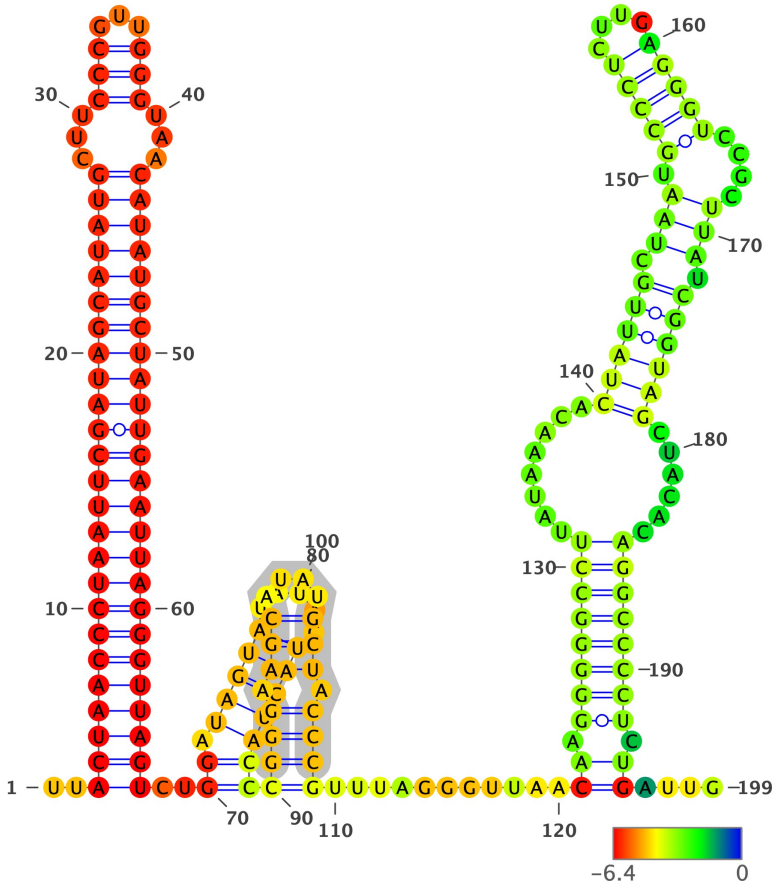
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 25 to 139--inverted_repeat, id-NC_007605.1:9021..9135, 9021-9135(+)

Attributes: ['ID=id-NC_007605.1:9021..9135', 'Note=dyad symmetry%2C binding site for EBNA-1 (site II)', 'gbkey=repeat_region', 'rpt_type=inverted']

NC_007605.1 (forward strand): Structure number 32 from nt 9107 to 9124 (nt 91 to 108)

```
5'-GGGAAGCAUAUGCUACCC-3'
5'-(((.(((....))).)))-3'
Motif MFE = -6.8; z-score = -3.89; 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 9017 to 9215 (motif highlighted in silver):

```
5'-UUACUAACCCUAAUUCGAUAGCAUAUGCUUCCCGUUGGGUAACAUAUGCUAUUGAAUUAGGGUUAGUCUGGAUAGUAUAUACUACUACCCGGGAAGCAUAUGCUACCCGUU
UAGGGUUAACAAGGGGGCCUUAUAAACACUAUUGCUAAUGCCCUCUUGAGGGUCCGCUUAUCGGUAGCUACACAGGCCCCUCUGAUUG-3
5'-..((((((((((((((((((((((((((...(((...)))...)))))))))))))))))))))))))))))..((.(((((.....)))))))((((.(((....))).)))).. 
.........((.(((((((.......((((((.(((.((((((....)))))....))).)))))).....)))))))).))....-3'
MFE = -81.9; z-score = -6.34; ED = 31.5
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

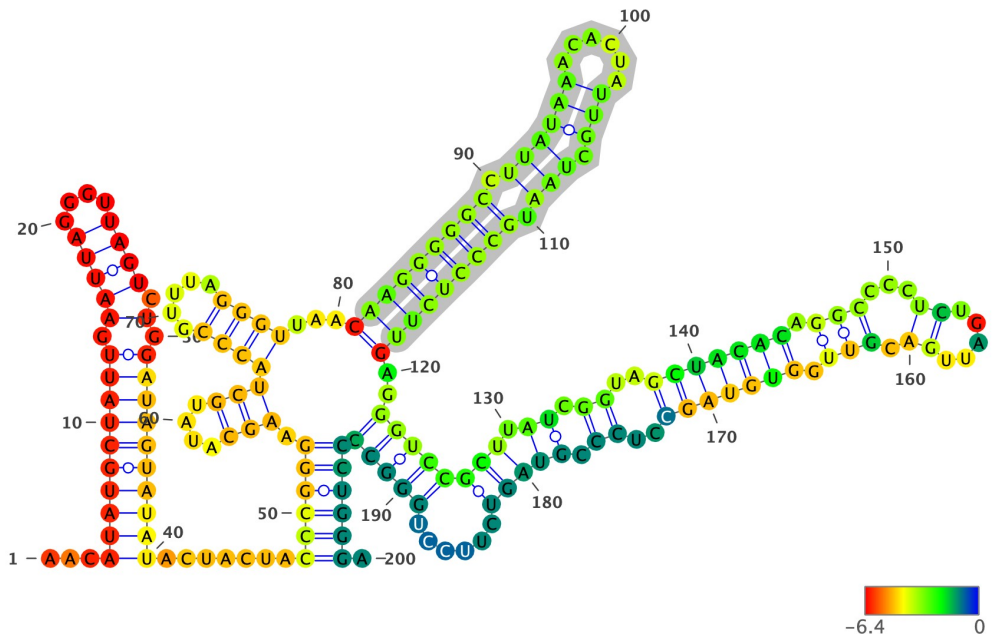
Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

3-- nt 5 to 119--inverted_repeat, id-NC_007605.1:9021..9135, 9021-9135(+)

Attributes: ['ID=id-NC_007605.1:9021..9135', 'Note=dyad symmetry%2C binding site for EBNA-1 (site II)', 'gbkey=repeat_region', 'rpt_type=inverted']

NC_007605.1 (forward strand): Structure number 33 from nt 9138 to 9174 (nt 82 to 118)

```
5'-AAGGGGGCCUUAUAAACACUAUUGCUAAUGCCCUCUU-3'
5'-(.(((((.(.................).))))))).)-3'
Motif MFE = -11.5; z-score = -3.33; 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 9057 to 9256 (motif highlighted in silver):

```
5'-AACAUAUGCUAUUGAAUUAGGGUUAGUCUGGAUAGUAUAUACUACUACCCGGGAAGCAUAUGCUACCCGUUUAGGGUUAACAAGGGGGCCUUAUAAACACUAUUGCUAAUG
CCCUCUUGAGGGUCCGCUUAUCGGUAGCUACACAGGCCCCUCUGAUUGACGUUGGUGUAGCCUCCCGUAGUCUUCCUGGGCCCCUGGGA-3
5'-...(((((((((.(((((....))))).).))))))))))).....((((((.(((....)))((((.....)))).....(((((((((.((((((.....)))).)))).)
)))))))).(((((((((.((.((..(((((((.(((...((.....)).))).)))))))..)).)))))).....)))))))))).-3'
MFE = -65.7; z-score = -2.28; ED = 22.09
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

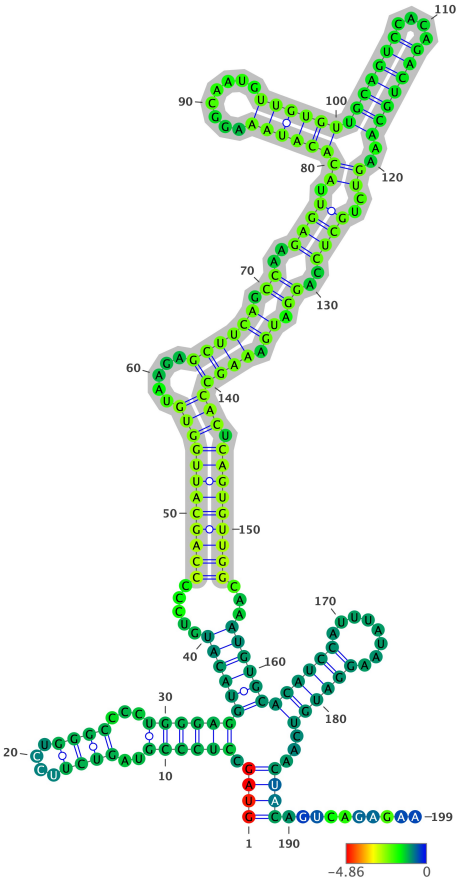
3-- nt 1 to 79--inverted_repeat, id-NC_007605.1:9021..9135, 9021-9135(+)

Attributes: ['ID=id-NC_007605.1:9021..9135', 'Note=dyad symmetry%2C binding site for EBNA-1 (site II)', 'gbkey=repeat_region', 'rpt_type=inverted']

NC_007605.1 (forward strand): Structure number 34 from nt 9269 to 9376 (nt 46 to 153)

```
5'-CCAGCAUUGGUGUAAGAGCUUCAGCCAAGAGUUACACAUAAAGGCAAUGUUGUGUUGCAGUCCACAGACUGCAAAGUCUGCUCCAGGAUGAAAGCCACUCAGUGUUGG-3'

5'-(((((((((((.....((((((.((..(((((.(((((((((.......)))))).....................)).)))))..)).)).)))))))).)))))))))-3'
Motif MFE = -36.4; z-score = -3.03; ED = 13.09
```



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 9224 to 9422 (motif highlighted in silver):

```
5'-GUAGCCUCCCGUAGUCUUCCUGGGCCCCUGGGAGGUACAUGUCCCCCAGCAUUGGUGUAAGAGCUUCAGCCAAGAGUUACACAUAAAGGCAAUGUUGUGUUGCAGUCCACA
GACUGCAAAGUCUGCUCCAGGAUGAAAGCCACUCAGUGUUGGCAAAUGUGCACAUCCAUUUAUAAGGAUGUCAACUACAGUCAGAGAA-3
5'-((((.((((((..((((....)))).....))))))((((((.....((((((((((((.....((((((.((..((((.((((((((.......)))))))((((((((....
)))))))..))..))))..)).)).)))))))).))))))))...))))))((((((.......)))))))...))))..........-3'
MFE = -65.5; z-score = -2.72; ED = 10.99
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

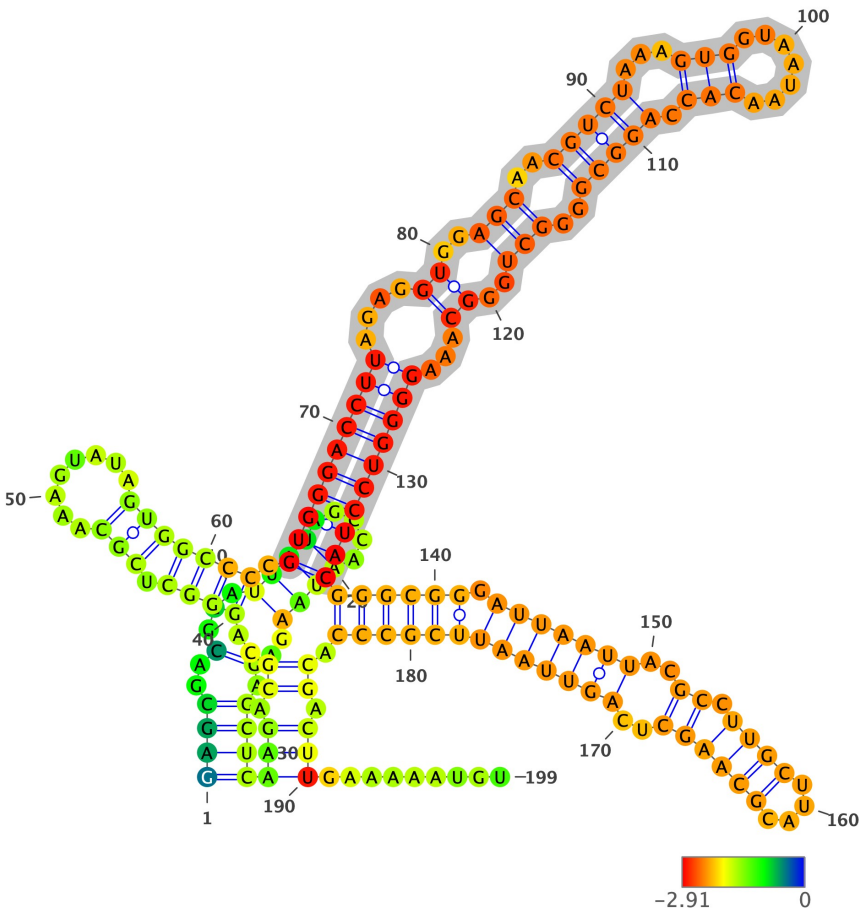
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 89--origin_of_replication, id-NC_007605.1:7315..9312, 7315-9312(+)

Attributes: ['ID=id-NC_007605.1:7315..9312', 'Note=region containing oriP%2C the latent cycle origin of DNA replication', 'gbkey=rep_origin']

NC_007605.1 (forward strand): Structure number 35 from nt 11122 to 11193 (nt 64 to 135)

```
5'-GUGGGACCUUAGAGGUGGAGCAACGUCUAAAGUGGUAAUAACACCAGGCGGGGCUGGGCAAAGGGGUCCUAC-3'
5'-((((((((((....((..((((..((((((...(((.......)))..))))))..)))..))...))))))))))-3'
Motif MFE = -29.9; z-score = -3.87; 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 11059 to 11257 (motif highlighted in silver):

```
5'-GAGCGACGGAUUAUAGCCAAUAAGAGAGCUCAAGACGCAGGGCUCGCAAAGUAUAGUGGCCCCGUGGGACCUUAGAGGUGGAGCAACGUCUAAAGUGGUAAUAACACCAGG
CGGGGCUGGGCAAAGGGGUCCUACGGGCGGGAUUAAUUACGCCUUGCUUACGCAAGCUCAGUUAAUUCGCCCACGACUUGAAAAAUGU-3
5'-((((..(...((((.....)))).).))))(((.((..((((.(((.......)))))))).((((((((((....((..(((..((((((...(((.......))).)))
)).))).))...))))))))))((((((.(((((((..((.((((....)))))).))))))))))))).)).))).........-3'
MFE = -68.4; z-score = -2.45; ED = 24.15
```

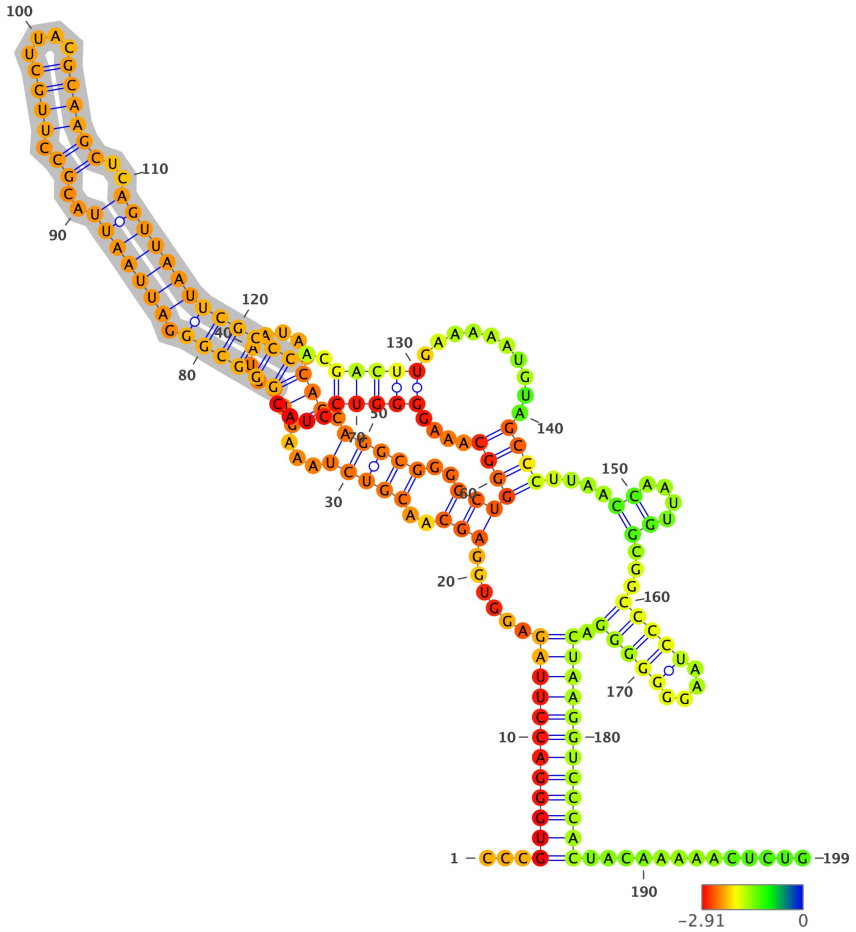
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 36 from nt 11194 to 11241 (nt 76 to 123)

```
5'-GGGCGGGAUUAAUUACGCCUUGCUUACGCAAGCUCAGUUAAUUCGCCC-3'
5'-((((((.(((((((..((.((((....)))))))..)))))))))))))-3'
Motif MFE = -19.4; z-score = -3.3; ED = 3.94
```



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 11119 to 11317 (motif highlighted in silver):

```
5'-CCCGUGGGACCUUAGAGGUGGAGCAACGUCUAAAGUGGUAAUAACACCAGGCGGGGCUGGGCAAAGGGGUCCUACGGGCGGGAUUAAUUACGCCUUGCUUACGCAAGCUCA
GUUAAUUCGCCCACGACUUGAAAAAUGUAGCCCUUAACCAAUUGGCGGCCCCUAAGGGGGGGACUAAGGUCCCACUACAAAAACUCUG-3
5'-...((((((((((((.....(((..((((((...(((.......))).)))))..)))((((....(((((....((((((.(((((((..((.((((....)))))))..)
))))))))))))..)))))).........))))....((....))...(((((....)))))).))))))))))))).............-3'
MFE = -74.6; z-score = -3.26; ED = 33.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 187 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 187 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

4-- nt 187 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

5-- nt 187 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

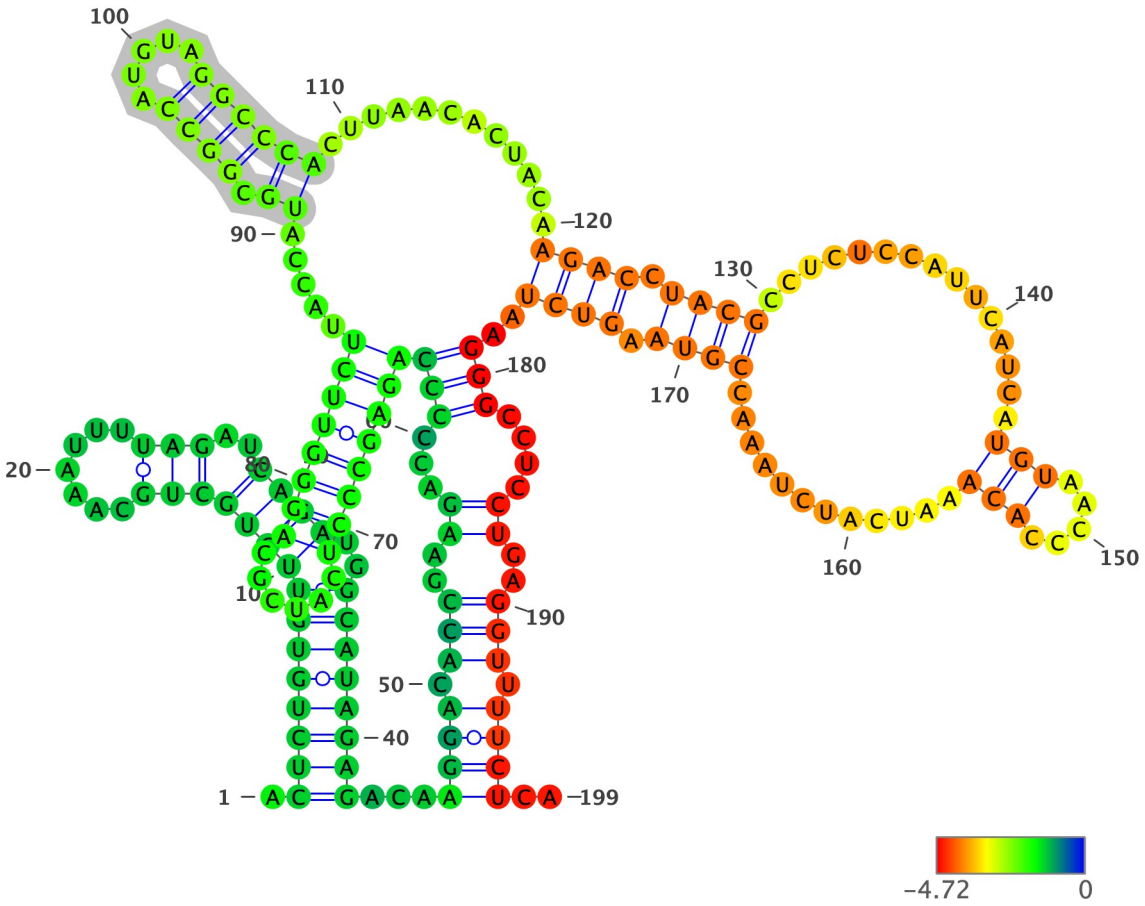
Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

6-- nt 187 to 192--TATA_box, id-HHV4_EBNA-2-2, 11305-11310(+)

Attributes: ['ID=id-HHV4_EBNA-2-2', 'Note=C promoter (Cp) used in latency III', 'gbkey=regulatory', 'regulatory_class=TATA_box']

NC_007605.1 (forward strand): Structure number 37 from nt 11402 to 11419 (nt 91 to 108)

```
5'-UGCGGCCAUGUAGGCCCA-3'
5'-((.((((.....))))))-3'
Motif MFE = -6.9; z-score = -2.31; ED = 0.94
```



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

Extracted structure model with flanking nucleotides 11312 to 11510 (motif highlighted in silver):

```
5'-ACUCUGUGUUCUGCUGCAAAUUUUAGAUCAGAUGGCAUAGAGACAAGGACACCGAAGACCCCCAGAGCCCUCAUCGCAGGGUUCUUACCAUGCGGCCAUGUAGGCCCACUU
AACACUACAAGACCUACGCCUCUCCAUUCAUCAUGUAACCCACAAAUCAUCUAAACCGUAAGUCUAAGGGCCUCCUGAGGUUUUCUCA-3
5'-.(((((((((((((((.......)))..)))))..)))))))))...((((.((((..(((...((((((((((((.....)))))))))).....((.((((.....)))))))...
.........((((.((((..............(((.....)))............))))).))))..)))....))..)))).))))..-3'
MFE = -45.8; z-score = -2.12; ED = 27.99
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 25 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 25 to 168--exon, exon-HHV4_EBNA-1.1-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-1', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

6-- nt 25 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 25 to 168--exon, exon-HHV4_EBNA-3B/EBNA-3C-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 25 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 25 to 168--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

10-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

11-- nt 25 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

12-- nt 25 to 168--exon, exon-HHV4_EBNA-3A-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

14-- nt 25 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

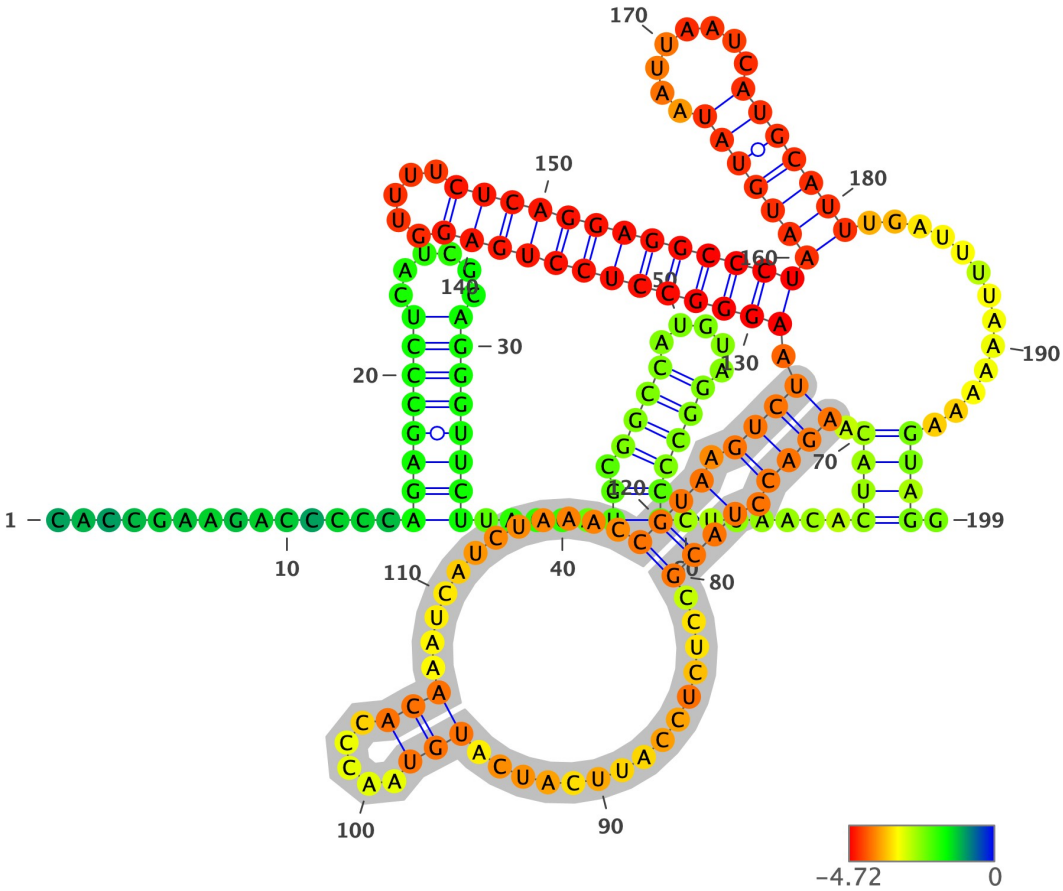
Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

15-- nt 25 to 168--exon, exon-HHV4_EBNA-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-2-1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

NC_007605.1 (forward strand): Structure number 38 from nt 11432 to 11487 (nt 72 to 127)

```
5'-AGACCUACGCCUCUCCAUUCAUCAUGUAACCCACAAAUCAUCUAAACCGUAAGUCU-3'
5'-((((.((((..............(((.....)))............)))).))))-3'
Motif MFE = -3.7; z-score = -1.28; ED = 3.63
```



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

Extracted structure model with flanking nucleotides 11361 to 11559 (motif highlighted in silver):

```
5'-CACCGAAGACCCCCAGAGCCCUCAUCGCAGGGUUCUUACCAUGCGGCCAUGUAGGCCCACUUAACACUACAAGACCUACGCCUCUCCAUUCAUCAUGUAACCCACAAAUCA
UCUAAACCGUAAGUCUAAGGGCCUCCUGAGGUUUUCUCAGGAGGCCCUAAUGUAUAAUUAAUCAUGCAUUUGAUUUUAAAAAAGUAGG-3
5'-..............(((((((((.....)))))))).....((.((((.....)))))).......((((.((((.(((((.............(((.....)))).....
.......))))).)))).((((((((((((.....)))))))))))))((((((.......)))))))............)))).-3'
MFE = -58.0; z-score = -4.72; ED = 15.08
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 119--exon, exon-HHV4_EBNA-1.1-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-1', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 119--exon, exon-HHV4_EBNA-3B/EBNA-3C-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 119--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

10-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

11-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

12-- nt 1 to 119--exon, exon-HHV4_EBNA-3A-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

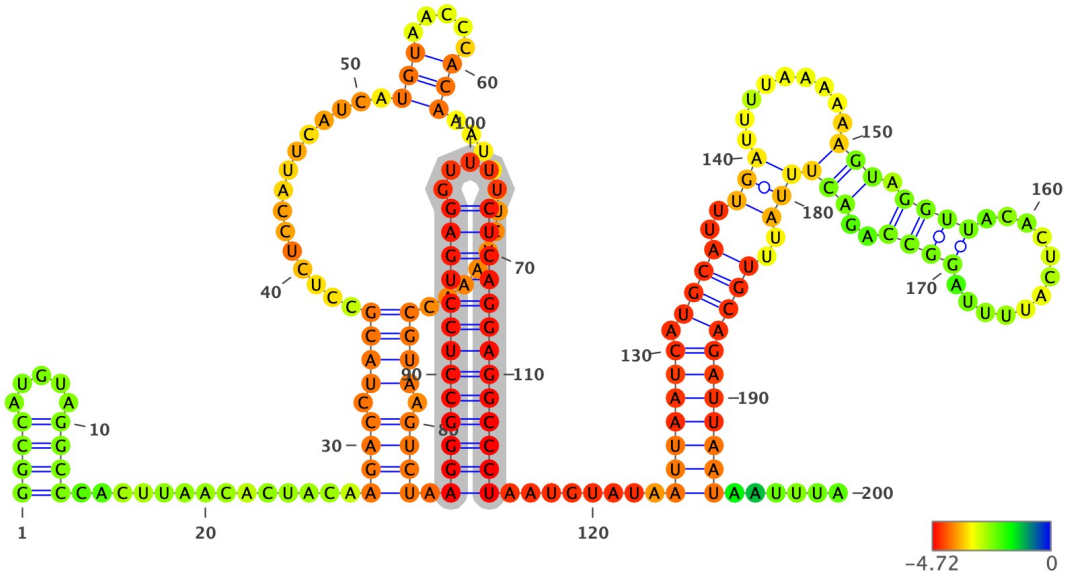
Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

15-- nt 1 to 119--exon, exon-HHV4_EBNA-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-2-1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

NC_007605.1 (forward strand): Structure number 39 from nt 11489 to 11519 (nt 85 to 115)

```
5'-AGGGCCUCCUGAGGUUUUCUCAGGAGGCCCU-3'
5'-(((((((((((((.....)))))))))))))-3'
Motif MFE = -27.2; z-score = -6.6; 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 11405 to 11604 (motif highlighted in silver):

```
5'-GGCCAUGUAGGCCCACUUAACACUACAAGACCUACGCCUCUCCAUUCAUCAUGUAACCCACAAAUCAUCUAAACCGUAAGUCUAAGGGCCUCCUGAGGUUUUCUCAGGAGG
CCCUAAUGUAUAAUUAAUCAUGCAUUUGAUUUUAAAAAAGUAGGUUACACUCAUUUUAGGCCAGACUUUAUUUGCAGAUUAAUAAUUUA-3
5'-((((.....))))..............((((.((((................(((.....)))............)))).)))).((((((((((((.....))))))))))
))))........(((((((.((((..(((.........(((.((((............))))..)))))))..)))))))))))).....-3'
MFE = -52.0; z-score = -4.66; ED = 45.19
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 75--exon, exon-HHV4_EBNA-1.1-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-1', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 75--exon, exon-HHV4_EBNA-3B/EBNA-3C-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 75--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

12-- nt 1 to 75--exon, exon-HHV4_EBNA-3A-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

13-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

14-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

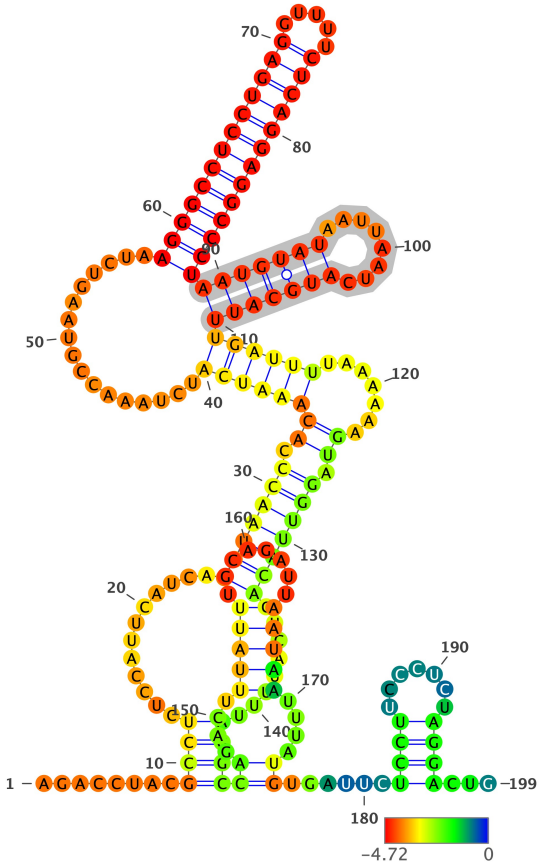
Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

15-- nt 1 to 75--exon, exon-HHV4_EBNA-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-2-1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

NC_007605.1 (forward strand): Structure number 40 from nt 11520 to 11541 (nt 89 to 110)

```
5'-AAUGUAUAAUUAAUCAUGCAUU-3'
5'-(((((((........)))))))-3'
Motif MFE = -3.0; z-score = -3.97; 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 11432 to 11630 (motif highlighted in silver):

```
5'-AGACCUACGCCUCUCCAUUCAUCAUGUAACCCACAAAUCAUCUAAACCGUAAGUCUAAGGGCCUCCUGAGGUUUUCUCAGGAGGCCCUAAUGUAUAAUUAAUCAUGCAUUU
GAUUUUAAAAAAGUAGGUUACACUCAUUUUAGGCCAGACUUUAUUUGCAGAUUAAUAAUUUAUGUGAUUCUCCUUCCCUCUAGGACUG-3
5'-........((((............(((((((.(((((((.................((((((((((((.....)))))))))))))))(((((((........)))))))
)))))).......)).)))))))........))))((....(((((........)))))....)).....((((.......)))).....-3'
MFE = -47.0; z-score = -3.6; ED = 45.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 48--exon, exon-HHV4_EBNA-1.1-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-1', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 195 to 199--exon, exon-HHV4_EBNA-1.1-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-2', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

6-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

7-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 48--exon, exon-HHV4_EBNA-3B/EBNA-3C-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

9-- nt 195 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

11-- nt 1 to 48--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

12-- nt 195 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-2', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

15-- nt 1 to 48--exon, exon-HHV4_EBNA-3A-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

16-- nt 195 to 199--exon, exon-HHV4_EBNA-3A-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-2', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

17-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

18-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

19-- nt 1 to 48--exon, exon-HHV4_EBNA-2-1, 11336-11479(+)

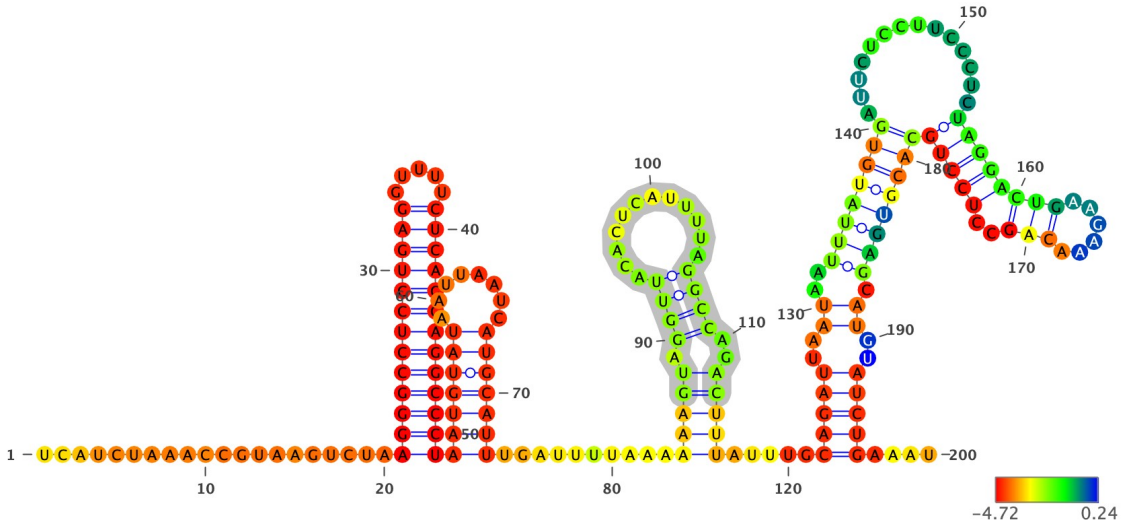
Attributes: ['ID=exon-HHV4_EBNA-2-1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

20-- nt 195 to 199--exon, exon-HHV4_EBNA-2-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-2-2', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

NC_007605.1 (forward strand): Structure number 41 from nt 11555 to 11581 (nt 87 to 113)

```
5'-GUAGGUUACACUCAUUUUAGGCCAGAC-3'
5'-((.((((...........))))..))-3'
Motif MFE = -1.6; z-score = 0.68; 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 11469 to 11668 (motif highlighted in silver):

```
5'-UCAUCUAAACCGUAAGUCUAAGGGCCUCCUGAGGUUUUCUCAGGAGGCCCUAAUGUAUAAUUAAUCAUGCAUUUGAUUUUAAAAAAGUAGGUUACACUCAUUUUAGGCCAG
ACUUUAUUUGCAGAUUAAUAAUUUAUGUGAUUCUCCUUCCCUCUAGGACUGAAGAAACAGCCUCCUGCACGUGAGCAUGUAUCUGAAAU-3
5'-....................(((((((((((((.....)))))))))))))(((((((.........)))))))..........(((((.((((............)))).
)))))).....(((((..((..(((((((((.............((((((((......)))..)))))))))))))).))..)))))....-3'
MFE = -51.6; z-score = -3.63; ED = 49.95
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 11--exon, exon-HHV4_EBNA-1.1-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-1', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 158 to 189--exon, exon-HHV4_EBNA-1.1-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-2', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

6-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 11--exon, exon-HHV4_EBNA-3B/EBNA-3C-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

9-- nt 158 to 189--exon, exon-HHV4_EBNA-3B/EBNA-3C-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

11-- nt 1 to 11--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

12-- nt 158 to 189--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-2', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

13-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

14-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

15-- nt 1 to 11--exon, exon-HHV4_EBNA-3A-1, 11336-11479(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

16-- nt 158 to 189--exon, exon-HHV4_EBNA-3A-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-2', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

17-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

18-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

19-- nt 1 to 11--exon, exon-HHV4_EBNA-2-1, 11336-11479(+)

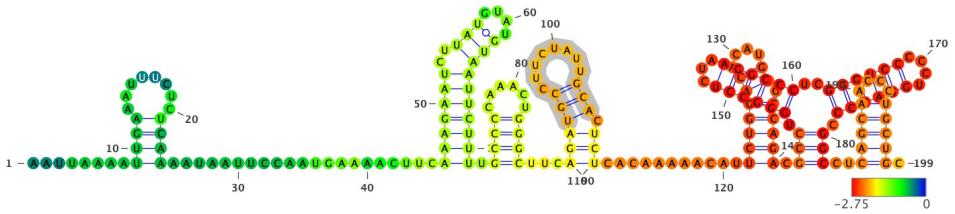
Attributes: ['ID=exon-HHV4_EBNA-2-1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

20-- nt 158 to 189--exon, exon-HHV4_EBNA-2-2, 11626-11657(+)

Attributes: ['ID=exon-HHV4_EBNA-2-2', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

NC_007605.1 (forward strand): Structure number 42 from nt 11971 to 11984 (nt 93 to 106)

```
5'-UGCCUUCUAUUGCA-3'
5'-(((........)))-3'
Motif MFE = -0.3; z-score = -1.17; 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 11879 to 12077 (motif highlighted in silver):

```
5'-AAUUAAAAUUGAAAUUUCUCUCAAAAUAAUUCCAAUGAAAACUUCAAAGAAUCUUAUGUAUGUAAUUCUUUUGCCCCAAACUGGGCUUCAGAUGCCUUCUAUUGCACUCUC
ACAAAAACAUUCUGGACACAUGUGCCAGACGCCUGGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGC-3
5'-........((((........)))).....................(((((((..(((....)))))))))).((((......)))).....(((((((.........))).))).
..........(((((((....)).))))).(((.(((((((...)))))))..(((((((....)))))))..)))..(((((....))))).-3'
MFE = -48.0; z-score = -3.0; ED = 29.6
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 123 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

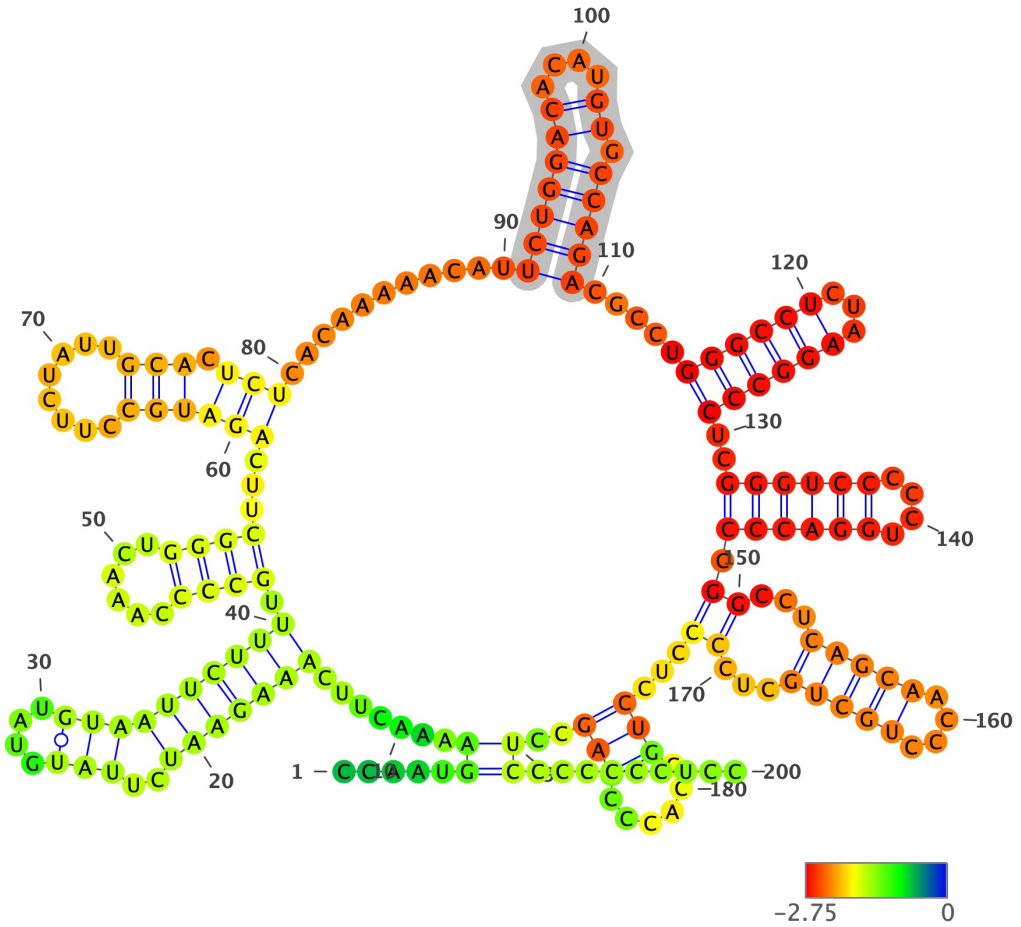
Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 123 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 43 from nt 12000 to 12018 (nt 91 to 109)

```
5'-UCUGGACACAUGUGCCAGA-3'
5'-(((((((....)).)))))-3'
Motif MFE = -6.1; z-score = -2.74; ED = 2.29
```



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

Extracted structure model with flanking nucleotides 11910 to 12109 (motif highlighted in silver):

```
5'-CCAAUGAAAACUUCAAAGAAUCUUAUGUAUGUAAUUCUUUUGCCCCAAACUGGGCUUCAGAUGCCUUCUAUUGCACUCUCACAAAAACAUUCUGGACACAUGUGCCAGACG
CCUGGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCC-3
5'-.....((.......((((((((..((((....)))))))))).((((.....)))).....((((((.......))).))).....((((((((....)).)))))).
...((((((...)))))).((((((((....)))))).((...((((((....)))))...)).....(((.....))).)).)).....-3'
MFE = -49.3; z-score = -3.27; ED = 27.45
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 92 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

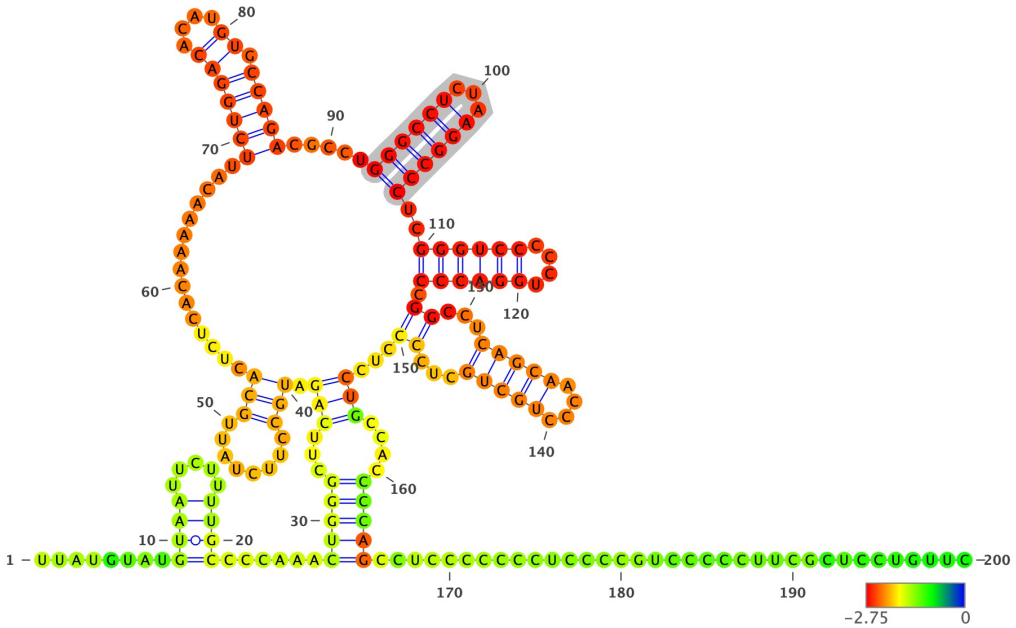
Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 92 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 44 from nt 12024 to 12038 (nt 93 to 107)

```
5'-GGGCCUCUAAGGCCC-3'
5'-((((((...)))))))-3'
Motif MFE = -9.5; z-score = -4.31; 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 11932 to 12131 (motif highlighted in silver):

```
5'-UUAUGUAUGUAAUUCUUUUGCCCCAAACUGGGCUUCAGAUGCCUUCUAUUGCACUCUCACAAAAACAUUCUGGACACAUGUGCCAGACGCCUGGGCCUCUAAGGCCCUCGG
GUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGUUC-3
5'-........((((.....)))).....(((((...(((.(((........)))..............(((((((....).)))))).....((((((...)))))))..((
((((....)))))).((...(((((....)))))...)).)...)))....)))))....................................-3'
MFE = -47.9; z-score = -2.63; ED = 29.86
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 70 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

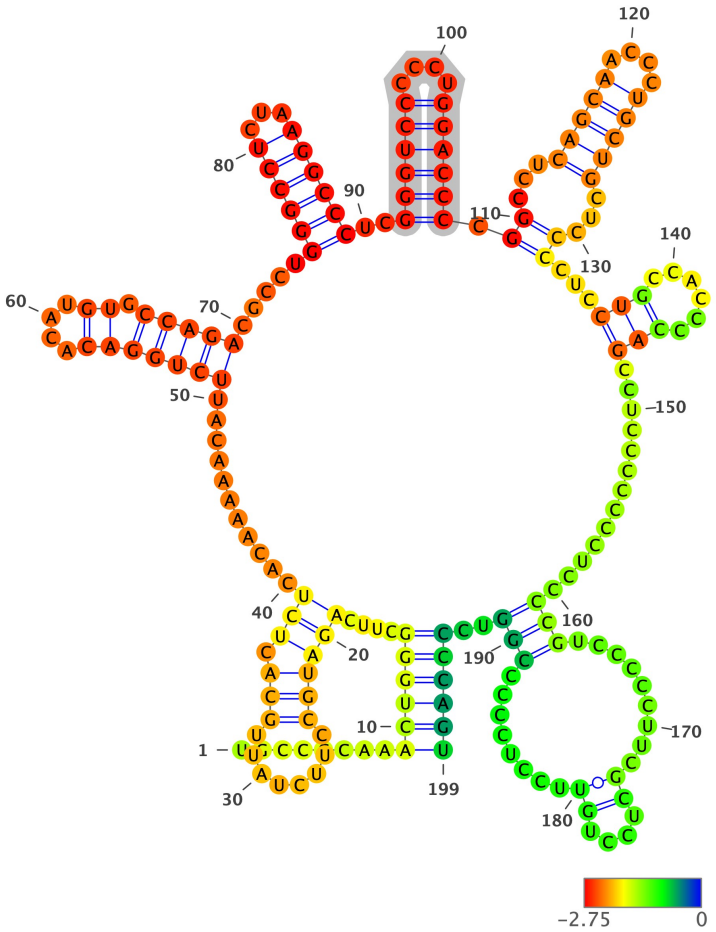
Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 70 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 45 from nt 12041 to 12056 (nt 92 to 107)

```
5'-GGGUCCCCCUGGACCC-3'
5'-((((((....)))))))-3'
Motif MFE = -9.7; z-score = -3.66; ED = 0.08
```



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 11950 to 12148 (motif highlighted in silver):

```
5'-UGCCCCAAACUGGGCUUCAGAUGCCUUCUAUUGCACUCUCACAAAAACAUUCUGGACACAUGUGCCAGACGCCUGGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGC
CUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGUUCCUCCCCCGGUCCCCAGU-3
5'-........((((((....((((((........))).)))...........(((((((....)).)))))).....((((((...)))))))..((((((....)))))))..((.
..((((((....)))))...))...(((......)))............(((.........((....)).......)))..)))))))-3'
MFE = -50.9; z-score = -2.72; ED = 28.39
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 52 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

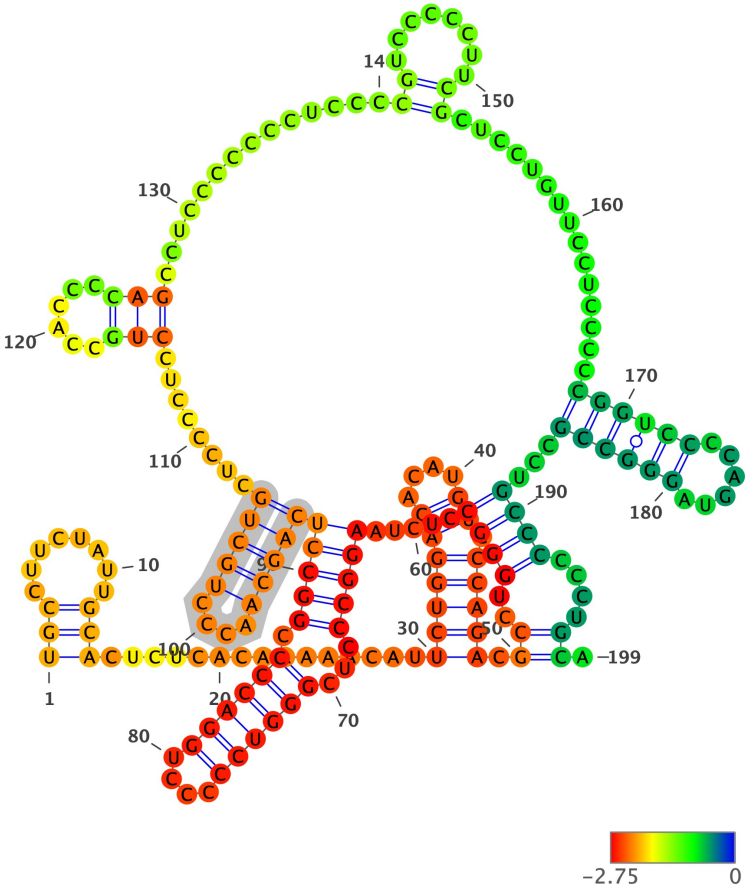
Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 52 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 46 from nt 12063 to 12076 (nt 93 to 106)

```
5'-CAGCAACCCUGCUG-3'
5'-(((((....)))))-3'
Motif MFE = -4.6; z-score = -4.36; 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 11971 to 12169 (motif highlighted in silver):

```
5'-UGCCUUCUAUUGCACUCUCACAAAAACAUUCUGGACACAUGUGCCAGACGCCUGGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCC
CUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGUUCCUCCCCCGGUCCCCAGUAGGGCCGCCUGCCCCCCUGCA-3
5'-((........)))...............(((((((....)).)))))..((..((((.....(((((...((((((....)))))).)))))(((((....)))))).....
...(((......)))..............((........))...............((((((.....))))))...)))))....)).-3'
MFE = -49.7; z-score = -2.05; ED = 34.67
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 31 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

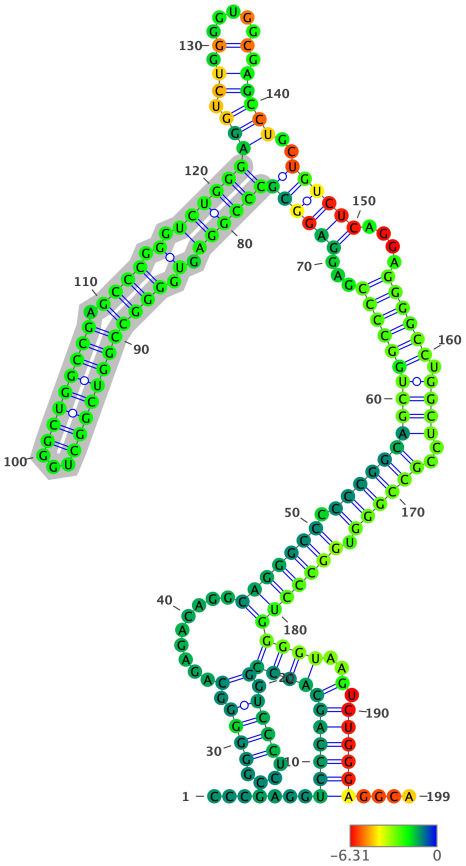
Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 31 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 47 from nt 12430 to 12475 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))))).).)))))))-3'
Motif MFE = -35.3; z-score = -3.8; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 12354 to 12552 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).)........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.6; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 188 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

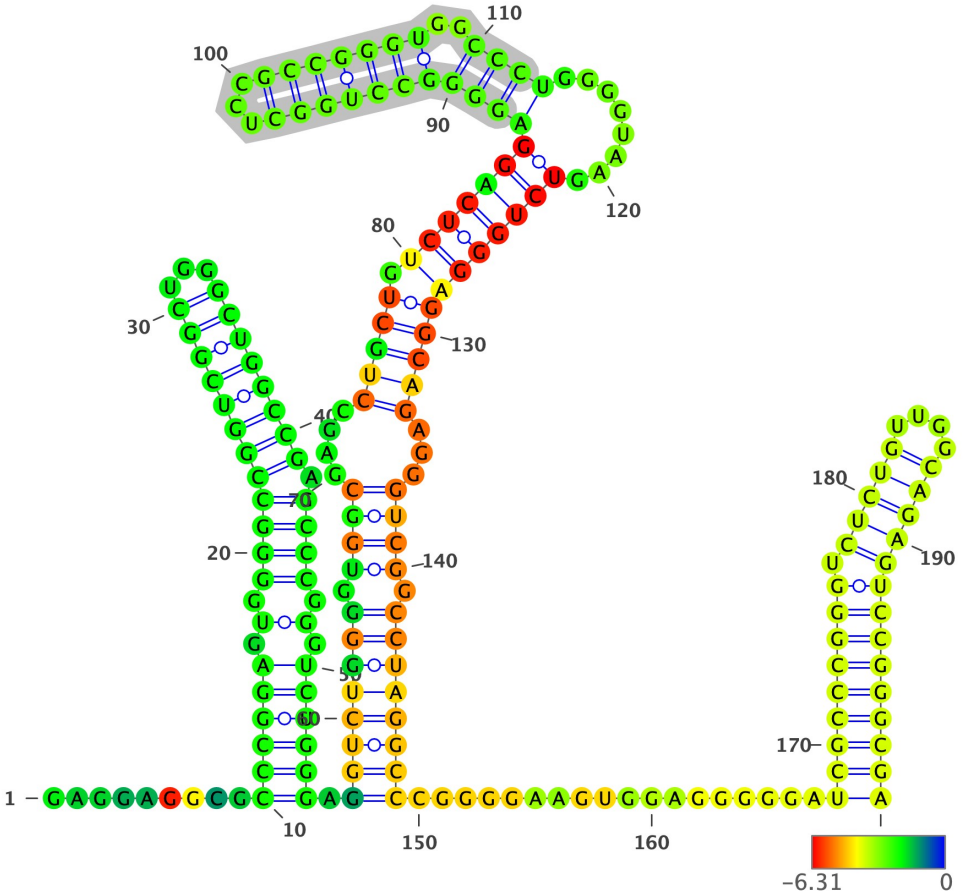
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 188 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 48 from nt 12508 to 12532 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.78; 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 12421 to 12620 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.02; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 121 to 200--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

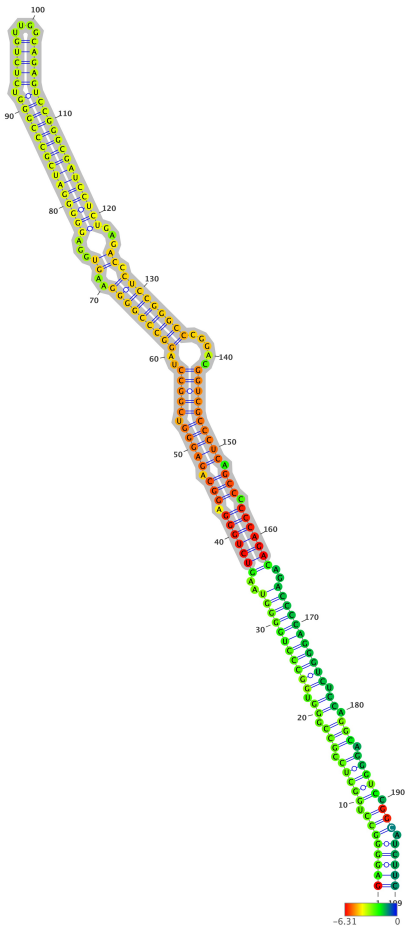
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 121 to 200--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 49 from nt 12542 to 12667 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((((.(((((....)))))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -5.8; ED = 3.47
```



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 12506 to 12704 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.((((.((.(((((((((((..(((((((.((((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).))))))))).....))))))))).))).))))))..))))))))))).)).))).))))).))).))))-3'
MFE = -149.6; z-score = -6.73; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 36 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

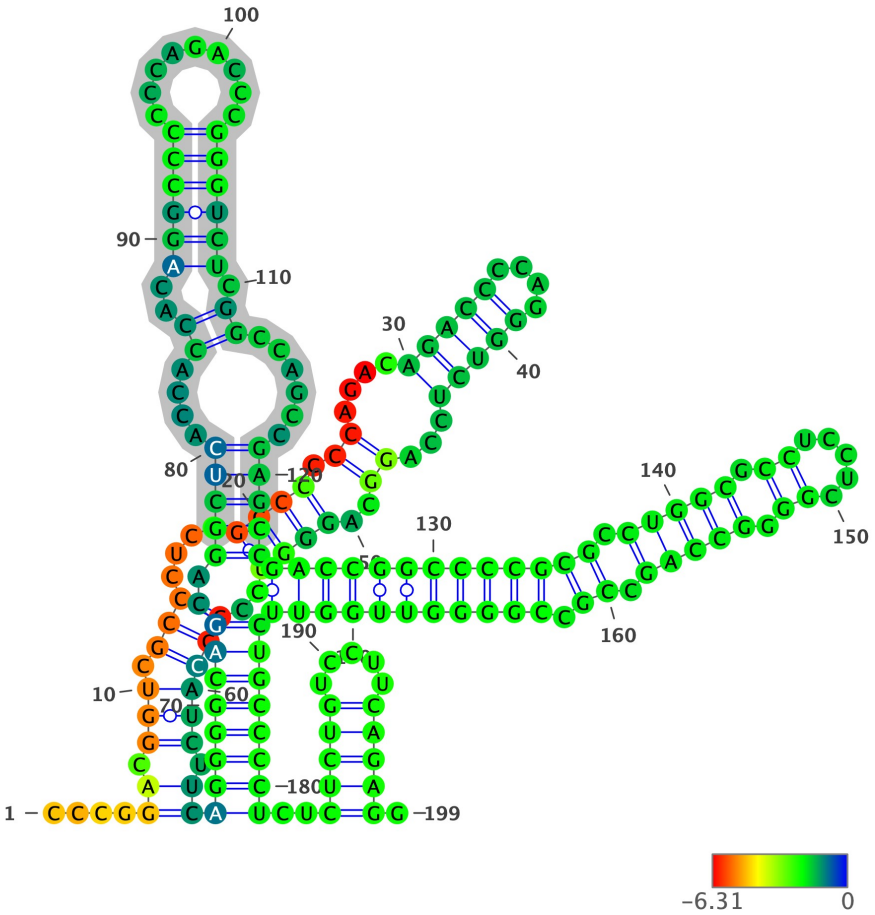
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 36 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 50 from nt 12716 to 12761 (nt 77 to 122)

```
5'-GCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGC-3'
5'-(..............(((.........)))...............)-3'
Motif MFE = -11.9; z-score = 0.05; ED = 11.49
```



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 12640 to 12838 (motif highlighted in silver):

```
5'-CCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCG
GCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-....((.(((.(((....((((.((....((((((....)))))...))..)))))..)))))).))(((((((..(((((....((..((((((.........)))))).)
).....)))))((((((((((((.(((((.((.....)).)))))).)).)))))))))))))))))..(((((.....)))))).-3'
MFE = -93.4; z-score = -1.77; ED = 25.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

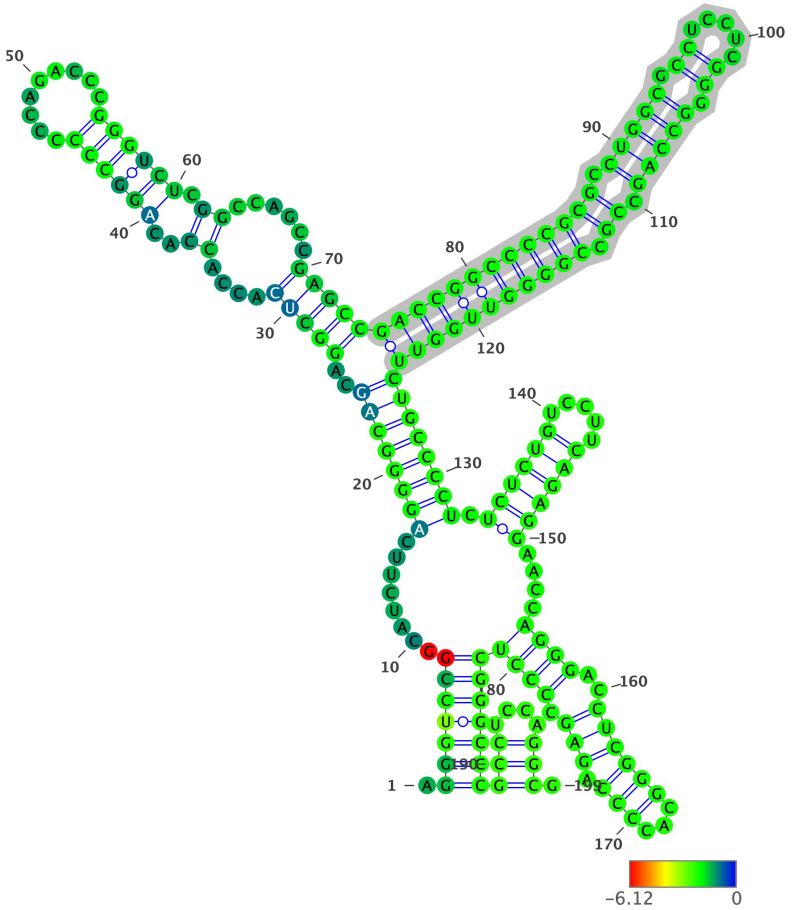
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 51 from nt 12763 to 12812 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.51; ED = 2.52
```



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 12689 to 12887 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -2.81; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

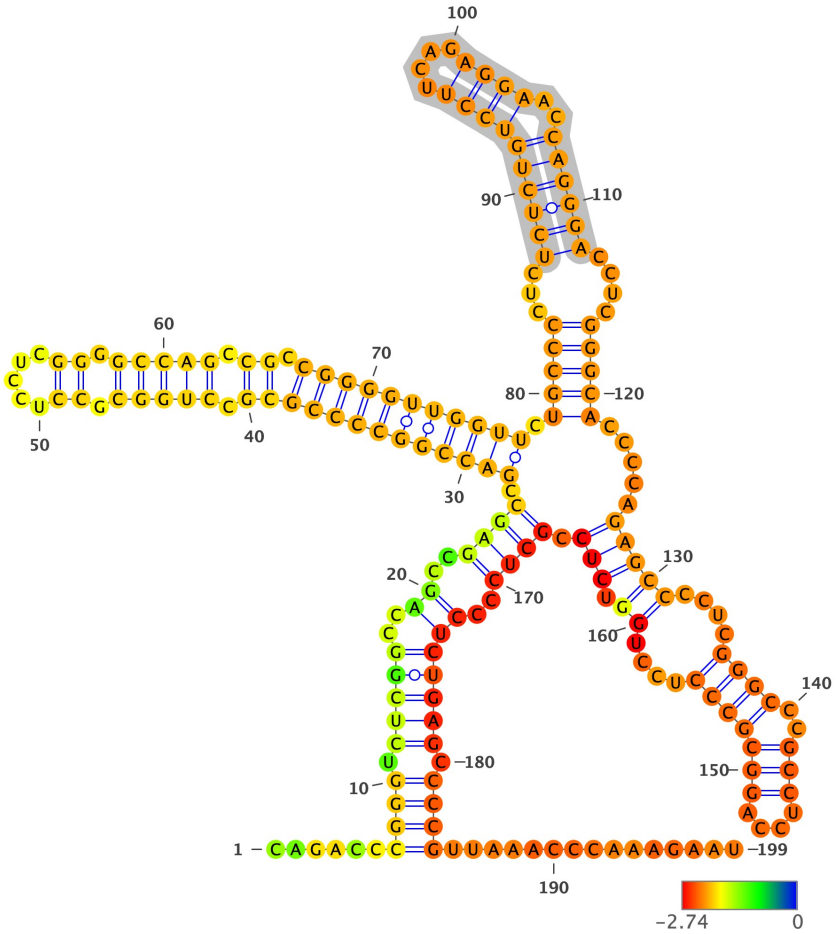
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 52 from nt 12822 to 12847 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-(((((((.......))..)))))-3'
Motif MFE = -8.8; z-score = -2.28; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 12736 to 12934 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.27; ED = 36.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

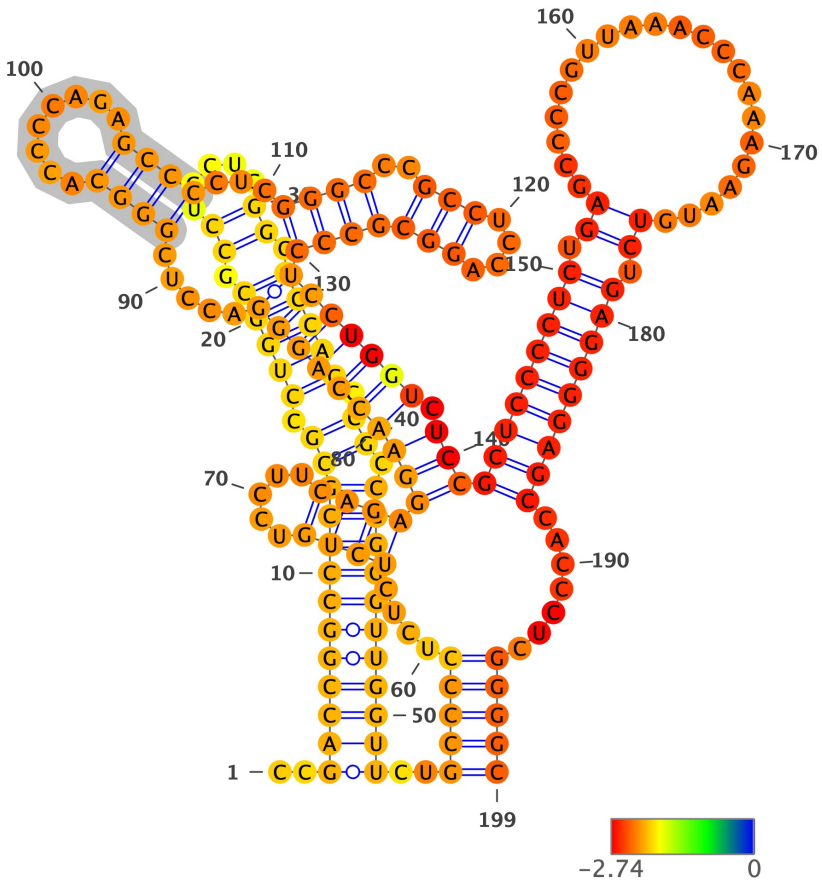
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 53 from nt 12852 to 12867 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-(((((........))))-3'
Motif MFE = -6.0; z-score = -1.84; 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 12761 to 12959 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -3.97; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

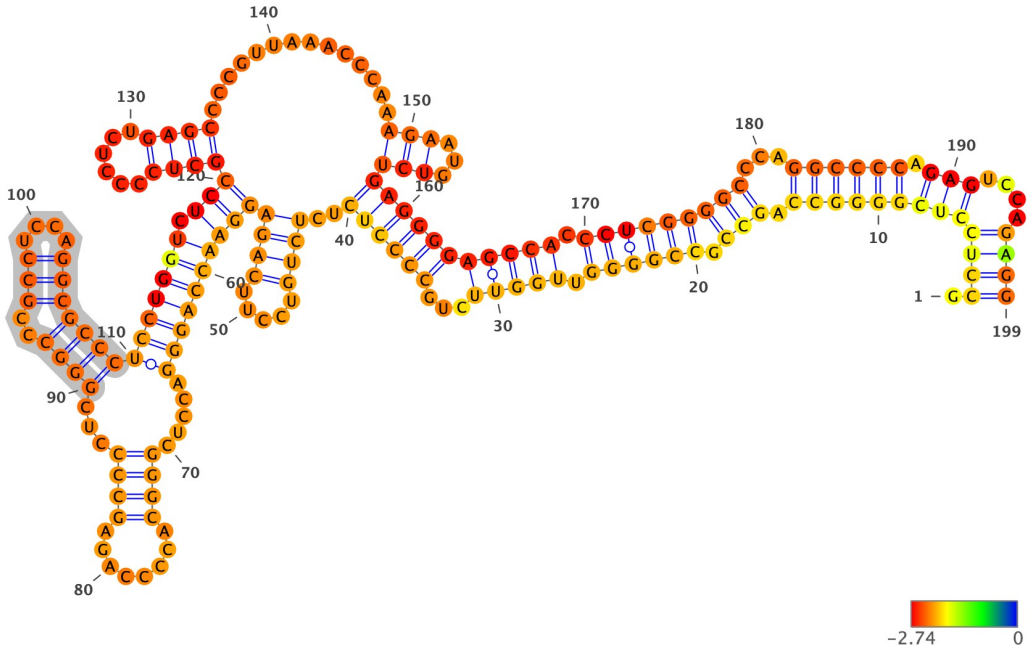
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 54 from nt 12871 to 12890 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..((((....)))))))-3'
Motif MFE = -9.3; z-score = -1.74; 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 12782 to 12980 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........))))...((((..((((....)))))))))
)))))).)))((((.....))))..............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.76; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

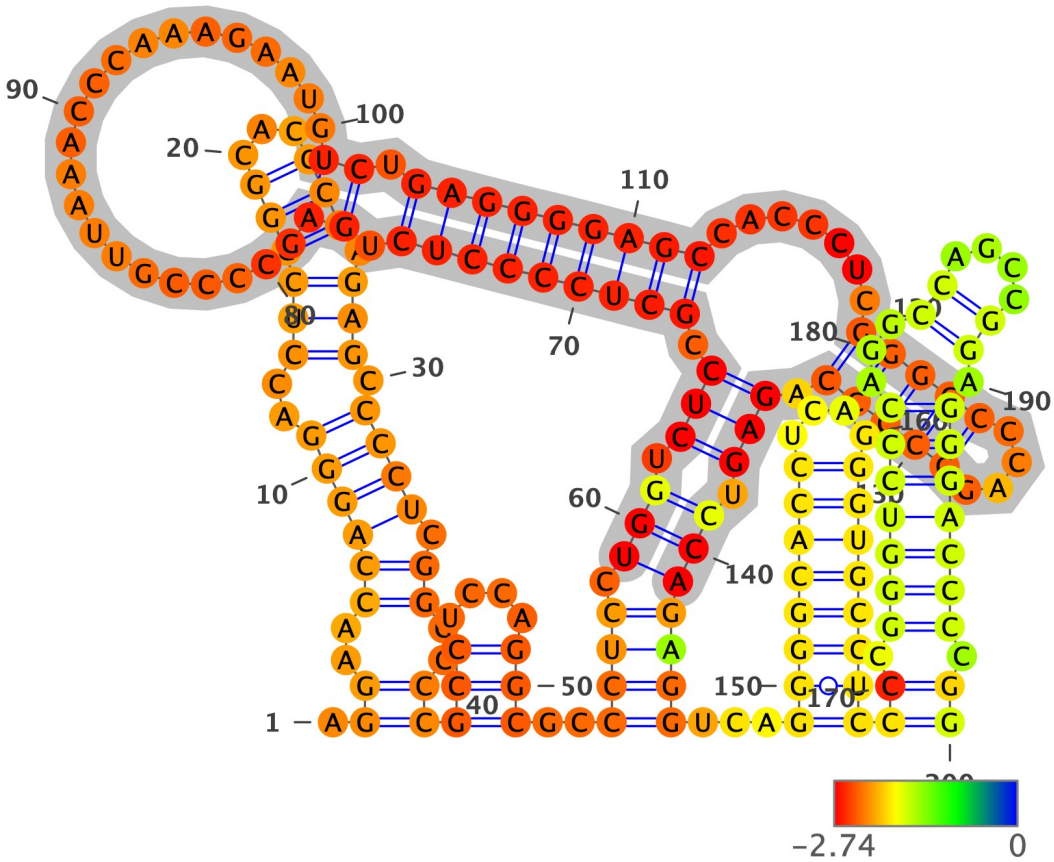
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 199--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 55 from nt 12894 to 12976 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.13; ED = 6.59
```



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 12836 to 13035 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.45; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 200--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

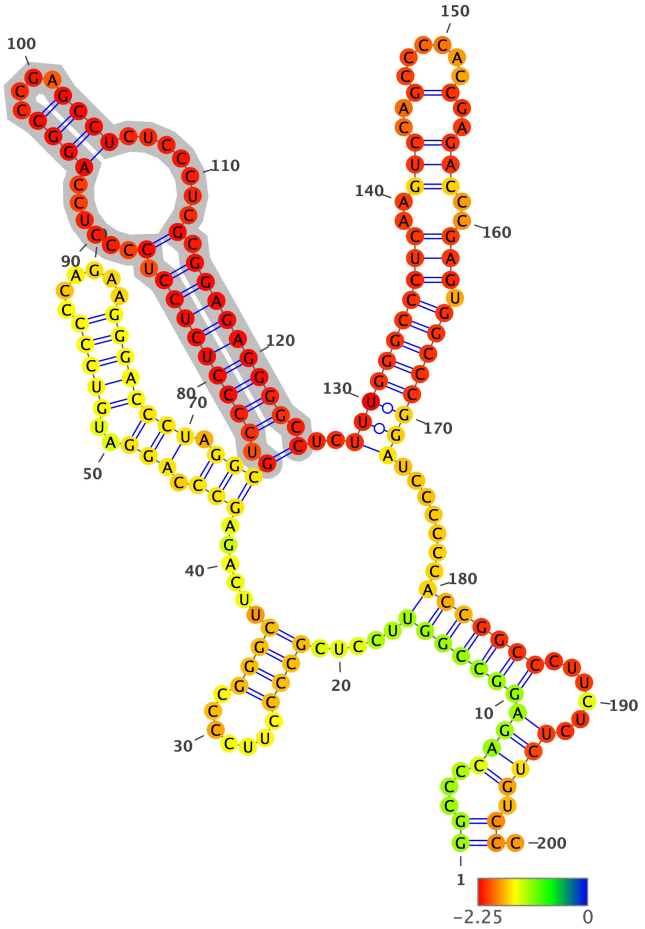
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 200--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 56 from nt 13120 to 13170 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -2.74; 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 13046 to 13245 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..))))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.9; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 200--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

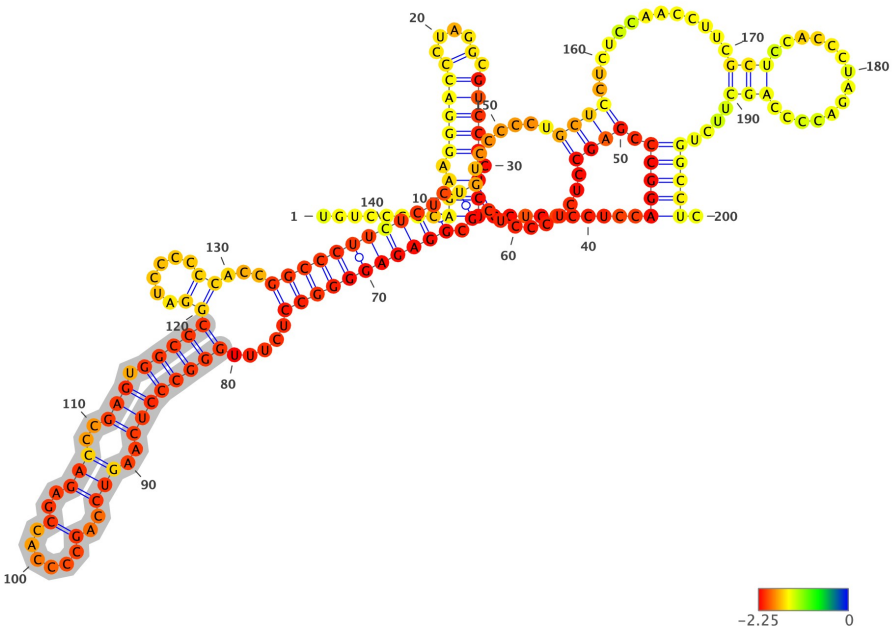
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 200--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 57 from nt 13176 to 13214 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -2.0; ED = 1.4
```



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

Extracted structure model with flanking nucleotides 13096 to 13295 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............))).....)))))).-3'
MFE = -60.2; z-score = -2.19; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 200--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

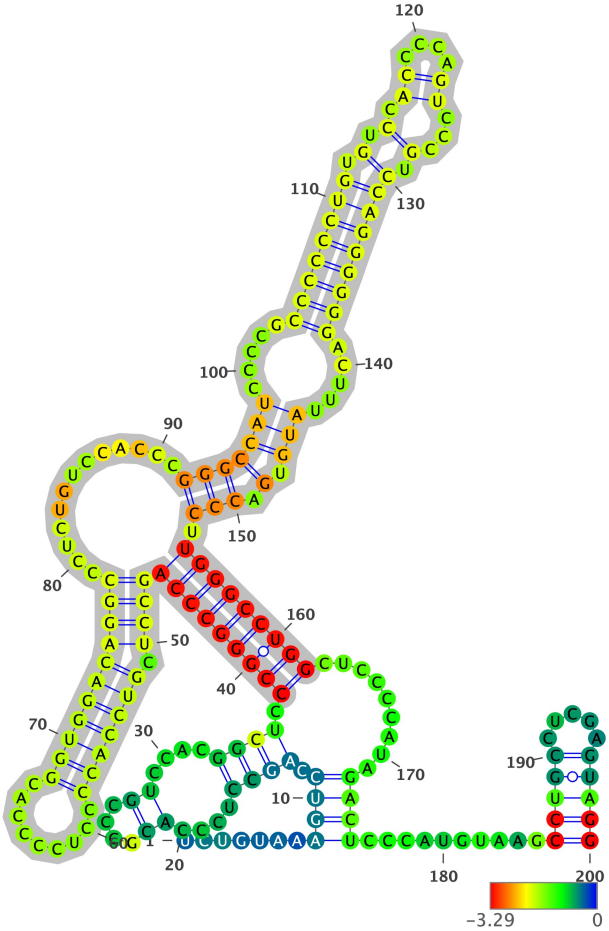
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 200--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 58 from nt 13581 to 13705 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....(((((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.55; ED = 23.92
```



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 13544 to 13743 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).))))))))).....))).).))).)))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.55; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 149--gene, gene-HHV4_BWRF1.1, 12541-13692(+)

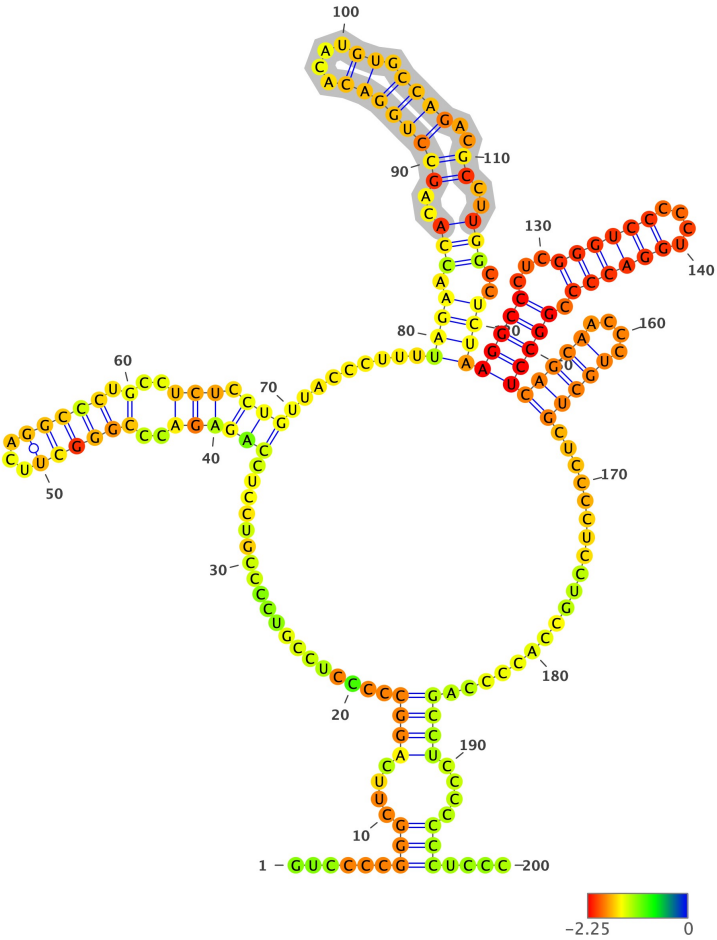
Attributes: ['ID=gene-HHV4_BWRF1.1', 'Dbxref=GeneID:3783691', 'Name=BWRF1', 'Note=originally called BCRF2', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'start_range=.,12541']

14-- nt 1 to 149--CDS, cds-YP_401635.1, 12541-13692(+)

Attributes: ['ID=cds-YP_401635.1', 'Parent=gene-HHV4_BWRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q8AZK8,Genbank:YP_401635.1,GeneID:3783691', 'Name=YP_401635.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.1', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401635.1', 'start_range=.,12541']

NC_007605.1 (forward strand): Structure number 59 from nt 15068 to 15096 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..(.....................)..)-3'
Motif MFE = -5.8; z-score = -0.76; ED = 3.21
```



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 14983 to 15182 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))................))))....)))....-3'
MFE = -58.0; z-score = -2.0; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

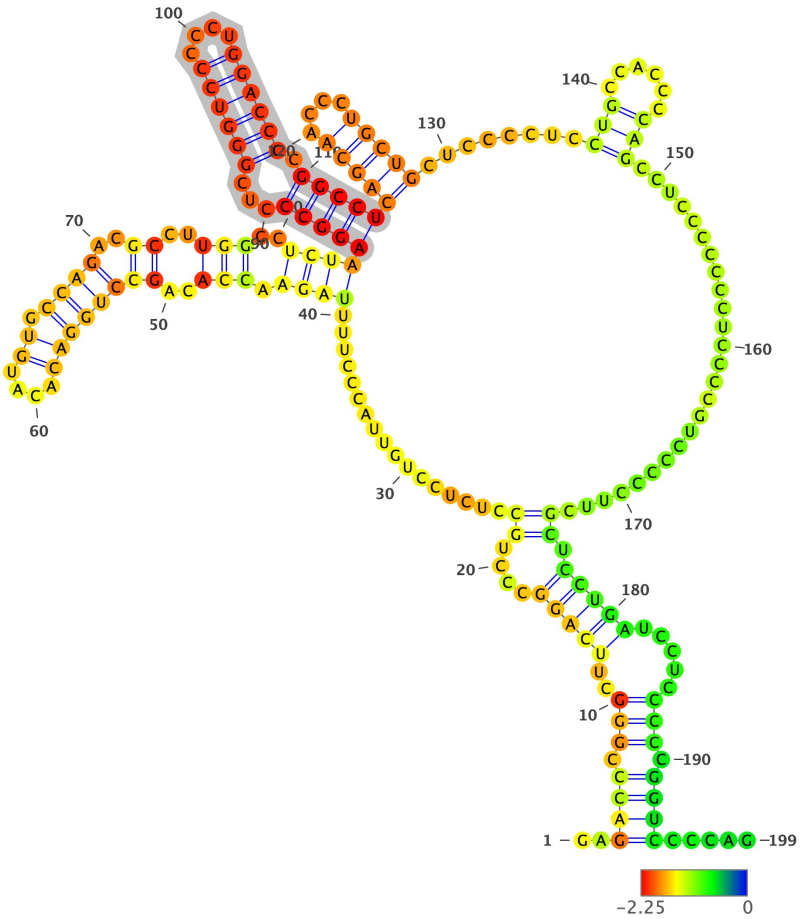
Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 60 from nt 15105 to 15134 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -4.2; 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 15021 to 15219 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..)))..)))))((((((...((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....)))).)))).....-3'
MFE = -53.6; z-score = -1.77; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-2-3, 12001-15072(+)

Attributes: ['ID=id-HHV4_EBNA-2-3', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

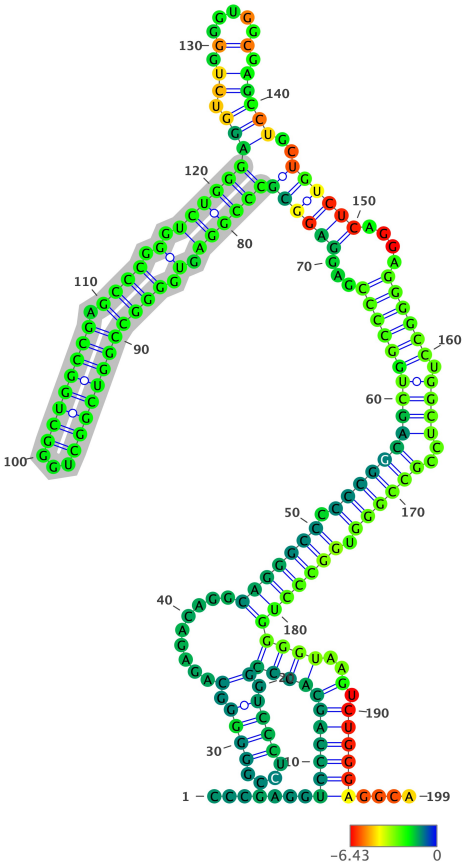
Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 61 from nt 15502 to 15547 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -3.75; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 15426 to 15624 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).)........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.97; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

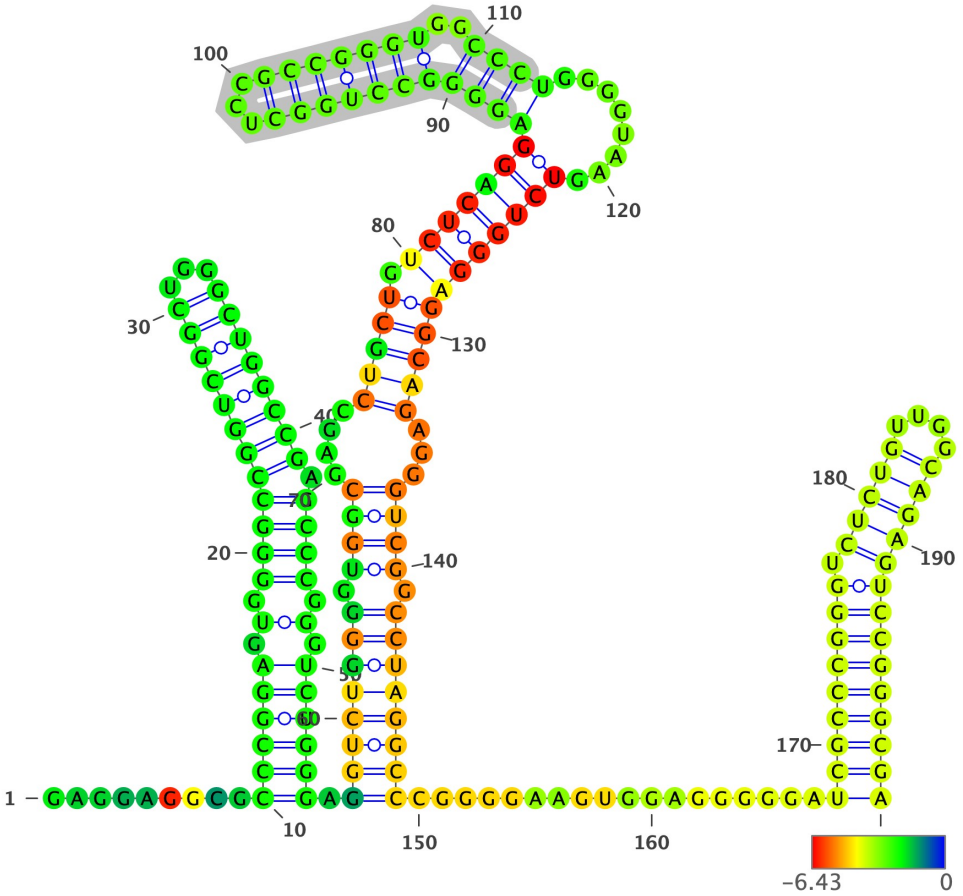
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 188 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 62 from nt 15580 to 15604 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.73; 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 15493 to 15692 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.09; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

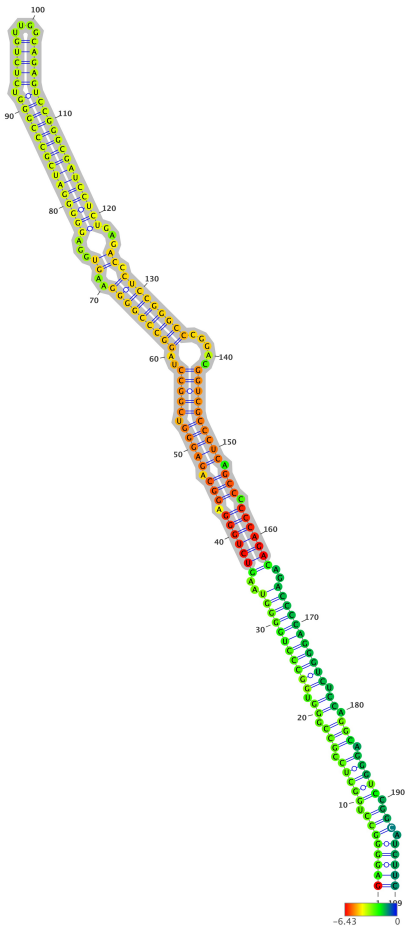
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 121 to 200--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 63 from nt 15614 to 15739 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((((.(((((....)))))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.5; ED = 3.47
```



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 15578 to 15776 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.(((.((.(((((((((((..(((((((.(((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
)))))))))...)).)))))))))).....))))))))).)))).))))))).))))))))))..))).))).))))).))).))))-3'
MFE = -149.6; z-score = -6.79; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

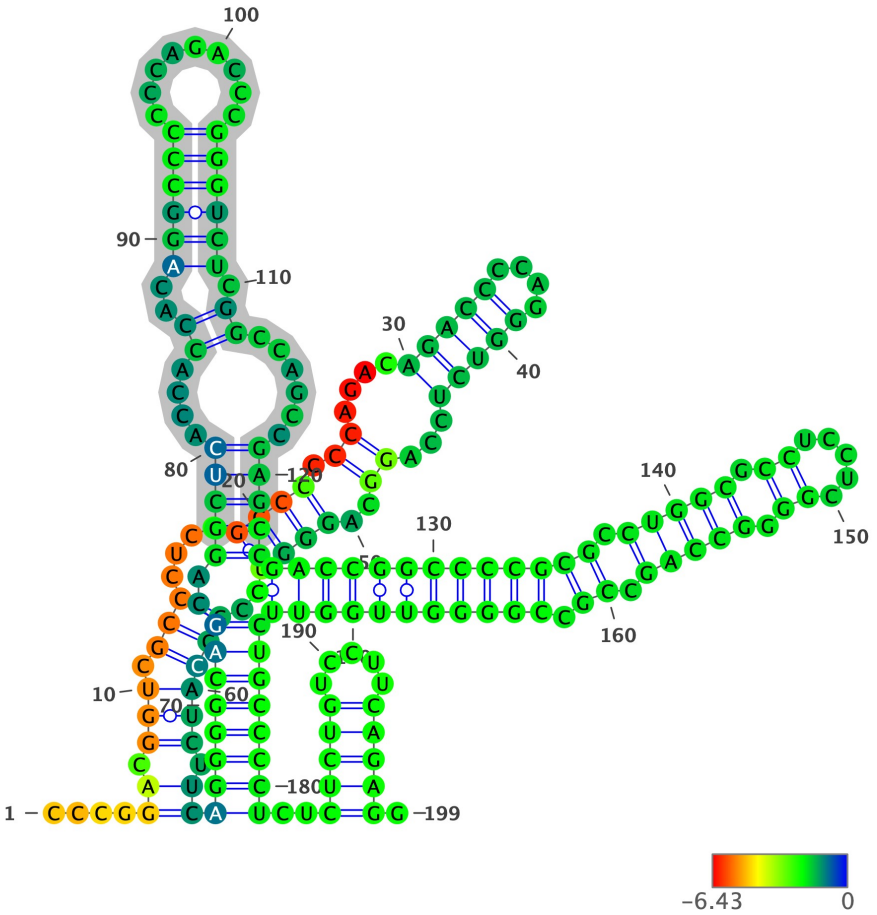
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 36 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 64 from nt 15788 to 15833 (nt 77 to 122)

```
5'-GCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGC-3'
5'-(..............(((.........)))...............)-3'
Motif MFE = -11.9; z-score = -0.18; ED = 11.49
```



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 15712 to 15910 (motif highlighted in silver):

```
5'-CCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCG
GCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-....((.((((.((((....(((((.((....((((((....)))))...))..)))))..)))))).))((((((((..((((((....((..((((((.........)))))).)
).....)))))((((((((((((.(((((.((.....)).)))))).)).)))))))))))))))))..(((((.....)))))).-3'
MFE = -93.4; z-score = -1.51; ED = 25.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

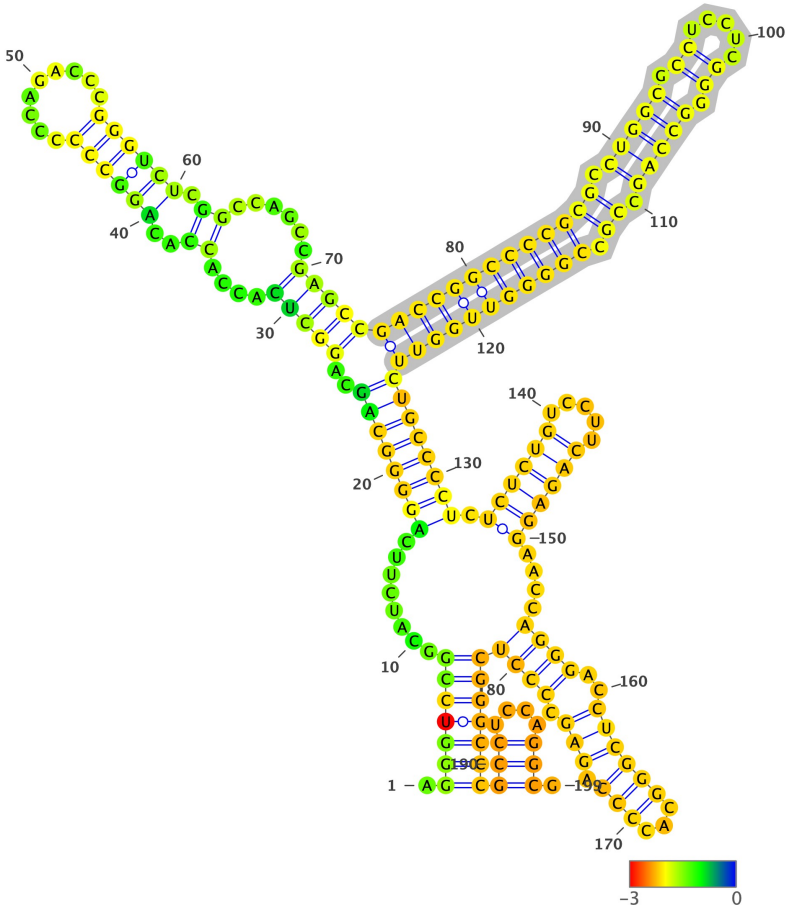
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 65 from nt 15835 to 15884 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.14; ED = 2.52
```



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 15761 to 15959 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).)))))))))))((....)).-3'
MFE = -101.9; z-score = -2.83; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

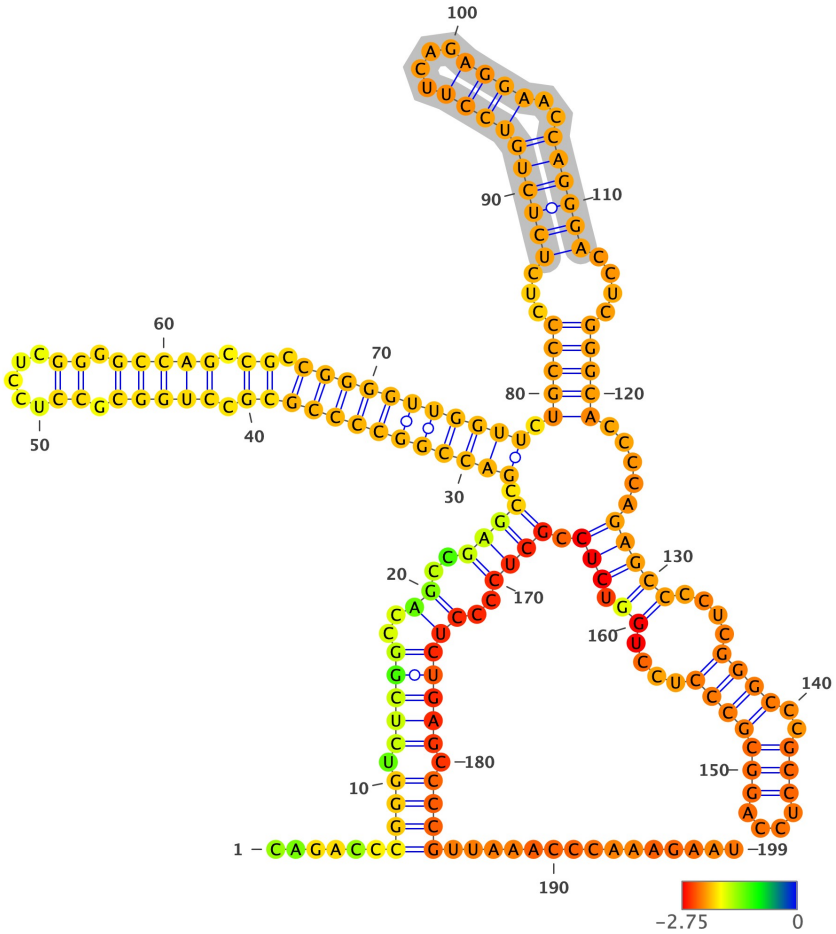
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 66 from nt 15894 to 15919 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-(((((((.......))..)))))-3'
Motif MFE = -8.8; z-score = -2.88; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 15808 to 16006 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.24; ED = 36.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

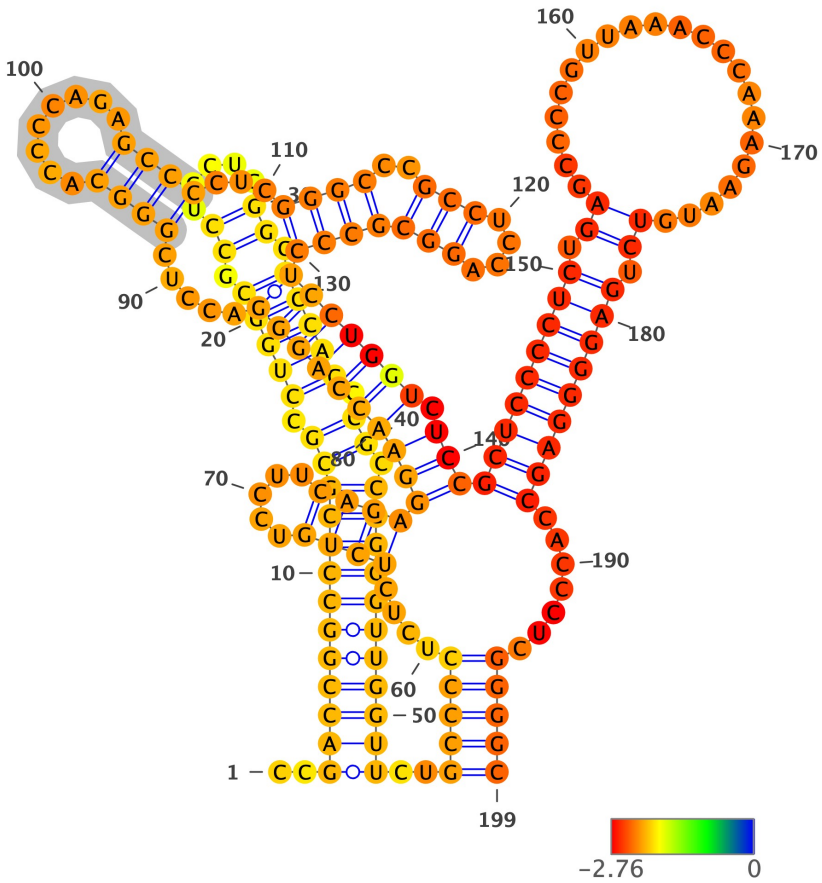
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 67 from nt 15924 to 15939 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-(((((........))))-3'
Motif MFE = -6.0; z-score = -2.26; 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 15833 to 16031 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -4.35; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

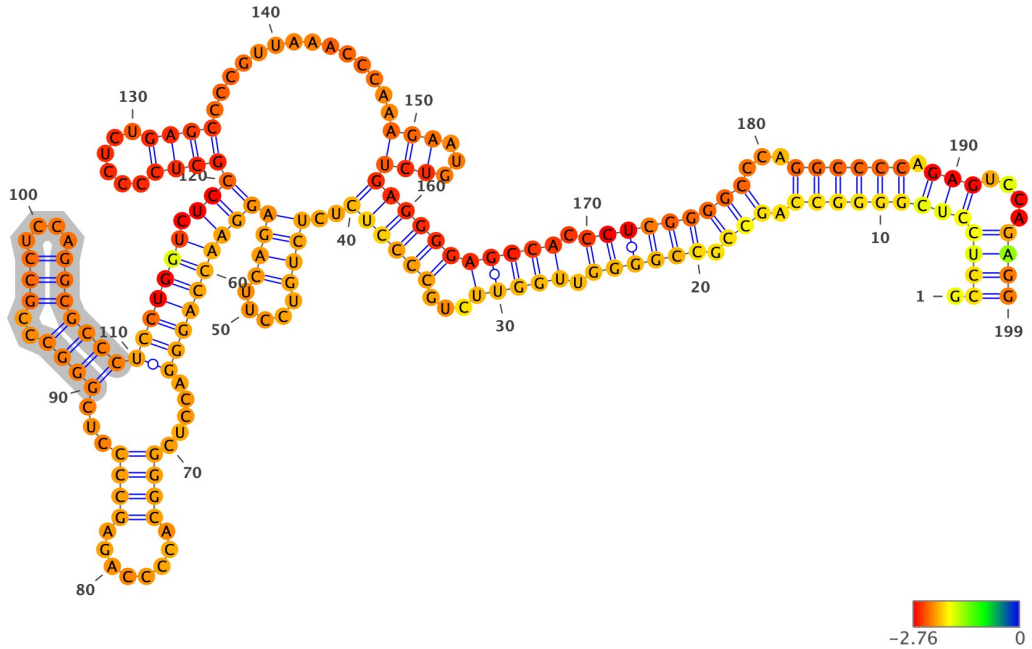
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 68 from nt 15943 to 15962 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..((((....)))))))-3'
Motif MFE = -9.3; z-score = -1.45; 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 15854 to 16052 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........))))...((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.44; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

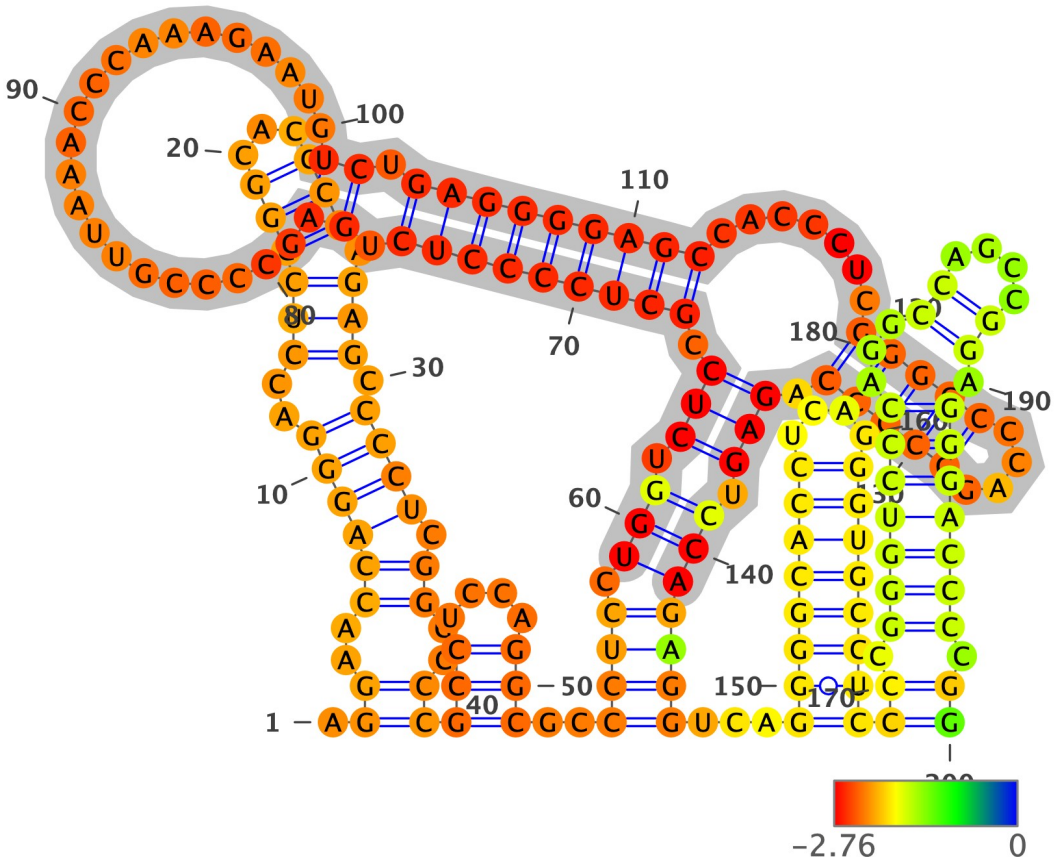
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 199--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 69 from nt 15966 to 16048 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.4; ED = 6.59
```



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 15908 to 16107 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).))..))(((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.3; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

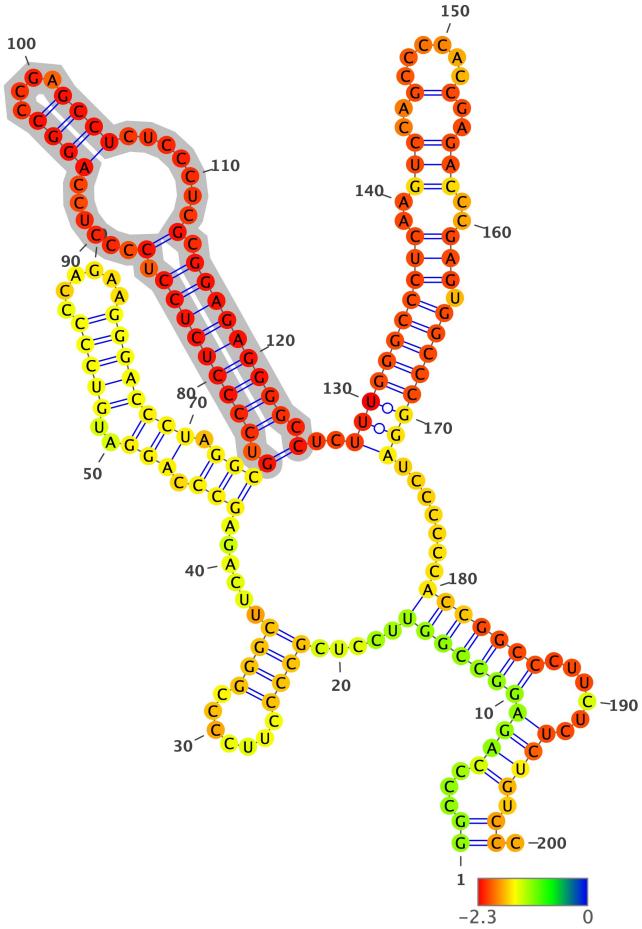
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 200--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 70 from nt 16192 to 16242 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.03; 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 16118 to 16317 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.68; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

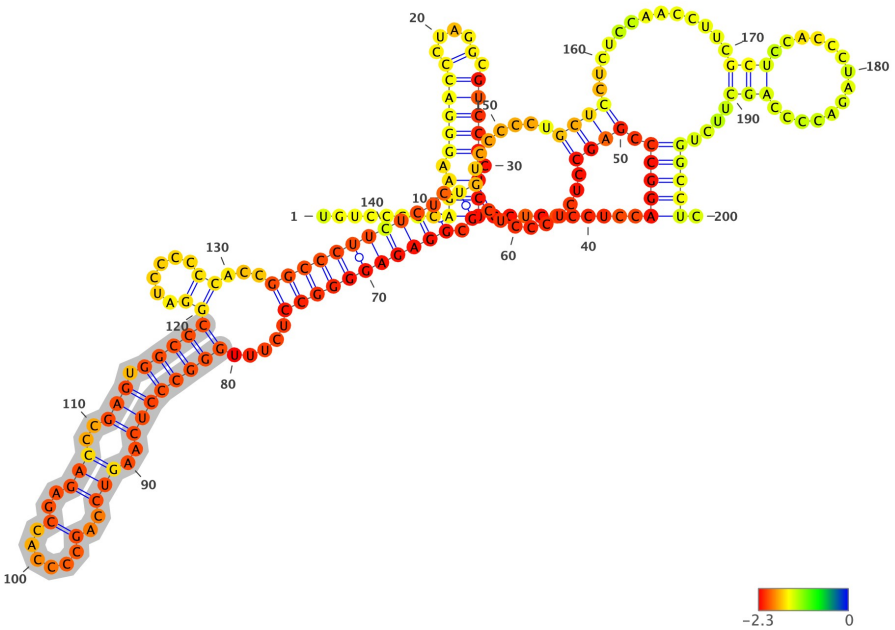
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 200--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 71 from nt 16248 to 16286 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -1.86; 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 16168 to 16367 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).)))..........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.53; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

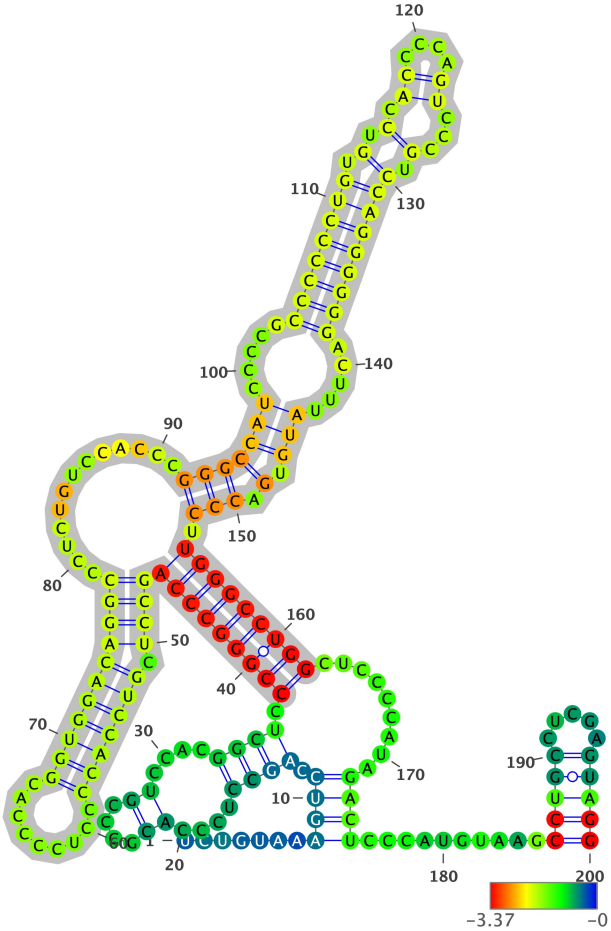
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 200--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 72 from nt 16653 to 16777 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....(((((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.73; ED = 23.92
```



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 16616 to 16815 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).))))))))).....))).).))).))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.3; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.2, 15613-16764(+)

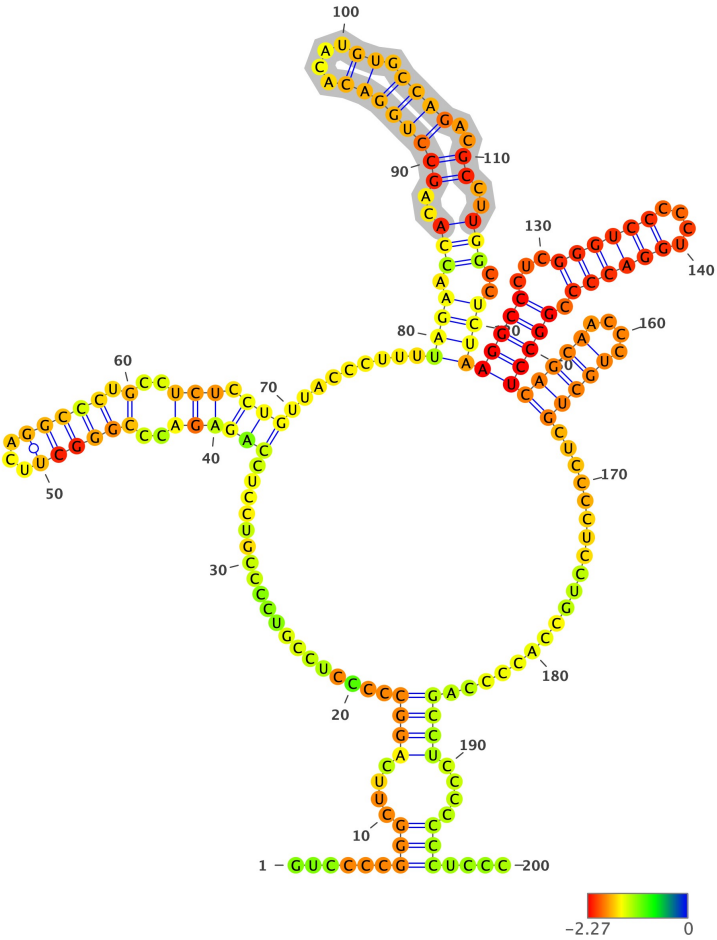
Attributes: ['ID=gene-HHV4_BWRF1.2', 'Dbxref=GeneID:3783734', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'start_range=.,15613']

16-- nt 1 to 149--CDS, cds-YP_401637.1, 15613-16764(+)

Attributes: ['ID=cds-YP_401637.1', 'Parent=gene-HHV4_BWRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZK6,Genbank:YP_401637.1,GeneID:3783734', 'Name=YP_401637.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.2', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401637.1', 'start_range=.,15613']

NC_007605.1 (forward strand): Structure number 73 from nt 18140 to 18168 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..((.................))..)-3'
Motif MFE = -5.8; z-score = -0.75; ED = 3.21
```



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 18055 to 18254 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))................))))....)))....-3'
MFE = -58.0; z-score = -2.5; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

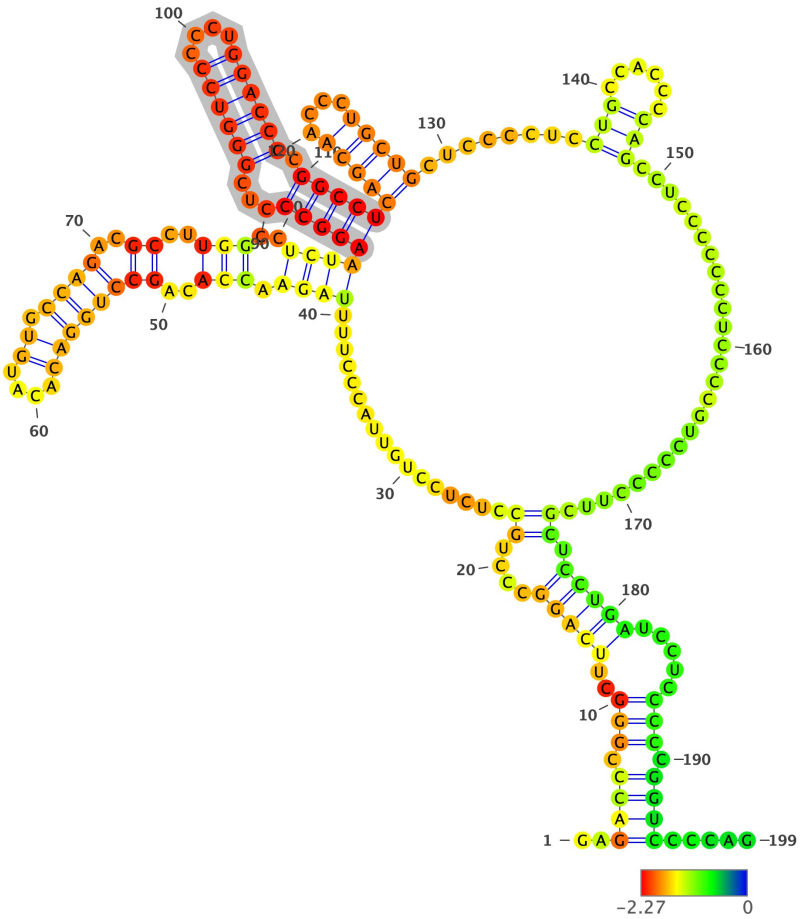
Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 74 from nt 18177 to 18206 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -3.73; ED = 0.48
```



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

Extracted structure model with flanking nucleotides 18093 to 18291 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..))))..))))((((((...(((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....))).)))).....-3'
MFE = -53.6; z-score = -2.02; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-11, 15073-18144(+)

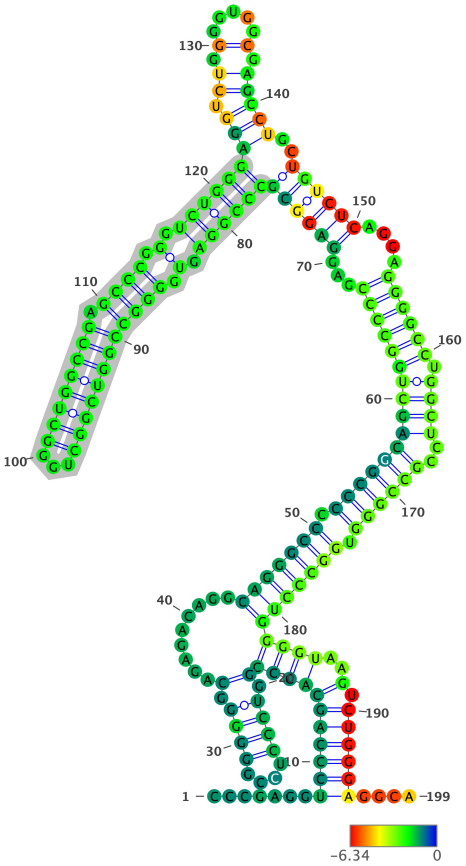
Attributes: ['ID=id-HHV4_EBNA-LP-11', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 75 from nt 18574 to 18619 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -4.06; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 18498 to 18696 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).)........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)..)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.82; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

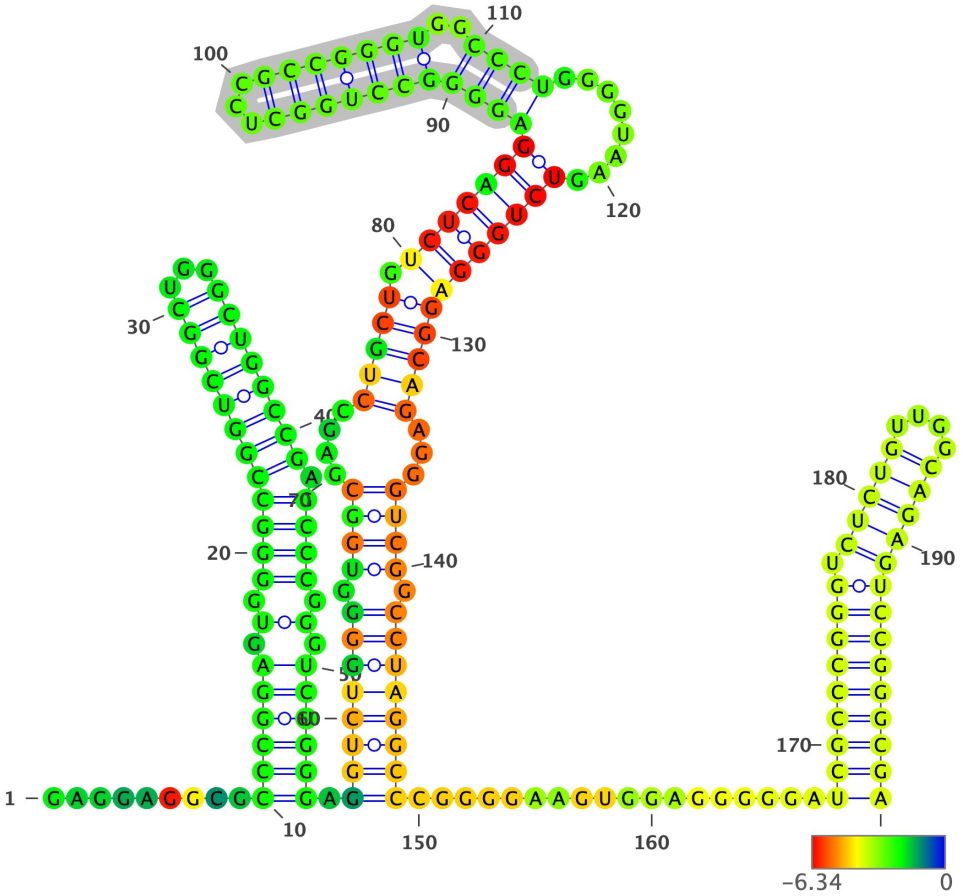
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 188 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 76 from nt 18652 to 18676 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.88; 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 18565 to 18764 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -2.97; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

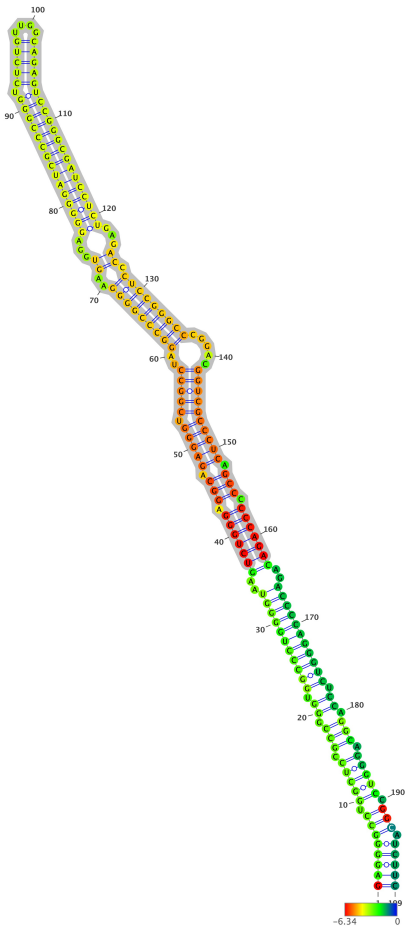
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 121 to 200--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 77 from nt 18686 to 18811 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((.(((((....)))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -5.43; ED = 3.47
```



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 18650 to 18848 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-((((((((.(((((.((((.((.(((((((((((..((((((((.((((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).)))))))))).....))))))))).))).))))))).))))))..))))))))))).))).))).))))).))).))))))-3'
MFE = -149.6; z-score = -7.32; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

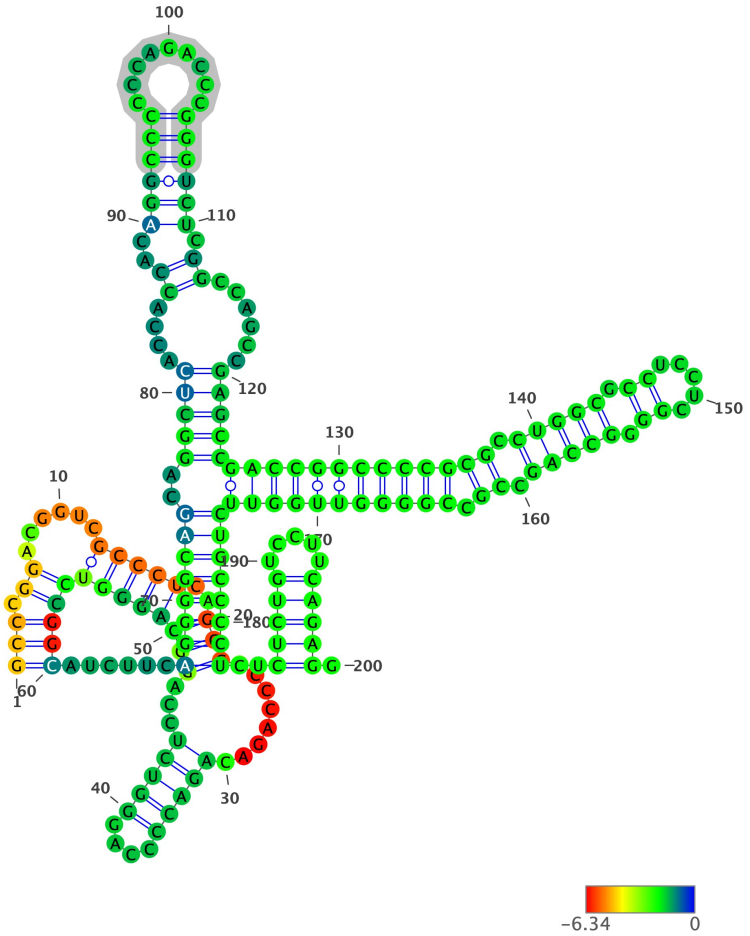
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 36 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 78 from nt 18875 to 18889 (nt 93 to 107)

```
5'-CCCCCCAGACCCGGG-3'
5'-(((.........)))-3'
Motif MFE = -3.0; z-score = -1.16; 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 18783 to 18982 (motif highlighted in silver):

```
5'-GCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUC
GGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-(((.((......((((((..((((........((((((....))))))...)))))))))))))).....(((((((..((((((....((..((((((.........)))))).
))......)))))((((((((((((.(((((.(.....)).)))))).)).)))))))))))))))..(((((.....))))).-3'
MFE = -93.8; z-score = -1.28; ED = 24.16
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

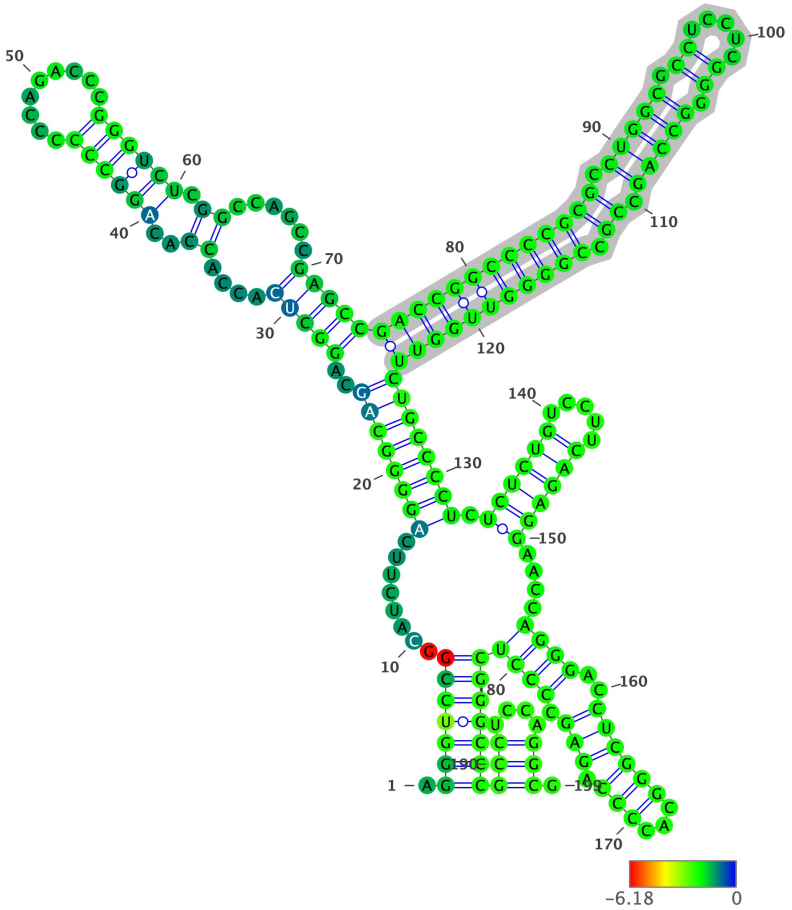
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 200--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 79 from nt 18907 to 18956 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.62; ED = 2.52
```



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 18833 to 19031 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -2.39; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

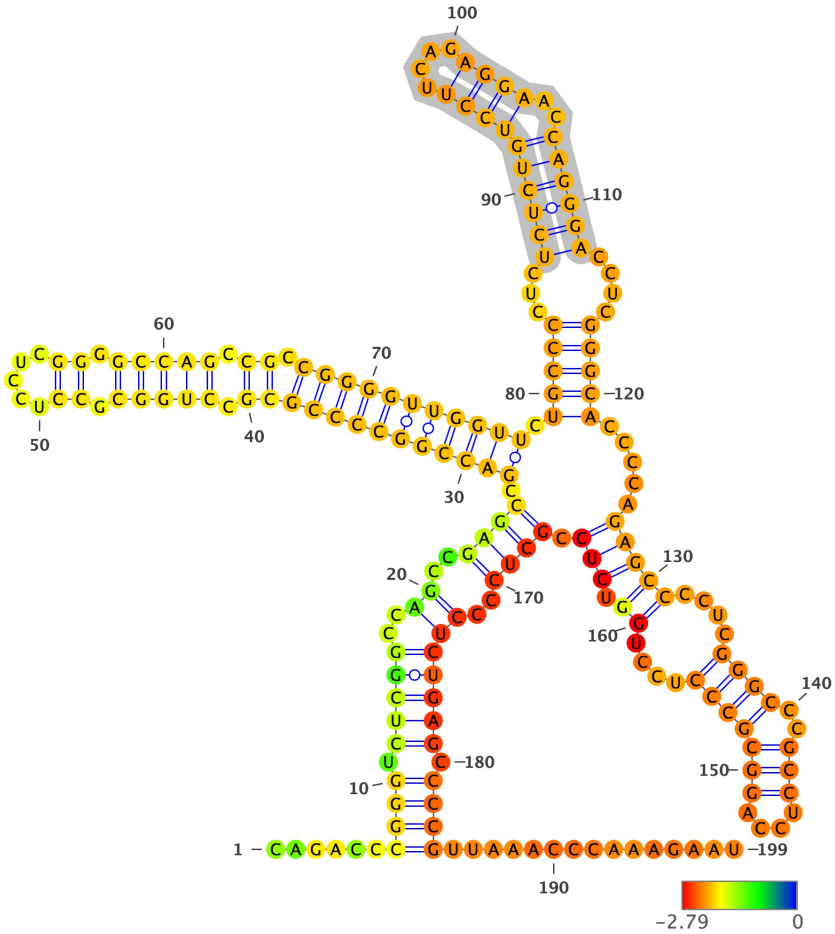
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 80 from nt 18966 to 18991 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-(((((((.......))..)))))-3'
Motif MFE = -8.8; z-score = -2.28; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 18880 to 19078 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.96; ED = 36.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

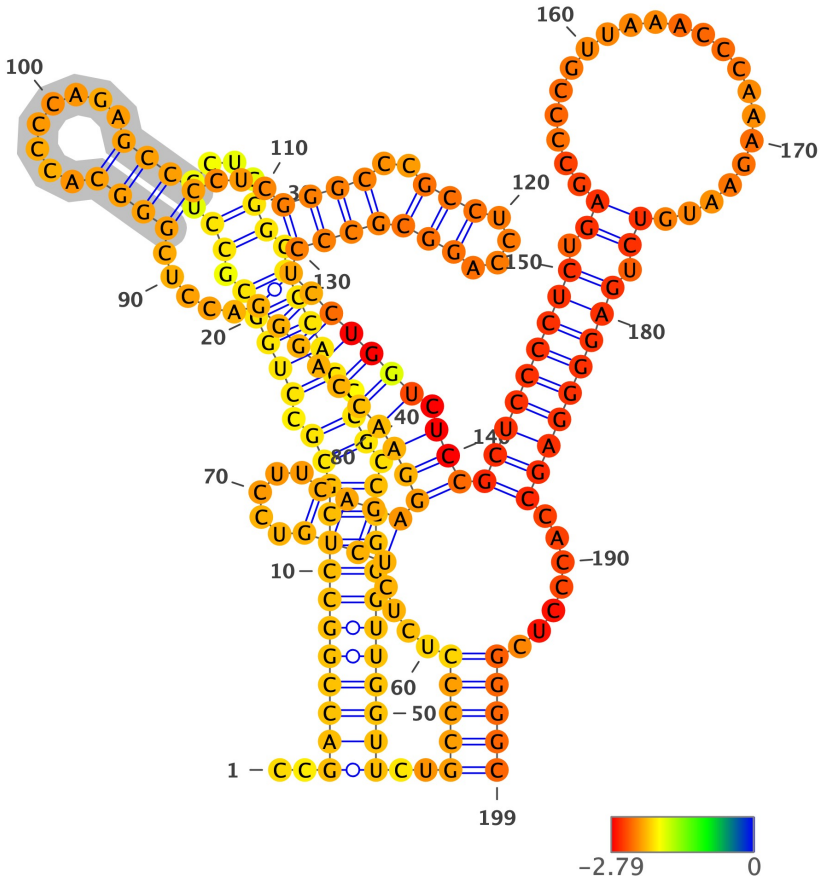
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 81 from nt 18996 to 19011 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-((((........))))-3'
Motif MFE = -6.0; z-score = -2.16; 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 18905 to 19103 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -3.95; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

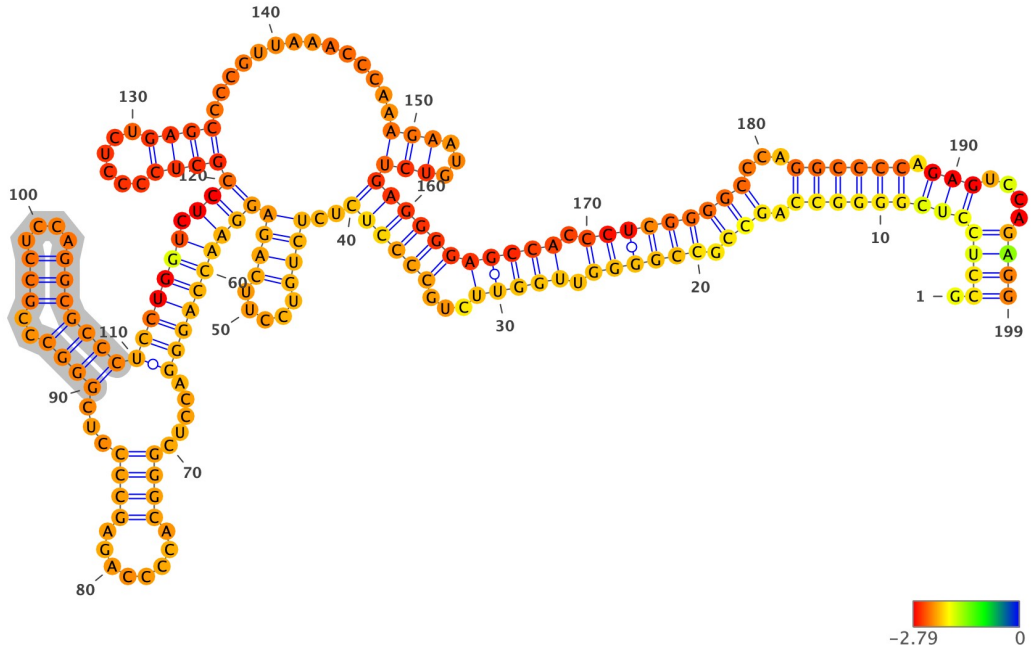
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 82 from nt 19015 to 19034 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..((((....)))))))-3'
Motif MFE = -9.3; z-score = -0.87; 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 18926 to 19124 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........))))...((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).)))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.57; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

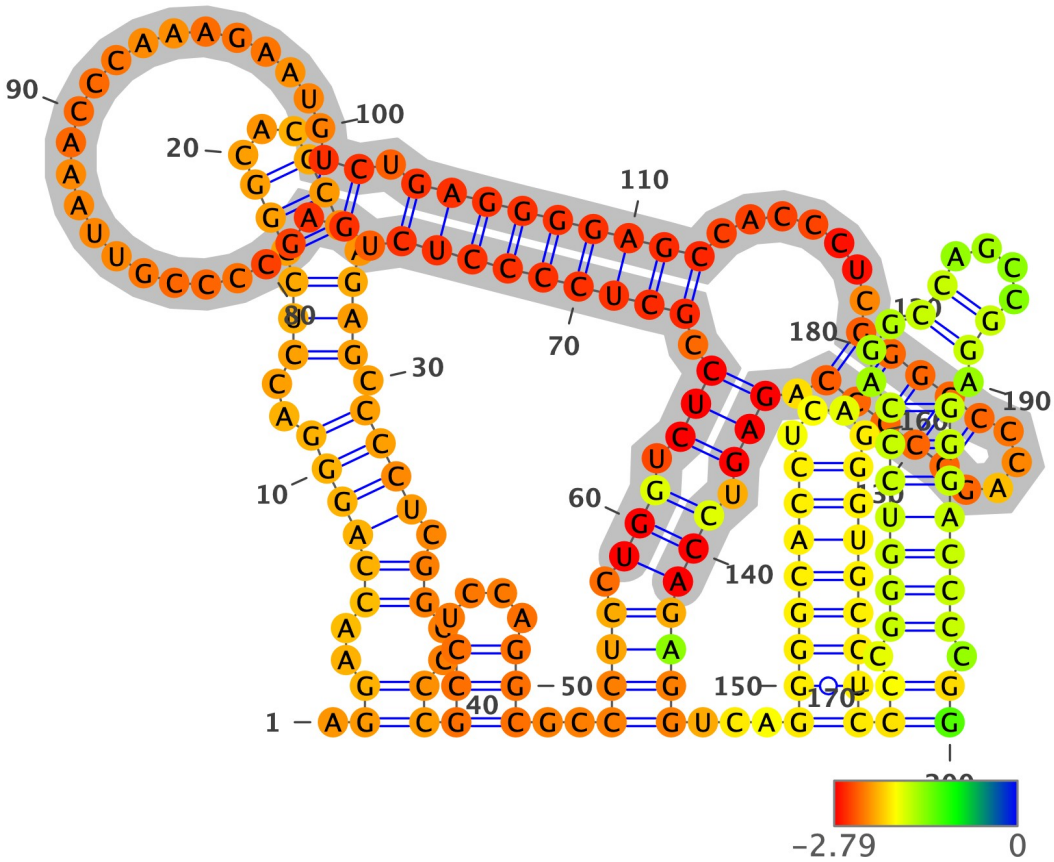
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 199--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 83 from nt 19038 to 19120 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.65; ED = 6.59
```



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 18980 to 19179 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.2; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

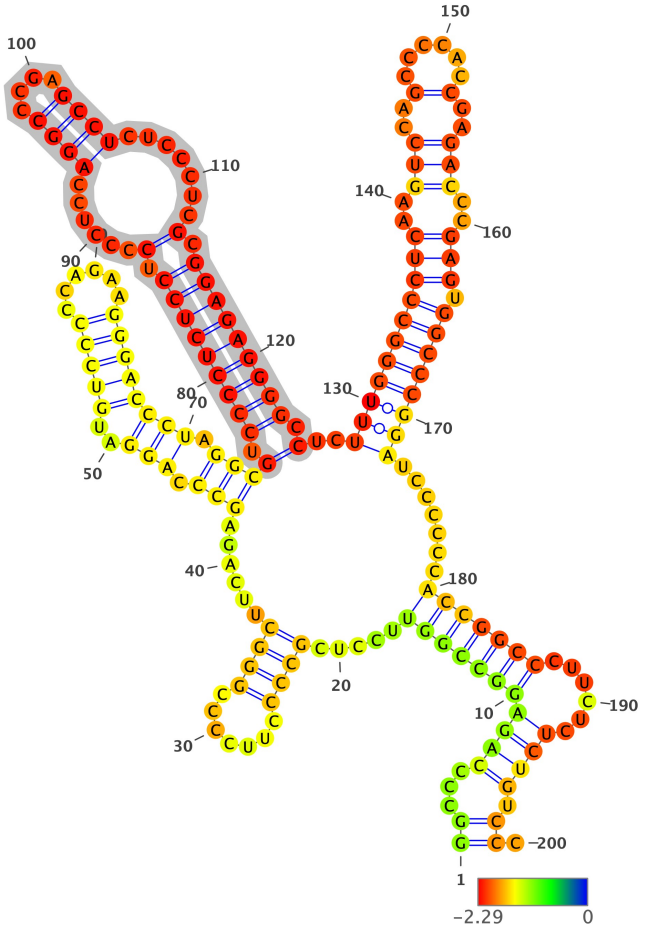
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 200--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 84 from nt 19264 to 19314 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.01; 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 19190 to 19389 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.((((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..((((..(.....)..)))).)))).))))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -3.09; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

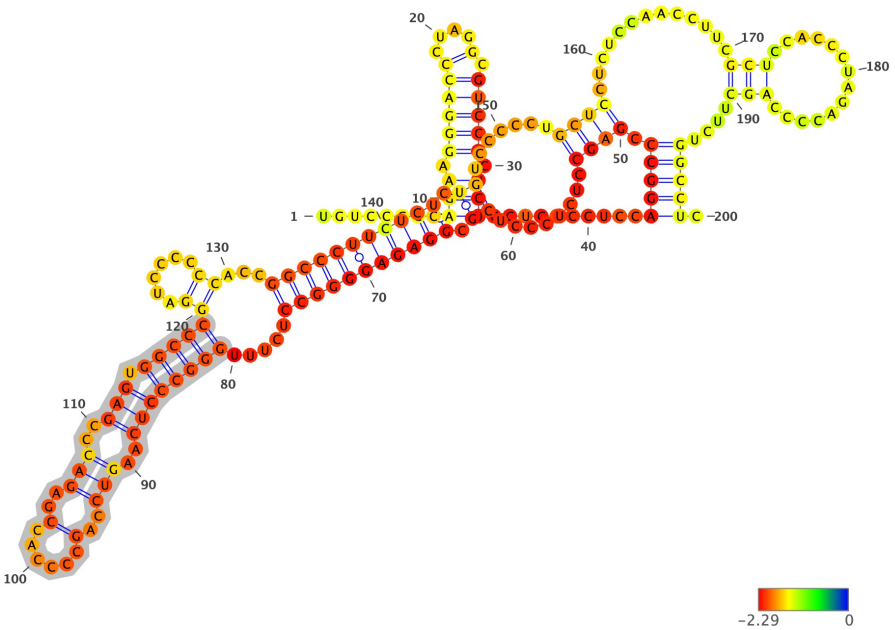
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 200--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 85 from nt 19320 to 19358 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -2.07; 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 19240 to 19439 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.43; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

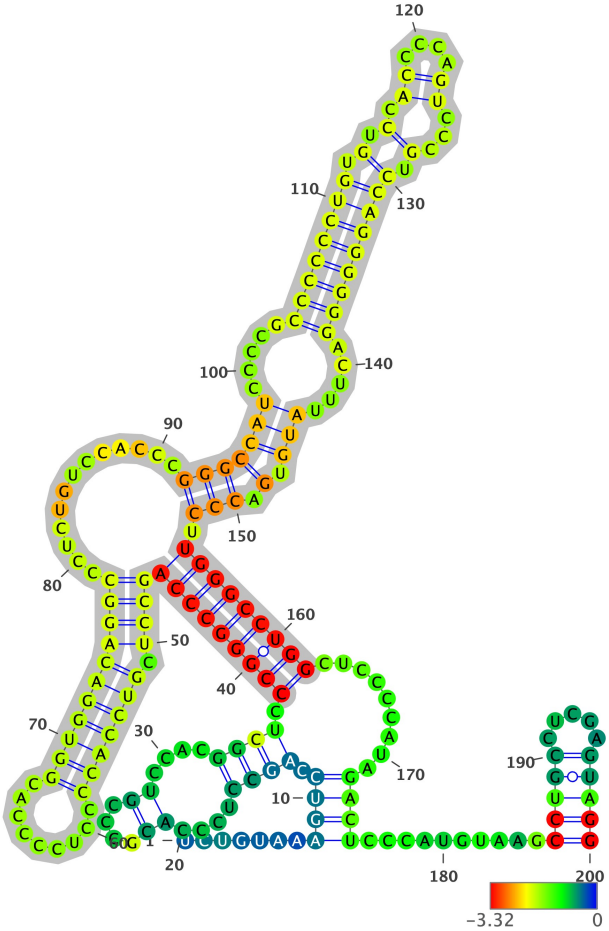
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 200--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 86 from nt 19725 to 19849 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................)))).............(((((((.....(((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.31; ED = 23.92
```



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 19688 to 19887 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).))))))))).....))).).))).))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.52; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.3, 18685-19836(+)

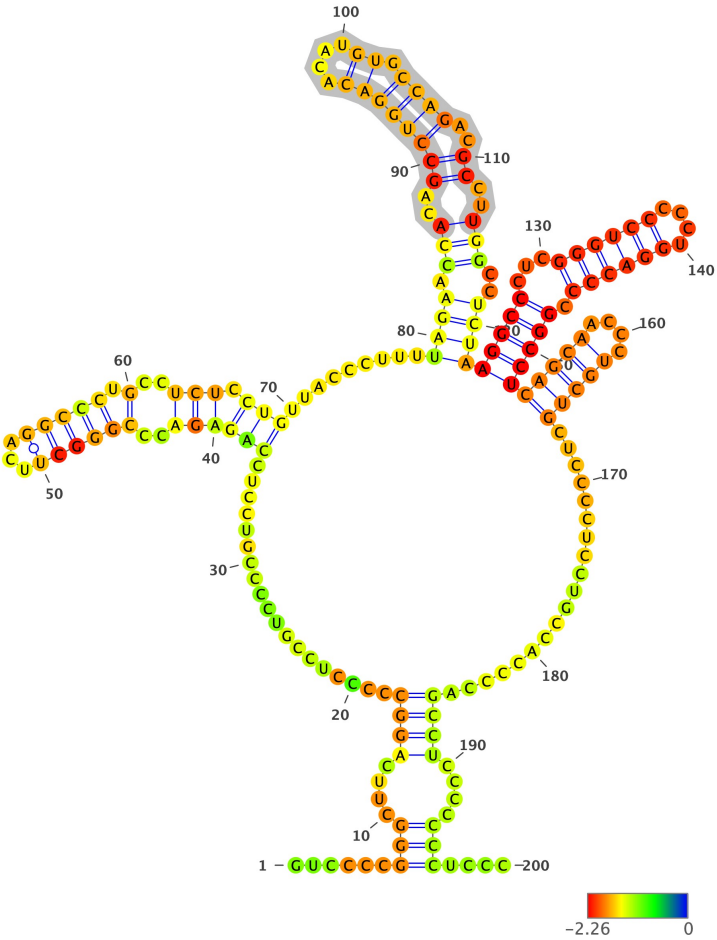
Attributes: ['ID=gene-HHV4_BWRF1.3', 'Dbxref=GeneID:3783735', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'start_range=.,18685']

16-- nt 1 to 149--CDS, cds-YP_401638.1, 18685-19836(+)

Attributes: ['ID=cds-YP_401638.1', 'Parent=gene-HHV4_BWRF1.3', 'Dbxref=UniProtKB/TrEMBL:Q8AZK5,Genbank:YP_401638.1,GeneID:3783735', 'Name=YP_401638.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.3', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401638.1', 'start_range=.,18685']

NC_007605.1 (forward strand): Structure number 87 from nt 21212 to 21240 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..((.................))..)-3'
Motif MFE = -5.8; z-score = -0.8; ED = 3.21
```



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 21127 to 21326 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))................))))....)))....-3'
MFE = -58.0; z-score = -2.04; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

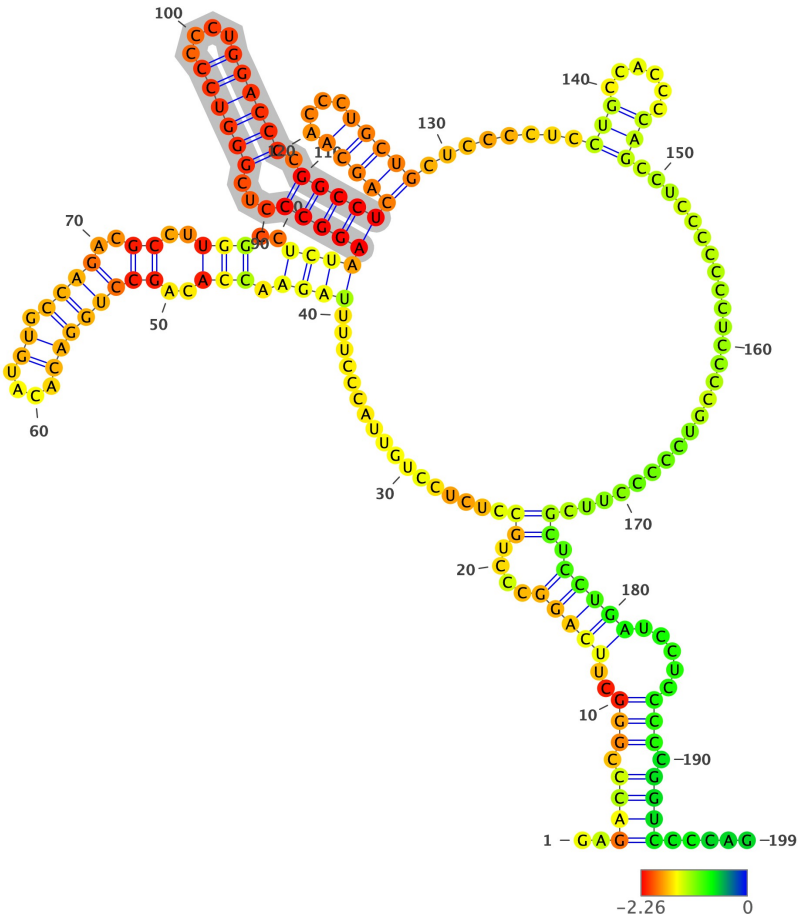
Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 88 from nt 21249 to 21278 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -4.15; 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 21165 to 21363 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..)))..)))))((((((...((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....)))).)))).....-3'
MFE = -53.6; z-score = -2.12; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-12, 18145-21216(+)

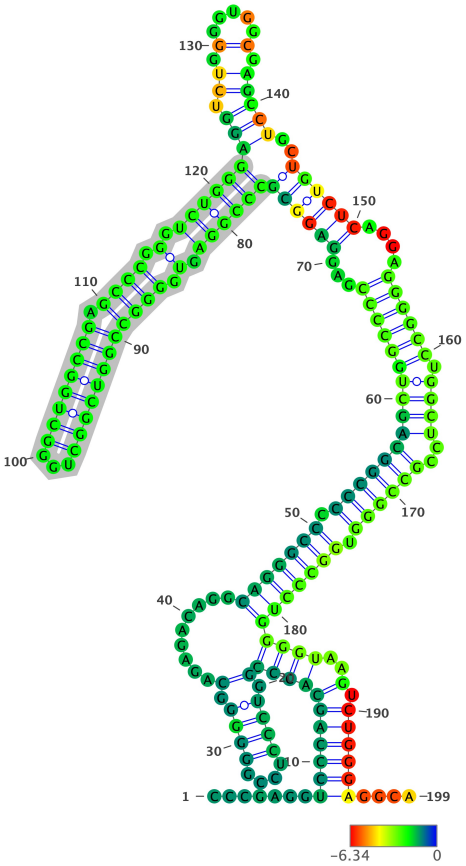
Attributes: ['ID=id-HHV4_EBNA-LP-12', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 89 from nt 21646 to 21691 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -3.7; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 21570 to 21768 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).).........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -2.03; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

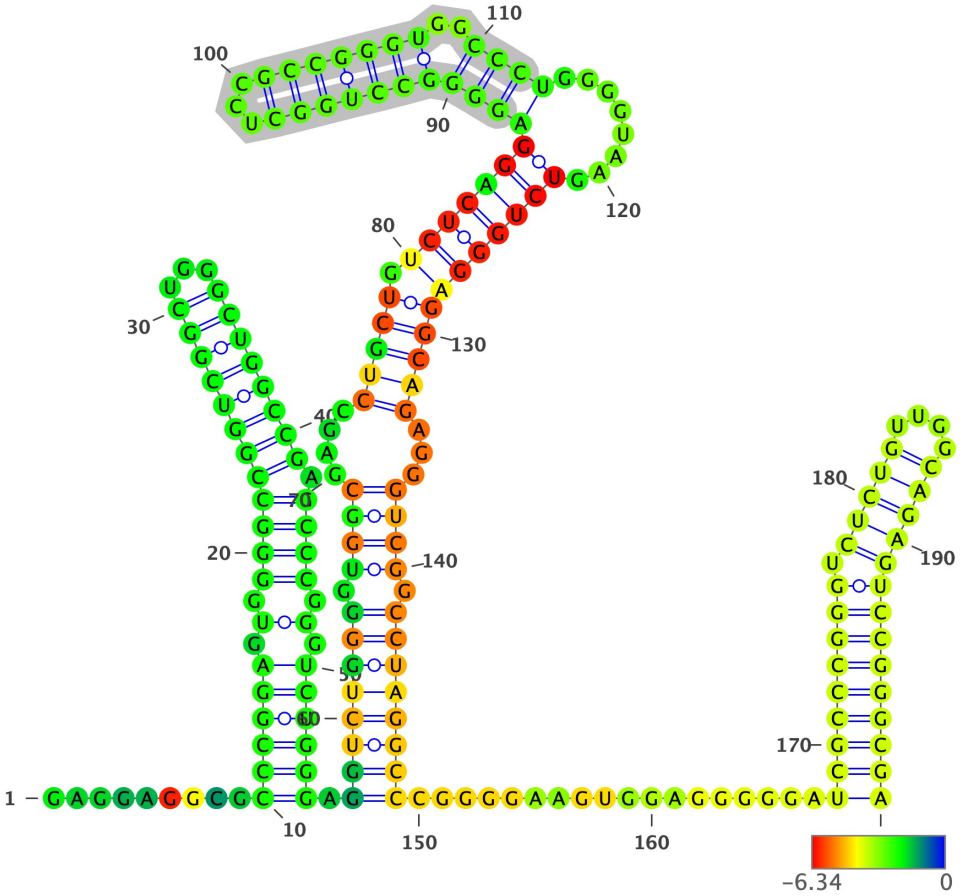
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 188 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 90 from nt 21724 to 21748 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -1.18; 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 21637 to 21836 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.01; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

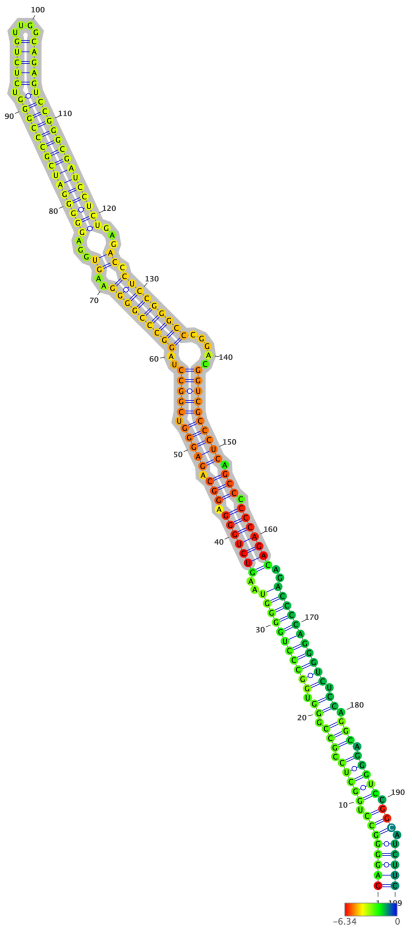
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 121 to 200--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 91 from nt 21758 to 21883 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((((.(((((....)))))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.44; ED = 3.47
```



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 21722 to 21920 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-((((((((.(((((.((((.((.(((((((((((..(((((((.((((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).)))))))))).....))))))))).))).))))))).))))))..))))))))))).))).))).))))).))).))))))-3'
MFE = -149.6; z-score = -7.38; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

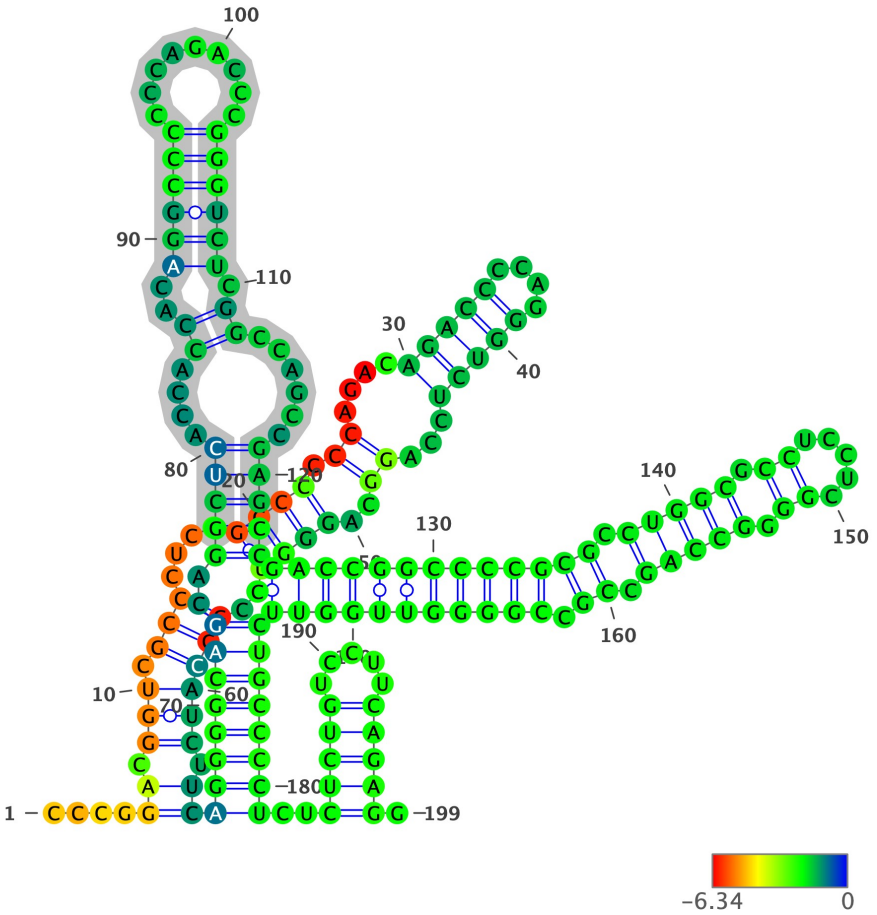
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 36 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 92 from nt 21932 to 21977 (nt 77 to 122)

```
5'-GCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGC-3'
5'-(..............(((.........)))...............)-3'
Motif MFE = -11.9; z-score = -0.16; ED = 11.49
```



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 21856 to 22054 (motif highlighted in silver):

```
5'-CCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCG
GCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-....((.((((.(((....((((.((....((((((....)))))...))..)))))..)))))).))(((((((..(((((....((..((((((.........)))))).)
).....)))))((((((((((((.(((((.((.....)).)))))).)).)))))))))))))))))..(((((.....)))))).-3'
MFE = -93.4; z-score = -1.57; ED = 25.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

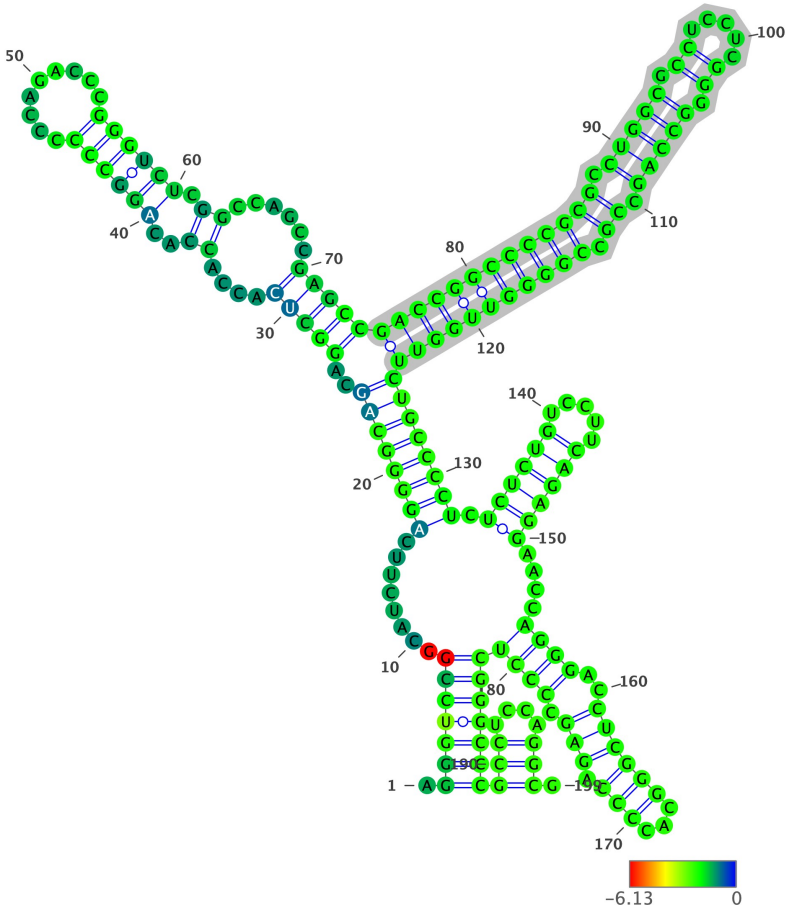
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 93 from nt 21979 to 22028 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.48; ED = 2.52
```



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 21905 to 22103 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).))......)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -2.69; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

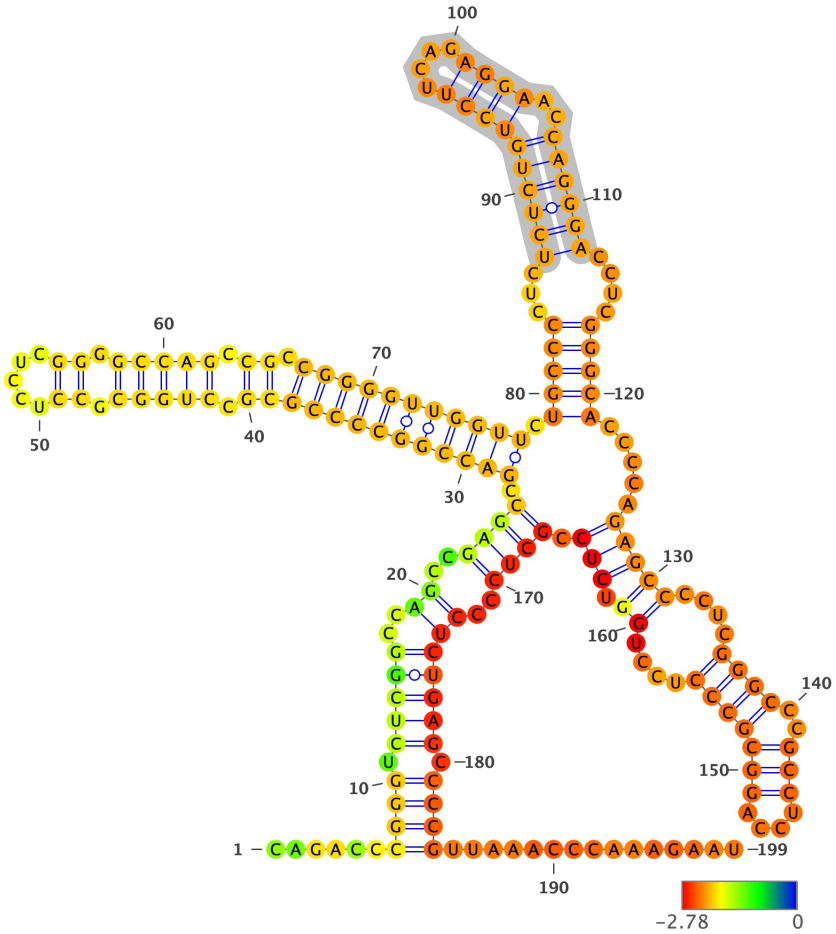
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 94 from nt 22038 to 22063 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-((((((.(........)...)))))))-3'
Motif MFE = -8.8; z-score = -2.29; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 21952 to 22150 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.91; ED = 36.45
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

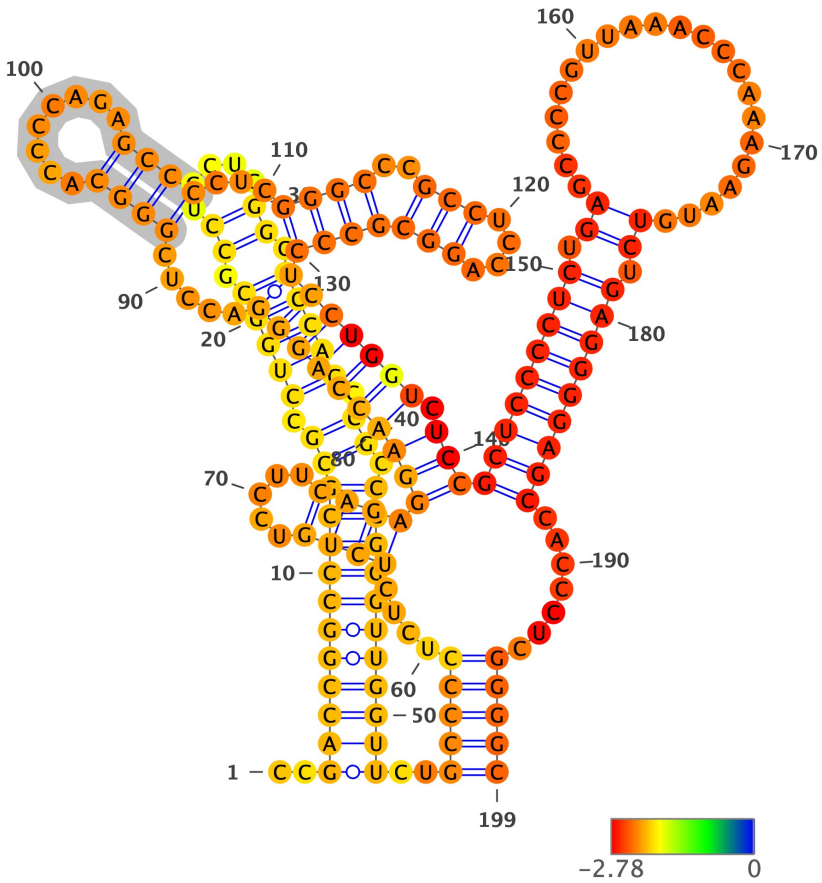
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 95 from nt 22068 to 22083 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-(((((........))))-3'
Motif MFE = -6.0; z-score = -1.84; 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 21977 to 22175 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -3.74; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

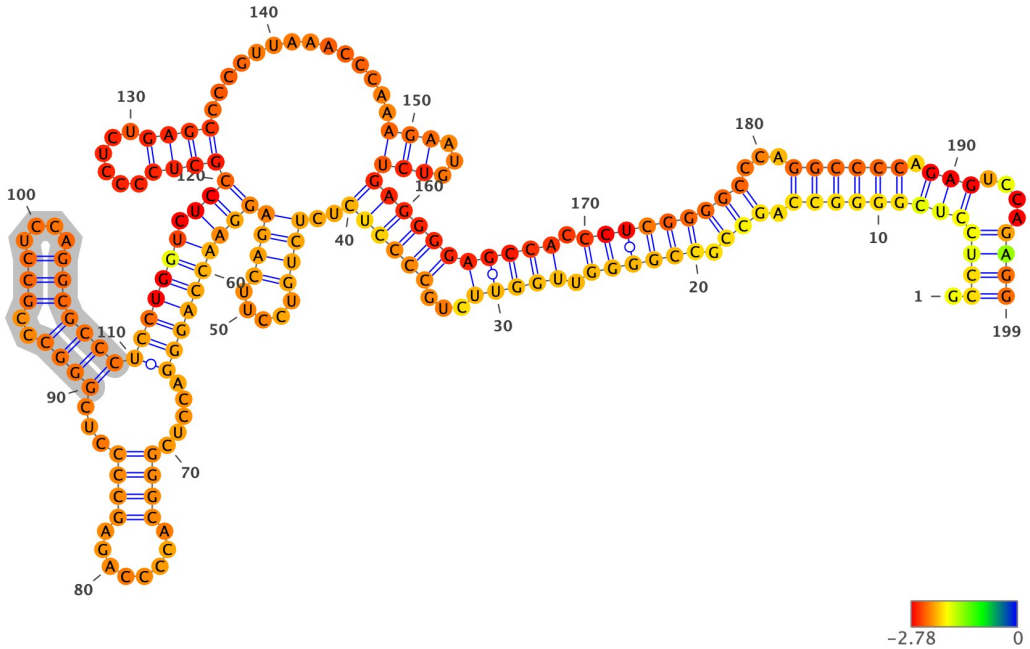
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 96 from nt 22087 to 22106 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..(((....)))))))-3'
Motif MFE = -9.3; z-score = -1.43; 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 21998 to 22196 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........)))).....((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -3.04; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

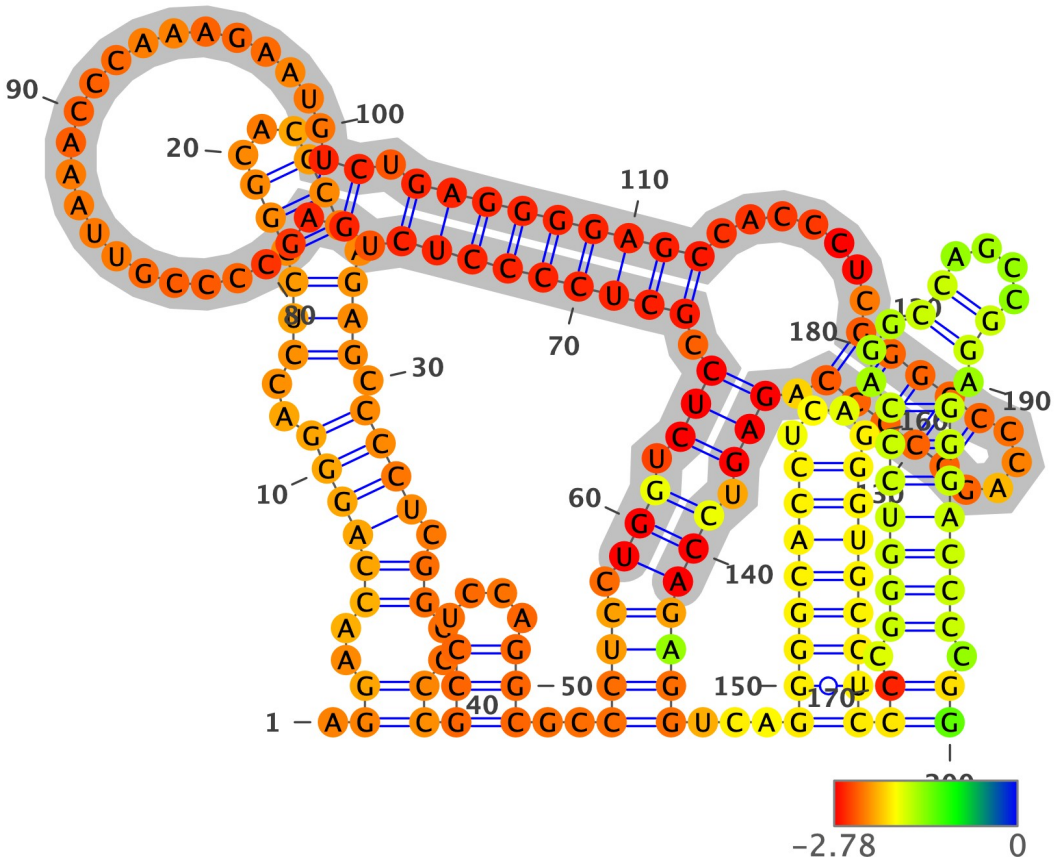
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 199--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 97 from nt 22110 to 22192 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.5; ED = 6.59
```



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 22052 to 22251 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.63; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

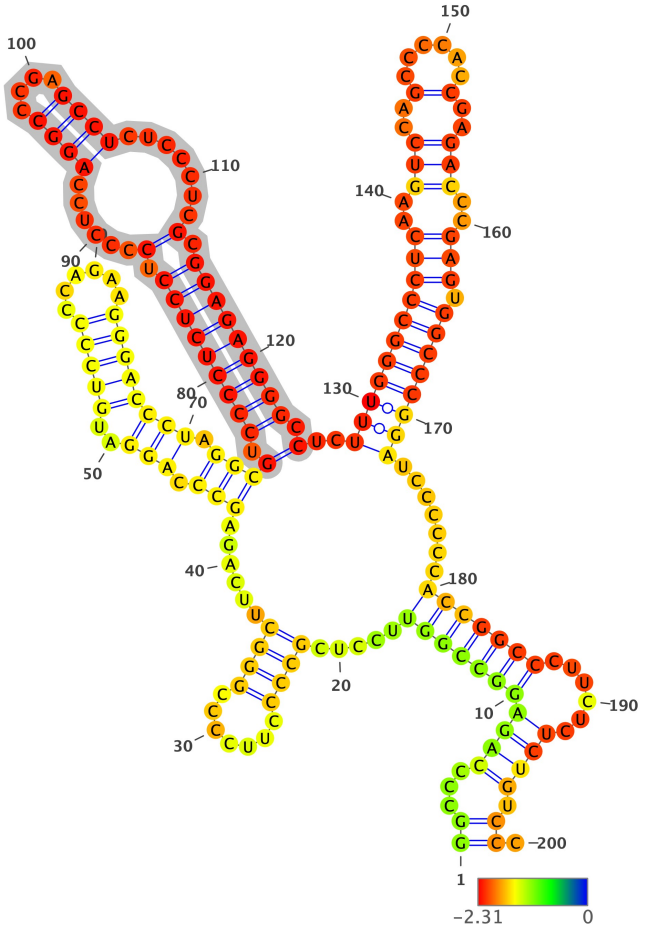
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 200--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 98 from nt 22336 to 22386 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.37; 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 22262 to 22461 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.74; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

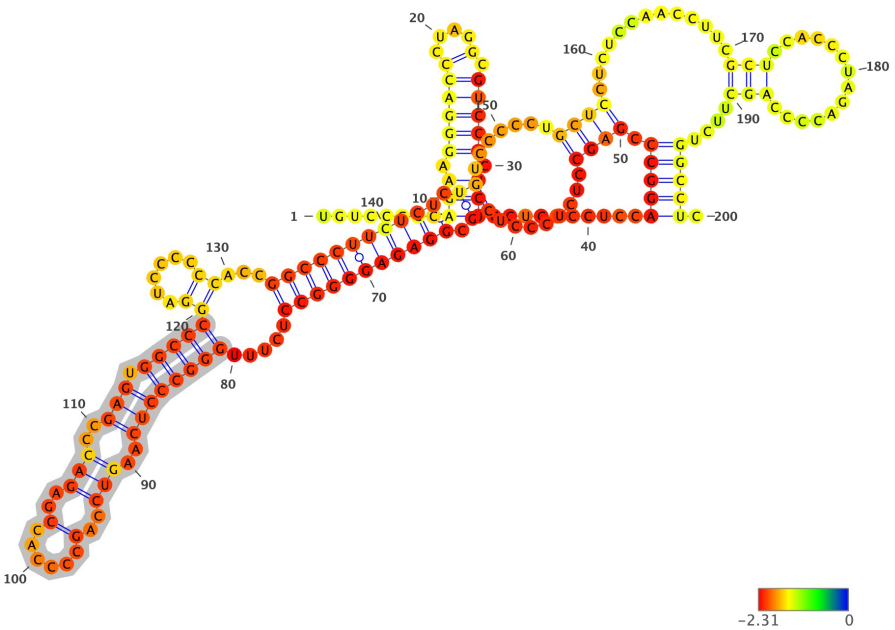
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 200--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 99 from nt 22392 to 22430 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-((((((.....((..(......)..)).....).))))))-3'
Motif MFE = -15.5; z-score = -1.83; 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 22312 to 22511 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.24; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

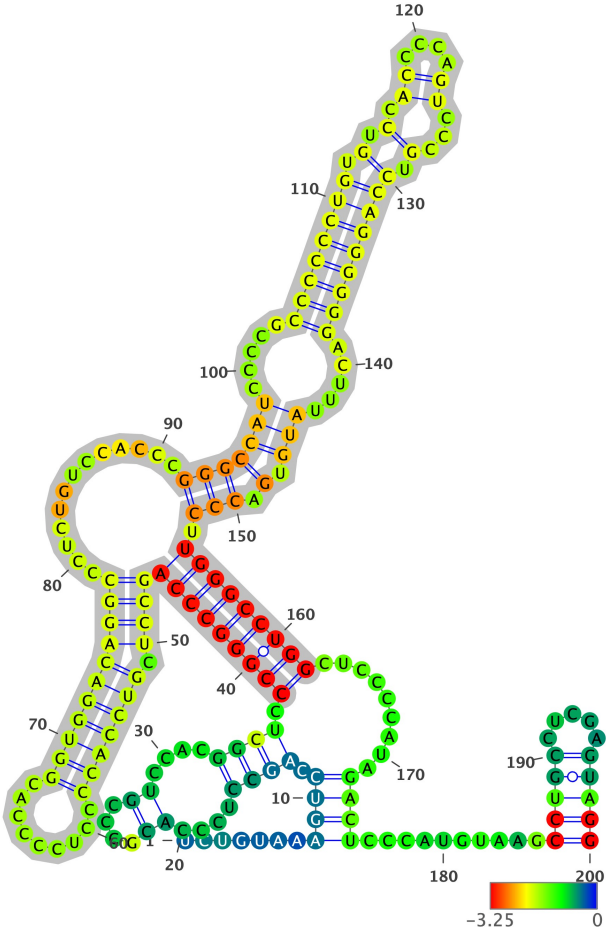
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 200--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 100 from nt 22797 to 22921 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................)))).............(((((((.....(((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.8; ED = 23.92
```



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 22760 to 22959 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).))))))))).....))).).))).)))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.86; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.4, 21757-22908(+)

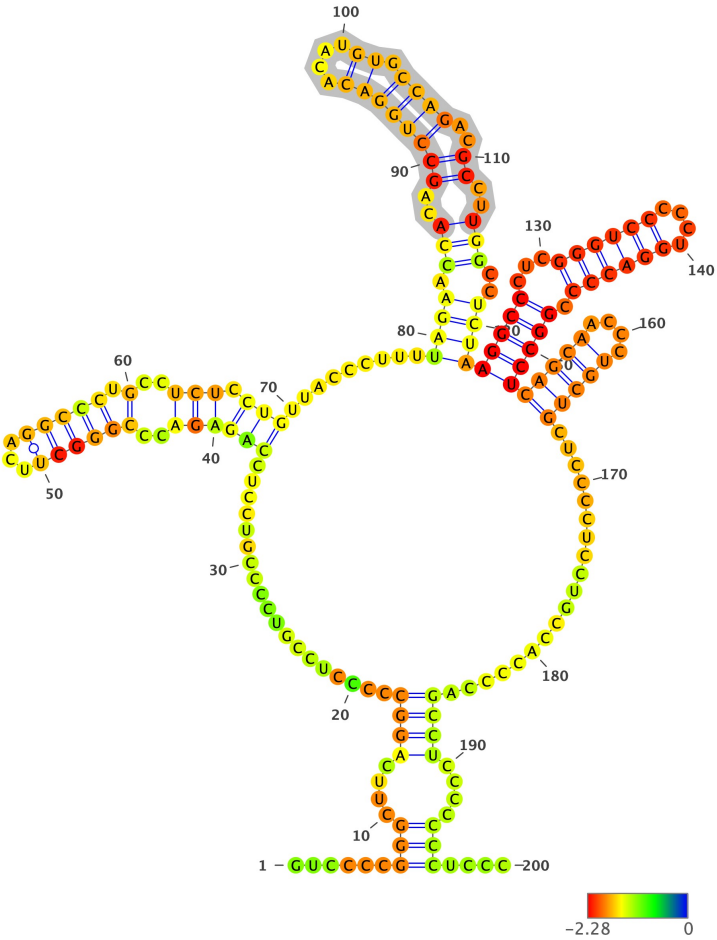
Attributes: ['ID=gene-HHV4_BWRF1.4', 'Dbxref=GeneID:3783736', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'start_range=.,21757']

16-- nt 1 to 149--CDS, cds-YP_401639.1, 21757-22908(+)

Attributes: ['ID=cds-YP_401639.1', 'Parent=gene-HHV4_BWRF1.4', 'Dbxref=UniProtKB/TrEMBL:Q8AZK4,Genbank:YP_401639.1,GeneID:3783736', 'Name=YP_401639.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.4', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401639.1', 'start_range=.,21757']

NC_007605.1 (forward strand): Structure number 101 from nt 24284 to 24312 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..((.................))..)-3'
Motif MFE = -5.8; z-score = -0.46; ED = 3.21
```



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 24199 to 24398 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))................))))....)))....-3'
MFE = -58.0; z-score = -2.23; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

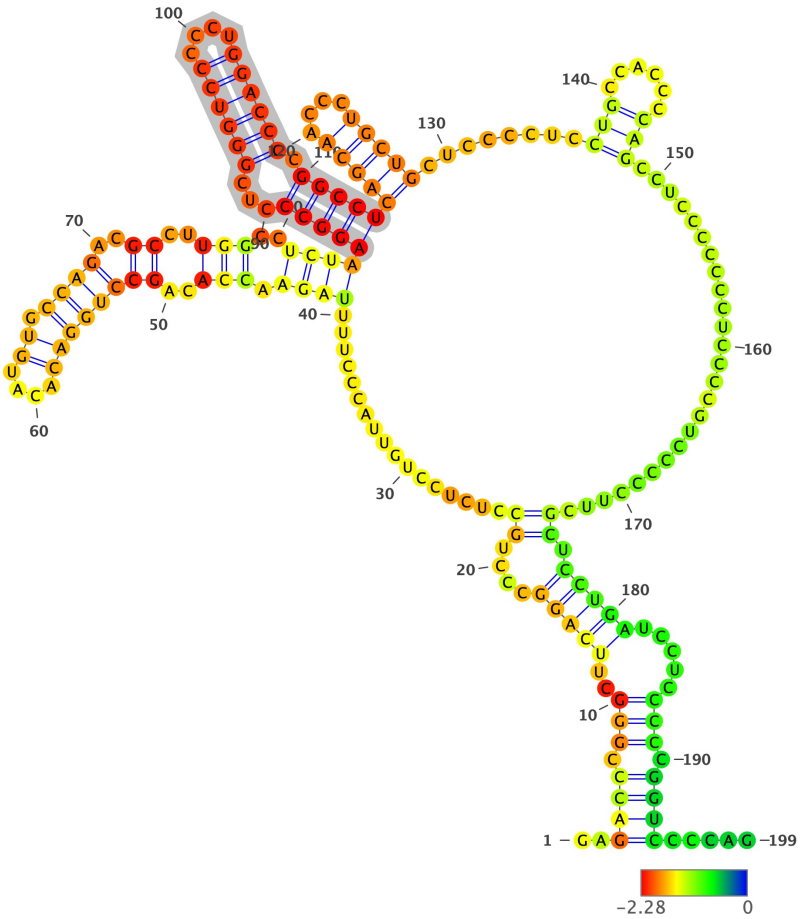
Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 102 from nt 24321 to 24350 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -4.28; 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 24237 to 24435 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..))))..))))((((((...((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....))).)))).....-3'
MFE = -53.6; z-score = -1.9; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-13, 21217-24288(+)

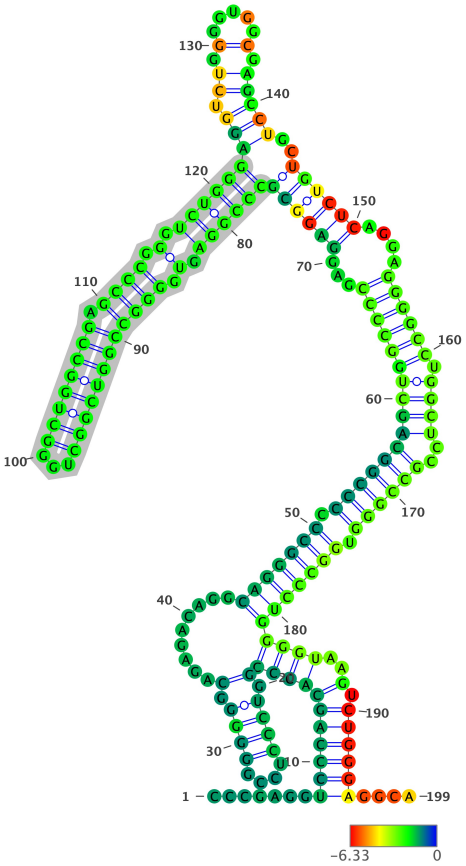
Attributes: ['ID=id-HHV4_EBNA-LP-13', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 103 from nt 24718 to 24763 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -4.27; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 24642 to 24840 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).)........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)..)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.62; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

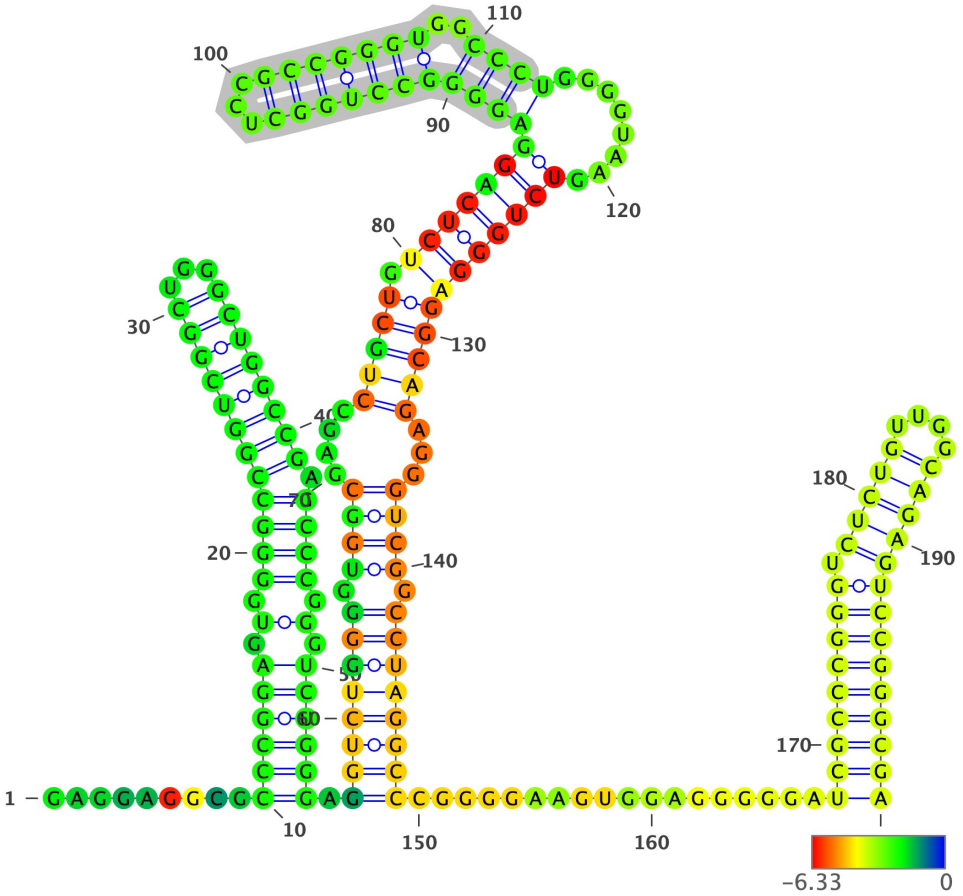
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 188 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 104 from nt 24796 to 24820 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.97; 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 24709 to 24908 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.01; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

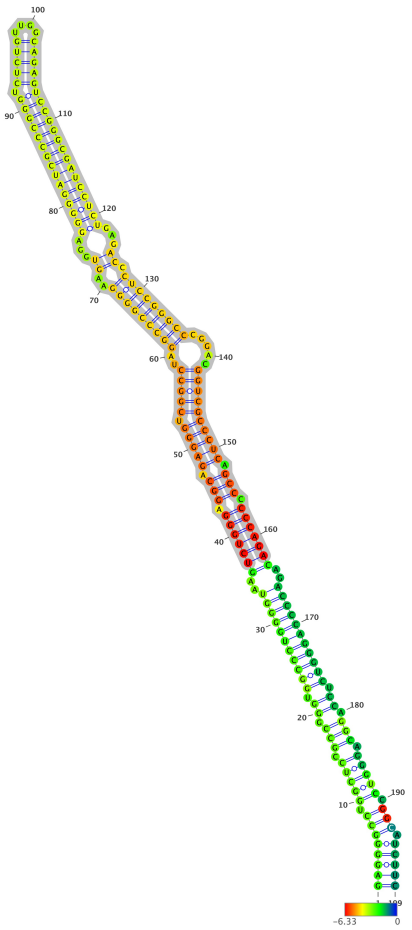
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 121 to 200--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 105 from nt 24830 to 24955 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((.(((((....)))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.28; ED = 3.47
```



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 24794 to 24992 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.((((.((.(((((((((((..(((((((.((((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).))))))))).....))))))))).))).))))))..))))))))))).)).))).))))).))).))))-3'
MFE = -149.6; z-score = -7.25; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

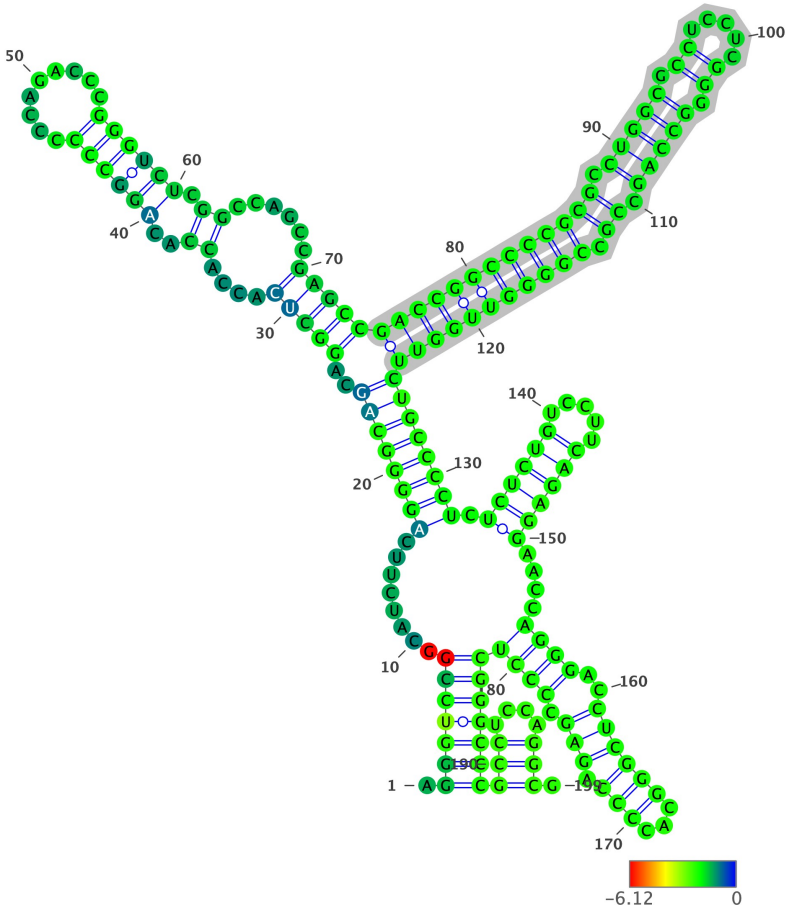
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 36 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 106 from nt 25051 to 25100 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -4.04; ED = 2.52
```



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 24977 to 25175 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -2.47; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

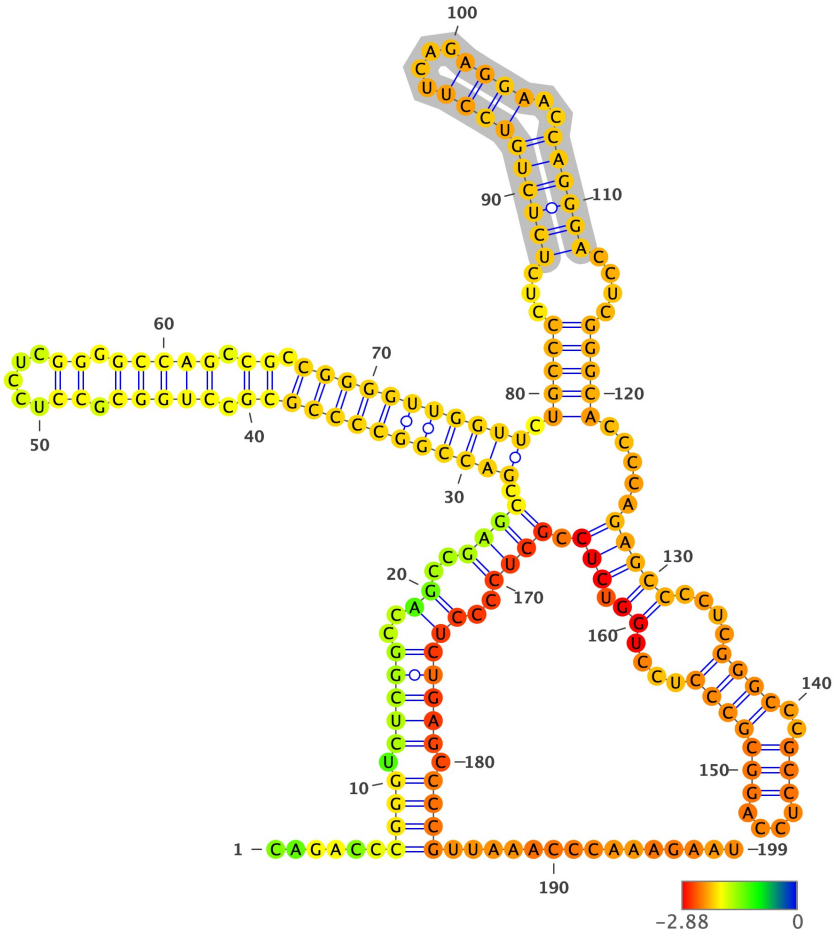
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 107 from nt 25110 to 25135 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-((((((.(........)...)))))))-3'
Motif MFE = -8.8; z-score = -2.13; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 25024 to 25222 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.26; ED = 36.45
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

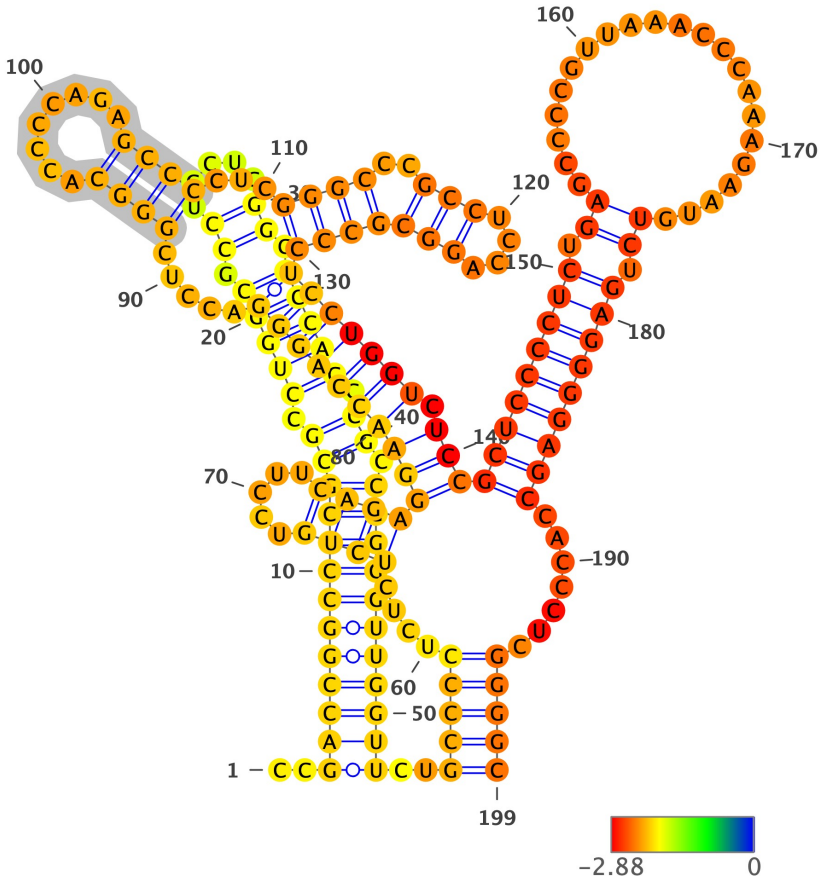
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 108 from nt 25140 to 25155 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-((((........))))-3'
Motif MFE = -6.0; z-score = -1.86; 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 25049 to 25247 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -4.09; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

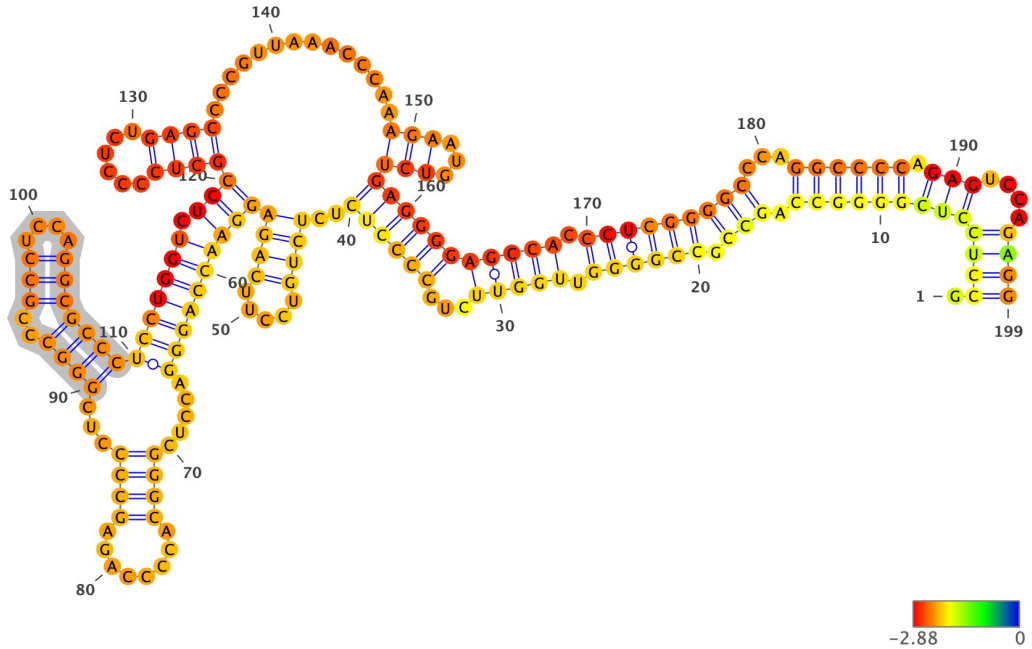
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 109 from nt 25159 to 25178 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..(((....)))))))-3'
Motif MFE = -9.3; z-score = -1.12; 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 25070 to 25268 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........))))...(((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -3.0; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

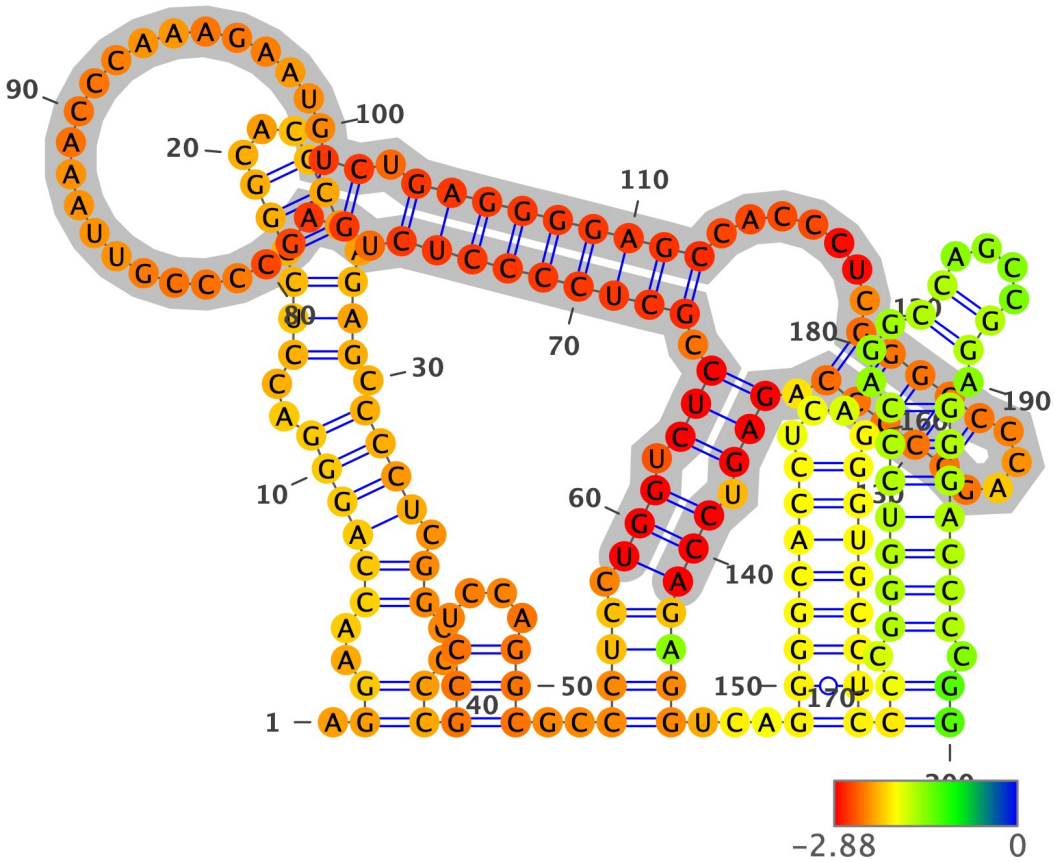
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 199--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 110 from nt 25182 to 25264 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-(((.(((.(((((((((.((.....................)).)))))))))).....(((((....))))).))).)))-3'
Motif MFE = -35.0; z-score = -3.11; ED = 6.59
```



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 25124 to 25323 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.25; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

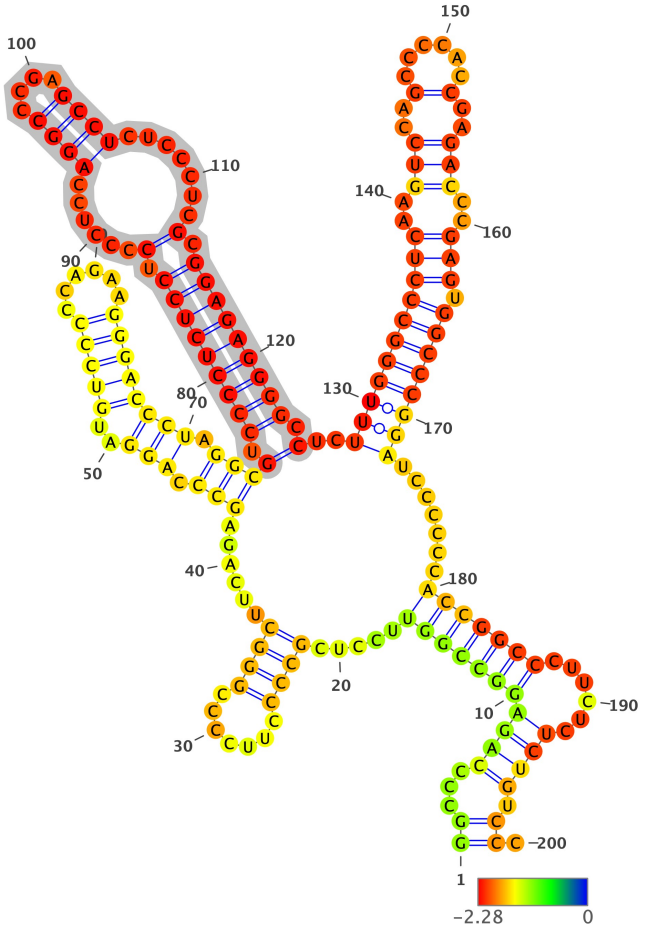
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 200--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 111 from nt 25408 to 25458 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.12; 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 25334 to 25533 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.79; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

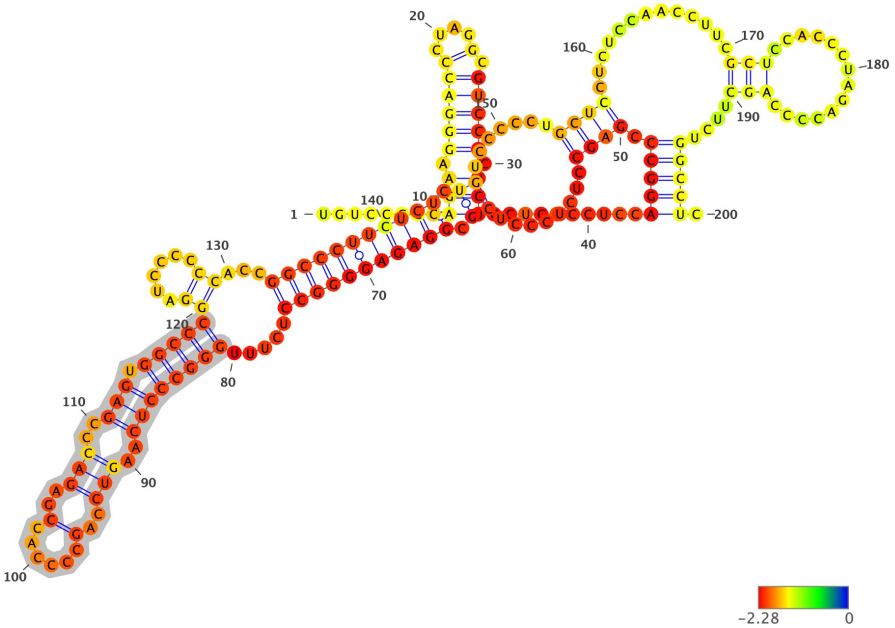
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 200--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 112 from nt 25464 to 25502 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -2.18; ED = 1.4
```



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

Extracted structure model with flanking nucleotides 25384 to 25583 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.42; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

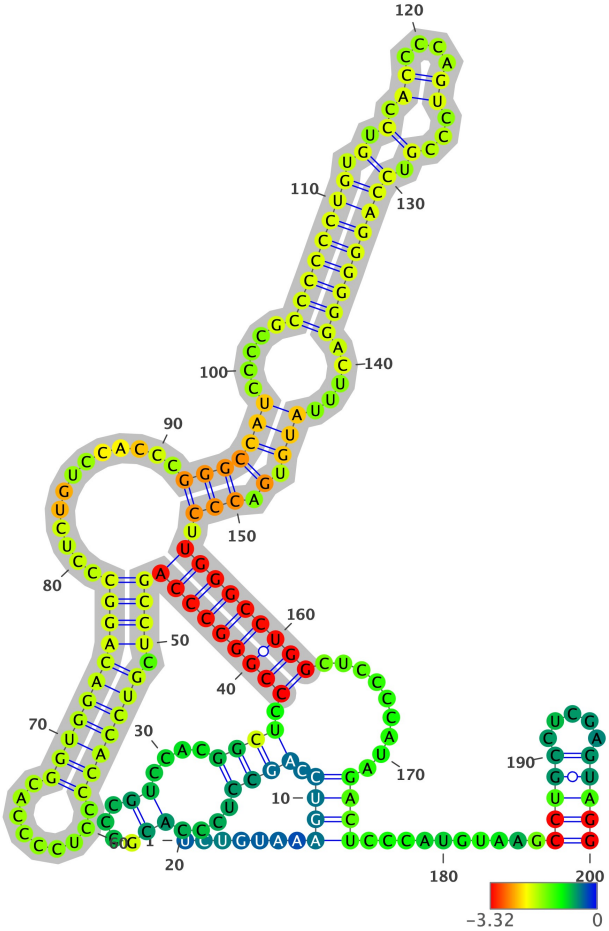
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 200--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 113 from nt 25869 to 25993 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....((((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -4.09; ED = 23.92
```



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 25832 to 26031 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).))))))))).....))).).))).))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.64; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.5, 24829-25980(+)

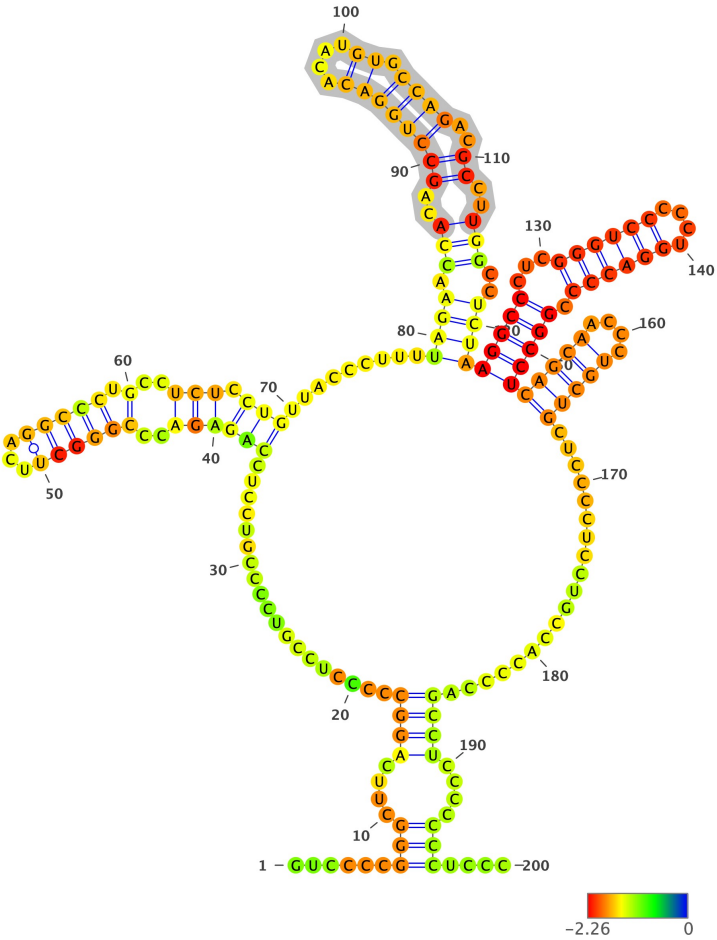
Attributes: ['ID=gene-HHV4_BWRF1.5', 'Dbxref=GeneID:3783737', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'start_range=.,24829']

16-- nt 1 to 149--CDS, cds-YP_401640.1, 24829-25980(+)

Attributes: ['ID=cds-YP_401640.1', 'Parent=gene-HHV4_BWRF1.5', 'Dbxref=UniProtKB/TrEMBL:Q8AZK3,Genbank:YP_401640.1,GeneID:3783737', 'Name=YP_401640.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.5', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401640.1', 'start_range=.,24829']

NC_007605.1 (forward strand): Structure number 114 from nt 27356 to 27384 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..((.................))..)-3'
Motif MFE = -5.8; z-score = -0.73; ED = 3.21
```



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 27271 to 27470 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))................))))....)))....-3'
MFE = -58.0; z-score = -2.44; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

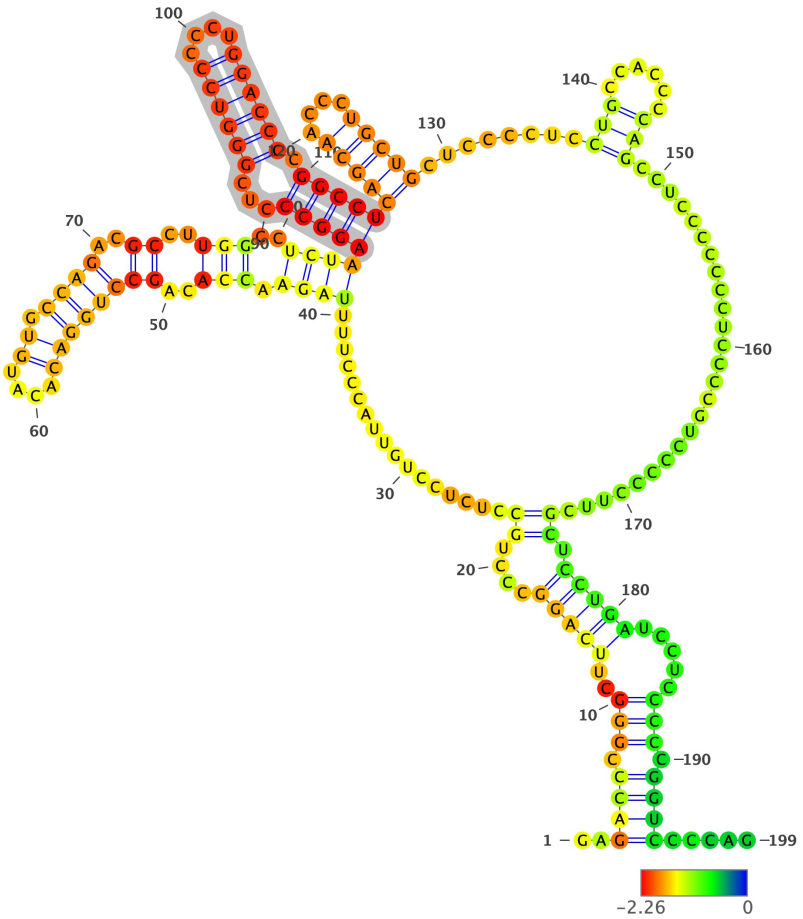
Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 115 from nt 27393 to 27422 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -3.77; 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 27309 to 27507 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..))))..))))((((((...(((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....))).)))).....-3'
MFE = -53.6; z-score = -2.25; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-14, 24289-27360(+)

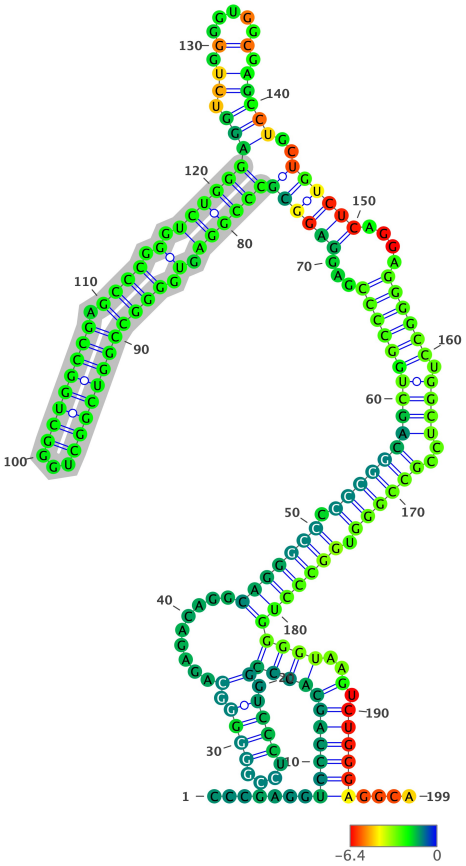
Attributes: ['ID=id-HHV4_EBNA-LP-14', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 116 from nt 27790 to 27835 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -4.09; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 27714 to 27912 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).).........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.72; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

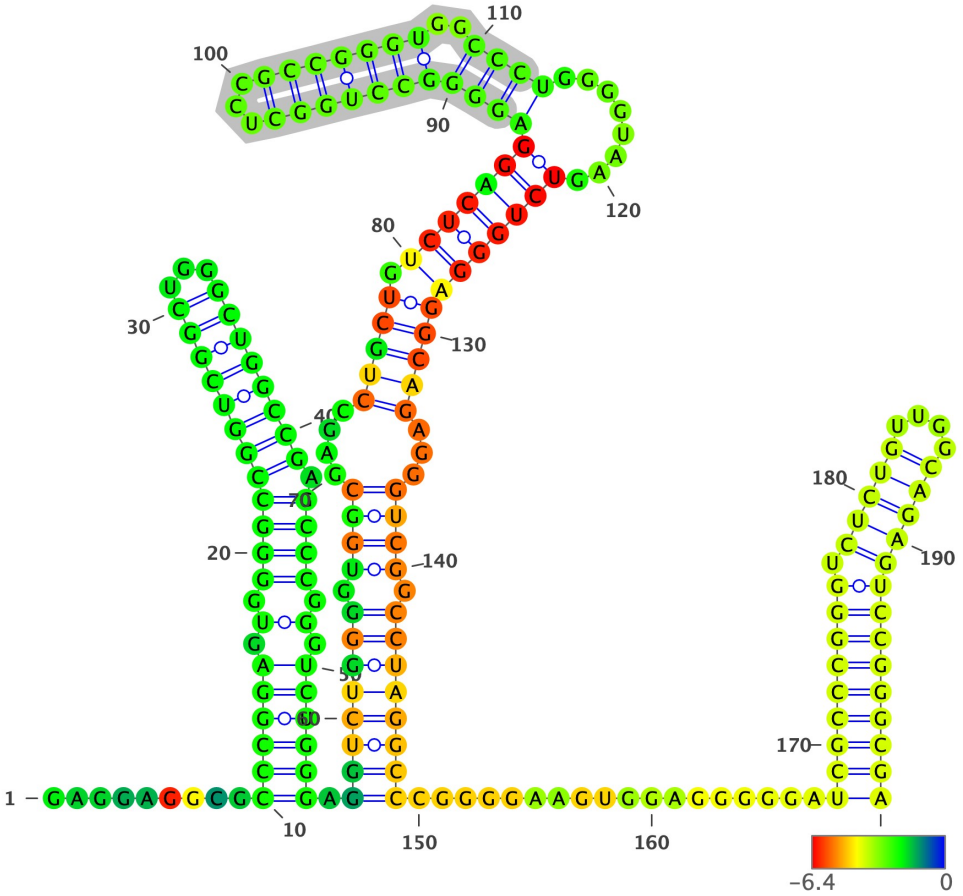
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 188 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 117 from nt 27868 to 27892 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.92; 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 27781 to 27980 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).((((((((.((((....(((((.((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.43; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

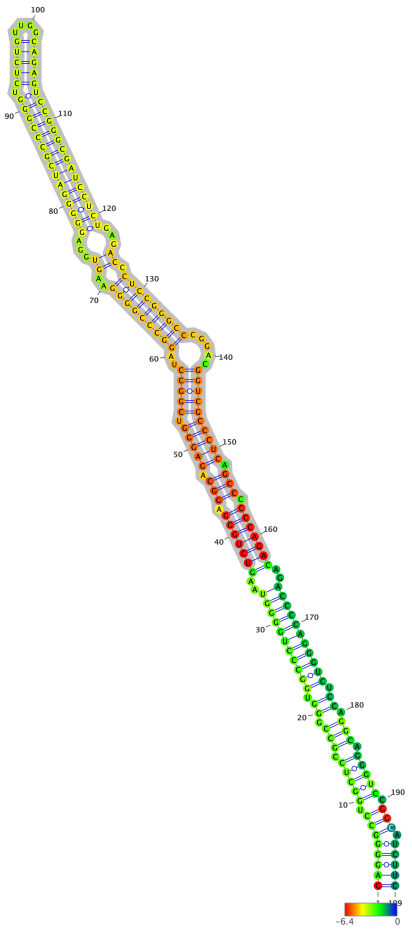
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 121 to 200--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 118 from nt 27902 to 28027 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((.(((((....)))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.23; ED = 3.47
```



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 27866 to 28064 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.(((.((.(((((((((((..(((((((.(((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).))))))))).....))))))))).))).))))))..))))))))))).)).))).))))).))).))))-3'
MFE = -149.6; z-score = -7.08; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

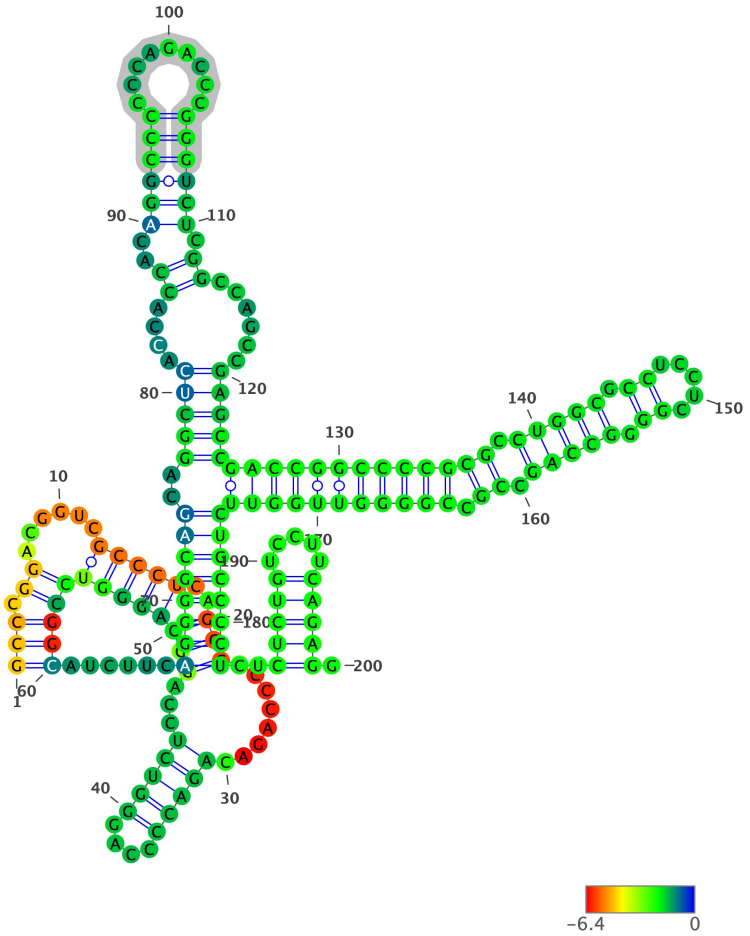
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 36 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 119 from nt 28091 to 28105 (nt 93 to 107)

```
5'-CCCCCCAGACCCGGG-3'
5'-(((.........)))-3'
Motif MFE = -3.0; z-score = -0.87; ED = 3.45
```



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

Extracted structure model with flanking nucleotides 27999 to 28198 (motif highlighted in silver):

```
5'-GCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUC
GGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-(((.((......((((((..((((........(((((....)))))...)))))))))))))).....(((((((..((((((....((..((((((.........)))))).
))......)))))((((((((((((.(((((.(.....)).)))))).)).)))))))))))))))..(((((.....))))).-3'
MFE = -93.8; z-score = -1.23; ED = 24.16
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

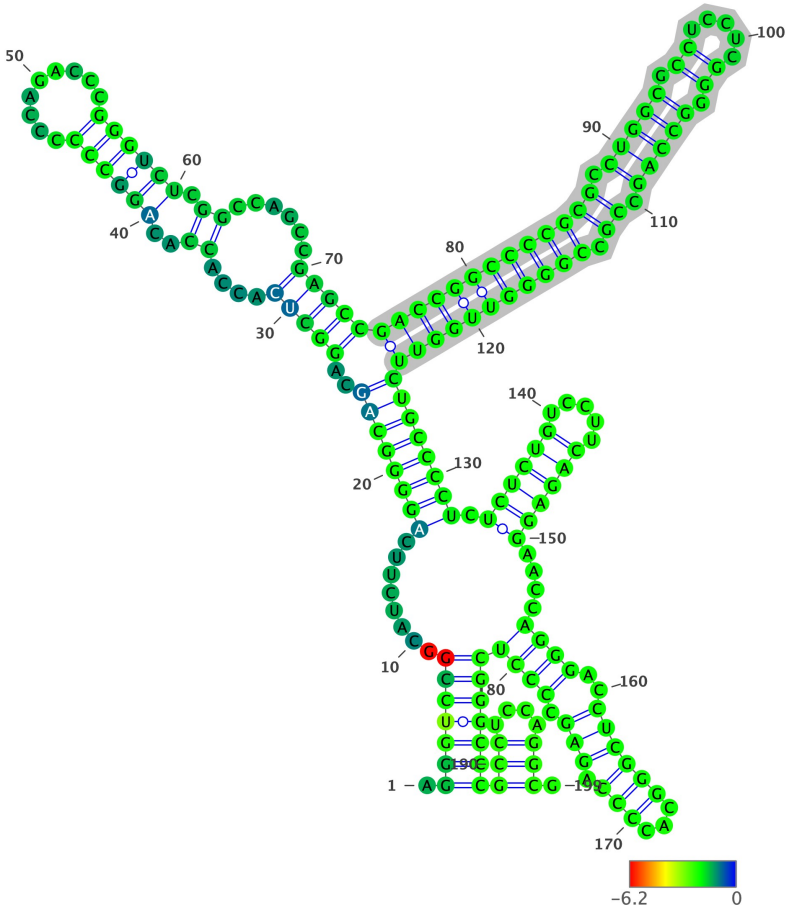
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 200--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 120 from nt 28123 to 28172 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.87; ED = 2.52
```



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 28049 to 28247 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -3.32; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

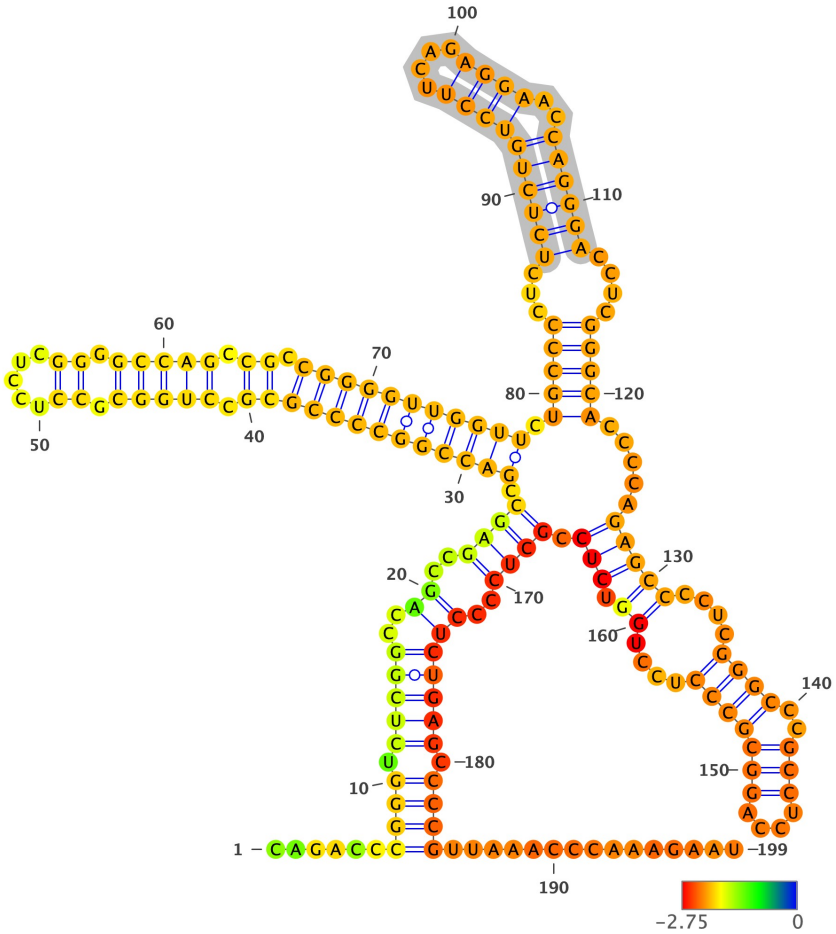
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 121 from nt 28182 to 28207 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-(((((((.......))..)))))-3'
Motif MFE = -8.8; z-score = -2.66; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 28096 to 28294 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.71; ED = 36.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

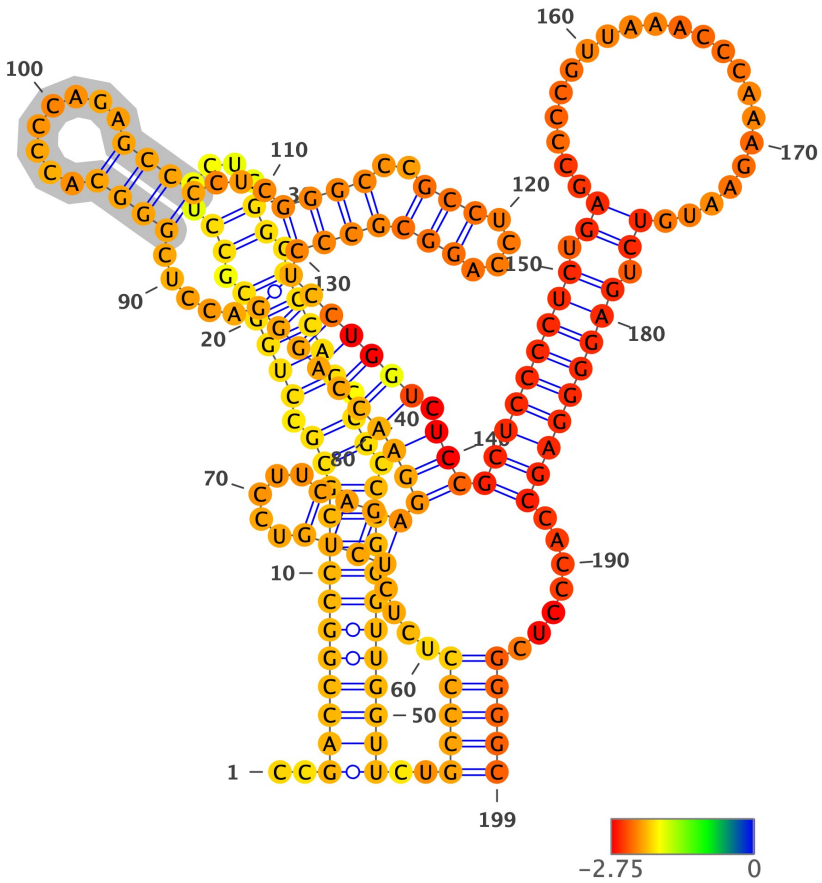
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 122 from nt 28212 to 28227 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-((((........))))-3'
Motif MFE = -6.0; z-score = -2.43; 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 28121 to 28319 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -3.34; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

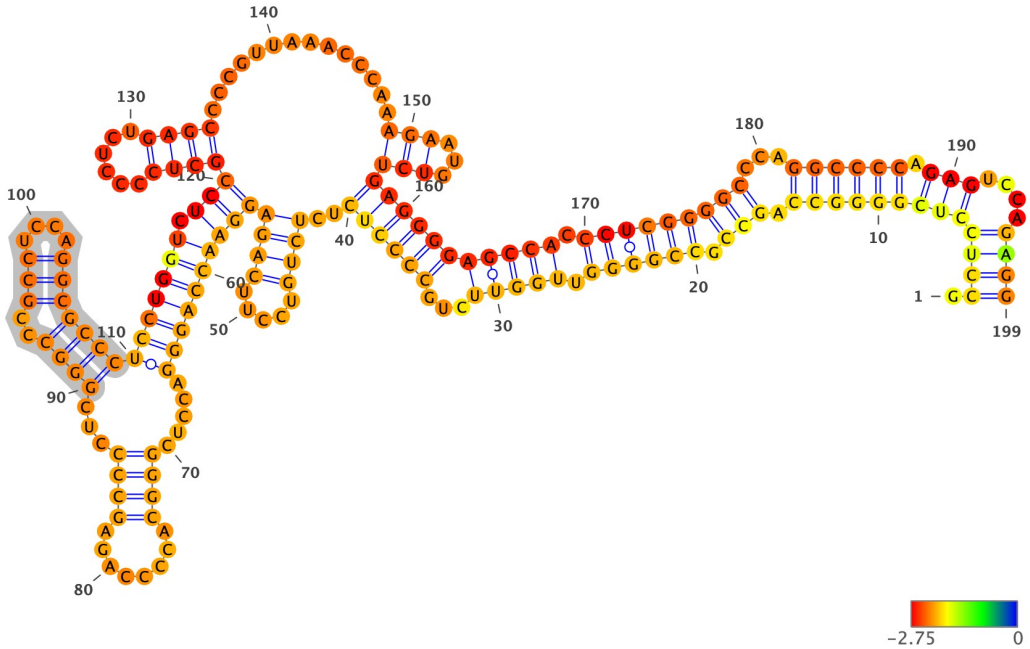
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 123 from nt 28231 to 28250 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..(((....)))))))-3'
Motif MFE = -9.3; z-score = -1.21; 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 28142 to 28340 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........)))).....((((..(((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.6; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

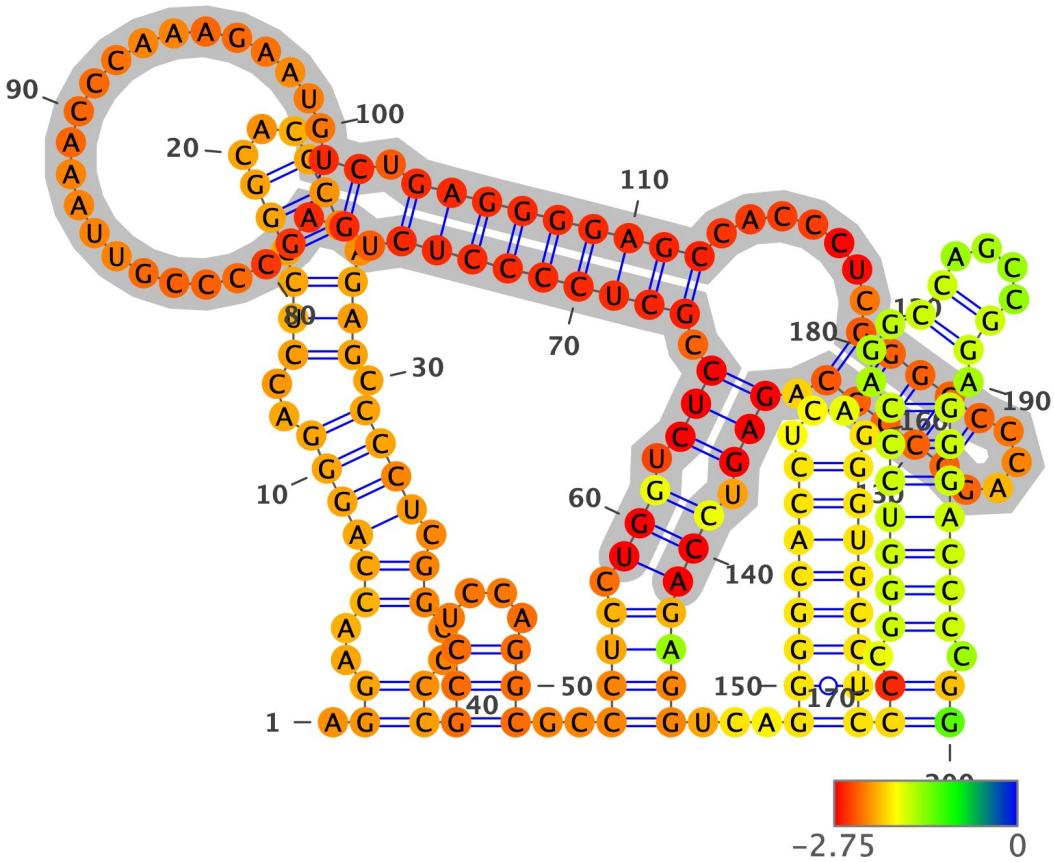
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 199--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 124 from nt 28254 to 28336 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.06; ED = 6.59
```



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 28196 to 28395 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.56; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

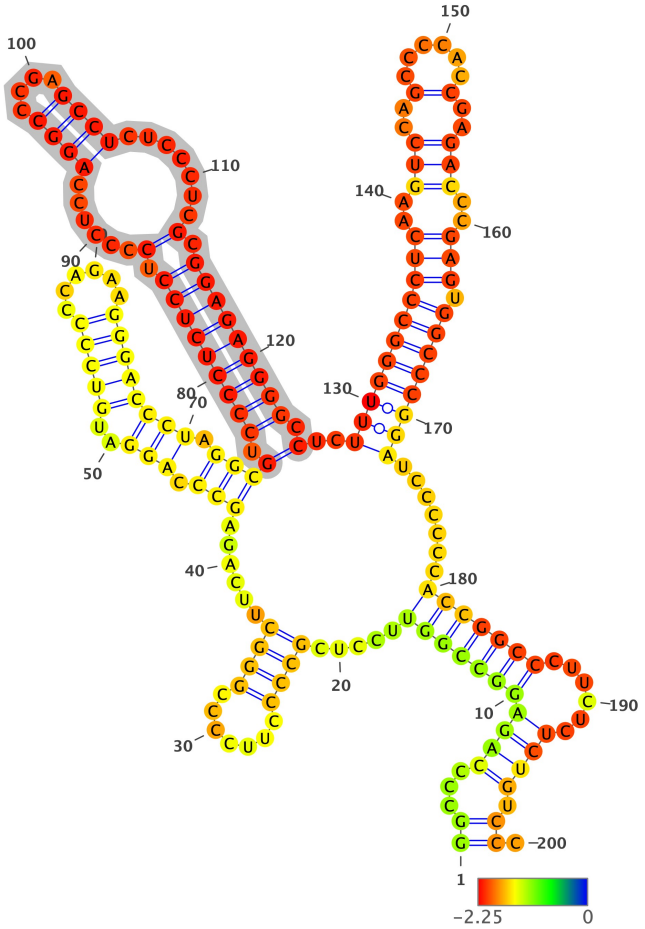
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 200--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 125 from nt 28480 to 28530 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.42; 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 28406 to 28605 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.79; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

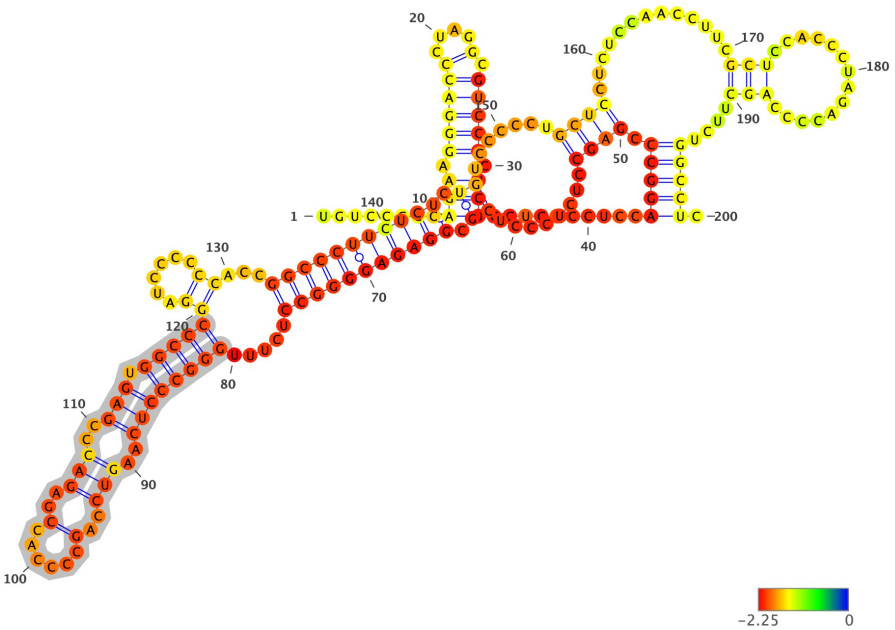
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 200--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 126 from nt 28536 to 28574 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -1.98; 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 28456 to 28655 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............))).....)))))).-3'
MFE = -60.2; z-score = -2.4; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

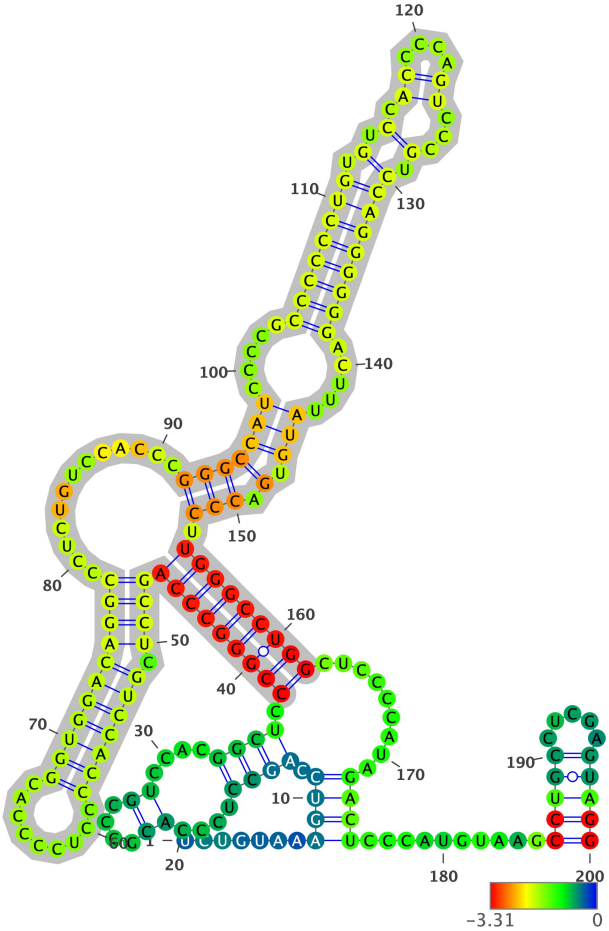
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 200--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 127 from nt 28941 to 29065 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....(((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.4; ED = 23.92
```



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 28904 to 29103 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.(((....)))...).))))))))).....)))).).))).)))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.54; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.6, 27901-29052(+)

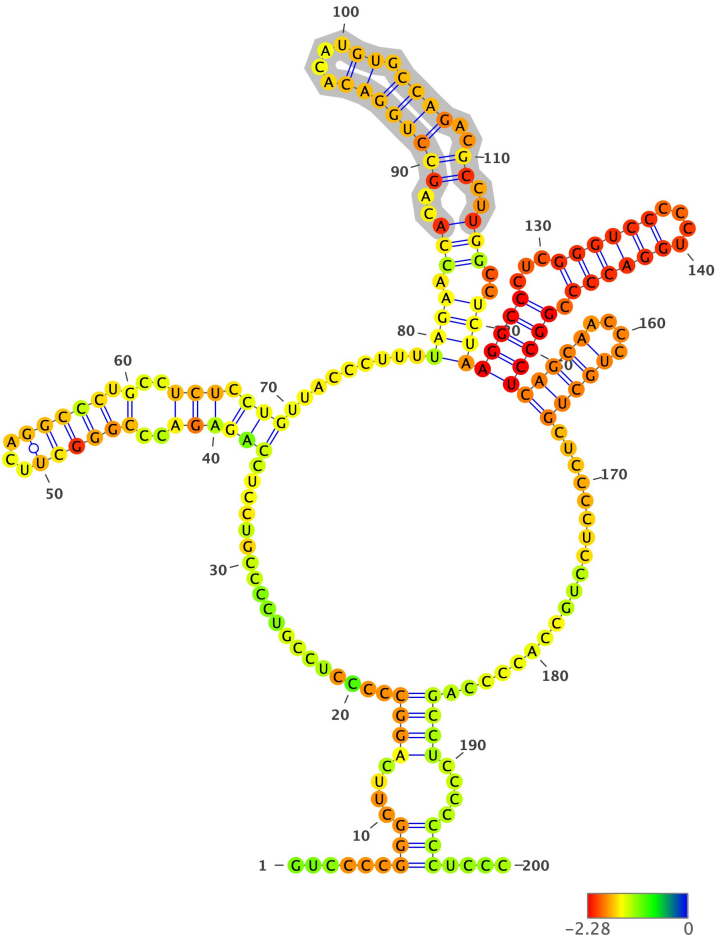
Attributes: ['ID=gene-HHV4_BWRF1.6', 'Dbxref=GeneID:3783738', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'start_range=.,27901']

16-- nt 1 to 149--CDS, cds-YP_401641.1, 27901-29052(+)

Attributes: ['ID=cds-YP_401641.1', 'Parent=gene-HHV4_BWRF1.6', 'Dbxref=UniProtKB/TrEMBL:Q8AZK2,Genbank:YP_401641.1,GeneID:3783738', 'Name=YP_401641.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.6', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401641.1', 'start_range=.,27901']

NC_007605.1 (forward strand): Structure number 128 from nt 30428 to 30456 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..(.....................)..)-3'
Motif MFE = -5.8; z-score = -0.64; ED = 3.21
```



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 30343 to 30542 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))..................))))....)))....-3'
MFE = -58.0; z-score = -2.32; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

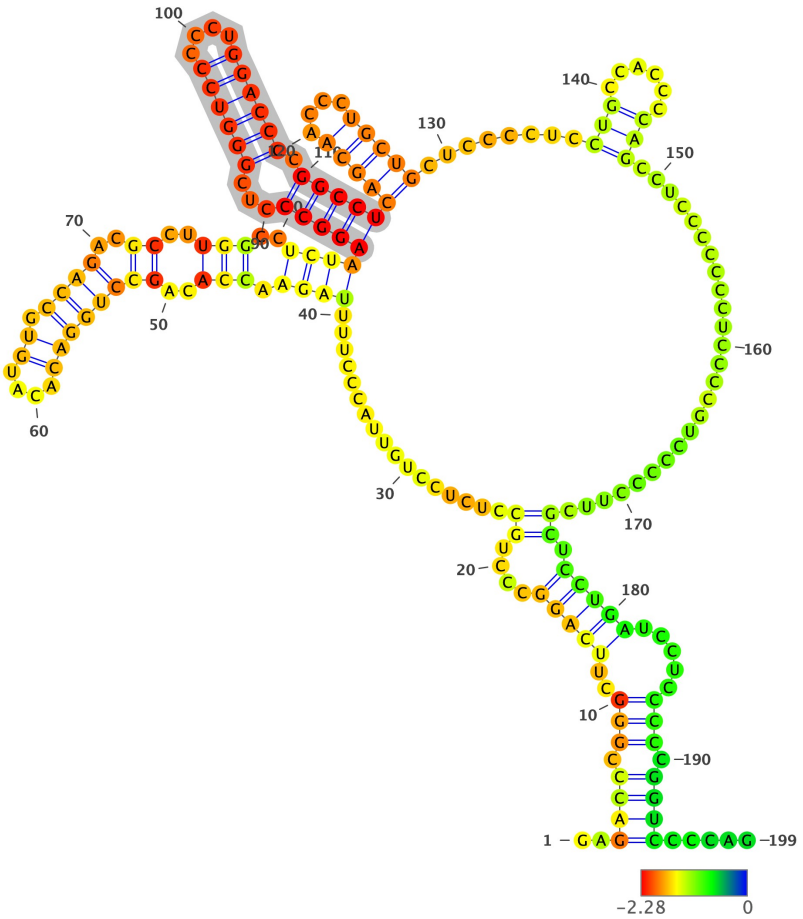
Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 129 from nt 30465 to 30494 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -4.0; 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 30381 to 30579 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..)))..)))))((((((...((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....)))).)))).....-3'
MFE = -53.6; z-score = -1.83; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-15, 27361-30432(+)

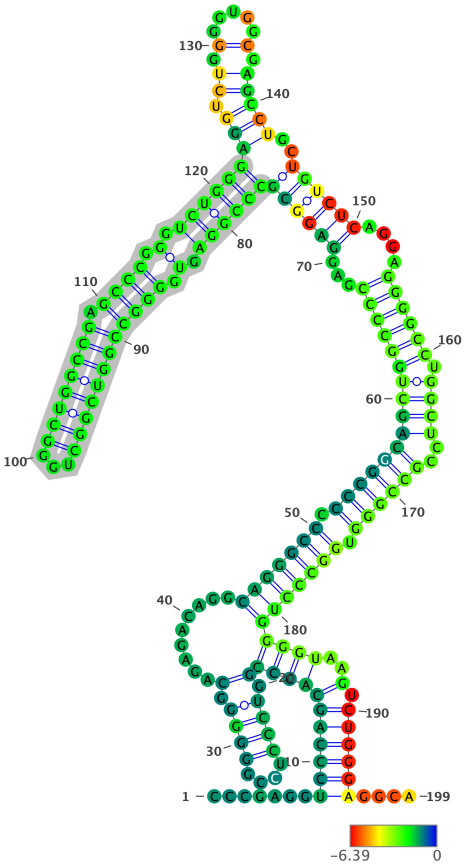
Attributes: ['ID=id-HHV4_EBNA-LP-15', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 130 from nt 30862 to 30907 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))).).)))))))-3'
Motif MFE = -35.3; z-score = -4.61; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 30786 to 30984 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).).........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.64; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

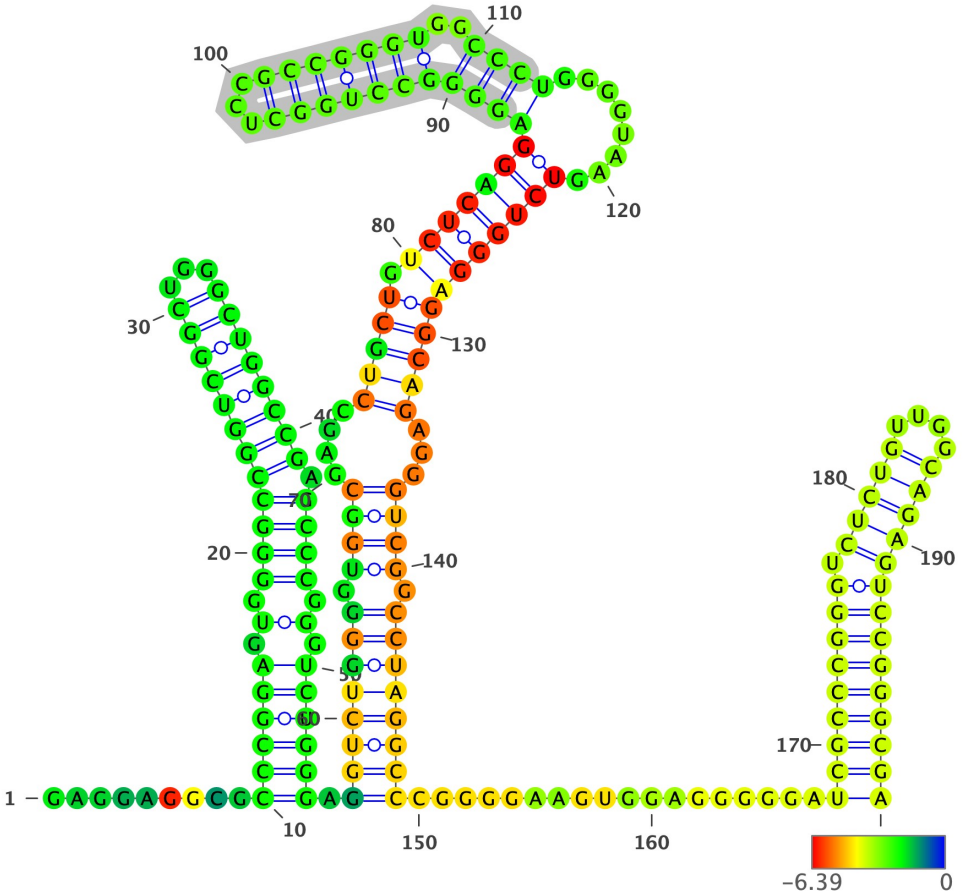
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 188 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 131 from nt 30940 to 30964 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.78; 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 30853 to 31052 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).(((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -3.14; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

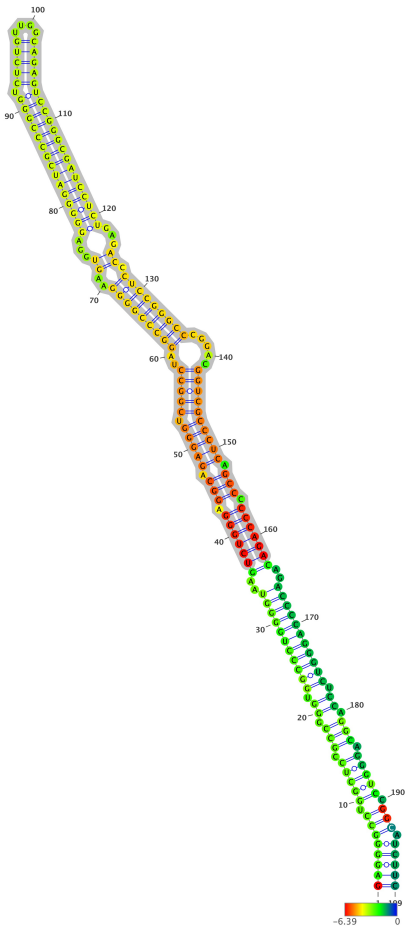
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 121 to 200--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 132 from nt 30974 to 31099 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((.(((((....)))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.37; ED = 3.47
```



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 30938 to 31136 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.((((.((.(((((((((((..(((((((.((((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
))))))))))...)).))))))))).....))))))))).))).))))))..))))))))))).))).))).))))).))).))))-3'
MFE = -149.6; z-score = -6.71; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

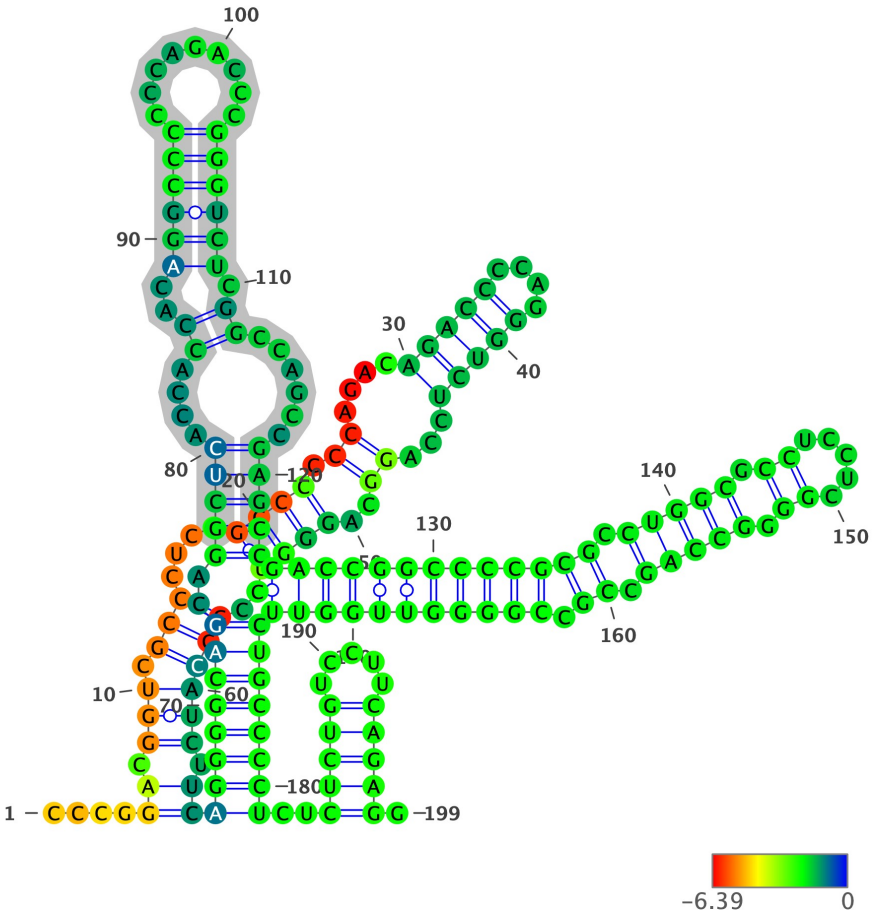
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 36 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 133 from nt 31148 to 31193 (nt 77 to 122)

```
5'-GCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGC-3'
5'-(..............(((.........)))...............)-3'
Motif MFE = -11.9; z-score = -0.14; ED = 11.49
```



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 31072 to 31270 (motif highlighted in silver):

```
5'-CCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCG
GCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-....((.(((.(((....((((.((....((((((....)))))...))..)))))..)))))).))(((((((..(((((....((..((((((.........)))))).)
).....)))))((((((((((((.(((((.((.....)).)))))).)).)))))))))))))))))..(((((.....)))))).-3'
MFE = -93.4; z-score = -1.34; ED = 25.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

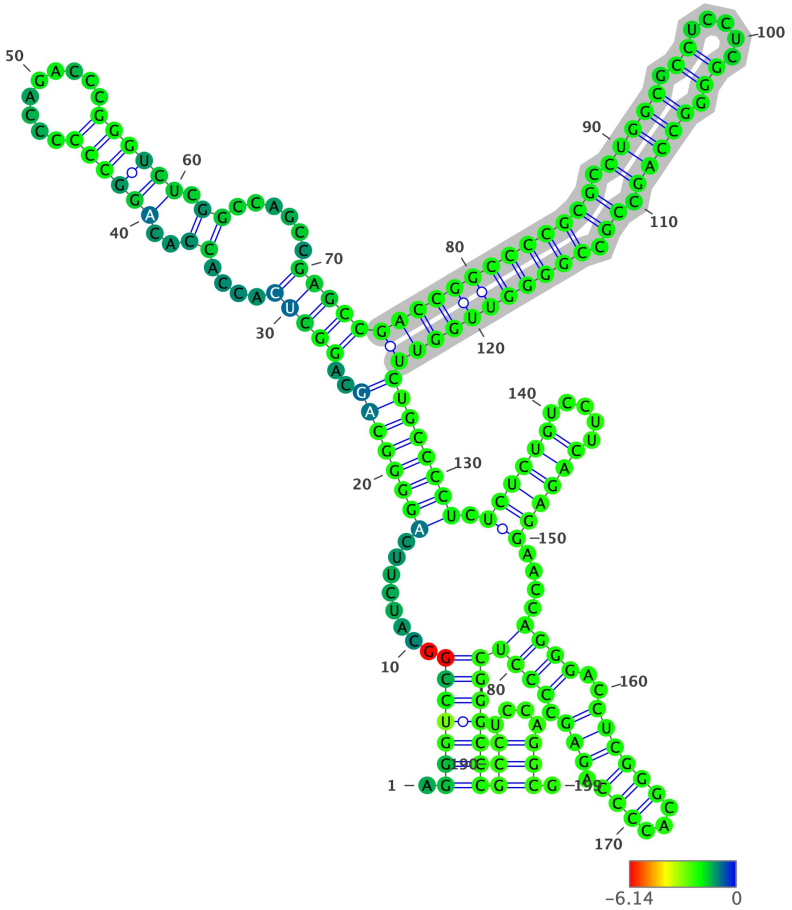
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 134 from nt 31195 to 31244 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.88; ED = 2.52
```



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 31121 to 31319 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).)))))))))))((....)).-3'
MFE = -101.9; z-score = -2.44; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

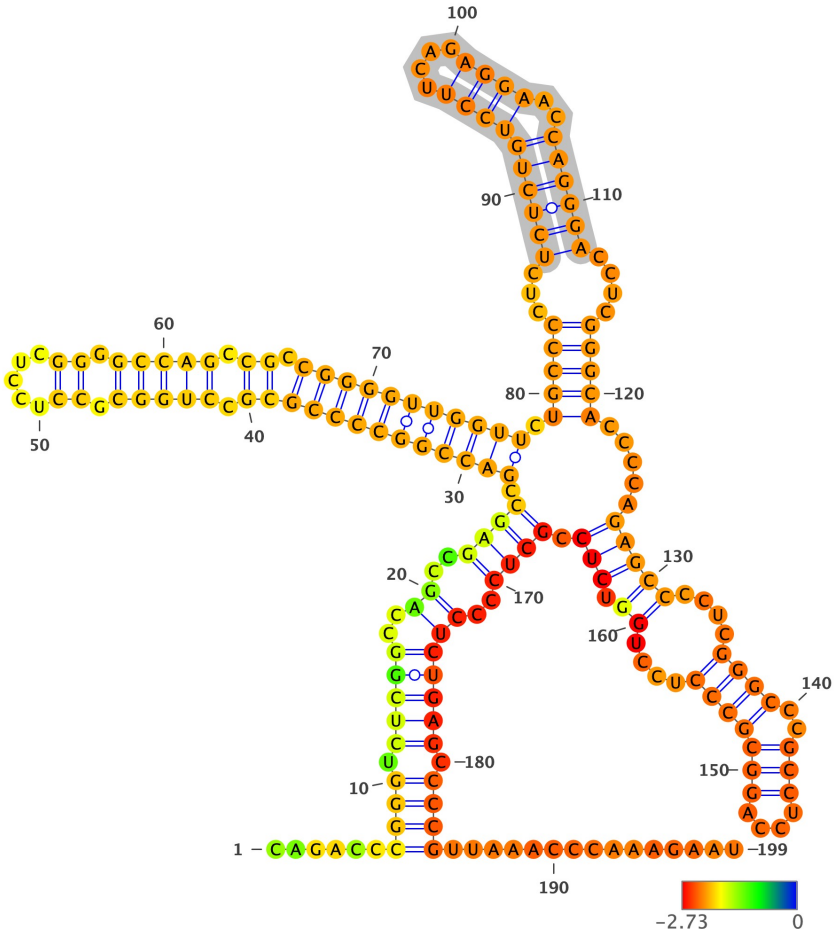
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 135 from nt 31254 to 31279 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-(((((((.......))..)))))-3'
Motif MFE = -8.8; z-score = -2.19; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 31168 to 31366 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((((.(((((.(.....)).)))))).)).))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.73; ED = 36.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

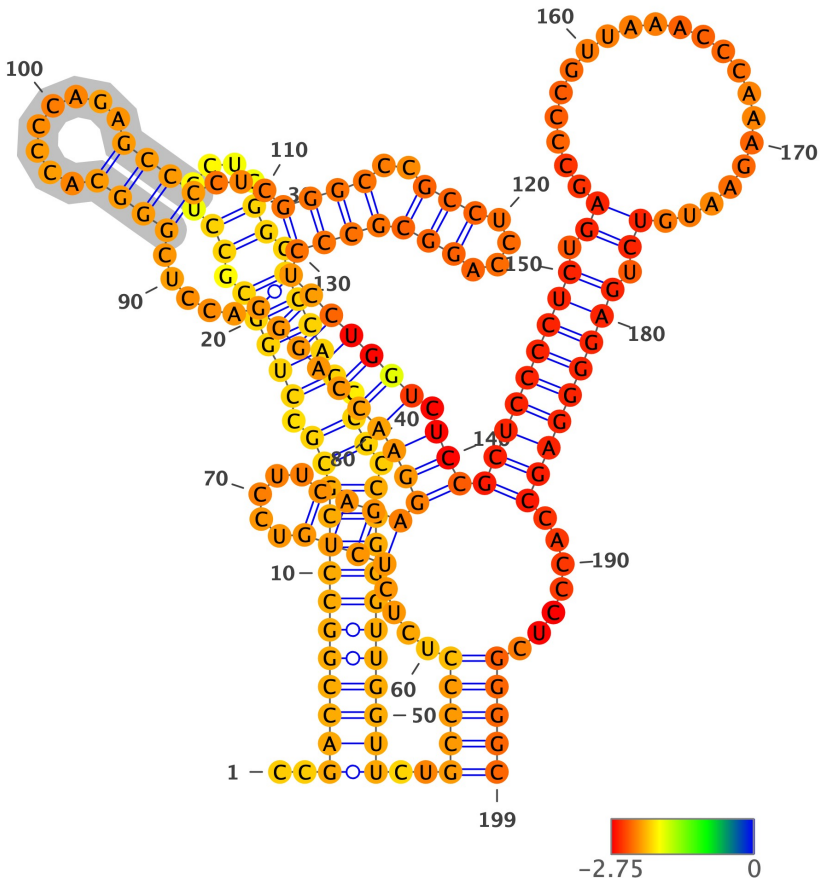
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 136 from nt 31284 to 31299 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-((((........))))-3'
Motif MFE = -6.0; z-score = -2.08; 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 31193 to 31391 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -3.04; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

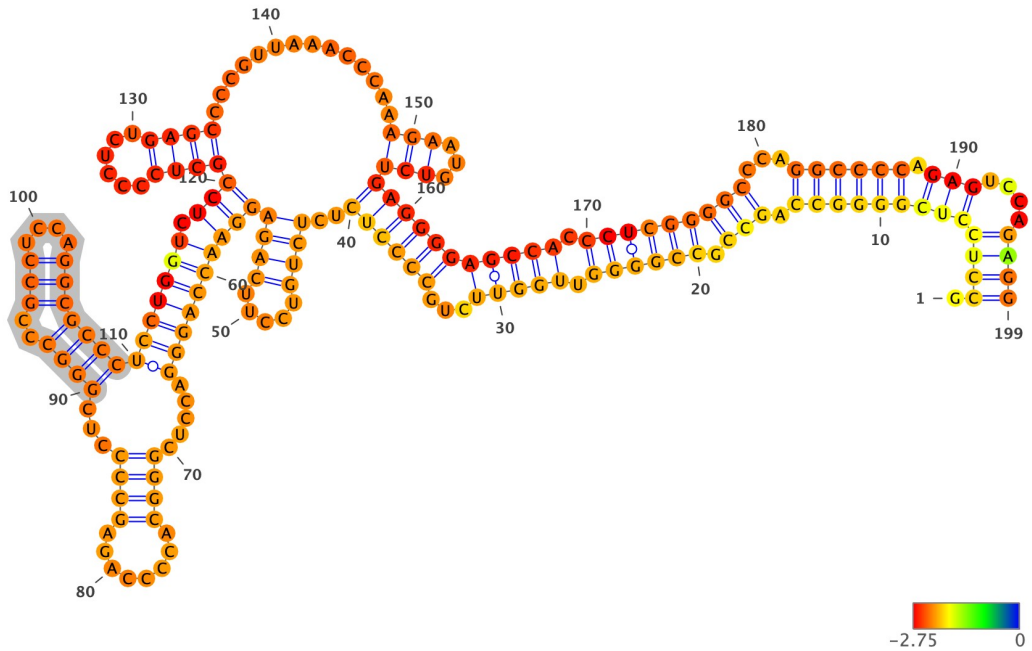
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 137 from nt 31303 to 31322 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..(((....)))))))-3'
Motif MFE = -9.3; z-score = -1.61; 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 31214 to 31412 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........)))).....((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.87; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

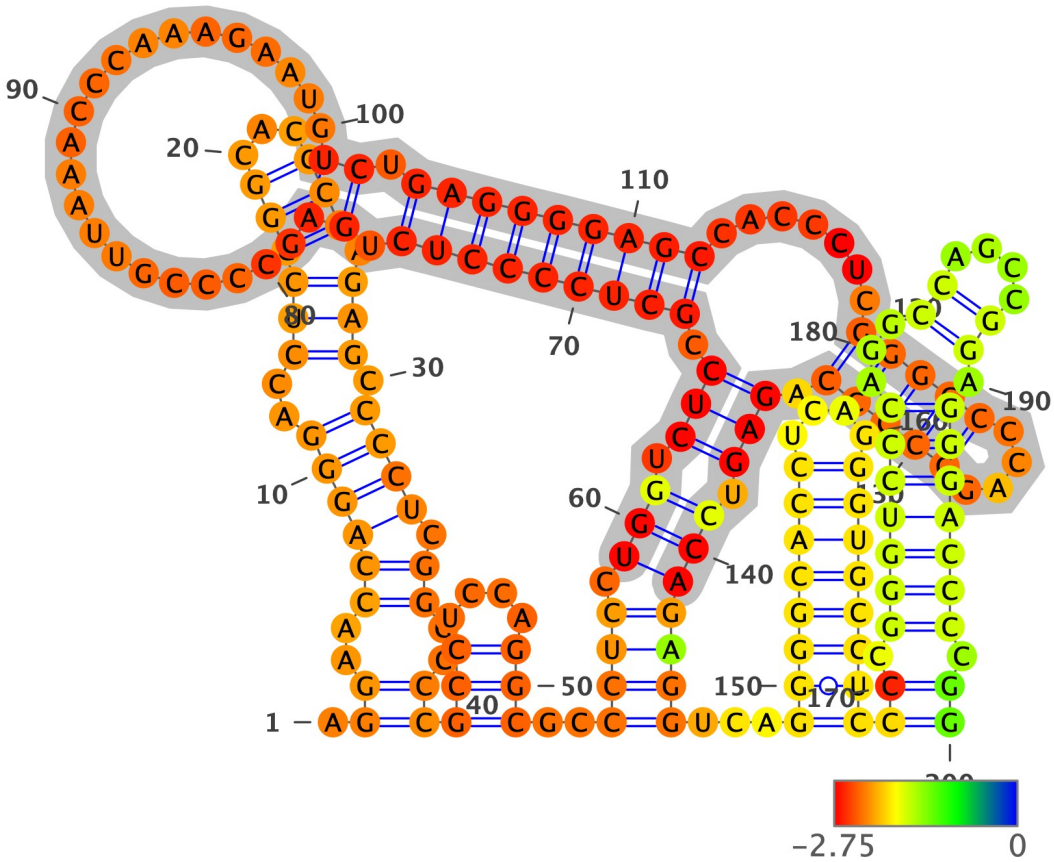
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 199--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 138 from nt 31326 to 31408 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.46; ED = 6.59
```



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 31268 to 31467 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.68; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

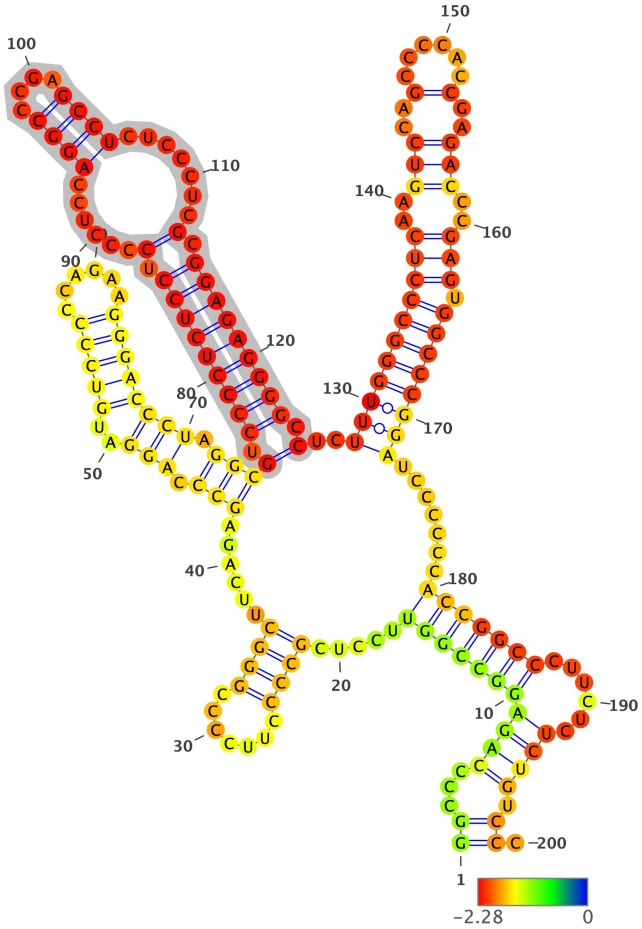
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 200--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 139 from nt 31552 to 31602 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.05; 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 31478 to 31677 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -3.0; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

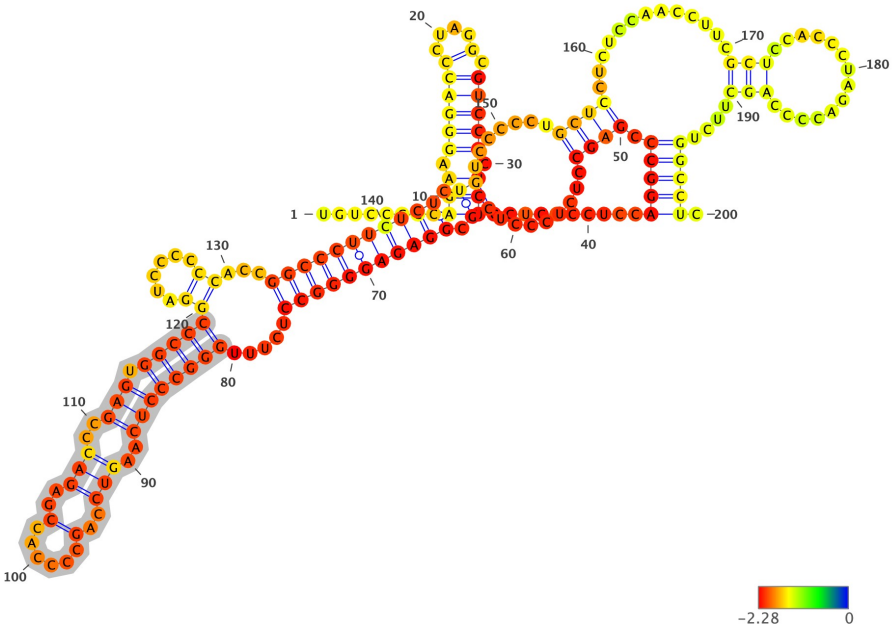
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 200--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 140 from nt 31608 to 31646 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-(((((......((..(......)..)).......)))))-3'
Motif MFE = -15.5; z-score = -1.77; 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 31528 to 31727 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.34; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

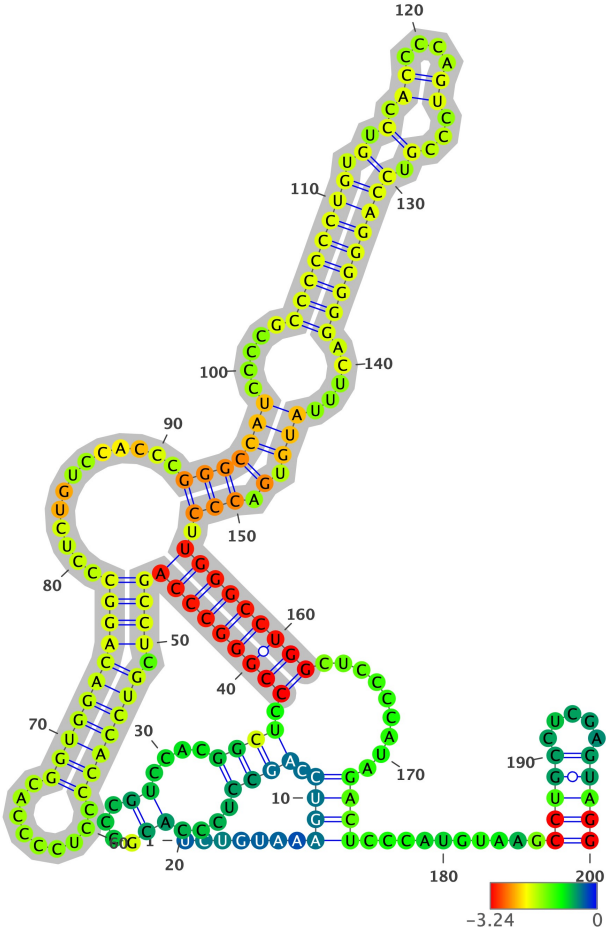
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 200--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 141 from nt 32013 to 32137 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....(.(((((((.(.(.((....)).)).).)))))))).).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -4.01; ED = 23.92
```



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 31976 to 32175 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).).))))))))).....)))).).))).))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.75; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.7, 30973-32124(+)

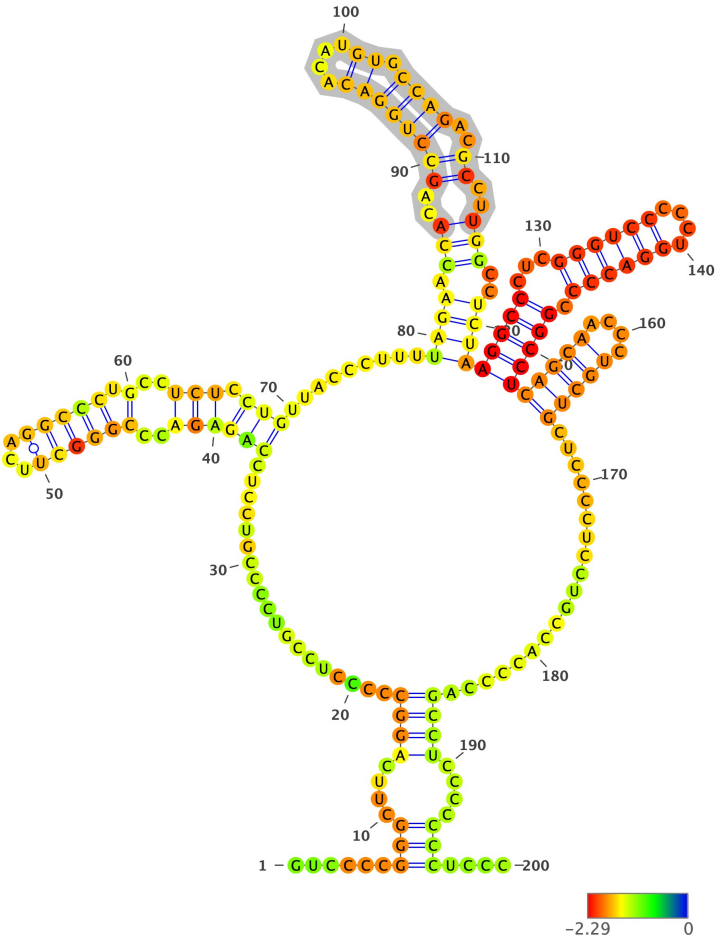
Attributes: ['ID=gene-HHV4_BWRF1.7', 'Dbxref=GeneID:3783739', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'start_range=.,30973']

16-- nt 1 to 149--CDS, cds-YP_401642.1, 30973-32124(+)

Attributes: ['ID=cds-YP_401642.1', 'Parent=gene-HHV4_BWRF1.7', 'Dbxref=UniProtKB/TrEMBL:Q8AZK1,Genbank:YP_401642.1,GeneID:3783739', 'Name=YP_401642.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.7', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401642.1', 'start_range=.,30973']

NC_007605.1 (forward strand): Structure number 142 from nt 33500 to 33528 (nt 86 to 114)

```
5'-ACAGCCUGGACACAUGUGCCAGACGCCUU-3'
5'-(..(.....................)..)-3'
Motif MFE = -5.8; z-score = -0.63; ED = 3.21
```



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 33415 to 33614 (motif highlighted in silver):

```
5'-GUCCCCGGGCUUCAGGCCCCCUCCGUCCCCGUCCUCCAGAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGC
CUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGGCCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCC-3
5'-......(((....((((.................(((((..((((((...)))))).)..))).))).........((((.(((..(((((((....)).)))))..))
..)))..)))))((((...((((((....)))))).)))))((((....)))))..................))))....)))....-3'
MFE = -58.0; z-score = -2.55; ED = 29.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 90--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

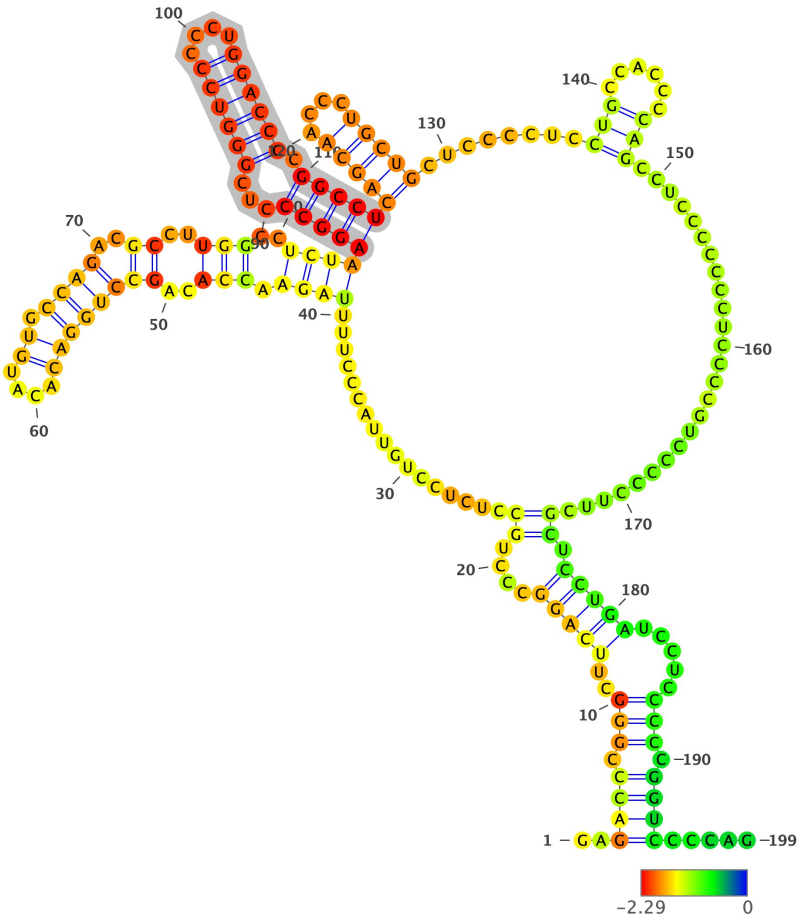
Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 91 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 143 from nt 33537 to 33566 (nt 85 to 114)

```
5'-AGGCCCUCGGGUCCCCCUGGACCCCGGCCU-3'
5'-(((((...(((((((....)))))))..)))))-3'
Motif MFE = -19.0; z-score = -3.72; 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 33453 to 33651 (motif highlighted in silver):

```
5'-GAGACCCGGGCUUCAGGCCCUGCCUCUCCUGUUACCCUUUUAGAACCACAGCCUGGACACAUGUGCCAGACGCCUUGGCCUCUAAGGCCCUCGGGUCCCCCUGGACCCCGG
CCUCAGCAACCCUGCUGCUCCCCUCCUGCCACCCCAGCCUCCCCCCCUCCCCGUCCCCCUUCGCUCCUGAUCCUCCCCCGGUCCCCAG-3
5'-..(((((.((((..((((((....(((................((((.((((..(((((((((....)).)))))..))..))))..))))((((((...(((((((....)))))))..))
)))((((((....)))))).......(((......))).......................)).)))))).....)))).)))).....-3'
MFE = -53.6; z-score = -1.75; ED = 31.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 52--direct_repeat, id-HHV4_EBNA-LP-16, 30433-33504(+)

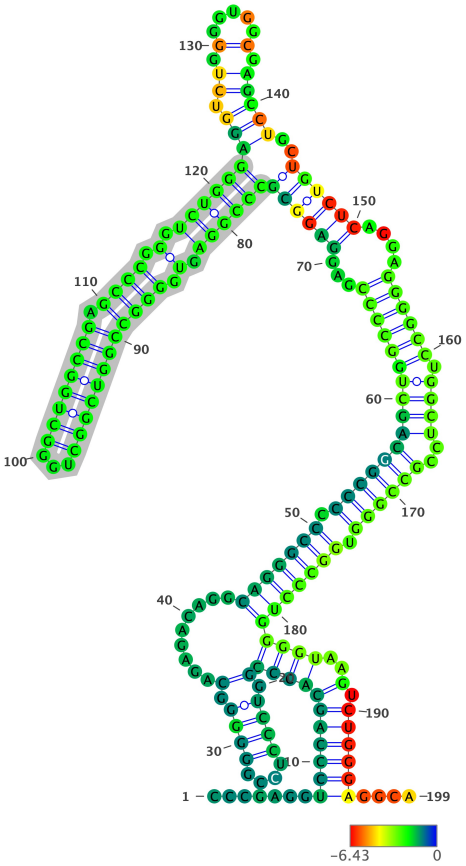
Attributes: ['ID=id-HHV4_EBNA-LP-16', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 53 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 144 from nt 33934 to 33979 (nt 77 to 122)

```
5'-CCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGG-3'
5'-((((((.(.(((((((((((...)))))))))).)))))).).)))))))-3'
Motif MFE = -35.3; z-score = -3.9; ED = 0.17
```



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

Extracted structure model with flanking nucleotides 33858 to 34056 (motif highlighted in silver):

```
5'-CCCGAGGUCCCAGCACCCGGUCCCUCCGGGGGGCAGAGACAGGCAGGGCCCCCCGGCAGCUGGCCCCGAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGC
CCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCA-3
5'-.......((((((((((((.((((....)))).)........(((((((.(((((((((((((((((...((((((((((((.(.((((((((((...)))))))))).))
)).).)))))))((.((.(.....).)))))..)))))).....)))))).)))).)).)))))).))))))))))))..).)))))))....-3'
MFE = -119.3; z-score = -1.9; ED = 55.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 188 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

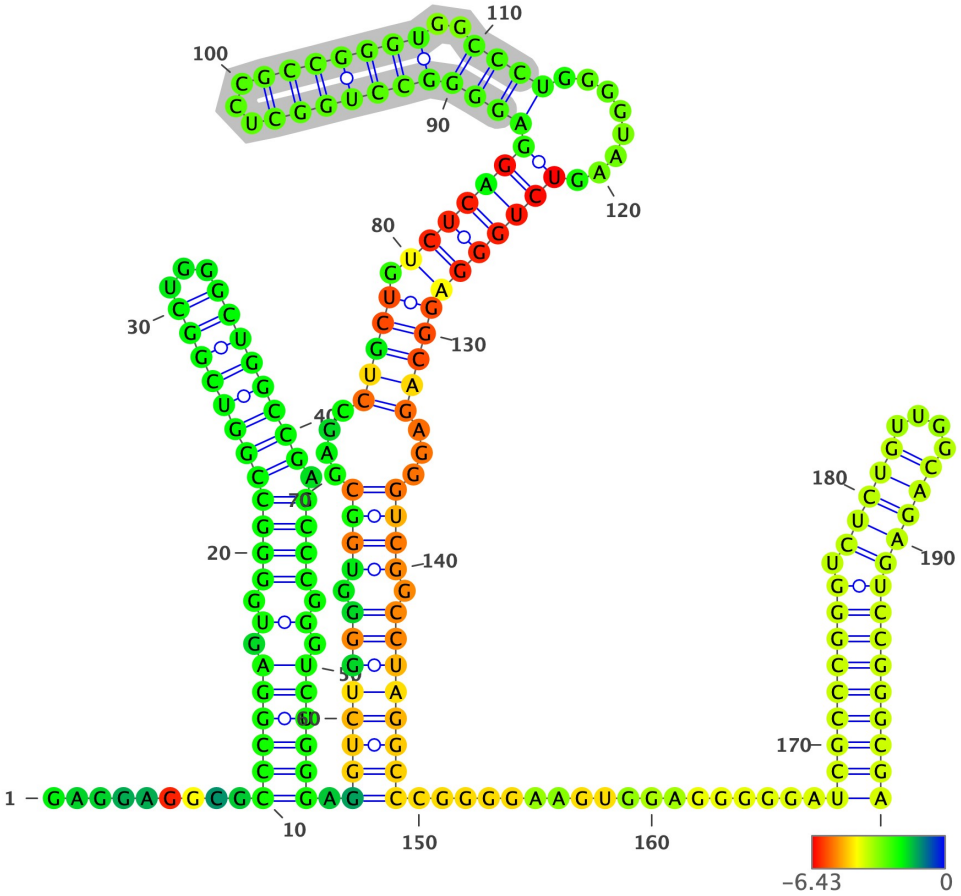
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 188 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 145 from nt 34012 to 34036 (nt 88 to 112)

```
5'-GGGGCCUGGCUCCGCCGGGUGGCCC-3'
5'-(((.(((((((...)))))))...)))-3'
Motif MFE = -13.9; z-score = -0.85; 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 33925 to 34124 (motif highlighted in silver):

```
5'-GAGGAGGCGCCCGGAGUGGGGCCGGUCGGCUGGGCUGGCCGAGCCCGGGUCUGGGAGGUCUGGGGUGGCGAGCCUGCUGUCUCAGGAGGGGCCUGGCUCCGCCGGGUGGCC
CUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGA-3
5'-.........((((((.(.(((((((((((...)))))))).)))).).)))))).((((((((.((((....(((((.(((((((((((((((((...)))))))..))
)).......)))))))))))...)))).)))))))).................(((((((((.((((....)))))))))))))-3'
MFE = -111.7; z-score = -2.95; ED = 36.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 121 to 200--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

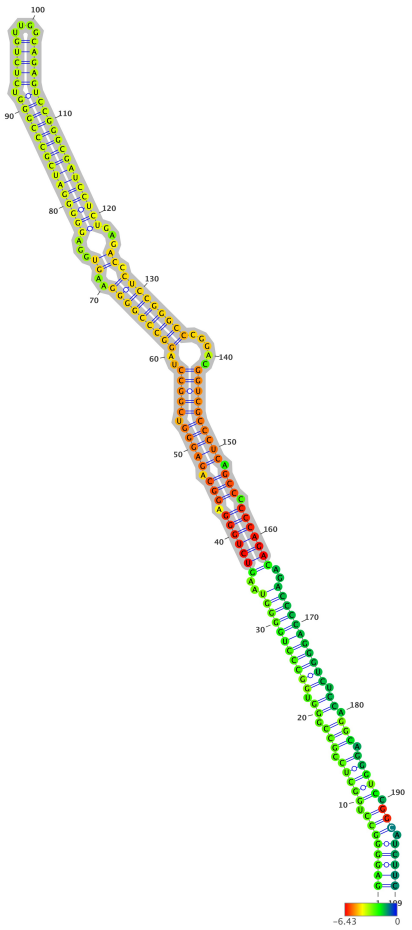
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 121 to 200--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 146 from nt 34046 to 34171 (nt 37 to 162)

```
5'-UCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGGGCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGC
CCUCAGCCCCCCAGA-3'
5'-((((((.(((.(((((.(((((..((((((((((..((...((((((((((((((((.(((((....)))))))))))))))))))))...)).)))))))))).....))))))
))))).))).)))))))-3'
Motif MFE = -93.2; z-score = -6.32; ED = 3.47
```



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 34010 to 34208 (motif highlighted in silver):

```
5'-GAGGGGCCUGGCUCCGCCGGGUGGCCCUGGGGUAAGUCUGGGAGGCAGAGGGUCGGCCUAGGCCCGGGGAAGUGGAGGGGGAUCGCCCGGGUCUCUGUUGGCAGAGUCCGG
GCGAUCCUCUGAGACCCUCCGGGCCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUC-3
5'-(((((((.(((((.(((.((.(((((((((((..(((((((.(((.(((((.(((((..(((((((((..((...((((((((((((((.(((((....)))))))))
)))))))))...)).)))))))))).....))))))))).)))).)))))))..)))))))))))).)).))).))))).))).))))-3'
MFE = -149.6; z-score = -7.27; ED = 5.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 36 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

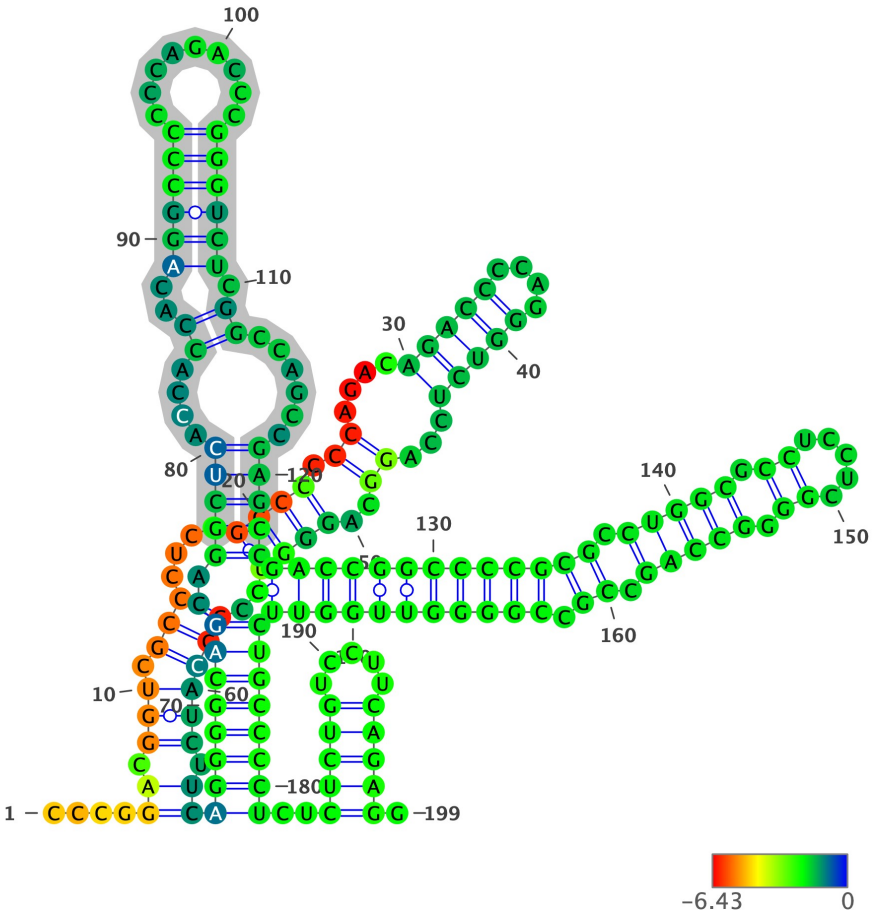
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 36 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 147 from nt 34220 to 34265 (nt 77 to 122)

```
5'-GCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGC-3'
5'-(..............(((.........)))...............)-3'
Motif MFE = -11.9; z-score = -0.1; ED = 11.49
```



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 34144 to 34342 (motif highlighted in silver):

```
5'-CCCGGACGGUCGCCCUCAGCCCCCCAGACAGACCCCAGGGUCUCCAGGCAGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCG
GCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGG-3
5'-....((.((((.((((....((((.((....((((((....)))))...))..)))))..)))))).))((((((((..((((((....((..((((((.........)))))).)
).....)))))((((((((((((.(((((.((.....)).)))))).)).)))))))))))))))))..(((((.....)))))).-3'
MFE = -93.4; z-score = -1.58; ED = 25.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

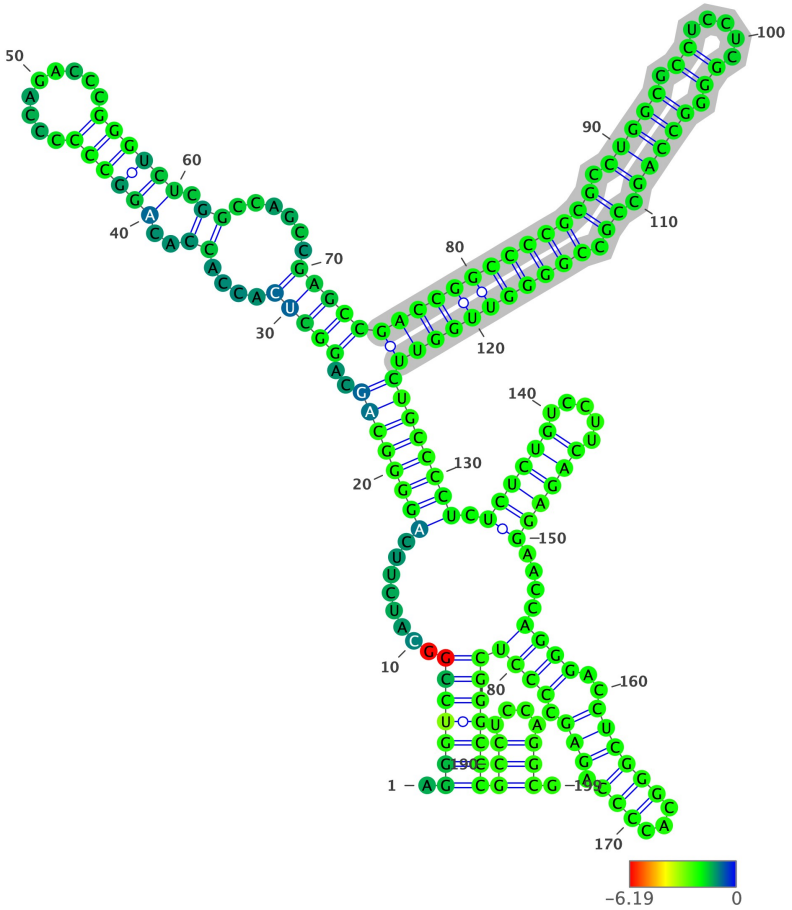
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 148 from nt 34267 to 34316 (nt 75 to 124)

```
5'-GACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUU-3'
5'-(((((((((((.............................)))))))))))-3'
Motif MFE = -36.6; z-score = -3.58; ED = 2.52
```



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 34193 to 34391 (motif highlighted in silver):

```
5'-AGGGUCCGGCAUCUUCAGGGGCAGCAGGCUCACCACCACAGGCCCCCCAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCC
GCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCG-3
5'-.(((((((.......((((((((..((((((....((..((((((.........)))))).)).....)))))((((((((((((.(((((.((.....)).)))))).)
).))))))))))))))))).((((((.....)))))).....((((..((((((...)))).))).))))))))))))((....)).-3'
MFE = -101.9; z-score = -2.14; ED = 28.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

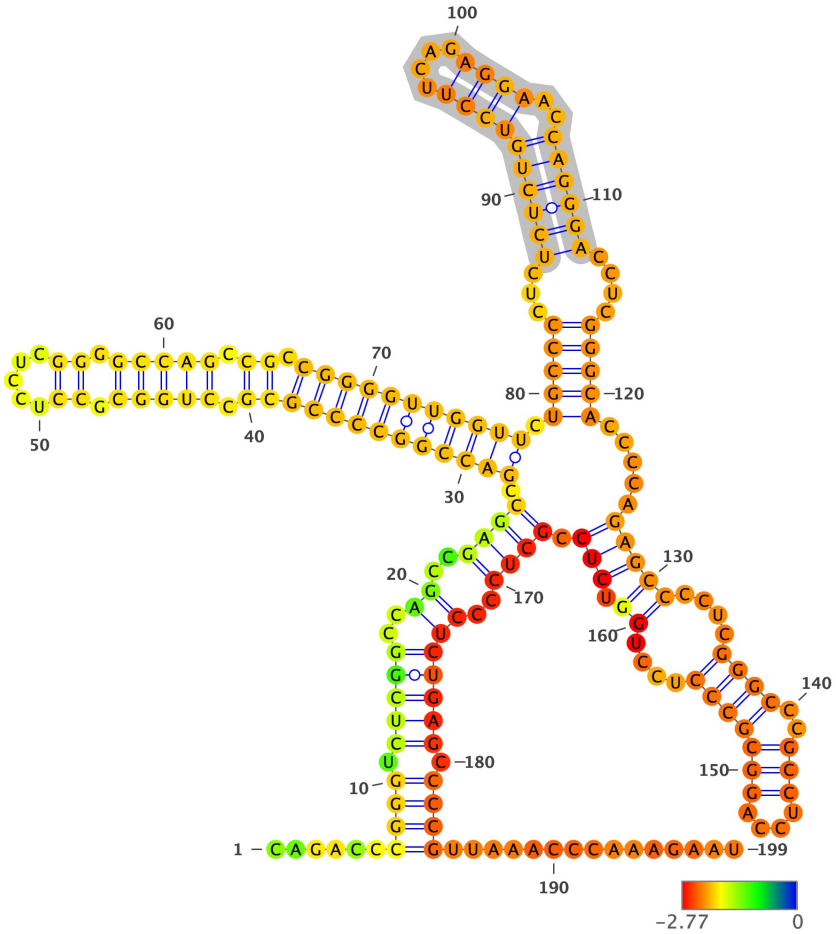
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 149 from nt 34326 to 34351 (nt 87 to 112)

```
5'-UCUCUGUCCUUCAGAGGAACCAGGGA-3'
5'-((((((.(........)...)))))))-3'
Motif MFE = -8.8; z-score = -2.76; ED = 1.81
```



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

Extracted structure model with flanking nucleotides 34240 to 34438 (motif highlighted in silver):

```
5'-CAGACCCGGGUCUCGGCCAGCCGAGCCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGG
ACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAU-3
5'-......((((.(((((..((..(((((.((((((((((((.(((((.(.....)).)))))).)).)))))))))))).(((((...((((((((((....)))))..)))))
)....)))))).....(((((....((((..(((....)))))))....)).))).)))))..)))))))).))))................-3'
MFE = -89.1; z-score = -2.68; ED = 36.45
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

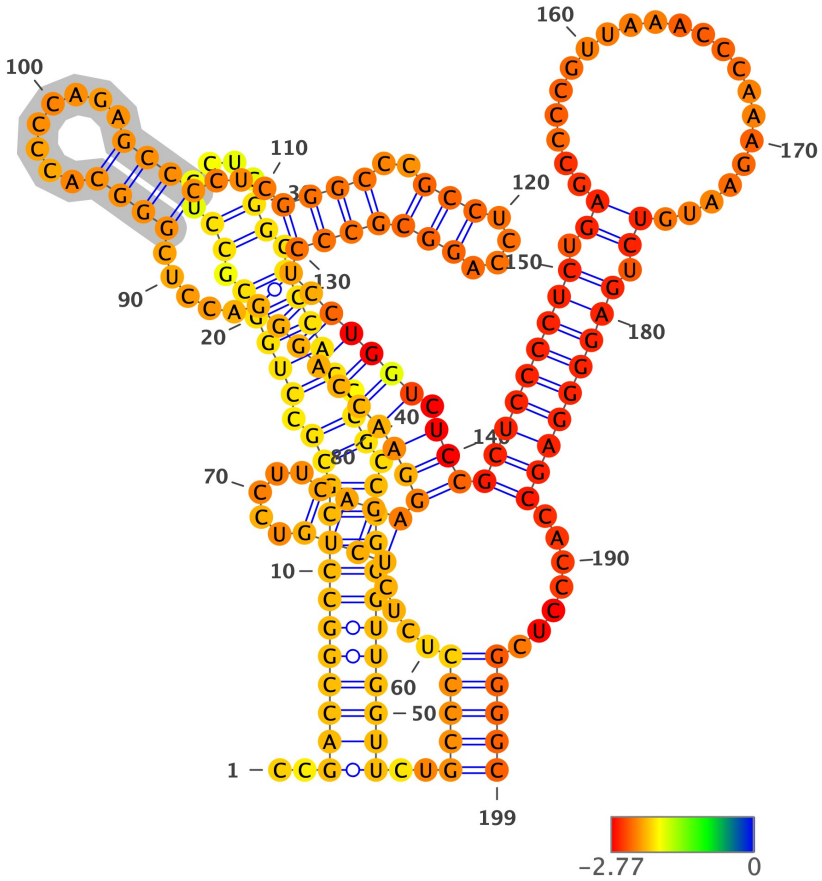
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 150 from nt 34356 to 34371 (nt 92 to 107)

```
5'-GGGCACCCCAGAGCCC-3'
5'-((((........))))-3'
Motif MFE = -6.0; z-score = -2.2; 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 34265 to 34463 (motif highlighted in silver):

```
5'-CCGACCGGCCCCGCGCCUGGCGCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCG
GGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGC-3
5'-..(((((((((((((.(((((.((.....)).)))))).)).)))))))))))..(((((....((((.....))))((((((((((.....((((........)))))...(
(((..((((....))))))))))))))).)))(((((((((.((.....................)).)))))))))).....)))))-3'
MFE = -98.8; z-score = -4.08; ED = 14.87
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

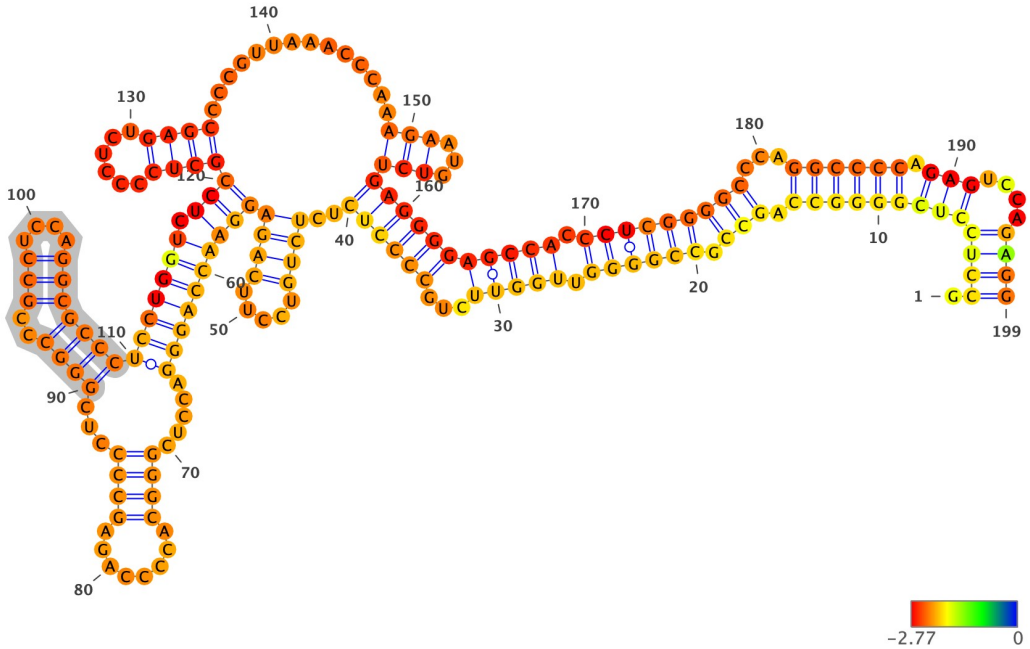
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 151 from nt 34375 to 34394 (nt 90 to 109)

```
5'-GGGCCCGCCUCCAGGCGCCC-3'
5'-(((((..(((....)))))))-3'
Motif MFE = -9.3; z-score = -1.56; 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 34286 to 34484 (motif highlighted in silver):

```
5'-GCCUCCUCGGGGCCAGCCGCCGGGGUUGGUUCUGCCCCUCUCUCUGUCCUUCAGAGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUC
CUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGG-3
5'-.(((((((((((((.(((.((((((.(((((...((((((..((((.....)))))((((((((((.....((((........)))).....((((..((((....)))))))))
)))))).)))((((.....)))).............(((...)))))))))))))).))))))))...)))))).)))....))))-3'
MFE = -92.0; z-score = -2.79; ED = 43.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 199--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

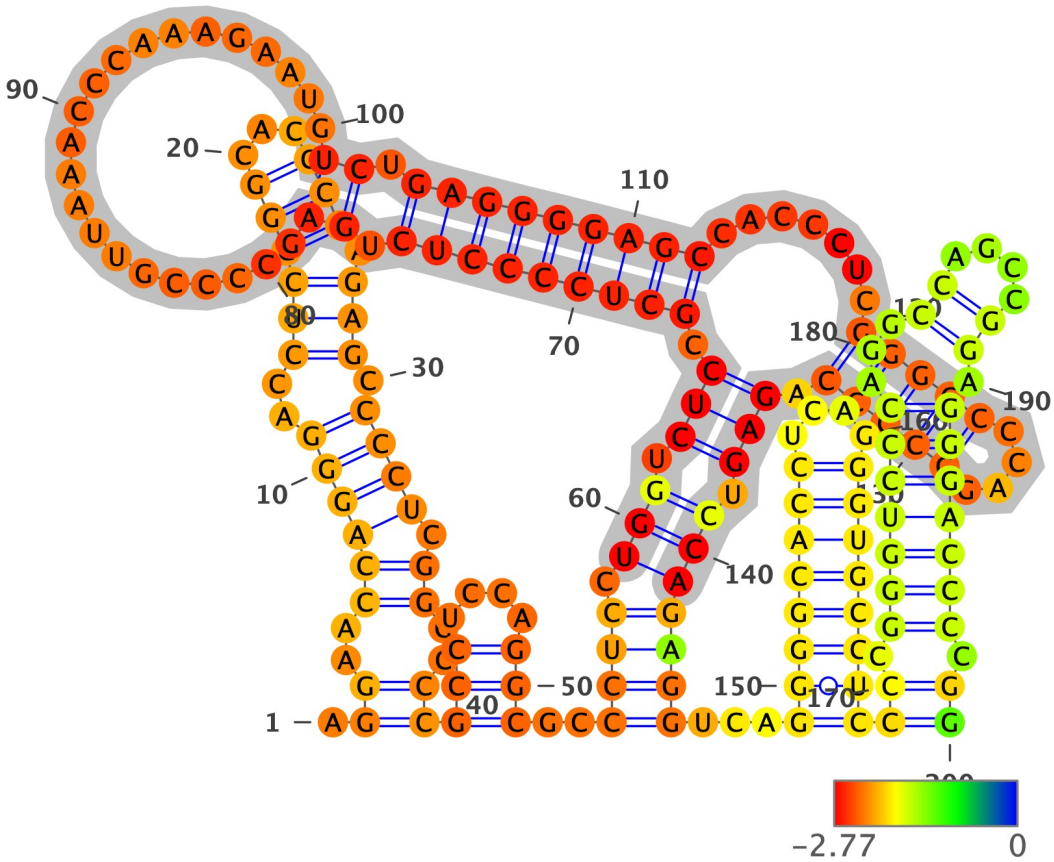
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 199--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 152 from nt 34398 to 34480 (nt 59 to 141)

```
5'-UGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAGCCACCCUCGGGGCCCAGGCCCCAGAGUCCA-3'
5'-((..(((.(((((((((.((.....................)).)))))))))).....(((((....))))).)))..))-3'
Motif MFE = -35.0; z-score = -3.28; ED = 6.59
```



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 34340 to 34539 (motif highlighted in silver):

```
5'-AGGAACCAGGGACCUCGGGCACCCCAGAGCCCCUCGGGCCCGCCUCCAGGCGCCCUCCUGGUCUCCGCUCCCCUCUGAGCCCCGUUAAACCCAAAGAAUGUCUGAGGGGAG
CCACCCUCGGGGCCCAGGCCCCAGAGUCCAGAGGUCAGGGGCACCUCAGGGUGCCUCCCCGGGUCCCAGGCCAGCCGGAGGGACCCCGG-3
5'-.((..(((((((..(((((((...))).))).))))).)).)..))((((....)))..((((.((((.((((.(((((((((.((.....................)).)))))))))
).....(((((....))))).))).)))))))...((((((((....)))))))))((.(((((((...((....)).)))))))).))-3'
MFE = -97.0; z-score = -2.52; ED = 47.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

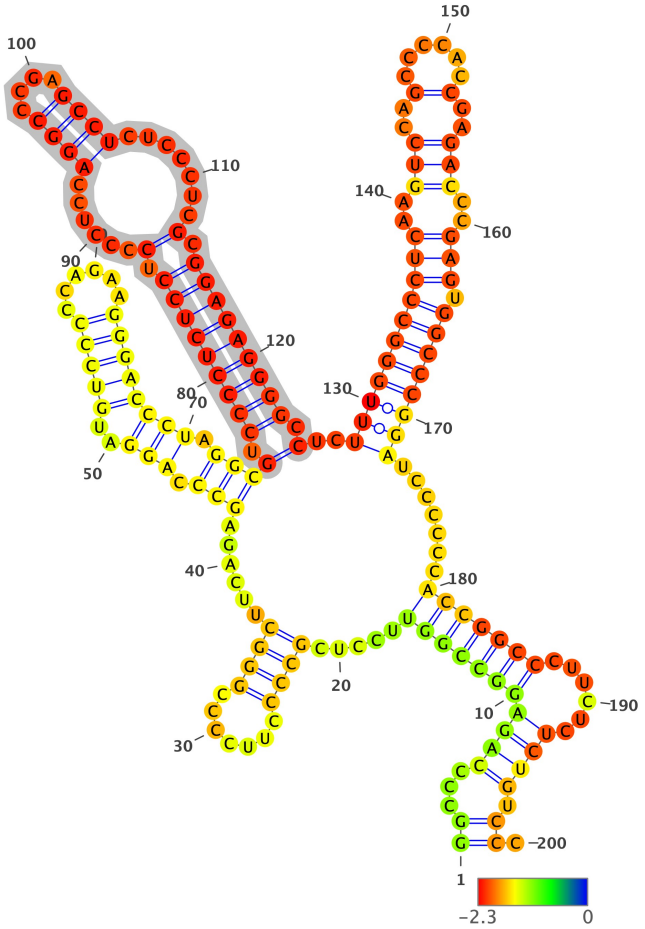
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 200--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 153 from nt 34624 to 34674 (nt 75 to 125)

```
5'-GUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCC-3'
5'-(.(((((((((.(.....((((....)))).....).))))))))).)-3'
Motif MFE = -22.8; z-score = -3.38; 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 34550 to 34749 (motif highlighted in silver):

```
5'-GGCCCCAGAGGCCGGUUCCUCGCCCCUUCCCCGGGCUUCAGAGCCCAGGAUGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCU
CGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCC-3
5'-((...(((((((((((.....((((.......))))).....(((.(((..(((((.....)))))))).)))(.(((((((((.(.....((((....)))).....
.).))))))))).)..((((((((((..(((..(.....)..)))..))).)))))))).....)))))))).....)))).)).-3'
MFE = -81.7; z-score = -2.83; ED = 16.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

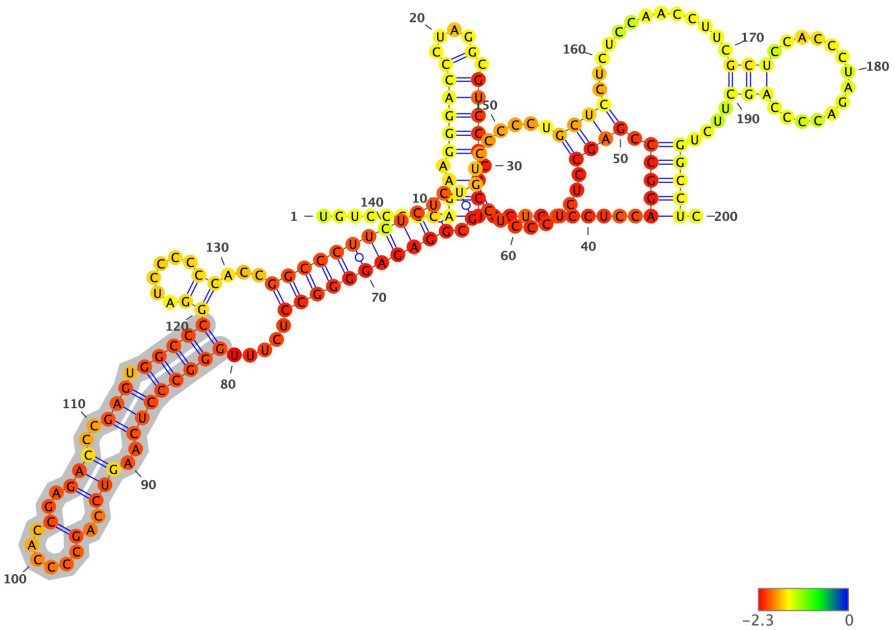
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 200--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 154 from nt 34680 to 34718 (nt 81 to 119)

```
5'-GGGCCCUCAAGUCCAGCCCCACCGAGACCCGAGUGGCCC-3'
5'-((((((.....((..(......)..)).....).))))))-3'
Motif MFE = -15.5; z-score = -1.81; 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 34600 to 34799 (motif highlighted in silver):

```
5'-UGUCCCCCAGAAGGGACCCUAGGCGUCCCCUCUCCUCCCCUCCAGGCCCGAGCCUCUCCCUCGCGGAGAGGGGCCUCUUUGGGCCCUCAAGUCCAGCCCCACCGAGACCCG
AGUGGCCCGGAUCCCCCCACCGGCCCUUCUCUCUGUCCCCCUGCUCCUCUCCAACCUUCGCUCCACCCUAGACCCCAGCUUCUGGCCUC-3
5'-........(((.((((((....).)))))).))).........(((((.((((........((.(((((((((((.....((((((((..(((..(......)..)))..)
)).)))))((......))...))))))))))).)).......))))).............(((.............)))....)))))).-3'
MFE = -60.2; z-score = -2.42; ED = 48.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 200--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

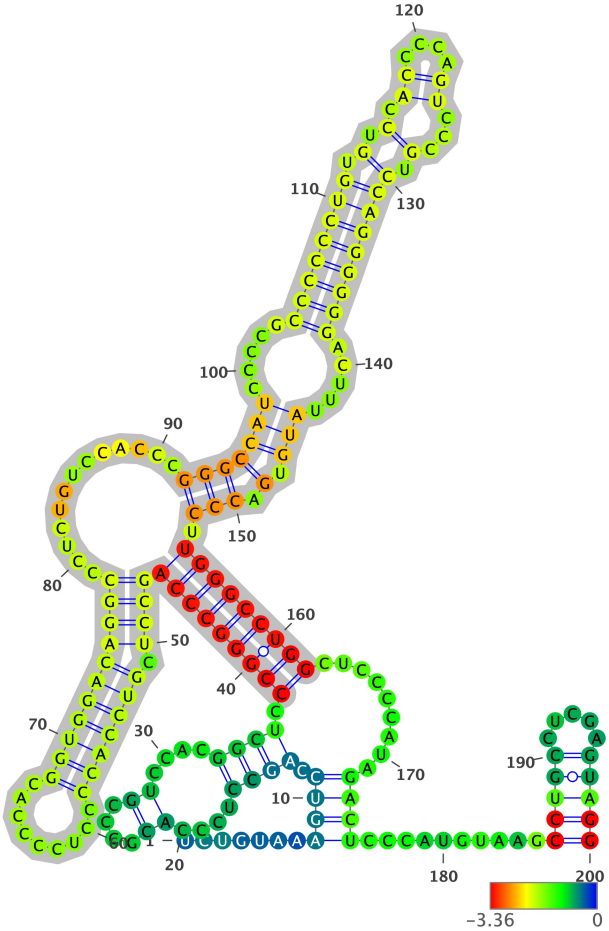
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 200--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 155 from nt 35085 to 35209 (nt 38 to 162)

```
5'-CCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUGUGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUG
ACCCUUGGGCCUGG-3'
5'-(((((((((((.......................))))).............(((((((.....(((((((((.(.(.((....)).)).).))))))))).....))).)
.))).)))))))))-3'
Motif MFE = -57.7; z-score = -3.77; ED = 23.92
```



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 35048 to 35247 (motif highlighted in silver):

```
5'-UCUGUAAAGUCCAGCCUCCCACGCCCGUCCACGGCUCCCGGGCCCAGCCUCGUCCACCCCUCCCCACGGUGGACAGGCCCUCUGUCCACCCGGGCCAUCCCCGCCCCCCUG
UGUCCACCCCAGUCCCGUCCAGGGGGGACUUUAUGUGACCCUUGGGCCUGGCUCCCCAUAGACUCCCAUGUAAGCCUGCCUCGAGUAGG-3
5'-.......((((.((((....((....))....)))).((((((((((((.(((((((.........)))))))))))).............(((((((.....(((((((
.(.(.((....)).)).).))))))))).....))).).))).))))))))).........))))..........(((((.....)))))-3'
MFE = -68.1; z-score = -1.4; ED = 17.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-2, 12001-35355(+)

Attributes: ['ID=id-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'gbkey=repeat_region', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'rpt_family=IR1%3B W', 'rpt_type=direct', 'rpt_unit_range=12001..15072 (3072 bp)']

12-- nt 1 to 200--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

13-- nt 1 to 200--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-LP-17, 33505-35355(+)

Attributes: ['ID=id-HHV4_EBNA-LP-17', 'Note=partial copy', 'gbkey=repeat_region', 'rpt_family=IR1%3B W', 'rpt_type=direct']

15-- nt 1 to 149--gene, gene-HHV4_BWRF1.8, 34045-35196(+)

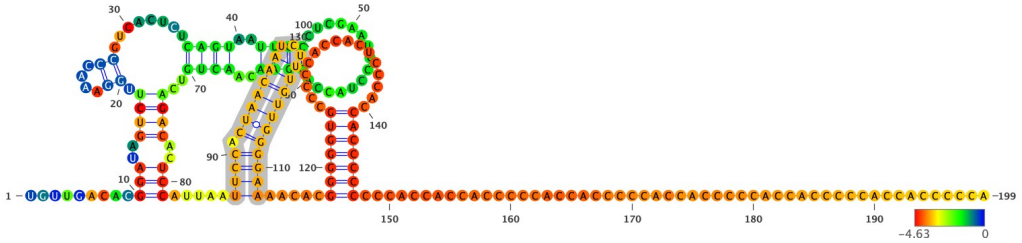
Attributes: ['ID=gene-HHV4_BWRF1.8', 'Dbxref=GeneID:3783740', 'Name=BWRF1', 'gbkey=Gene', 'gene=BWRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'start_range=.,34045']

16-- nt 1 to 149--CDS, cds-YP_401643.1, 34045-35196(+)

Attributes: ['ID=cds-YP_401643.1', 'Parent=gene-HHV4_BWRF1.8', 'Dbxref=UniProtKB/TrEMBL:Q8AZK0,Genbank:YP_401643.1,GeneID:3783740', 'Name=YP_401643.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=BWRF1', 'locus_tag=HHV4_BWRF1.8', 'partial=true', 'product=protein BWRF1', 'protein_id=YP_401643.1', 'start_range=.,34045']

NC_007605.1 (forward strand): Structure number 156 from nt 36352 to 36377 (nt 87 to 112)

```
5'-UUCCACUAACAAUCUUUGUUGGGGAA-3'
5'-((((.(((((((...)))))))))))-3'
Motif MFE = -9.0; z-score = -3.42; 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 36266 to 36464 (motif highlighted in silver):

```
5'-UGUUGACACGGAUAGUCUUGGAAACCCGUCACUCUCAGUAAUUCCCUCGAAUCCCUACCAGGAACAACUGUCAGACACUCCAUUAAUUCCACUAACAAUCUUUGUUGGGGA
AAACACGGGGGUGCCCCCACCACUCCCACCACCCCCCCCACCACCACCCCCACCACCCCCACCACCCCCACCACCCCCACCACCCCCA-3
5'-.........(((..((((.((....)).......((((..((((.............))))..)))))..)))))..)))).....((((.(((((((...)))))))))
).....(((((((.............)))))))..............................................................-3'
MFE = -33.6; z-score = -3.21; ED = 36.81
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--exon, exon-HHV4_EBNA-2-19, 36098-37744(+)

Attributes: ['ID=exon-HHV4_EBNA-2-19', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

12-- nt 1 to 199--CDS, cds-YP_401644.1, 36216-37679(+)

Attributes: ['ID=cds-YP_401644.1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=UniProtKB/TrEMBL:Q777H1,Genbank:YP_401644.1,GeneID:3783761', 'Name=YP_401644.1', 'gbkey=CDS', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'product=nuclear antigen EBNA-2', 'protein_id=YP_401644.1']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

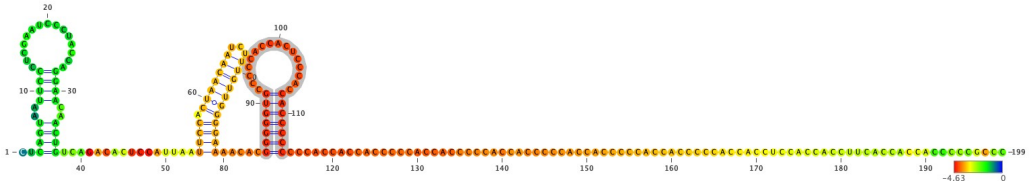
Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

15-- nt 125 to 199--repeat_region, id-HHV4_EBNA-LP, 36390-36512(+)

Attributes: ['ID=id-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'gbkey=repeat_region', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP', 'rpt_unit_range=36390..36398']

NC_007605.1 (forward strand): Structure number 157 from nt 36383 to 36412 (nt 85 to 114)

```
5'-GGGGGUGCCCCCACCACUCCCACCACCCCC-3'
5'-(((((((.............)))))))-3'
Motif MFE = -11.2; z-score = -3.38; 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 36299 to 36497 (motif highlighted in silver):

```
5'-CUCAGUAAUUCCCUCGAAUCCCUACCAGGAACAACUGUCAGACACUCCAUUAAUUCCACUAACAAUCUUUGUUGGGGAAAACACGGGGGUGCCCCCACCACUCCCACCACC
CCCCCCACCACCACCCCCACCACCCCCACCACCCCCACCACCCCCACCACCCCCACCACCUCCACCACCUUCACCACCACCCCCGCCC-3
5'-..(((((..((((.............))))..))))................((((.(((((((...)))))))))))).....(((((((.................))))
)))).....................................................................................-3'
MFE = -27.3; z-score = -4.87; ED = 9.21
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--exon, exon-HHV4_EBNA-2-19, 36098-37744(+)

Attributes: ['ID=exon-HHV4_EBNA-2-19', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

12-- nt 1 to 199--CDS, cds-YP_401644.1, 36216-37679(+)

Attributes: ['ID=cds-YP_401644.1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=UniProtKB/TrEMBL:Q777H1,Genbank:YP_401644.1,GeneID:3783761', 'Name=YP_401644.1', 'gbkey=CDS', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'product=nuclear antigen EBNA-2', 'protein_id=YP_401644.1']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

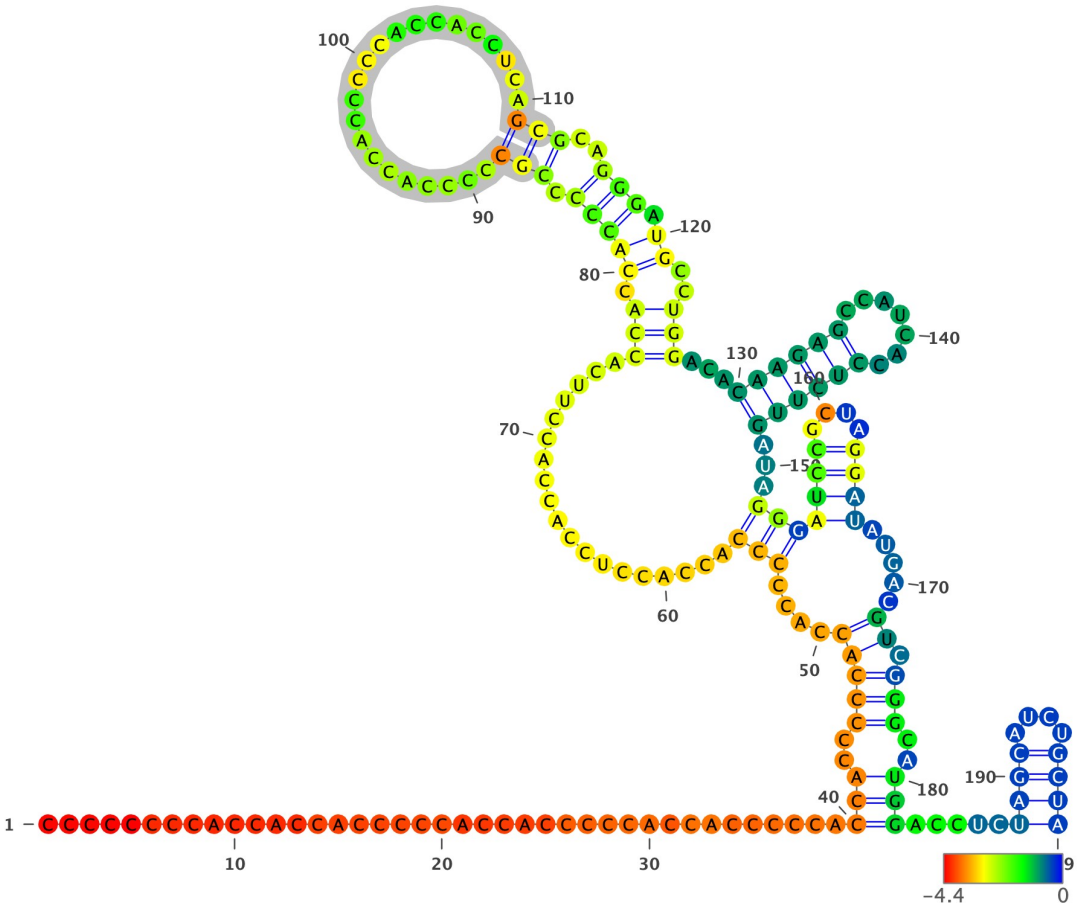
Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

15-- nt 92 to 199--repeat_region, id-HHV4_EBNA-LP, 36390-36512(+)

Attributes: ['ID=id-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'gbkey=repeat_region', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP', 'rpt_unit_range=36390..36398']

NC_007605.1 (forward strand): Structure number 158 from nt 36494 to 36519 (nt 87 to 112)

```
5'-GCCCCCACCACCCCCACCACCUCAGC-3'
5'-(........................)-3'
Motif MFE = 0.0; z-score = 0.37; ED = 0.1
```



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 36408 to 36606 (motif highlighted in silver):

```
5'-CCCCCCCCACCACCACCCCCACCACCCCCACCACCCCCACCACCCCCACCACCCCCACCACCUCCACCACCUUCACCACCACCCCCGCCCCCACCACCCCCACCACCUCAG
CGCAGGGAUGCCUGGACACAAGAGCCAUCACCUCUUGAUAGGGAUCCGCUAGGAUAUGACGUCGGGCAUGGACCUCUAGCAUCUGCUA-3
5'-.........................................(((..(((((....(((....................(((.(((((.(((.....................)
))..)))).))..)))...((((((.......)))))).....))))((....))))).....)).)))..))).....((((....))))-3'
MFE = -29.1; z-score = -1.76; ED = 26.17
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--exon, exon-HHV4_EBNA-2-19, 36098-37744(+)

Attributes: ['ID=exon-HHV4_EBNA-2-19', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

12-- nt 1 to 199--CDS, cds-YP_401644.1, 36216-37679(+)

Attributes: ['ID=cds-YP_401644.1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=UniProtKB/TrEMBL:Q777H1,Genbank:YP_401644.1,GeneID:3783761', 'Name=YP_401644.1', 'gbkey=CDS', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'product=nuclear antigen EBNA-2', 'protein_id=YP_401644.1']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

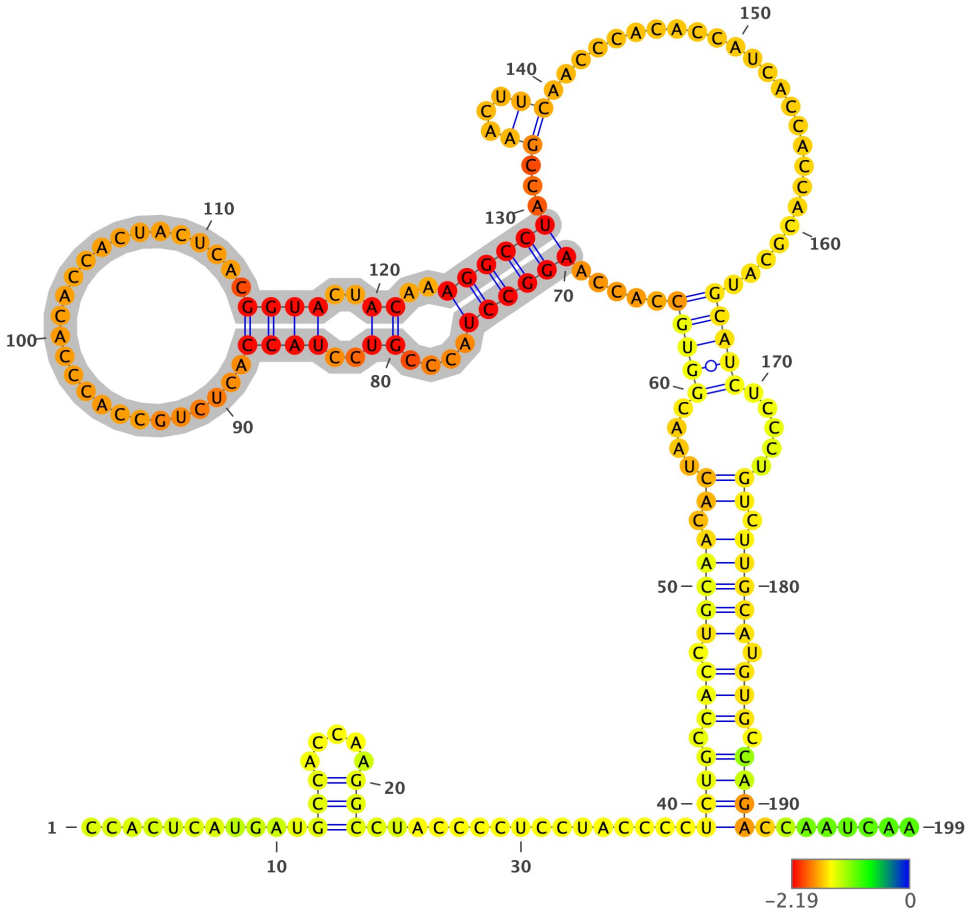
Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

15-- nt 1 to 105--repeat_region, id-HHV4_EBNA-LP, 36390-36512(+)

Attributes: ['ID=id-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'gbkey=repeat_region', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP', 'rpt_unit_range=36390..36398']

NC_007605.1 (forward strand): Structure number 159 from nt 36861 to 36920 (nt 70 to 129)

```
5'-AGGCCUACCCGUCCUACCACUCUGCCACCCACACCACUACUCACGGUACUACAAAGGCCU-3'
5'-((((((....((..((((.........................))))..))..)))))))-3'
Motif MFE = -10.5; z-score = -2.47; 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 36792 to 36990 (motif highlighted in silver):

```
5'-CCACUCAUGAUGCCACCAAGGCCUACCCCUCCUACCCCUCUGCCACCUGCAACACUAACGGUGCCACCAAGGCCUACCCGUCCUACCACUCUGCCACCCACACCACUACUC
ACGGUACUACAAAGGCCUACCGAACUUCAACCCACACCAUCACCACCACGCAUGCAUCUCCCUGUCUUGCAUGUGCCAGACCAAUCAA-3
5'-...........(((.....)))................((((.(((.(((((.((....(((((.....(((((....((..((((.......................
..))))..))..)))))))...((...)).......................)))))).....)).)))))).))).))))........-3'
MFE = -31.2; z-score = -2.45; ED = 27.18
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-2, 11305-37739(+)

Attributes: ['ID=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Name=EBNA-2', 'gbkey=Gene', 'gene=EBNA-2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-2, 11336-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-2', 'Parent=gene-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

11-- nt 1 to 199--exon, exon-HHV4_EBNA-2-19, 36098-37744(+)

Attributes: ['ID=exon-HHV4_EBNA-2-19', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=GeneID:3783761', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2']

12-- nt 1 to 199--CDS, cds-YP_401644.1, 36216-37679(+)

Attributes: ['ID=cds-YP_401644.1', 'Parent=rna-HHV4_EBNA-2', 'Dbxref=UniProtKB/TrEMBL:Q777H1,Genbank:YP_401644.1,GeneID:3783761', 'Name=YP_401644.1', 'gbkey=CDS', 'gene=EBNA-2', 'locus_tag=HHV4_EBNA-2', 'product=nuclear antigen EBNA-2', 'protein_id=YP_401644.1']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-LP, 14352-37744(+)

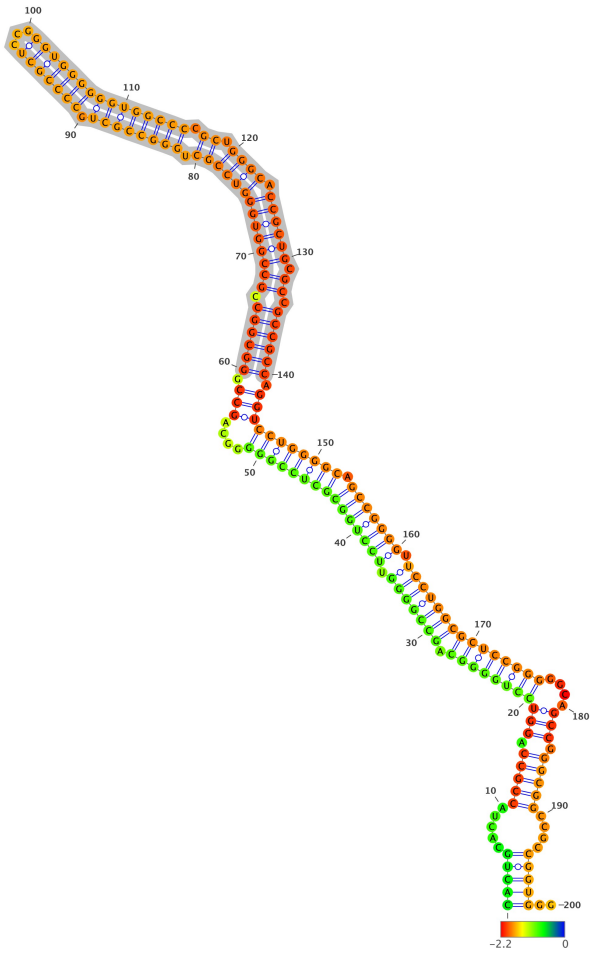
Attributes: ['ID=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Name=EBNA-LP', 'gbkey=Gene', 'gene=EBNA-LP', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-LP']

14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-LP, 14384-37744(+)

Attributes: ['ID=rna-HHV4_EBNA-LP', 'Parent=gene-HHV4_EBNA-LP', 'Dbxref=GeneID:3783746', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-LP', 'locus_tag=HHV4_EBNA-LP']

NC_007605.1 (forward strand): Structure number 160 from nt 38339 to 38419 (nt 60 to 140)

```
5'-GGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCC-3'
5'-((((((.......................................................................))))))-3'
Motif MFE = -64.2; z-score = -2.83; ED = 3.63
```



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

Extracted structure model with flanking nucleotides 38280 to 38479 (motif highlighted in silver):

```
5'-CACUGCACUACCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUG
GCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCCGGGCGGCCGCCGGUGGG-3
5'-(((((.....((((((.(((((((((((.(((((((.(((((((((((((((....((((.((((((.(((((((((((((.((((((((.(((((((...)))))))))))
))))).)).)))).)))))))..)).)))))).))))))))))))).))))))).))))))))))))))))....))).)))))....)))))..-3'
MFE = -145.3; z-score = -2.87; ED = 10.31
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

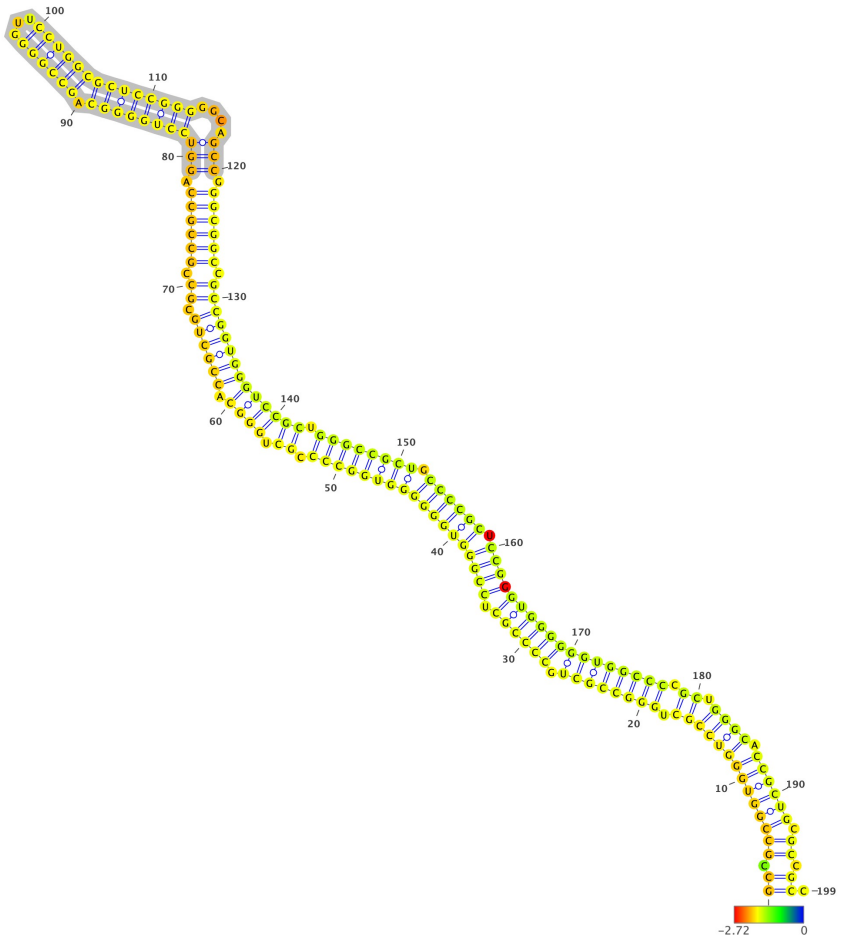
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 11 to 200--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 161 from nt 38421 to 38462 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.67; 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 38343 to 38541 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.88; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

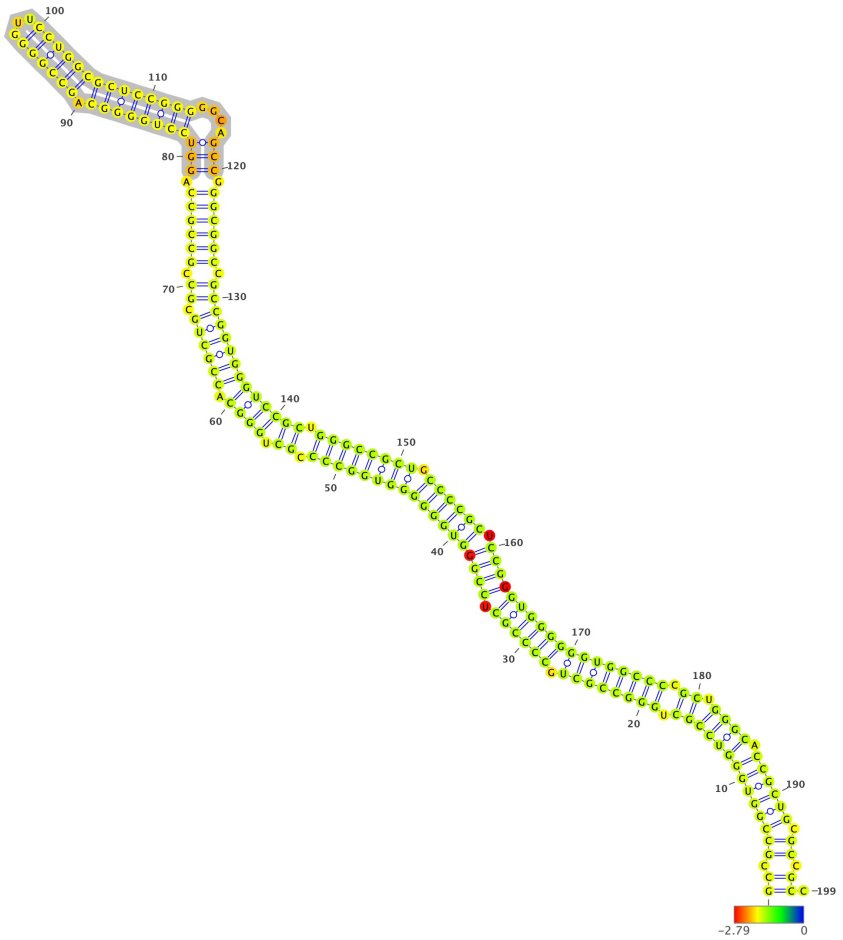
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 162 from nt 38546 to 38587 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.67; 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 38468 to 38666 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.69; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

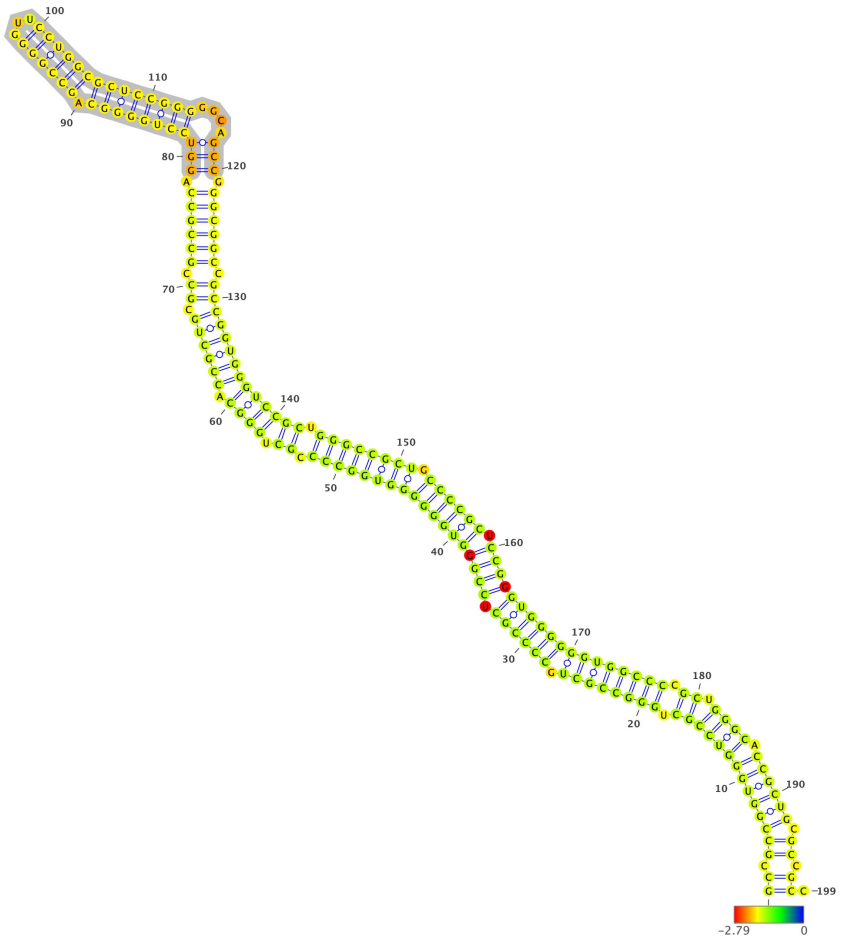
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 163 from nt 38671 to 38712 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.88; 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 38593 to 38791 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.35; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

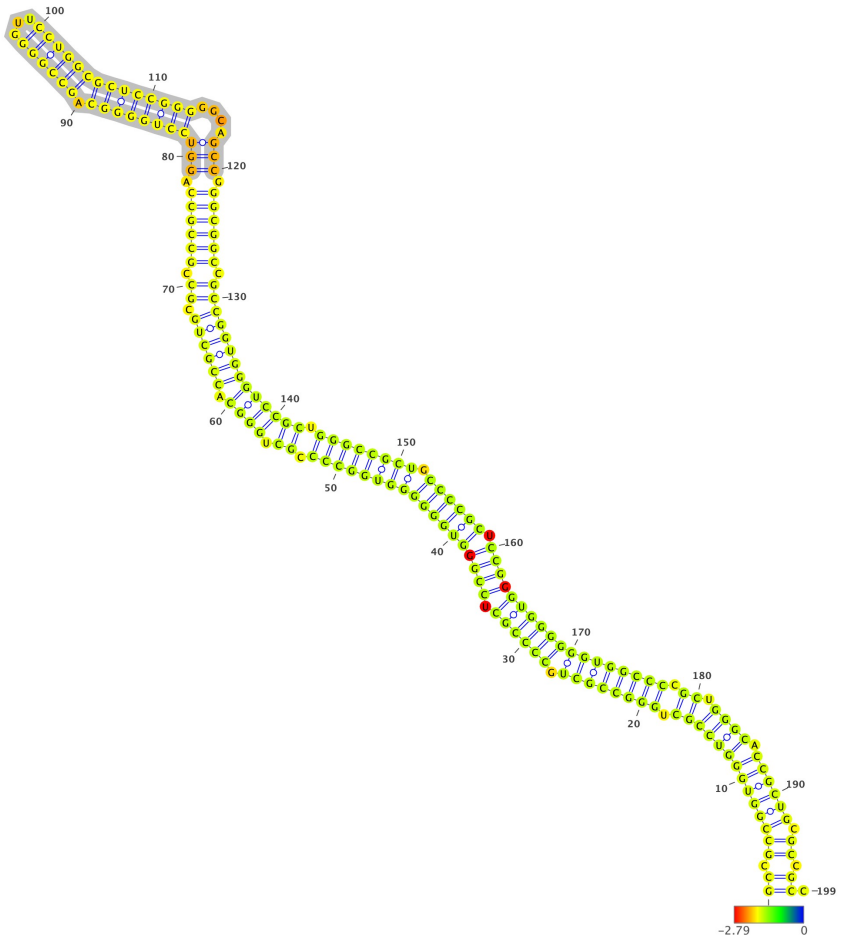
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 164 from nt 38796 to 38837 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.66; 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 38718 to 38916 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.34; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

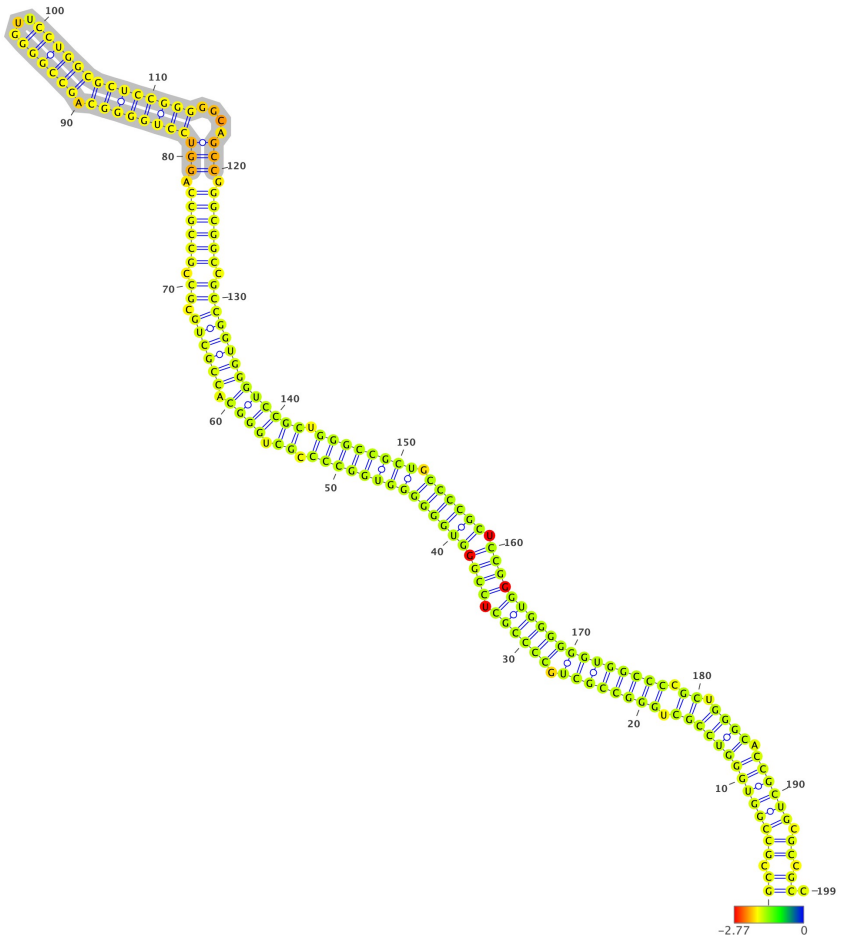
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 165 from nt 38921 to 38962 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -3.02; 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 38843 to 39041 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))))).)))))).))))))))))))))))))))).))).)))).)))))))).)).)).-3'
MFE = -157.4; z-score = -4.0; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

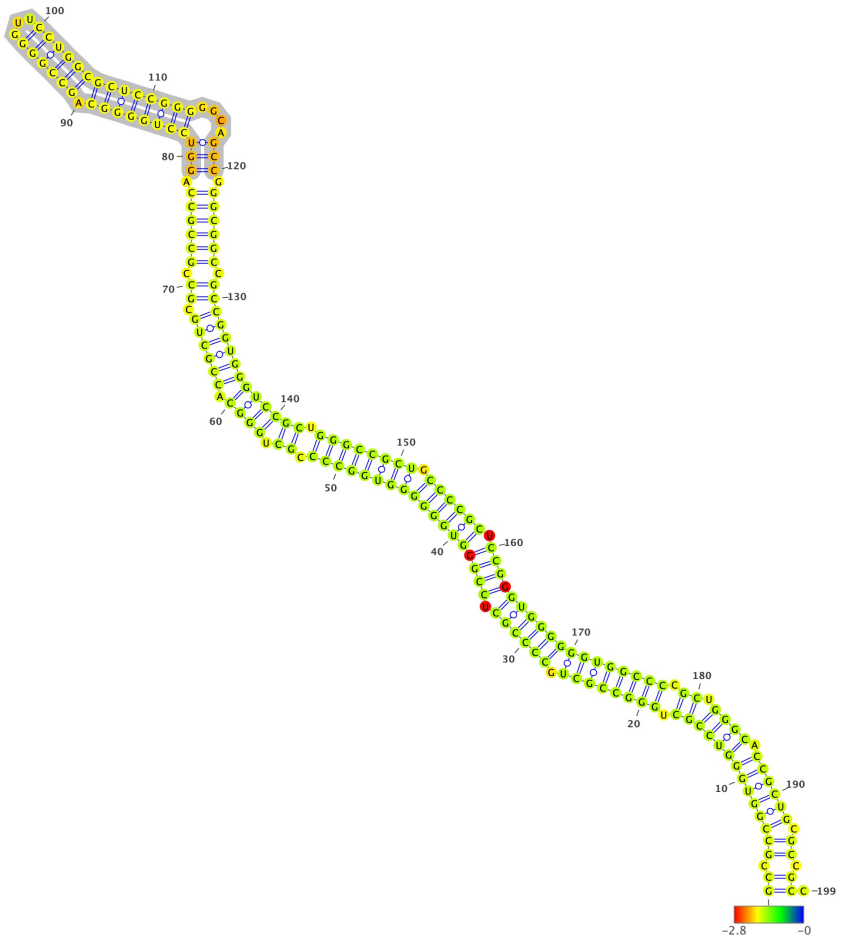
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 166 from nt 39046 to 39087 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.41; 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 38968 to 39166 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.82; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

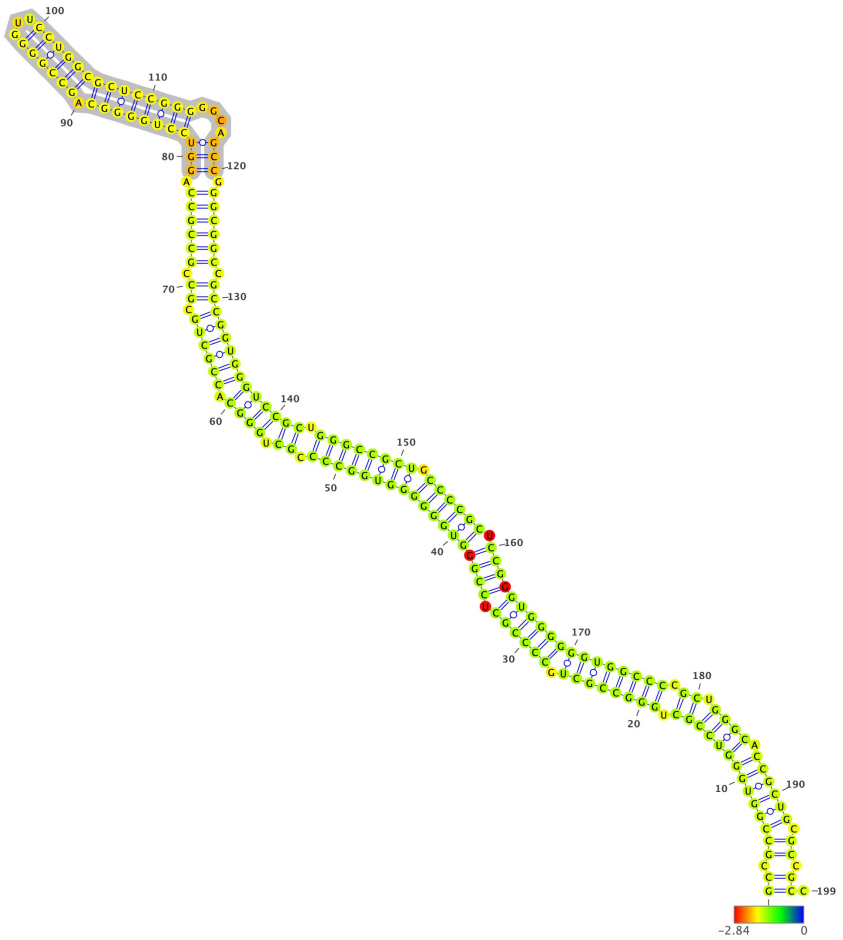
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 167 from nt 39171 to 39212 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.97; 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 39093 to 39291 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.9; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

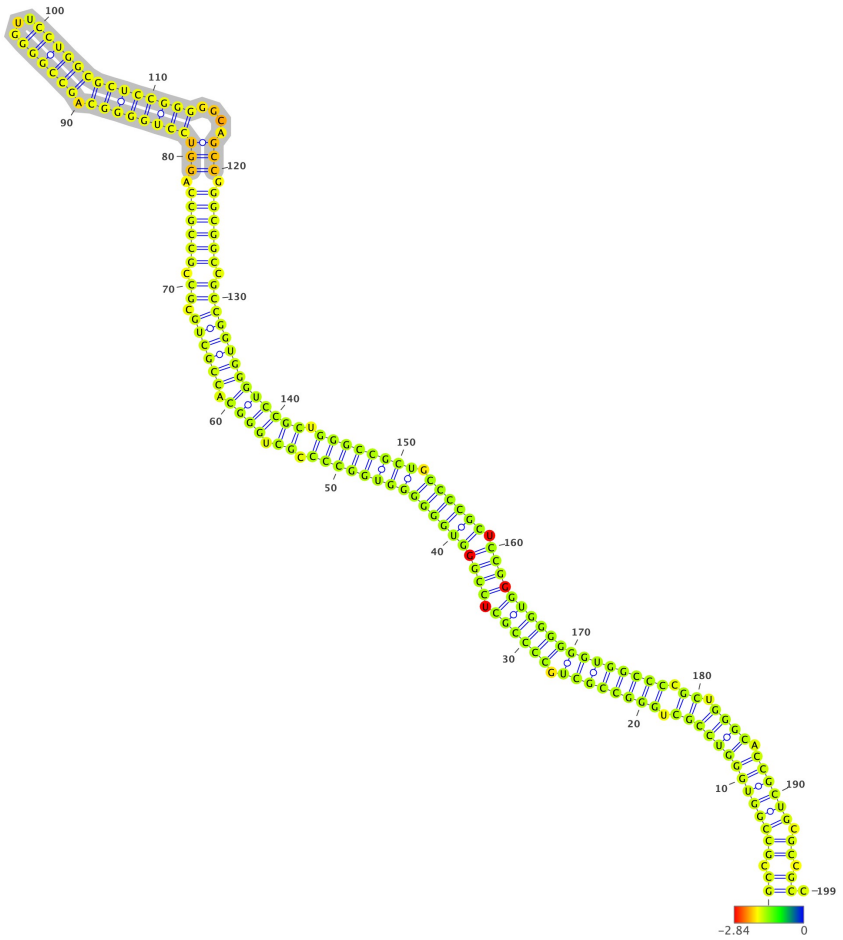
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 168 from nt 39296 to 39337 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....................................)))-3'
Motif MFE = -28.4; z-score = -2.55; 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 39218 to 39416 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.46; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

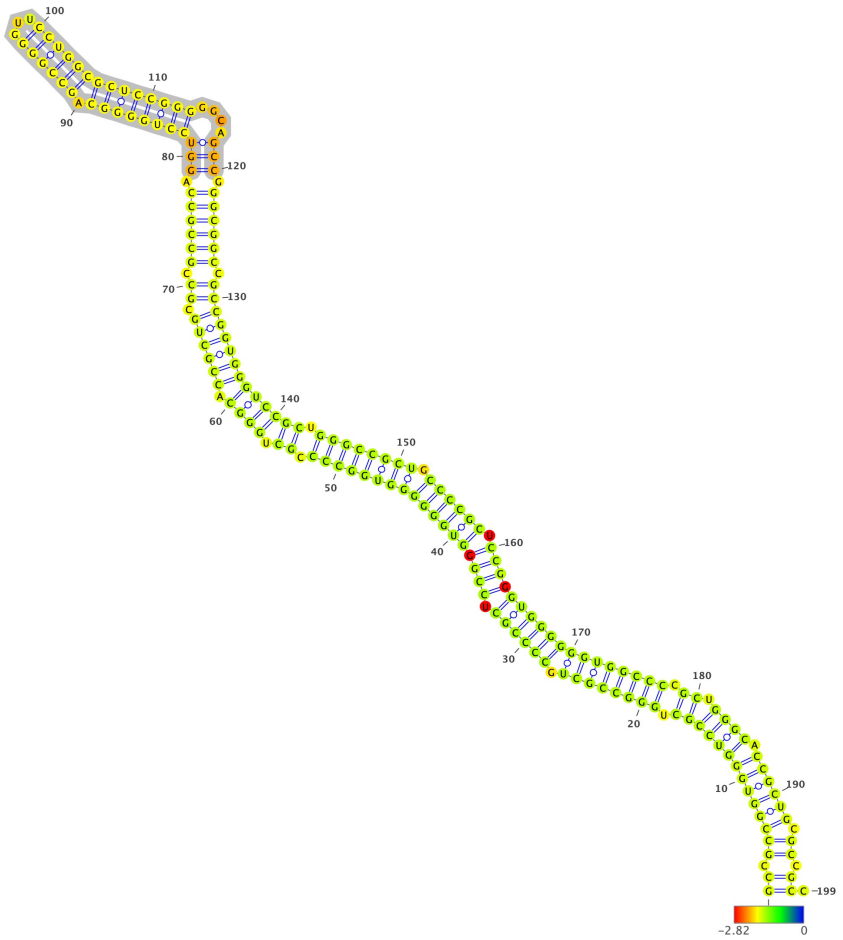
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 169 from nt 39421 to 39462 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.92; 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 39343 to 39541 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.75; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

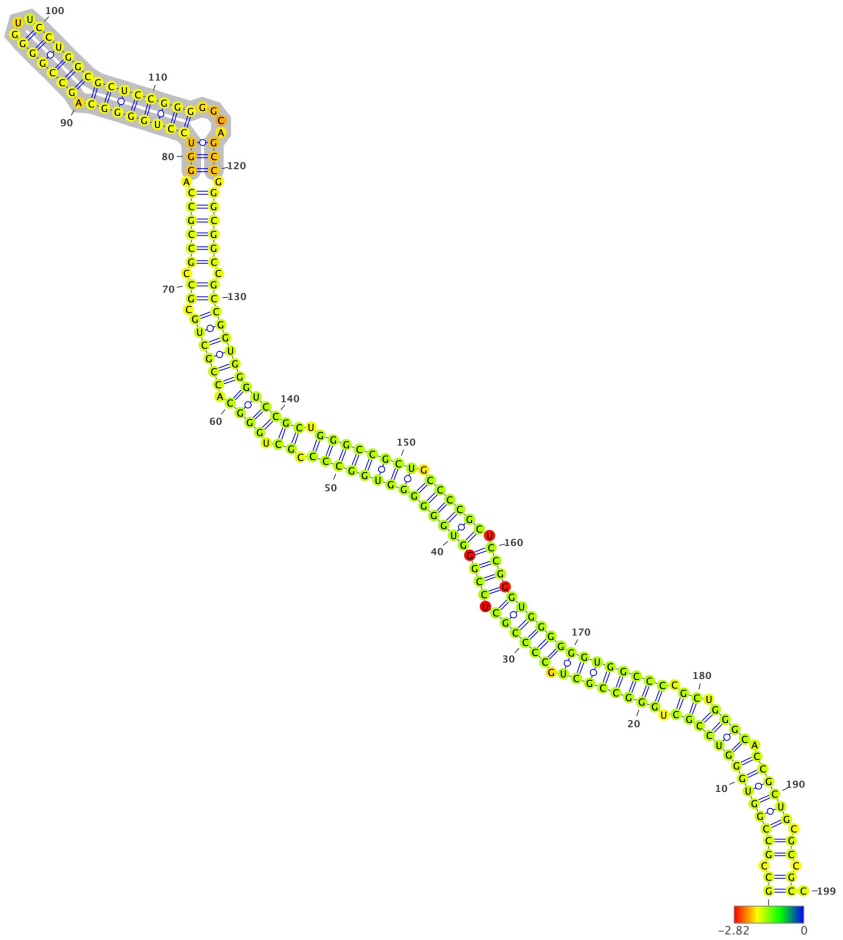
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 170 from nt 39546 to 39587 (nt 79 to 120)

```
5'-GGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCC-3'
5'-(((.....)))-3'
Motif MFE = -28.4; z-score = -2.85; 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 39468 to 39666 (motif highlighted in silver):

```
5'-GCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCG
GGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCC-3
5'-((.(((((((((((((.(((((((.((((((.((((((((((((((((((.((.((((.((((((.((.((((((.((((((((((((.((((((...)))))))))))))
))....))).)))))).))))))))))))))).))))))).))))))).))))))))))))))))))).))).))))).)))))).)).)).-3'
MFE = -157.4; z-score = -3.45; ED = 4.04
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

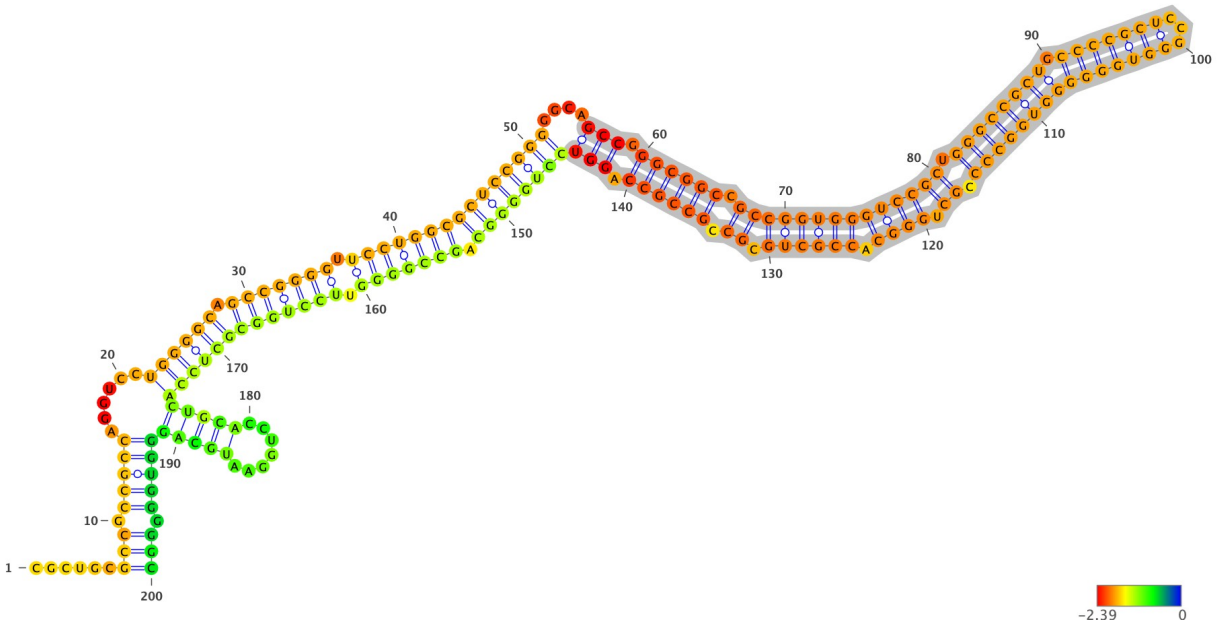
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 171 from nt 39710 to 39798 (nt 56 to 144)

```
5'-GCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUGGCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGU-3'
5'-(((.(((((((.(((((((((.....................................................)))))))..)).)))))))..)))-3'
Motif MFE = -69.0; z-score = -2.85; ED = 1.91
```



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

Extracted structure model with flanking nucleotides 39655 to 39854 (motif highlighted in silver):

```
5'-CGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCGGGGGCAGCCGGGCGGCCGCCGGUGGGUCCGCUGGGCCGCUGCCCCGCUCCGGGUGGGGGGUG
GCCCCGCUGGGCACCGCUGCGCCGCCGCCAGGUCCUGGGGCAGCCGGGGUUCCUGGCGCUCCACUGCACCUGGAAUGCAGGGUGGGGGC-3
5'-......(((.(((((.....((((((.(((((((.(((((((((((((((....(((.((((((.((((((((((((((.(((((((.(((((((...)))))))))))
))))).)).)))).)))))).)).)))))).))))))))))).)))))))).))))))))))))))(((((.......)))))))))).)))-3'
MFE = -141.0; z-score = -2.43; ED = 20.67
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

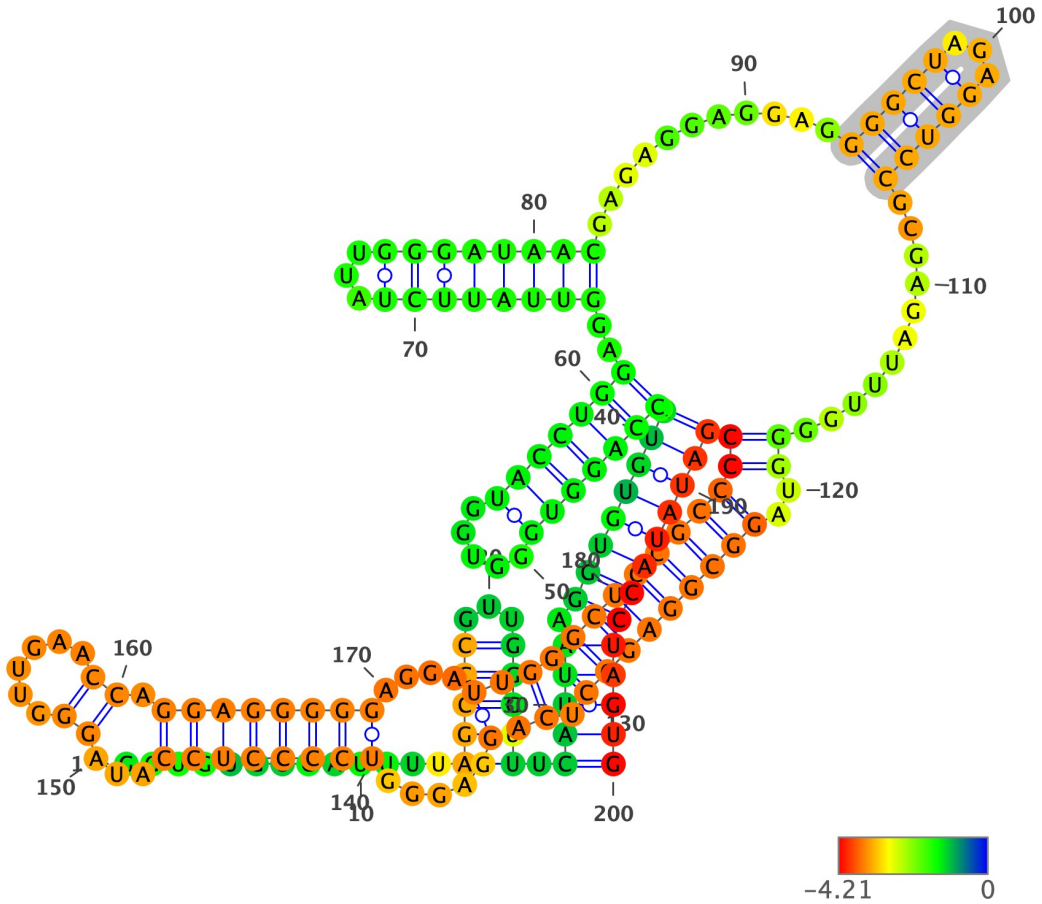
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 173--direct_repeat, id-HHV4_EBNA-3A, 38290-39827(+)

Attributes: ['ID=id-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=repeat_region', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'rpt_family=IR2%3B NotI', 'rpt_type=direct', 'rpt_unit_range=38290..38414']

NC_007605.1 (forward strand): Structure number 172 from nt 40693 to 40705 (nt 94 to 106)

```
5'-GGGCUAGAGGUCC-3'
5'-(((((...)))))-3'
Motif MFE = -3.5; z-score = -2.5; 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 40600 to 40799 (motif highlighted in silver):

```
5'-GGUGUGUCAUUUUAGCCCGUUGGGUUUCAUUAAGGUGUGUCACCAGGUGGGUGGUACCUGGAGGUUAUUCUAUUGGGAUAACGAGAGGAGGAGGGGCUAGAGGUCCGCGAG
AUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAGGGGGAGGAUUGGGCUCCGCCCCGAUAUACCUAGUG-3
5'-............(((((...))))).(((((.(((((((.(((((((.....)))))))..((((((((...)))))))).........(((((...))))).....
......((..(((((((((.(((.....(((((((...((......)).)))))))....))))))))))))))))))))))))))))))))))))-3'
MFE = -81.8; z-score = -4.13; ED = 30.44
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

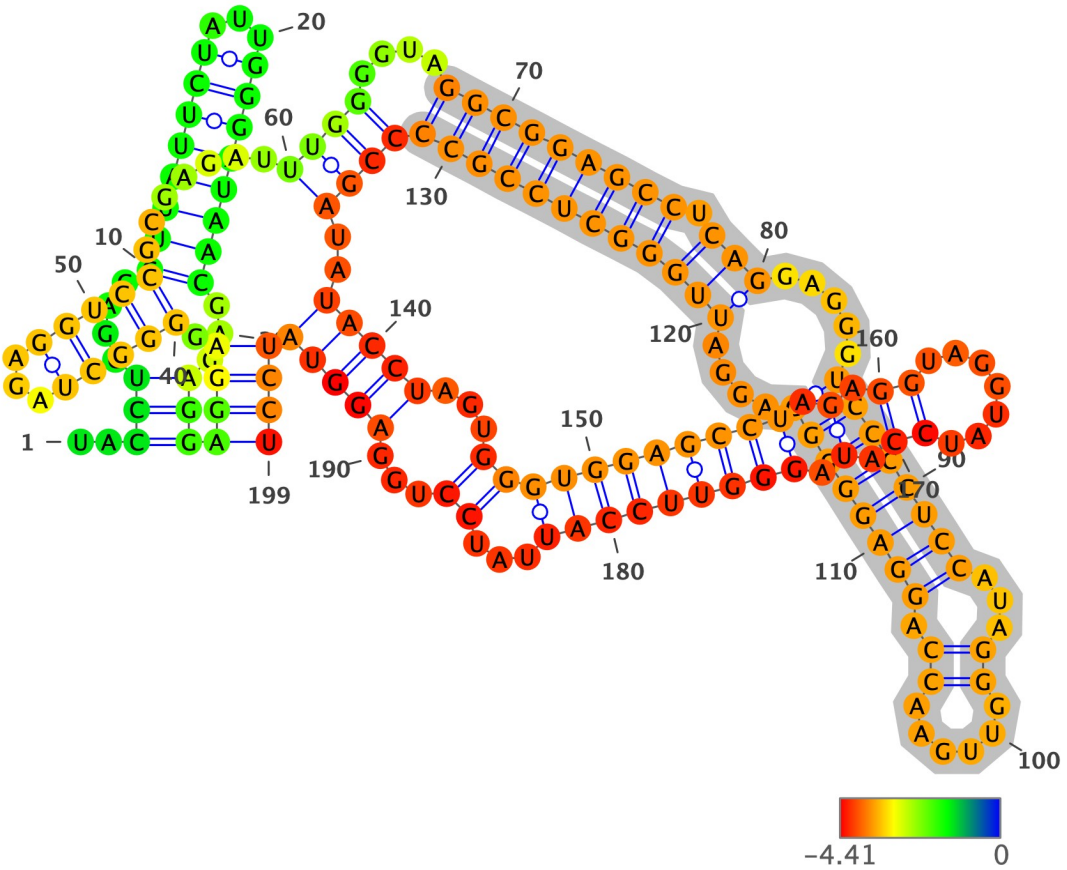
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 173 from nt 40721 to 40784 (nt 68 to 131)

```
5'-GGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAGGGGGAGGAUUGGGCUCCGCC-3'
5'-(((((((((.(((.....(((((((((...((......)).)))))))).....)))))))))))))-3'
Motif MFE = -40.5; z-score = -5.45; ED = 1.91
```



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

Extracted structure model with flanking nucleotides 40654 to 40852 (motif highlighted in silver):

```
5'-UACCUGGAGGUUAUUCUAUUGGGAUAACGAGAGGAGGAGGGGCUAGAGGUCCGCGAGAUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAG
GGGGAGGAUUGGGCUCCGCCCCGAUAUACCUAGUGGGUGGAGCCUAGAGGUAGGUAUCCAUAGGGUUCCAUUAUCCUGGAGGUAUCCU-3
5'-..(((....(((((((((...)))))))))...)))((((.(((((...)))))).......((((....(((((((((.(((.....((((((((...((......)).))))
))))).....))))))))))))))..((((((...((((((((((.(.((.......)).).))))))))))...))...)))))))))-3'
MFE = -81.6; z-score = -3.9; ED = 47.89
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

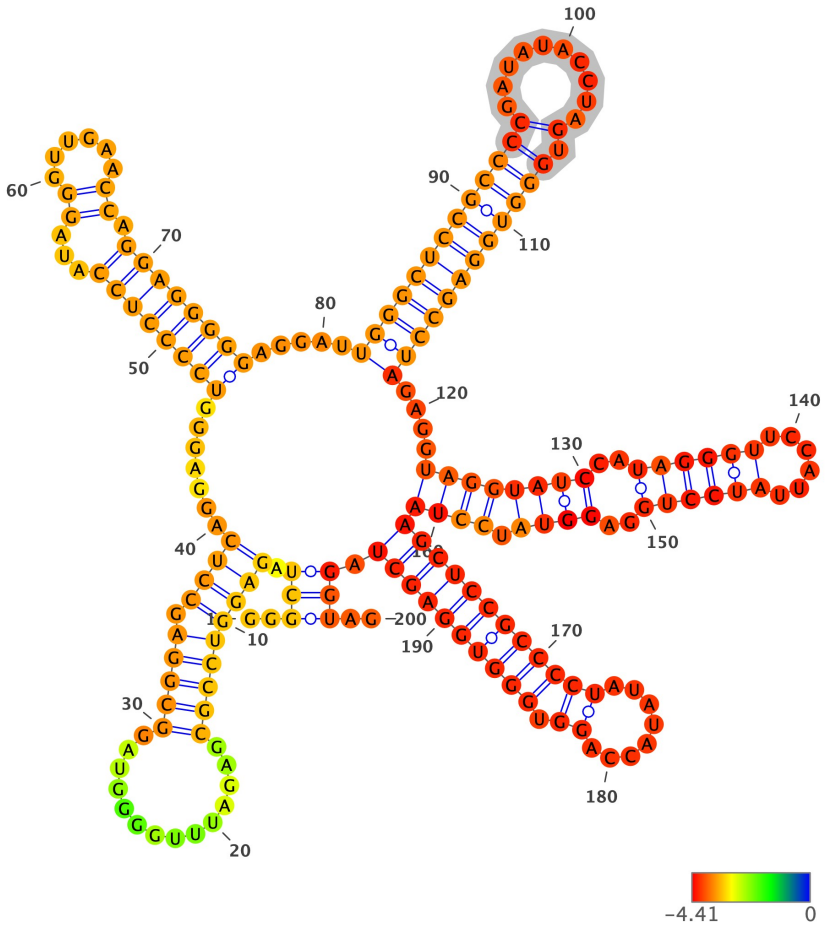
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 174 from nt 40785 to 40799 (nt 93 to 107)

```
5'-CCGAUAUACCUAGUG-3'
5'-((.........).)-3'
Motif MFE = 0.0; z-score = 0.61; 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 40693 to 40892 (motif highlighted in silver):

```
5'-GGGCUAGAGGUCCGCGAGAUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAGGGGGAGGAUUGGGCUCCGCCCCGAUAUACCUAGUGGGUG
GAGCCUAGAGGUAGGUAUCCAUAGGGUUCCAUUAUCCUGGAGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAG-3
5'-..(((.(((((((((.............)))))).))))).......(((((((((...((......)).)))))))))).....((((((((((((.........).)))))
)))))))....(((((((..((((((.....))))))..)))).)))))(((((((((((((.......)).)))))))))).))).--3'
MFE = -91.9; z-score = -4.62; ED = 43.33
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

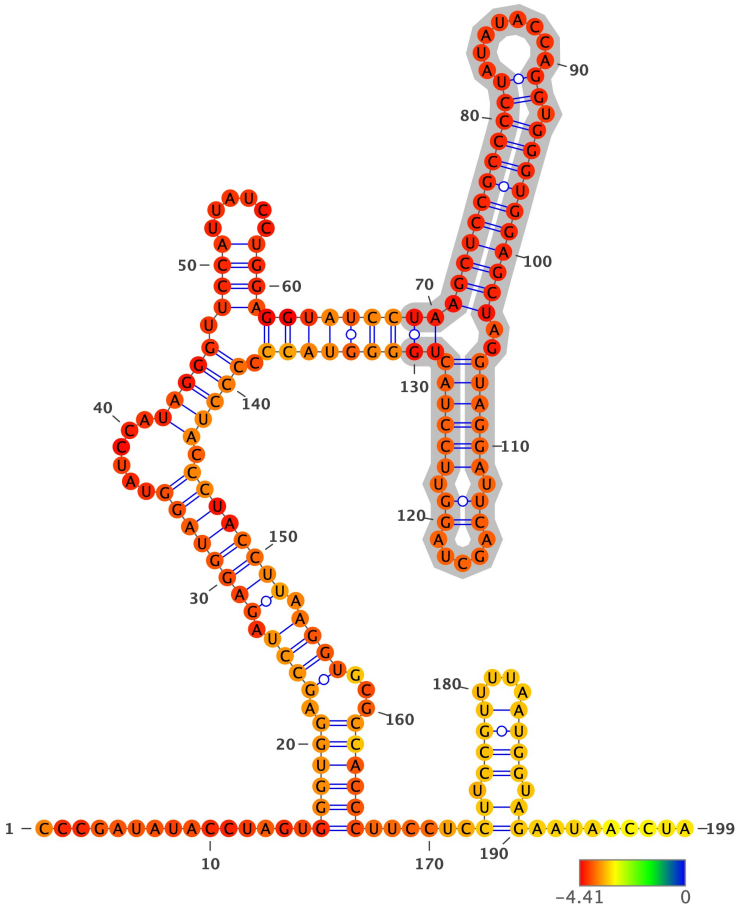
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 175 from nt 40852 to 40913 (nt 69 to 130)

```
5'-UAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUG-3'
5'-(.(((((((((((.......)).)))))))))..((((((.(.....)).)))))).)-3'
Motif MFE = -30.4; z-score = -4.26; ED = 1.57
```



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

Extracted structure model with flanking nucleotides 40784 to 40982 (motif highlighted in silver):

```
5'-CCCGAUAUACCUAGUGGGUGGAGCCUAGAGGUAGGUAUCCAUAGGGUUCCAUUAUCCUGGAGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGA
UUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUA-3
5'-...............((((((.((((.(((((((.....(((((.((((.....)))))((((((((((((((((((((.......)).)))))))))))..((((((
.((.....)).))))))))))))))).)))))).))))))).))))...)))))).....((.((((....)))).)).........-3'
MFE = -79.2; z-score = -5.08; ED = 20.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

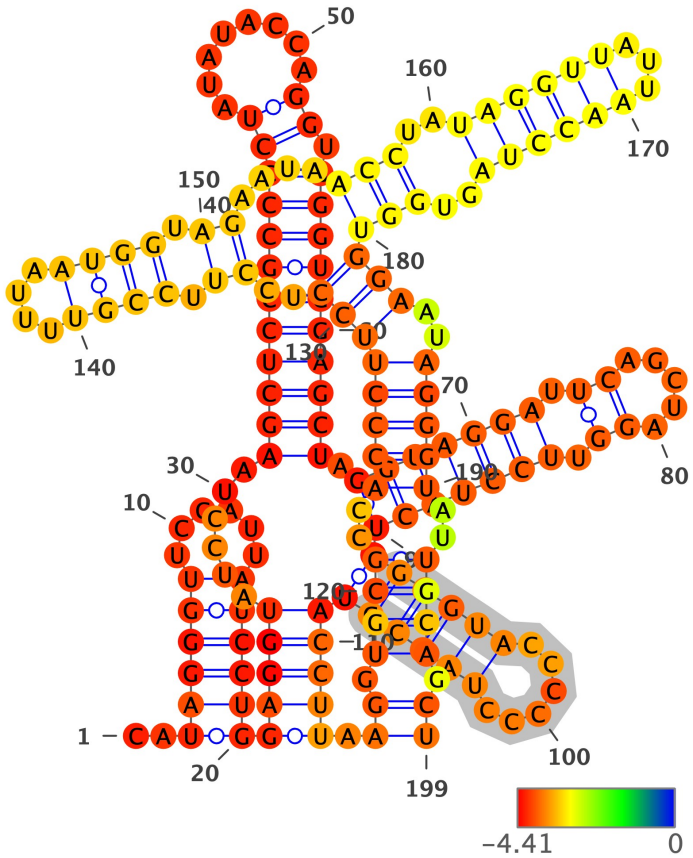
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 176 from nt 40914 to 40929 (nt 92 to 107)

```
5'-GGGUACCCCCCUACCC-3'
5'-((.((......)).))-3'
Motif MFE = -4.9; z-score = -4.13; 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 40823 to 41021 (motif highlighted in silver):

```
5'-CAUAGGGUUCCAUUAUCCUGGAGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACC
UUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCU-3
5'-..((((((.....))))))((((.....((((((((((((.......)).)))))))))).(((((((.(.....).)))))))((((((.....)))))))))
)).((.(((((..(((((((((..((.((((....)))).)).....(((..((((((...)))))))..)))))))..)))))..)))).))-3'
MFE = -74.3; z-score = -5.02; ED = 34.44
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

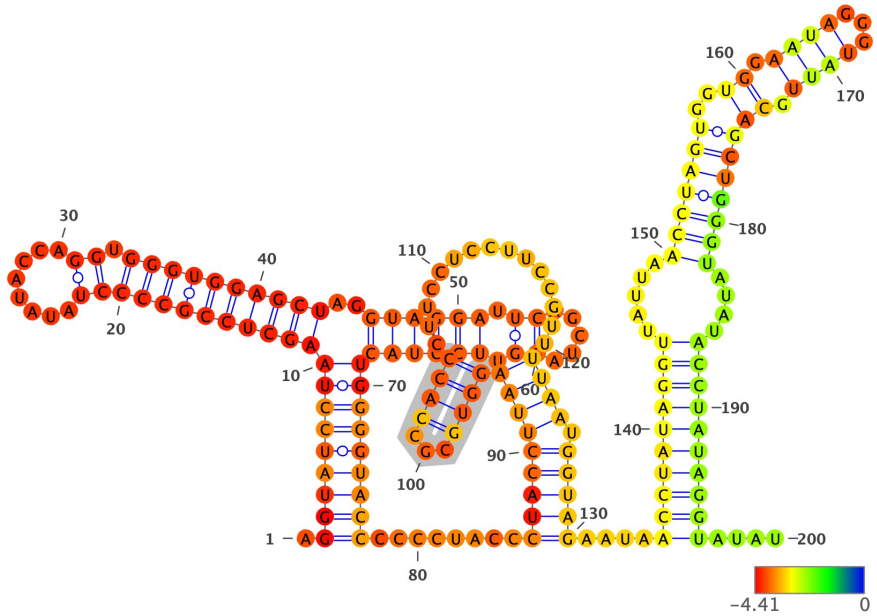
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 177 from nt 40938 to 40948 (nt 95 to 105)

```
5'-GGUGCGCCACC-3'
5'-(((.....)))-3'
Motif MFE = -2.2; z-score = -1.99; 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 40844 to 41043 (motif highlighted in silver):

```
5'-AGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCU
CCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAU-3
5'-.(((((((((((((((((((((.......)).)))))))))).((((((.(.....)).))))))))))))))).......((((((((((((...)))).....
.........)))).)))))....((((((((((.....(((((((..((.((((...)))).)))))))))....)))))))))).....-3'
MFE = -74.3; z-score = -5.33; ED = 40.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

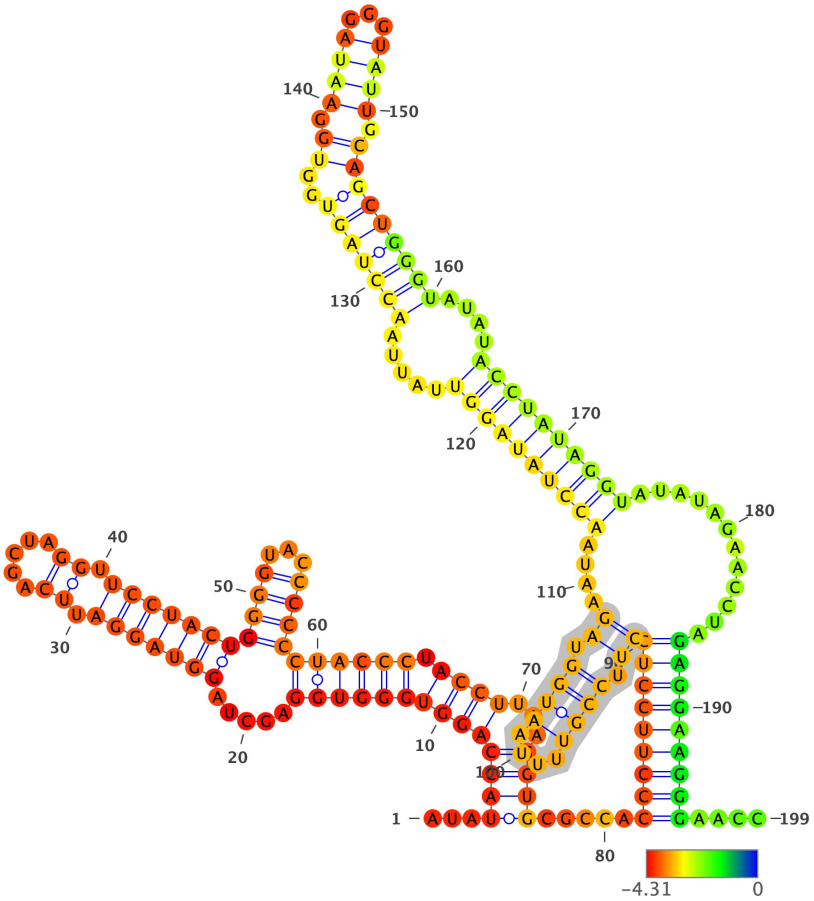
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 178 from nt 40956 to 40973 (nt 91 to 108)

```
5'-CUUCCGUUUUAAUGGUAG-3'
5'-((.((((....)))).))-3'
Motif MFE = -1.6; z-score = -1.49; ED = 1.79
```



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

Extracted structure model with flanking nucleotides 40866 to 41064 (motif highlighted in silver):

```
5'-AUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAU
AACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAACCUAGAGGAAGGGAACC-3
5'-...(((((((((((((.....(((((((.((.....)).)))))))((((...)))))))))).))))...))))).....((((((((((.((((....)))).)).)...
.((((((((((.....(((((((..((.((((...)))).)))))))))....))))))))))..............)))))))))....-3'
MFE = -74.7; z-score = -4.45; ED = 17.26
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

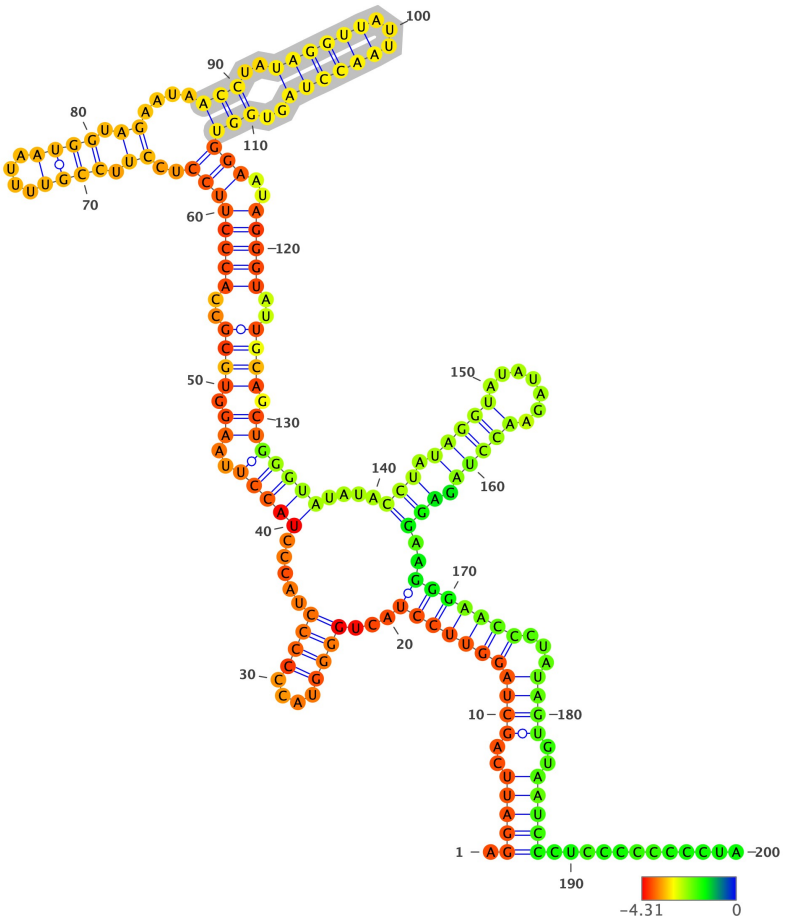
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 199--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 179 from nt 40978 to 41002 (nt 88 to 112)

```
5'-ACCUAUAGGUUAUUAACCUAGUGGU-3'
5'-(((..(((((((...)))))))..)))-3'
Motif MFE = -8.9; z-score = -4.14; 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 40891 to 41090 (motif highlighted in silver):

```
5'-AGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGG
UGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAACCUAGAGGAAGGGAACCCUAUAGUGUAAUCCCUCCCCCCCCUA-3
5'-.(((((..(((((((((((...((((....))))).....((((..((.((((..(((((((((..((.((((....)))).)).....((((..(((((((...)))))))..))
))))).)))))..)))).)))))))....(((.(((((.......)))))..))).)).)))))))...)))))..)))))............-3'
MFE = -65.9; z-score = -4.09; ED = 39.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

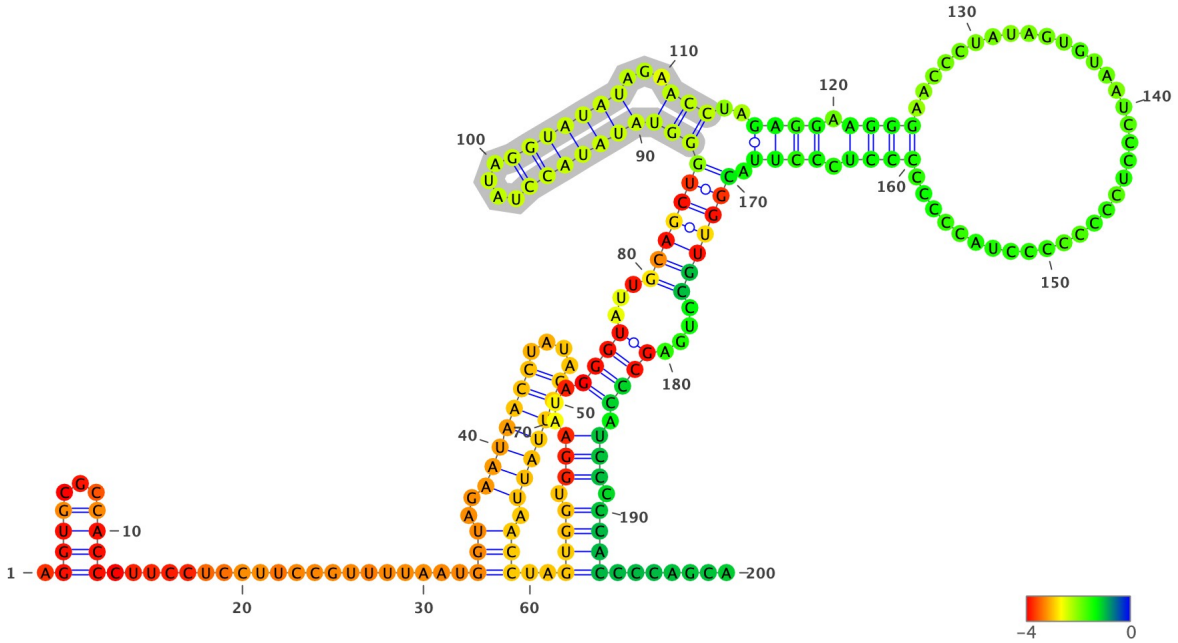
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 180 from nt 41023 to 41049 (nt 87 to 113)

```
5'-GGUAUAUACCUAUAGGUAUAUAGAACC-3'
5'-((((((((((....)))))))...)))-3'
Motif MFE = -7.3; z-score = -3.11; 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 40937 to 41136 (motif highlighted in silver):

```
5'-AGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAA
CCUAGAGGAAGGGAACCCUAUAGUGUAAUCCCUCCCCCCCCUACCCCCCCCUCCCUUACGGUUGCCUGAGCCCAUCCCCCACCCCAGCA-3
5'-.((((...)))).....................(((..(((((((....)))))))).))).((((.(((...((((...(((((((((((((((....)))))))))...)
)).((((.((((.....................................)))).)))).)))))))....)))).))).))))........-3'
MFE = -52.24; z-score = -2.27; ED = 48.07
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--origin_of_replication, id-HHV4_EBNA-3A-5, 40301-41293(+)

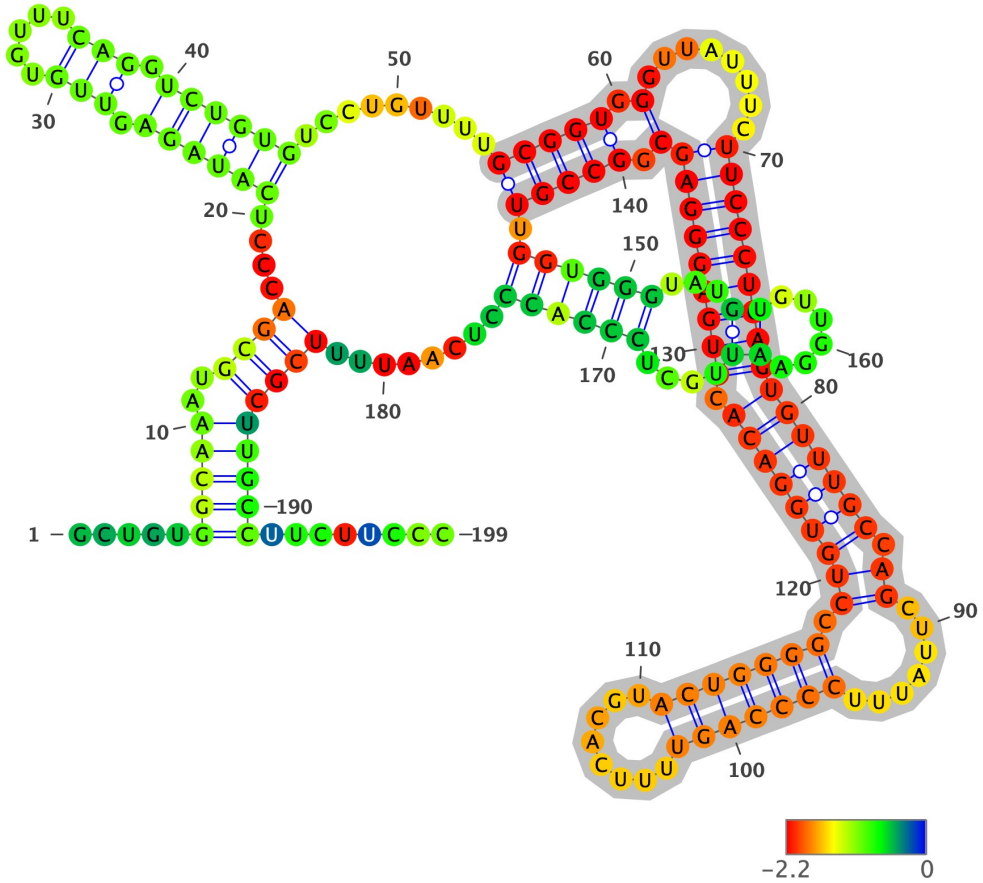
Attributes: ['ID=id-HHV4_EBNA-3A-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

10-- nt 1 to 200--direct_repeat, id-HHV4_EBNA-3A-6, 40366-41409(+)

Attributes: ['ID=id-HHV4_EBNA-3A-6', 'Note=DRleft%2C similar to 143272..144328', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 181 from nt 41807 to 41896 (nt 55 to 144)

```
5'-GCGGUGGGUUAUUUCUUCCCUCAGUGUUUGCCAGCUUAUUUCCCCAGUUUUCACGUACUGGGGCCUGUGGACACCUGAGGGAGCGGCCGU-3'
5'-(((((.(........(((((((((((((((.((.............................)))))))))).)))))))))).)))))-3'
Motif MFE = -38.2; z-score = -3.95; ED = 6.34
```



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 41753 to 41951 (motif highlighted in silver):

```
5'-GCUGUGGCAAAUGCGACCCUCAUAGAGUUGUGUUUCAGGUCUGUGUCCUGUUUUGCGGUGGGUUAUUUCUUCCCUCAGUGUUUGCCAGCUUAUUUCCCCAGUUUUCACGUA
CUGGGGCCUGUGGACACCUGAGGGAGCGGCCGUUGGUGGGUAUGUGUUGGAAUUGCUCCCACCCUCAAUUUUCGCUUGCCUUCUUCCC-3
5'-.....((((((..((((....((((((.(((.....))).)))))).........(((((.(........((((((((((((((((.((.......(((((((........)
))))))).)))))))))).))))))))))).)))))).(((((((...((......))....)))))).........)))))))))........-3'
MFE = -68.3; z-score = -2.58; ED = 7.3
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_BHRF1, 41471-43251(+)

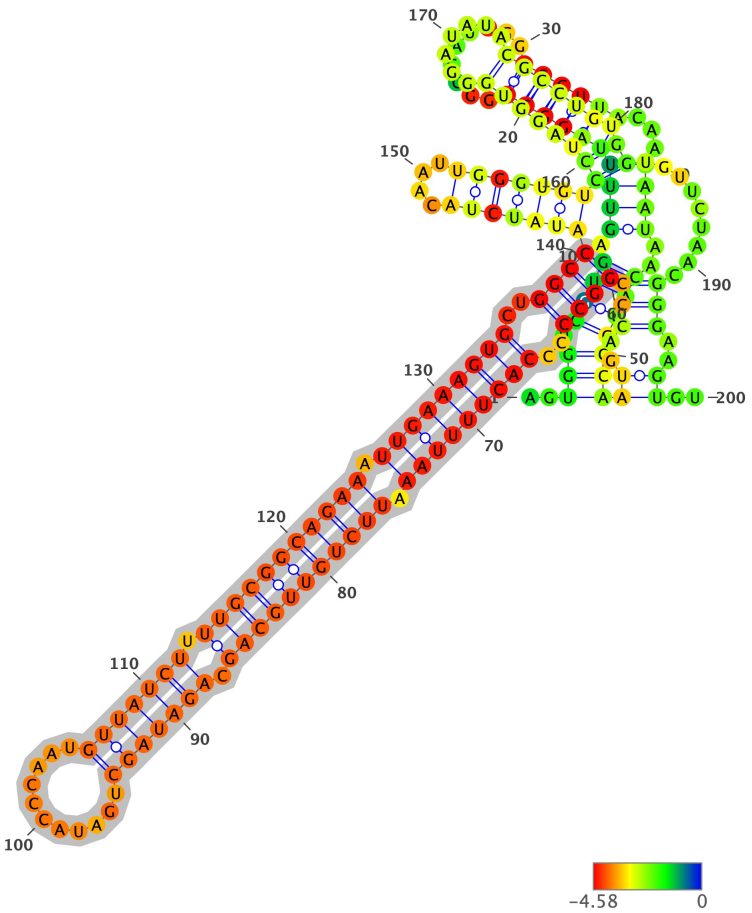
Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 1 to 199--intron, id-HHV4_BHRF1, 41629-42046(+)

Attributes: ['ID=id-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Note=spliced in some BHRF1 transcripts%3B acceptor site is utilised by latent transcripts', 'gbkey=intron', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1']

NC_007605.1 (forward strand): Structure number 182 from nt 42840 to 42920 (nt 60 to 140)

```
5'-GGCCCCCACUUUUAAAUUCUGUUGCAGCAGAUAGCUGAUACCCAAUGUUAUCUUUUGCGGCAGAAAUUGAAAGUGCUGGCC-3'
5'-((((..(((((((((.((((((((((.(((((((.........)))))))).)))))))))))).)))))))))..))))-3'
Motif MFE = -39.9; z-score = -6.78; 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 42781 to 42980 (motif highlighted in silver):

```
5'-AGUGGUCGUGAGUUUUAGGCCGGCCAUGGGGGCUUACAAGAAUAACAUGCCAAUGACCCGGCCCCCACUUUUAAAUUCUGUUGCAGCAGAUAGCUGAUACCCAAUGUUAUC
UUUUGCGGCAGAAAUUGAAAGUGCUGGCCAUAUCUACAAUUGGGUGUCCUAGGUGGGAUAUACGCCUGUGGUGUUCUAACGGGAAGUGU-3
5'-..(((.((((.((((((((((.........)))))).....)))).)).))))))))((..(((((((..(((((((((.((((((((((.(((((((.........)))))))
).)))))))))).)))))))))..))))(((((((....)))))))((((((((.......)))))).)).........)))..))..-3'
MFE = -71.0; z-score = -3.32; ED = 39.09
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_BHRF1, 41471-43251(+)

Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 73 to 94--miRNA, rna-HHV4_BHRF1-2, 42853-42874(+)

Attributes: ['ID=rna-HHV4_BHRF1-2', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

11-- nt 73 to 94--exon, exon-HHV4_BHRF1-2-1, 42853-42874(+)

Attributes: ['ID=exon-HHV4_BHRF1-2-1', 'Parent=rna-HHV4_BHRF1-2', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

12-- nt 108 to 129--miRNA, rna-HHV4_BHRF1-3, 42888-42909(+)

Attributes: ['ID=rna-HHV4_BHRF1-3', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

13-- nt 108 to 129--exon, exon-HHV4_BHRF1-3-1, 42888-42909(+)

Attributes: ['ID=exon-HHV4_BHRF1-3-1', 'Parent=rna-HHV4_BHRF1-3', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

14-- nt 188 to 200--miRNA, rna-HHV4_BHRF1-4, 42968-42989(+)

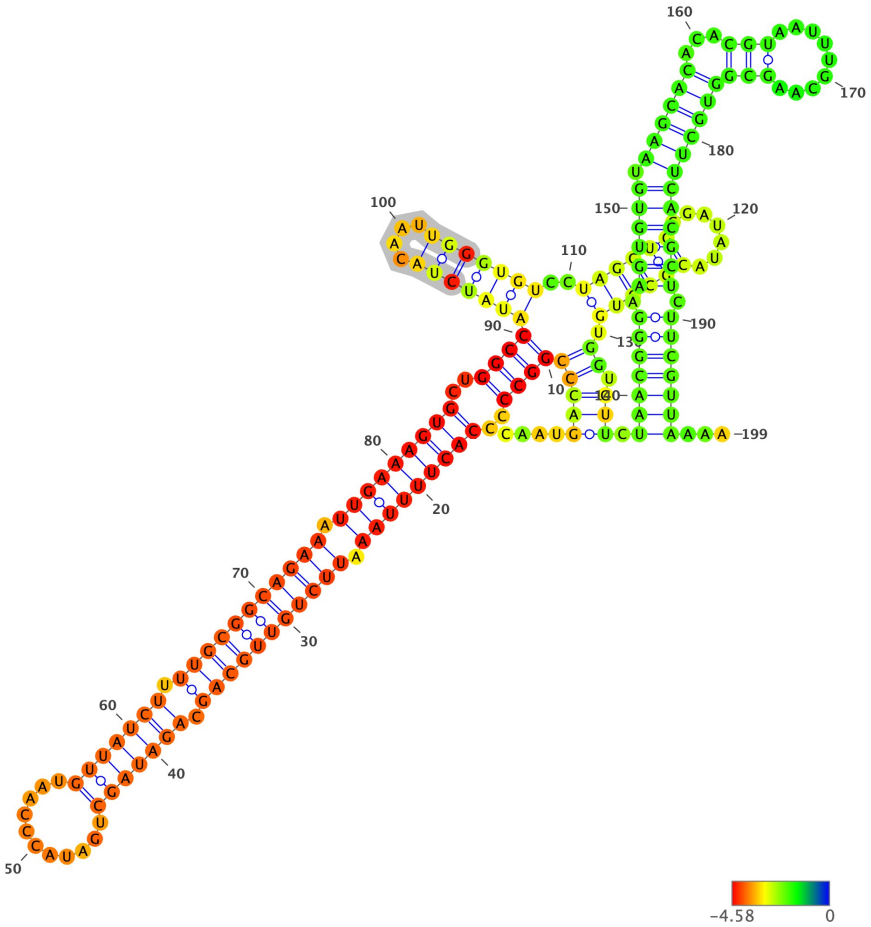
Attributes: ['ID=rna-HHV4_BHRF1-4', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

15-- nt 188 to 200--exon, exon-HHV4_BHRF1-4-1, 42968-42989(+)

Attributes: ['ID=exon-HHV4_BHRF1-4-1', 'Parent=rna-HHV4_BHRF1-4', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

NC_007605.1 (forward strand): Structure number 183 from nt 42925 to 42934 (nt 95 to 104)

```
5'-CUACAAUUGG-3'
5'-(........)-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 42831 to 43029 (motif highlighted in silver):

```
5'-CAAUGACCCGGCCCCCACUUUUAAAUUCUGUUGCAGCAGAUAGCUGAUACCCAAUGUUAUCUUUUGCGGCAGAAAUUGAAAGUGCUGGCCAUAUCUACAAUUGGGUGUCCU
AGGUGGGAUAUACGCCUGUGGUGUUCUAACGGGAAGUGUGUAAGCACACACGUAAUUUGCAAGCGGUGCUUCACGCUCUUCGUUAAAA-3
5'-....(((((((((..(((((((((.((((((((((.(((((((.........)))))))).)))))))))))).)))))))))..))))(((((((....)))))))..(
(((((.......)))))).)).))).(((((((.((((((.((((((...(((.........)))))))))))))))))).)))))))...-3'
MFE = -76.5; z-score = -5.24; ED = 15.53
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_BHRF1, 41471-43251(+)

Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 23 to 44--miRNA, rna-HHV4_BHRF1-2, 42853-42874(+)

Attributes: ['ID=rna-HHV4_BHRF1-2', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

11-- nt 23 to 44--exon, exon-HHV4_BHRF1-2-1, 42853-42874(+)

Attributes: ['ID=exon-HHV4_BHRF1-2-1', 'Parent=rna-HHV4_BHRF1-2', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

12-- nt 58 to 79--miRNA, rna-HHV4_BHRF1-3, 42888-42909(+)

Attributes: ['ID=rna-HHV4_BHRF1-3', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

13-- nt 58 to 79--exon, exon-HHV4_BHRF1-3-1, 42888-42909(+)

Attributes: ['ID=exon-HHV4_BHRF1-3-1', 'Parent=rna-HHV4_BHRF1-3', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

14-- nt 138 to 159--miRNA, rna-HHV4_BHRF1-4, 42968-42989(+)

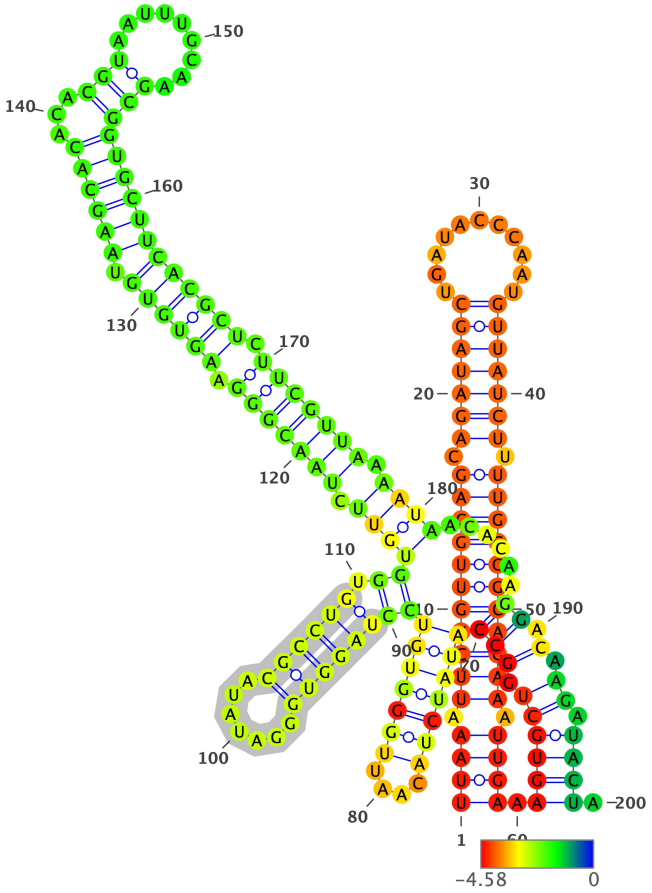
Attributes: ['ID=rna-HHV4_BHRF1-4', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

15-- nt 138 to 159--exon, exon-HHV4_BHRF1-4-1, 42968-42989(+)

Attributes: ['ID=exon-HHV4_BHRF1-4-1', 'Parent=rna-HHV4_BHRF1-4', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

NC_007605.1 (forward strand): Structure number 184 from nt 42941 to 42959 (nt 91 to 109)

```
5'-UAGGUGGGAUAUACGCCUG-3'
5'-((((((.......))))))-3'
Motif MFE = -6.3; z-score = -3.24; 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 42851 to 43050 (motif highlighted in silver):

```
5'-UUAAAUUCUGUUGCAGCAGAUAGCUGAUACCCAAUGUUAUCUUUUGCGGCAGAAAUUGAAAGUGCUGGCCAUAUCUACAAUUGGGUGUCCUAGGUGGGAUAUACGCCUGUG
GUGUUCUAACGGGAAGUGUGUAAGCACACACGUAAUUUGCAAGCGGUGCUUCACGCUCUUCGUUAAAAUAACACAAGGACAAGAUACUA-3
5'-((((.(((((((((((.(((((((.........)))))))).)))))))))))).)))).((((((.((((((((((....)))))))))(((((((.......)))))))).)
)(((((.(((((((.((((((.((((((...(((.........)))))))))))))))).)))))))).)))).....)).).)).)))).-3'
MFE = -63.5; z-score = -4.3; ED = 24.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_BHRF1, 41471-43251(+)

Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 3 to 24--miRNA, rna-HHV4_BHRF1-2, 42853-42874(+)

Attributes: ['ID=rna-HHV4_BHRF1-2', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

11-- nt 3 to 24--exon, exon-HHV4_BHRF1-2-1, 42853-42874(+)

Attributes: ['ID=exon-HHV4_BHRF1-2-1', 'Parent=rna-HHV4_BHRF1-2', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2*']

12-- nt 38 to 59--miRNA, rna-HHV4_BHRF1-3, 42888-42909(+)

Attributes: ['ID=rna-HHV4_BHRF1-3', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

13-- nt 38 to 59--exon, exon-HHV4_BHRF1-3-1, 42888-42909(+)

Attributes: ['ID=exon-HHV4_BHRF1-3-1', 'Parent=rna-HHV4_BHRF1-3', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

14-- nt 118 to 139--miRNA, rna-HHV4_BHRF1-4, 42968-42989(+)

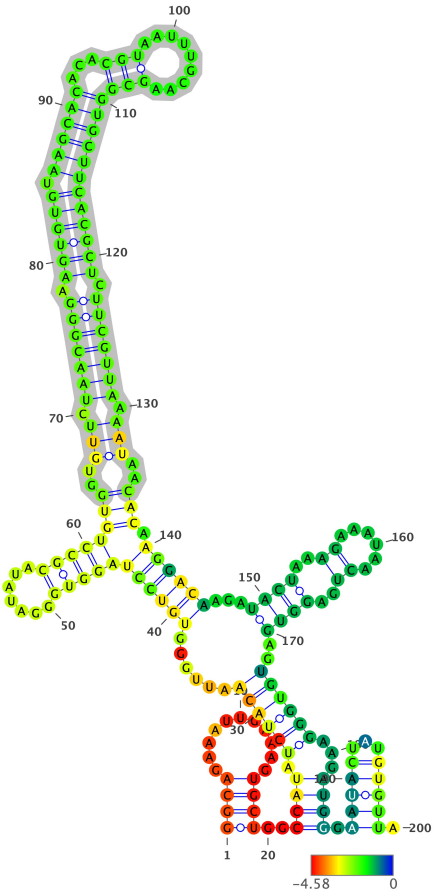
Attributes: ['ID=rna-HHV4_BHRF1-4', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

15-- nt 118 to 139--exon, exon-HHV4_BHRF1-4-1, 42968-42989(+)

Attributes: ['ID=exon-HHV4_BHRF1-4-1', 'Parent=rna-HHV4_BHRF1-4', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

NC_007605.1 (forward strand): Structure number 185 from nt 42961 to 43033 (nt 64 to 136)

```
5'-GGUGUUCUAACGGGAAGUGUGUAAGCACACACGUAAUUUGCAAGCGGUGCUUCACGCUCUUCGUUAAAAUAAC-3'
5'-(....(.(((((((.(.........................................).)))))))).)....)-3'
Motif MFE = -24.0; z-score = -3.58; ED = 7.2
```



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 42898 to 43097 (motif highlighted in silver):

```
5'-GGCAGAAAUUGAAAGUGCUGGCCAUAUCUACAAUUGGGUGUCCUAGGUGGGAUAUACGCCUGUGGUGUUCUAACGGGAAGUGUGUAAGCACACACGUAAUUUGCAAGCGGU
GCUUCACGCUCUUCGUUAAAAUAACACAAGGACAAGAUACUAAAGAAAUAACUGAGGUGAGUGUGGGAAGAUGGGAAUACUAUGUGUUA-3
5'-(((((...........))))).((((.((((((.....((((((((((.......)))))))((..((((.(((((((.((((((.((((((...((((.........)))))
))))))))))).)))))))).))))..))).)))))).....((((..((......))..)))))..)))))))...)))).((((((...)))))).-3'
MFE = -52.1; z-score = -1.68; ED = 43.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_BHRF1, 41471-43251(+)

Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 1 to 12--miRNA, rna-HHV4_BHRF1-3, 42888-42909(+)

Attributes: ['ID=rna-HHV4_BHRF1-3', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

11-- nt 1 to 12--exon, exon-HHV4_BHRF1-3-1, 42888-42909(+)

Attributes: ['ID=exon-HHV4_BHRF1-3-1', 'Parent=rna-HHV4_BHRF1-3', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-2']

12-- nt 71 to 92--miRNA, rna-HHV4_BHRF1-4, 42968-42989(+)

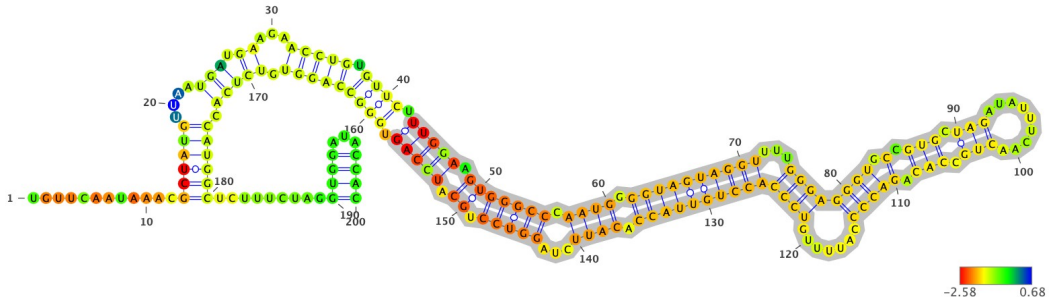
Attributes: ['ID=rna-HHV4_BHRF1-4', 'Parent=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

13-- nt 71 to 92--exon, exon-HHV4_BHRF1-4-1, 42968-42989(+)

Attributes: ['ID=exon-HHV4_BHRF1-4-1', 'Parent=rna-HHV4_BHRF1-4', 'Dbxref=GeneID:3783706', 'gbkey=ncRNA', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'product=ebv-miR-BHRF1-3']

NC_007605.1 (forward strand): Structure number 186 from nt 43267 to 43381 (nt 43 to 157)

```
5'-UUGGAAGUGGGCCCAAUGGGGUAGUAGGUUUUGGGAGGGUGCCGUGCUAGAUAUUUCAACUGCCACAGACCCCAUUUUGUCCCACCUGUUACCACAUUCUAGGUCCUGCAU
CCAG-3'
5'-(((.(.(((((((.....................................................................................)))))).)).)
.)))-3'
Motif MFE = -41.1; z-score = -2.5; ED = 11.81
```



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 43225 to 43424 (motif highlighted in silver):

```
5'-UGUUCAAUAAACGCUAUGUUAAUGAUGAAGAACCUGUGUUCUUUGGAAGUGGGCCCAAUGGGGUAGUAGGUUUUGGGAGGGUGCCGUGCUAGAUAUUUCAACUGCCACAGA
CCCCAUUUUGUCCCACCUGUUACCACAUUCUAGGUCCUGCAUCCAGUGGGCCAGGUGUCUCACCAUGGCUCUUUCUAGGUGGAUACCAC-3
5'-............(((((.....(((.((...(((((.((((.(((((.(((((((.((((.(((((((((((...((((((((.(.(((.(((.........)))).)))).))
)))).......)))))))))))))).))))...)))))).)).)))))).)))))))))).)))))).)))))).........((((...))))-3'
MFE = -64.1; z-score = -1.85; ED = 31.97
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 27--gene, gene-HHV4_BHRF1, 41471-43251(+)

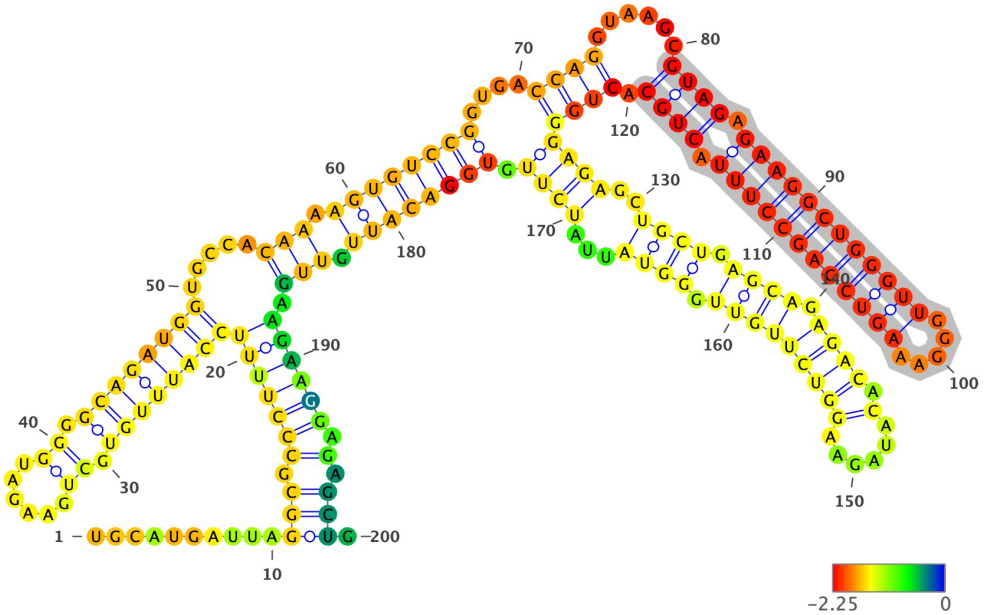
Attributes: ['ID=gene-HHV4_BHRF1', 'Dbxref=GeneID:3783706', 'Name=BHRF1', 'Note=Bcl-2 family%3B can also be expressed from Cp or Wp type of spliced RNA', 'gbkey=Gene', 'gene=BHRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BHRF1']

10-- nt 6 to 11--polyA_signal_sequence, id-HHV4_BHRF1-3, 43230-43235(+)

Attributes: ['ID=id-HHV4_BHRF1-3', 'Dbxref=GeneID:3783706', 'gbkey=regulatory', 'gene=BHRF1', 'locus_tag=HHV4_BHRF1', 'regulatory_class=polyA_signal_sequence']

NC_007605.1 (forward strand): Structure number 187 from nt 44039 to 44077 (nt 81 to 119)

```
5'-GUAGAGAAGGCUGGGUUGGGAAAGUCCAGCCUUUACUGC-3'
5'-((((.(((((((((((.....)))))))))))).))))-3'
Motif MFE = -19.1; z-score = -5.01; 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 43959 to 44158 (motif highlighted in silver):

```
5'-UGCAUGAUUAGGCGCCCUUUUCCAUUUGUGCUGAAGAUGGGGCAGAUGGUGCCACAAAAGUGUCCGGUGACCAGGUAAGCGUAGAGAAGGCUGGGUUGGGAAAGUCCAGCC
UUUACUGCACUGGGAGAGCUGCUGAGCAGAGACACAUAGAAGGUCUUGUUGGGUAUUAUCUUGUGGACAUUGUUGAAGAAGGAGAGCUG-3
5'-..........(((.((((((((((((((.((......)).)))))))).....(((.(((((((....((((......((((.((((((((((((....)))))))))
)))).)))).)))))((((..((((.((((.((((.(......)))))))))).)))).....)))).)))))))).))).)))))).).))).-3'
MFE = -65.5; z-score = -2.04; ED = 33.2
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

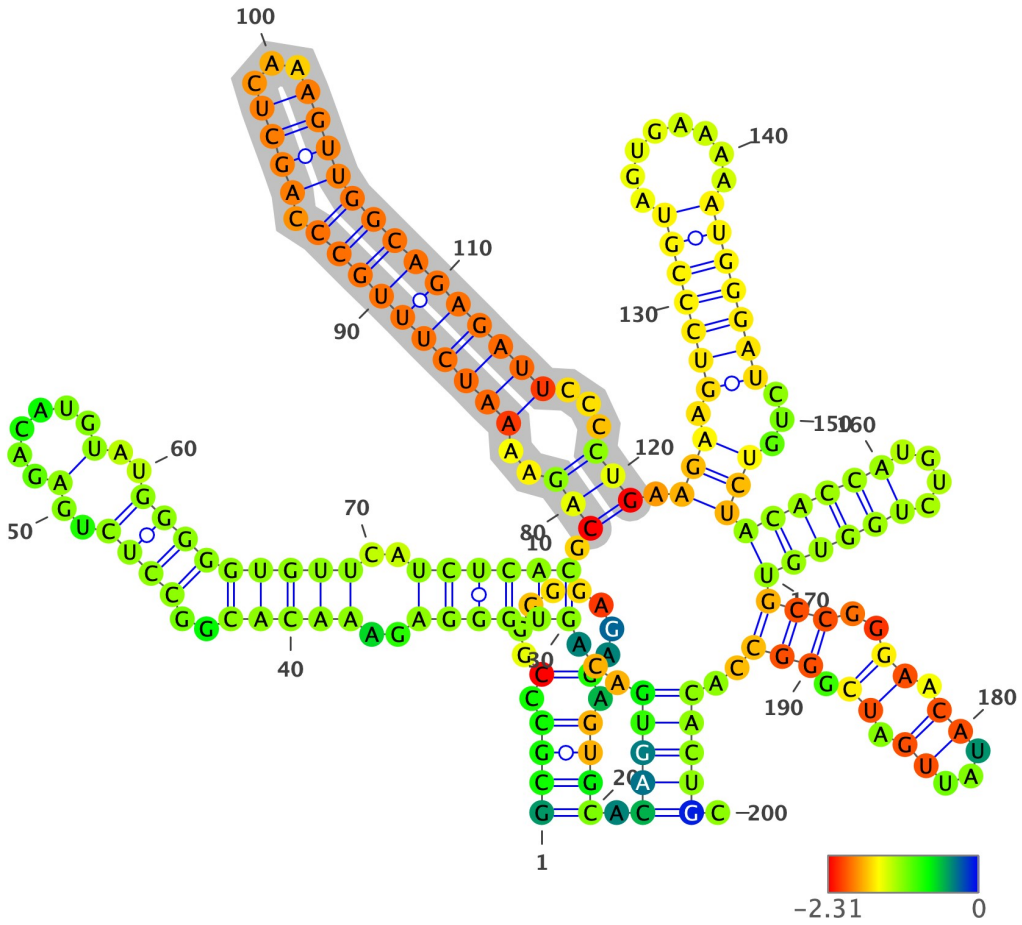
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 188 from nt 44342 to 44384 (nt 79 to 121)

```
5'-CAGAAAAUCUUUGCCCAGCUCAAAGUUGGCAGAGAUUCCCCUG-3'
5'-(....((.............................)).....)-3'
Motif MFE = -15.7; z-score = -3.75; 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 44264 to 44463 (motif highlighted in silver):

```
5'-GCGCCCGGGGGAGAGAGUGCACAGUGACAGUGGGAGAAACACGGCCUCUGAGACAUGUAUGGGGGUGUUCAUCUCACGCAGAAAAUCUUUGCCCAGCUCAAAGUUGGCAGA
GAUUCCCCUGAAGAAGUCCCGUAGUGAAAAAUGGGAUCUGUCUACACCAUGUCUGGUGUGCCGGGAACAUAUUGAUCGGGCCACACUGC-3
5'-((((.(........).)))).(((((...(((((((..((((((..((((..(......)..)))))))))..)))))).(((..((((((((((.((((...)))))))))))
))))...))).(((.(((((((.......)))))))...)))((((((....)))))))((..((.((...)).)).)))..)))))).-3'
MFE = -67.1; z-score = -1.28; ED = 19.69
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

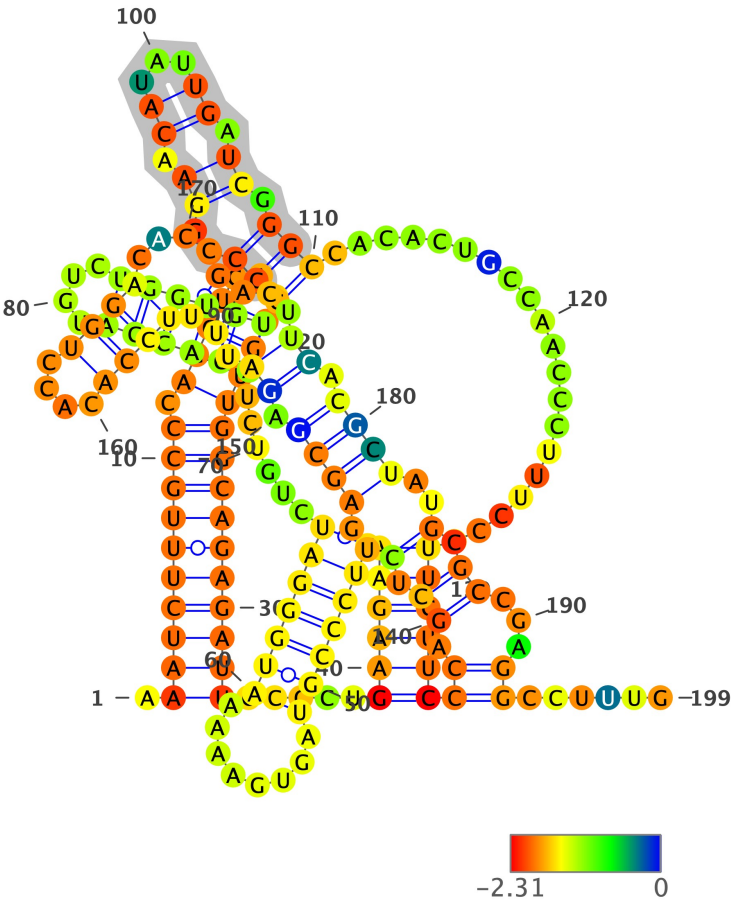
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 189 from nt 44435 to 44454 (nt 90 to 109)

```
5'-CCGGGAACAUAUUGAUCGGG-3'
5'-((...(.((...)).)..))-3'
Motif MFE = -2.9; z-score = -0.42; 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 44346 to 44544 (motif highlighted in silver):

```
5'-AAAUCUUUGCCCAGCUCAAAGUUGGCAGAGAUUCCCCUGAAGAAGUCCCGUAGUGAAAAAUGGGAUCUGUCUACACCAUGUCUGGUGUGCCGGGAACAUAUUGAUCGGGCC
ACACUGCCAACCCUUUCCAUUCUUCCCAGCUCUGAGCGAGAUUUUCCACACCUGGACACCGACUUCACGCUAUGCGCCGAGGCCUUUG-3
5'-.((((((((((.((((...)))))))))))))).....((((((((((((.......)))))))).....((((((....)))))))((..((.((...)).)).)))).
.................)))))))(.((.(..(((((.((.((((((....))))....)).)).)))))..).)).....)).....-3'
MFE = -48.6; z-score = -0.75; ED = 45.02
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

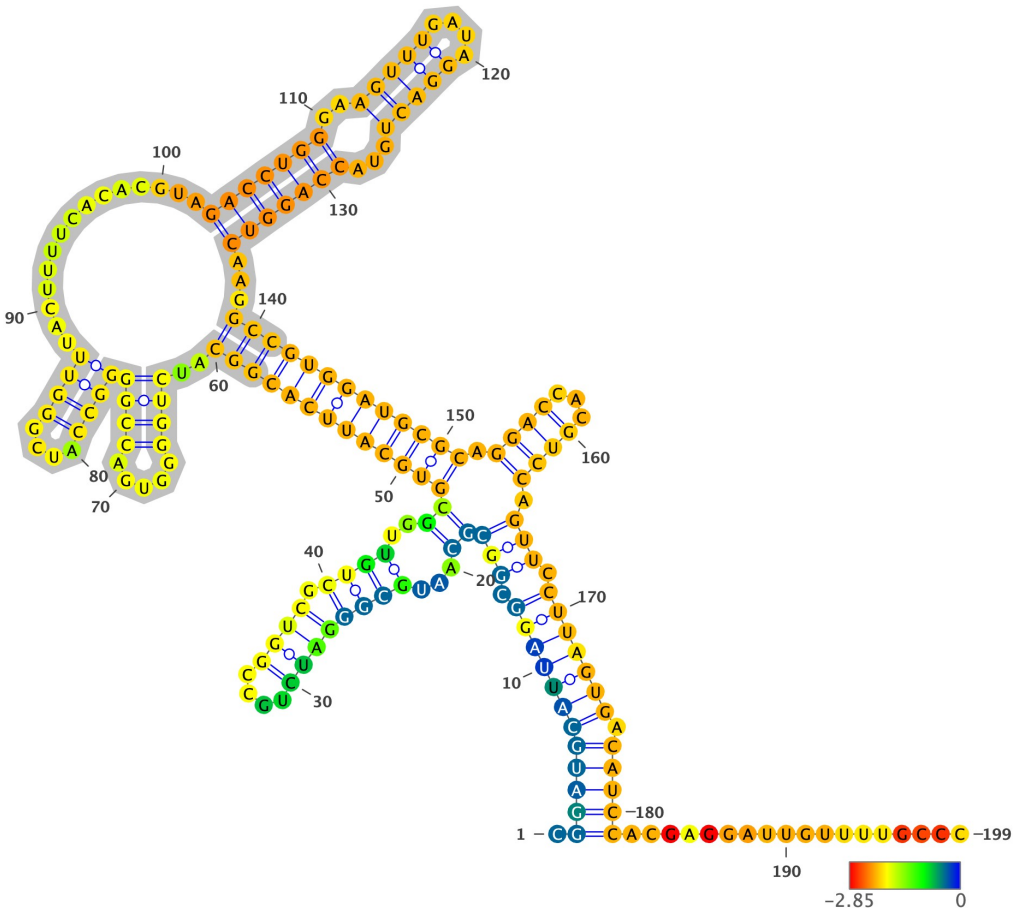
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 190 from nt 44624 to 44707 (nt 58 to 141)

```
5'-GGCAUCUGGGGUGACCGGGGCCAUCGGGUUUACUUUUCACACGUAGACCUGGGAAGUUUGAUAGGACUGUACCAGGUCAAGGCC-3'
5'-(((.........................................(((((((..((((((....)))))...)))))))...)))-3'
Motif MFE = -29.1; z-score = -1.3; ED = 12.8
```



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 44567 to 44765 (motif highlighted in silver):

```
5'-CGGAUGCAUUAGGCGGCGCAAUGCGGGAUCUGCCGGUCGCUGUUGGCGUGCAUUCACGGCAUCUGGGGUGACCGGGGCCAUCGGGUUUACUUUUCACACGUAGACCUGGGA
AGUUUGAUAGGACUGUACCAGGUCAAGGCCGUGGAUGCGCAGGACCACGUCCAGUUCCUUAGUGACAUCCACGAGGAUUGUUUUGCCC-3
5'-.(((((((((((.((((...(((((((((....)))).)))))..))((((((((((((..((((.....)))))((((....)))).............(((((((..
(((((....)))))...)))))))...))))))))))))).((((...)))).))).)))))))).))))).................-3'
MFE = -77.2; z-score = -1.4; ED = 40.23
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

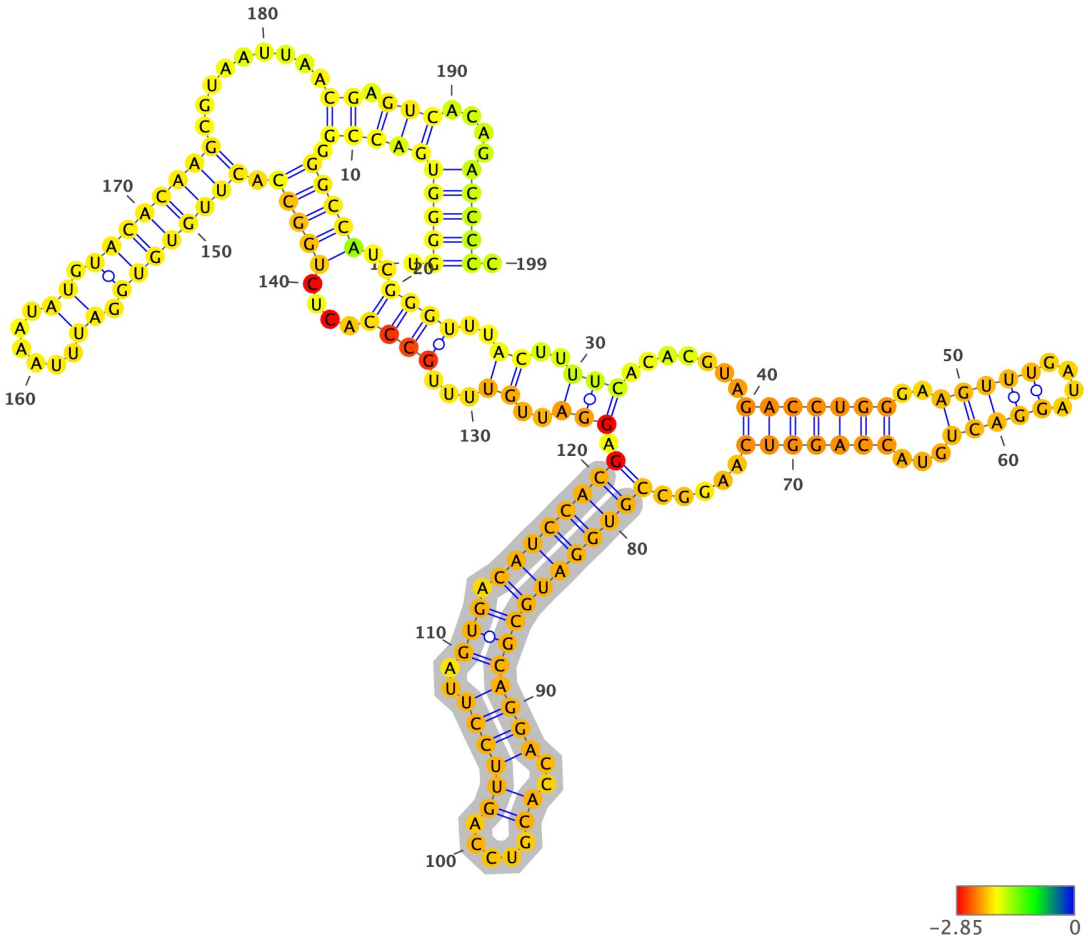
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 191 from nt 44708 to 44749 (nt 79 to 120)

```
5'-GUGGAUGCGCAGGACCACGUCCAGUUCCUUAGUGACAUCCAC-3'
5'-(((((((((((((..((.....)))))))..))).)))))))-3'
Motif MFE = -16.2; z-score = -3.04; ED = 2.7
```



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 44630 to 44828 (motif highlighted in silver):

```
5'-UGGGGUGACCGGGGCCAUCGGGUUUACUUUUCACACGUAGACCUGGGAAGUUUGAUAGGACUGUACCAGGUCAAGGCCGUGGAUGCGCAGGACCACGUCCAGUUCCUUAGU
GACAUCCACGAGGAUUGUUUUGCCCACUCUGGCCACUUGUGUGGAUUUAAAUAUGUACACAAGCGUAAUUAACGAGUCACAGACCCCC-3
5'-.((((((((((.(((((..(((((..((..(((.......(((((((..((((((....)))))).....))))))).....((((((((((((((..((.....)))))))..))
).)))))))).))))..))...))))....)))))).((((((((.((......)).)))))))).........)).))).....)))))).-3'
MFE = -73.8; z-score = -3.31; ED = 11.68
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

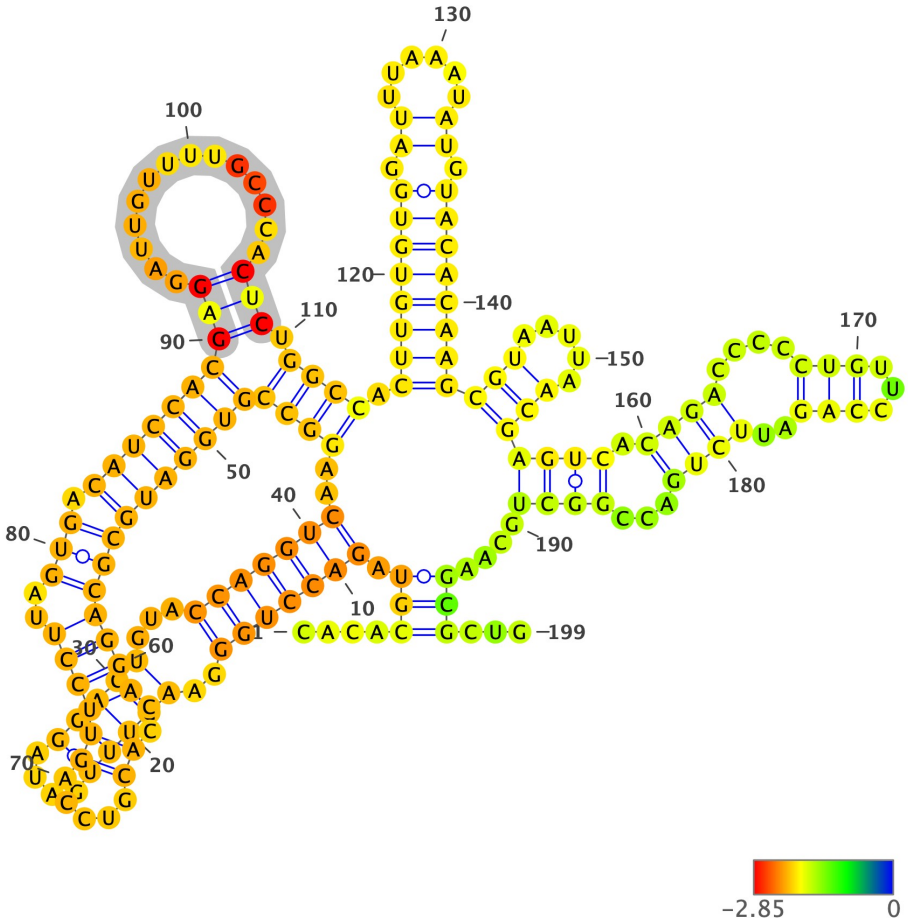
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 192 from nt 44750 to 44769 (nt 90 to 109)

```
5'-GAGGAUUGUUUUGCCCACUC-3'
5'-(.(..............).)-3'
Motif MFE = -0.1; z-score = 0.87; ED = 4.04
```



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 44661 to 44859 (motif highlighted in silver):

```
5'-CACACGUAGACCUGGGAAGUUUGAUAGGACUGUACCAGGUCAAGGCCGUGGAUGCGCAGGACCACGUCCAGUUCCUUAGUGACAUCCACGAGGAUUGUUUUGCCCACUCUG
GCCACUUGUGUGGAUUUAAAUAUGUACACAAGCGUAAUUAACGAGUCACAGACCCCCUGUUCCAGAUUCUGACCGGCUGCAAGCGCUG-3
5'-....(((.(((((((..((((((....)))))...)))))))..((((((((((((((((((..((.....)))))))..))).)))))))((.............)))).)
)))).((((((((.(((.....)).)))))))))((.....)))((((.((((....(((...)))..)))))...)))))....)))...-3'
MFE = -63.2; z-score = -1.8; ED = 24.85
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

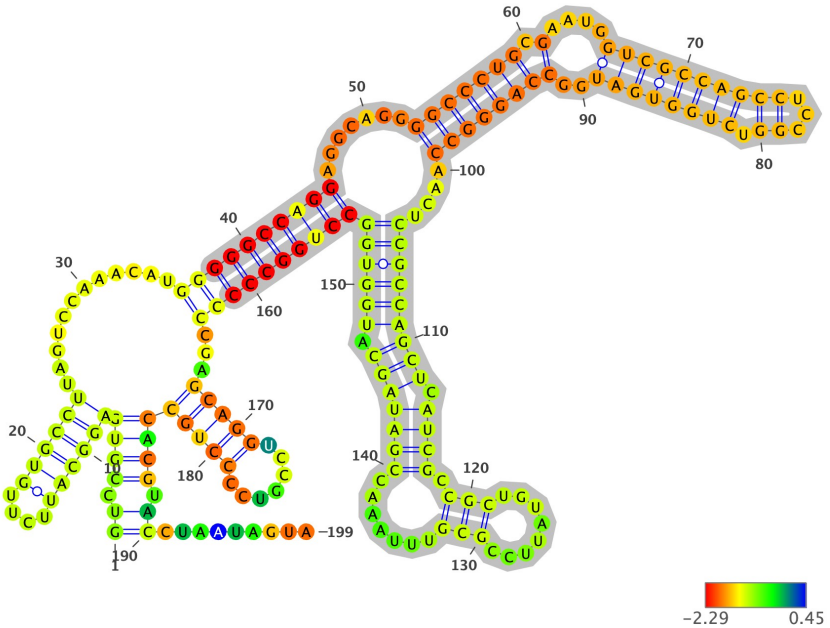
Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 193 from nt 45211 to 45334 (nt 38 to 161)

```
5'-GGGCCAGGAGGCAGGGGCCCUGCGAAUGGUCGCCAGCCUCCGGUCUGGUGAUGGCCAGGGCCAACUCCGCCAGCUCAUCGCCGCUGUAUUCCGCGUUUAAACCGAUAGCAU
GGUGGCCUGGCCC-3'
5'-(((((.((.......................................................................................................
.....)).)))))-3'
Motif MFE = -61.2; z-score = -2.74; ED = 8.6
```



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 45174 to 45372 (motif highlighted in silver):

```
5'-GUCCGUGAGGCAUUCUUGUGCCUUAGUCCAAACAUGGGGGCCAGGAGGCAGGGGCCCUGCGAAUGGUCGCCAGCCUCCGGUCUGGUGAUGGCCAGGGCCAACUCCGCCAGC
UCAUCGCCGCUGUAUUCCGCGUUUAAACCGAUAGCAUGGUGGCCUGGCCCCCCGAGCAGGUCCGUCCCCUGCCACGUACCUAAUAGUA-3
5'-((.(((((((((....))))))).............((((((((((.......(((((((.(....((((((((((...)).)))))))).))))))))....((((((((
(.((((.(((........)))).......)))))))).))))))))))))))...(((((.......)))))))))).))..........-3'
MFE = -87.6; z-score = -2.46; ED = 12.72
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

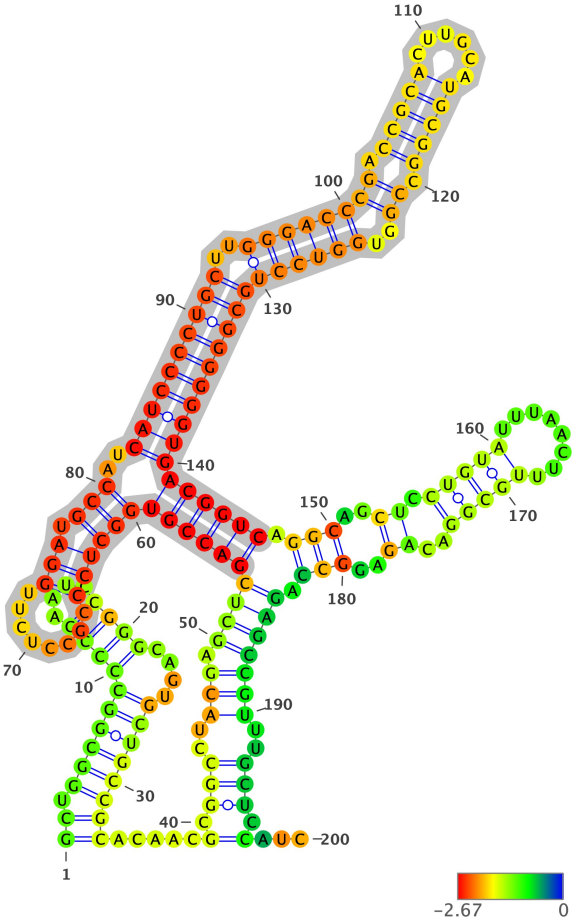
8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

NC_007605.1 (forward strand): Structure number 194 from nt 48951 to 49043 (nt 54 to 146)

5'-GACCGUGGCUCCCGCCUCUUGGAUGCCAUCAUCCCCUGCUUGGGACCCGACCGCACUUGCAUGCGGCCGGUGGUCCUGCGGGGGGUGACGGUC-3'

5'-(((((((((((.....))).)))..((((((((((..((((((((.....)).)))))))))))))))))))))-3'
Motif MFE = -52.4; z-score = -3.48; ED = 7.55



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

Extracted structure model with flanking nucleotides 48898 to 49097 (motif highlighted in silver):

5'-GCUGGCGGCCCCGAAUCCGGGCAGUGCUGCCGCACAACGCGGCCUACGAGCUCGACCGUGGCUCCCGCCUCUUGGAUGCCAUCAUCCCCUGCUUGGGACCCGACCGCACUUGCAUGCGGCCGGUGGUCCUGCGGGGGGUGACGGUCAGGCAGCUCCUGUAUUUAACUUUGCGGACAGAGGCCAGAGCCGUUUGCUCCAUC-3
5'-((.((((((((((....)))).....))))))).....(.((((..((((.((((((((((((((((.....)))).))))..((((((((((..((((((((.(((((...
...)))))).))..))))))))))))))))))))).((((..((.(((((.....)))))..))..)))).)))))))..)))).)...-3'
MFE = -94.6; z-score = -2.58; ED = 23.42

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_BFRF1A, 46236-49786(+)

Attributes: ['ID=gene-HHV4_BFRF1A', 'Dbxref=GeneID:3783759', 'Name=BFRF1A', 'Note=core gene', 'gbkey=Gene', 'gene=BFRF1A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF1A']

10-- nt 1 to 200--gene, gene-HHV4_BFRF1, 46544-49786(+)

Attributes: ['ID=gene-HHV4_BFRF1', 'Dbxref=GeneID:3783699', 'Name=BFRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BFRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF1']

11-- nt 1 to 200--gene, gene-HHV4_BFRF2, 47520-49786(+)

Attributes: ['ID=gene-HHV4_BFRF2', 'Dbxref=GeneID:3783700', 'Name=BFRF2', 'Note=betagamma gene', 'gbkey=Gene', 'gene=BFRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF2']

12-- nt 1 to 200--CDS, cds-YP_401650.1, 47520-49295(+)

Attributes: ['ID=cds-YP_401650.1', 'Parent=gene-HHV4_BFRF2', 'Dbxref=UniProtKB/TrEMBL:Q777G6,Genbank:YP_401650.1,GeneID:3783700', 'Name=YP_401650.1', 'gbkey=CDS', 'gene=BFRF2', 'locus_tag=HHV4_BFRF2', 'product=protein UL49', 'protein_id=YP_401650.1']

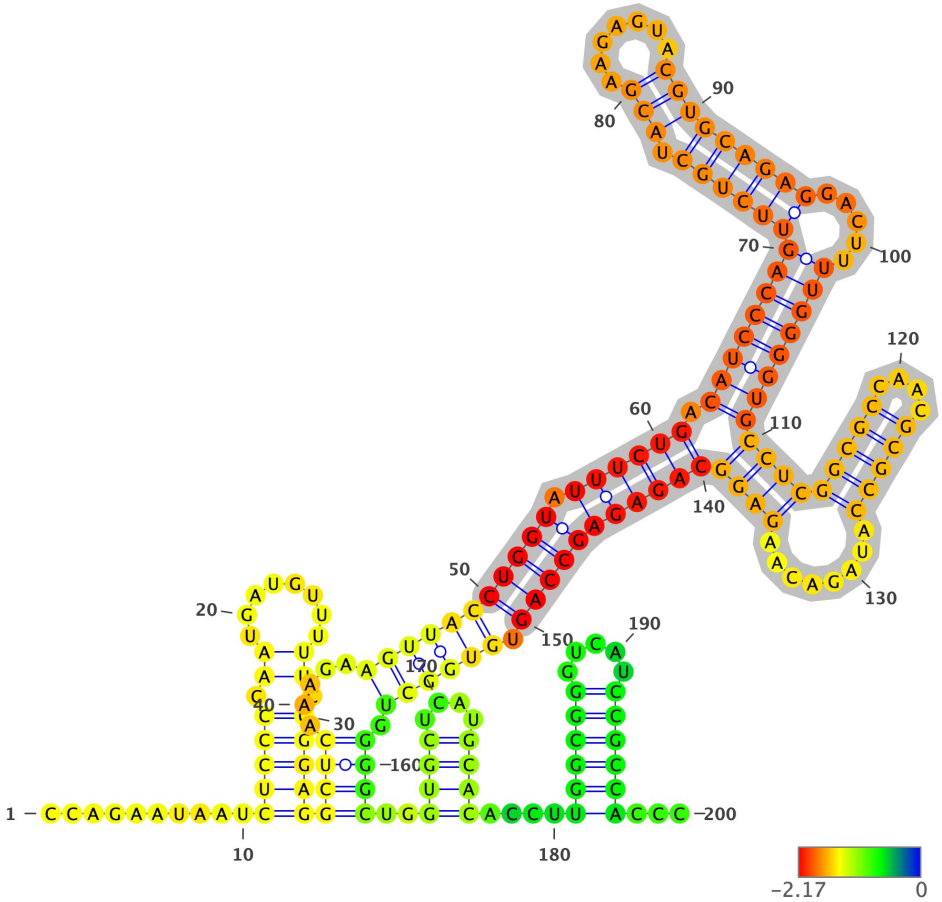
13-- nt 159 to 164--TATA_box, id-HHV4_BFRF3, 49056-49061(+)

Attributes: ['ID=id-HHV4_BFRF3', 'Dbxref=GeneID:3783701', 'gbkey=regulatory', 'gene=BFRF3', 'regulatory_class=TATA_box']

NC_007605.1 (forward strand): Structure number 195 from nt 49360 to 49460 (nt 50 to 150)

```
5'-CUGGUAUUUCUGACAUCCCAGUUCUGCUACGAAGAGUACGUGCAGAGGACUUUUGGGGUGCCUCGGCGCCAACGCGCCAUAGACAAGAGGCAGAGAGCCAG-3'

5'-(((((.((((((.....................................................................................))))))))))-3'
Motif MFE = -41.2; z-score = -2.81; ED = 4.94
```



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

Extracted structure model with flanking nucleotides 49311 to 49510 (motif highlighted in silver):

```
5'-CCAGAAUAAUCUCCCCAAUGAUGUUUUUCGGGAGGCUCAAAGAAGUUACCUGGUAUUUCUGACAUCCCAGUUCUGCUACGAAGAGUACGUGCAGAGGACUUUUGGGGUGCC
UCGGCGCCAACGCGCCAUAGACAAGAGGCAGAGAGCCAGUGUGGCUGGGGCUGGUGCUCAUGCACACCUUGGCGGGUCAUCCGCCACCC-3
5'-..........(((((.((........)).)))))((((.....((((((((((.(((((((.(((((((((((((.(((.......)))))))))).....)))))))))((
(((((((....)))))).......)))))))))))))).)))))).))))..((((....)))).....((((((.....)))))).....-3'
MFE = -76.0; z-score = -2.58; ED = 19.11
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_BFRF1A, 46236-49786(+)

Attributes: ['ID=gene-HHV4_BFRF1A', 'Dbxref=GeneID:3783759', 'Name=BFRF1A', 'Note=core gene', 'gbkey=Gene', 'gene=BFRF1A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF1A']

10-- nt 1 to 200--gene, gene-HHV4_BFRF1, 46544-49786(+)

Attributes: ['ID=gene-HHV4_BFRF1', 'Dbxref=GeneID:3783699', 'Name=BFRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BFRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF1']

11-- nt 1 to 200--gene, gene-HHV4_BFRF2, 47520-49786(+)

Attributes: ['ID=gene-HHV4_BFRF2', 'Dbxref=GeneID:3783700', 'Name=BFRF2', 'Note=betagamma gene', 'gbkey=Gene', 'gene=BFRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF2']

12-- nt 1 to 200--gene, gene-HHV4_BFRF3, 49219-49786(+)

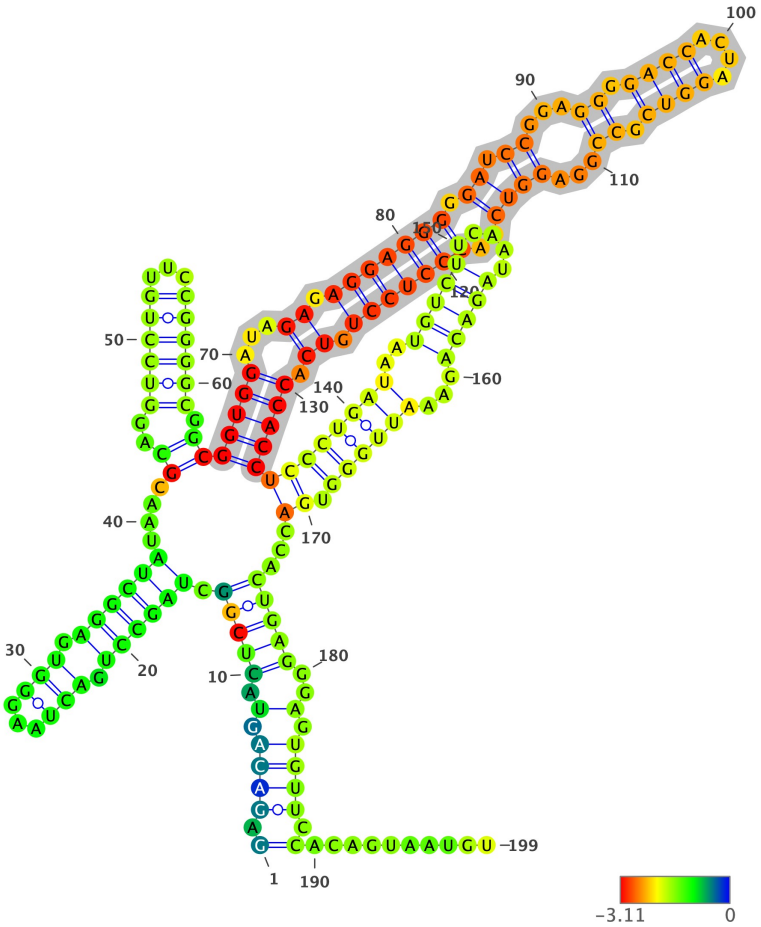
Attributes: ['ID=gene-HHV4_BFRF3', 'Dbxref=GeneID:3783701', 'Name=BFRF3', 'Note=core gene', 'gbkey=Gene', 'gene=BFRF3', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BFRF3']

13-- nt 1 to 200--CDS, cds-YP_401651.1, 49219-49749(+)

Attributes: ['ID=cds-YP_401651.1', 'Parent=gene-HHV4_BFRF3', 'Dbxref=UniProtKB/TrEMBL:Q777G5,Genbank:YP_401651.1,GeneID:3783701', 'Name=YP_401651.1', 'gbkey=CDS', 'gene=BFRF3', 'locus_tag=HHV4_BFRF3', 'product=small capsid protein', 'protein_id=YP_401651.1']

NC_007605.1 (forward strand): Structure number 196 from nt 49943 to 50012 (nt 65 to 134)

```
5'-GGUGGAUAGAGAGGAGGGGGAUCCGGAGGGGACCACUAGGUCGCCGGAGGUCGACCCUCCUGUCACCACC-3'
5'-(((((...((.(((((((.((.(((...((.((((....)))).)).)))..)))))..)))))))).)).)))))-3'
Motif MFE = -40.5; z-score = -4.06; 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 49879 to 50077 (motif highlighted in silver):

```
5'-GAGACAGUACUCGGCUAGCCUGACUAAGGGUGAGGCUAUAACGCAGGUCCUGUUCCGGGGCGGCGGUGGAUAGAGAGGAGGGGGAUCCGGAGGGGACCACUAGGUCGCCGG
AGGUCGACCCUCCUGUCACCACCUCCCUGAUAAUGUCUUCAAUAGACAGAAAUUGGGUGACCACUGAGGGAGUGUUCCACAGUAAUGU-3
5'-(.(((((.(.(((((.((((((.(((...))).)))))).....((..(((((((...)))))))..))((((((...((.(((((((.((.((...((.((((....)))))..)).)).
.))))..)))))))).)).)))))((((((((..(((((.....)))))...)))))).))...)))))..).)))).).........-3'
MFE = -82.6; z-score = -3.21; ED = 26.5
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

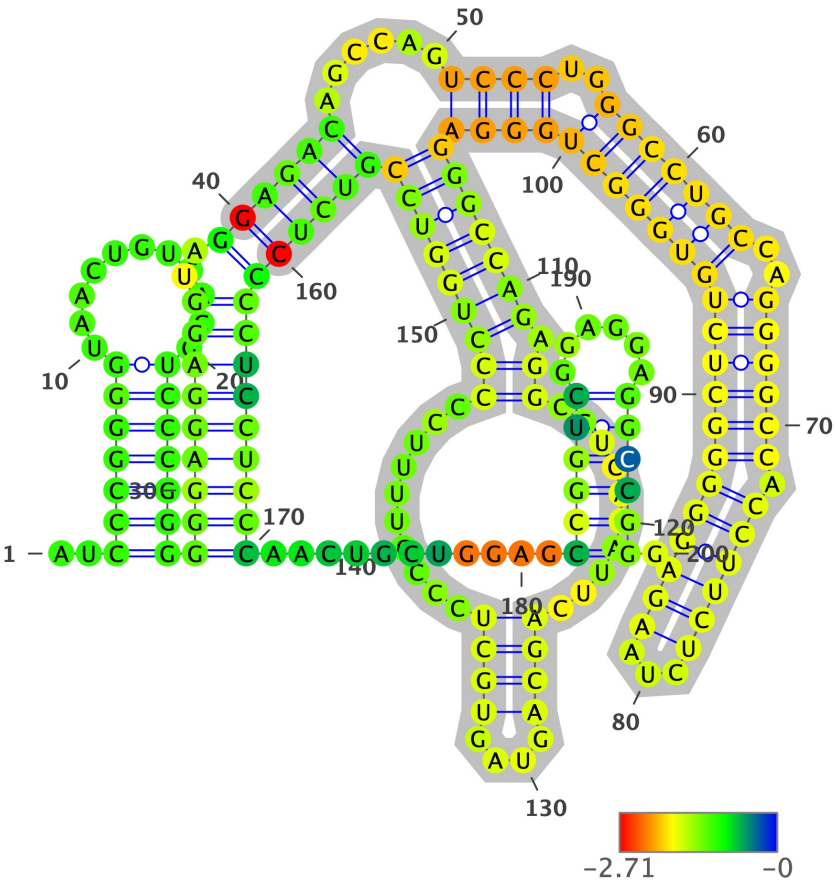
Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 65 to 199--exon, id-HHV4_EBNA-3A-7, 49943-50170(+)

Attributes: ['ID=id-HHV4_EBNA-3A-7', 'Note=Fp first exon of splice RNAs induced in lytic cycle%2C some spliced to EBNA-1', 'gbkey=exon']

NC_007605.1 (forward strand): Structure number 197 from nt 51292 to 51412 (nt 40 to 160)

```
5'-GAGACAGCCAGUCCCUGGGCCUGCCAGGGGCCACCUUCUCUAAGAGGGGGCUCUGUGGGCUGGGAGGGCCAGAGGCCUCAGAUUCAGCAGUAGUGCUCCCCUUUUCCCCCU
GGUCCGUCUC-3'
5'-(..........(((((..((.........................................))))))).....................................................
.........)-3'
Motif MFE = -54.4; z-score = -1.84; ED = 30.49
```



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 51253 to 51452 (motif highlighted in silver):

```
5'-AUCCCGGGGUAACUGUCACGUCCCGGGGGGAGGAGGUAGGAGACAGCCAGUCCCUGGGCCUGCCAGGGGCCACCUUCUCUAAGAGGGGGCUCUGUGGGCUGGGAGGGCCAG
AGGCCUCAGAUUCAGCAGUAGUGCUCCCCUUUUCCCCCUGGUCCGUCUCCCCUCCUCCCAACUGCUGGAGCCGGUCGGAGGAGGCCGGG-3
5'-..(((((((.........)))))))(((((((((..((((((.....((((..(((((((..((((((.(((((((...)))))))))))))))))))))))))))))
.((.........((((....))))..........)))))))))))))))))))))))).........(((((.....)))))).-3'
MFE = -101.9; z-score = -2.62; ED = 16.82
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

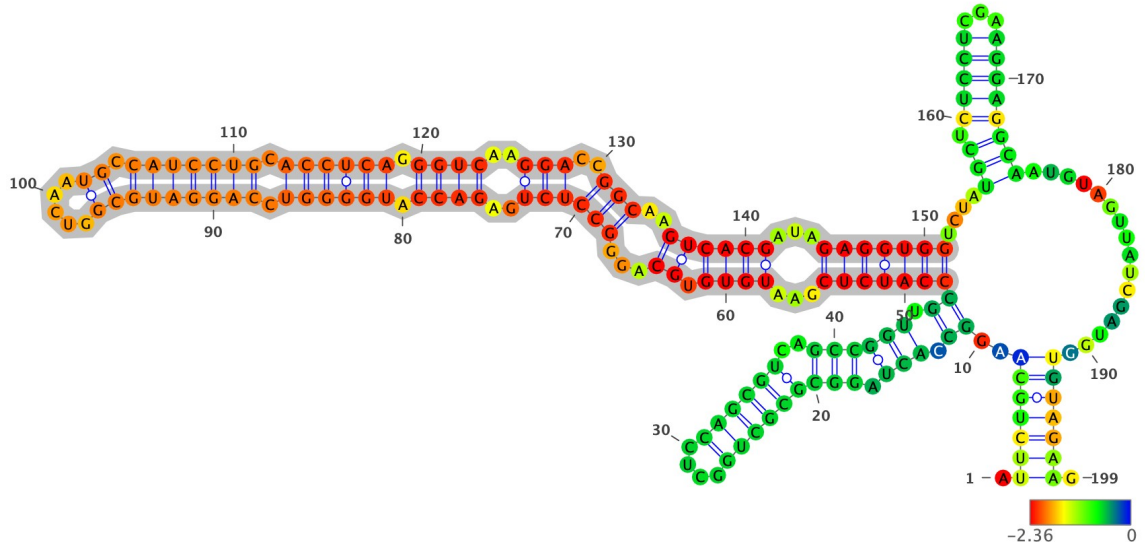
10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 198 from nt 55426 to 55529 (nt 48 to 151)

5'-CCAUCUCGAAUGUGUGCAGGGCCUCUGAGACCAUGGGGUCCAGGAUGCGGUCAAUGCCAUCCUGCACCUCAGGGUCAAGGACCGGCAAGUCACGAUAGAGGUGG-3'

5'-(((((((...(((((.((...(((((((..(((((.((((((.....)))))).))))..)))).))).))))))...)))))))-3'
Motif MFE = -48.3; z-score = -3.74; ED = 14.19



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 55379 to 55577 (motif highlighted in silver):

5'-AUUCUGCAAGGCCACUAGGCGCGCUGGCUCCAGCGUCAGCCGGUUGCCCAUCUCGAAUGUGUGCAGGGCCUCUGAGACCAUGGGGUCCAGGAUGCGGUCAAUGCCAUCCUG
CACCUCAGGGUCAAGGACCGGCAAGUCACGAUAGAGGUGGUCUAUGCUCUCCUCGAAGGAGGCAAUGUAGUUAUCGAUGGUGUAGAAG-3
5'-.(((((((..((.(((.(((((((((....)))))).))))))).))))))).))(((((((...(((((.((...(((((((..((((.(((((((.(((((((((.....)).)))))))
.)))))).)))).))).)).))).))))))...)))))))....(((.((((((...)))))))).....))))))).-3'
MFE = -81.4; z-score = -2.46; ED = 24.19

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

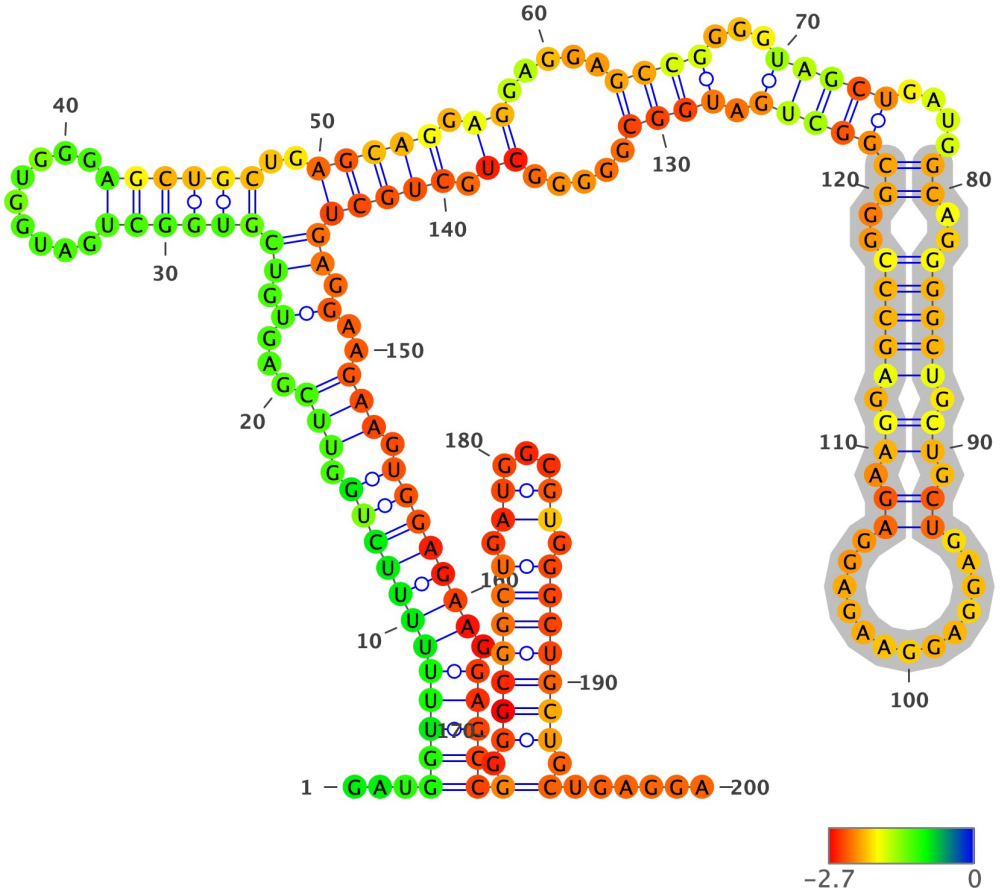
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 199 from nt 57448 to 57490 (nt 79 to 121)

```
5'-GCAGGGGCUGCUGCUGAGGAGGAAGAGGAGAAGGAGCCCGGGC-3'
5'-((...(((...(.................)...)))...))-3'
Motif MFE = -14.6; z-score = -2.2; ED = 1.44
```



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

Extracted structure model with flanking nucleotides 57370 to 57569 (motif highlighted in silver):

```
5'-GAUGGUUUUUUUCUGGUUCGAGUGUCGUGGCUGAUGGUGGGAGCUGCUGAGCAGGAGGAGGAGCCGGGGUAGCUGAUGGCAGGGGCUGCUGCUGAGGAGGAAGAGGAGAAG
GAGCCCGGGCGGCUGAUGGCGGGGGCUGCUGCUGAGGAAGAAGUGGAGAAGGAGCCGGGGCGGCUGAUGGCGUGGGCUGCUGCUGAGGA-3
5'-...(((((((((((.(((...(.(((((((((.........)))))))..(((((.((.....((((...((((((....((..((((((.((.(((.............)).))
.)))))..)))))))).))))....)).)))))))).)..)))).)))))))).))))))(.(((((((.((...)).)))))))).......-3'
MFE = -69.5; z-score = -2.22; ED = 24.31
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

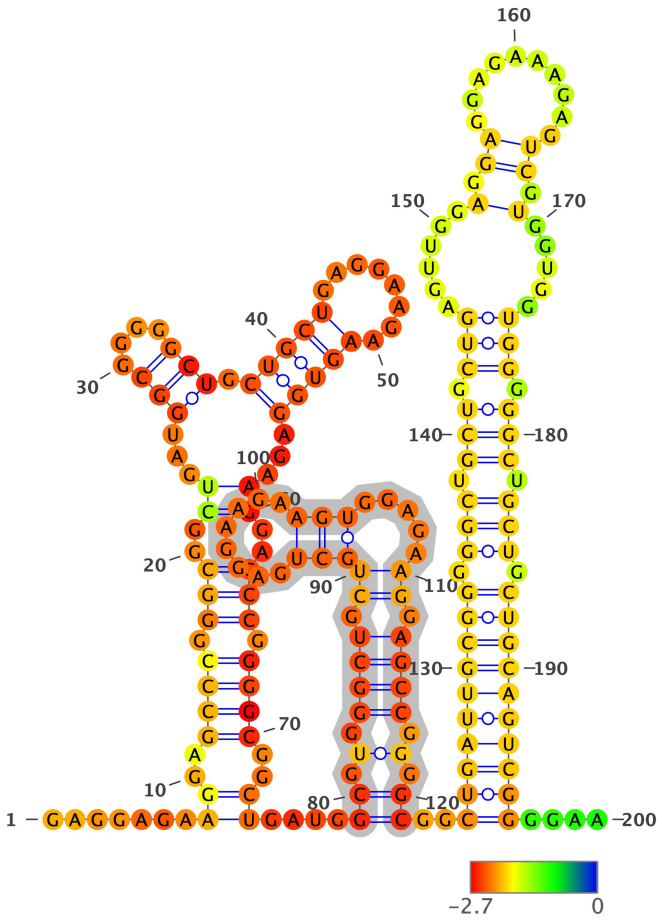
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 27 to 200--repeat_region, id-HHV4_EBNA-1.2, 57396-57642(+)

Attributes: ['ID=id-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=57396..57446']

NC_007605.1 (forward strand): Structure number 200 from nt 57550 to 57592 (nt 79 to 121)

```
5'-GCGUGGGCUGCUGCUGAGGAAGAAGUGGAGAAGGAGCCGGGGC-3'
5'-((...((((...(((........)))........))))...))-3'
Motif MFE = -14.1; z-score = -2.63; ED = 3.27
```



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

Extracted structure model with flanking nucleotides 57472 to 57671 (motif highlighted in silver):

```
5'-GAGGAGAAGGAGCCCGGGCGGCUGAUGGCGGGGGCUGCUGCUGAGGAAGAAGUGGAGAAGGAGCCGGGGCGGCUGAUGGCGUGGGCUGCUGCUGAGGAAGAAGUGGAGAAG
GAGCCGGGGCGGCUGAUUGCGGGGGCUGCUGCUGAGUUGGAGGAGGAGAAAGAGUCGUGGUGGUGGGGGCUGCUGCUGCAGUCGGGGAA-3
5'-.......((..((((.((((..((...((((....)))).(((((........)))))...)).)).)))).))....((.(.((((.((((((........)))).....))
.)))).)..))..((((((((((.(((.(((.(((.....(.((..........)).).....))).))).))).))).))))))))))....-3'
MFE = -68.6; z-score = -3.24; ED = 32.98
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

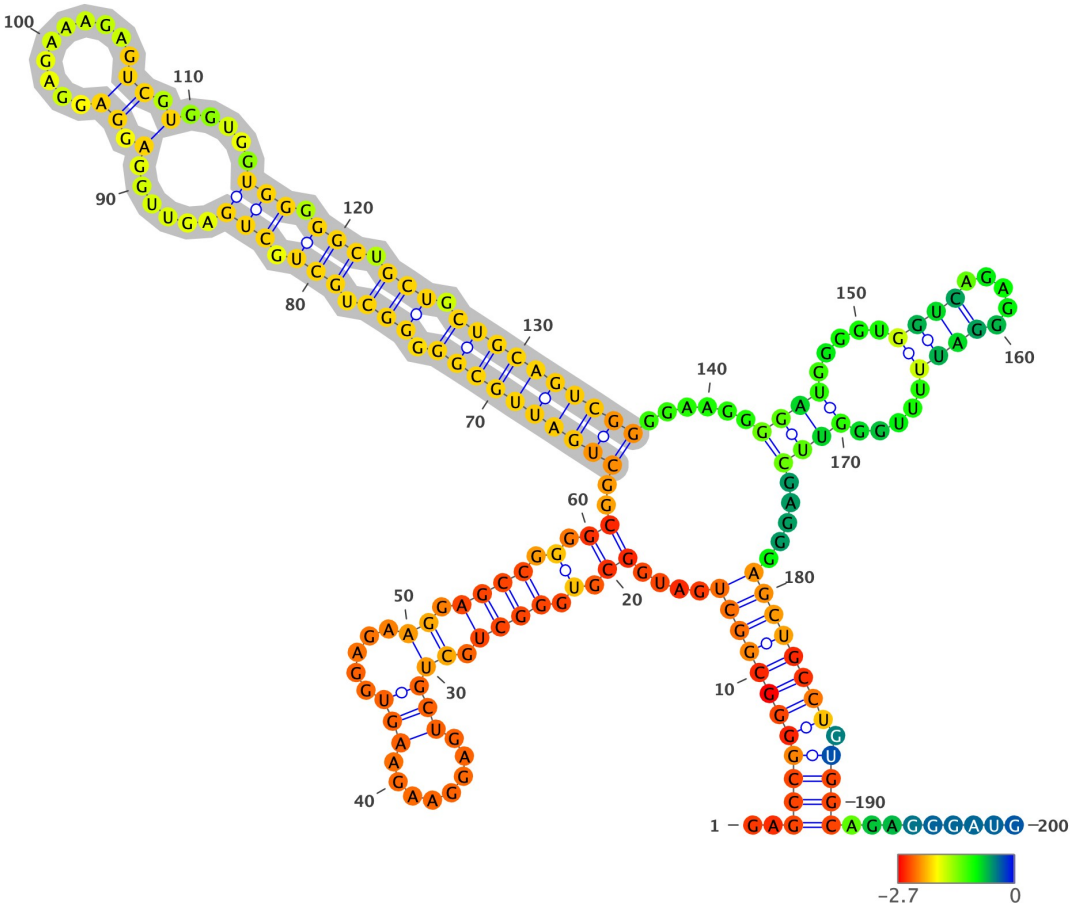
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 171--repeat_region, id-HHV4_EBNA-1.2, 57396-57642(+)

Attributes: ['ID=id-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=57396..57446']

NC_007605.1 (forward strand): Structure number 201 from nt 57595 to 57667 (nt 64 to 136)

```
5'-CUGAUUGCGGGGGCUGCUGCUGAGUUGGAGGAGGAGAAAGAGUCGUGGUGGUGGGGGCUGCUGCUGCAGUCGG-3'
5'-((.....))-3'
Motif MFE = -27.7; z-score = -2.76; ED = 5.83
```



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 57532 to 57731 (motif highlighted in silver):

```
5'-GAGCCGGGGCGGCUGAUGGCGUGGGCUGCUGCUGAGGAAGAAGUGGAGAAGGAGCCGGGGCGGCUGAUUGCGGGGGCUGCUGCUGAGUUGGAGGAGGAGAAAGAGUCGUGG
UGGUGGGGGCUGCUGCUGCAGUCGGGGAAGGGGAUGGGGUGGUCAGAGGGAUUUUUGGGUUCGAGGGAGCUGCCUGUGGCAGAGGGAUG-3
5'-..(((((((((((....((.(.((((.(((((........)))).....)).)))).).)).(((((((((.(((.(((.(((......(.((.........)).).....)))).))).))).))))))))).....(((.....(((.....)))).....)))).....)))))))).))))).........-3'
MFE = -67.4; z-score = -2.86; ED = 21.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

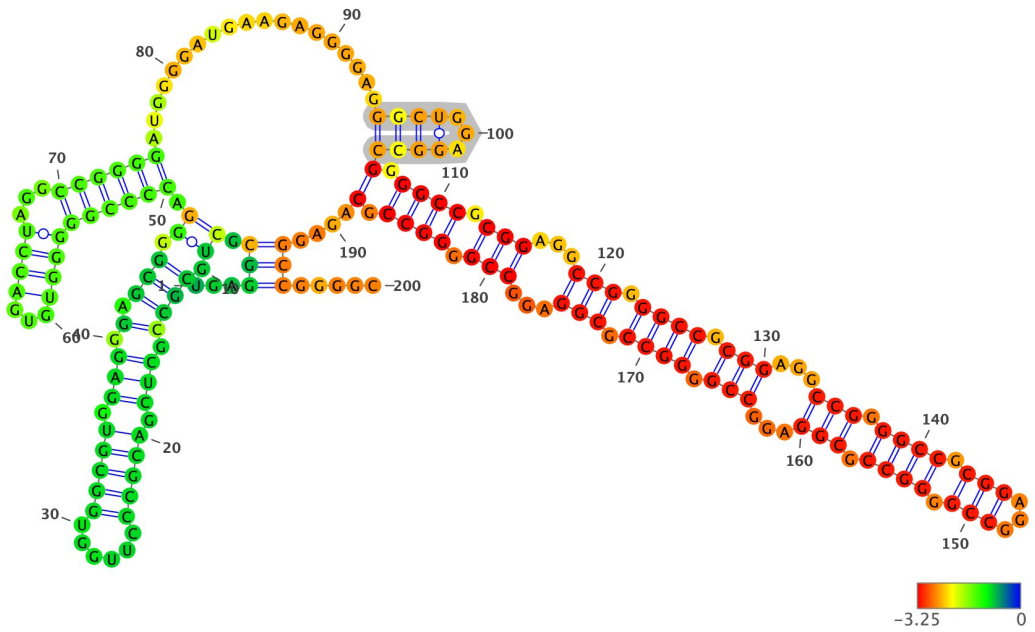
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 111--repeat_region, id-HHV4_EBNA-1.2, 57396-57642(+)

Attributes: ['ID=id-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=57396..57446']

NC_007605.1 (forward strand): Structure number 202 from nt 58105 to 58115 (nt 95 to 105)

```
5'-GGCUGGAGGCC-3'
5'-(.((...)).)-3'
Motif MFE = -2.9; z-score = -2.82; 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 58011 to 58210 (motif highlighted in silver):

```
5'-UGAGGCGCUGCGCCGCUCGACGCCCUUGGUGGCGUGGAGGGAGCGGGGACCCCGGGGGUGUGACCUAGGCCGGGGAUGGGGAUGAAGAGGGGAGGGCUGGAGGCCGGGGCC
GCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCAGAGGCCGGGGC-3
5'-...(((.((.((((.(((.(((((.....))))).))).).))).)).((((((((((...)))).....)))))).................((((...))))(.((((
.(((...((((.((((.(((...(((.((((.(((...))).)))).)))...)))).)))).)))...)))).)))).).....)))).....-3'
MFE = -116.0; z-score = -2.19; ED = 18.32
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

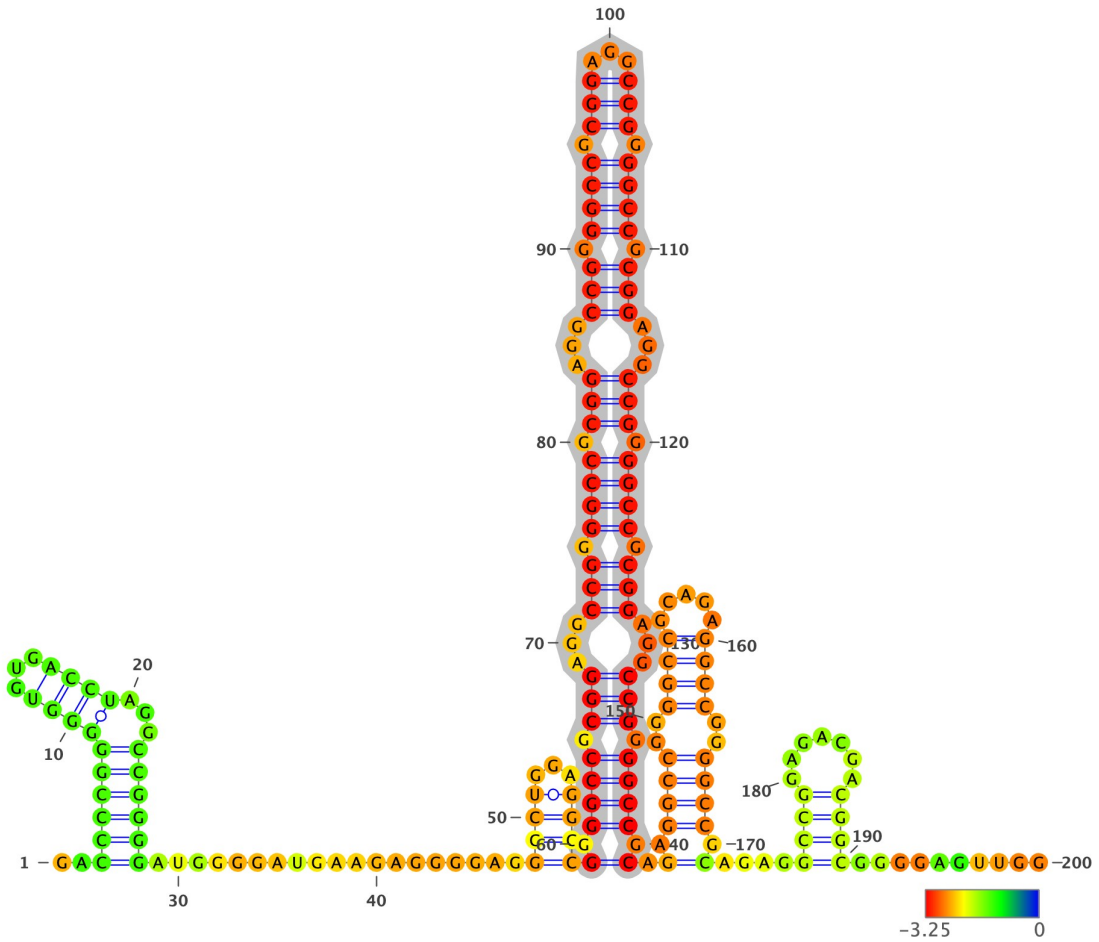
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 89 to 200--repeat_region, id-HHV4_EBNA-1.2-2, 58099-58233(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=58099..58113']

NC_007605.1 (forward strand): Structure number 203 from nt 58116 to 58198 (nt 59 to 141)

```
5'-GGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGC-3'
5'-(.(((((.(((...(((.(((((.(((...(((.(((((.(((...))).))))).)))...))).)))).)))...))).)))))-3'
Motif MFE = -65.5; z-score = -3.85; 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 58058 to 58257 (motif highlighted in silver):

```
5'-GACCCCGGGGGUGUGACCUAGGCCGGGGAUGGGGAUGAAGAGGGGAGGGCUGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGC
GGAGGCCGGGGCCGCGGAGGCCGGGGCCGCAGAGGCCGGGGCCGCAGAGGCCGGGGCCGCAGAGGCCGGAGACGACGGCGGGGAGUUGG-3
5'-..((((((((((...)))))...)))))).................((((...))))).(((((.(((...(((.((((.(((...(((.((((.(((...)))).)))))).)
))...))).)))).)))...))).)))).).(.(((((..((((.....))))).)))).).....((((.......))))..........-3'
MFE = -110.8; z-score = -2.76; ED = 28.22
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

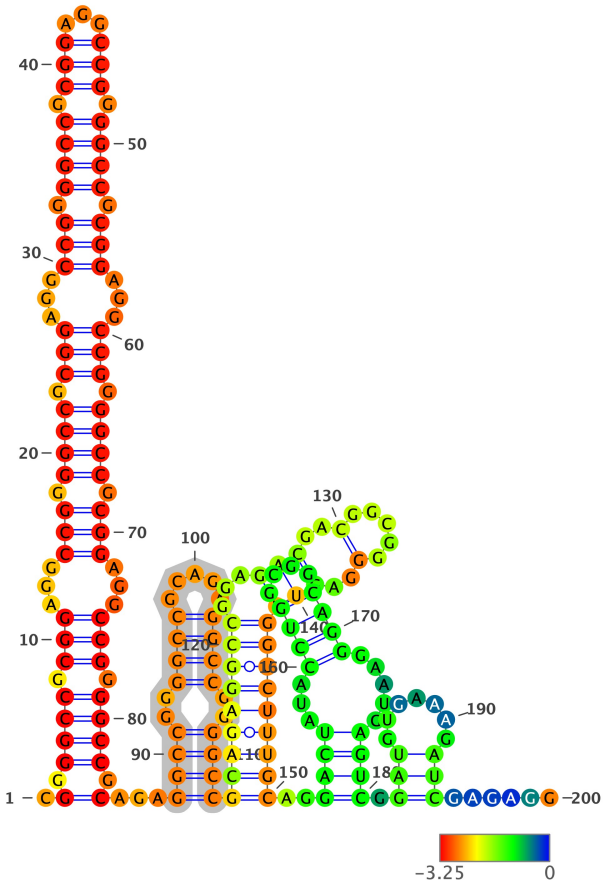
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 42 to 176--repeat_region, id-HHV4_EBNA-1.2-2, 58099-58233(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=58099..58113']

NC_007605.1 (forward strand): Structure number 204 from nt 58202 to 58226 (nt 88 to 112)

```
5'-GGCCGGGGCCGCAGAGGCCGGGGCC-3'
5'-(((((..((((.....))))..)))))-3'
Motif MFE = -15.8; z-score = -2.13; 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 58115 to 58314 (motif highlighted in silver):

```
5'-CGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCGGAGGCCGGGGCCGCAGAGGCCGGGGCCGCAGAGGCCGGGGC
CGCAGAGGCCGGAGACGACGGCGGGGAGUUGGUCUUUGCAGGACUAUACCUGGCGGCAGGGAAUGAGUCGGAUGUGAAAGAUCGAGAGG-3
5'-.(.((((.(((...(((.((((.(((...(((.((((.(((...))).)))).)))...))).)))).)))...))).)))).)...((((..((((.....))))..)))
)(((((((((...((((..(.....)..)))))))))))).((((...((((....))))).....)))).(((.......)))......-3'
MFE = -111.3; z-score = -3.75; ED = 18.61
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

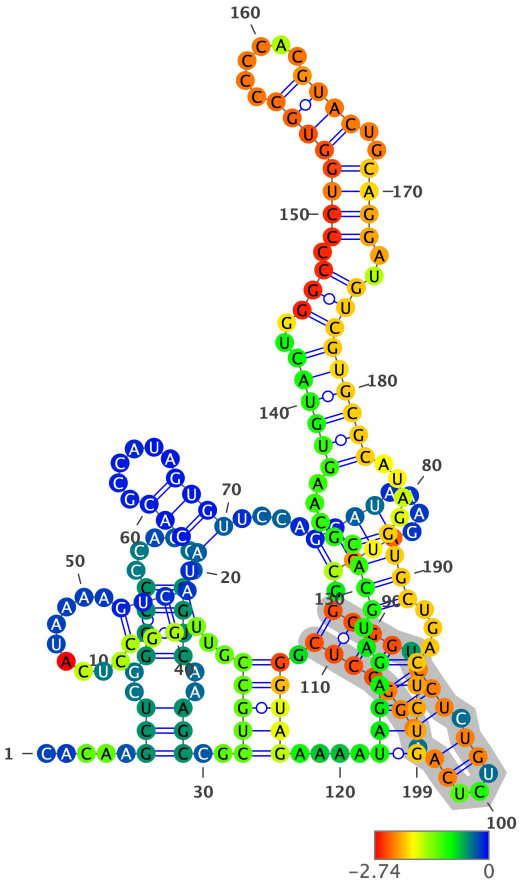
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 119--repeat_region, id-HHV4_EBNA-1.2-2, 58099-58233(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-2', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=58099..58113']

NC_007605.1 (forward strand): Structure number 205 from nt 58505 to 58528 (nt 88 to 111)

```
5'-GGGGUCCUCUGUCUCAAAGGCCUC-3'
5'-((((.(((.((...)).)))))))-3'
Motif MFE = -6.7; z-score = -1.46; 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 58418 to 58616 (motif highlighted in silver):

```
5'-CACAAGCUCGGGCCCCACCAGGUCAAAGCCGCUGCCGUUGGCCUCAUAAAAGUCAUACACGCCAUAGUGUUCCAGCAUAAAGAUGCGGGGGUCCUCUGUCUCAAAGGCCUC
GGGUAGAAAAUAGAGAUGCACGCAAGUGUACUGGGCCCCUGGUGCCCCCACGUACUGCAGGAUGUCGUGCGCAUAGGUGCUGACUCUG-3
5'-.....(((..((((.....))))..)))..(((((..((((.........)))).((((.....)))).....((((....)))).((((.(((.((...)).)))))))
.)))))....(((((..((((....((((((..(((.(((((((.....)))).)))))..)))))..)))))))))....)))))...)))))-3'
MFE = -57.5; z-score = 0.56; ED = 49.55
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

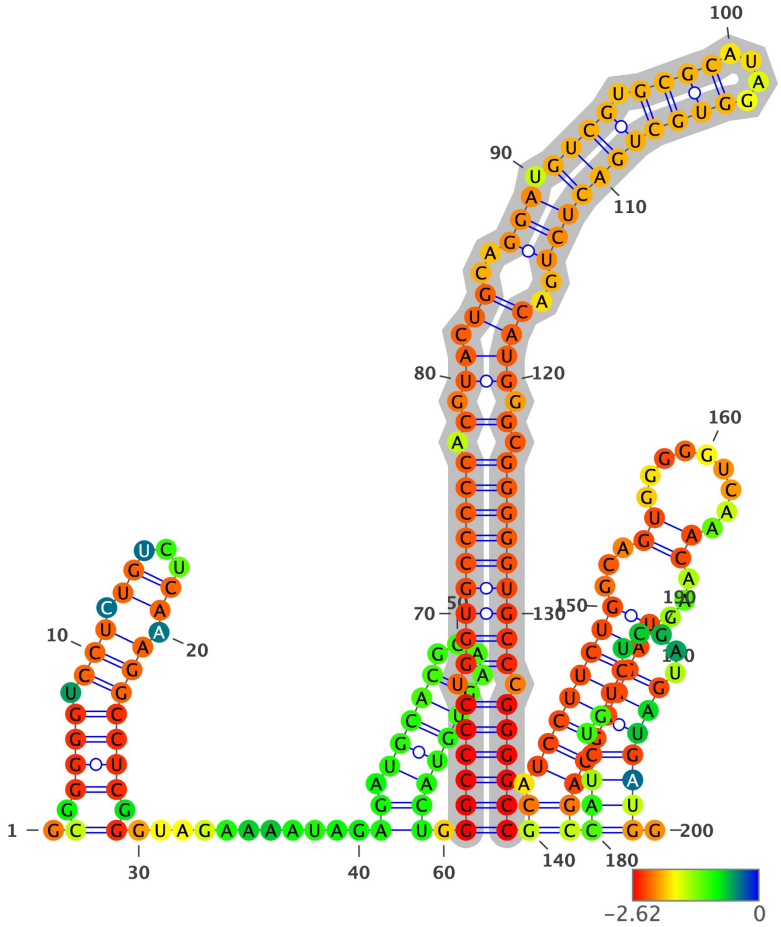
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 206 from nt 58562 to 58640 (nt 61 to 139)

```
5'-GGCCCCUGGUGCCCCCACGUACUGCAGGAUGUCGUGCGCAUAGGUGCUGACUCUGACAUGGGCGGGGGUGCCCGGGGCC-3'
5'-((((((.(((((((((.(.((.((..((((.((((.............)))))))..)))).).))))))))).)))))))-3'
Motif MFE = -49.2; z-score = -3.84; 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 58502 to 58701 (motif highlighted in silver):

```
5'-GCGGGGGUCCUCUGUCUCAAAGGCCUCGGGUAGAAAAUAGAGAUGCACGCAAGUGUACUGGGCCCCUGGUGCCCCCACGUACUGCAGGAUGUCGUGCGCAUAGGUGCUGAC
UCUGACAUGGGCGGGGGUGCCCGGGGCCGCAUCCUUCUGGCAGUGGGGGUCAAACAAGUAGAAGGAGCCAUCUGUCUCGAUGAUGAUGG-3
5'-.(.((((.((((.((...)).)))))).).........((.(((((....))))))).((((((.(((((((((.(.((.((..((((.((((.((((....)))))))
)))..)))).).)))))))))).))))))((.(((((((...((.........)).)))))))))))((((.(((.....)))))))).-3'
MFE = -83.5; z-score = -1.75; ED = 24.42
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

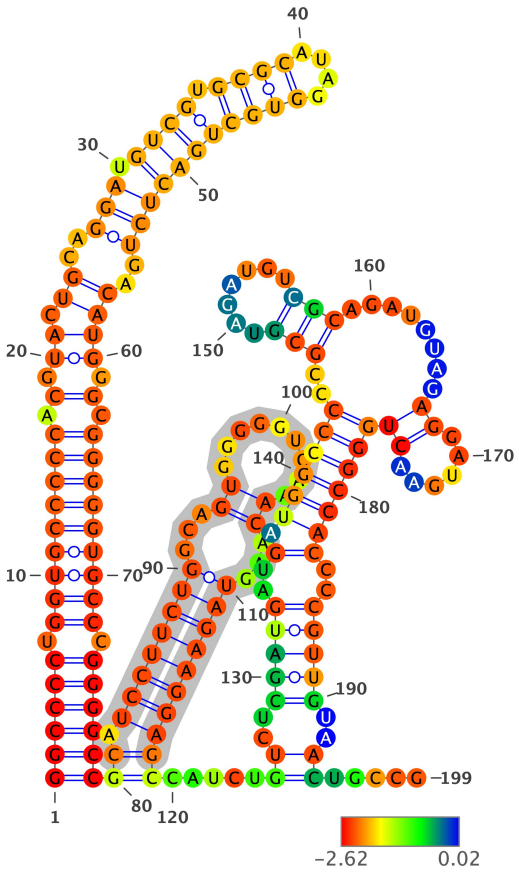
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 207 from nt 58642 to 58679 (nt 81 to 118)

```
5'-CAUCCUUCUGGCAGUGGGGGUCAAACAAGUAGAAGGAG-3'
5'-(.(((((((...((.........))...)))))))))-3'
Motif MFE = -10.1; z-score = -1.53; ED = 3.72
```



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 58562 to 58760 (motif highlighted in silver):

```
5'-GGCCCCUGGUGCCCCCACGUACUGCAGGAUGUCGUGCGCAUAGGUGCUGACUCUGACAUGGGCGGGGGUGCCCGGGGCCGCAUCCUUCUGGCAGUGGGGGUCAAACAAGUA
GAAGGAGCCAUCUGUCUCGAUGAUGAUGGCCCCCGCGUAGAUGUCGCAGAUGUAGAGGAUGAACUGGGCCACCCCGUUGUAACUGCCG-3
5'-((((((.(((((((((.(.((.((..((((.((((.((((....)))))))))))..)))))).).))))))))).)))))))((.(((((((((...((.........)))...))
)))))))).....((..((((((..(.((((((..(((.......)))).........((......)))))))))..)))))..)).....-3'
MFE = -81.4; z-score = -1.88; ED = 32.02
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

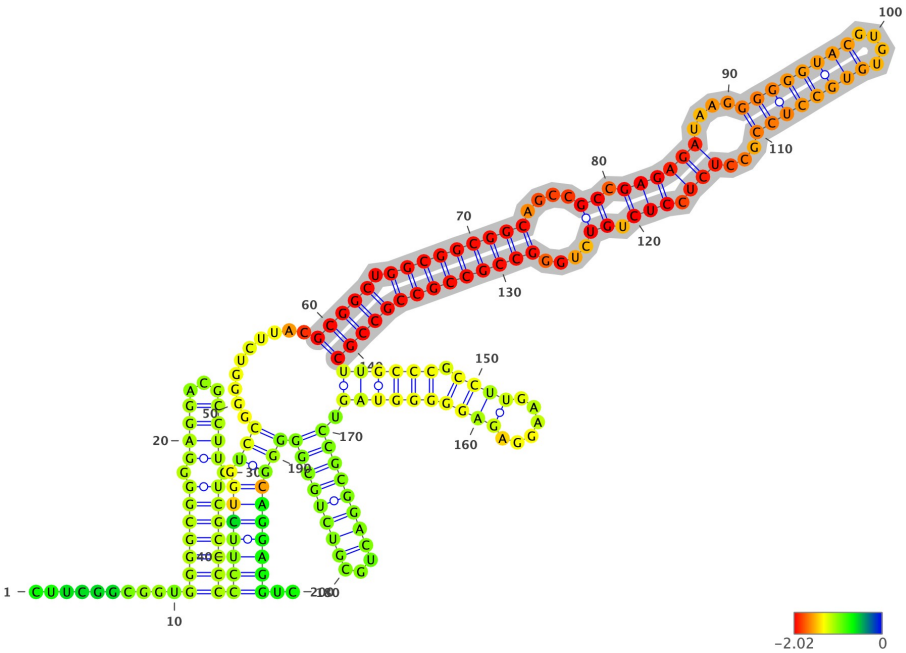
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 208 from nt 59298 to 59380 (nt 59 to 141)

```
5'-GCGGCUGGCGGCGGCAGCCGCCGAGAGAUAAGGGGGGUACGUGUGUGCCUCCGCCUCUCCUCUGUCUGGGCCGCCGCCGCCGC-3'
5'-(((((.............((.((((.....................................))).)).............)))))-3'
Motif MFE = -52.8; z-score = -3.5; ED = 9.66
```



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

Extracted structure model with flanking nucleotides 59240 to 59439 (motif highlighted in silver):

```
5'-CUUCGGCGGUGGGGCGGGGAGGACGCCUUGUCGCCCCCCUUCUGGUCCGGGGUCUUACGCGGCUGGCGGCGGCAGCCGCCGAGAGAUAAGGGGGGUACGUGUGUGCCUCCG
CCUCUCCUCUGUCUGGGCCGCCGCCGCCGCUUGCCCGCCUUGAAGGAGAGGGGGUAGUCCGCGGACUGCGUCUGCGGGGGCAGGAGGUC-3
5'-..........(((((((.((((...)))).)))))))(((((((.(((..........(((((.(((((((((....((.((((((....(((((((((....)))))))))..
..)))).)))).)).....))))))))))))))(((((.((((.....)))))))))).((((((((...)))))))))))))))))..-3'
MFE = -113.0; z-score = -1.97; ED = 24.81
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

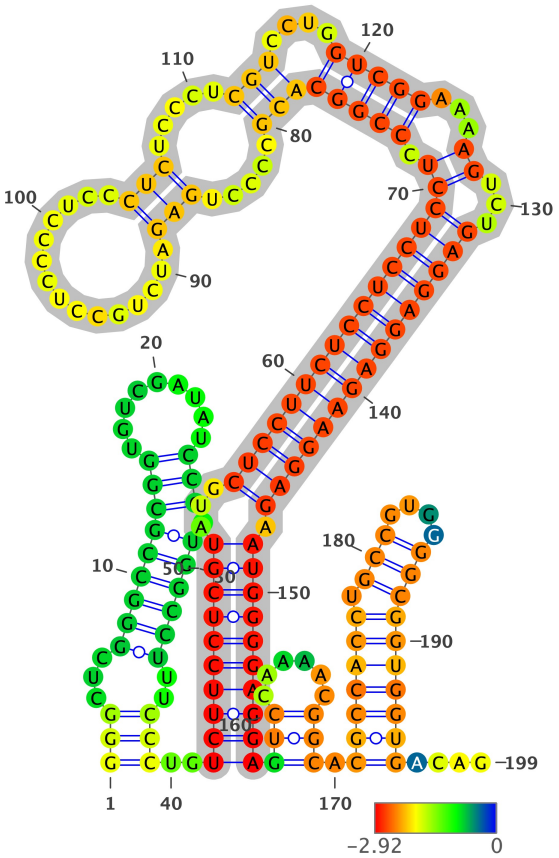
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 209 from nt 59491 to 59606 (nt 42 to 157)

```
5'-UCUUCCUCGUAUGCUCCUUCUCCUCCUCCUCCCGGCACGCCCCUGAGAUCUGCCUCCCCUCCCUCUCCCUCGUCCUGGUCGGAAAAGUCUGAGGAGGAGAAGGAGAAUGGG
GAGGA-3'
5'-((((((((((...((((((((((((((((.((((((((.....(((.............)))).....)))....)))))...))...))))))))))))))).))))
))))))-3'
Motif MFE = -50.3; z-score = -4.42; ED = 15.98
```



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 59450 to 59648 (motif highlighted in silver):

```
5'-GGGCUCGGGCCGCGGUGUCGAUAUCCGAUGGCCUUUCCCUGUCUUCCUCGUAUGCUCCUUCUCCUCCUCCUCCCGGCACGCCCCUGAGAUCUGCCUCCCCUCCCUCUCCCU
CGUCCUGGUCGGAAAAGUCUGAGGAGGAGAAGGAGAAUGGGGAGGAGUCCAAAACGGCACGCCACCUGCCGUGGGGCGGUGGUGACAG-3
5'-(((...(((((((((.........)))).)))))))..)))..((((((((((...((((((((((((((((.((((((((.....(((.............)))).....
)))....)))))...))...))))))))))))))).))))))))))((.......)))).(((((((.((....)))))))))....-3'
MFE = -87.9; z-score = -2.1; ED = 6.67
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

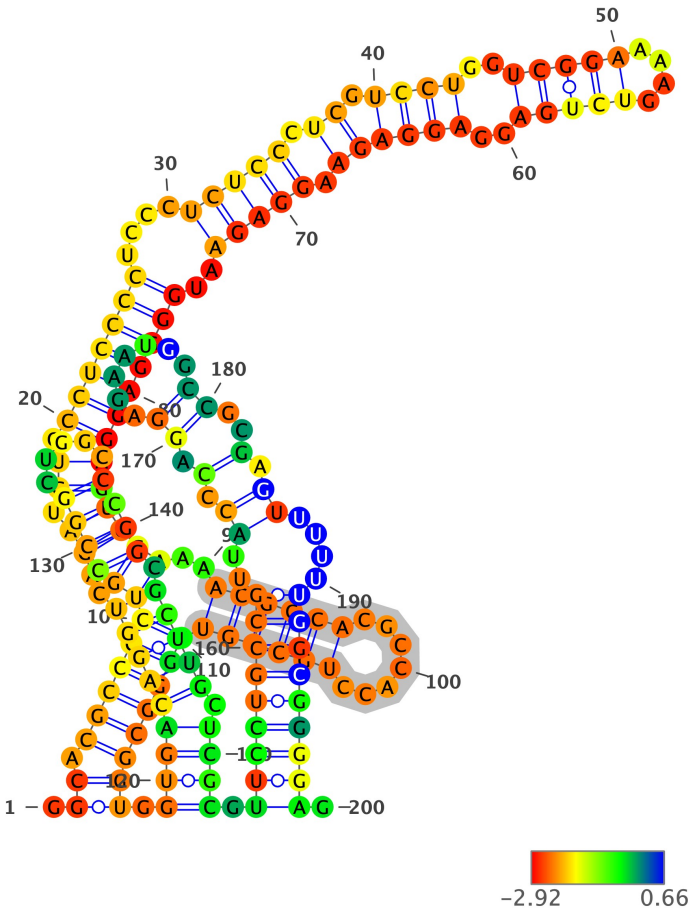
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 210 from nt 59614 to 59632 (nt 91 to 109)

```
5'-ACGGCACGCCACCUGCCGU-3'
5'-((((((.......))))))-3'
Motif MFE = -7.1; z-score = -2.45; ED = 1.13
```



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 59524 to 59723 (motif highlighted in silver):

```
5'-GGCACGCCCCUGAGAUCUGCCUCCCCUCCCUCUCCCUCGUCCUGGUCGGAAAAGUCUGAGGAGGAGAAGGAGAAUGGGGAGGAGUCCAAAACGGCACGCCACCUGCCGUGG
GGCGGUGGUGACAGGUCCCGGCUGGCCCGGCGCUUGCUCGCGUUCCUGCCGUUACCCAGGAGAAUGGCCGCGAGUUUUUUGGCGGGGAG-3
5'-.((.(((((((((.((.((.(((((((....(((((.((.(((((..((((((....)))))..)))))).)))))..))))))))))))))..((((((.......)))))))
))))))).(((((((((.((((.....)))).)))))).)))).(((((((((..((.(.(((.......))..).)).....)))))))))).-3'
MFE = -87.6; z-score = -0.97; ED = 42.93
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

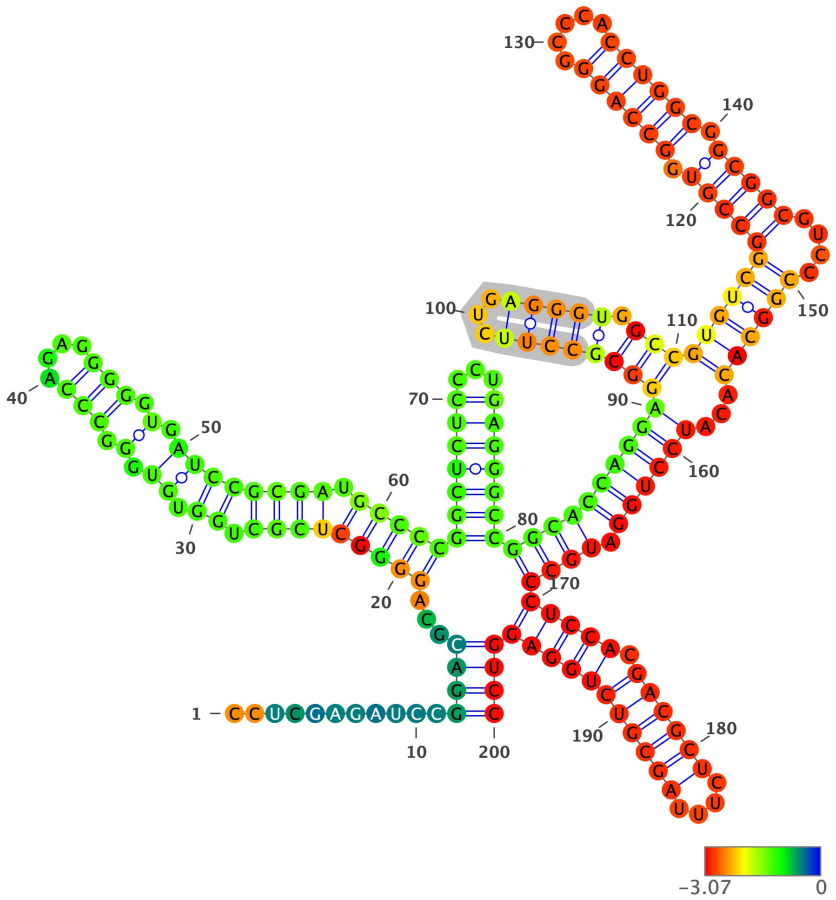
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 211 from nt 60327 to 60337 (nt 95 to 105)

```
5'-CCUUCUGAGGG-3'
5'-((.......))-3'
Motif MFE = -1.3; z-score = -2.35; ED = 2.26
```



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

Extracted structure model with flanking nucleotides 60233 to 60432 (motif highlighted in silver):

```
5'-CCUCGAGAUCCGGACGCAGGGGCUCGCUGGUGUGGGCCCAGAGGGGGUGAUCCGCGAUGCCCCGGCUCUCCCUGAGGGCCGGCACCAGGAGGCGCCUUCUGAGGGUGGCCG
UGUCGGCCGUGGCCAGGGCCCACCUGGCGGCGGCGUCCCGGCACACAUCCUGGAUGCCCUCCACGACGCUCUUUAGCGUCUGGAGGUCC-3
5'-...........((((...(((((((((.((.((.(.((((....)))).).)))))))).)))))(((((((...)))))))(((((((((((((((...)))))).)))(
((((((((((.((((((.....)))))).)))))....)))))).....)))))).))))((((.((((((....)))))))))))))))-3'
MFE = -115.3; z-score = -3.02; ED = 30.06
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

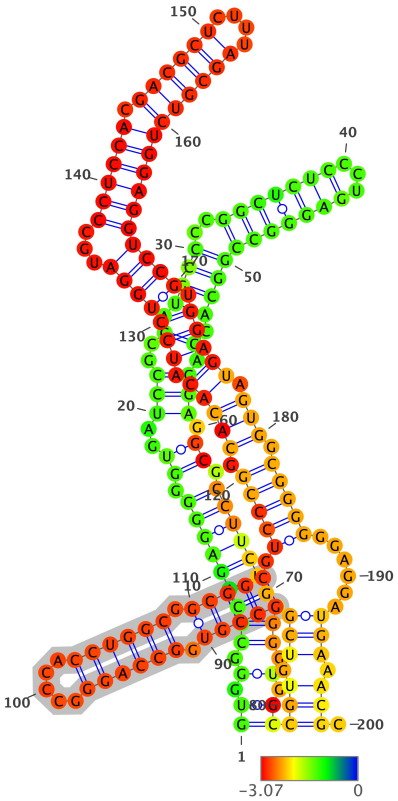
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 212 from nt 60349 to 60377 (nt 86 to 114)

```
5'-GCCGUGGCCAGGGCCCACCUGGCGGCGGC-3'
5'-(((((.(((((((.....)))))))..)))))-3'
Motif MFE = -24.0; z-score = -3.59; ED = 0.06
```



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

Extracted structure model with flanking nucleotides 60264 to 60463 (motif highlighted in silver):

```
5'-GUGGGCCCAGAGGGGGUGAUCCGCGAUGCCCCGGCUCUCCCUGAGGGCCGGCACCAGGAGGCGCCUUCUGAGGGUGGCCGUGUCGGCCGUGGCCAGGGCCCACCUGGCGGC
GGCGUCCCGGCACACAUCCUGGAUGCCCUCCACGACGCUCUUUAGCGUCUGGAGGUCCGUGGAGUAGUGGCGGGGGGAGGAUGAAACGC-3
5'-((.(.(((((((((.((..((((..(.((((..(((((((...)))))))))))).).))).)).)))))))).)).).))(((.(((((((((.((((((.....)))))))).))
))).(((((.(((((.(((((((...((((((.((((((....)))))))))))))))))).)))))).))).)))))......))).))).-3'
MFE = -110.0; z-score = -2.17; ED = 25.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

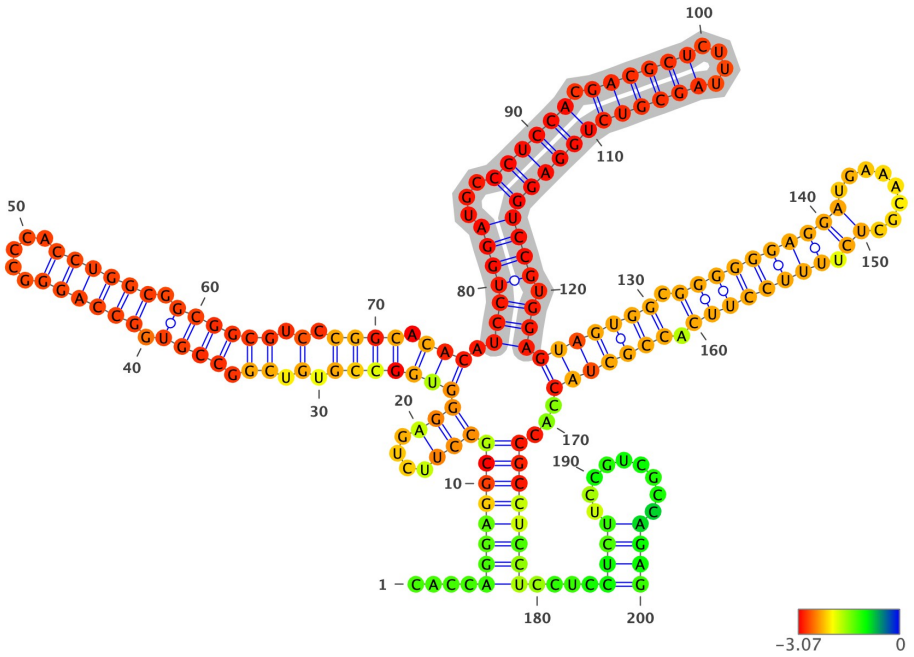
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 213 from nt 60391 to 60437 (nt 77 to 123)

```
5'-UCCUGGAUGCCCUCCACGACGCUCUUUAGCGUCUGGAGGUCCGUGGA-3'
5'-(((((((...((((((.((((((....)))))))))))))))).)))-3'
Motif MFE = -25.3; z-score = -4.76; ED = 1.48
```



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

Extracted structure model with flanking nucleotides 60315 to 60514 (motif highlighted in silver):

```
5'-CACCAGGAGGCGCCUUCUGAGGGUGGCCGUGUCGGCCGUGGCCAGGGCCCACCUGGCGGCGGCGUCCCGGCACACAUCCUGGAUGCCCUCCACGACGCUCUUUAGCGUCUG
GAGGUCCGUGGAGUAGUGGCGGGGGGAGGAUGAAACGCUCUUUUCCUUCACCGCUACCACCGCCUCCUCCUCCUCUUCCGUCGCCAGAG-3
5'-....(((((((((((....)))))))(((((.(.((.((((.((((((.....)))))).)))))).).)))).))).(((((((...((((((.((((((....)))))))))
))))))))).)))(((((((.((((((((((........)).)))))))).)))))))...)))))))))....((((.........))))-3'
MFE = -100.5; z-score = -4.21; ED = 27.54
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

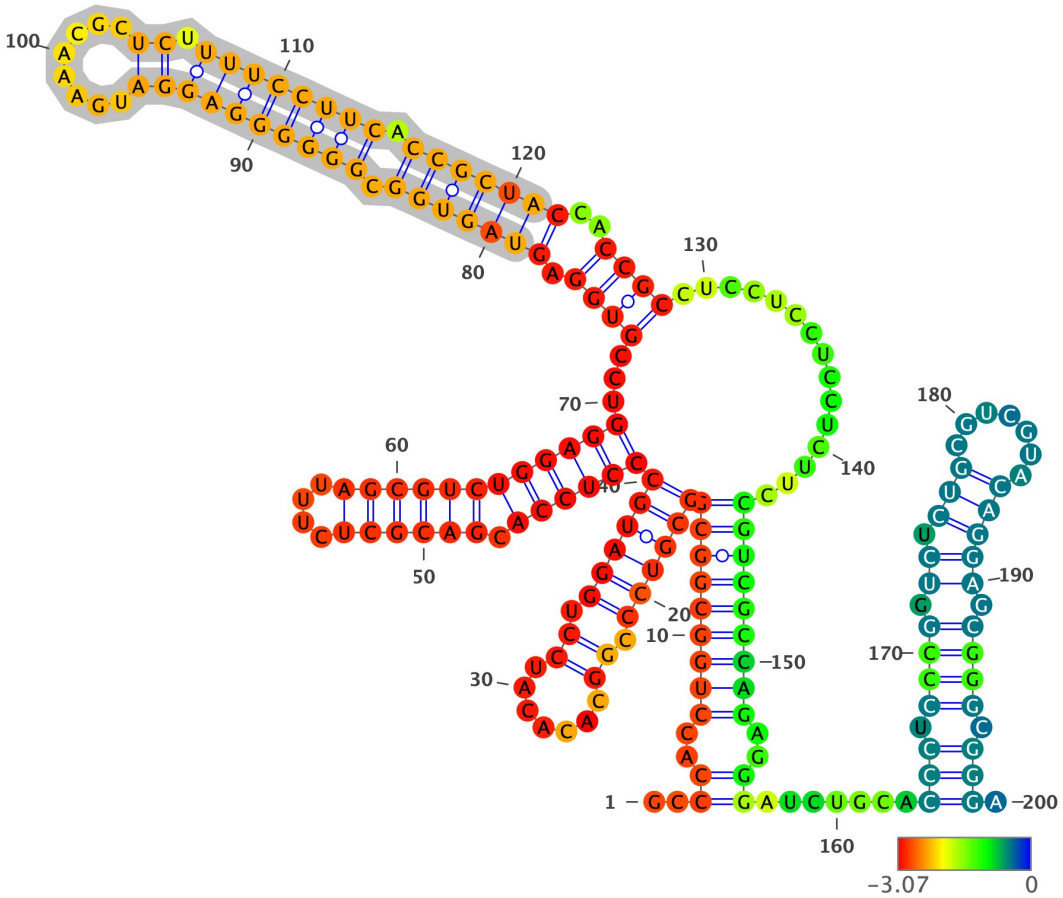
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 214 from nt 60439 to 60481 (nt 79 to 121)

```
5'-UAGUGGCGGGGGGAGGAUGAAACGCUCUUUUCCUUCACCGCUA-3'
5'-(.((((.(((((((((((........)).)))))))).)))).)-3'
Motif MFE = -16.8; z-score = -2.17; ED = 13.36
```



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 60361 to 60560 (motif highlighted in silver):

```
5'-GCCCACCUGGCGGCGGCGUCCCGGCACACAUCCUGGAUGCCCUCCACGACGCUCUUUAGCGUCUGGAGGUCCGUGGAGUAGUGGCGGGGGGAGGAUGAAACGCUCUUUUCC
UUCACCGCUACCACCGCCUCCUCCUCCUCUUCCGUCGCCAGAGGGAUCUGCACCCUCCCGGUCUCUGCGUCGUACAGGAGCGGGCGGGA-3
5'-..((..(((((((((((((((.((.......)).)))))))((((((.((((((....)))))))))))))...((((.(((((((.((((((((((.......)).)))))
)))).)))))))..))))..............)))))))))..)).......(((.((((.((.(((.......)))))).)))).)))).-3'
MFE = -95.7; z-score = -3.19; ED = 13.34
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

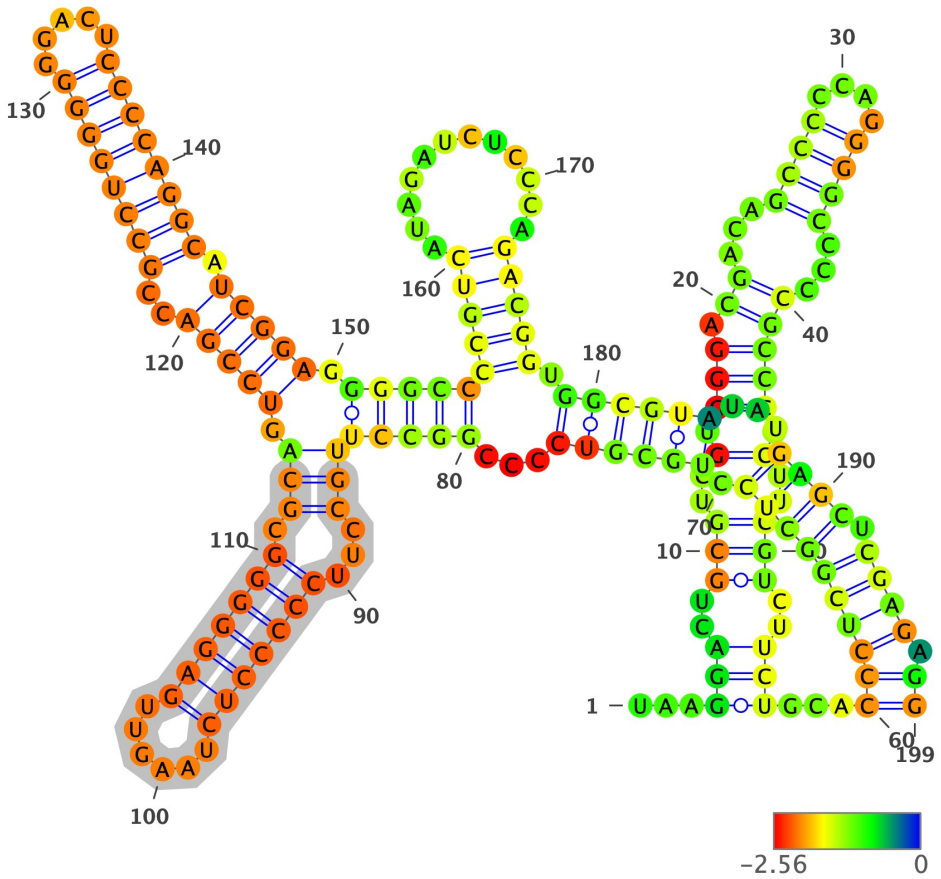
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 215 from nt 60885 to 60912 (nt 86 to 113)

```
5'-GCCUUCCCCCUCUAAGUUGAGGGGGCGC-3'
5'-((...(((((((.....)))))))).))-3'
Motif MFE = -15.5; z-score = -3.16; 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 60800 to 60998 (motif highlighted in silver):

```
5'-UAAGGACUGCGUCGUGGGACGACAGCCCCCAGGGGCCCCCGCCCUCUUCGUCUUCUGCACCCUCGGCUCCUGCGUCCCCGGCCUUGCCUUCCCCCUCUAAGUUGAGGGGGC
GCAGUCCGACCGCCUGGGGGGACUCCCCAGGCAUCGGAGGGGCCCCGUCAUAGAUCUCCCAGACGGUGGCGUAUAUGAGCUCGAGAGG-3
5'-...(((..((((..(.((((.((...((((....))))...))))))..)..)))..)))...((((((((((.((((((...((((((((...(((((((.....)))))))).
))).((((((..((((((((.....)))))))).)))))).)))))((((((.............)))))).)))))))...)))).)))).))-3'
MFE = -93.8; z-score = -2.36; ED = 26.46
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

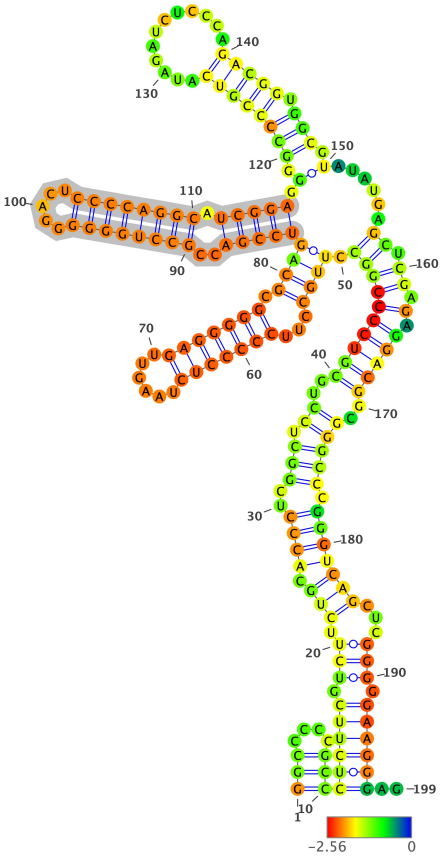
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 216 from nt 60915 to 60948 (nt 83 to 116)

```
5'-UCCGACCGCCUGGGGGGACUCCCCAGGCAUCGGA-3'
5'-(((((..(((((((((.....)))))))))..)))))-3'
Motif MFE = -23.6; z-score = -4.44; 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 60833 to 61031 (motif highlighted in silver):

```
5'-GGCCCCCGCCCUCUUCGUCUUCUGCACCCUCGGCUCCUGCGUCCCCGGCCUUGCCUUCCCCCUCUAAGUUGAGGGGGCGCAGUCCGACCGCCUGGGGGGACUCCCCAGGCA
UCGGAGGGGCCCCGUCAUAGAUCUCCCAGACGGUGGCGUAUAUGAGCUCGAGAGGACGGCGGGCCCGGGUCAGCUCGGGGGAAGGGAG-3
5'-((((....))))))))(((.(((.(((.(((((..((((.((..((((((((((.((((...(((((((.....)))))))).))))))))(((..(((((((((.....)))))))))).
)))))).(.(((((((((.............)))))).))))..).....)).)).).)))))..)))))).))))))).....)))).)))))))..-3'
MFE = -101.0; z-score = -1.74; ED = 10.97
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

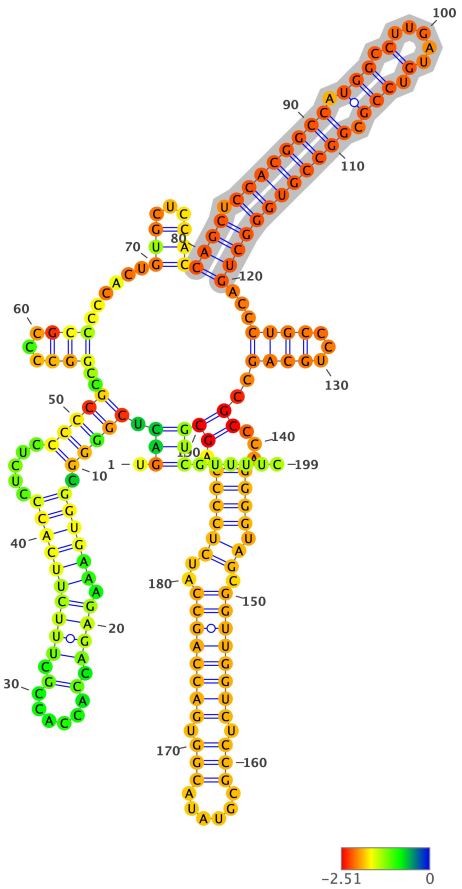
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 217 from nt 62220 to 62261 (nt 79 to 120)

```
5'-CAGCUCCACGGCCAUGGCCUUGAUGUCCGCGGCCGUGGGCUG-3'
5'-((((.(((((((((.(((.(.....).))).)))))))))))))-3'
Motif MFE = -27.2; z-score = -3.57; 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 62142 to 62340 (motif highlighted in silver):

```
5'-UGACUCGGGGCGGUGAAAGAGACCACCACCGCUUUCUUCACCCUCUCCCCCGCCGGCCCCGCCCCCACUGUGCUCCACCAGCUCCACGGCCAUGGCCUUGAUGUCCGCGGC
CGUGGGCUGACCCUGCCCUGCAGCCGCCCAGGGGUAGCGGUUGGUCUCCGCGUAUACGGUGACCAGCCAUCUCCCCAGCGUCGUUUUC-3
5'-.((((.(((((.((((((.((((.(.......).)))))))))).....)))))..(((...))).......(((...)))((((.(((((((((.(((.(.....).))).)))
)))))))))...((((...)))))..((...((((.((.(((((((((.((.....)).)))))))).))))))..)))))).)))))......-3'
MFE = -83.8; z-score = -2.56; ED = 33.07
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

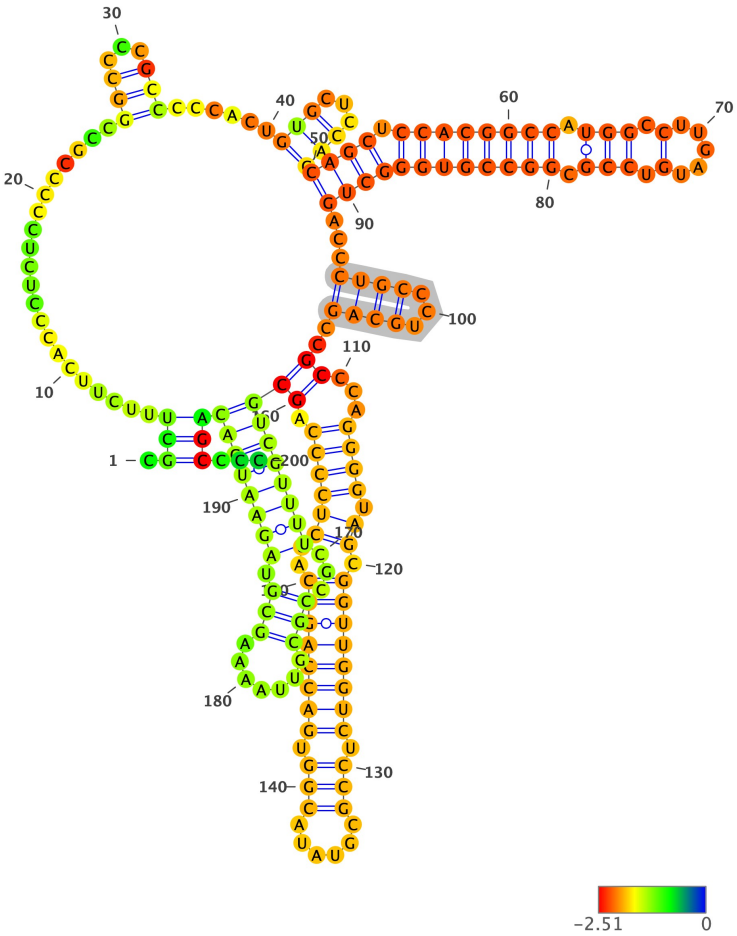
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 218 from nt 62265 to 62275 (nt 95 to 105)

```
5'-CUGCCCUGCAG-3'
5'-(((((...)))))-3'
Motif MFE = -2.2; z-score = -2.64; 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 62171 to 62370 (motif highlighted in silver):

```
5'-CGCUUUCUUCACCCUCUCCCCCGCCGGCCCCGCCCCCACUGUGCUCCACCAGCUCCACGGCCAUGGCCUUGAUGUCCGCGGCCGUGGGCUGACCCUGCCCUGCAGCCGCCC
AGGGGUAGCGGUUGGUCUCCGCGUAUACGGUGACCAGCCAUCUCCCCAGCGUCGUUUUCGCCGCGUUAAAAGCGUAGAAUGACAGCCCC-3
5'-.(((.....................(((...))).....(((...)))(((((.(((((((((.(((.(.....).))).))))))))))))...(((((...)))))..((..
.(((((.((.(((((((((.((.....))).)))))))).)).))))))).))))))))))...(((.......))).))))))))))))...-3'
MFE = -77.0; z-score = -2.14; ED = 27.8
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

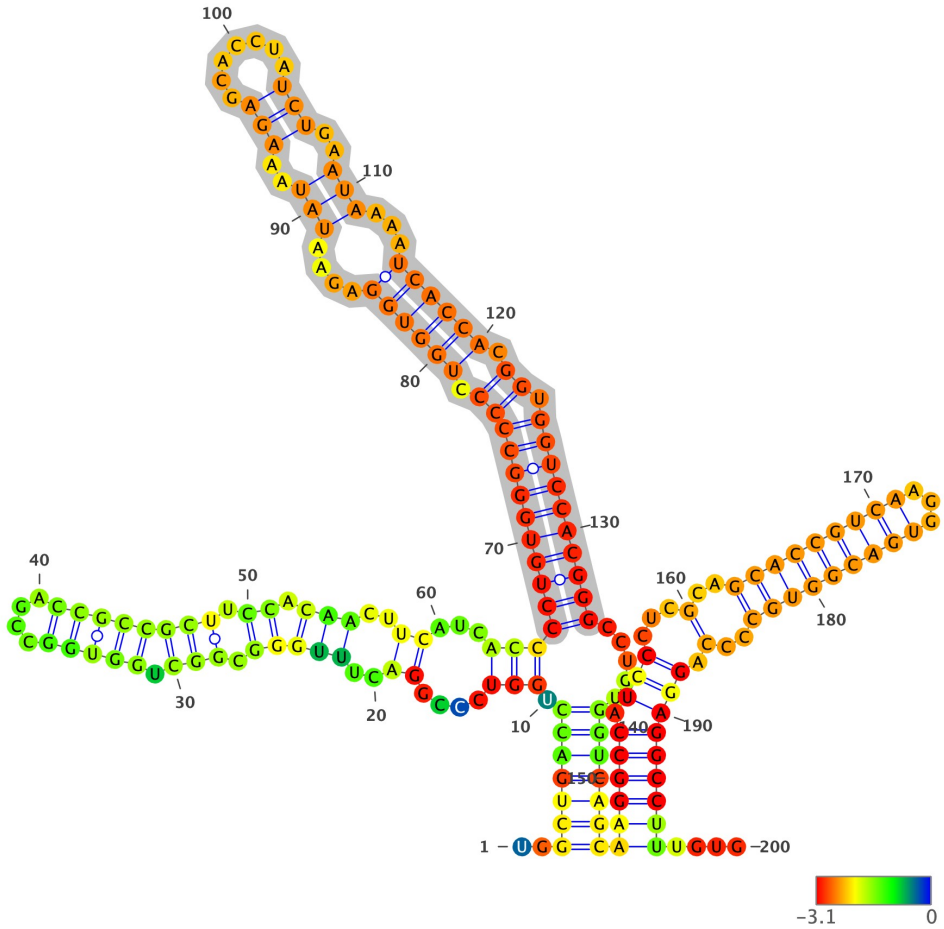
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 219 from nt 63508 to 63576 (nt 66 to 134)

```
5'-CCUGUGGGCCCCCUGGUGGAGAAUAUAAAGAGCACCUAUCUGAAUAAAAUCACCACGGUGGUCCACGGG-3'
5'-(((((((((((.((((((....(((..(((.......)))..)))...)))))).)).)))))))))-3'
Motif MFE = -30.8; z-score = -4.29; ED = 4.33
```



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 63443 to 63642 (motif highlighted in silver):

```
5'-UGGCUGACCUGGUCCCGGACUUUGGGCGGCUGGUGGCCGACCGCCGCUUCCACAACUUCAUCACCCCUGUGGGCCCCCUGGUGGAGAAUAUAAAGAGCACCUAUCUGAAUA
AAAUCACCACGGUGGUCCACGGGCCUGUGGUCAGCAAGGCCAUCCCUCGCAGCACCGUCAAGGUGACGGUGCCCCAGGAGGCCUUUGUG-3
5'-..(((((((.(((....((..((((((.((((.(((((....)))))))).)).))))..))...)))((((((((((.((((((....(((..(((.......)))..)))
...)))))).)).))))))))))).....)))))))((((((.(((...(..((((((((((...)))))))))..).)))))))))....-3'
MFE = -89.4; z-score = -3.46; ED = 27.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BORF1, 62729-66600(+)

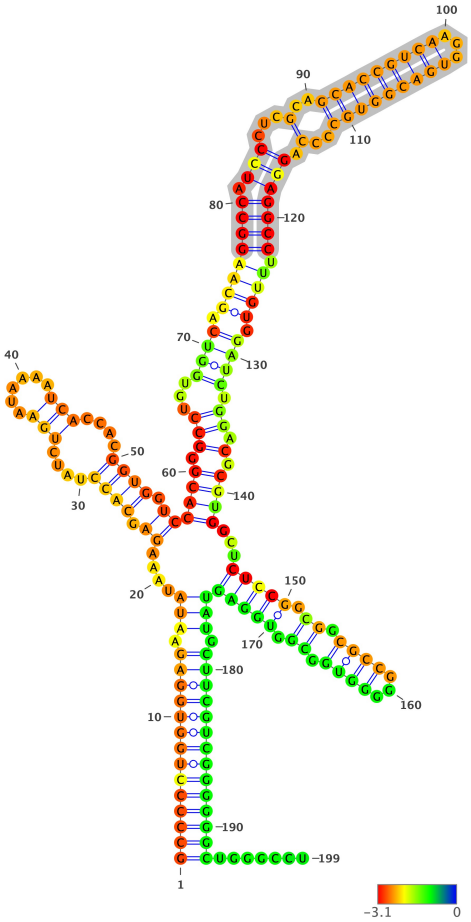
Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 200--CDS, cds-YP_401654.1, 62950-64044(+)

Attributes: ['ID=cds-YP_401654.1', 'Parent=gene-HHV4_BORF1', 'Dbxref=UniProtKB/TrEMBL:Q777G2,Genbank:YP_401654.1,GeneID:3783724', 'Name=YP_401654.1', 'gbkey=CDS', 'gene=BORF1', 'locus_tag=HHV4_BORF1', 'product=capsid triplex subunit 1', 'protein_id=YP_401654.1']

NC_007605.1 (forward strand): Structure number 220 from nt 63591 to 63636 (nt 77 to 122)

```
5'-GGCCAUCCCUCGCAGCACCGUCAAGGUGACGGUGCCCCAGGAGGCC-3'
5'-(((((.(.(...(..((((((((((...)))))))))..).).).)))))-3'
Motif MFE = -24.9; z-score = -3.29; 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 63515 to 63713 (motif highlighted in silver):

```
5'-GCCCCCUGGUGGAGAAUAUAAAGAGCACCUAUCUGAAUAAAAUCACCACGGUGGUCCACGGGCCUGUGGUCAGCAAGGCCAUCCCUCGCAGCACCGUCAAGGUGACGGUGC
CCCAGGAGGCCUUUGUGGAUCUGGACGCGUGGCUCUCCGGCGGCGCCGGGGGUGGCGGUGGAGUAUGCUUCGUCGGGGGGCUGGGCCU-3
5'-(((((((((((((.(((....((.((((....((((.....)))).....)))).))))(.((((...((((.(((((((((.((((...(..((((((((...)))))))))
..).)))))))).)))).)))).)).).)))))...((((((.((.((((...)))).)).)))))))).))))))))))))))).......-3'
MFE = -93.8; z-score = -2.32; ED = 20.63
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

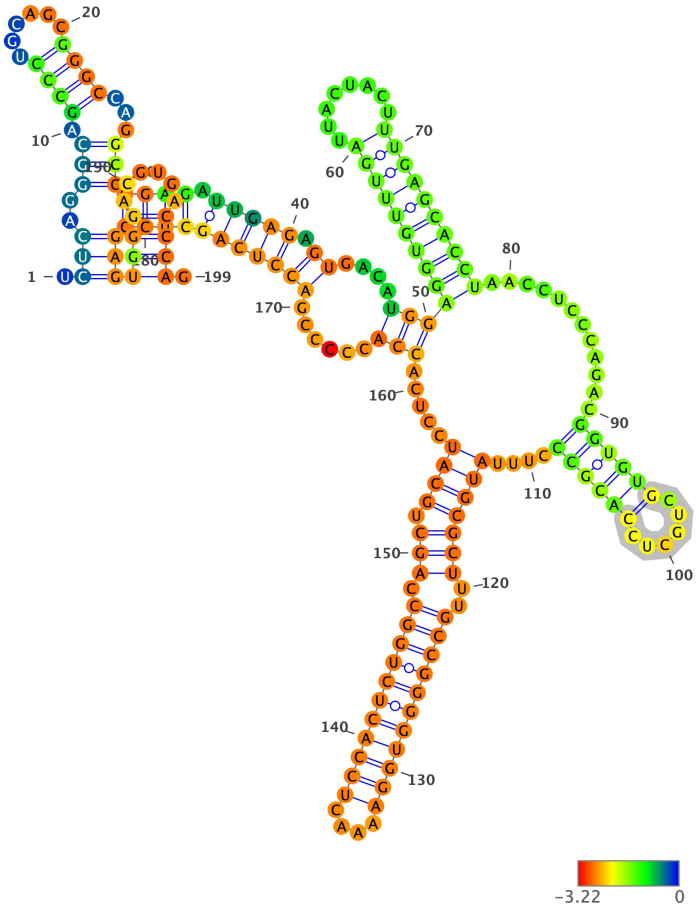
Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--CDS, cds-YP_401654.1, 62950-64044(+)

Attributes: ['ID=cds-YP_401654.1', 'Parent=gene-HHV4_BORF1', 'Dbxref=UniProtKB/TrEMBL:Q777G2,Genbank:YP_401654.1,GeneID:3783724', 'Name=YP_401654.1', 'gbkey=CDS', 'gene=BORF1', 'locus_tag=HHV4_BORF1', 'product=capsid triplex subunit 1', 'protein_id=YP_401654.1']

NC_007605.1 (forward strand): Structure number 221 from nt 64621 to 64628 (nt 96 to 103)

```
5'-GCUGCUCC-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 64526 to 64724 (motif highlighted in silver):

```
5'-UCUCAGGGCAGCCCUGCAGCGGGCCAGGCCGGAGAUUGAGAGUGACAUGGAGGUGUUUGAUUACUACUUUGAGCACCUAACCUCCCAGACGGUGUGCUGCUCCACGCCCUU
UAUGCGCUUUGCCGGGGUGGAAAACUCCACUCUGGCCAGCUGCAUCCUCACCACCCCCGACCUCAGCUCCGAGUGGGACGUGACCCAG-3
5'-.((((..((((.((((......))))...)))))((((.(((((.((....((((((((((((((.........)))))))))))).............((((((.....))))))).
.(((((((..((((((((((((....)))))))))))).)))).)))).....)))......))))))))))))))((((.....)))).-3'
MFE = -76.1; z-score = -1.54; ED = 36.55
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--gene, gene-HHV4_BORF2, 63881-66600(+)

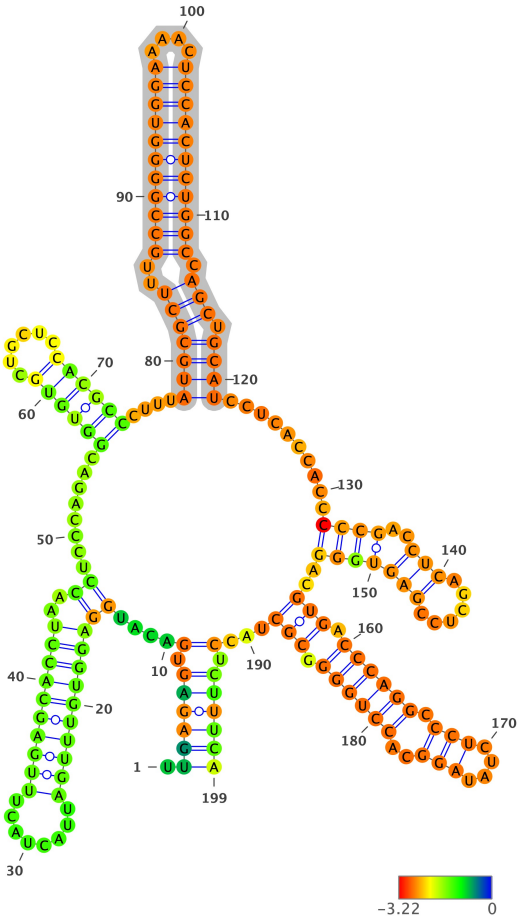
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 199--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 222 from nt 64638 to 64681 (nt 78 to 121)

```
5'-AUGCGCUUUGCCGGGGUGGAAAACUCCACUCUGGCCAGCUGCAU-3'
5'-(((((((..((((((((((....)))))))))))).))).))))-3'
Motif MFE = -25.9; z-score = -5.11; ED = 1.7
```



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

Extracted structure model with flanking nucleotides 64561 to 64759 (motif highlighted in silver):

```
5'-UUGAGAGUGACAUGGAGGUGUUUGAUUACUACUUUGAGCACCUAACCUCCCAGACGGUGUGCUGCUCCACGCCCUUUAUGCGCUUUGCCGGGGUGGAAAACUCCACUCUGG
CCAGCUGCAUCCUCACCACCCCCGACCUCAGCUCCGAGUGGGACGUGACCCAGGCCCUCUAUAGGCACCUGGGGCGCUACCUCUUUCA-3
5'-.(((((((.(....((((((((((((.......)))))))))))..)).......((((((.....))))))....(((((((..((((((((((....)))))))))))
).))).)))).........((((..(((.....)))))))..((((.((((((.(((....)))..)))))).)))...).)))))-3'
MFE = -75.4; z-score = -3.39; ED = 25.52
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--gene, gene-HHV4_BORF2, 63881-66600(+)

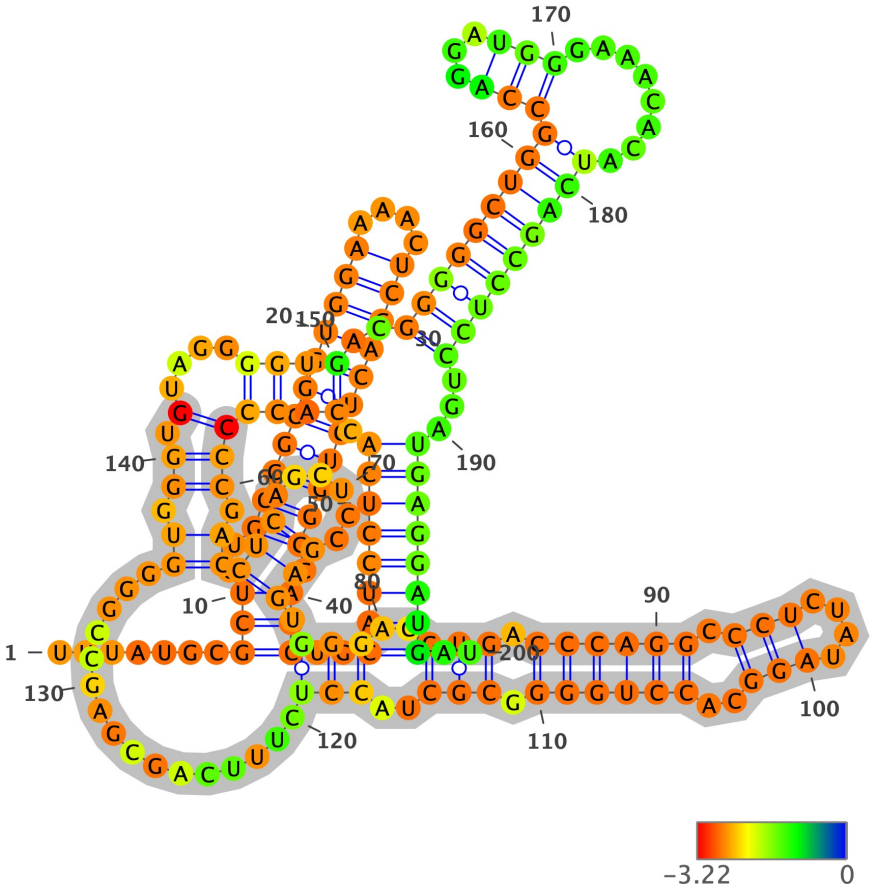
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 199--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 223 from nt 64692 to 64776 (nt 58 to 142)

```
5'-CCCGACCUCAGCUCCGAGUGGGACGUGACCCAGGCCCUCUAUAGGCACCUGGGGCGCUACCUCUUUCAGCGAGCCGGGGUGGGUG-3'
5'-(.(...(((......)))..(...((((.(((((((.((((....)))).)))))))).)))...)....................)..)-3'
Motif MFE = -39.3; z-score = -1.94; ED = 10.21
```



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 64635 to 64834 (motif highlighted in silver):

```
5'-UUUAUGCGCUUUGCCGGGGUGGAAAACUCCACUCUGGCCAGCUGCAUCCUCACCACCCCCGACCUCAGCUCCGAGUGGGACGUGACCCAGGCCCUCUAUAGGCACCUGGGG
CGCUACCUCUUUCAGCGAGCCGGGGUGGGUGUAGGGGUGACGGGGGCUGGCCAGGAUGGGAAACACAUCAGCCUCCUGAUGAGGAUGAU-3
5'-.......(((..((((((((((((....)))))))))))).)))..(((((((.(((((((.(((((......))).(((..(((.((((((.(((....)))).)).)))))).
)))..)))................)).)).)....)))))..((((((((((((...)))........)))))))))...)))))))..-3'
MFE = -74.8; z-score = -3.56; ED = 26.21
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 200--gene, gene-HHV4_BORF2, 63881-66600(+)

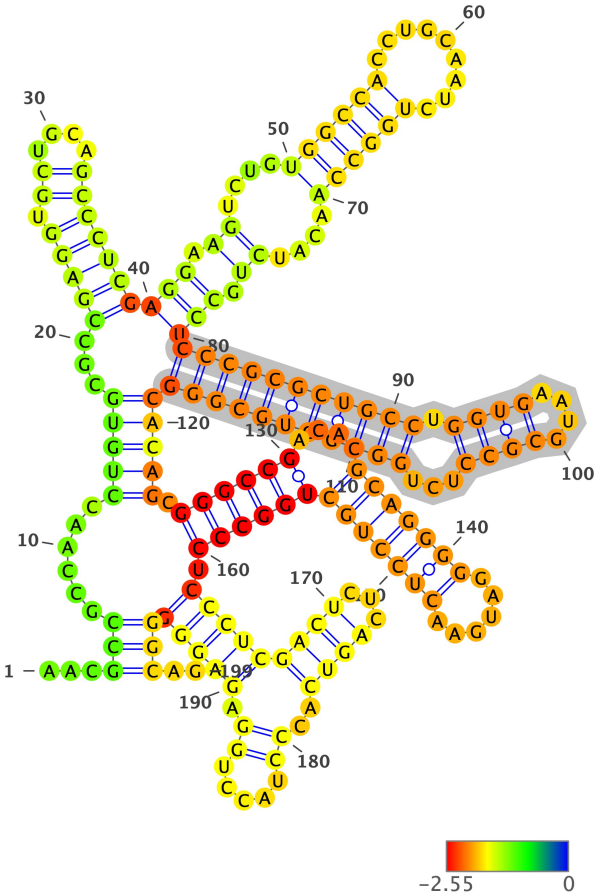
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 200--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 224 from nt 65348 to 65385 (nt 81 to 118)

```
5'-CCCGCGCUGCCUGGUGAAUGCGCCUCUGGCGGUGCGGG-3'
5'-(((((((((((.((((....))))...)))))))))))-3'
Motif MFE = -27.1; z-score = -3.9; 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 65268 to 65466 (motif highlighted in silver):

```
5'-AACGCCGCCAACCUGUGCGCCGAGGUGCUGCAGCCCUCGAGGAAGUCUGUGGCCACCUGCAAUCUGGCCAACAUCUGCCUCCCGCGCUGCCUGGUGAAUGCGCCUCUGGCG
GUGCGGGCACAGCGGGCCGACACGCAGGGGGAUGAACUCCUGCUGGCCCUCCCUCGACUCUCAGUCACCCUACCUGGAGAGGGGGCAG-3
5'-...(((.....((((((...(((((.((....)))))))((((.((....((((((.........)))))).....)).)))((((((((((.((((....)))).)))))
))))))))))).((((((....((((((.....)))))))))))))).(((((((((...)))).)).((.....)).)))))))..-3'
MFE = -93.7; z-score = -2.68; ED = 29.57
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--gene, gene-HHV4_BORF2, 63881-66600(+)

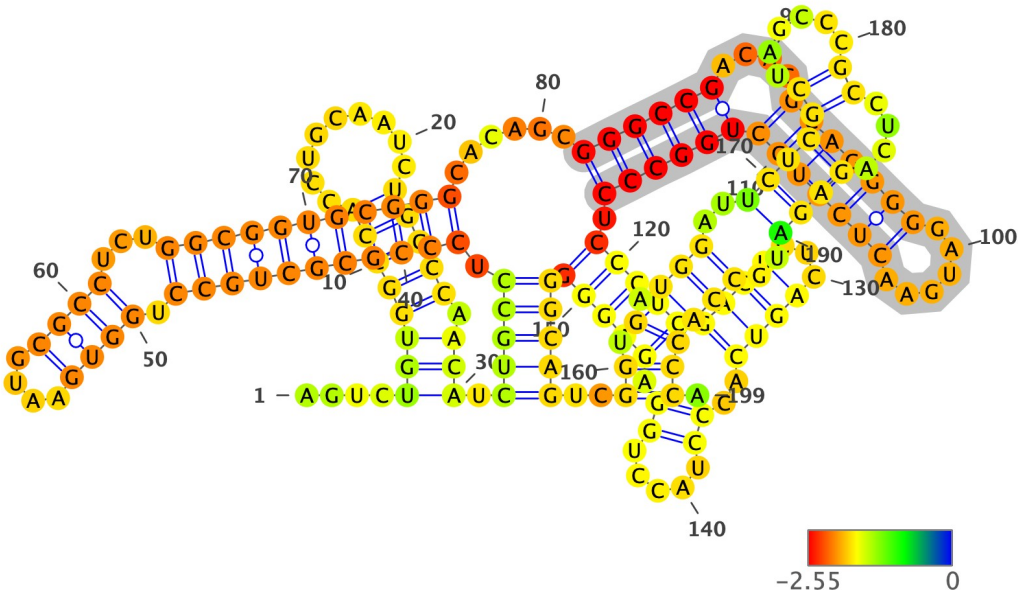
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 199--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 225 from nt 65392 to 65427 (nt 82 to 117)

```
5'-GGGCCGACACGCAGGGGGAUGAACUCCUGCUGGCCC-3'
5'-((((((....(((((((.....)))))))))))))-3'
Motif MFE = -22.2; z-score = -3.71; 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 65311 to 65509 (motif highlighted in silver):

```
5'-AGUCUGUGGCCACCUGCAAUCUGGCCAACAUCUGCCUCCCGCGCUGCCUGGUGAAUGCGCCUCUGGCGGUGCGGGCACAGCGGGCCGACACGCAGGGGGAUGAACUCCUGC
UGGCCCUCCCUCGACUCUCAGUCACCCUACCUGGAGAGGGGGCAGUCGGUGAUGGAUUCUCGCUAGCCCGCCUCAGAGAUGCCACCCA-3
5'-....(((((((((.........))))).))).(((((.(((((((((((.((((....))))...)))))))))))).....((((((....(((((((.....)))))))
))))))).((((((((...)))))..((.....)).))))))))))..((.(.((((..((((((.....)).....)))))..)))))).-3'
MFE = -88.9; z-score = -2.09; ED = 26.71
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--gene, gene-HHV4_BORF2, 63881-66600(+)

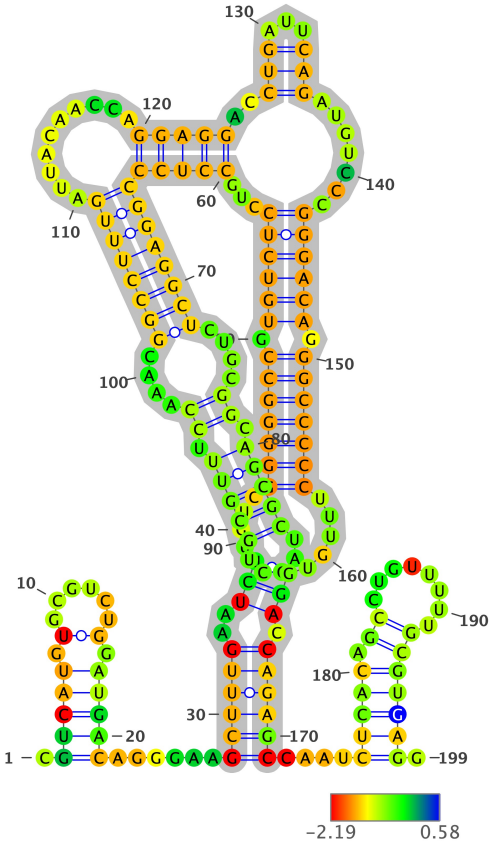
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 199--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 226 from nt 66045 to 66188 (nt 28 to 171)

```
5'-GCUUUGAAUCUUGUCGGGGGCCGUGUCUCCUGCCUCCCGGAGGCUCUGCGGCAGCGCUACCUGCGUUUCCAAACGGCCUUUGAUUACAACCAGGAGGACCUGAUUCAGAUG
UCCCGGGACAGGGCCCCCUUUGUGGACCAGAGC-3'
5'-(....(..(.......................................................................................................
.........................).)....)-3'
Motif MFE = -60.3; z-score = -2.47; ED = 17.77
```



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 66018 to 66216 (motif highlighted in silver):

```
5'-CGUCAUGUGCGUCUGGAUGACAGGGAAGCUUUGAAUCUUGUCGGGGGCCGUGUCUCCUGCCUCCCGGAGGCUCUGCGGCAGCGCUACCUGCGUUUCCAAACGGCCUUUGAU
UACAACCAGGAGGACCUGAUUCAGAUGUCCCGGGACAGGGCCCCCUUUGUGGACCAGAGCCAAUCUCACAGCCUGUUUUUGCGUGAGG-3
5'-.(((((.(......).))))).....(((((..(((....(((((((.((((((...(((((((((((((....((.(((((.....)))))).)).....)))))))).
........)))))..(((...))).......)))))).)))))))).....))).)))))).....(((((.((........)))))))).-3'
MFE = -73.8; z-score = -0.92; ED = 33.52
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 199--gene, gene-HHV4_BORF2, 63881-66600(+)

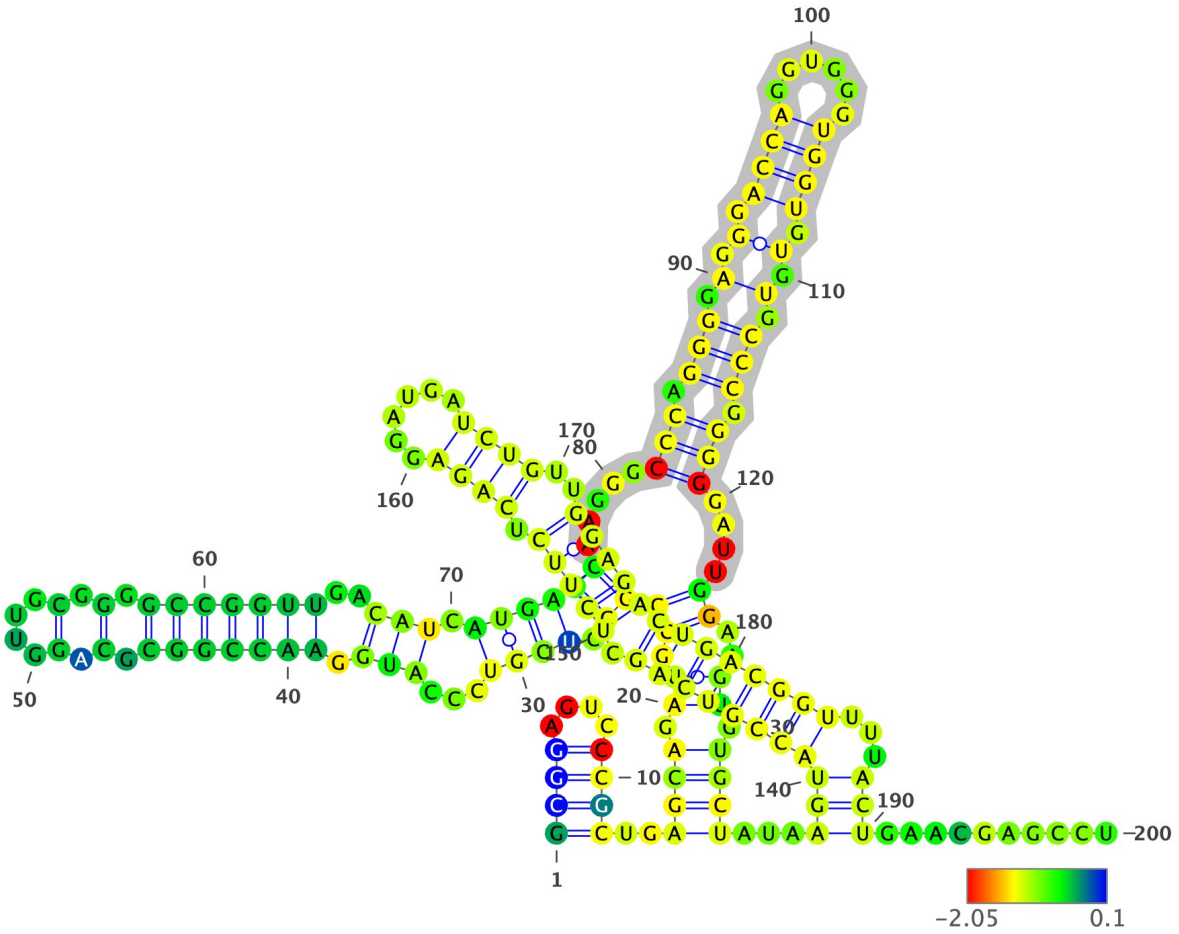
Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 199--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

NC_007605.1 (forward strand): Structure number 227 from nt 66459 to 66505 (nt 77 to 123)

```
5'-AAGGGCCCAGGGGAGGGACCAGGUGGGUGGUGUGUGCCCGGGGGAUU-3'
5'-((...(.....)..))-3'
Motif MFE = -20.2; z-score = -3.32; 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 66383 to 66582 (motif highlighted in silver):

```
5'-GCGGAGUCCCGCUGAGCAGAUGCCGCCUCGUCCCAUGGAACCGGCGCAGGUUGCGGGGCCGGUUGACAUCAUGAGCAAGGGCCCAGGGGAGGGACCAGGUGGGUGGUGUGU
GCCCGGGGGAUUGGAAGUGUGCUAUAAGUACCGUCAGCUCUUCUCAGAGGAUGAUCUGUUGGAGACUGACGGUUUUACUGAACGAGCCU-3
5'-((((....)))).((((.((.(((((.((((...(((.(((((((.(.(....).).)))))))..)))).)))))).....(((.(((.(.(.((((.....)))).).).
.))).)))....)).)).)))).....((((((((((.(((((.((((.....)))).)).))))))))))))...))).........-3'
MFE = -76.9; z-score = -1.95; ED = 44.78
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BORF1, 62729-66600(+)

Attributes: ['ID=gene-HHV4_BORF1', 'Dbxref=GeneID:3783724', 'Name=BORF1', 'Note=core gene', 'gbkey=Gene', 'gene=BORF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF1']

12-- nt 1 to 200--gene, gene-HHV4_BORF2, 63881-66600(+)

Attributes: ['ID=gene-HHV4_BORF2', 'Dbxref=GeneID:3783725', 'Name=BORF2', 'Note=core gene', 'gbkey=Gene', 'gene=BORF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BORF2']

13-- nt 1 to 200--CDS, cds-YP_401655.1, 64119-66599(+)

Attributes: ['ID=cds-YP_401655.1', 'Parent=gene-HHV4_BORF2', 'Dbxref=UniProtKB/TrEMBL:Q777G1,Genbank:YP_401655.1,GeneID:3783725', 'Name=YP_401655.1', 'gbkey=CDS', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'product=ribonucleotide reductase subunit 1', 'protein_id=YP_401655.1']

14-- nt 134 to 139--TATA_box, id-HHV4_BORF2-2, 66516-66521(+)

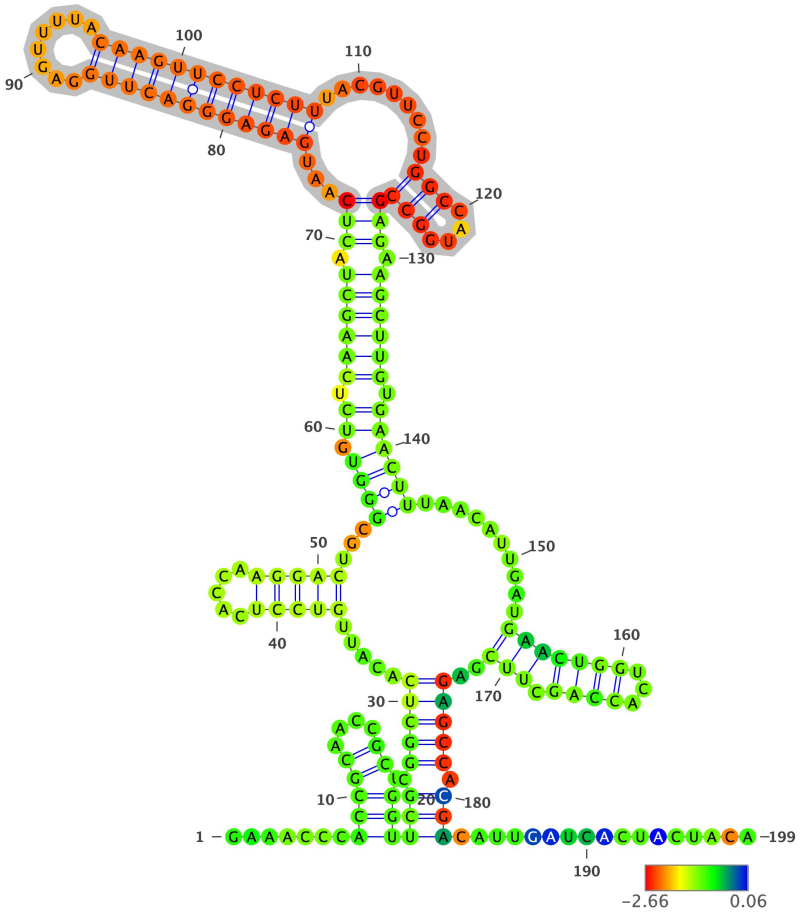
Attributes: ['ID=id-HHV4_BORF2-2', 'Dbxref=GeneID:3783725', 'gbkey=regulatory', 'gene=BORF2', 'locus_tag=HHV4_BORF2', 'regulatory_class=TATA_box']

15-- nt 134 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

NC_007605.1 (forward strand): Structure number 228 from nt 66737 to 66792 (nt 72 to 127)

```
5'-CAAUGAGAGGGACUUGGAGUUUUACAAGUUCCUCUUUACGUUCCUGGCCAUGGCCG-3'
5'-(...((((((((((((.......)))))))))))).........(((....))))-3'
Motif MFE = -21.9; z-score = -2.91; ED = 2.25
```



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

Extracted structure model with flanking nucleotides 66666 to 66864 (motif highlighted in silver):

```
5'-GAAACCCACCGCAACCGCUGGUUCGCGGCUCACAUUGUCCUCACCAAGGACUGCGGGUGUCUCAAGCUACUCAAUGAGAGGGACUUGGAGUUUUACAAGUUCCUCUUUACG
UUCCUGGCCAUGGCCGAGAAGCUUGUGAACUUUAACAUUGAUGAACUGGUCACCAGCUUCGAGAGCCACGACAUUGAUCACUACUACA-3
5'-.......(((((....)).)))((((.(((((.....(((((.....)))))...(((((.((.(((((((.(((...(((((((((((.......)))))))))))).....
.....((((....)))))).)))))).)))))).........(((((((...)))).)))..)))))).)))................-3'
MFE = -62.1; z-score = -2.65; ED = 19.36
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

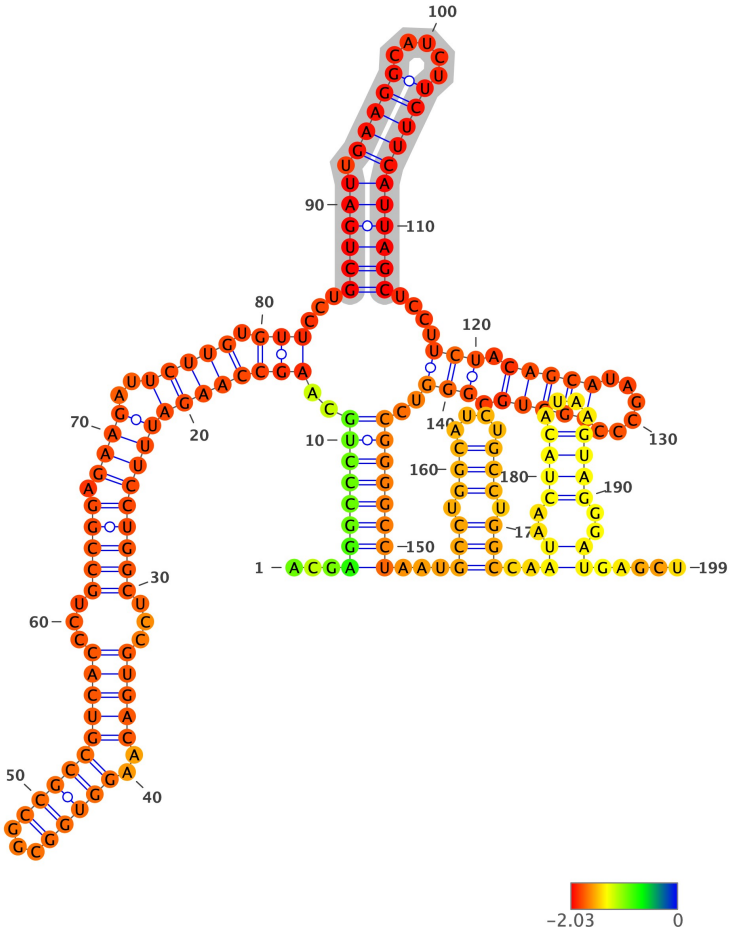
Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 199--CDS, cds-YP_401656.1, 66612-67520(+)

Attributes: ['ID=cds-YP_401656.1', 'Parent=gene-HHV4_BaRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q777G0,Genbank:YP_401656.1,GeneID:3783683', 'Name=YP_401656.1', 'gbkey=CDS', 'gene=BaRF1', 'locus_tag=HHV4_BaRF1.1', 'product=ribonucleotide reductase subunit 2', 'protein_id=YP_401656.1']

NC_007605.1 (forward strand): Structure number 229 from nt 67064 to 67091 (nt 86 to 113)

```
5'-GCUGAUUGAAGGCAUCUUCUUCAUUAGC-3'
5'-((((((.............))))))-3'
Motif MFE = -8.6; z-score = -2.79; ED = 2.19
```



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

Extracted structure model with flanking nucleotides 66979 to 67177 (motif highlighted in silver):

```
5'-ACGAGGCCCUGCAAGCCAAGAUUUCCUGGCUCCGUGACAAGGUGGCGGCCGCCGUCACCCUGCCGGAGAAGAUUCUUGUGUUCCUGCUGAUUGAAGGCAUCUUCUUCAUUA
GCUCCUUCUACAGCAUAGCCCUGCUGCGGGUCCGGGGCCUAAUGCCUGGCAUCUGCCUGGCCAAUAACUACAUAAGUAGGGAUGAGCU-3
5'-...(((((((((..((((((((((((((((((...(((((..(((((...)))))))))))...)))))).))))..)))))).))))...((((((.(((((.....)))))))))
))....(((.(((((.....))))).)))..))))))))...((((.((((....)))).)))..((..((((....))))..)).....-3'
MFE = -75.0; z-score = -2.49; ED = 32.16
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

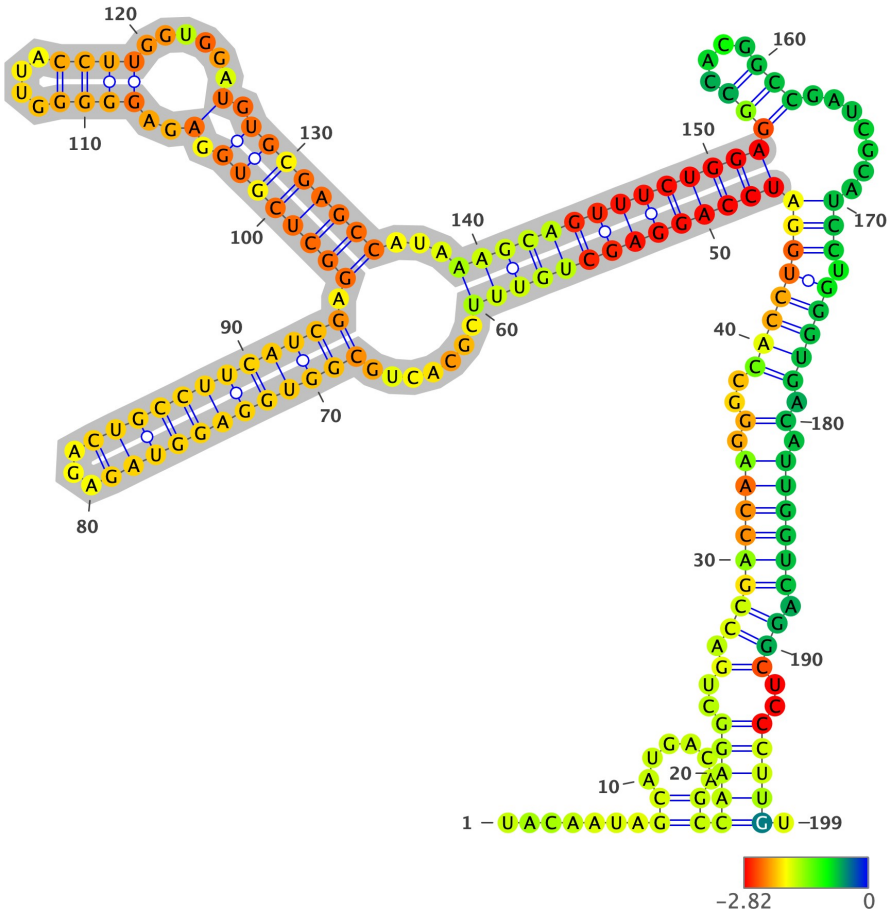
12-- nt 1 to 199--CDS, cds-YP_401656.1, 66612-67520(+)

Attributes: ['ID=cds-YP_401656.1', 'Parent=gene-HHV4_BaRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q777G0,Genbank:YP_401656.1,GeneID:3783683', 'Name=YP_401656.1', 'gbkey=CDS', 'gene=BaRF1', 'locus_tag=HHV4_BaRF1.1', 'product=ribonucleotide reductase subunit 2', 'protein_id=YP_401656.1']

NC_007605.1 (forward strand): Structure number 230 from nt 67252 to 67357 (nt 47 to 152)

```
5'-UCCAGGAGCUGUUUCGCACUGCGGUGGAGGUAGAGACUGCCUUCAUCGAGGCUCGUGGAGAGGGGGUUACCUUGGUGGAUGUGCGAGCCAUAAAGCAGUUUCUGGA-3'

5'-(((((((((.........((((((((((((...)))))))))))).(((((.((.(..((((....))))).....).)).)))))........)))))))))-3'
Motif MFE = -50.9; z-score = -4.93; 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 67206 to 67404 (motif highlighted in silver):

```
5'-UACAAUAGCAUGACAGCCAAGGCUGACCGACCAAGGGCCACCUGGAUCCAGGAGCUGUUUCGCACUGCGGUGGAGGUAGAGACUGCCUUCAUCGAGGCUCGUGGAGAGGGG
GUUACCUUGGUGGAUGUGCGAGCCAUAAAGCAGUUUCUGGAGGCCACGGCCGAUCGCAUCCUGGGUGACAUUGGUCAGGCUCCCUUGU-3
5'-.......((......))((((((..(.(((((((((.(..((((((((((((((((((((((((.......((((((((((...)))))))))))).(((((((((.(..((((
....)))).....).))))))))...))))))))))))))((....)))).......))).)))))).).)))))).)))..)))))).-3'
MFE = -82.3; z-score = -2.48; ED = 15.74
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

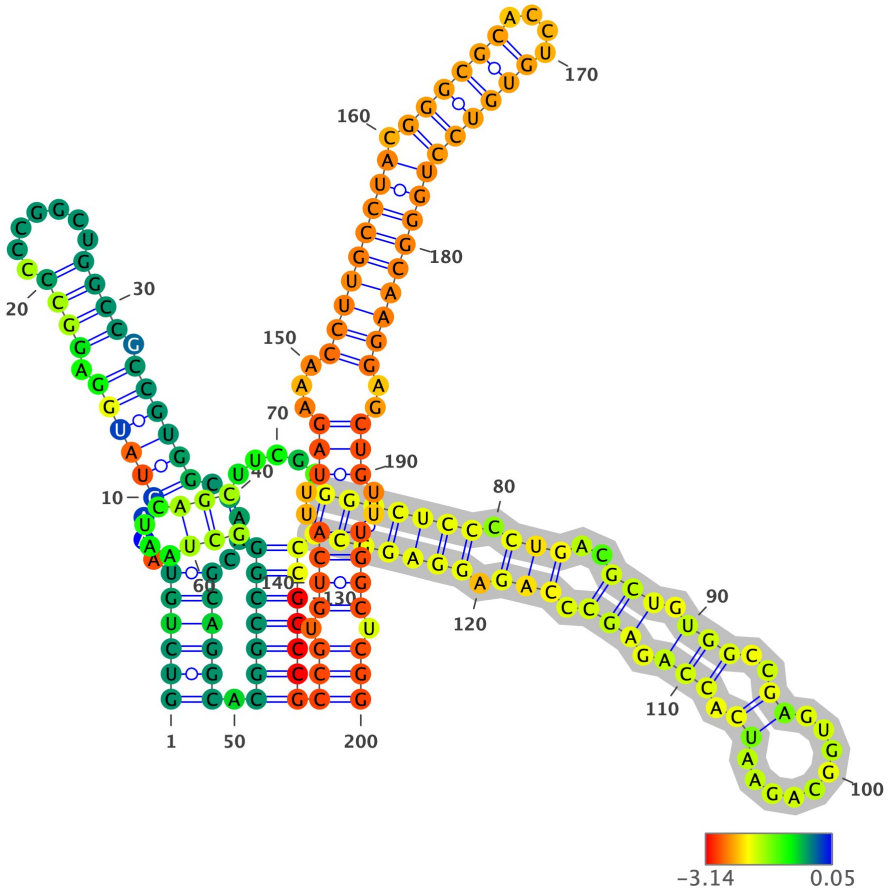
Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 199--CDS, cds-YP_401656.1, 66612-67520(+)

Attributes: ['ID=cds-YP_401656.1', 'Parent=gene-HHV4_BaRF1.1', 'Dbxref=UniProtKB/TrEMBL:Q777G0,Genbank:YP_401656.1,GeneID:3783683', 'Name=YP_401656.1', 'gbkey=CDS', 'gene=BaRF1', 'locus_tag=HHV4_BaRF1.1', 'product=ribonucleotide reductase subunit 2', 'protein_id=YP_401656.1']

NC_007605.1 (forward strand): Structure number 231 from nt 67796 to 67850 (nt 73 to 127)

```
5'-GGUCUCCCCUGACGCUGUGGCCGAGUGGCAGAAUCACCAGAGCCCAGAGGAGGCC-3'
5'-(((((((.(.............(...........).........).)))))))-3'
Motif MFE = -23.8; z-score = -1.93; 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 67724 to 67923 (motif highlighted in silver):

```
5'-GUCUGUAAACUAUGGAGGCCCCCGGCUGGCCGCCGUGGCCAACGCAGGCACGGCCGGGCUAAUCAGCUUCGAGGUCUCCCCUGACGCUGUGGCCGAGUGGCAGAAUCACCA
GAGCCCAGAGGAGGCCCCGGCCGCCGUGUCAUUUAGAAACCUUGCCUACGGGCGCACCUGUGUCCUGGGCAAGGAGCUGUUUGGCUCGG-3
5'-((((((...((((((.((((.......)))).)))))).....)))))).((((((((((....)))).....(((((((.(((..(((.(((..((.........)).)))
.))).))).))))))))))))))((.(((((..(((...(((((((((.((((((....)))))))))))))))..)))..)))))..)))-3'
MFE = -96.6; z-score = -3.09; ED = 15.04
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 200--gene, gene-HHV4_BMRF1, 67552-69916(+)

Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

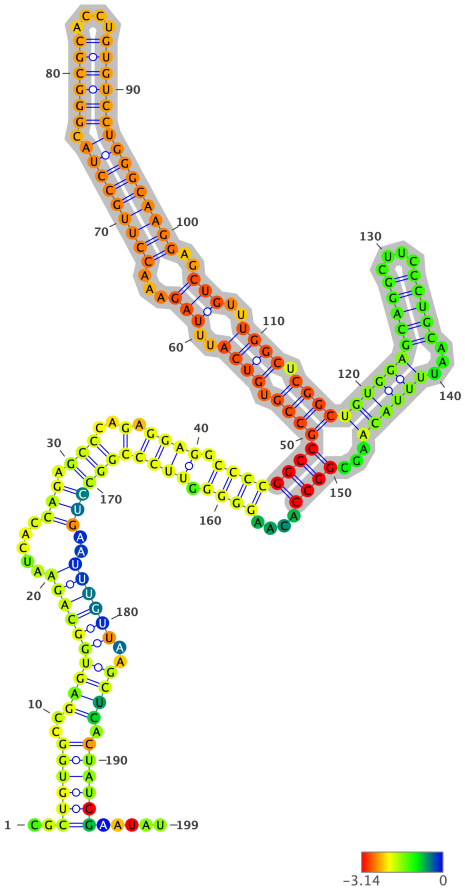
13-- nt 1 to 200--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 232 from nt 67853 to 67960 (nt 46 to 153)

```
5'-GGCCGCCGUGUCAUUUAGAAACCUUGCCUACGGGCGCACCUGUGUCCUGGGCAAGGAGCUGUUUGGCUCGGCUGUGGAGCAGGCUUCCCUGCAAUUUUACAAGCGGCC-3'

5'-(((((((.((((..(((...(((((((((.((((((....)))))))))))))))..)))..)))).)))).................................))))-3'
Motif MFE = -53.6; z-score = -4.77; 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 67808 to 68006 (motif highlighted in silver):

```
5'-CGCUGUGGCCGAGUGGCAGAAUCACCAGAGCCCAGAGGAGGCCCCGGCCGCCGUGUCAUUUAGAAACCUUGCCUACGGGCGCACCUGUGUCCUGGGCAAGGAGCUGUUUGG
CUCGGCUGUGGAGCAGGCUUCCCUGCAAUUUUACAAGCGGCCACAAGGGGGUUCCCGGCCUGAAUUUGUUAAGCUCACUAUGGAAUAU-3
5'-..((((((..(((((((((((.....(((.((((..(.((((.(((((((((((((.(((((..(((...(((((((((.((((((....)))))))))))))))..)))..)))
).))))((((((((((((....)))))...)))))))...))))....)))).))))))))))))..)))))))..)))).)))))))).....-3'
MFE = -86.2; z-score = -3.49; ED = 10.88
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 199--gene, gene-HHV4_BMRF1, 67552-69916(+)

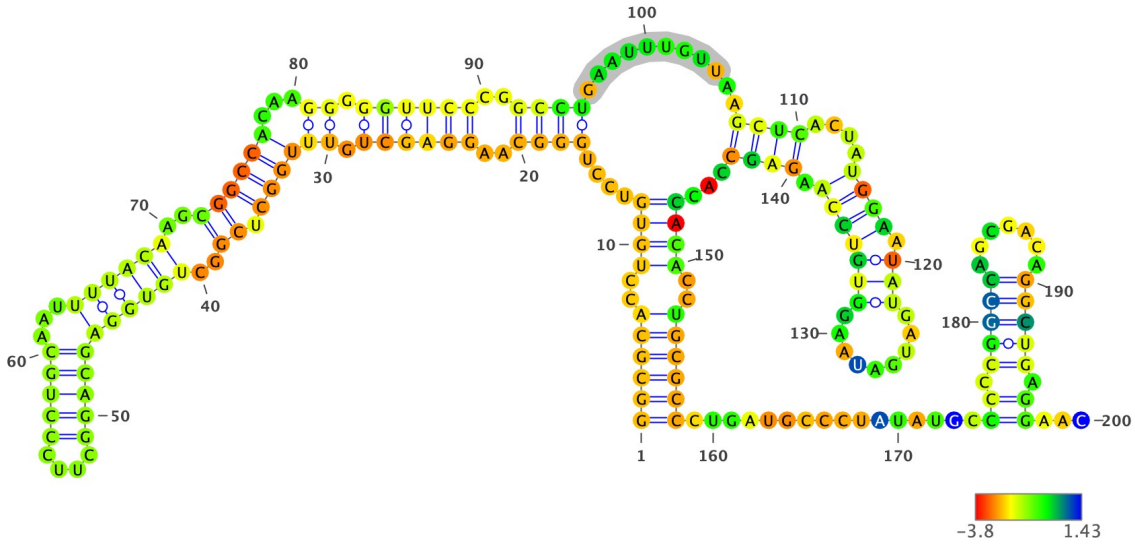
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 199--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 233 from nt 67980 to 67988 (nt 96 to 104)

```
5'-GAAUUUGUU-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 67885 to 68084 (motif highlighted in silver):

```
5'-GGCGCACCUGUGUCCUGGGCAAGGAGCUGUUUGGCUCGGCUGUGGAGCAGGCUUCCCUGCAAUUUUACAAGCGGCCACAAGGGGGUUCCCGGCCUGAAUUUGUUAAGCUCA
CUAUGGAAUAUGAUGAUAAGGUGUCCAAGAGCCACCACACCUGCGCCCUGAUGCCCUAUAUGCCCCCGGCCAGCGACAGGCUGAGGAAC-3
5'-(((((((..((((....((((..((((((.((((((.((..((((((((((((....)))))...)))))))..)))))))...)).)))))))..))))).....((((.
...((((.(((........)))))))..))))...)))))..)))))).....................((.(((((.......))))).)).....-3'
MFE = -67.5; z-score = 0.07; ED = 27.79
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 200--gene, gene-HHV4_BMRF1, 67552-69916(+)

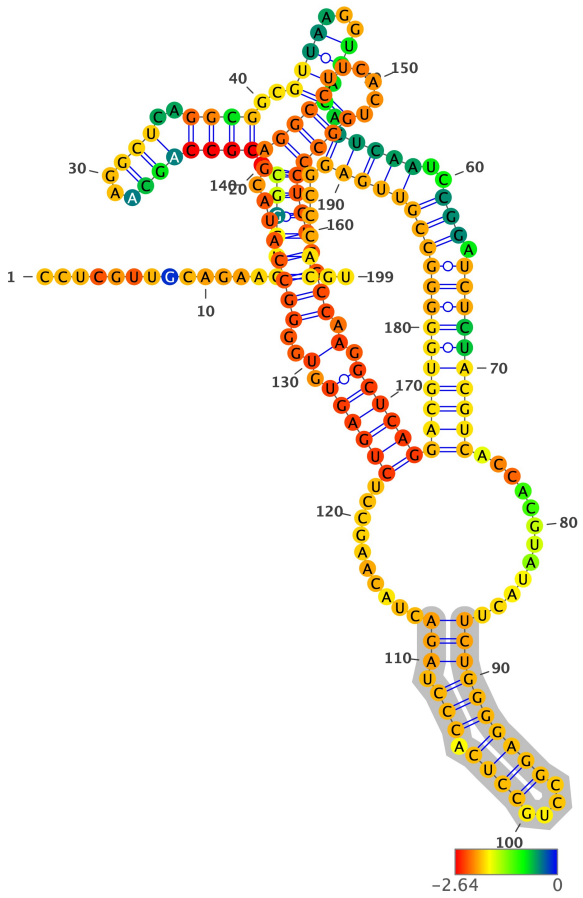
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 200--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 234 from nt 68214 to 68239 (nt 87 to 112)

```
5'-UCUGGGGAGGCCUGCCUCACCCUAGA-3'
5'-((((((.............))).)))-3'
Motif MFE = -11.7; z-score = -2.76; ED = 4.75
```



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 68128 to 68326 (motif highlighted in silver):

```
5'-CCUCGUUGCAGAAGUGGGCACGCCAGCAAGGCUCAGGCGGCGUUAAGGUGACACUCAAUCCGGAUCUCUACGUCACCACGUAUACUUCUGGGGAGGCCUGCCUCACCCUAG
ACUACAAGCCUCUGAGUGUGGGGCCAUACGAGGCCUUCACUGGCCCUGUGGCCAAGGCUCAGGACGUGGGGGCCGUUGAGGCCCACGU-3
5'-.............((((((.(((((((...))).)).))))..((((...)))).((((((..(((.((((((((((.............((((((((((....)))))).))).))
).........((((((.(..(((((((.(.((((.....)))))))))))).).)).))))))))))))))))))))))))))))))))))..-3'
MFE = -84.3; z-score = -2.11; ED = 16.89
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 199--gene, gene-HHV4_BMRF1, 67552-69916(+)

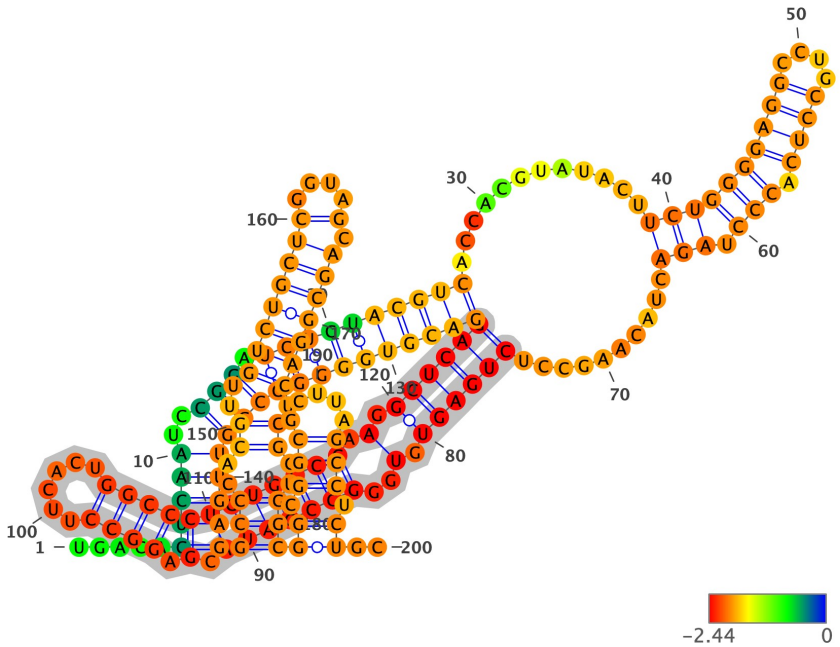
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 199--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 235 from nt 68250 to 68300 (nt 75 to 125)

```
5'-CUGAGUGUGGGGCCAUACGAGGCCUUCACUGGCCCUGUGGCCAAGGCUCAG-3'
5'-((((((.(..(((((((.(.((((.....)))))))))))).).)))))))-3'
Motif MFE = -29.0; z-score = -4.47; 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 68176 to 68375 (motif highlighted in silver):

```
5'-UGACACUCAAUCCGGAUCUCUACGUCACCACGUAUACUUCUGGGGAGGCCUGCCUCACCCUAGACUACAAGCCUCUGAGUGUGGGGCCAUACGAGGCCUUCACUGGCCCUG
UGGCCAAGGCUCAGGACGUGGGGGCCGUUGAGGCCCACGUUGUCUGCUCGGUAGCAGCGGACUCGCUGGCGGCGGCGCUUAGCCUCUGC-3
5'-.....(((((..(((.(((((((((((.............((((((((((....)))).)))).)))..........((((((.(..(((((((.(.((((.....)))))))
)))))).).))))))))))))))))))))))))((..((..(((((((((....).)))))))..))..)))((.((((.....)))).)).-3'
MFE = -88.0; z-score = -2.32; ED = 20.08
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 200--gene, gene-HHV4_BMRF1, 67552-69916(+)

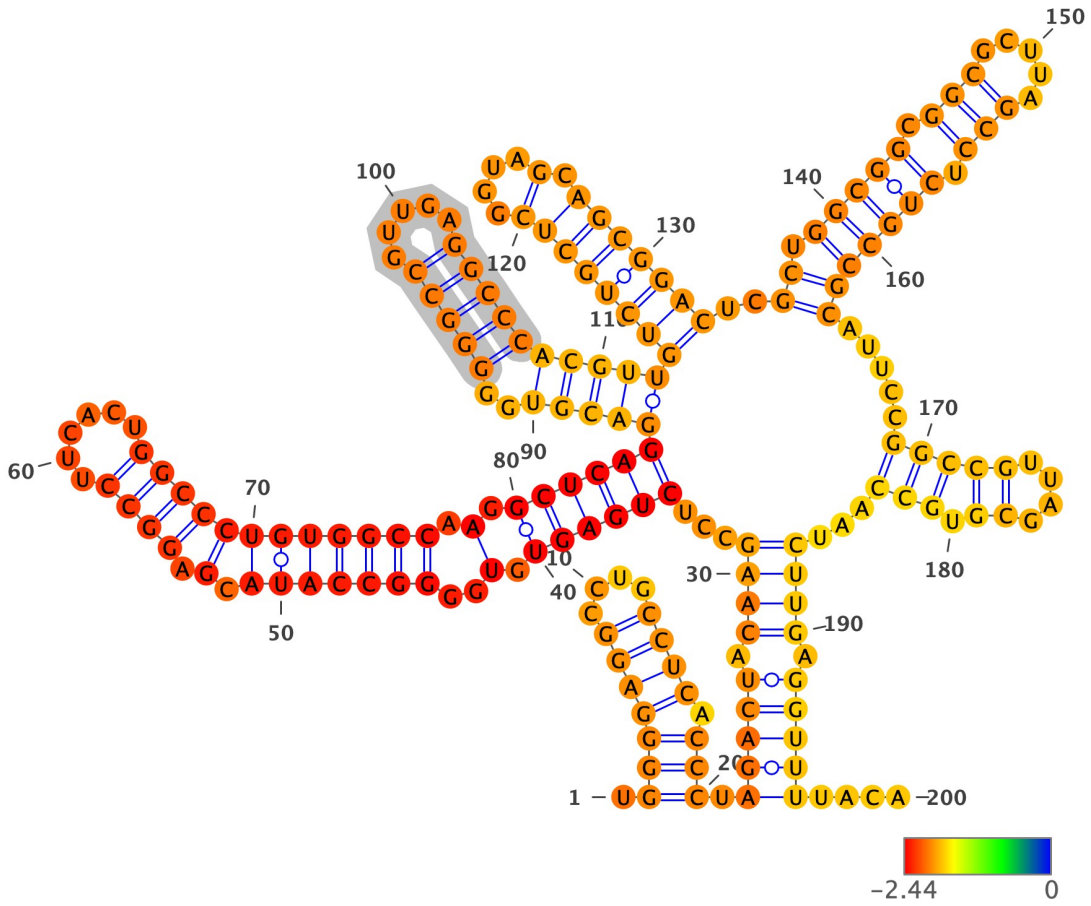
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 200--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 236 from nt 68308 to 68322 (nt 93 to 107)

```
5'-GGGCCGUUGAGGCCC-3'
5'-(((((.....)))))-3'
Motif MFE = -9.9; z-score = -3.75; 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 68216 to 68415 (motif highlighted in silver):

```
5'-UGGGGAGGCCUGCCUCACCCUAGACUACAAGCCUCUGAGUGUGGGGCCAUACGAGGCCUUCACUGGCCCUGUGGCCAAGGCUCAGGACGUGGGGGCCGUUGAGGCCCACGU
UGUCUGCUCGGUAGCAGCGGACUCGCUGGCGGCGGCGCUUAGCCUCUGCCGCAUUCCGGCCGUUAGCGUGCCAAUCUUGAGGUUUUACA-3
5'-.(((((((....)))).))).(((((.((((...((((((.(..(((((((.(.((((.....)))))))))))).).))))))((((..(((((.....)))))))))
)((((((((....).)))))))..((.(((((.((.....)).)))))).....((((....)).)))...)))).)))))....-3'
MFE = -95.1; z-score = -3.03; ED = 25.4
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 200--gene, gene-HHV4_BMRF1, 67552-69916(+)

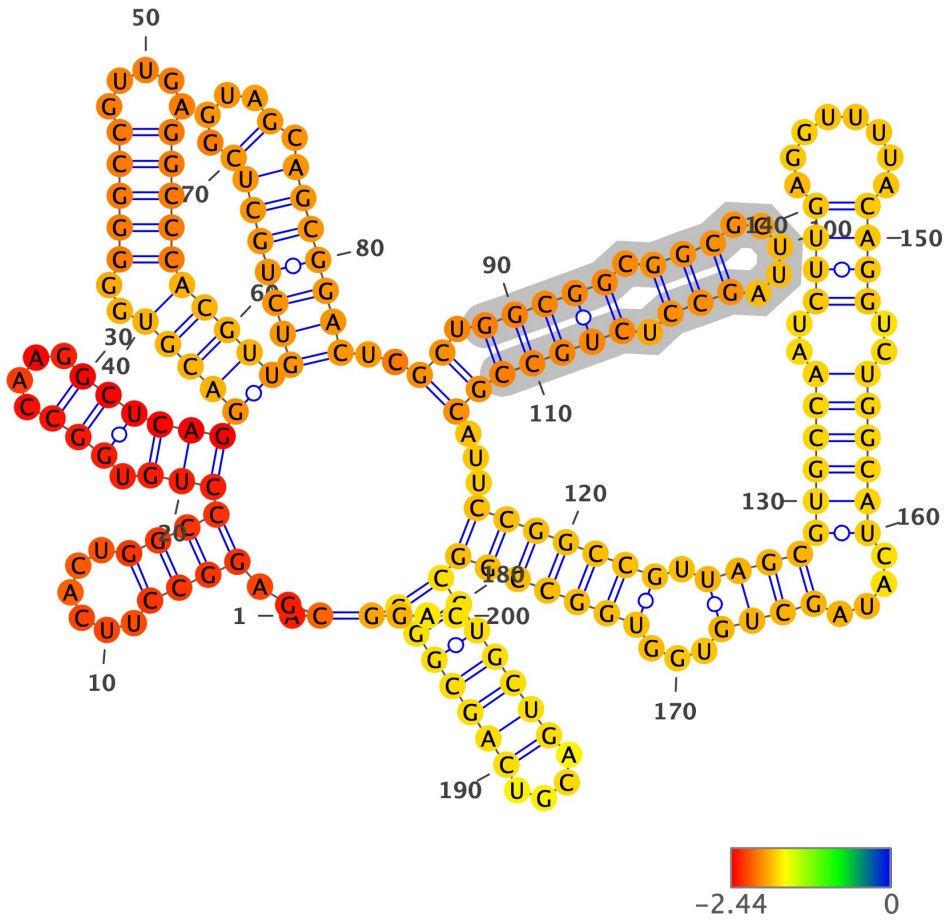
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 200--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 237 from nt 68354 to 68376 (nt 89 to 111)

```
5'-GGCGGCGGCGCUUAGCCUCUGCC-3'
5'-(((((.............)))))-3'
Motif MFE = -13.5; z-score = -3.15; ED = 0.06
```



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

Extracted structure model with flanking nucleotides 68266 to 68465 (motif highlighted in silver):

```
5'-ACGAGGCCUUCACUGGCCCUGUGGCCAAGGCUCAGGACGUGGGGGCCGUUGAGGCCCACGUUGUCUGCUCGGUAGCAGCGGACUCGCUGGCGGCGGCGCUUAGCCUCUGCC
GCAUUCCGGCCGUUAGCGUGCCAAUCUUGAGGUUUUACAGGUCUGGCAUCAUAGCUGUGGUGGCCGGCCUGCUGACGUCAGCGGGGGAC-3
5'-.(..((((.....))))((((.((((....))))))(((((..(((((.....)))))))))))(((((((((....).))))))).((.(((((.((((.....)))).)))))
)).....(((((((.((((((((((..((((........))))..))))))).....)))))...)))))))(((((((....)))))))).....-3'
MFE = -96.2; z-score = -1.91; ED = 23.55
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 200--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 200--gene, gene-HHV4_BMRF1, 67552-69916(+)

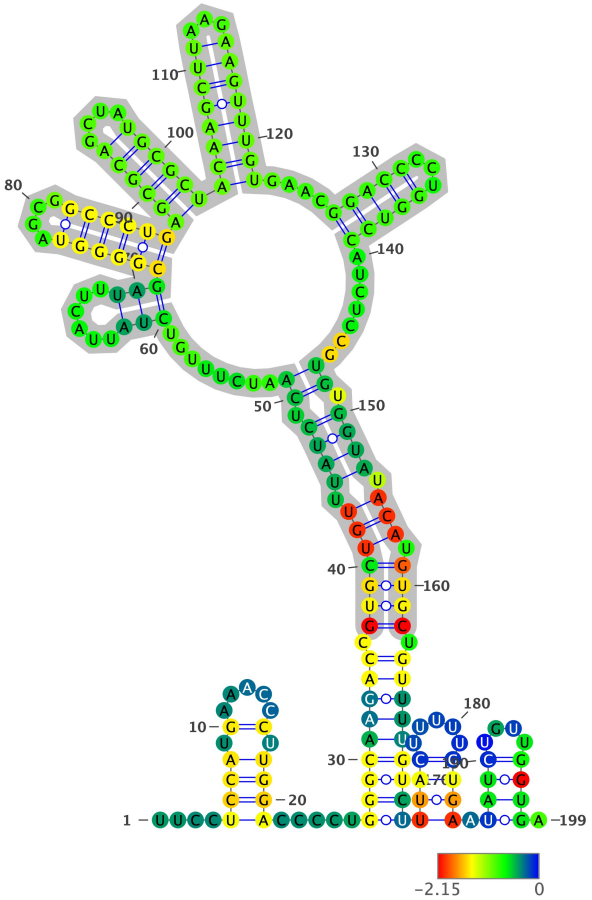
Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 200--CDS, cds-YP_401657.1, 67611-68825(+)

Attributes: ['ID=cds-YP_401657.1', 'Parent=gene-HHV4_BMRF1', 'Dbxref=UniProtKB/TrEMBL:Q777F9,Genbank:YP_401657.1,GeneID:3783718', 'Name=YP_401657.1', 'gbkey=CDS', 'gene=BMRF1', 'locus_tag=HHV4_BMRF1', 'product=DNA polymerase processivity subunit', 'protein_id=YP_401657.1']

NC_007605.1 (forward strand): Structure number 238 from nt 69724 to 69849 (nt 37 to 162)

```
5'-GUGCUGUUUAUCUCAAUCUUUGUCUAUUACUUUAGCGGGGUAGCGGCCCUGAGCGCAGCUAUGCGCUACAAGCUUAAGAAGUUUGUGAACGGACCCCUGGUCCAUCUCCGU
GUGGUAUACAUGUGC-3'
5'-(...(((.......................................................................................................
.......)))....)-3'
Motif MFE = -39.8; z-score = -1.73; ED = 7.36
```



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 69688 to 69886 (motif highlighted in silver):

```
5'-UUCCUCCAUGAAACCCUUGGACCCCUGGGCAAGACCGUGCUGUUUAUCUCAAUCUUUGUCUAUUACUUUAGCGGGGUAGCGGCCCUGAGCGCAGCUAUGCGCUACAAGCUU
AAGAAGUUUGUGAACGGACCCCUGGUCCAUCUCCGUGUGGUAUACAUGUGCUGUUUUGUCUUUACUUUUUGUGAAUAUCUGUUGGUGA-3
5'-....(((((.(.....).))))).....(((((((((.(((((((.((((.(((........(((.....)))(((((((....)))))))(((((((....)))))))(((((((
...)))))))).....(((((...)))))).......)).)))).))).)))).))))))))))((((.....)))).((((....)))).-3'
MFE = -57.1; z-score = -1.18; ED = 15.33
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 1 to 199--gene, gene-HHV4_BaRF1.1, 66516-69916(+)

Attributes: ['ID=gene-HHV4_BaRF1.1', 'Dbxref=GeneID:3783683', 'Name=BaRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BaRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BaRF1.1']

12-- nt 1 to 199--gene, gene-HHV4_BMRF1, 67552-69916(+)

Attributes: ['ID=gene-HHV4_BMRF1', 'Dbxref=GeneID:3783718', 'Name=BMRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF1']

13-- nt 1 to 199--gene, gene-HHV4_BMRF2, 68491-69916(+)

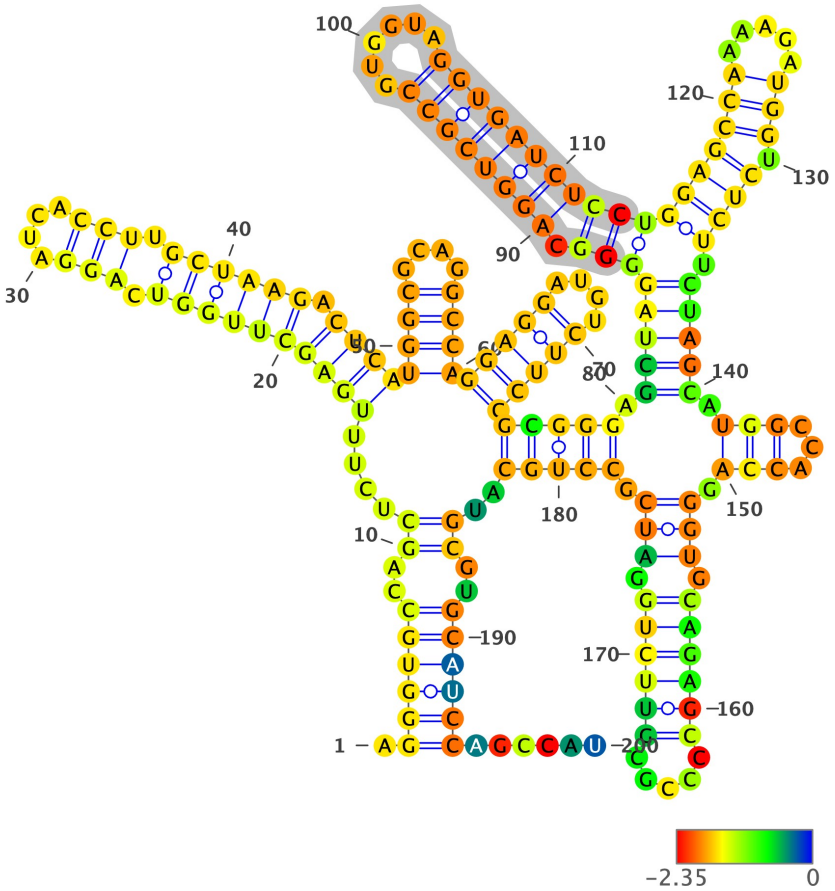
Attributes: ['ID=gene-HHV4_BMRF2', 'Dbxref=GeneID:3783719', 'Name=BMRF2', 'Note=core gene', 'gbkey=Gene', 'gene=BMRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BMRF2']

14-- nt 1 to 199--CDS, cds-YP_401658.1, 68830-69903(+)

Attributes: ['ID=cds-YP_401658.1', 'Parent=gene-HHV4_BMRF2', 'Dbxref=UniProtKB/TrEMBL:Q777F8,Genbank:YP_401658.1,GeneID:3783719', 'Name=YP_401658.1', 'gbkey=CDS', 'gene=BMRF2', 'locus_tag=HHV4_BMRF2', 'product=envelope protein UL43', 'protein_id=YP_401658.1']

NC_007605.1 (forward strand): Structure number 239 from nt 70921 to 70947 (nt 87 to 113)

```
5'-GGCAGGUCGCCGUGGUAGGUGAUCUCC-3'
5'-(..((.................)).)-3'
Motif MFE = -13.4; z-score = -2.69; ED = 0.33
```



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 70835 to 71034 (motif highlighted in silver):

```
5'-AGGGUGCCAGCUCUUUGAGCUUGGUCAGGAUCACCUUGCUAAGACUCAUGGCGCAGGCCAGGAGGAUGUCUUCCGCGGGAGCUAGGGGCAGGUCGCCGUGGUAGGUGAUCU
CCUGGAGCCAAAAGAUGGUCUCUUCUAGCAUGGCCACCAGGGUGCAGAGCCCCGCGUUCUGGAUCGCCUGCAUGCGUGCAUCCAGCCAU-3
5'-.(((((((..((....((((((((((.((((....)))).)))))).))))((((....))))((((((....))))))(((((.((((((((.((((((((.....)))))))))
)))(((((((.....))).)))).)))))).((((...))).((((.((((((.....)))))))).))).)))))..))..)))))).......-3'
MFE = -83.7; z-score = -2.87; ED = 45.13
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

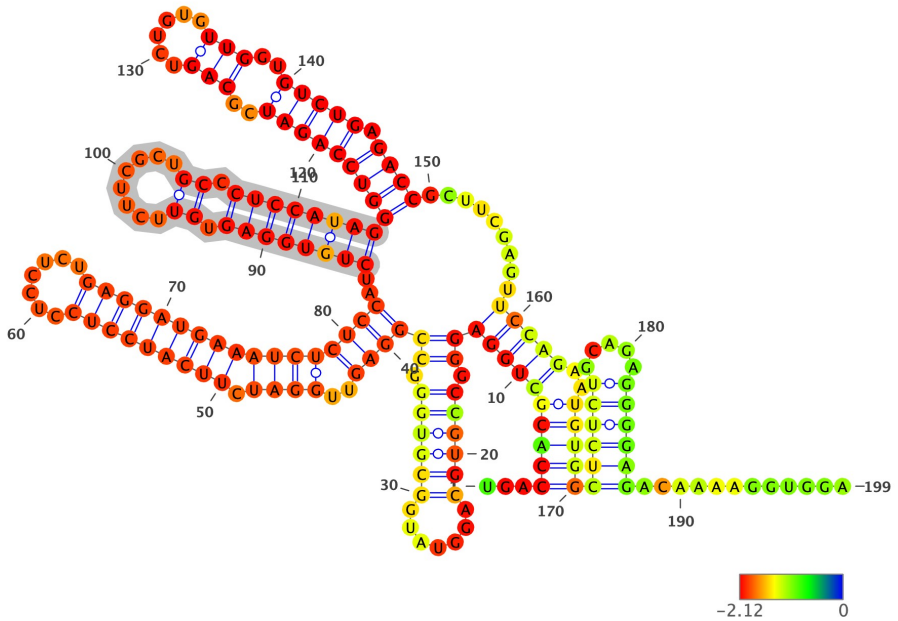
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 240 from nt 71744 to 71773 (nt 85 to 114)

```
5'-CUGUGGAGUGUUCUUCGCUGCCCUCCAUAG-3'
5'-((.(((((.((........)).)))))).))-3'
Motif MFE = -11.7; z-score = -3.1; 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 71660 to 71858 (motif highlighted in silver):

```
5'-UGACCACGCUGGAGGGCCGUGCAGGUAUGGCGUGGGCCGGAGUUGGAUCUUCAUCCUCCUCCUCUGAGGAUGAAAUCUCUCCAUCUGUGGAGUGUUCUUCGCUGCCCUCCA
UAGGGUCCAGAUCGCAGUCUGUGUUGGUGUCUGAGACCGCUUCGAGUUCCAGAAUGUGGCUCUCUGCAGAGGGGAGACAAAAGGUGGA-3
5'-...(((((((((((.((((((.......)))))).))((((..((((.(((((((((.......)))))))))))))))))..((((((((.((........)).)))))
)))((((((((..(((.....)))..)))))..)))).........)))))..)))))((((((.....)))))).............-3'
MFE = -77.0; z-score = -1.43; ED = 29.61
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

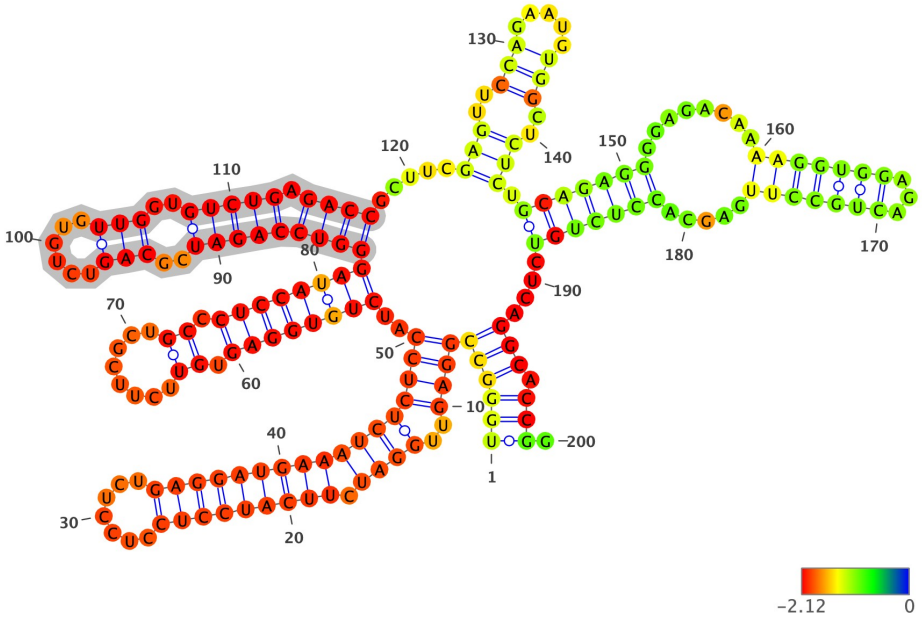
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 241 from nt 71774 to 71808 (nt 83 to 117)

```
5'-GGUCCAGAUCGCAGUCUGUGUUGGUGUCUGAGACC-3'
5'-(((((((((..(((.....)))..)))))).))))-3'
Motif MFE = -12.3; z-score = -2.27; 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 71692 to 71891 (motif highlighted in silver):

```
5'-UGGGCCGGAGUUGGAUCUUCAUCCUCCUCCUCUGAGGAUGAAAUCUCUCCAUCUGUGGAGUGUUCUUCGCUGCCCUCCAUAGGGUCCAGAUCGCAGUCUGUGUUGGUGUCU
GAGACCGCUUCGAGUUCCAGAAUGUGGCUCUCUGCAGAGGGGAGACAAAAGGUGGAGACUGCCUUGAGCACCUCUGUCUCAGGCACCGG-3
5'-((((((((((..((((.(((((((((.......)))))))))))))))))..((((((((.((........)).)))))))))((((((((..(((......)))..))))
).))))).....(((..(((.....)))..))).(((((((.......(((((((...)))))))).....)))))))....))).)))).-3'
MFE = -78.8; z-score = -2.92; ED = 27.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

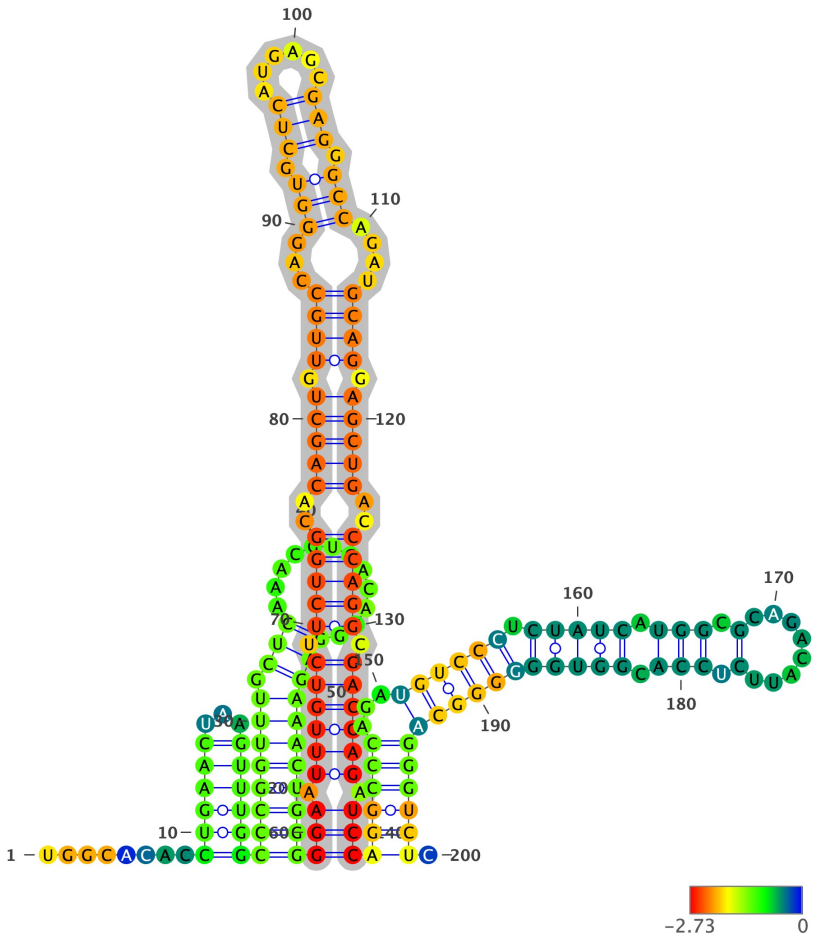
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 242 from nt 72319 to 72401 (nt 59 to 141)

```
5'-GGAAUUUGUCUUCUGGCACAGCUGUUGCCAGGGUGCUCAUGAGCGAGGGCCAGAUGCAGGAGCUGACCCAGGCGACGAGAUCC-3'
5'-(((.(((((((.(((((..(((((.(((((...((((.((((......)))).)))....)))))..)))))..)))))).)))))).)))-3'
Motif MFE = -40.9; z-score = -3.94; 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 72261 to 72460 (motif highlighted in silver):

```
5'-UGGCACACCUGAACUAAGUUUGGCCCGGUUUGCUCAAACGUGACAUGGAGAAACUGGGGGAAUUUGUCUUCUGGCACAGCUGUUGCCAGGGUGCUCAUGAGCGAGGGCCAG
AUGCAGGAGCUGACCCAGGCGACGAGAUCCAGGCCCAGAUGUCCCUCUAUCAUGGCGCAGACAUUCUCCACGGUGGGGGGCAGGGUCUC-3
5'-........((((((...)))))))(((((((.(((.............)))))))))))((.((((((.(((((..(((((.((((...(((.(((......))).))).)).
..))))).)))))..)))))).)))))).)))((((((...((((((.(((((.(((.(........).))).)))))))))))))))).-3'
MFE = -83.6; z-score = -2.63; ED = 14.07
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

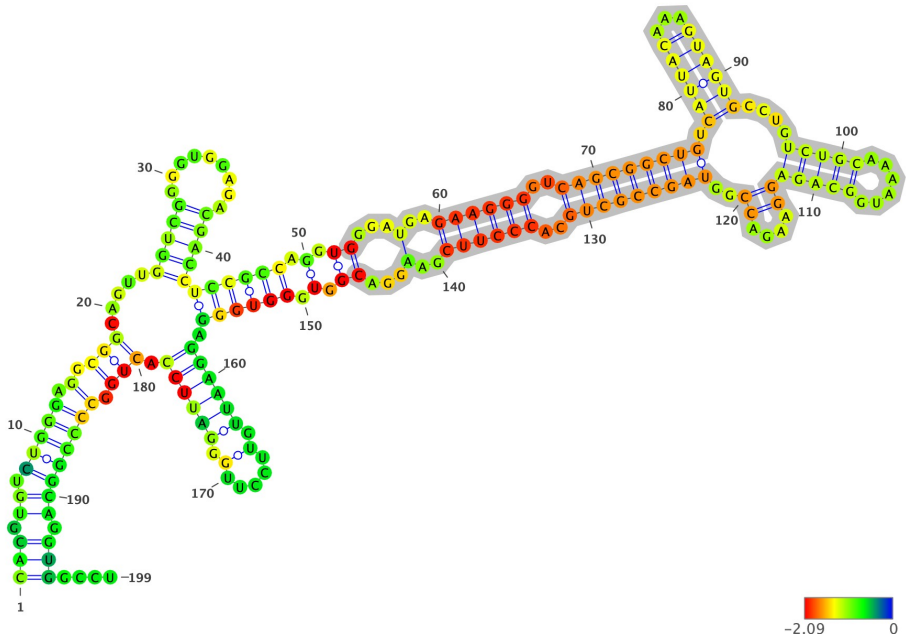
10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 243 from nt 73261 to 73354 (nt 53 to 146)

```
5'-GGGAUGAGAAGGGGUCAGCGGCUGUCAUUACAAAGUAGUGCCUGUCUGCAAAAUGGCAGAGGAAGACCGGUAGCCGCUGCACCCUUCGAAGGAC-3'

5'-(.......................................................................................)-3'
Motif MFE = -36.9; z-score = -3.26; ED = 11.34
```



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 73209 to 73407 (motif highlighted in silver):

```
5'-CACGUGUCUGGGAGGCGGCAGUUGGUCGGGGUGGAGACGACCUCCGCCAGGUGGGAUGAGAAGGGGUCAGCGGCUGUCAUUACAAAGUAGUGCCUGUCUGCAAAAUGGCAG
AGGAAGACCGGUAGCCGCUGCACCCUUCGAAGGACGGUGGGUGGGAGGAAUUGUUCCUUGGGAUUCCACUGGCCCCGGCAGGUGGCCU-3
5'-(((.((.(((((.(.(((.....(((((.........)))))((((((.(.((...(..((((((..(((((((((.((((((...)))))).....(((((......))))
)((....))..))))))))).))))))..)...)).).)))))).((((((.(.....).)))))).))).)))))))).)))....-3'
MFE = -81.7; z-score = -1.94; ED = 53.79
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

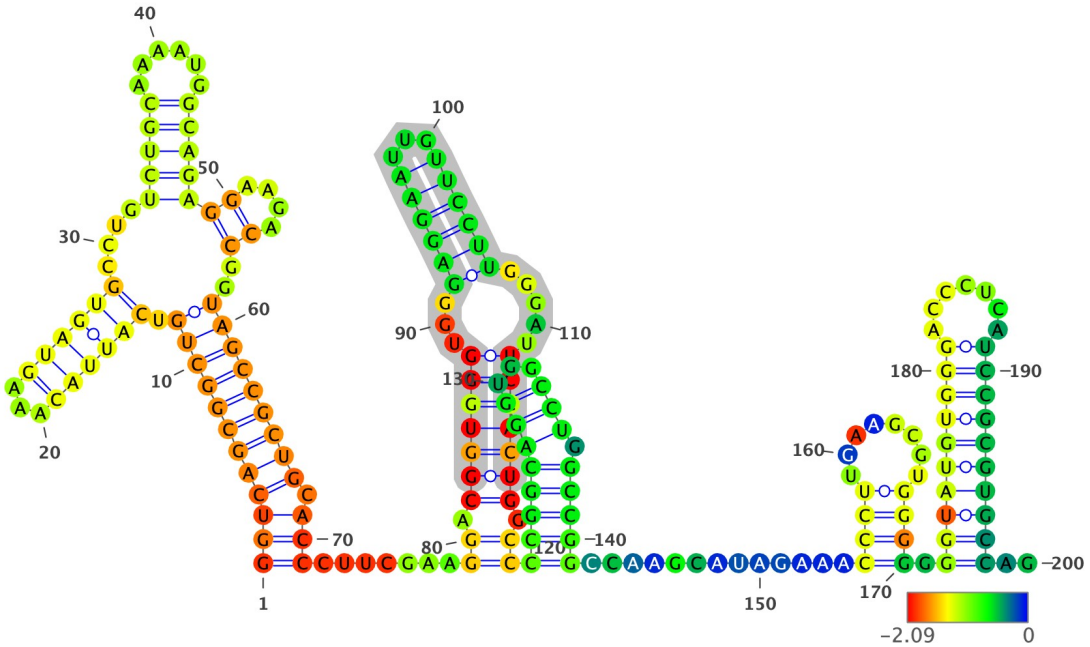
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 244 from nt 73355 to 73389 (nt 83 to 117)

```
5'-GGUGGGUGGGAGGAAUUGUUCCUUGGGAUUCCACU-3'
5'-(.(.((.......................)).).)-3'
Motif MFE = -11.5; z-score = -2.25; ED = 2.18
```



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

Extracted structure model with flanking nucleotides 73273 to 73472 (motif highlighted in silver):

```
5'-GGUCAGCGGCUGUCAUUACAAAGUAGUGCCUGUCUGCAAAAUGGCAGAGGAAGACCGGUAGCCGCUGCACCCUUCGAAGGACGGUGGGUGGGAGGAAUUGUUCCUUGGGAU
UCCACUGGCCCCGGCAGGUGGCCUGGCCGGCCAAGCAUAGAAACCCUUGAAGCGUGGGGGGGUAUGUGGGACCCUCAUCCGCGUGCCAG-3
5'-(((((((((((.((((((...)))))))....(((((......)))))))(....)).)))))))))).))).......((.(((((((...((((((...)))))))).....
)))))))).))((((((((...))).)))))..............((((........)))).((((((((((.......))))))))))..-3'
MFE = -76.1; z-score = -1.31; ED = 46.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

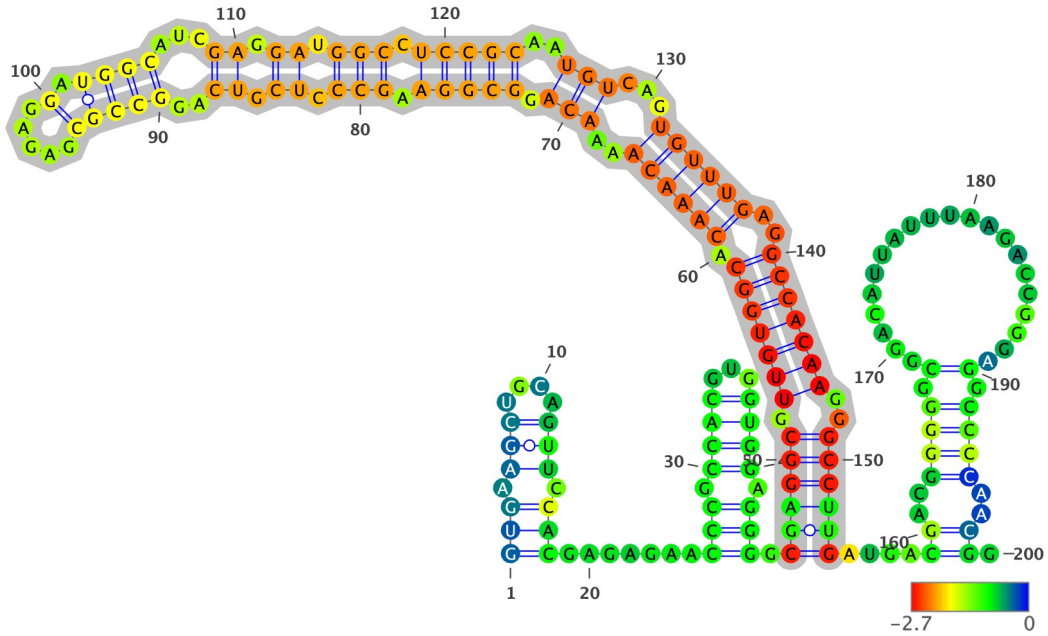
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 245 from nt 74465 to 74573 (nt 46 to 154)

```
5'-CGAGGCGUUGUGGCACAAACAAAACAGGCGGAAGCCCUCGUCAGGCCGCGAGAGGAUGGCAUCGAGGAUGGCCUCCGCAAUGUCAGUGUUUGAGGCCACAAGGGCCUUG-3
'
5'-(..(((.(((((((.((((((..(((.(((((.(((.((.((.....................)).)).))).)))))..)))...)))))))..)))))))..)))..)-3
'
Motif MFE = -52.5; z-score = -4.22; ED = 7.39
```



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 74420 to 74619 (motif highlighted in silver):

```
5'-GUGAAGCUGCAGUUCCACGAGAGAACCCGCCACGUGGUGGAGGGGCGAGGCGUUGUGGCACAAACAAAACAGGCGGAAGCCCUCGUCAGGCCGCGAGAGGAUGGCAUCGAG
GAUGGCCUCCGCAAUGUCAGUGUUUGAGGCCACAAGGGCCUUGAUGACGACGGGGGCGGACAUUAUUUAAGACCGGGAGGCCCCAACGG-3
5'-(((.(((....))).)))........(((.((((...)))))..))).((((((.(((((((.((((((..(((.(((((.(((.((.((..(((((.....).))))...)).
)).))).)))))..)))...)))))).)))))))..)))))).....((..(((((.(.....................).)))))..)).-3'
MFE = -78.2; z-score = -1.86; ED = 16.5
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

11-- nt 175 to 200--gene, gene-HHV4_BSRF1, 74594-75316(+)

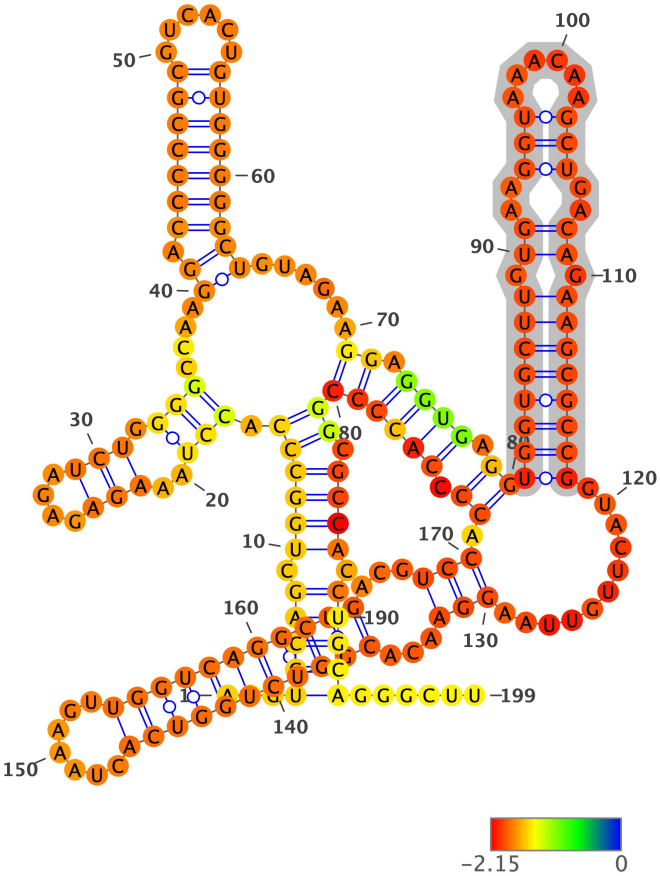
Attributes: ['ID=gene-HHV4_BSRF1', 'Dbxref=GeneID:3783731', 'Name=BSRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BSRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BSRF1']

12-- nt 175 to 180--TATA_box, id-HHV4_BSRF1, 74594-74599(+)

Attributes: ['ID=id-HHV4_BSRF1', 'Dbxref=GeneID:3783731', 'gbkey=regulatory', 'gene=BSRF1', 'locus_tag=HHV4_BSRF1', 'regulatory_class=TATA_box']

NC_007605.1 (forward strand): Structure number 246 from nt 75525 to 75562 (nt 81 to 118)

```
5'-UGGUGCUUGUGAAGGUAAACAAGCUGACAGAAGCGCCG-3'
5'-(....................................)-3'
Motif MFE = -16.8; z-score = -4.49; 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 75445 to 75643 (motif highlighted in silver):

```
5'-AGGUGCAGCUGGCCCACCUAAAGAGAGAUCUGGGGCCAAGGACCCCCGCGUCACUGUGGGGGCUGUAGAAGGAGGUGAGGUGGUGCUUGUGAAGGUAAACAAGCUGACAGA
AGCGCCGGUACUUGUUAAGGAACACGGUCUGGUCACUAAAGUUGGUCAGGCUGACGUCCACCCCACCCCGGCGCCACCUGCAGGGCUU-3
5'-...(((((.(((((((.(((..(((....))).))).....((.(((((((.....)))))))))).....((.((((.((((((((((.((..(((.....)))).)).)).)
)))))))...........(((...((((((((((.....)))))))))))...))).)).)))))))).))))).))))).....-3'
MFE = -76.4; z-score = -1.51; ED = 30.7
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

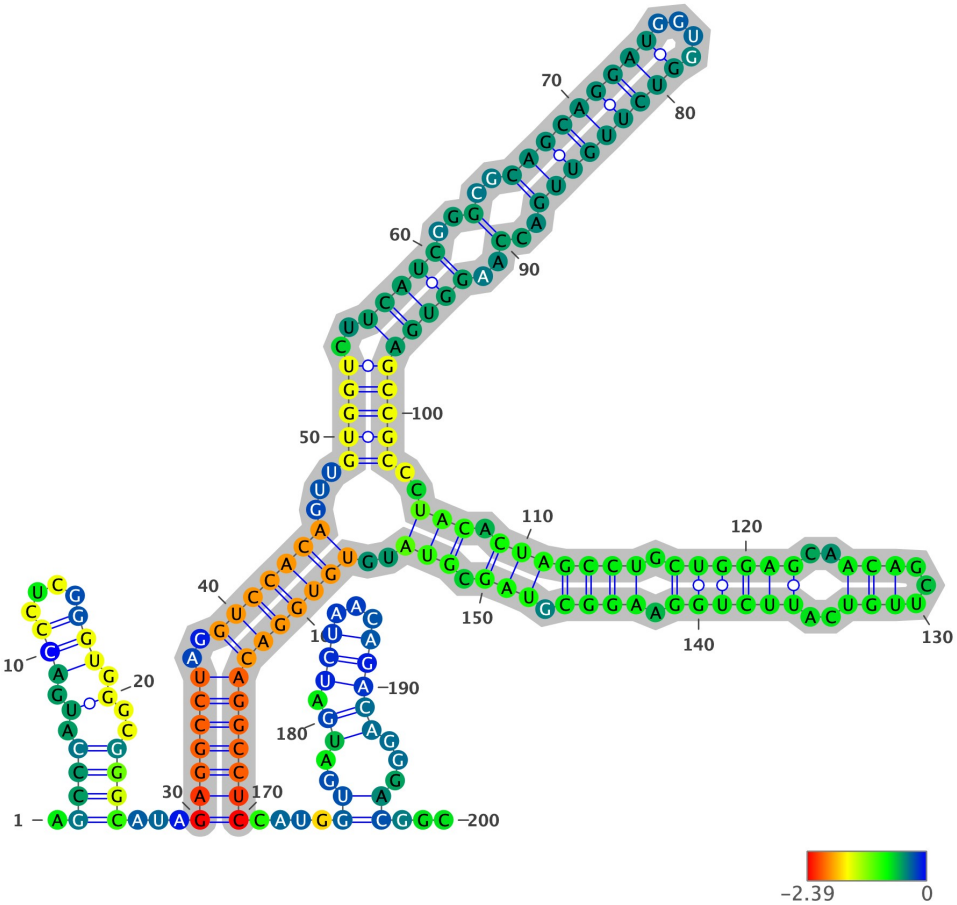
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 247 from nt 76043 to 76183 (nt 30 to 170)

```
5'-GAGGCCUAGGUCCACAGUUGUGGUCUUCAUCGGGCGCAGCAGGAUGGUGGUCUUGUUGACCAAGGUGAGCCGCCCUACACUAGCCUGCUGGAGCAACAGCUUGUCAUUCUG
GAAGGCGUAGCGUAUGUGUGGACAGGCCUC-3'
5'-(((((((.....................................................................................................
.......................)))))))-3'
Motif MFE = -61.1; z-score = -3.07; ED = 11.03
```



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 76014 to 76213 (motif highlighted in silver):

```
5'-AGCCCAUGACCCUCGGGUGGGCGGGCAUAGAGGCCUAGGUCCACAGUUGUGGUCUUCAUCGGGCGCAGCAGGAUGGUGGUCUUGUUGACCAAGGUGAGCCGCCCUACACUA
GCCUGCUGGAGCAACAGCUUGUCAUUCUGGAAGGCGUAGCGUAUGUGUGGACAGGCCUCCAUGGUGAUGAUCUAACAGACAGGGACGGC-3
5'-.((((.(.(((....))).)..)))).....(((((((..(((((((...(((((..(((((..(..((((((((((....)))))))))..)..))))))))))..(((.(((
((((.((((((..(((...))).)..)))))).)))).))).))..))))))))))))))....((..((.(((...)))))...)).....-3'
MFE = -76.1; z-score = -0.7; ED = 26.36
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

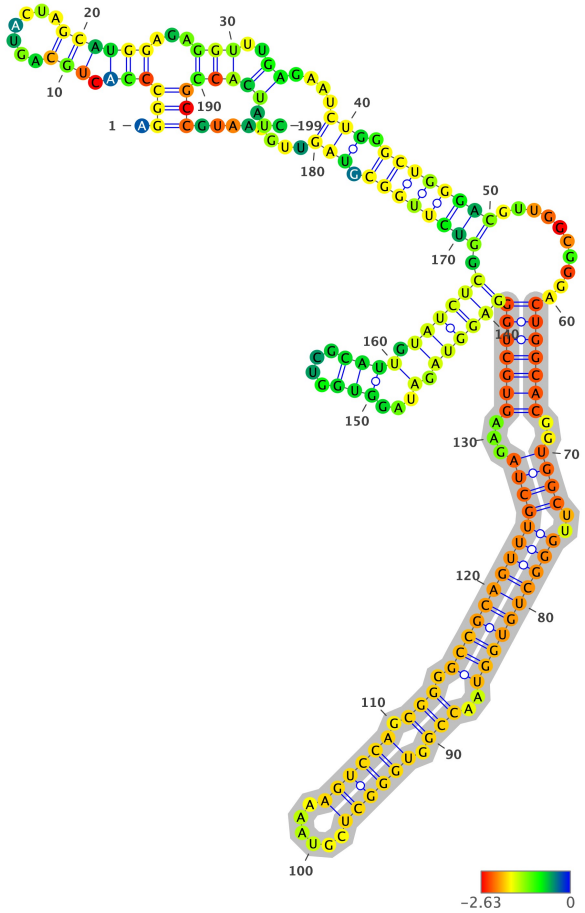
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 248 from nt 77324 to 77401 (nt 61 to 138)

```
5'-CUGGCACGGUGGCUUGGGCUGUGGUAACCGGUGGGCUCGUAAAAGUCCAGCGGGGCCGCAGUUUGCUAGAAGUGCUGG-3'
5'-(((((((..(((((..(((((((((((.............................)))))))))))))...)))))))-3'
Motif MFE = -42.2; z-score = -4.61; 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 77264 to 77462 (motif highlighted in silver):

```
5'-AGGCCCACUGCAGUACUAGCAUGGAGAGGUUUGAGAAUCUGGGCUGGGACGUUGGCGGGACUGGCACGGUGGCUUGGGCUGUGGUAACCGGUGGGCUCGUAAAAGUCCAGC
GGGGCCGCAGUUUGCUAGAAGUGCUGGGAGGUAGAUAGGUGGUCGCAUUGUAUCUCGGUCUUGGCGUAGUUGAAUCACCGCCGUAAUC-3
5'-.(((((((.(((.......)))))))...((((..((....((((.(((((((((..........((((((((..(((((..((((((((((..(((.((((((.....)))))))).
)).)))))))))))))))...)))))))((((((.(...((((....)))).)))))).)))))))).)))).....)))))))).....-3'
MFE = -74.3; z-score = -1.36; ED = 38.31
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

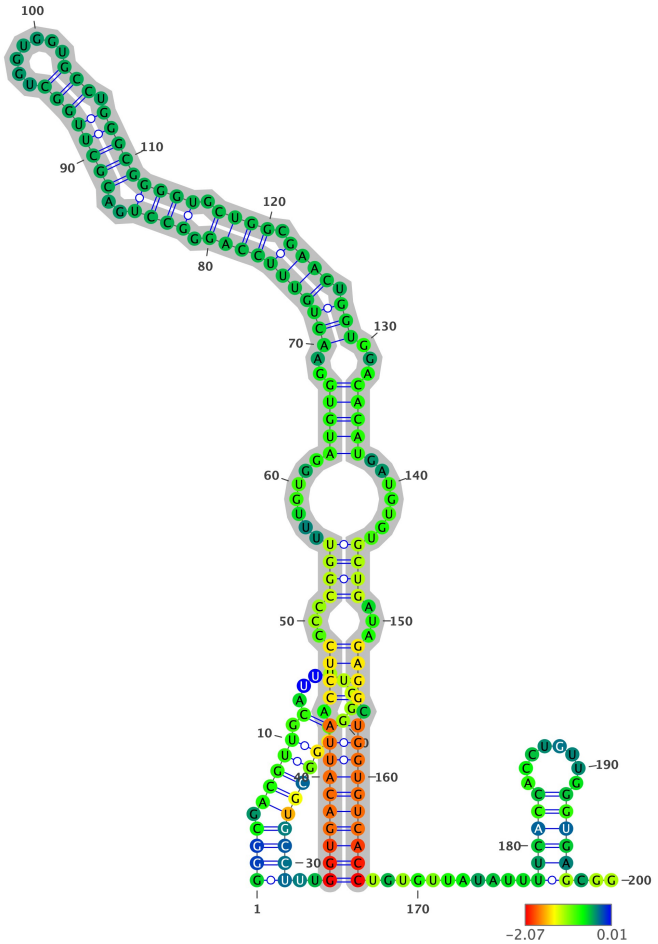
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 249 from nt 77622 to 77754 (nt 34 to 166)

```
5'-GGUGACAUUAACCUCCCCCGGUUUUGUGGAUGUGGAACUGUUUCCAGGGCCUGACGCUUGGCUGGUGGUGCCUGGGCGGGGUGCUGGCGAACUGGUGGACACAUGAUGUGU
GCUGAUAGAGGCUGGUGUCACC-3'
5'-(.....)-3'
Motif MFE = -57.9; z-score = -2.99; ED = 3.71
```



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

Extracted structure model with flanking nucleotides 77589 to 77788 (motif highlighted in silver):

```
5'-GGGCGACGUUGCAUUUUGGGGGGGCGUGCCUUUGGUGACAUUAACCUCCCCCGGUUUUGUGGAUGUGGAACUGUUUCCAGGGCCUGACGCUUGGCUGGUGGUGCCUGGGCG
GGGUGCUGGCGAACUGGUGGACACAUGAUGUGUGCUGAUAGAGGCUGGUGUCACCUGUGUUAUAUUUUCACCACCUGUUGGGUGAGCGG-3
5'-((((.(((((.(........).)))))))))..((((((((((.((((...((((.......(((((..(((((((((((.((((..((((((((.......)))).)))))
))))).)))).)))).)))...)))))).......)))).)))).))))))))))..........((((((.......)))))).....-3'
MFE = -77.4; z-score = -1.23; ED = 10.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

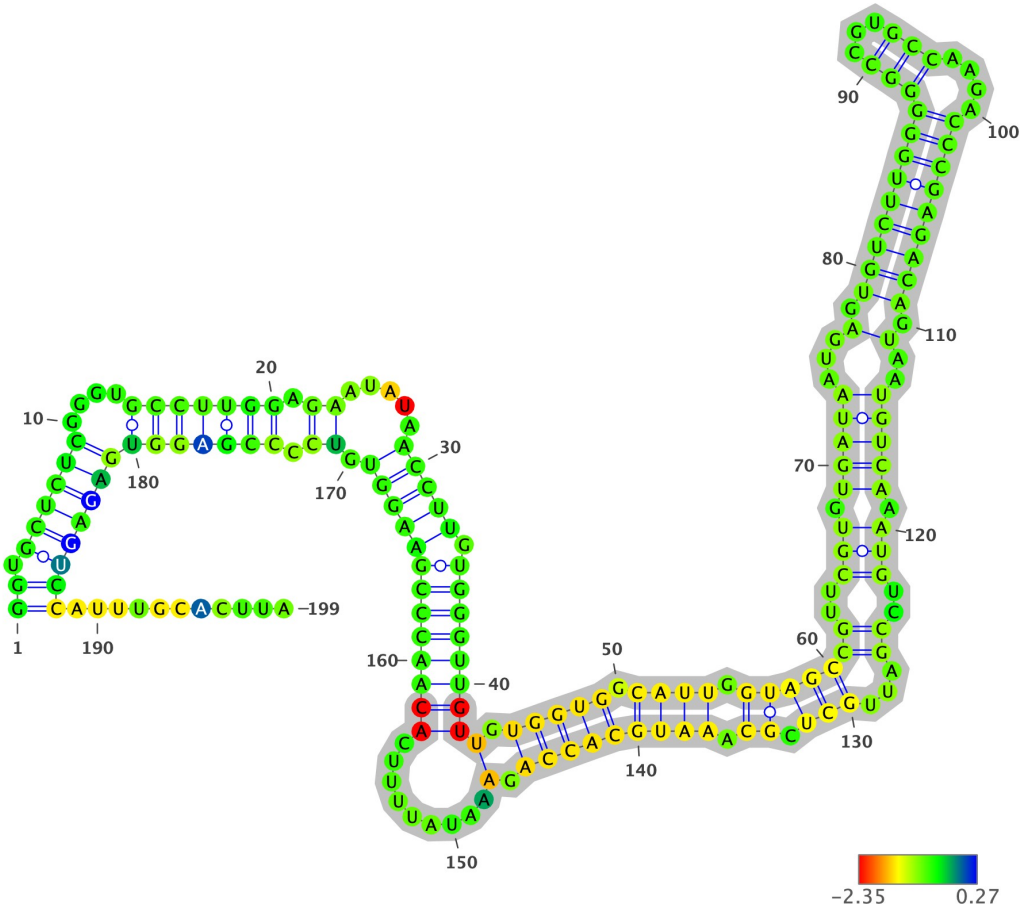
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 250 from nt 78622 to 78739 (nt 41 to 158)

```
5'-GUUGUGGUGGCAUUGGUAGCCGUUCGUGUGAUAAUGAGUGUCUUGGGGGCCGUGCCAAGACCCGAGACAGUAAUGUCAAAUGUCCGAUUGCUCGCAAAUGCACCAGAAAUA
UUUUCAC-3'
5'-((.....................................................................................................................
.....))-3'
Motif MFE = -39.1; z-score = -2.38; ED = 12.1
```



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 78582 to 78780 (motif highlighted in silver):

```
5'-GGUGCUCUCGGGUGCCUUGGAGAAUAUAACCUUGUGGGUUGUUGUGGUGGCAUUGGUAGCCGUUCGUGUGAUAAUGAGUGUCUUGGGGGCCGUGCCAAGACCCGAGACAGU
AAUGUCAAAUGUCCGAUUGCUCGCAAAUGCACCAGAAAUAUUUUCACAACCCGAAGGUGUCCCCGAGGUGAGAGUCCAUUUGCACUUA-3
5'-((.(((((((....(((((((.((.....(((((.(((((((((.(((((.(((((.(((((((..((((.(((((...(.(((((((((((...)))....))))))))).)
..))))).))).))...))).)).))))))))).).........))))))))))))).)).))))))))))))))))))).....-3'
MFE = -73.8; z-score = -2.97; ED = 18.25
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

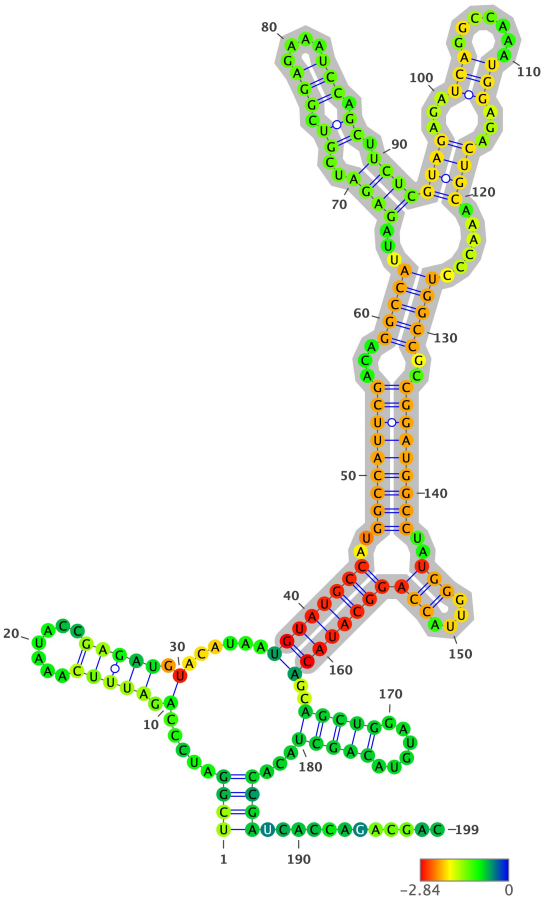
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 251 from nt 80450 to 80573 (nt 38 to 161)

```
5'-GUAUGCCAUGGCCAUUCGACAGGCCAUUAGAGAUCGUCGGAGAAAUCCAGCUUCUCGUAGAGAUCAGGCCAAAUGGAGACUGCAAACCCUGGCCGCCGGAUGGCCUAUGGG
UUACCAGGCAUAC-3'
5'-(((((((..(((((((((...(((((.....))))).))))))))))..(((.
...)))))))))-3'
Motif MFE = -46.6; z-score = -3.14; ED = 22.4
```



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 80413 to 80611 (motif highlighted in silver):

```
5'-UCGGAUCCCAGAUUUCAAAUACCGAGAUGUACAUAAUGUAUGCCAUGGCCAUUCGACAGGCCAUUAGAGAUCGUCGGAGAAAUCCAGCUUCUCGUAGAGAUCAGGCCAAAU
GGAGACUGCAAACCCUGGCCGCCGGAUGGCCUAUGGGUUACCAGGCAUACAGCAGCUGGAUGUACAGCUACACCGAUCACCAGACGAC-3
5'-((((.....(.(((((.......))))).).....(((((((..(((((((((...(((((...(((((..((.((((....)))).)).))))((((...(((.......)
))...))))......)))))..)))))))))..(((....)))))))))))..(((((.....)))))...))))............-3'
MFE = -61.6; z-score = -2.25; ED = 15.98
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--exon, exon-HHV4_EBNA-3A-21, 80382-82962(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-21', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

10-- nt 1 to 199--CDS, cds-YP_401669.1, 80382-82877(+)

Attributes: ['ID=cds-YP_401669.1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=UniProtKB/TrEMBL:Q8AZJ8,Genbank:YP_401669.1,GeneID:3783762', 'Name=YP_401669.1', 'gbkey=CDS', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'product=nuclear antigen EBNA-3A', 'protein_id=YP_401669.1']

11-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

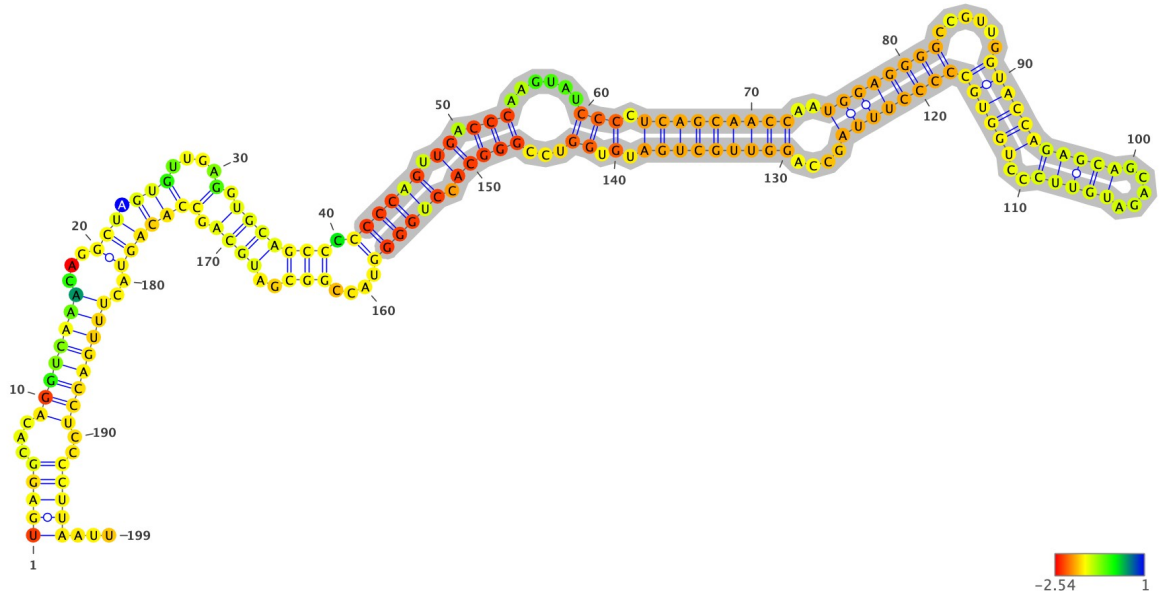
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

12-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 252 from nt 81901 to 82016 (nt 42 to 157)

```
5'-CCCAGUUGACCCAAGUAUCCCCUCAGCAACCAAUGGAGGGGCCGUUGGUACCAGAGCAGCAGAUGUUCCCUGGUGCCCCCUUUAGCCAGGUUGCUGAUGUGGUCCGGGCAC
CUGGG-3'
5'-(((.(.((.(((.....(((.....................................................................................).)).....))))).
).)))-3'
Motif MFE = -52.8; z-score = -3.47; ED = 16.66
```



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 81860 to 82058 (motif highlighted in silver):

```
5'-UGAGGCACAGGUCAAACAGGCUAGUGUUGAGGUGCAGCCCCCCCAGUUGACCCAAGUAUCCCCUCAGCAACCAAUGGAGGGGCCGUUGGUACCAGAGCAGCAGAUGUUCCC
UGGUGCCCCCUUUAGCCAGGUUGCUGAUGUGGUCCGGGCACCUGGGGUACCGGCGAUGCAGCCACAGUACUUUGACCUCCCCUUAAUU-3
5'-(((((...(((((((...(((.(((....(.(((((((.((((((.((.(((.....(((.(((((((((..((((((((.....((((((((((.....)))))).
)))))))))))))....)))))))).).))...)))))).)))))).....)))..)))).)))))))..)))))))..)))))...-3'
MFE = -83.4; z-score = -3.54; ED = 34.38
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--exon, exon-HHV4_EBNA-3A-21, 80382-82962(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-21', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

10-- nt 1 to 199--CDS, cds-YP_401669.1, 80382-82877(+)

Attributes: ['ID=cds-YP_401669.1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=UniProtKB/TrEMBL:Q8AZJ8,Genbank:YP_401669.1,GeneID:3783762', 'Name=YP_401669.1', 'gbkey=CDS', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'product=nuclear antigen EBNA-3A', 'protein_id=YP_401669.1']

11-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

12-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

13-- nt 61 to 130--repeat_region, id-HHV4_EBNA-1.2-6, 81920-81989(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-6', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type A']

14-- nt 134 to 159--repeat_region, id-HHV4_EBNA-1.2-7, 81993-82018(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-7', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type B']

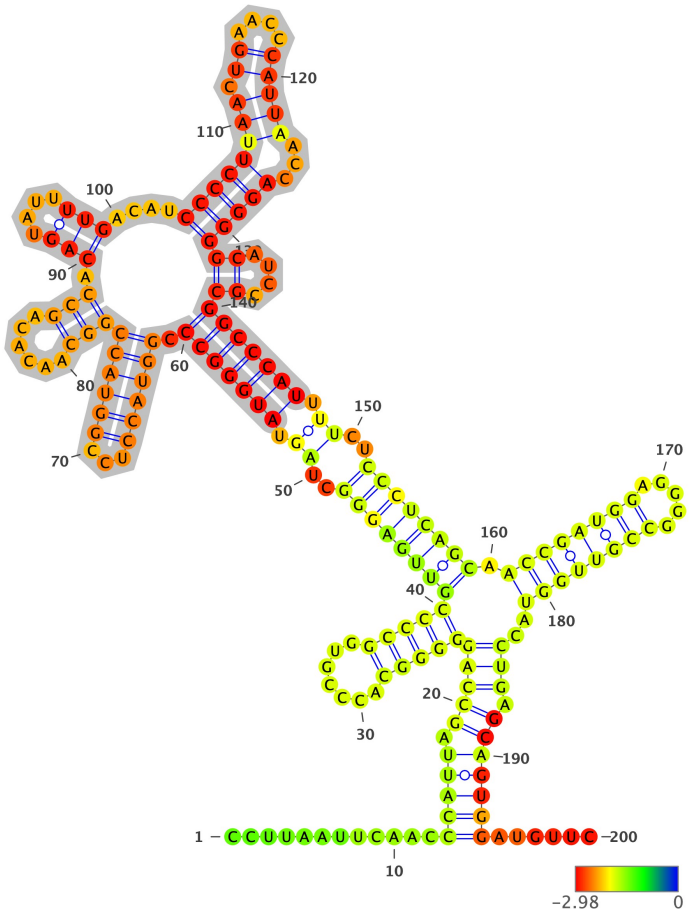
15-- nt 160 to 199--repeat_region, id-HHV4_EBNA-1.2-8, 82019-82093(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-8', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type C']

NC_007605.1 (forward strand): Structure number 253 from nt 82104 to 82196 (nt 54 to 146)

5'-AUGGGCCCGGUACCUCCGGUACCGGCAACACAGCCACAGUAUUUUGACAUCCCCUUAACUGAACCCAUUAACCAGGGGGCAUCCGCGGCCCAU-3'

5'-(((((((.((((((...)))))))((.....)))).(((....))))....(((((.((.((....))))).....)))))((....)))))))))-3'
Motif MFE = -32.8; z-score = -3.5; ED = 15.79



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 82051 to 82250 (motif highlighted in silver):

5'-CCUUAAUUCAACCCAUUAGCCAGGGGGCACCCGUGGCCCCGUUGAGGGCUAGUAUGGGCCCGGUACCUCCGGUACCGGCAACACAGCCACAGUAUUUUGACAUCCCCUUAA
CUGAACCCAUUAACCAGGGGGCAUCCGCGGCCCAUUUUCUCCCUCAGCAACCGAUGGAGGGGCCGUUGGUACCUGAGCAGUGGAUGUUC-3
5'-.....(((((.((((((((((.....)))))))))))))))..((.(((((((.((((((...)))))))((.....))).(((....))).....((((((((
.((....)))))...)))))((....)))))))))..))..)))))))).((((((((.....)))))))))..))).)))))))).....-3'
MFE = -79.3; z-score = -3.53; ED = 11.19

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 200--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 200--exon, exon-HHV4_EBNA-3A-21, 80382-82962(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-21', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

10-- nt 1 to 200--CDS, cds-YP_401669.1, 80382-82877(+)

Attributes: ['ID=cds-YP_401669.1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=UniProtKB/TrEMBL:Q8AZJ8,Genbank:YP_401669.1,GeneID:3783762', 'Name=YP_401669.1', 'gbkey=CDS', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'product=nuclear antigen EBNA-3A', 'protein_id=YP_401669.1']

11-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

12-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

13-- nt 1 to 43--repeat_region, id-HHV4_EBNA-1.2-8, 82019-82093(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-8', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type C']

14-- nt 48 to 73--repeat_region, id-HHV4_EBNA-1.2-9, 82098-82123(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-9', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type B']

15-- nt 74 to 151--repeat_region, id-HHV4_EBNA-1.2-10, 82124-82201(+)

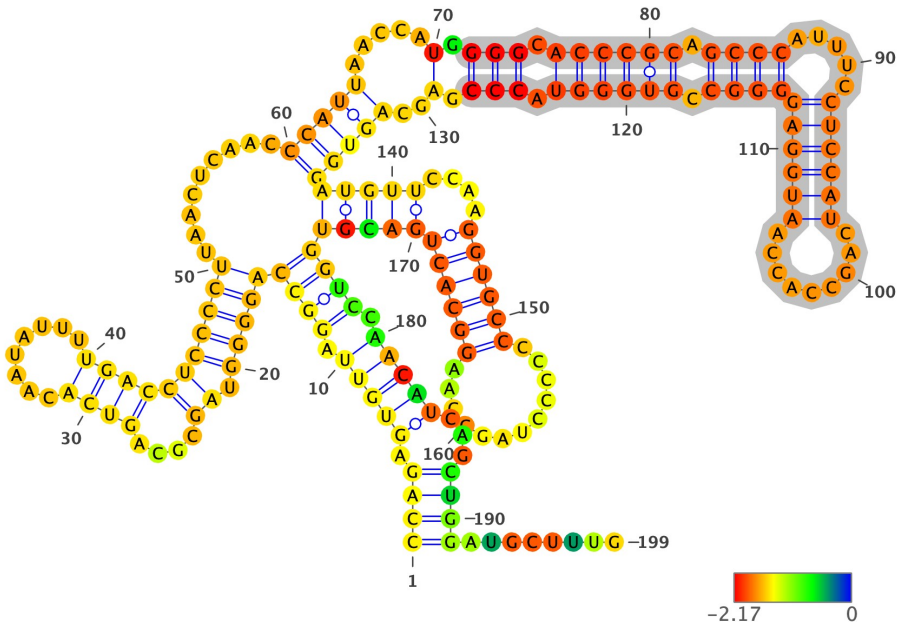
Attributes: ['ID=id-HHV4_EBNA-1.2-10', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type C']

16-- nt 152 to 200--repeat_region, id-HHV4_EBNA-1.2-11, 82202-82272(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-11', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type A']

NC_007605.1 (forward strand): Structure number 254 from nt 82339 to 82394 (nt 72 to 127)

```
5'-GGGCACCCGCAGCCCAUUUCCUCCAUCAGCCACCAAUGGAGGGGCCGUGGGUACCC-3'
5'-(((.................................................)))-3'
Motif MFE = -28.4; z-score = -3.55; ED = 2.06
```



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

Extracted structure model with flanking nucleotides 82268 to 82466 (motif highlighted in silver):

```
5'-CCAGAGUGUUAGGCCAGGGGUAGCGCAGUCACAAUAUUUUGACCUCCCCUUAACUCAACCCAUUAACCAUGGGGCACCCGCAGCCCAUUUCCUCCAUCAGCCACCAAUGGA
GGGGCCGUGGGUACCCGAGCAGUGGAUGUUCCAAGGUGCCCCCCCUAGCCAAGGCACUGACGUGGUCCAACAUCAGCUGGAUGCUUUG-3
5'-((((.(((((.(((((((((.((....((((........)))))))))).........(((((.....(.(((.((((((.((((.....((((((.........)))))
)))))).)))))).))).)..)))))((((....((((((.............)))))))))))))).)))))...))))........-3'
MFE = -68.9; z-score = -2.21; ED = 46.81
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

7-- nt 1 to 199--gene, gene-HHV4_EBNA-3A, 11305-82962(+)

Attributes: ['ID=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'Name=EBNA-3A', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3A', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3A']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3A, 11336-82962(+)

Attributes: ['ID=rna-HHV4_EBNA-3A', 'Parent=gene-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

9-- nt 1 to 199--exon, exon-HHV4_EBNA-3A-21, 80382-82962(+)

Attributes: ['ID=exon-HHV4_EBNA-3A-21', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=GeneID:3783762', 'gbkey=mRNA', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A']

10-- nt 1 to 199--CDS, cds-YP_401669.1, 80382-82877(+)

Attributes: ['ID=cds-YP_401669.1', 'Parent=rna-HHV4_EBNA-3A', 'Dbxref=UniProtKB/TrEMBL:Q8AZJ8,Genbank:YP_401669.1,GeneID:3783762', 'Name=YP_401669.1', 'gbkey=CDS', 'gene=EBNA-3A', 'locus_tag=HHV4_EBNA-3A', 'product=nuclear antigen EBNA-3A', 'protein_id=YP_401669.1']

11-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

12-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

13-- nt 1 to 5--repeat_region, id-HHV4_EBNA-1.2-11, 82202-82272(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-11', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type A']

14-- nt 16 to 93--repeat_region, id-HHV4_EBNA-1.2-12, 82283-82360(+)

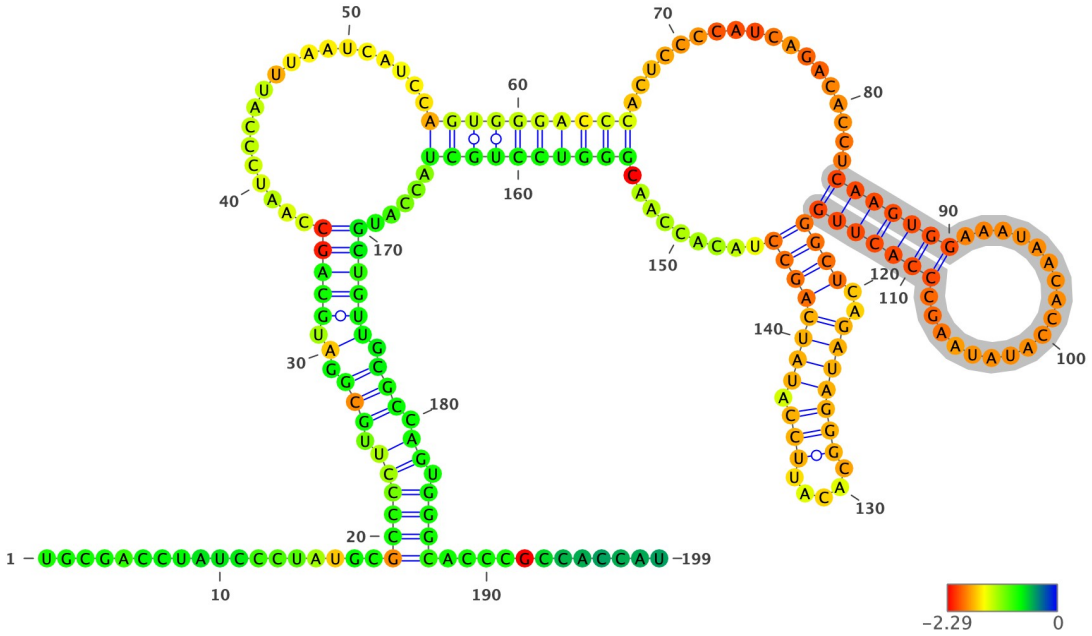
Attributes: ['ID=id-HHV4_EBNA-1.2-12', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type C']

15-- nt 94 to 164--repeat_region, id-HHV4_EBNA-1.2-13, 82361-82431(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-13', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_family=type A']

NC_007605.1 (forward strand): Structure number 255 from nt 85108 to 85139 (nt 84 to 115)

```
5'-CAAGUGGAAAUAACACCAUAUAAGCCCACUUG-3'
5'-(((((((.................)))))))-3'
Motif MFE = -7.1; z-score = -3.56; 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 85025 to 85223 (motif highlighted in silver):

```
5'-UGCGACCUAUCCCUAUGCGCCCCUUGCGGAUGCAGCCAAUCCCAUUUAAUCAUCCAGUGGGACCCACUCCCCAUCAGACACCUCAAGUGGAAAUAACACCAUAUAAGCCCA
CUUGGGCUCAGAUAGGGCACAUUCCAUAUCAGCCUACACCAACGGGUCCUGCUACCAUGCUGUUGCGCCAGUGGGCACCCGCCACCAU-3
5'-..................((((((.(((.(.(((((...................(((((((((.................((((((.................)))
))))))((((..(((((((.....))).)))))))).........))))))))))....)))))).))).)).)))).............-3'
MFE = -52.1; z-score = -2.17; ED = 31.65
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 199--CDS, cds-YP_401670.1, 83500-85959(+)

Attributes: ['ID=cds-YP_401670.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=UniProtKB/TrEMBL:Q777E8,Genbank:YP_401670.1,GeneID:3783763', 'Name=YP_401670.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3B', 'protein_id=YP_401670.1']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

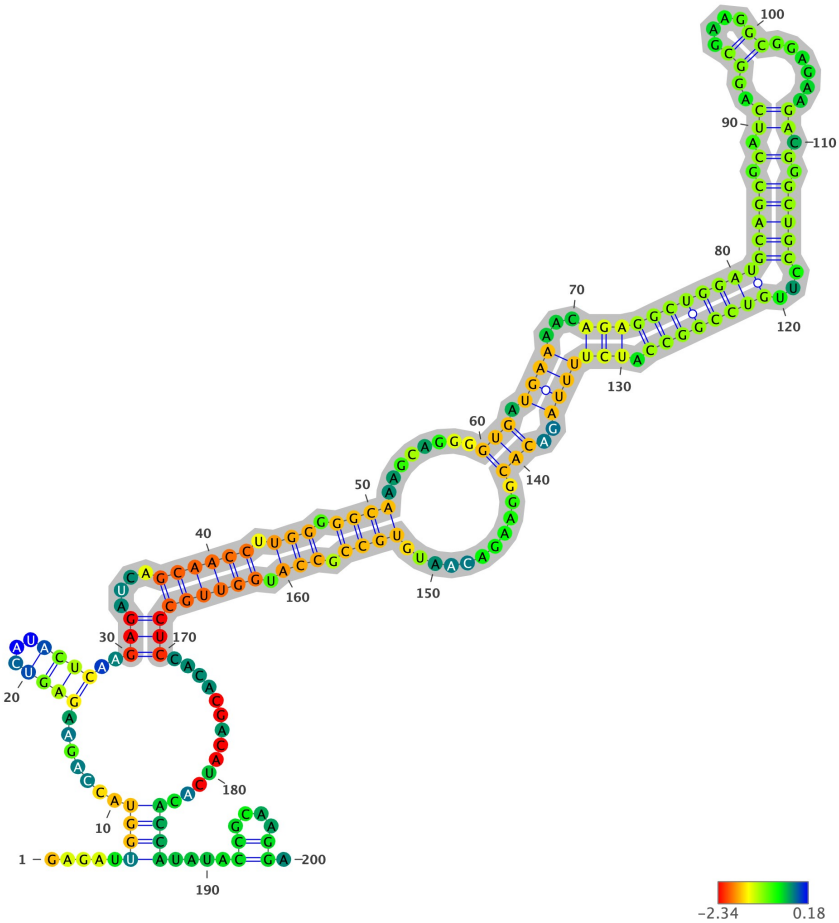
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 256 from nt 86240 to 86380 (nt 30 to 170)

```
5'-GAGAUCAGCAACCUUGGGGGCAAAGCAGGGGUGAUGAAAACAGAGGCUGGAUGCAGCGCAUCAGGCGAAGGCGGAGAAGACGGGCUGCCUUGUCCGGCCAUCUUUUAGACA
CGGAAGACAAUGUGCCGCCAUGGUUGCCUC-3'
5'-(......((((.....................................................................................................
.......................))))..)-3'
Motif MFE = -53.3; z-score = -2.36; ED = 13.9
```



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 86211 to 86410 (motif highlighted in silver):

```
5'-GAGAUUGGUACCAGAAGAGUCAUACUCAAGAGAUCAGCAACCUUGGGGGCAAAGCAGGGGUGAUGAAAACAGAGGCUGGAUGCAGCGCAUCAGGCGAAGGCGGAGAAGACG
GGCUGCCUUGUCCGGCCAUCUUUUAGACACGGAAGACAAUGUGCCGCCAUGGUUGCCUCCACACGACAUCACACCAUAUACCGCAAGGA-3
5'-.....((((.......((((...)))))..((((....((((((.(((.((((........(((.((((((...(((((((((((((((.(.((..((....)).....)).)
.)))))...))))))))).))))))).))).....))))).))).))))))))).............))))....((....)).-3'
MFE = -59.2; z-score = -0.59; ED = 22.57
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--exon, exon-HHV4_EBNA-1.1-20, 86076-86442(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-20', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C',

'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

6-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-20, 86076-86442(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-20', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

10-- nt 1 to 200--CDS, cds-YP_401671.1, 86083-86442(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

11-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

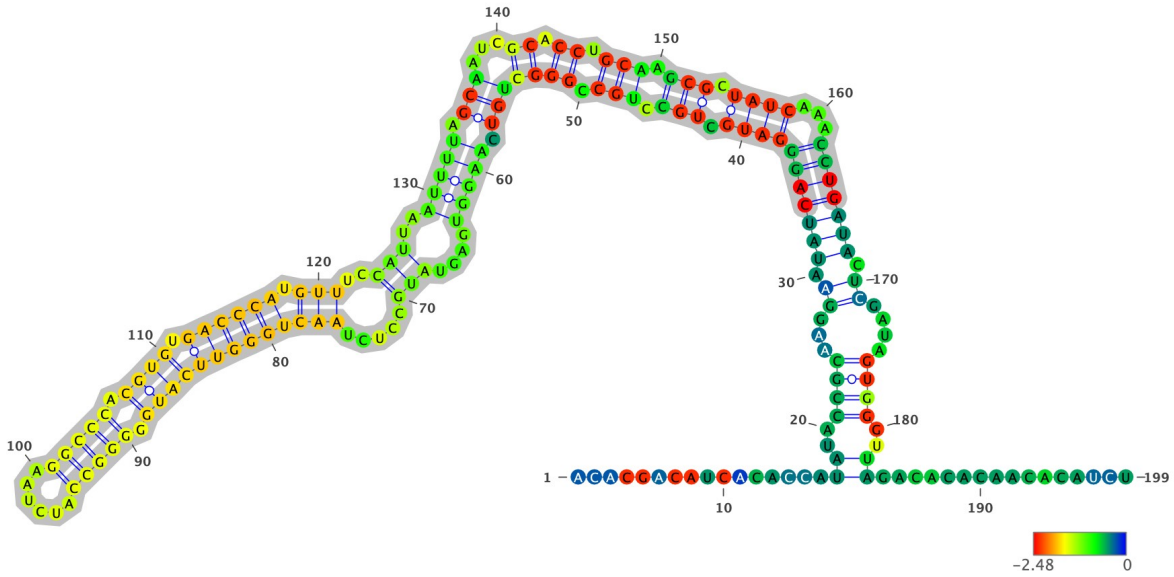
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

12-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 257 from nt 86415 to 86546 (nt 34 to 165)

```
5'-CAGGGAUGCUGCCUGCCGGGCUGUCAAGGUGAGUAUGCCUCUAACUGGGUUCAUGGGGGCCAUCUAAGGCCCACGUGUGACCCAUGUUUCCAUUAAUUUUAGCAAUCGCAC
CUGCAAGCGCUAUCAAACCUG-3'
5'-((..(((((.((...((.(((..((.....................................................................................)).....).)
).)).....)).)))).....))-3'
Motif MFE = -45.4; z-score = -2.25; ED = 23.94
```



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 86382 to 86580 (motif highlighted in silver):

```
5'-ACACGACAUCACACCAUAUACCGCAAGGAAUAUCAGGGAUGCUGCCUGCCGGGCUGUCAAGGUGAGUAUGCCUCUAACUGGGUUCAUGGGGGCCAUCUAAGGCCCACGUGU
GACCCAUGUUUCCAUUAAUUUUAGCAAUCGCACCUGCAAGCGCUAUCAAACCUGAUACUCGAUAGUGGGUUAGACACACAACACAUCU-3
5'-................((..((((...((.(((((((((((.(((.(((.(((((((.(((((....(((.....((((((((((((.(((((......)))))).)))))
))))))).)))..)))..)))))).)))...)).)).)))).)))).))))...)))))))).)).....))))..)).................-3'
MFE = -58.8; z-score = -2.41; ED = 12.69
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 61--exon, exon-HHV4_EBNA-1.1-20, 86076-86442(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-20', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

8-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 61--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-20, 86076-86442(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-20', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

10-- nt 136 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

11-- nt 1 to 61--CDS, cds-YP_401671.1, 86083-86442(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

12-- nt 136 to 199--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

13-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

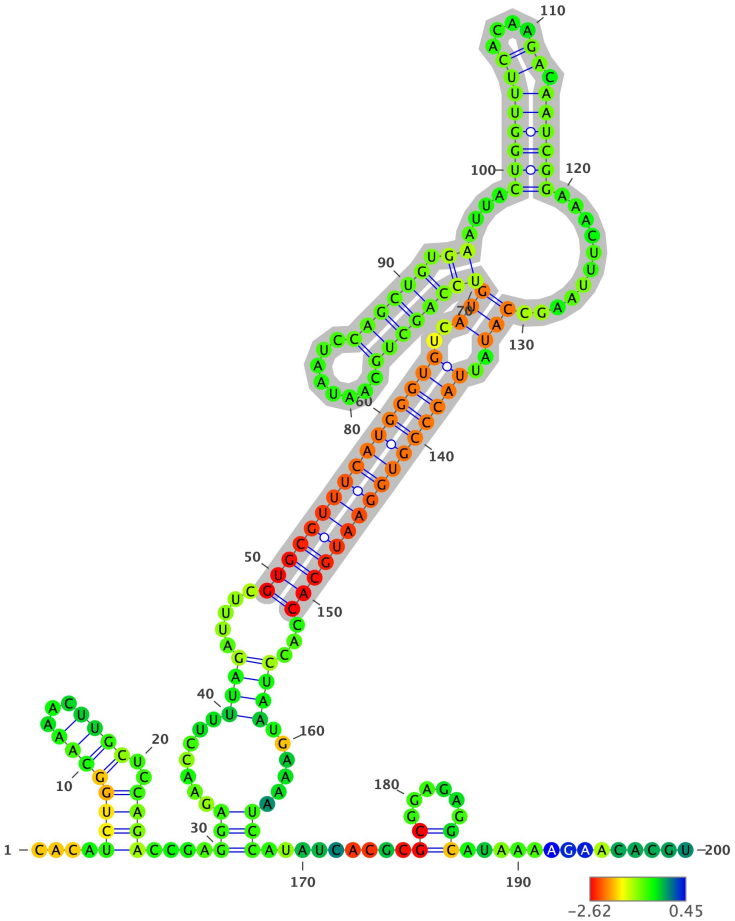
14-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 258 from nt 87018 to 87120 (nt 49 to 151)

```
5'-GUGCGUUUCAUGGGUGUCAUGUCCAGCUGCAAUAAUCCAGCUGUGAAUUACUGGUUUCACAAGACAAUCGGAAACUUUAAGCCAUAUUACCCGUGGAAUGCAC-3'

5'-(((((((((((((((..(((.....))))..))))))))))))))))-3'
Motif MFE = -36.4; z-score = -4.34; ED = 15.17
```



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 86970 to 87169 (motif highlighted in silver):

```
5'-CACAUCUGGCAAAACUUGCUCCAGACCGAGGAGAACCUUUUAGAUUUCGUGCGUUUCAUGGGUGUCAUGUCCAGCUGCAAUAAUCCAGCUGUGAAUUACUGGUUUCACAAG
ACAAUCGGAAACUUUAAGCCAUAUUACCCGUGGAAUGCACCACCUAAUGAAAAUCCAUAUCACGCGCGGAGAGGCAUAAAAGAACACGU-3
5'-....(((((((...)))))..)))).....(((.......(((.....((((((((((((((..((((((((((.......)))))))).))....(((((((....)
).))))))...........)))..))))))))))))))...))))......)))........((......)).............-3'
MFE = -47.5; z-score = -0.98; ED = 36.43
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

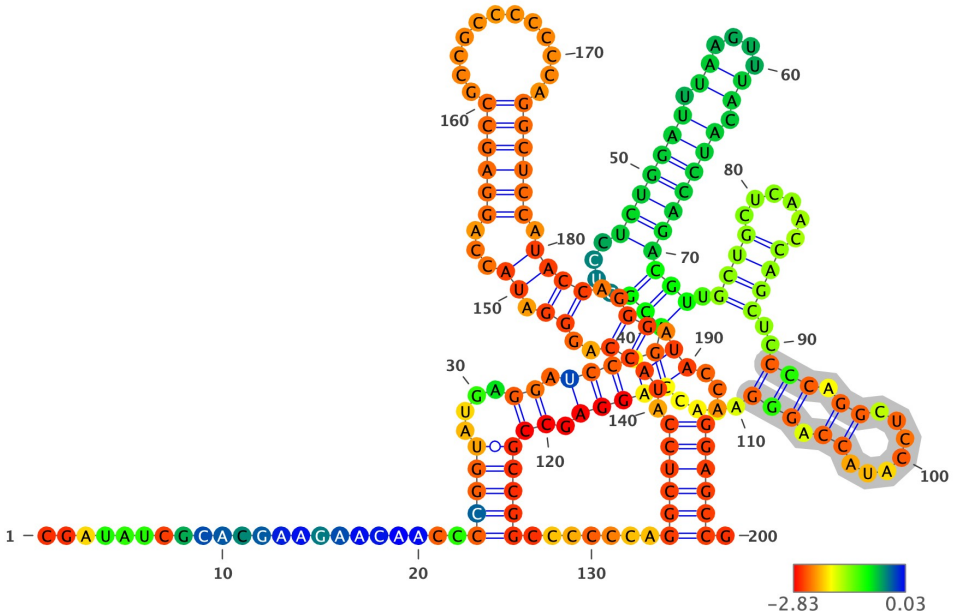
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 259 from nt 88384 to 88402 (nt 91 to 109)

```
5'-CCCAGGCUCCAUACCAGGG-3'
5'-(.(.((.......)).).)-3'
Motif MFE = -4.1; z-score = -0.89; 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 88294 to 88493 (motif highlighted in silver):

```
5'-CGAUAUCGCACGAAGAACAACCCCGGUAUGAGGAUCCUGACGCUCCUCUGGAUUUAAGUUUACAUCCAGACGUUGCUGCUCAACCAGCUCCCCAGGCUCCAUACCAGGGAU
ACCAGGAGCCGCCGGCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGCCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCG-3
5'-......................(((((....((.(((((((((....(((((((.((....)).)))))))))).((((......)))))..(((.(((.......)).)))).
.))))).)))))))).......((((((.((((..((.((...((((((.............)))))).)))).)).))...)))))).-3'
MFE = -60.7; z-score = -1.58; ED = 52.46
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS',

'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

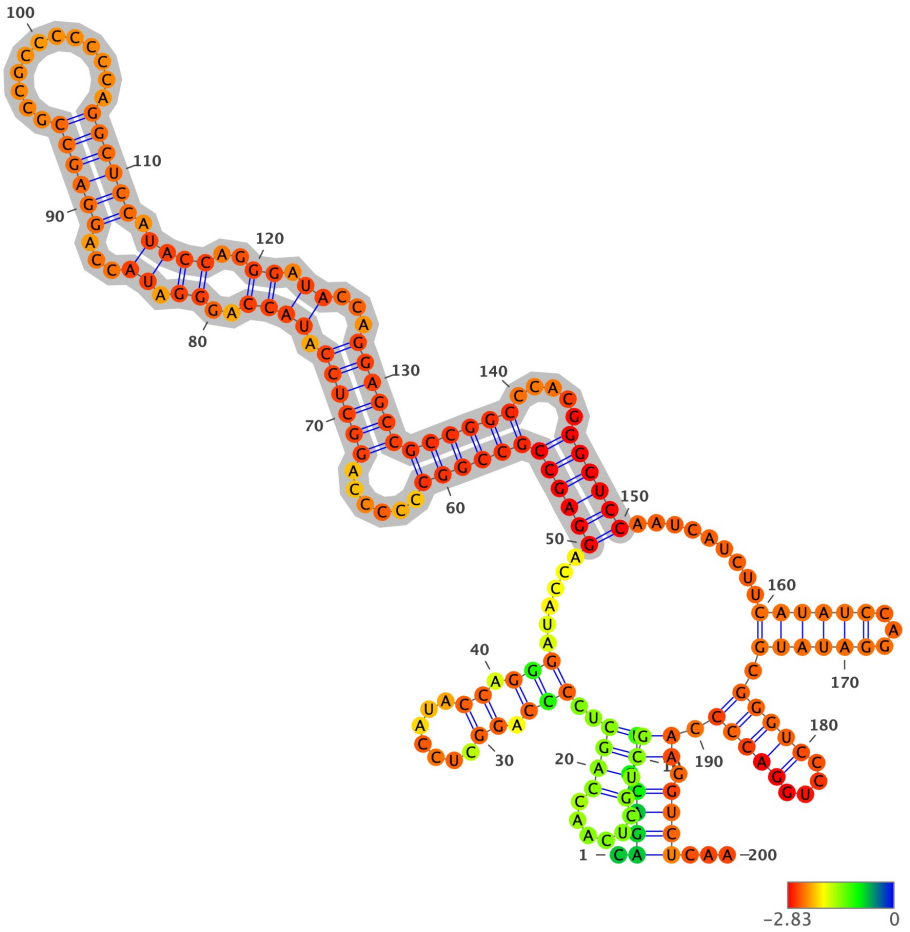
12-- nt 84 to 200--repeat_region, id-HHV4_EBNA-1.2-18, 88377-88493(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-18', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=88377..88415']

NC_007605.1 (forward strand): Structure number 260 from nt 88409 to 88509 (nt 50 to 150)

```
5'-GGAGCCGCCGGCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGCCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGGCCCACGGGCUCC-3'

5'-(((((((((((.....((((((.(((((..((.((...((((((.............)))))).)))))..)).)).)...)))))))))))).....))))))-3'
Motif MFE = -47.2; z-score = -2.81; ED = 9.9
```



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 88360 to 88559 (motif highlighted in silver):

```
5'-CAGACGUUGCUGCUCAACCAGCUCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGGCCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGCCCCCCCAGGCUC
CAUACCAGGGAUACCAGGAGCCGCCGGCCCACGGGCUCCAAUCAUCUUCAUAUCCAGGAUAUGCGGGUCCCUGGACCCCAAGGUCUCAA-3
5'-.((((.((((((.....)))))..(((.(((.......)).))).....((((((((((((.....((((((.(((((..((.((...((((((.............)))))
).))))..)).)).)...))))))))))))).....)))))).........((((((...)))))).(((((....)))))).)).))))...-3'
MFE = -74.7; z-score = -2.66; ED = 24.98
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

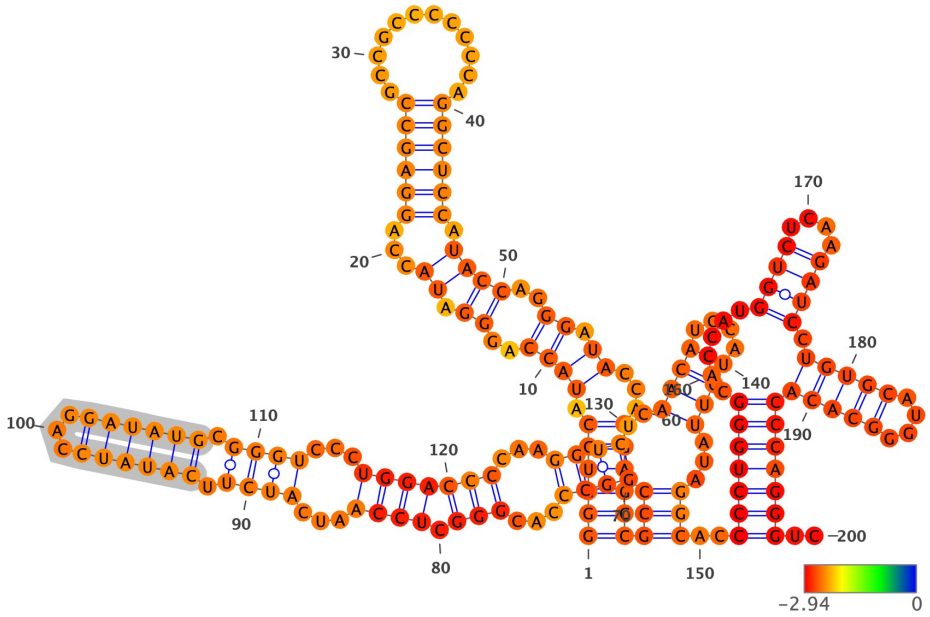
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

12-- nt 18 to 134--repeat_region, id-HHV4_EBNA-1.2-18, 88377-88493(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-18', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=88377..88415']

NC_007605.1 (forward strand): Structure number 261 from nt 88519 to 88533 (nt 93 to 107)

```
5'-CAUAUCCAGGAUAUG-3'
5'-((((((...)))))))-3'
Motif MFE = -2.6; z-score = -3.31; 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 88427 to 88626 (motif highlighted in silver):

```
5'-GGCUCCAUACCAGGGAUACCAGGAGCCGCCGCCCCCCCAGGCUCCAUACCAGGGAUACCAGGAGCCGCCGGCCCACGGGCUCCAAUCAUCUUCAUAUCCAGGAUAUGCGGG
UCCCUGGACCCCAAGGUCUCAACAUCCAUGUUAUAGGCACCCCUGGGCACCAUGGUCUCAAGAUCCUGUGCAUGGGCACACCCAGGGUC-3
5'-((((((.((((..((.((...((((((.............)))))).)))))..)).)).....)))))))(((((((...(((.((((...((((.(((((((...)))))))).)))
)...)))))))...)))))..((((....))))...)))..(((((((.....((((....)))).(((((....)))))))))))))..-3'
MFE = -72.7; z-score = -2.37; ED = 57.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS',

'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

12-- nt 1 to 67--repeat_region, id-HHV4_EBNA-1.2-18, 88377-88493(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-18', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=88377..88415']

NC_007605.1 (forward strand): Structure number 262 from nt 88554 to 88574 (nt 90 to 110)

```
5'-UCUCAACAUCCAUGUUAUAGG-3'
5'-((..((((....))))...))-3'
Motif MFE = 0.0; z-score = 0.67; ED = 3.28
```

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 88465 to 88664 (motif highlighted in silver):

```
5'-AGGCUCCAUACCAGGGAUACCAGGAGCCGCCGGCCCACGGGCUCCAAUCAUCUUCAUAUCCAGGAUAUGCGGGUCCCUGGACCCCAAGGUCUCAACAUCCAUGUUAUAGGC
ACCCCUGGGCACCAUGGUCUCAAGAUCCUGUGCAUGGGCACACCCAGGGUCCAUGGGAUCCCAGGGCACCACAUCUCCCACCUCAGUGG-3
5'-.(((.....(((((((.((.(((((((..((.....)))))))).........((((((...)))))).)))))))))).........((((.((((....)))).)))))
..(((((((..((((((.(((.....((((....)))))....))).)))))).....)))))))..)).....((((....))))-3'
MFE = -70.7; z-score = -3.16; ED = 29.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS',

'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

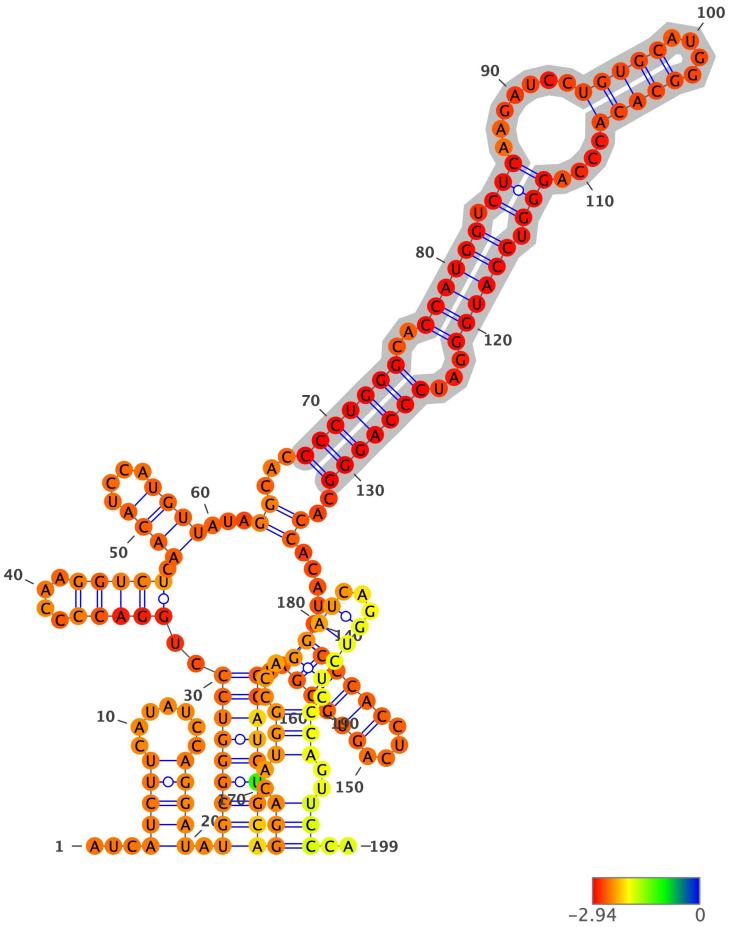
Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

12-- nt 1 to 29--repeat_region, id-HHV4_EBNA-1.2-18, 88377-88493(+)

Attributes: ['ID=id-HHV4_EBNA-1.2-18', 'Dbxref=GeneID:3783774', 'gbkey=repeat_region', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'rpt_unit_range=88377..88415']

NC_007605.1 (forward strand): Structure number 263 from nt 88578 to 88641 (nt 68 to 131)

```
5'-CCCUGGGCACCAUGGUCUCAAGAUCCUGUGCAUGGGCACACCCAGGGUCCAUGGGAUCCCAGGG-3'
5'-(((((((..(((((((.(((.......(((((....)))))....))).)))))))...)))))))-3'
Motif MFE = -32.6; z-score = -3.55; 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 88511 to 88709 (motif highlighted in silver):

```
5'-AUCAUCUUCAUAUCCAGGAUAUGCGGGUCCCUGGACCCCAAGGUCUCAACAUCCAUGUUAUAGGCACCCCUGGGCACCAUGGUCUCAAGAUCCUGUGCAUGGGCACACCCA
GGGUCCAUGGGAUCCCAGGGCACCACAUCUCCCACCUCAGUGGGAUGGAUCUGCAGGACAUGGCCAGGAUCAGGUCUCCCAGUUCCCA-3
5'-...(((((.......)))))..(((((((((..(((((....)))))).(((....)))))...((...(((((((..((((((.(((.......(((((....)))))))....
)))).)))))))...)))))))..))).....((((((....)))))).))))))))))((((..((((...((((...)))).)))..)))..-3'
MFE = -70.9; z-score = -2.72; ED = 38.03
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 199--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

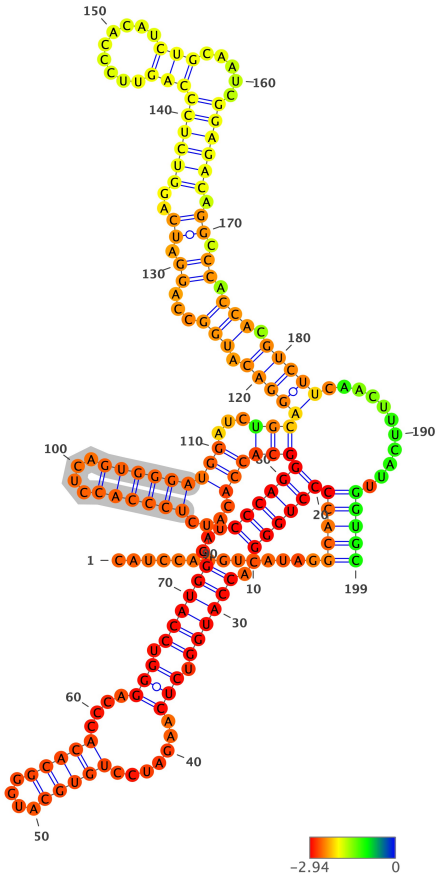
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 264 from nt 88651 to 88666 (nt 92 to 107)

```
5'-UCCCACCUCAGUGGGA-3'
5'-((((((....)))))))-3'
Motif MFE = -8.2; z-score = -4.56; ED = 0.49
```



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 88560 to 88758 (motif highlighted in silver):

```
5'-CAUCCAUGUUAUAGGCACCCCUGGGCACCAUGGUCUCAAGAUCCUGUGCAUGGGCACACCCAGGGUCCAUGGGAUCCCAGGGCACCACAUCUCCCACCUCAGUGGGAUGGA
UCUGCAGGACAUGGCCAGGAUCAGGUCUCCCAGUUCCCACAUCUGCAAUCGGAGACAGGCCCACCACGUCUUCAACUUUCAUUGGUGC-3
5'-..............((((((((((..((((((.(((.......(((((....)))))....))).)))))).))))))(((((....((((((....)))))))))).
..)))(((((.(((...((.((..((((((((.........)))).....)))))).)).)).)).)))).)))))..........)))))-3'
MFE = -69.2; z-score = -2.42; ED = 45.9
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 199--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

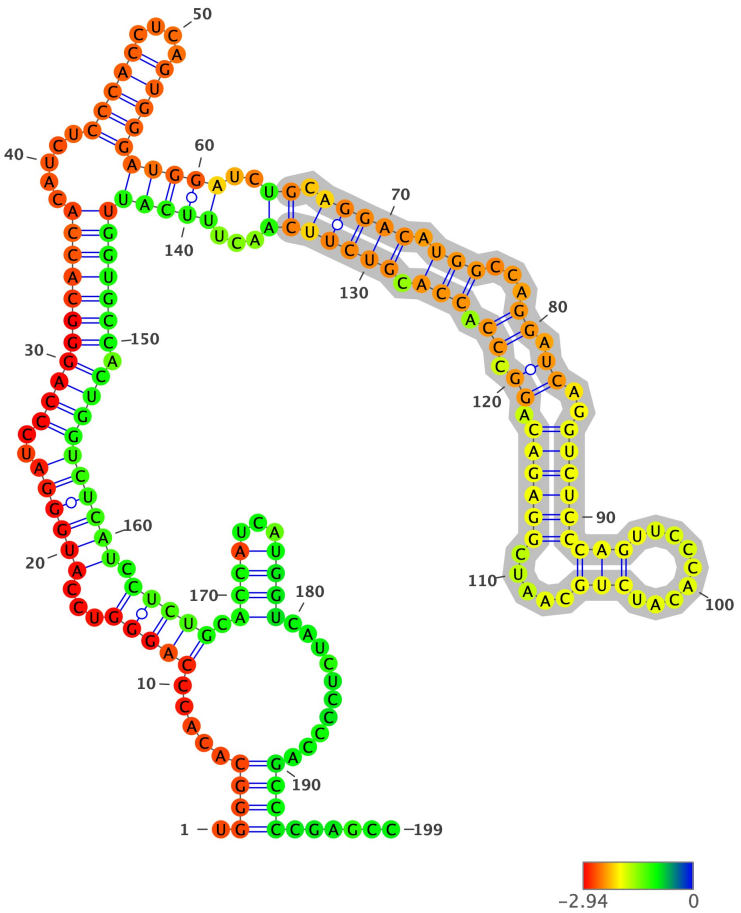
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 265 from nt 88674 to 88743 (nt 65 to 134)

```
5'-GCAGGACAUGGCCAGGAUCAGGUCUCCCAGUUCCCACAUCUGCAAUCGGAGACAGGCCCACCACGUCUUC-3'
5'-(..((((.(((...((.((.....................................)).)).))).)))))..)-3'
Motif MFE = -19.6; z-score = -1.21; ED = 6.19
```



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

Extracted structure model with flanking nucleotides 88610 to 88808 (motif highlighted in silver):

```
5'-UGGGCACACCCAGGGUCCAUGGGAUCCCAGGGCACCACAUCUCCCACCUCAGUGGGAUGGAUCUGCAGGACAUGGCCAGGAUCAGGUCUCCCAGUUCCCACAUCUGCAAUC
GGAGACAGGCCCACCACGUCUUCAACUUUCAUUGGUGCCACUGGUCUCAUCCUCUGCACCAUCAUGGUCAUCUCCCCAGCCCCGAGCC-3
5'-.((((.....((((((...((((((..(((((((((((.....((((((....)))))))))((((..((.(((((.(((...((.((..(((((((((.........)))).....
))))))).)).)).))).)))))))...))))))))))))).))))))))))).)))))).((((...)))).........))))......-3'
MFE = -66.4; z-score = -2.38; ED = 26.27
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 199--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 199--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 199--CDS, cds-YP_401671.1, 86517-89135(+)

Attributes: ['ID=cds-YP_401671.1', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=UniProtKB/TrEMBL:Q777E7,Genbank:YP_401671.1,GeneID:3783763', 'Name=YP_401671.1', 'gbkey=CDS', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=nuclear antigen EBNA-3C', 'protein_id=YP_401671.1']

10-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

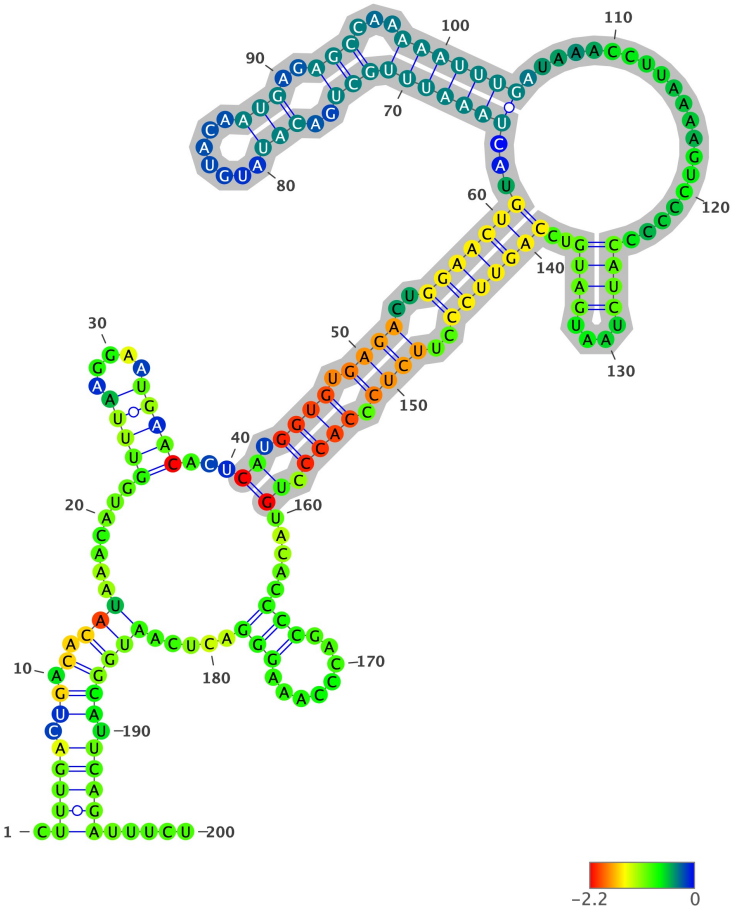
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

11-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 266 from nt 89210 to 89328 (nt 41 to 159)

```
5'-CAUGGUGUGAGACUGGAACUGUACUAAAUUUGCUGACAUAUGUACAAUGAGAGCCAAAAAUUUGAUAAACCUUAAAAGUCCCCCCAUCUAAUGAUGUCCAGUUCCCUUCUC
CCACCCUG-3'
5'-(..(((.....................................................................................................
..)))..)-3'
Motif MFE = -28.5; z-score = -2.69; ED = 10.08
```



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 89170 to 89369 (motif highlighted in silver):

```
5'-CUUUGACUGACACAUAAACAUGGUUUAAGGAAUGAACACUCAUGGUGUGAGACUGGAACUGUACUAAAUUUGCUGACAUAUGUACAAUGAGAGCCAAAAAUUUGAUAAACC
UUAAAAGUCCCCCCAUCUAAUGAUGUCCAGUUCCCUUCUCCCACCCUGUACACCCCGACCCAAAGGGACUCAAUGGCAUUCAGAUUUCU-3
5'-.(((((.((.(.(((.......((((.....)))))...((.((((.((((..(((((((...((((((((((..(((.......)))..)))...)))))))).......
.............((((....))))..)))))))..)))).)))).)).....(((........)))....)))))).)))))).....-3'
MFE = -39.5; z-score = -1.41; ED = 26.29
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-3B/EBNA-3C, 11305-89482(+)

Attributes: ['ID=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Name=EBNA-3B/EBNA-3C', 'Note=EBNA-3 family', 'gbkey=Gene', 'gene=EBNA-3B/EBNA-3C', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-3B/EBNA-3C']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C',

'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

6-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-21, 83500-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3B']

7-- nt 1 to 200--mRNA, rna-HHV4_EBNA-3B/EBNA-3C-2, 11336-89482(+)

Attributes: ['ID=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Parent=gene-HHV4_EBNA-3B/EBNA-3C', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

8-- nt 1 to 200--exon, exon-HHV4_EBNA-3B/EBNA-3C-2-21, 86517-89482(+)

Attributes: ['ID=exon-HHV4_EBNA-3B/EBNA-3C-2-21', 'Parent=rna-HHV4_EBNA-3B/EBNA-3C-2', 'Dbxref=GeneID:3783763', 'Note=can start from Cp or any Wp', 'gbkey=mRNA', 'gene=EBNA-3B/EBNA-3C', 'locus_tag=HHV4_EBNA-3B/EBNA-3C', 'product=EBNA-3C']

9-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

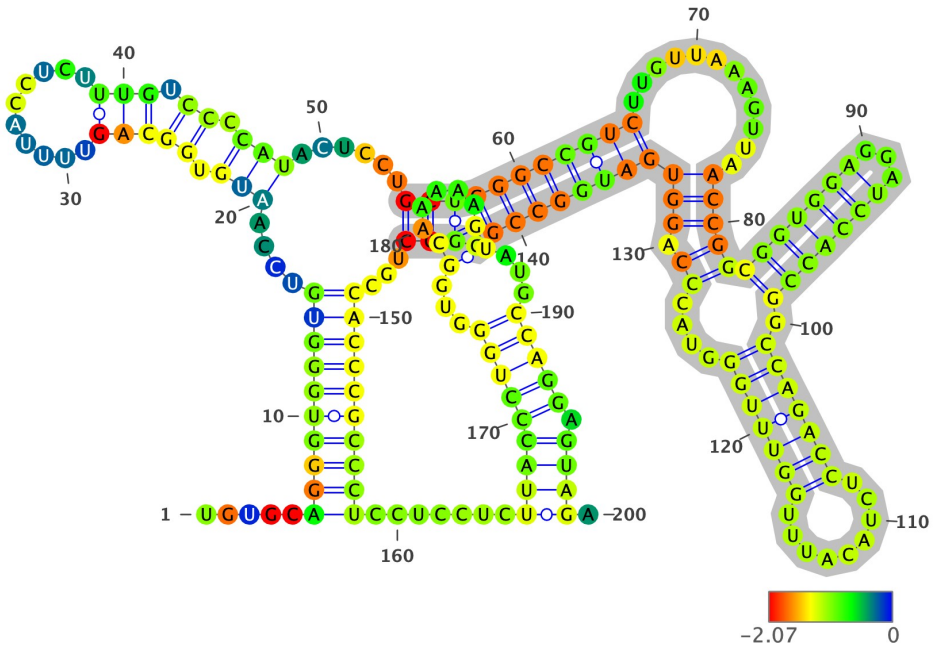
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

10-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 267 from nt 89624 to 89714 (nt 55 to 145)

```
5'-GCUCGGCCGUCUUGUUAAAGUUAACCGGCGGUGGAGGAUCCACCGGCCAGACCUCUACAUUUGGUUUGGGUACCCAGGUGAUGGCCGCGGC-3'
5'-((.....))-3'
Motif MFE = -37.8; z-score = -2.13; ED = 10.85
```



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

Extracted structure model with flanking nucleotides 89570 to 89769 (motif highlighted in silver):

```
5'-UGUGCAGGGUGGGUGUCCAAUGUGGCAGUUUUACCUCUUUGUCCCCAUACUCCUGCUCGGCCGUCUUGUUAAAGUUAACCGGCGGUGGAGGAUCCACCGGCCAGACCUCUA
CAUUUGGUUUGGGUACCCAGGUGAUGGCCGCGGCUGCCACCCGCCCUCCUCCUCUUACCCUGGGUGGCAAAAAGUAUGCCAGGAGUAGA-3
5'-.....((((((((((....(((.(((((..........))).)).))).)).....((((((((((.........((((((((((...)))))))).(((((((....
.....)))))))....)).))))))))))).)))...))))))))))).....((((((((...((.....))...)))))).)))).-3'
MFE = -72.5; z-score = -1.45; ED = 24.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

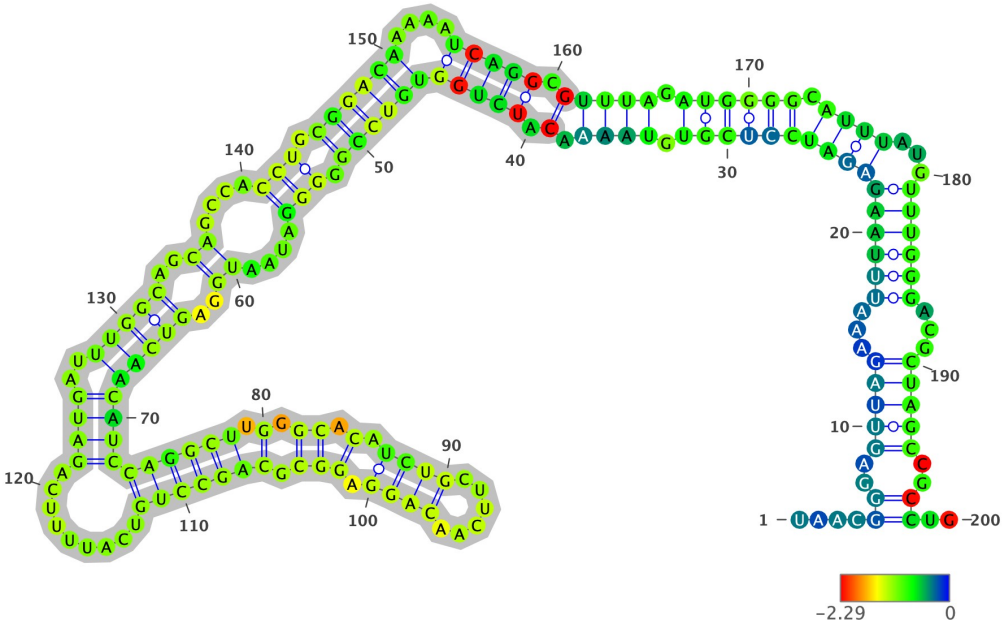
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 268 from nt 89951 to 90073 (nt 39 to 161)

```
5'-CAUCUGGUGUCCGGGGGAUAAUGGAGUCAACAUCCAGGCUUGGGCACAUCUGCUUCAACAGGAGGCGCAGCCUGUCAUUUUCAGAUGAUUUGGCAGCAGCCACCUGCGGAC
AAAAAUCAGGCG-3'
5'-(.(..(.....................................................................................................
......)..).)-3'
Motif MFE = -44.0; z-score = -2.14; ED = 20.78
```



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 89913 to 90112 (motif highlighted in silver):

```
5'-UAACGGGAGUUAGAAAUUUAAGAGAUCCUCGUGUAAAACAUCUGGUGUCCGGGGGAUAAUGGAGUCAACAUCCAGGCUUGGGCACAUCUGCUUCAACAGGAGGCGCAGCCU
GUCAUUUUCAGAUGAUUUGGCAGCAGCCACCUGCGGACAAAAAUCAGGCGUUUAGAUGGGGCAUUUAUGUUUGGGACGCUAGCCGCCUG-3
5'-....((..(((((...(((((((((((((((.((((.(.((((((((((.(((....((..((((((((((((((.(.((.(.((((......)))).))).))))))
).........))))..))))))..)).....))).)))))).....)))))).)))))).)))))).))))...)))))).....)))))..)).-3'
MFE = -65.9; z-score = -1.9; ED = 29.32
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

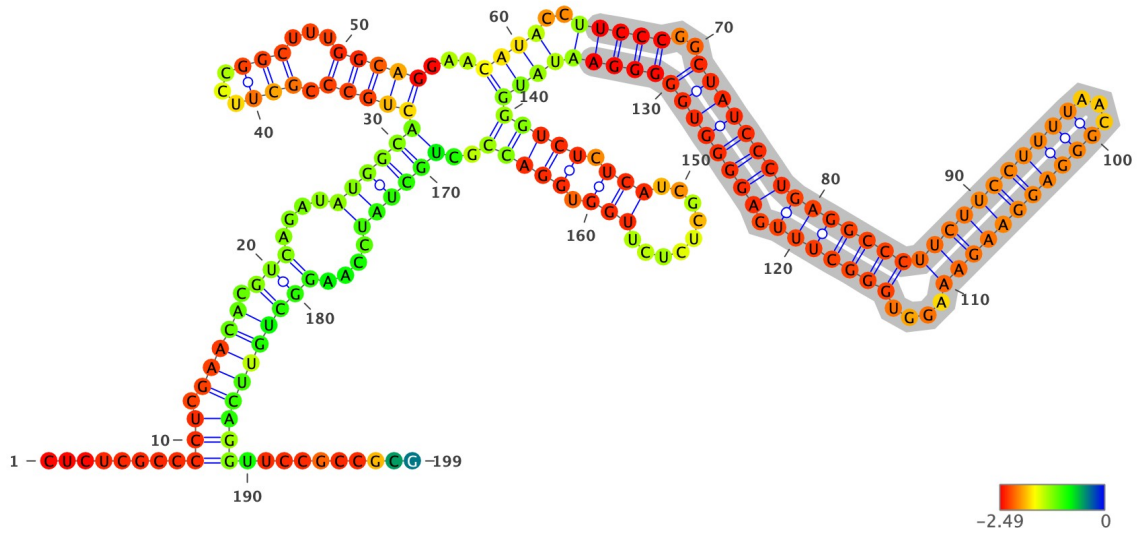
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 269 from nt 91637 to 91706 (nt 65 to 134)

```
5'-UCCCGGCUAUCCCUGAGGCCCUUCUUCCUUUUAACGGGAGGAAGAAAGGUGGGCUUUGAGGGGUGGGGGA-3'
5'-((((..(((((((((((((((((((((((...)))))))))))))....)))))))).))))))))))))-3'
Motif MFE = -38.0; z-score = -5.29; ED = 4.05
```



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 91573 to 91771 (motif highlighted in silver):

```
5'-CUCUCGCCCCUCGAACACGUCAGAUAUGGCACUGCCCGCUUCCGGCUUUGGCAGGAACAUACCUUCCCGGCUAUCCCUGAGGCCCUUCUUCCUUUUAACGGGAGGAAGAAA
GGUGGGCUUUGAGGGGUGGGGGAAUAUGGGUCUCUCAUCGCUCUCUUGGUGGACCGCUGCUAUCCAAGGCUGUUCAGGUUCCGCCGCG-3
5'-........(((.(((((.(((....(((((((((((.(((...))).)))))...(((((..((((((..(((((((((((((((((((((((((...)))))))))))).
...)))))))).))))))))))))))))(((((.(((.........))).)))))..)))))).....))))))))))).........-3'
MFE = -75.4; z-score = -2.61; ED = 22.8
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

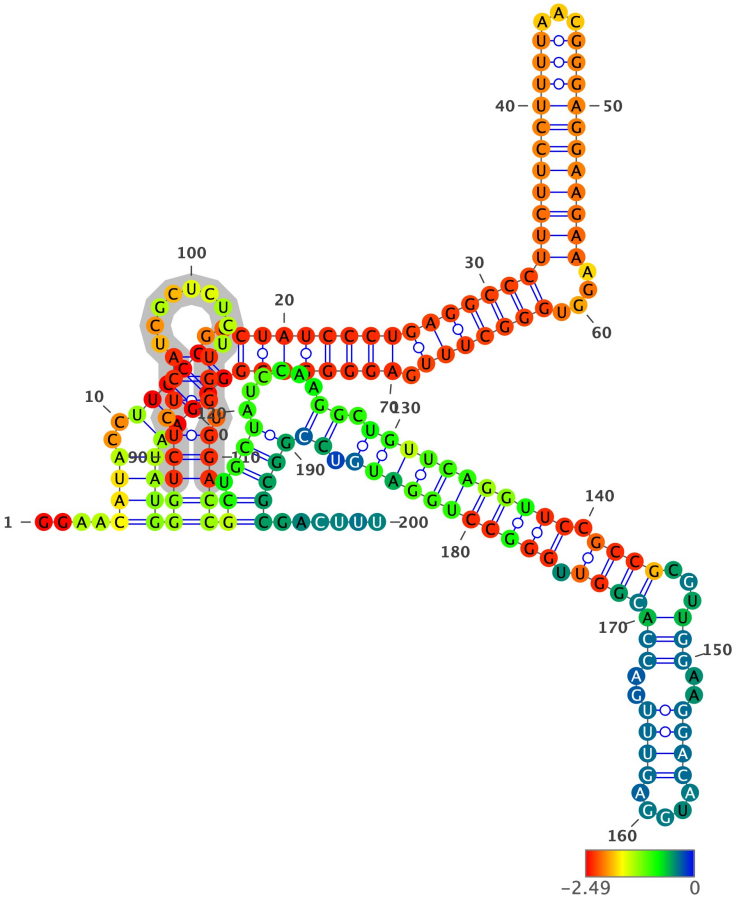
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 270 from nt 91714 to 91736 (nt 89 to 111)

```
5'-UCUCUCAUCGCUCUCUUGGUGGA-3'
5'-(((.(((.........))).)))-3'
Motif MFE = -3.2; z-score = -0.95; 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 91626 to 91825 (motif highlighted in silver):

```
5'-GGAACAUACCUUCCCGGCUAUCCCUGAGGCCCUUCUUCCUUUUAACGGGAGGAAGAAAGGUGGGCUUUGAGGGGUGGGGGAAUAUGGGUCUCUCAUCGCUCUCUUGGUGGA
CCGCUGCUAUCCAAGGCUGUUCAGGUUCCGCCGCGUUGGAAGGACAUGGAGUUUGACCACGGUUGGGCCUGGAUGUCCGGCGCGACUUU-3
5'-....(((((..((((((..(((((((((((((((((((((((((...)))))))))))).....))))))).))))))))))))))))))(((((.(((.........))).)))
))))(((.(((......((.((((((((((.((((...((((..((((.....))))..)))))))).))))))))))).))))))).....-3'
MFE = -79.6; z-score = -1.68; ED = 25.72
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 200--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

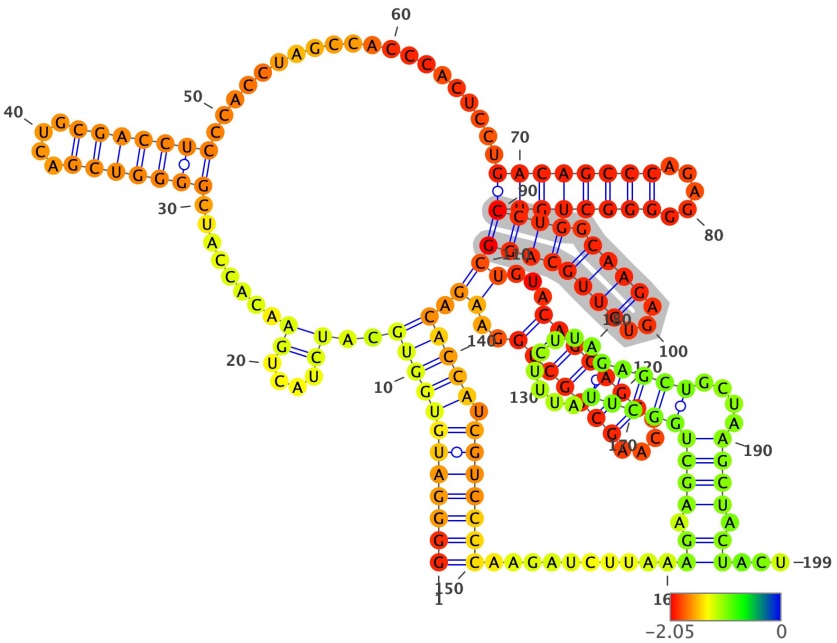
Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 200--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

NC_007605.1 (forward strand): Structure number 271 from nt 93064 to 93083 (nt 90 to 109)

```
5'-CCUGGCAAGAGUCUUGCAGG-3'
5'-(..................)-3'
Motif MFE = -6.8; z-score = -2.26; 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 92975 to 93173 (motif highlighted in silver):

```
5'-GGGGAUGUGGUGCAUCUACUGAACACCAUCGGGGUCGACUGCGACCUCCCACCUAGCCACCCACUCCUGACAGCCCAGAGGGGGCUGUUCCUGGCAAGAGUCUUGCAGGCU
GUACAGCAGCACAAGCUGCUGGAAGACACCAUCGUCCCCAAGAUCUUAAAGAAGCUGGCUUAUUUCUUAGAGCUGCUAAGCUACUACU-3
5'-(((((((((((..((....)).......(((((((....)))))))).....................(((((((.....)))))))))))((((.(((((...)))))))))((
...(((((((....)))))))..)).)))))..)))))))..........((.(((((((((.......)))))))....)))))..)).....-3'
MFE = -74.5; z-score = -3.74; ED = 30.79
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

6-- nt 1 to 199--gene, gene-HHV4_BRRF1, 92728-93827(+)

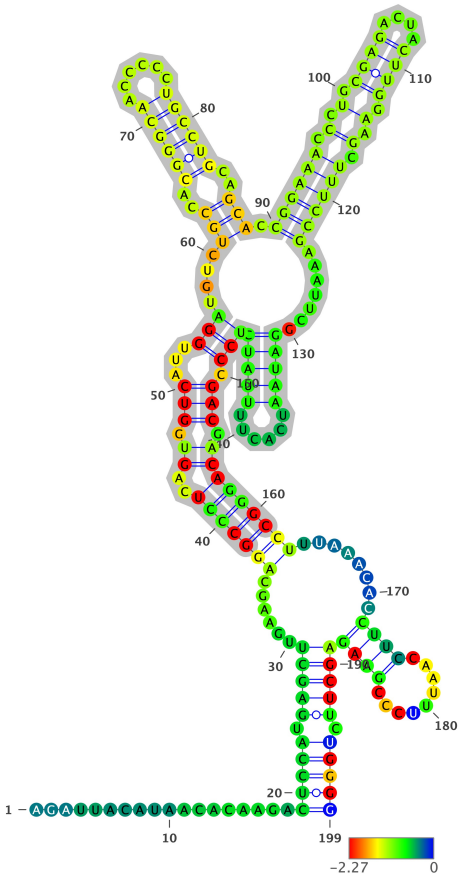
Attributes: ['ID=gene-HHV4_BRRF1', 'Dbxref=GeneID:3783728', 'Name=BRRF1', 'Note=gamma gene', 'gbkey=Gene', 'gene=BRRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BRRF1']

7-- nt 1 to 199--CDS, cds-YP_401675.1, 92894-93826(+)

Attributes: ['ID=cds-YP_401675.1', 'Parent=gene-HHV4_BRRF1', 'Dbxref=UniProtKB/TrEMBL:Q777E3,Genbank:YP_401675.1,GeneID:3783728', 'Name=YP_401675.1', 'gbkey=CDS', 'gene=BRRF1', 'locus_tag=HHV4_BRRF1', 'product=protein G49', 'protein_id=YP_401675.1']

NC_007605.1 (forward strand): Structure number 272 from nt 94728 to 94851 (nt 38 to 161)

```
5'-GCCCUCAGUGGUCAUUGGAUGUCUGCCACGGGCAACCCCCUGCCUGCAGCACCGGAAACCCUGCGAGACUACUUGGAAGCUUUCCGAAAUUCGGAUAAUCACUUUUAUCUC
CCGACGACAGGGC-3'
5'-((..(..(..(((...((.......................................................................................)
).)))..))..))-3'
Motif MFE = -40.3; z-score = -2.18; ED = 13.19
```



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 94691 to 94889 (motif highlighted in silver):

```
5'-AGAUUACAUAACACAAGACUCCAUGAGCUUGAAGCAGGCCCUCAGUGGUCAUUGGAUGUCUGCCACGGGCAACCCCCUGCCUGCAGCACCGGAAACCCUGCGAGACUACUU
GGAAGCUUUCCGAAAUUCGGAUAAUCACUUUUAUCUCCCGACGACAGGGCCUUUAAACACCUUCCAAUUUCCCGAAGAGCUUCUGGGG-3
5'-.................(((((.(((((.....(((((((..((.(((...(((....(((..((((((.....)))))).)))).((((((.(.(.((((....)))
).).).)))))).....((((.....)))))))).))).)))))))).....((((.........)))))))).)))))-3'
MFE = -57.5; z-score = -1.78; ED = 18.02
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

5-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

6-- nt 1 to 199--gene, gene-HHV4_BRRF2, 93955-95631(+)

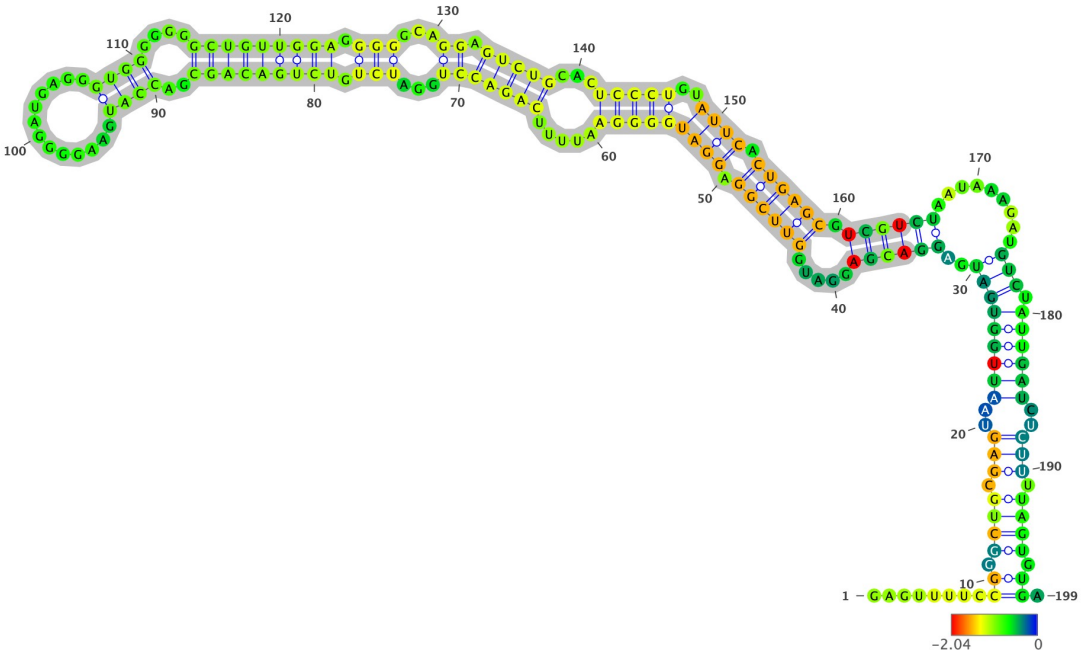
Attributes: ['ID=gene-HHV4_BRRF2', 'Dbxref=GeneID:3783729', 'Name=BRRF2', 'Note=gamma gene', 'gbkey=Gene', 'gene=BRRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BRRF2']

7-- nt 1 to 199--CDS, cds-YP_401676.1, 94014-95627(+)

Attributes: ['ID=cds-YP_401676.1', 'Parent=gene-HHV4_BRRF2', 'Dbxref=UniProtKB/TrEMBL:Q777E2,Genbank:YP_401676.1,GeneID:3783729', 'Name=YP_401676.1', 'gbkey=CDS', 'gene=BRRF2', 'locus_tag=HHV4_BRRF2', 'product=tegument protein G48', 'protein_id=YP_401676.1']

NC_007605.1 (forward strand): Structure number 273 from nt 95494 to 95623 (nt 35 to 164)

```
5'-ACGAGGAUGGUUCGGAGGAUGGGGAAUUUUCAGACCUGGAUCUGUCUGACAGCGACCAUGAAGGGGAUGAGGGUGGGGGGGCUGUUGGAGGGGGCAGGAGUCUGCACUCCC
UGUAUUCACUGAGCGUCGU-3'
5'-(..(.....................................................................................................
...............)..)-3'
Motif MFE = -46.6; z-score = -1.55; ED = 13.77
```



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 95460 to 95658 (motif highlighted in silver):

```
5'-GAGUUUUCCGGGCUGCGAGUAAUUGGUGAUGAGGACGAGGAUGGUUCGGAGGAUGGGGAAUUUUCAGACCUGGAUCUGUCUGACAGCGACCAUGAAGGGGAUGAGGGUGGG
GGGGCUGUUGGAGGGGGCAGGAGUCUGCACUCCCUGUAUUCACUGAGCGUCGUCUAAUAAAGAUGUCUAUUGAUCUCUUUAGUGUGA-3
5'-........((.((((.((((..(((((((((..((((((.....((((((.(((((((((.....(((((((...(((.(((((((((..((((.............)))).
...)))))))))).)))...)).)))))...)))))..)))).)))))).)))))).........)))).)))))).)).))))).)).-3'
MFE = -59.1; z-score = -0.48; ED = 26.52
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 195 to 199--exon, exon-HHV4_EBNA-1.1-21, 95654-97654(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-21', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

7-- nt 195 to 199--exon, exon-HHV4_EBNA-1.2-3, 95654-97654(+)

Attributes: ['ID=exon-HHV4_EBNA-1.2-3', 'Parent=rna-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

8-- nt 1 to 172--gene, gene-HHV4_BRRF2, 93955-95631(+)

Attributes: ['ID=gene-HHV4_BRRF2', 'Dbxref=GeneID:3783729', 'Name=BRRF2', 'Note=gamma gene', 'gbkey=Gene', 'gene=BRRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BRRF2']

9-- nt 1 to 168--CDS, cds-YP_401676.1, 94014-95627(+)

Attributes: ['ID=cds-YP_401676.1', 'Parent=gene-HHV4_BRRF2', 'Dbxref=UniProtKB/TrEMBL:Q777E2,Genbank:YP_401676.1,GeneID:3783729', 'Name=YP_401676.1', 'gbkey=CDS', 'gene=BRRF2',

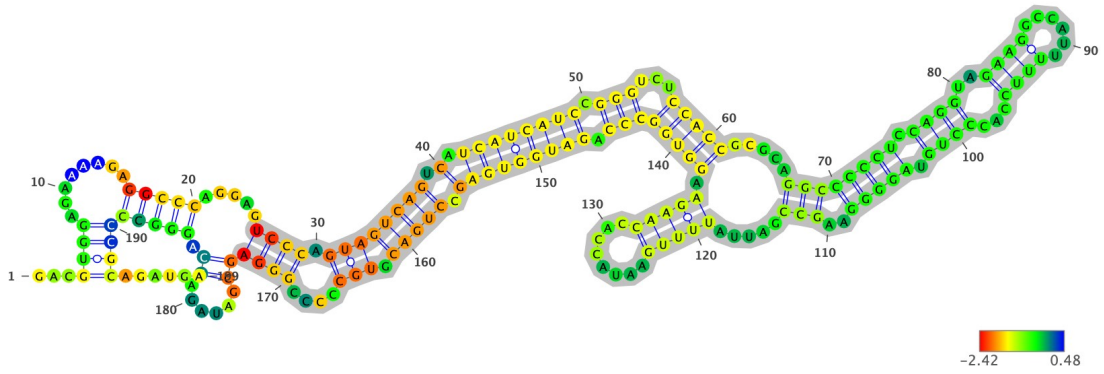
'locus_tag=HHV4_BRRF2', 'product=tegument protein G48', 'protein_id=YP_401676.1']

10-- nt 167 to 172--polyA_signal_sequence, id-HHV4_BRRF2-2, 95626-95631(+)

Attributes: ['ID=id-HHV4_BRRF2-2', 'Dbxref=GeneID:3783729', 'gbkey=regulatory', 'gene=BRRF2', 'locus_tag=HHV4_BRRF2', 'regulatory_class=polyA_signal_sequence']

NC_007605.1 (forward strand): Structure number 274 from nt 96810 to 96957 (nt 26 to 173)

```
5'-UCCCAGUAGUCAGUCAUCAUCAUCCGGGUCUCCACCGCGCAGGCCCCCUCCAGGUAGAAGGCCAUUUUUCCACCCUGUAGGGGAAGCCGAUUAUUUUGAAUACCACCAAGA
AGGUGGCCCAGAUGGUGAGCCUGACGUGCCCCCGGGA-3'
5'-((...(((.......................................................................................................
.........................)))......))-3'
Motif MFE = -55.9; z-score = -3.01; ED = 15.17
```



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 96785 to 96983 (motif highlighted in silver):

```
5'-GACGUGGAGAAAAGAGGCCCAGGAGUCCCAGUAGUCAGUCAUCAUCAUCCGGGUCUCCACCGCGCAGGCCCCCUCCAGGUAGAAGGCCAUUUUUCCACCCUGUAGGGGAAG
CCGAUUAUUUUGAAUACCACCAAGAAGGUGGCCCAGAUGGUGAGCCUGACGUGCCCCCGGGAGCGAUAGAGCAGGGCCCCGCAGAUGA-3
5'-...((((........((((.....((((.(((((((((.(.((((((((.(((...(((((.....((((((((.((((..((((......))))...)))))).)))))..)
)).....(((((........)))))..)))))))).))))))))).)))))).)))....)))))((.....)).)))))))))).....-3'
MFE = -70.7; z-score = -1.14; ED = 14.92
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_EBNA-1.1, 11305-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Name=EBNA-1', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=other', 'locus_tag=HHV4_EBNA-1.1']

3-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.1, 11336-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.1', 'Parent=gene-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

4-- nt 1 to 199--exon, exon-HHV4_EBNA-1.1-21, 95654-97654(+)

Attributes: ['ID=exon-HHV4_EBNA-1.1-21', 'Parent=rna-HHV4_EBNA-1.1', 'Dbxref=GeneID:3783709', 'Note=can start from Cp%2C Qp or any Wp', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.1']

5-- nt 1 to 199--gene, gene-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Name=EBNA-1', 'Note=latency I', 'gbkey=Gene', 'gene=EBNA-1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_EBNA-1.2']

6-- nt 1 to 199--mRNA, rna-HHV4_EBNA-1.2, 50134-97654(+)

Attributes: ['ID=rna-HHV4_EBNA-1.2', 'Parent=gene-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

7-- nt 1 to 199--exon, exon-HHV4_EBNA-1.2-3, 95654-97654(+)

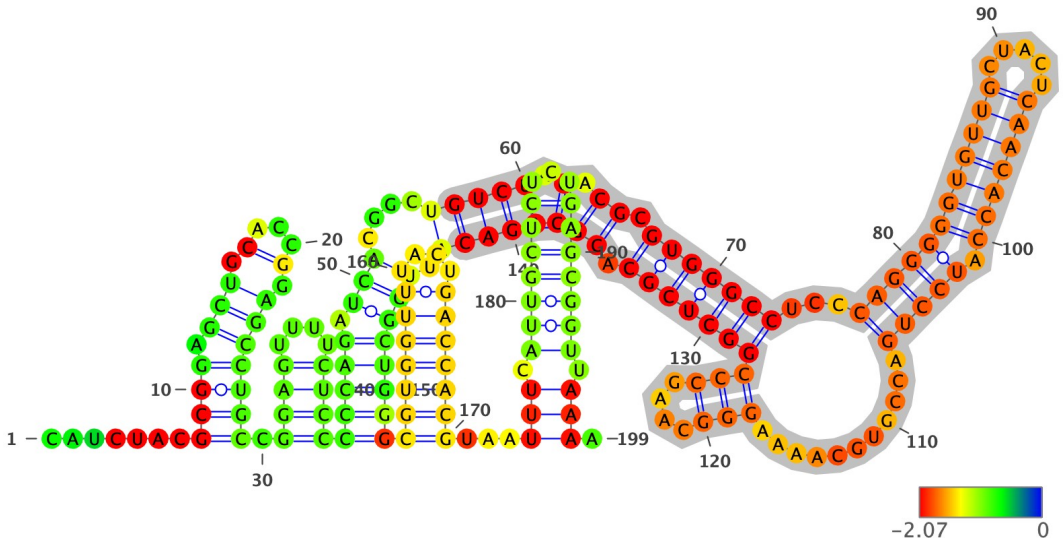
Attributes: ['ID=exon-HHV4_EBNA-1.2-3', 'Parent=rna-HHV4_EBNA-1.2', 'Dbxref=GeneID:3783774', 'Note=starts from the Q promoter (Qp) in latency I', 'gbkey=mRNA', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=EBNA-1%2C QUK transcript']

8-- nt 1 to 199--CDS, cds-YP_401677.1, 95662-97587(+)

Attributes: ['ID=cds-YP_401677.1', 'Parent=rna-HHV4_EBNA-1.2', 'Dbxref=UniProtKB/TrEMBL:Q777E1,Genbank:YP_401677.1,GeneID:3783774', 'Name=YP_401677.1', 'gbkey=CDS', 'gene=EBNA-1', 'locus_tag=HHV4_EBNA-1.2', 'product=nuclear antigen EBNA-1', 'protein_id=YP_401677.1']

NC_007605.1 (forward strand): Structure number 275 from nt 98471 to 98556 (nt 57 to 142)

```
5'-GUCUAGACGCGUGGGCCUCCCAGGGGGUGUUGCUACUCAACACCAUCCUGACCGUGCAAAAGGGCAAGCCCGGCUCGCACGCAGAC-3'
5'-(((((.(.((.(((((((.....................................................)))))))..)))))))-3'
Motif MFE = -36.3; z-score = -2.48; 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 98415 to 98613 (motif highlighted in silver):

```
5'-CAUCUACGCGGAGCUGCACCGGAGCCUGCCGGAGUUUUCUCCCCCAGAUCACGGCUGUCUAGACGCGUGGGCCUCCCAGGGGGUGUUGCUACUCAACACCAUCCUGACCGU
GCAAAAGGGCAAGCCCGGCUCGCACGCAGACAUUGGCUGGGCGUGGUUUACUGACCACGUAAUUUCAUUGCUCUCUGAGCGGUUAAAA-3
5'-.......((((.((((.(...).)))))).((((....))))((((.(((....(((((.(.((.(((((((...(((((((((((.....)))))))).))))).....
......(((....)))))))))).)))))))).))))))))((((((....)))))))...(((.(((((((...)))))))).))).-3'
MFE = -76.8; z-score = -2.97; ED = 23.38
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BKRF2, 97617-99504(+)

Attributes: ['ID=gene-HHV4_BKRF2', 'Dbxref=GeneID:3783710', 'Name=BKRF2', 'Note=core gene', 'gbkey=Gene', 'gene=BKRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BKRF2']

3-- nt 1 to 199--gene, gene-HHV4_BKRF3, 98065-99504(+)

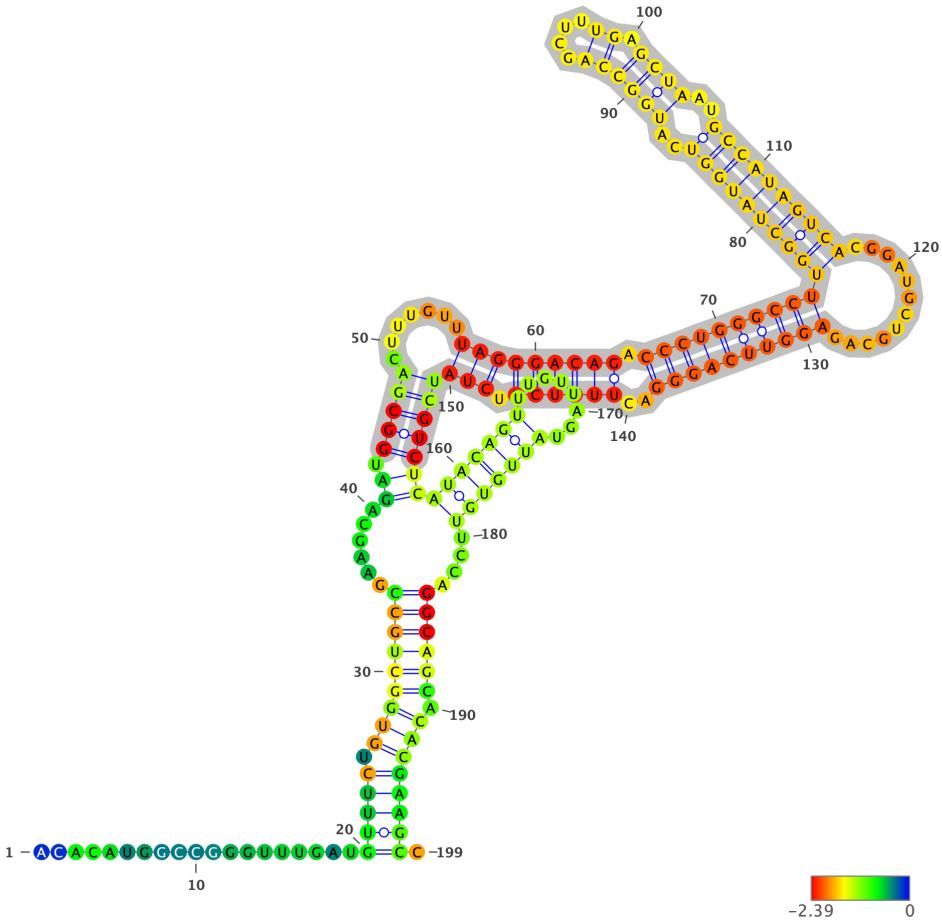
Attributes: ['ID=gene-HHV4_BKRF3', 'Dbxref=GeneID:3783711', 'Name=BKRF3', 'Note=core gene', 'gbkey=Gene', 'gene=BKRF3', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BKRF3']

4-- nt 1 to 199--CDS, cds-YP_401679.1, 98065-98832(+)

Attributes: ['ID=cds-YP_401679.1', 'Parent=gene-HHV4_BKRF3', 'Dbxref=UniProtKB/TrEMBL:Q777D9,Genbank:YP_401679.1,GeneID:3783711', 'Name=YP_401679.1', 'gbkey=CDS', 'gene=BKRF3', 'locus_tag=HHV4_BKRF3', 'product=uracil-DNA glycosylase', 'protein_id=YP_401679.1']

NC_007605.1 (forward strand): Structure number 276 from nt 99731 to 99842 (nt 44 to 155)

```
5'-GGCGACUUUGUUUAGGGACAGACCCUGGGCCUUGGCUAUGGUCAUGGCCAGCUUUGAGCUAAUGCCAUAGUCACGGAUGCUGCAGAGGUUCAGGGACUUGUCCUCUAUCGU
C-3'
5'-(((.........(((((((((.((((((((((.............................................................)))))))))).)))))))..)))
)-3'
Motif MFE = -47.0; z-score = -3.25; ED = 8.85
```



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 99688 to 99886 (motif highlighted in silver):

```
5'-ACACAUGGCCGGGUUUGAUGUUUCUGUGGCUGCCGAAGCAGAUGGCGACUUUGUUUAGGGACAGACCCUGGGCCUUGGCUAUGGUCAUGGCCAGCUUUGAGCUAAUGCCAU
AGUCACGGAUGCUGCAGAGGUUCAGGGACUUGUCCUCUAUCGUCUCAUACAGUUUGUUAGUAUUGUGUUCCAGGCAGCACACGAAGCC-3
5'-...................(((((.(((((((((.....((.(((((.......(((((((((.(((((((((((((((((((..((((((....)).)))))..)))))
)))))).............)))))))))).)))))).))))))))))((((((.......)))))))....)))))).))))))))).-3'
MFE = -72.1; z-score = -2.18; ED = 15.84
```

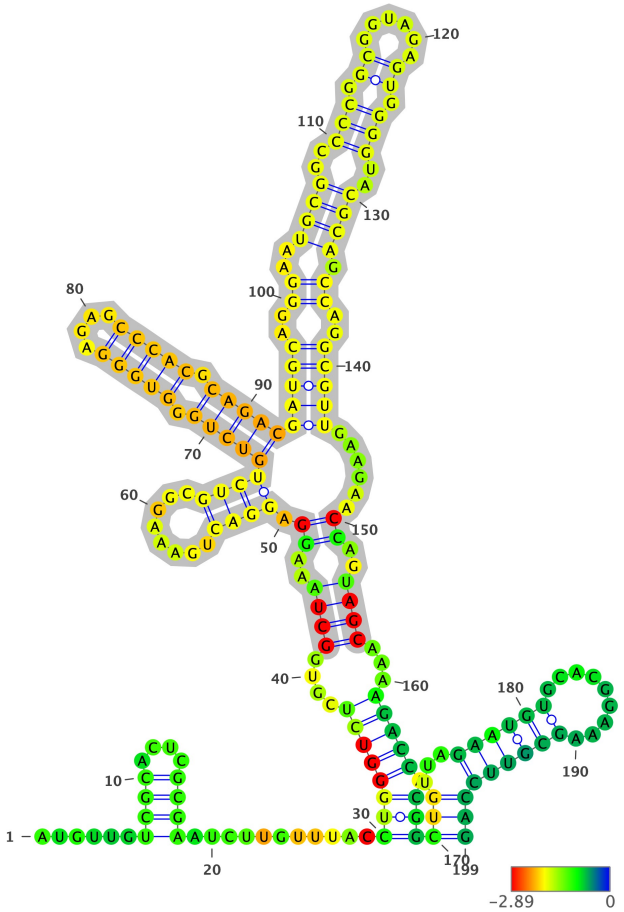
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 277 from nt 101204 to 101319 (nt 42 to 157)

```
5'-GCUAAAGGAGGACUGAAAGGCGUCUGUCUGGGUGGGAGAGCCCACGCAGACGAUGCAGGGAAUGCGGCCCCGGCGGUAGAGUGGGGUACGCAGCCAGGCGUUGAAGAACCA
GUAGC-3'
5'-(((....(................(((((.(((((....)))))).)))))..............................................................).
..)))-3'
Motif MFE = -51.2; z-score = -3.86; ED = 8.79
```



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 101163 to 101361 (motif highlighted in silver):

```
5'-AUGUUGUCGCACUCGCGAAUCUUGUUUACCUGGGUCUCGUGGCUAAAGGAGGACUGAAAGGCGUCUGUCUGGGUGGGAGAGCCCACGCAGACGAUGCAGGGAAUGCGGCCC
CGGCGGUAGAGUGGGGUACGCAGCCAGGCGUUGAAGAACCAGUAGCAAAAGACCACGGCUGUUAGAAUGUGCACGGAAAGCGUUCCAG-3
5'-......((((....))))..........(((((((((....((((..((.((((........)))))(((((.(((((....)))))).)))))(((((..((..(((((..((
(.(((.....)).)))..)))).)).)..)))))......)).)))))...)))))).)))((((...((((((.........)))))))))-3'
MFE = -71.0; z-score = -0.94; ED = 25.18
```

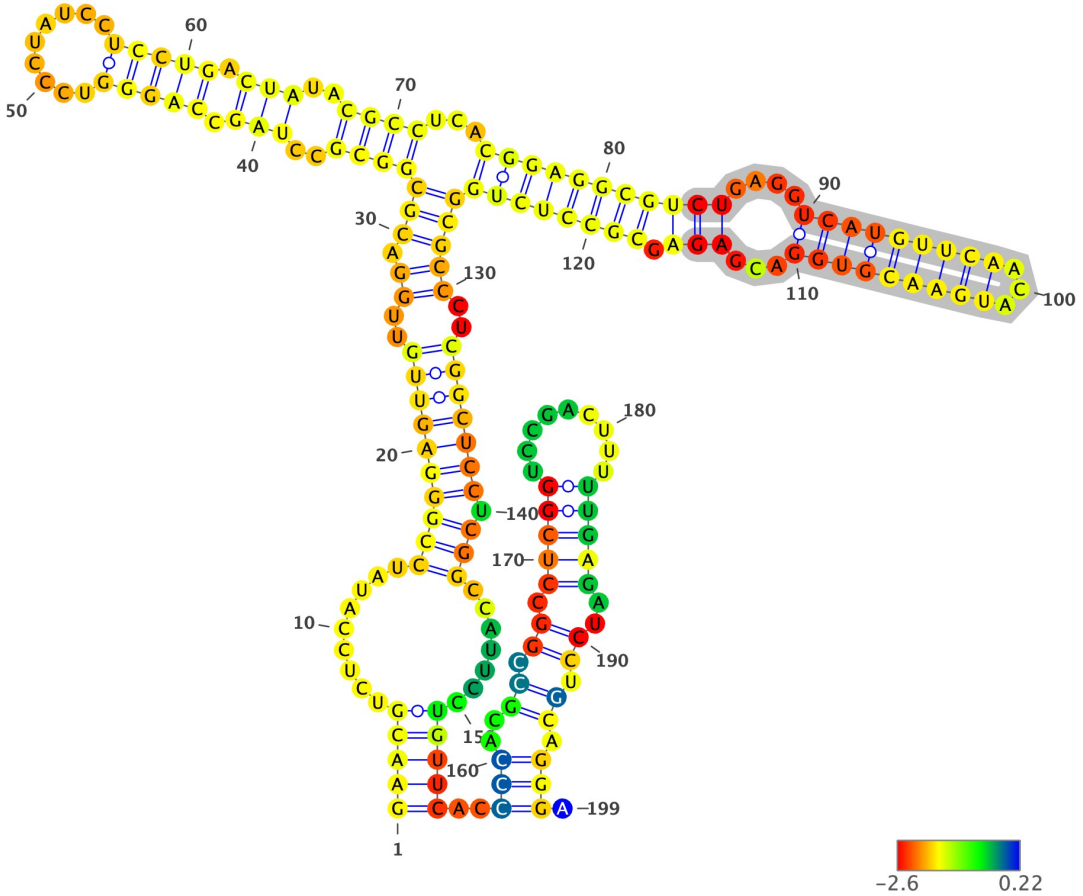
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 278 from nt 101908 to 101939 (nt 84 to 115)

```
5'-CUGAGGUCAUGUUCAACAUGAACGUGGACGAG-3'
5'-((....((((.............))))...))-3'
Motif MFE = -9.0; z-score = -1.89; ED = 3.56
```



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

Extracted structure model with flanking nucleotides 101825 to 102023 (motif highlighted in silver):

```
5'-GAACGUCUCCAUAUCCGGGAGUUGUUGGACGCGGCGCCUAGCCAGGGUCCCUAUCCUCCUGACUAUACGCCUCACGGAGGCGUCUGAGGUCAUGUUCAACAUGAACGUGGA
CGAGAGCGCCUCUGGCGCCCUCGGCUCCUCGGCCAUUCCUGUUCACCCCACGCCGGCCUCGGUCCGACUUUUUGAGAUCCUGCAGGGA-3
5'-(((((.........((((((((((..((.(((((((..(((.(((((.........)))))).)))..)))))...((((((((((....(((((((((...)))))))))).
..))).))))))))))))..)))))))).)))......)))))..((((..((.((.(((((.........)))))..)).)).)))).-3'
MFE = -77.3; z-score = -1.88; ED = 12.61
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BBRF1, 101588-104502(+)

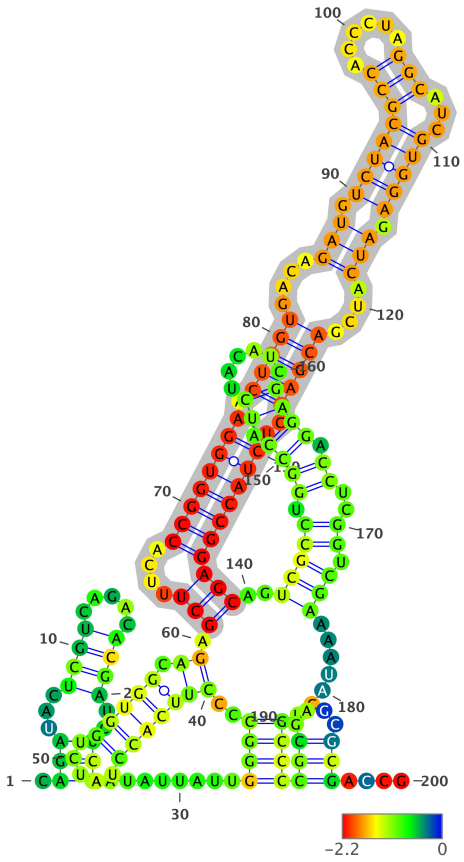
Attributes: ['ID=gene-HHV4_BBRF1', 'Dbxref=GeneID:3783764', 'Name=BBRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF1']

3-- nt 92 to 199--CDS, cds-YP_401682.1, 101916-103757(+)

Attributes: ['ID=cds-YP_401682.1', 'Parent=gene-HHV4_BBRF1', 'Dbxref=UniProtKB/TrEMBL:Q777D6,Genbank:YP_401682.1,GeneID:3783764', 'Name=YP_401682.1', 'gbkey=CDS', 'gene=BBRF1', 'locus_tag=HHV4_BBRF1', 'product=capsid portal protein', 'protein_id=YP_401682.1']

NC_007605.1 (forward strand): Structure number 279 from nt 103511 to 103589 (nt 61 to 139)

```
5'-GCUUUCACCGGUGGAACUCGUGACAGAUGUCUACGCCACCCUAGGCAUCGUGGAGAUCAUCGACGAGCUCUACCGGAGC-3'
5'-(((....(((((((((.......................................................)))))))))))-3'
Motif MFE = -35.5; z-score = -3.54; 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 103451 to 103650 (motif highlighted in silver):

```
5'-CAGAUACUCGUCAGACACGAUCUCUAUAUUAUUGGGCCCCUUCACCUAUCUGGUGGCAGAGCUUUCACCGGUGGAACUCGUGACAGAUGUCUACGCCACCCUAGGCAUCGU
GGAGAUCAUCGACGAGCUCUACCGGAGCAGUCGCCUGGCCAUCUACAUCGAGGACCUCGGUCGAAAAUACUGCCCCGCGAGCGCGACCG-3
5'-.(((...((((.....))))..))).......((((..(((((((.....))))).)).(((....((((((((.((((((....(((.(((((((.....)))).)))
))).)))....)))))).))))))))))..(((((.((((.((.....)))).))..)).))).))).....))))(((....)))).....-3'
MFE = -64.3; z-score = -0.88; ED = 40.34
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BBRF1, 101588-104502(+)

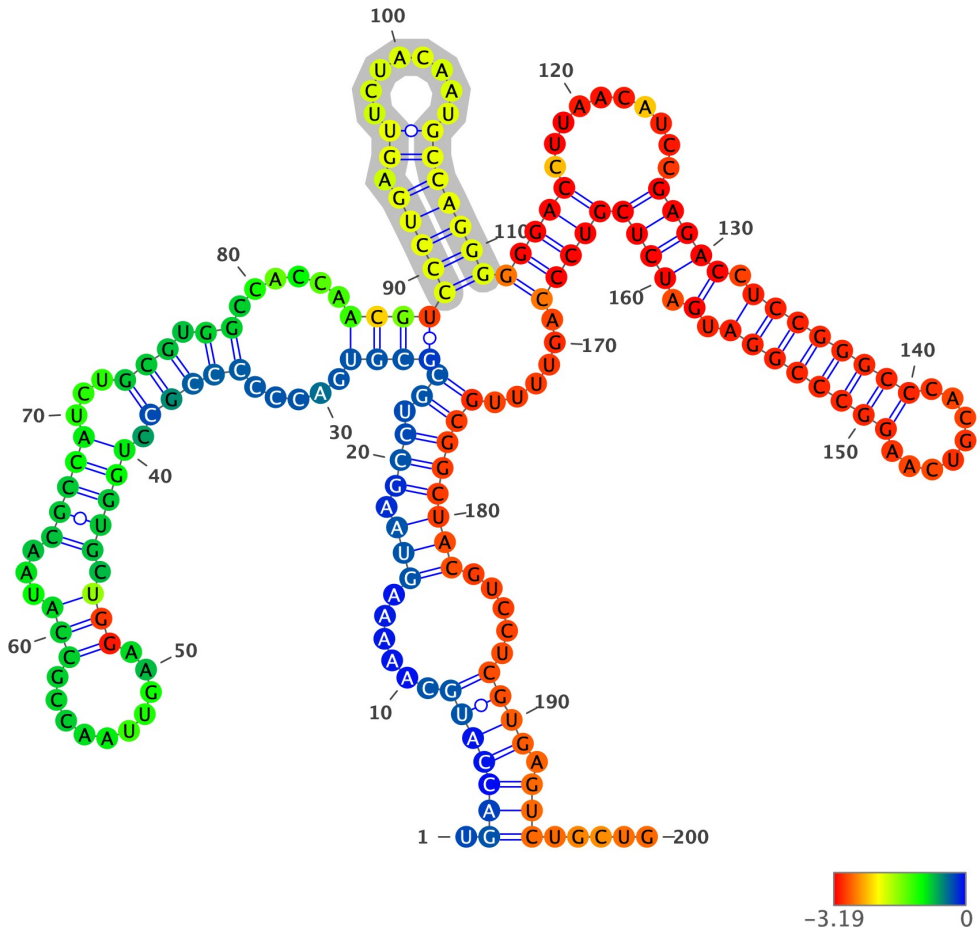
Attributes: ['ID=gene-HHV4_BBRF1', 'Dbxref=GeneID:3783764', 'Name=BBRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF1']

3-- nt 1 to 200--CDS, cds-YP_401682.1, 101916-103757(+)

Attributes: ['ID=cds-YP_401682.1', 'Parent=gene-HHV4_BBRF1', 'Dbxref=UniProtKB/TrEMBL:Q777D6,Genbank:YP_401682.1,GeneID:3783764', 'Name=YP_401682.1', 'gbkey=CDS', 'gene=BBRF1', 'locus_tag=HHV4_BBRF1', 'product=capsid portal protein', 'protein_id=YP_401682.1']

NC_007605.1 (forward strand): Structure number 280 from nt 103791 to 103813 (nt 89 to 111)

```
5'-CCCUGAGUUCUACAAUGCCAGGG-3'
5'-(((((.((.......)))))))-3'
Motif MFE = -8.2; z-score = -2.56; 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 103703 to 103902 (motif highlighted in silver):

```
5'-UGACCAUGCAAAAAGUAAGCCUGCGCGUGACCCCCCGCCUGGUGCUGGAAGUUAACCGCCAUAACGCCAUCUGCGUGGCCACCAACGUCCCUGAGUUCUACAAUGCCAGGG
GGGACCUUAACAUCCGAGACCUCCGGGCCCACGUCAAGGCCCGGAUGAUCUCGUCCCAGUUUUGCGGCUACGUCCUCGUGAGUCUGCUG-3
5'-.(((((((.....(((.(((.((((((.....(((((.((((((.(((..........)))...)))))).....))).)).....)))))((((.((.......)))))))
(((((.........(((((.((((((((.......)))))))).).))))))))).....)))))))).....)))).))).....-3'
MFE = -69.1; z-score = -1.06; ED = 36.43
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BBRF1, 101588-104502(+)

Attributes: ['ID=gene-HHV4_BBRF1', 'Dbxref=GeneID:3783764', 'Name=BBRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF1']

3-- nt 1 to 55--CDS, cds-YP_401682.1, 101916-103757(+)

Attributes: ['ID=cds-YP_401682.1', 'Parent=gene-HHV4_BBRF1', 'Dbxref=UniProtKB/TrEMBL:Q777D6,Genbank:YP_401682.1,GeneID:3783764', 'Name=YP_401682.1', 'gbkey=CDS', 'gene=BBRF1', 'locus_tag=HHV4_BBRF1', 'product=capsid portal protein', 'protein_id=YP_401682.1']

4-- nt 1 to 200--gene, gene-HHV4_BBRF2, 103660-104502(+)

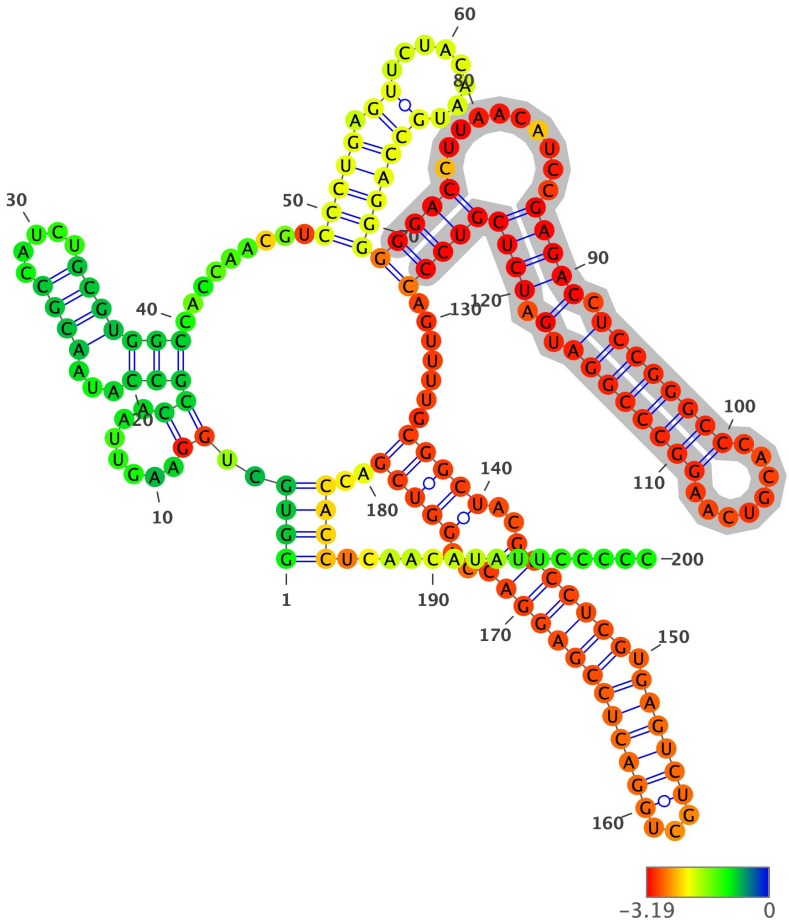
Attributes: ['ID=gene-HHV4_BBRF2', 'Dbxref=GeneID:3783686', 'Name=BBRF2', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF2']

5-- nt 1 to 200--CDS, cds-YP_401683.1, 103660-104496(+)

Attributes: ['ID=cds-YP_401683.1', 'Parent=gene-HHV4_BBRF2', 'Dbxref=UniProtKB/TrEMBL:Q777D5,Genbank:YP_401683.1,GeneID:3783686', 'Name=YP_401683.1', 'gbkey=CDS', 'gene=BBRF2', 'locus_tag=HHV4_BBRF2', 'product=tegument protein UL7', 'protein_id=YP_401683.1']

NC_007605.1 (forward strand): Structure number 281 from nt 103815 to 103869 (nt 73 to 127)

```
5'-GGACCUUAACAUCCGAGACCUCCGGGCCCACGUCAAGGCCCGGAUGAUCUCGUCC-3'
5'-(((((.........(((((.(((((((((.......)))))))))).).)))))))))-3'
Motif MFE = -24.5; z-score = -3.82; ED = 4.53
```



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 103743 to 103942 (motif highlighted in silver):

```
5'-GGUGCUGGAAGUUAACCGCCAUAACGCCAUCUGCGUGGCCACCAACGUCCCUGAGUUCUACAAUGCCAGGGGGGACCUUAACAUCCGAGACCUCCGGGCCCACGUCAAGGC
CCGGAUGAUCUCGUCCCAGUUUUGCGGCUACGUCCUCGUGAGUCUGCUGGACUCCGAGGACCAGGUCGACCACCUCAACAUAUUCCCCC-3
5'-(((((..(((.......)))((((...((((.....)))))))).........(((((.((........)))))))(((((..........(((((.(((((((((.......)))
)))))).).)))))))))).....(((((..(((((((.((((((...)))))))))))))))..)))))..))))...............-3'
MFE = -78.6; z-score = -3.08; ED = 20.03
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BBRF1, 101588-104502(+)

Attributes: ['ID=gene-HHV4_BBRF1', 'Dbxref=GeneID:3783764', 'Name=BBRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF1']

3-- nt 1 to 15--CDS, cds-YP_401682.1, 101916-103757(+)

Attributes: ['ID=cds-YP_401682.1', 'Parent=gene-HHV4_BBRF1', 'Dbxref=UniProtKB/TrEMBL:Q777D6,Genbank:YP_401682.1,GeneID:3783764', 'Name=YP_401682.1', 'gbkey=CDS', 'gene=BBRF1', 'locus_tag=HHV4_BBRF1', 'product=capsid portal protein', 'protein_id=YP_401682.1']

4-- nt 1 to 200--gene, gene-HHV4_BBRF2, 103660-104502(+)

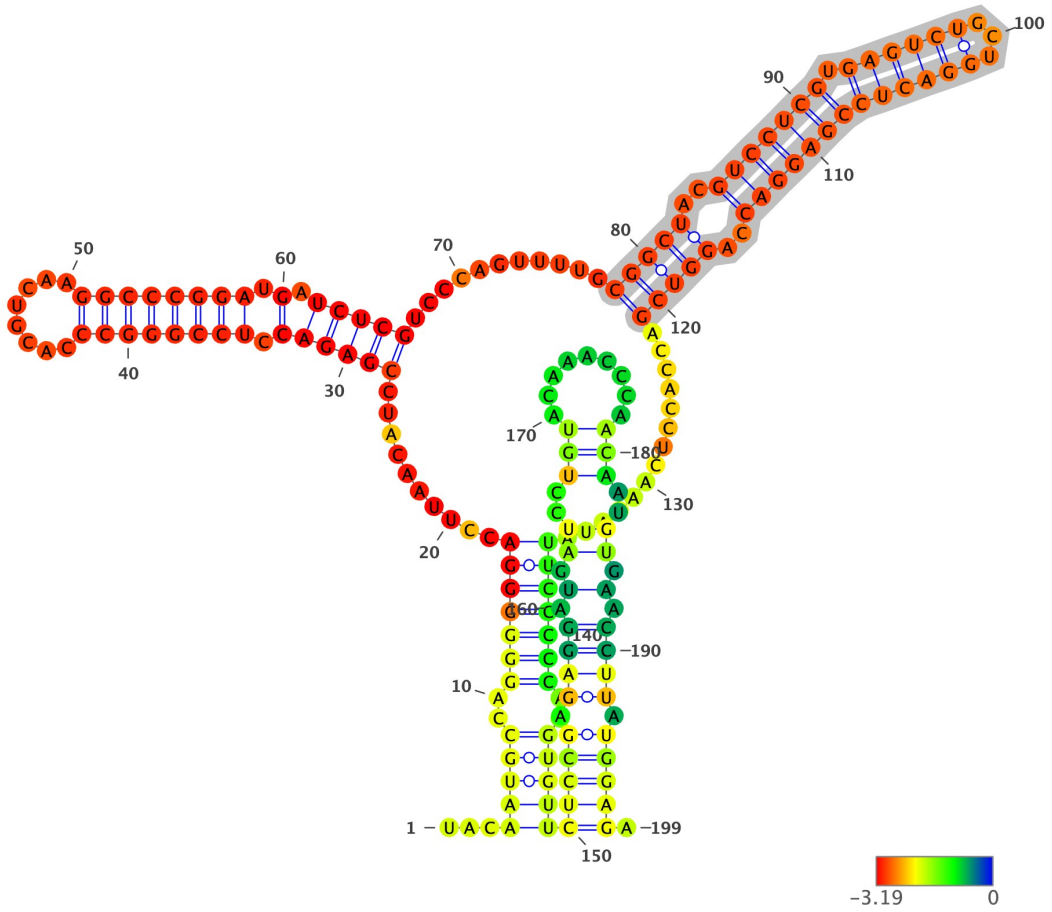
Attributes: ['ID=gene-HHV4_BBRF2', 'Dbxref=GeneID:3783686', 'Name=BBRF2', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF2']

5-- nt 1 to 200--CDS, cds-YP_401683.1, 103660-104496(+)

Attributes: ['ID=cds-YP_401683.1', 'Parent=gene-HHV4_BBRF2', 'Dbxref=UniProtKB/TrEMBL:Q777D5,Genbank:YP_401683.1,GeneID:3783686', 'Name=YP_401683.1', 'gbkey=CDS', 'gene=BBRF2', 'locus_tag=HHV4_BBRF2', 'product=tegument protein UL7', 'protein_id=YP_401683.1']

NC_007605.1 (forward strand): Structure number 282 from nt 103878 to 103921 (nt 78 to 121)

```
5'-CGGCUACGUCCUCGUGAGUCUGCUGGACUCCGAGGACCAGGUCG-3'
5'-(((((..(((((((.((((((...)))))))))))))..)))))-3'
Motif MFE = -26.2; z-score = -4.38; ED = 0.72
```



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

Extracted structure model with flanking nucleotides 103801 to 103999 (motif highlighted in silver):

```
5'-UACAAUGCCAGGGGGGACCUUAACAUCCGAGACCUCCGGGCCCACGUCAAGGCCCGGAUGAUCUCGUCCCAGUUUUGCGGCUACGUCCUCGUGAGUCUGCUGGACUCCGAG
GACCAGGUCGACCACCUCAACAUAUUCCCCCACGUGUUCUCCGAGAGGAUGAUCCUGUACAAACCCAACAAUGUGAACCUUAUGGAGA-3
5'-...(((((..(((((((.........((((((.(((((((.......)))))))).).)))))).........((((..(((((((.((((((...)))))))))))
)))..)))))............)))))))..)))))((((.((((.(.((..(((.........)))..)).).)))).)))))).-3'
MFE = -76.8; z-score = -4.07; ED = 15.32
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BBRF1, 101588-104502(+)

Attributes: ['ID=gene-HHV4_BBRF1', 'Dbxref=GeneID:3783764', 'Name=BBRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF1']

3-- nt 1 to 199--gene, gene-HHV4_BBRF2, 103660-104502(+)

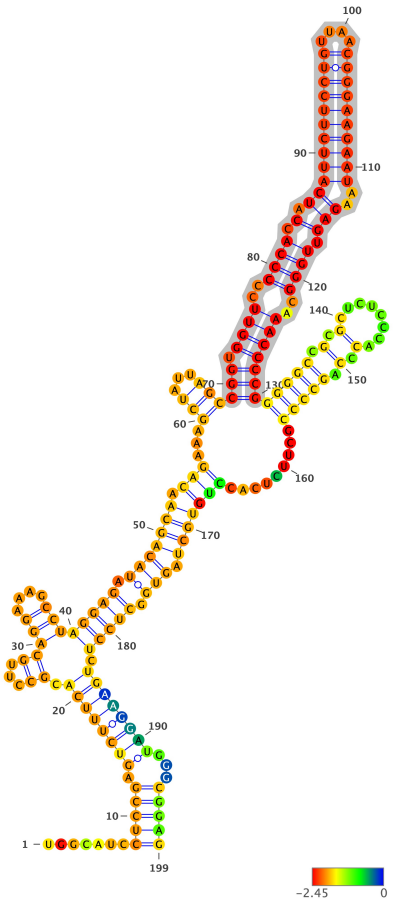
Attributes: ['ID=gene-HHV4_BBRF2', 'Dbxref=GeneID:3783686', 'Name=BBRF2', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF2', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF2']

4-- nt 1 to 199--CDS, cds-YP_401683.1, 103660-104496(+)

Attributes: ['ID=cds-YP_401683.1', 'Parent=gene-HHV4_BBRF2', 'Dbxref=UniProtKB/TrEMBL:Q777D5,Genbank:YP_401683.1,GeneID:3783686', 'Name=YP_401683.1', 'gbkey=CDS', 'gene=BBRF2', 'locus_tag=HHV4_BBRF2', 'product=tegument protein UL7', 'protein_id=YP_401683.1']

NC_007605.1 (forward strand): Structure number 283 from nt 105130 to 105191 (nt 69 to 130)

```
5'-CGGUGGUUCCCCCACCAUCAUUCUUCCUGUUAACGGGAAGAAUAAGAGUUGGGCAAACCCCG-3'
5'-(((.(((((..(((((.(.(((((((((((((....)))))))))))..)))).)))))..)))))))-3'
Motif MFE = -27.2; z-score = -4.48; ED = 4.49
```



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 105062 to 105260 (motif highlighted in silver):

```
5'-UGGCAUCCUCCGAGUCUUUCACGCCUUGCAGGAAAGCCUAGGAGAUACAGCAACAGAAAGCUAUUAGCCGGUGGUUCCCCCACCAUCAUUCUUCCUGUUAACGGGAAGAAU
AAGAGUUGGGCAAACCCCGGGGGCCGCGCUCUCCCACCCAGCCCCGCUUCUCACCUGUGCUAGUGGCUCCUCUGAAGGAUGGGCGGAG-3
5'-.......(((((.(((((((((.((...))))((....)))))))(((((.(((((((.((((...((((...)))))((.(((((..((((.(.((((((((((((....)))))))))))
..))).)))))..)))))))((((((.(.(........).).)))))........)))))))).))).)))))).))))))))...)))))-3'
MFE = -69.5; z-score = -1.38; ED = 30.51
```

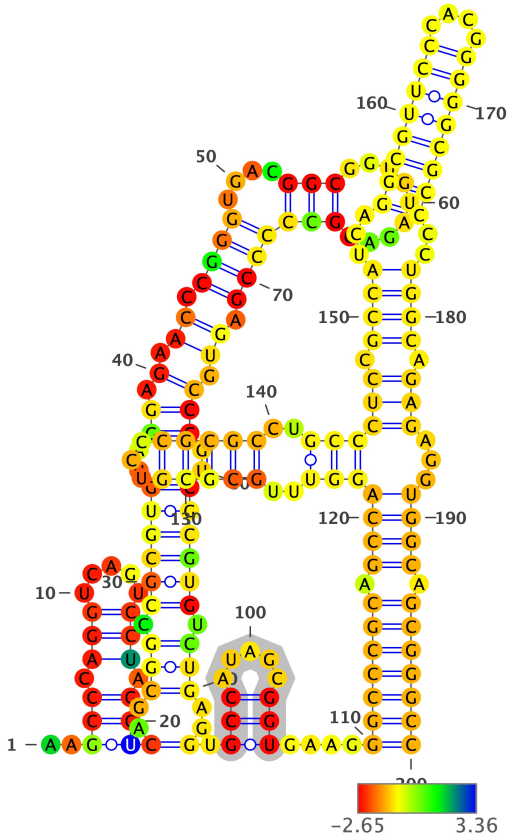
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 284 from nt 105392 to 105402 (nt 95 to 105)

```
5'-GCCAUAGCGGU-3'
5'-(((.....)))-3'
Motif MFE = -1.1; z-score = -1.6; 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 105298 to 105497 (motif highlighted in silver):

```
5'-AAGCCCAGGUCAGUCCUAGGUCAGCGGCCGCGUGUAGGAGAACCCGGGUGACGGCGGUGUAGAGGCCCCCGAGUGCCCGUCGCGUGUCUGAGGUGCCAUAGCGGUGAAGGG
CCCGCAGCCAGGUUUGCGCGUCCCGCGCCUGCCCUCCGCCAUCAGGCGUUCCCACGGGGGCGCCCCUGGCAGAGAGGUGGCAGCGGGCC-3
5'-..(((.((((.....)))).)))(..(((.(((((((..((.(.((.((((....(((.........)))))))).)).)))..)))))).)))..).((((.....)))....((
(((((.(((((((..((((((...)))))).))))((.((((...(((((((((....)))))))))..)))))).)))...)))))..)))))))-3'
MFE = -89.1; z-score = 1.04; ED = 38.62
```

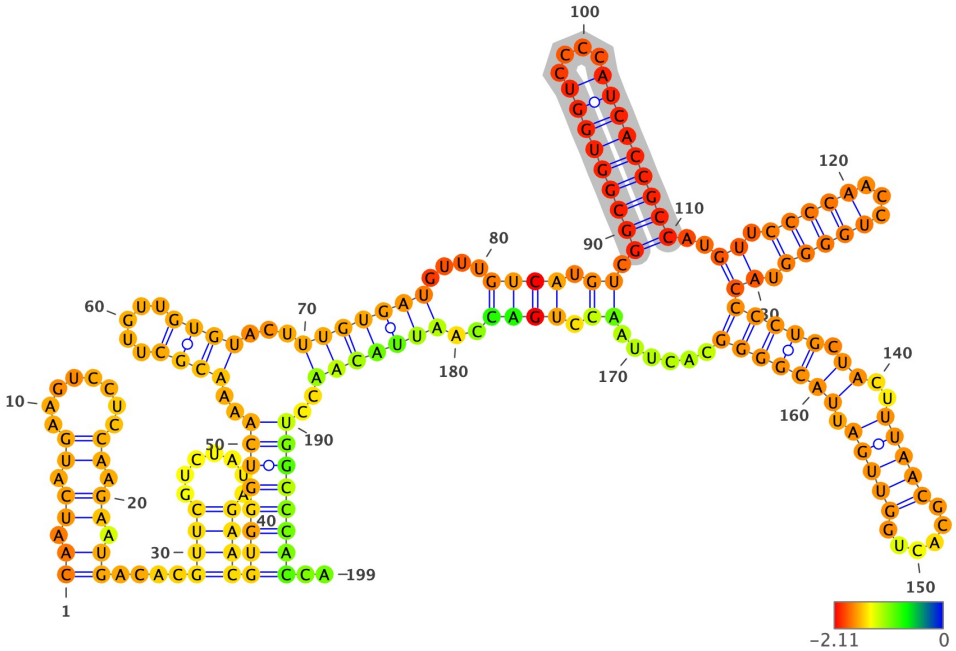
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 285 from nt 106932 to 106953 (nt 89 to 110)

```
5'-GGCGGUGGUCCCCAUCACCGCC-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -14.1; z-score = -3.41; 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 106844 to 107042 (motif highlighted in silver):

```
5'-CAAUCAUGAAGUCCUCCAAGAAUGACACGUUCGUCUAUAGAACGUGGGUCAAAACGCUUGUUGUGUACUUUGUGAUGUUUGUCAUGUCGGCGGUGGUCCCCAUCACCGCCA
UGUUCCCCAACCUGGGGUACCCCUGCUACUUUAACGCACUGGUUGAUUACGGGGCACUUAACCUGACCAAUUACAACCUGGCCCACCA-3
5'-((.((.((........)).)).)).....((((.......))))((((((((..((((.....)))).....(((((((.....((((.((.(((((((((....)))))))))).
.((.((((...)))))).))((((((.((..((((((.....)))))).)))))))).....)).)))))..)))))))..))))))))..-3'
MFE = -60.4; z-score = -2.83; ED = 38.37
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BBRF3, 106693-108075(+)

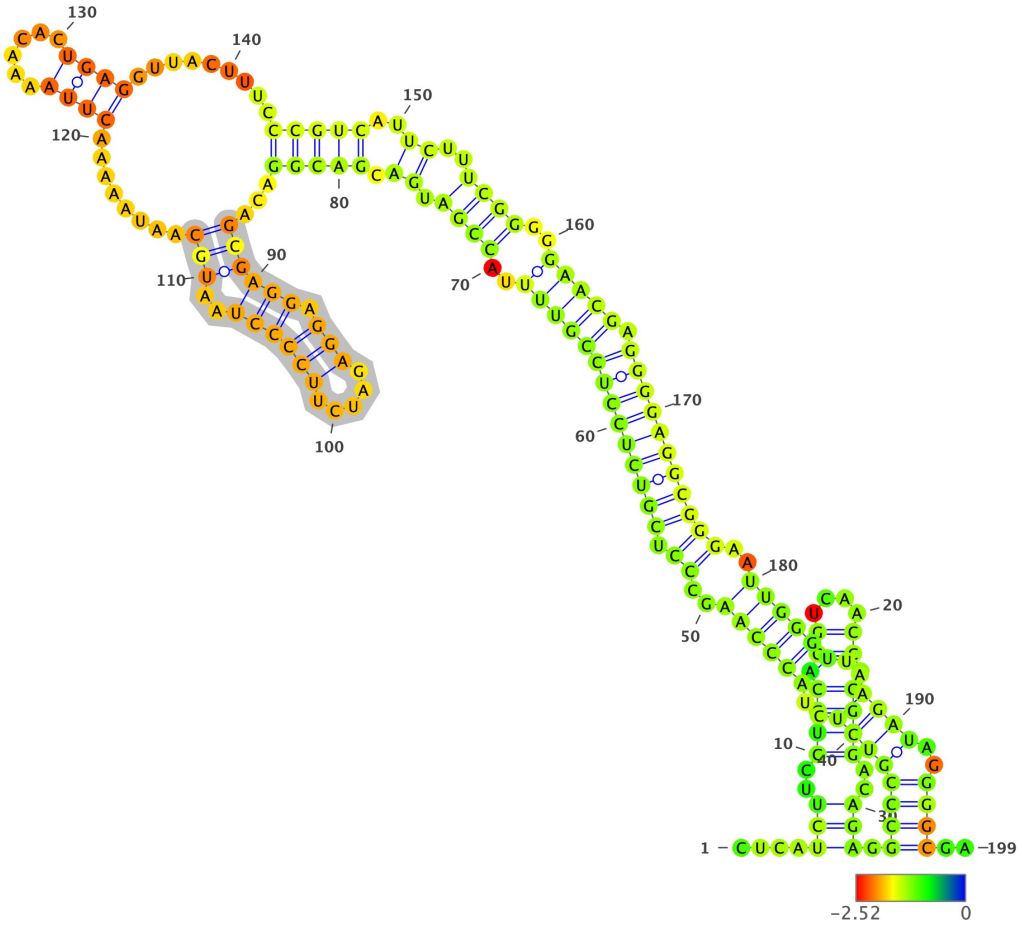
Attributes: ['ID=gene-HHV4_BBRF3', 'Dbxref=GeneID:3783687', 'Name=BBRF3', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF3', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF3']

3-- nt 6 to 199--CDS, cds-YP_401685.1, 106849-108066(+)

Attributes: ['ID=cds-YP_401685.1', 'Parent=gene-HHV4_BBRF3', 'Dbxref=UniProtKB/TrEMBL:Q777D4,Genbank:YP_401685.1,GeneID:3783687', 'Name=YP_401685.1', 'gbkey=CDS', 'gene=BBRF3', 'locus_tag=HHV4_BBRF3', 'product=envelope glycoprotein M', 'protein_id=YP_401685.1']

NC_007605.1 (forward strand): Structure number 286 from nt 108044 to 108069 (nt 87 to 112)

```
5'-GCGAGGAGGAGAUCUUCCCCUAAUGC-3'
5'-(.(....................).)-3'
Motif MFE = -6.4; z-score = -1.1; 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 107958 to 108156 (motif highlighted in silver):

```
5'-CUCAUCUUCCUCCAGGUCAACCAGGAGACAGAGGCCCGUCUCUACCCAAGCCCUCGUCUCCUCCGUUUUACCGAUGACGACGGACAGCGAGGAGGAGAUCUUCCCCUAAUG
CAAUAAAAACUUAAAACACUGAGGUUACUUUCCCGUCAUUCUUUCGGGGGAACGAGGGGAGGCGGGAAUUGGGUUAAGAUAGGGGCGA-3
5'-....(((..((((.((....)).)))).)).)).(((((((..((((((..((.(((((((((((((..(((((.((.(((((...((((((.((.....)))))))..))
)........(((.....)))).........)))))..))..)))))..)))))).))))))))))..)))))).))))..)))))..-3'
MFE = -78.9; z-score = -4.01; ED = 21.79
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 118--gene, gene-HHV4_BBRF3, 106693-108075(+)

Attributes: ['ID=gene-HHV4_BBRF3', 'Dbxref=GeneID:3783687', 'Name=BBRF3', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF3', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF3']

3-- nt 1 to 109--CDS, cds-YP_401685.1, 106849-108066(+)

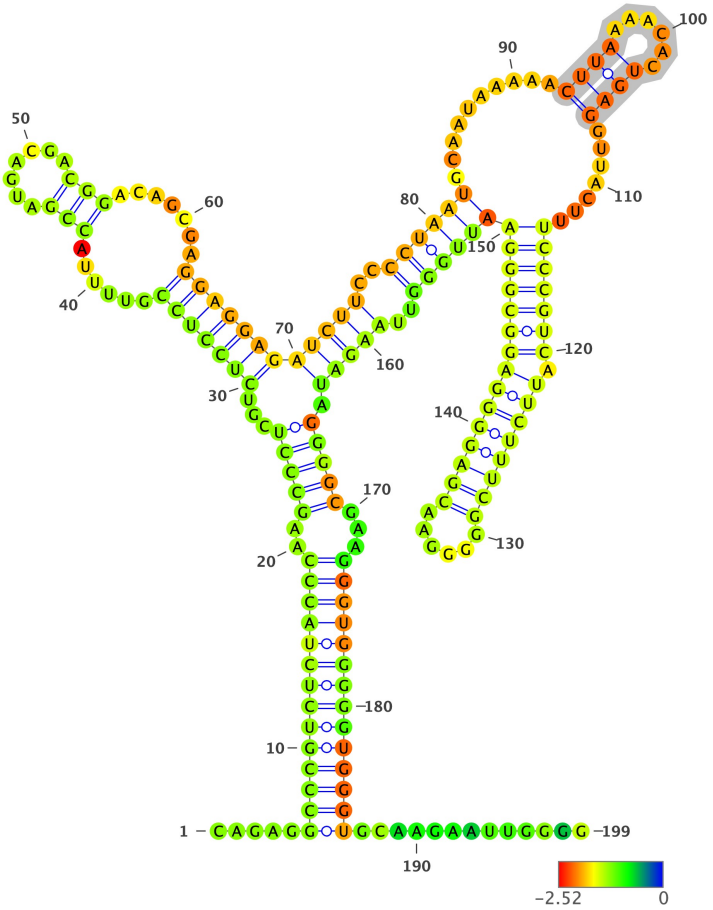
Attributes: ['ID=cds-YP_401685.1', 'Parent=gene-HHV4_BBRF3', 'Dbxref=UniProtKB/TrEMBL:Q777D4,Genbank:YP_401685.1,GeneID:3783687', 'Name=YP_401685.1', 'gbkey=CDS', 'gene=BBRF3', 'locus_tag=HHV4_BBRF3', 'product=envelope glycoprotein M', 'protein_id=YP_401685.1']

4-- nt 113 to 118--polyA_signal_sequence, id-HHV4_BBRF3-3, 108070-108075(+)

Attributes: ['ID=id-HHV4_BBRF3-3', 'Dbxref=GeneID:3783687', 'gbkey=regulatory', 'gene=BBRF3', 'locus_tag=HHV4_BBRF3', 'regulatory_class=polyA_signal_sequence']

NC_007605.1 (forward strand): Structure number 287 from nt 108078 to 108091 (nt 93 to 106)

```
5'-CUUAAAACACUGAG-3'
5'-((((.....))))-3'
Motif MFE = 0.0; z-score = 0.23; ED = 1.79
```



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

Extracted structure model with flanking nucleotides 107986 to 108184 (motif highlighted in silver):

```
5'-CAGAGGCCCGUCUCUACCCAAGCCCUCGUCUCCUCCGUUUUACCGAUGACGACGGACAGCGAGGAGGAGAUCUUCCCCUAAUGCAAUAAAAACUUAAAACACUGAGGUUAC
UUUCCCGUCAUUCUUUCGGGGGAACGAGGGGAGGCGGGAAUUGGGUUAAGAUAGGGGCGAAGGGUGGGGGUGGGUGCAAGAAUUGGGG-3
5'-.....(((((((((((((..((((((...(((((((.......((((.......)))).......)))))))((((((..((((((..........((((......)))).....
..(((((((.((((((((.....)))))))))))))))))))))..)))))).)))))...))))))))))))))).............-3'
MFE = -77.3; z-score = -2.8; ED = 21.99
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 90--gene, gene-HHV4_BBRF3, 106693-108075(+)

Attributes: ['ID=gene-HHV4_BBRF3', 'Dbxref=GeneID:3783687', 'Name=BBRF3', 'Note=core gene', 'gbkey=Gene', 'gene=BBRF3', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BBRF3']

3-- nt 1 to 81--CDS, cds-YP_401685.1, 106849-108066(+)

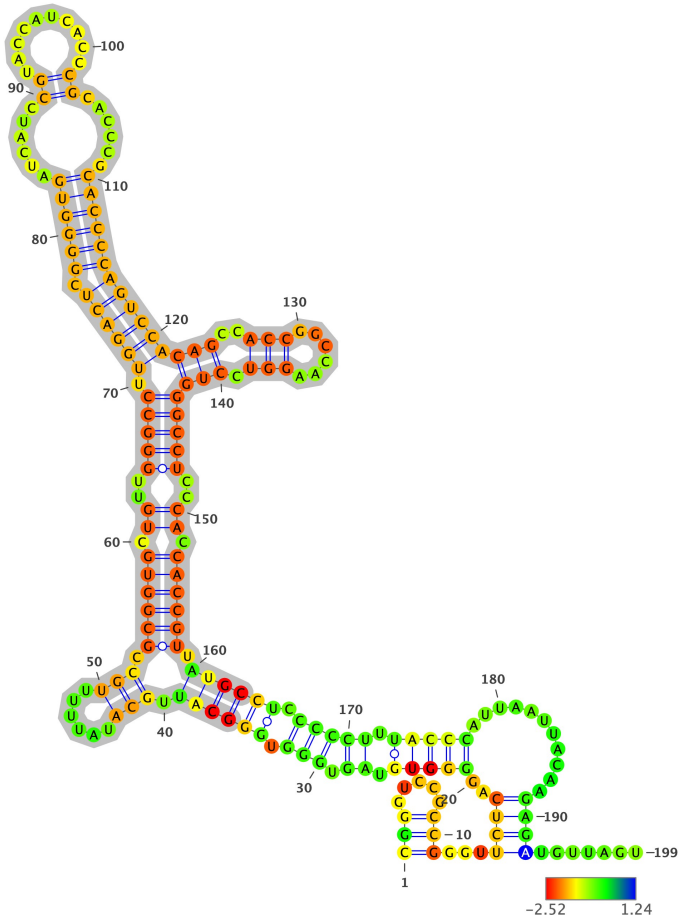
Attributes: ['ID=cds-YP_401685.1', 'Parent=gene-HHV4_BBRF3', 'Dbxref=UniProtKB/TrEMBL:Q777D4,Genbank:YP_401685.1,GeneID:3783687', 'Name=YP_401685.1', 'gbkey=CDS', 'gene=BBRF3', 'locus_tag=HHV4_BBRF3', 'product=envelope glycoprotein M', 'protein_id=YP_401685.1']

4-- nt 85 to 90--polyA_signal_sequence, id-HHV4_BBRF3-3, 108070-108075(+)

Attributes: ['ID=id-HHV4_BBRF3-3', 'Dbxref=GeneID:3783687', 'gbkey=regulatory', 'gene=BBRF3', 'locus_tag=HHV4_BBRF3', 'regulatory_class=polyA_signal_sequence']

NC_007605.1 (forward strand): Structure number 288 from nt 108300 to 108427 (nt 36 to 163)

```
5'-GCAUUGCAUAUUUUUGCCGCGGUGCUGUUGGGCCUUGGACUCGGGGUGAUCAUCCGUACCAUCACCCGCACCCGCACCCCAGUCCACAGCCACCGGCCAAGGUCCUGGGCC
UCCCACCACCGUUAUGC-3'
5'-((...............((((((.((..((((((.....................................................((((..((((......)))).)))))))
))..)).)))))))...))-3'
Motif MFE = -45.2; z-score = -1.81; ED = 27.01
```



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 108265 to 108463 (motif highlighted in silver):

```
5'-CGGGUCCGCCGGGUUCUCAGGGGUGUAGUGGGUGGGCAUUGCAUAUUUUUGCCGCGGUGCUGUUGGGCCUUGGACUCGGGGUGAUCAUCCGUACCAUCACCCGCACCCGCA
CCCCAGUCCACAGCCACCGGCCAAGGUCCUGGGCCUCCCACCACCGUUAUGCCUCCCCCUUUACCCAUUAAUUACAAGAGAUGUUAGU-3
5'-((.....)))...((((..(((((.((.(((.((((((.(((.....)))).((((((.((..(((((.((((((.((((((.....((..........)).....))
)))))))))))((..(((.....))).)))))))..)).)))))).)))))).)))))).....))))........-3'
MFE = -71.5; z-score = -1.38; ED = 15.87
```

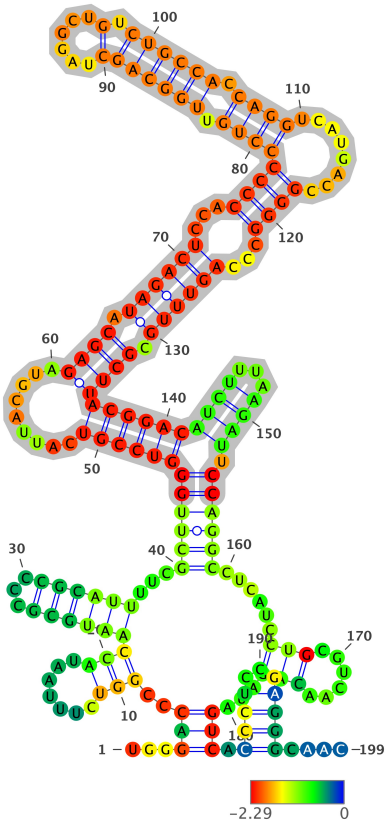
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 289 from nt 109068 to 109179 (nt 44 to 155)

```
5'-GGGUCCGUCAUUACGUAGAGCAUAGACUCCACCCCCCUGUUGGCAGCUAGGCUGUCUGCCACCAGGUCAUGACCGGGGCCCAGUUUGCGCUUACGGACAUCUUUAAGAUUC
C-3'
5'-(((((((.........((((.(((((((...((((.........................................)))).....)))))))..)))))))))))............
))-3'
Motif MFE = -39.7; z-score = -1.91; ED = 4.4
```



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 109025 to 109223 (motif highlighted in silver):

```
5'-UGGGACCCGGUCUUUAAUACCAAUGCGCCCCGCAUUUUCGCUUGGGUCCGUCAUUACGUAGAGCAUAGACUCCACCCCCCUGUUGGCAGCUAGGCUGUCUGCCACCAGGUC
AUGACCGGGGCCCAGUUUGCGCUUACGGACAUCUUUAAGAUUCCAGGCCUCAUCCUGCGUCAACAGAUAGUCACCCUCCGAGGGCAAC-3
5'-...(((..(((.......)))(((((((...)))))))...((((((((((((.........((((.((((((...((((((((.(((((((......).)))))).)))))..
......)))).....)))))).))))))))))((((...)))).)))))).....(((.....)))...))).((((...)))).....-3'
MFE = -60.1; z-score = -1.94; ED = 17.92
```

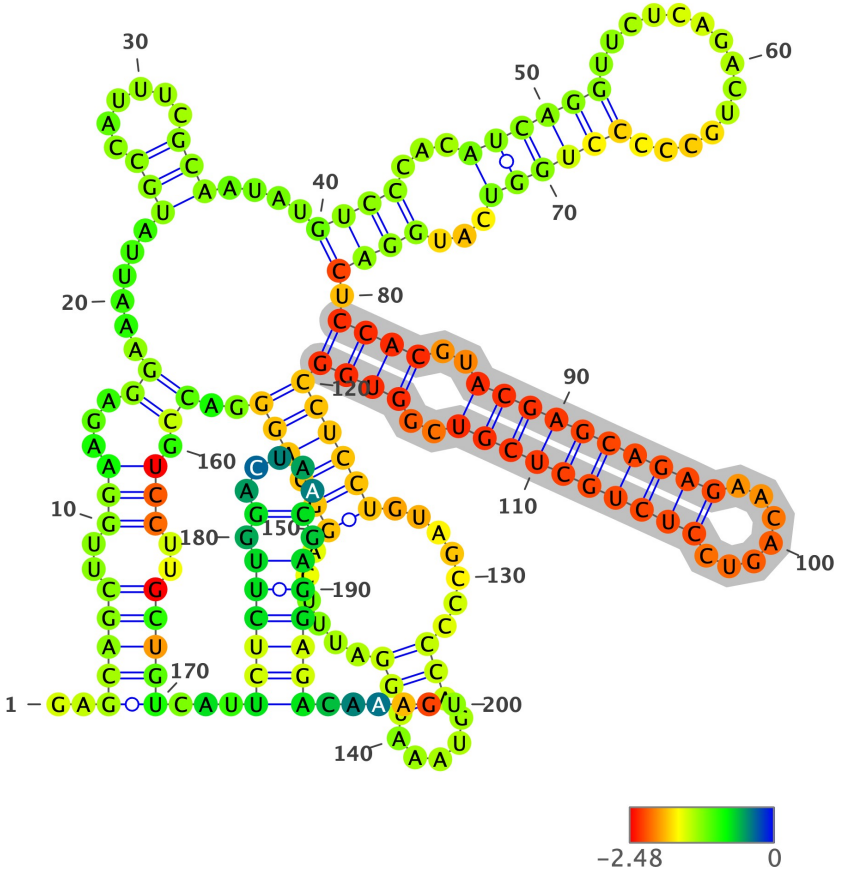
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 290 from nt 109735 to 109773 (nt 81 to 119)

```
5'-CCACGUACGAGCAGAGAACAGUCCUCUGCUCGUCGGUGG-3'
5'-(((((..((((((((((.......)))))))))))..)))))-3'
Motif MFE = -24.1; z-score = -5.05; 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 109655 to 109854 (motif highlighted in silver):

```
5'-GAGCAGCUUGGAAGAGGAAAUUAUGCCAUUUCGCAAUAUGUCCCACAUCAGGUUCUCAGACUGCCCCCUGGUCAUGGACUCCACGUACGAGCAGAGAACAGUCCUCUGCUC
GUCGGUGGCCUCCUGUAGCCCCCAGUAAAUGGAUUUCAGGGAGGGACCGUCCUUGCUGUCAUUCUCUUGGACUAACGAGGAGACAAAGU-3
5'-..((((((..(((...((......(((......)))....(((((...((((((.............)))))))...)))))).(((((..((((((((((.......))))))))
))..))))((((((.......(((.....)))......)))))))..)).))))..)))))...((((((.(.....).)))))).....-3'
MFE = -69.0; z-score = -2.34; ED = 43.45
```

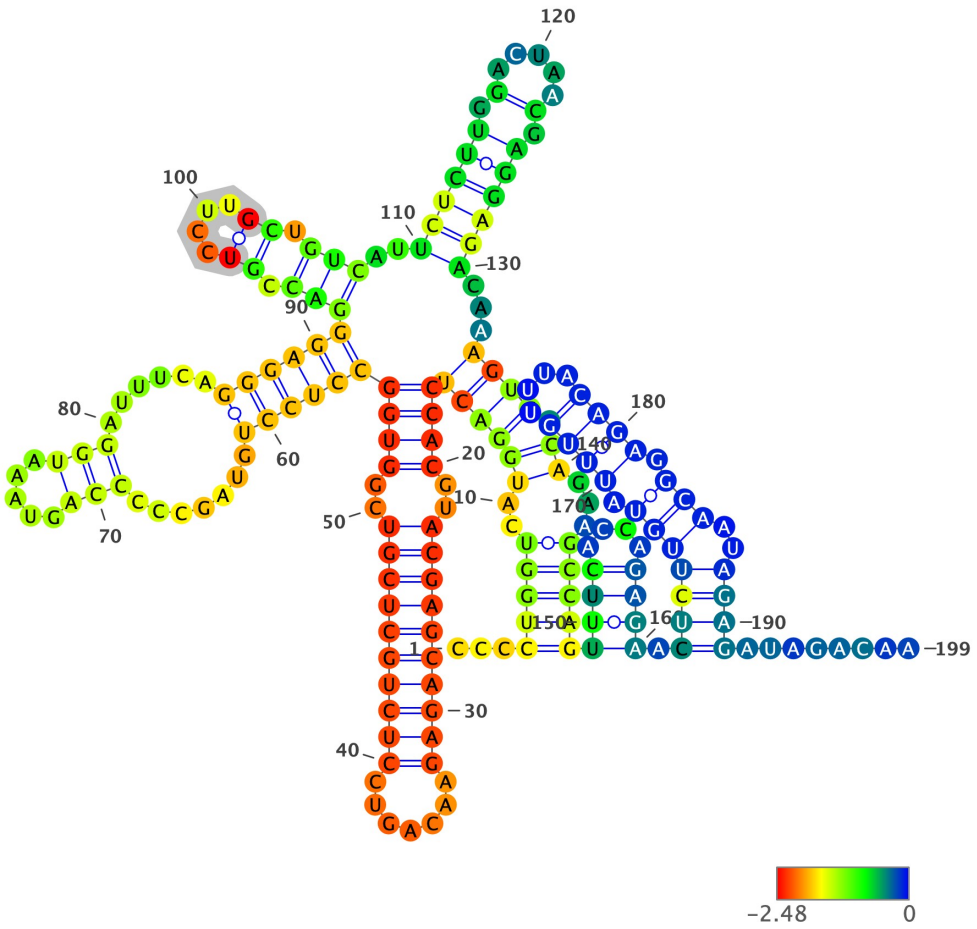
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 291 from nt 109815 to 109820 (nt 97 to 102)

```
5'-UCCUUG-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 109719 to 109917 (motif highlighted in silver):

```
5'-CCCCUGGUCAUGGACUCCACGUACGAGCAGAGAACAGUCCUCUGCUCGUCGGUGGCCUCCUGUAGCCCCCAGUAAAUGGAUUUCAGGGAGGGACCGUCCUUGCUGUCAUUC
UCUUGGACUAACGAGGAGACAAAGUCACAGAAGCCAGUUUCACCAGAGAACUCUUGUAUUUGUUUACAGAGGCAAUAGAGAUAGACAA-3
5'-...((((((..((((((((((..((((((((((.......))))))))))..))))((((((.......(((.....)))).....)))))))((.((....)).)))..((
((((.(.....).)))))).))...)))))((((....)))).(((((((.((((....)))).)))..))))........-3'
MFE = -64.4; z-score = -2.05; ED = 28.65
```

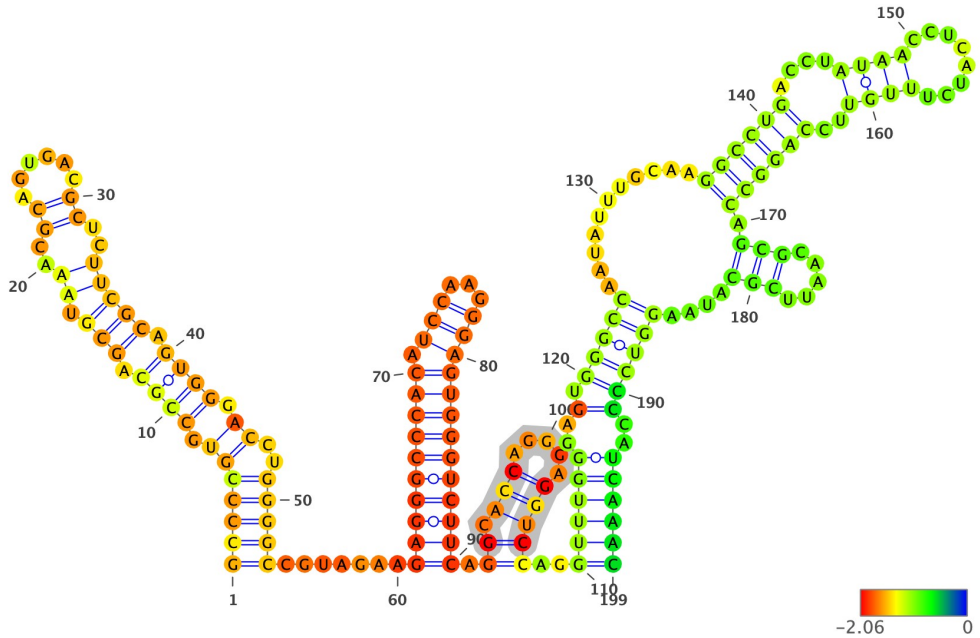
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 292 from nt 112183 to 112196 (nt 93 to 106)

```
5'-GCACCAGGGAGGUC-3'
5'-(...(.....)..)-3'
Motif MFE = -1.4; z-score = -0.13; ED = 0.8
```



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

Extracted structure model with flanking nucleotides 112091 to 112289 (motif highlighted in silver):

```
5'-GCCCCGUGCCGCAGCGUAAACGCAGUGACGCUCUUCGCAGUGGGACCUGGGGCCGUAGAAGAGGGCCCACAUCCAAGGGAGUGGGUCUUCAGGCACCAGGGAGGUCCAGGU
UUGGGAGUGGGCCAAUAUUUGCAAGGCCUGACCUAUAACCUCAUCUUUGUUCCAGGCCAGCGCAAUUCGCAUAAGGUCCCCAUCAAAC-3
5'-(((((((.((((.(((.((..((.....)).)))))).)))).)).)))))).....((((((((((.(((...)))))))))))))).((.((((.....)))))..((
((((..(.(((((.........((((((....((((.......))))).)))))).)))))).(((.....)))....)))))).)))))))-3'
MFE = -72.6; z-score = -1.29; ED = 45.25
```

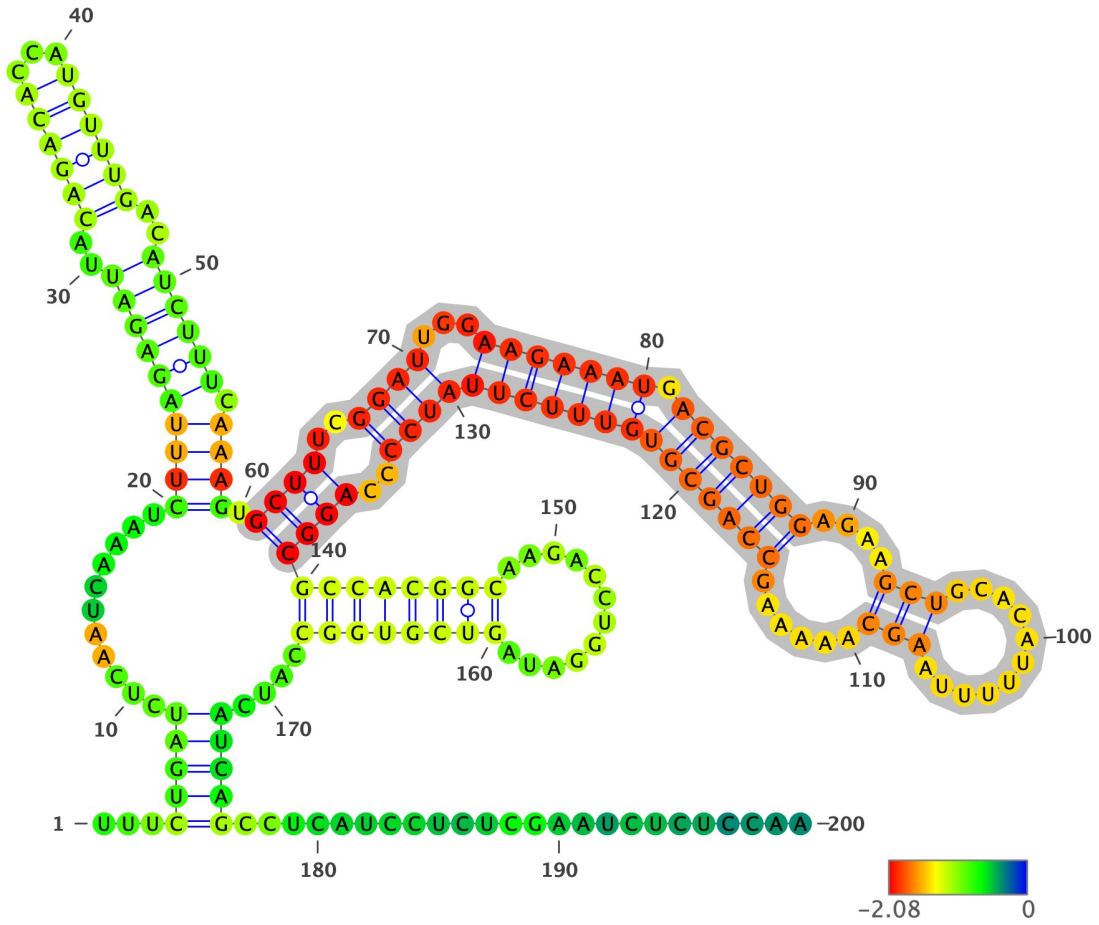
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 293 from nt 113256 to 113334 (nt 61 to 139)

```
5'-GCUUUCGGAUUGGAAGAAAUGACGCUGGAGAAGCUGCACAUUUUUAAGCAAAAAGCCAGCGUGUUUCUUAUCCCCAGGC-3'
5'-((((.........(.......................................................).......))))-3'
Motif MFE = -25.3; z-score = -2.85; 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 113196 to 113395 (motif highlighted in silver):

```
5'-UUUCUGAUCUCAAUCAAAUCUUUAGAGAUUACAGACACCAUGUUUGACAUCUUUCAAAGUGCUUUCGGAUUGGAAGAAAUGACGCUGGAGAAGCUGCACAUUUUUAAGCAA
AAAGCCAGCGUGUUUCUUAUCCCCAGGCGCCACGGCAAGACCUGGAUAGUCGUGGCCAUCAUCAGCCUCAUCCUCUCGAAUCUCUCCAA-3
5'-...(((((...........((((((((((..((((((...)))))).)))))).))))).(((((..(((((...(((((((.((((((....(((...........)))).
....))))))))))))))))..))))((((((((.............)))))))....)))))).......................-3'
MFE = -52.6; z-score = -2.26; ED = 16.43
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

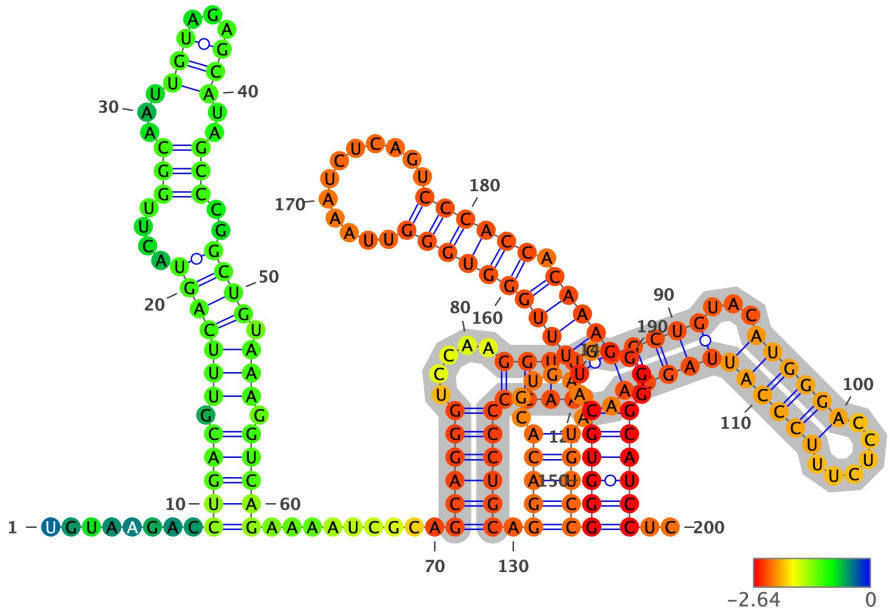
Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

3-- nt 1 to 200--CDS, cds-YP_401690.1, 112650-113585(+)

Attributes: ['ID=cds-YP_401690.1', 'Parent=gene-HHV4_BGRF1/BDRF1', 'Dbxref=UniProtKB/TrEMBL:Q777C9,Genbank:YP_401690.1,GeneID:3783767', 'Name=YP_401690.1', 'gbkey=CDS', 'gene=BGRF1/BDRF1', 'locus_tag=HHV4_BGRF1/BDRF1', 'product=DNA packaging terminase subunit 1', 'protein_id=YP_401690.1']

NC_007605.1 (forward strand): Structure number 294 from nt 113655 to 113713 (nt 71 to 129)

```
5'-GCAGGGUCCAAGGUUGUGCUGUACAUGGGACCUCUUUCCCAUUAGCAAGAACCCCCUGC-3'
5'-((((((.....((((.((((((...(((((((......)))))))))))..)))))))))))-3'
Motif MFE = -25.4; z-score = -3.77; 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 113585 to 113784 (motif highlighted in silver):

```
5'-UGUAAGACCUGACGUUUCAGUACUUGGCAAUUGUAGAGCAUAGCCCGGCUGUAAAGGUCAGAAAAUCGCAGCAGGGUCCAAGGUUGUGCUGUACAUGGGACCUCUUUCCCA
UUAGCAAGAACCCCCUGCAGGACACGUGACAUGUCCGGGUGCAUUUUGGGUGGGUUAAAUCUCAGUCCCACCACAAAGGGGGCAUCCUC-3
5'-........(((((.(((((((....(((...(((...)))..)))..)))).))).)))))........((((((.....((((.(((((...((((((......)))))
))))))..))))))))))).(((((.......)))))((((((.((((((((((.............)))))).)))))...)))))))..-3'
MFE = -73.7; z-score = -3.17; ED = 8.09
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

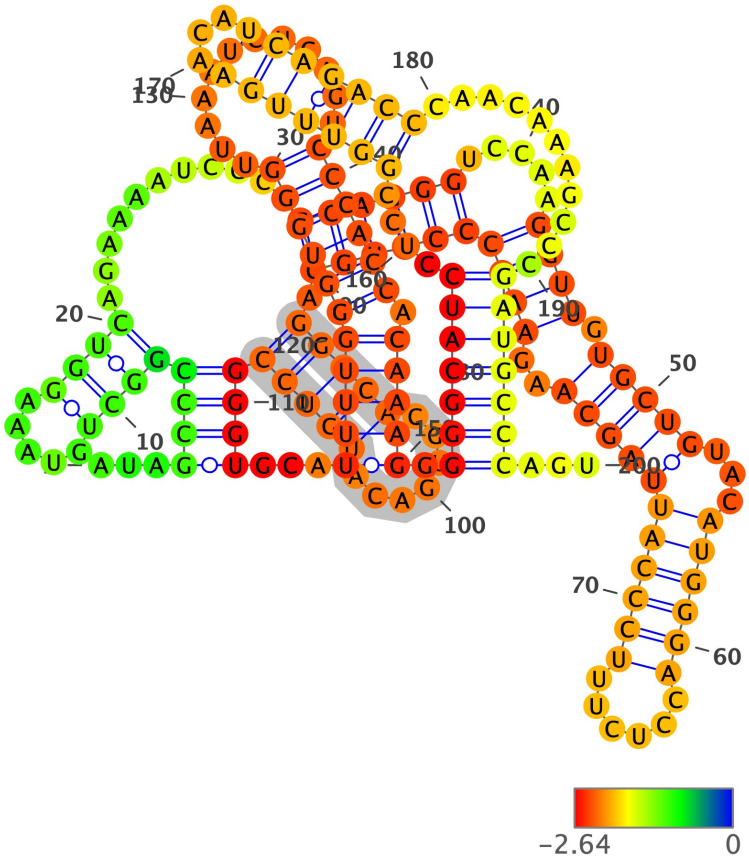
Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

3-- nt 1 to 1--CDS, cds-YP_401690.1, 112650-113585(+)

Attributes: ['ID=cds-YP_401690.1', 'Parent=gene-HHV4_BGRF1/BDRF1', 'Dbxref=UniProtKB/TrEMBL:Q777C9,Genbank:YP_401690.1,GeneID:3783767', 'Name=YP_401690.1', 'gbkey=CDS', 'gene=BGRF1/BDRF1', 'locus_tag=HHV4_BGRF1/BDRF1', 'product=DNA packaging terminase subunit 1', 'protein_id=YP_401690.1']

NC_007605.1 (forward strand): Structure number 295 from nt 113715 to 113731 (nt 92 to 108)

```
5'-GGACACGUGACAUGUCC-3'
5'-(((((.......)))))-3'
Motif MFE = -4.1; z-score = -1.39; 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 113624 to 113823 (motif highlighted in silver):

```
5'-AUAGCCCGGCUGUAAAGGUCAGAAAAUCGCAGCAGGGUCCAAGGUUGUGCUGUACAUGGGACCUCUUUCCCAUUAGCAAGAACCCCCUGCAGGACACGUGACAUGUCCGGG
UGCAUUUUGGGUGGGUUAAAUCUCAGUCCCACCACAAAGGGGGCAUCCUCCGGUUUGAACAUCAGACCCAACAAAGCCCGAUGCCCAGU-3
5'-...(((((((((.....)))).........((((((.....((((.((((((...((((((.....)))))))))))..)))))))))).(((((.......)))))))))
)...((((((((((.........)))))).)))))).(((((((....(((((((...)))))))).........)))))))...-3'
MFE = -70.4; z-score = -2.59; ED = 27.84
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

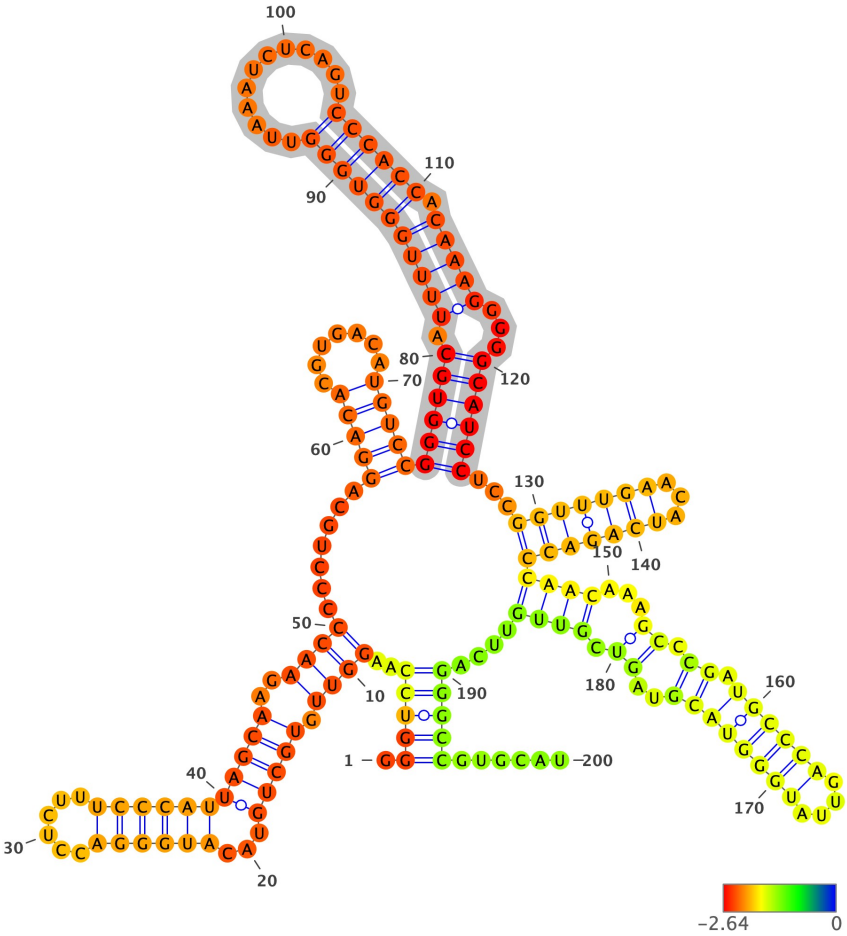
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 296 from nt 113732 to 113782 (nt 75 to 125)

```
5'-GGGUGCAUUUUGGGUGGGUUAAAUCUCAGUCCCACCACAAAGGGGGCAUCC-3'
5'-((((((.(((((((((((.....)))))))).)))))...)))))))-3'
Motif MFE = -21.8; z-score = -3.0; ED = 1.67
```



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

Extracted structure model with flanking nucleotides 113658 to 113857 (motif highlighted in silver):

```
5'-GGGUCCAAGGUUGUGCUGUACAUGGGACCUCUUUCCCAUUAGCAAGAACCCCCUGCAGGACACGUGACAUGUCCGGGUGCAUUUUGGGUGGGUUAAAUCUCAGUCCCACCA
CAAAGGGGGCAUCCUCCGGUUUGAACAUCAGACCCAACAAAGCCCGAUGCCCAGUUAUGGGUACGUAGUCGUUGUUCAGGGCCGUGCAU-3
5'-.((((((..((((.((((((...((((((.....)))))))))))..))))).......(((((.......)))))((((((.((((((((((.............)))))))).
)))))...)))))))...(((((((...)))))))((((...((.((.((((((....)))))))).)).)))).....)))))).......-3'
MFE = -73.6; z-score = -2.3; ED = 20.96
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

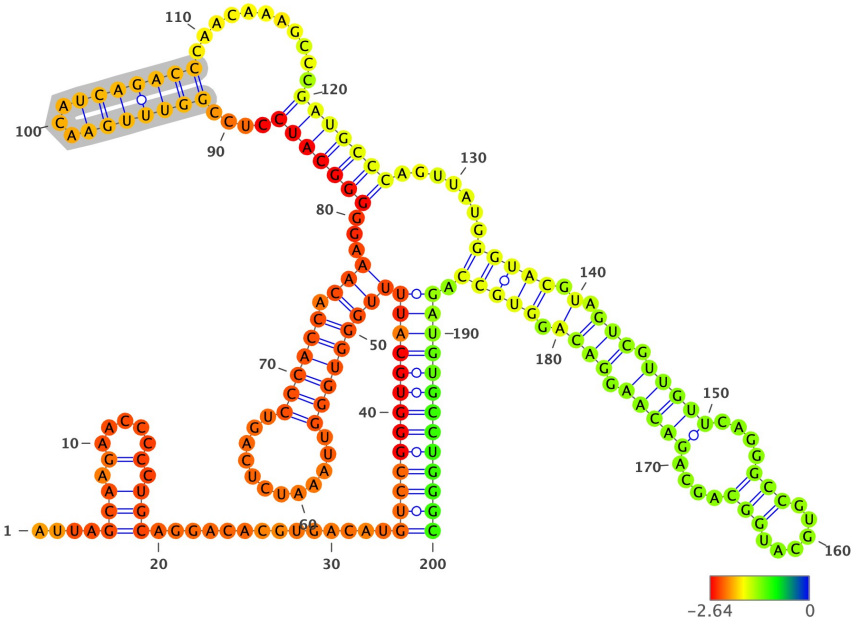
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 297 from nt 113786 to 113802 (nt 92 to 108)

```
5'-GGUUUGAACAUCAGACC-3'
5'-((.............))-3'
Motif MFE = -6.0; z-score = -4.72; 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 113695 to 113894 (motif highlighted in silver):

```
5'-AUUAGCAAGAACCCCCUGCAGGACACGUGACAUGUCCGGGUGCAUUUUGGGUGGGUUAAAUCUCAGUCCCACCACAAAGGGGGCAUCCUCCGGUUUGAACAUCAGACCCAA
CAAAGCCCGAUGCCCAGUUAUGGGUACGUAGUCGUUGUUCAGGGCCGUGCAUGGCAGCAGACAAGGACAGGUGCCAGAUGUGCCUGGGC-3
5'-....(((.(.....).))).............(((((((((((((((((((((.............)))))))).))))...(((((((....(((((((...)))))))).....))))))).....(((((.(.(((.(((((....((.....)))....)))))).)))).)))))).))))))))))))-3'
MFE = -71.8; z-score = -1.59; ED = 43.69
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

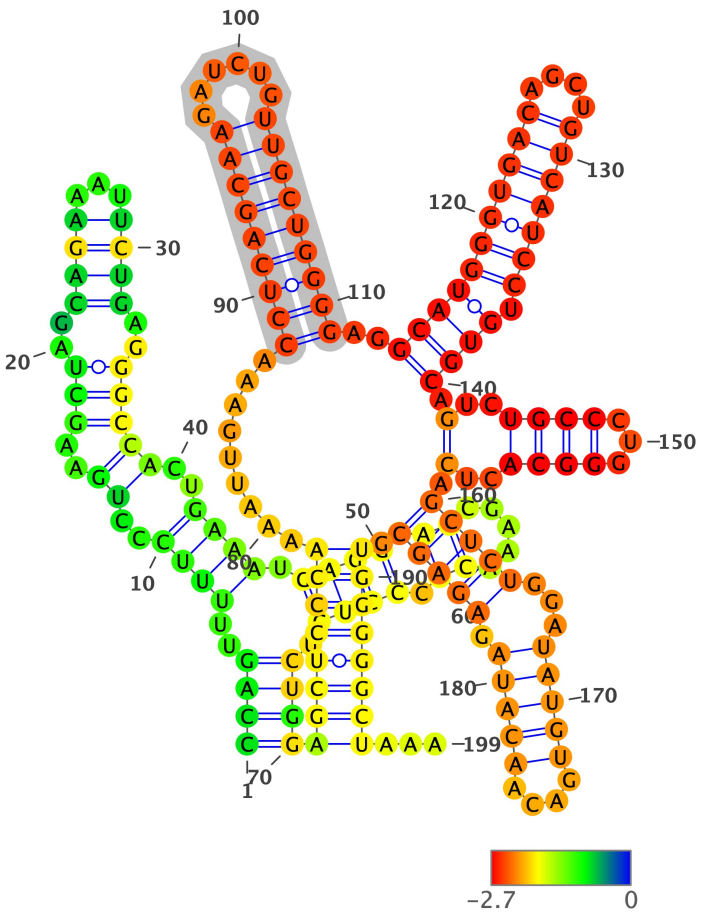
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 298 from nt 115102 to 115125 (nt 88 to 111)

```
5'-CCUCAGCAAGAUCUGUUGCUGGGG-3'
5'-(((((((((.....)))))))))-3'
Motif MFE = -13.2; z-score = -3.99; 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 115015 to 115213 (motif highlighted in silver):

```
5'-CCAGUUUUUCCCUGAAGCUAGCAGAAAUUCUGAGGGCCACUGAAAUGAGGAAGCGAAACUCCCUCUCUGGAGCUCCCAAAAUUGAAACCUCAGCAAGAUCUGUUGCUGGGG
AGGCAUGGGUGACAGCUGUCAUCCUGUGCAGUCUGCCCUGGGCACUCAGCUCUGGAUAUGUGACAACAUAGAGAGCGUGGGGGCUAAA-3
5'-((((..((((..((..((((..((((...)))).))))))..)))).((((.(.....).)))).))))((((((((.........((((((((.....)))))))))
..((((((((((....)))))))).)))).(..((((...)))))..).((((...((((((....)))))).)))))).))))))))...-3'
MFE = -72.3; z-score = -2.96; ED = 17.76
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

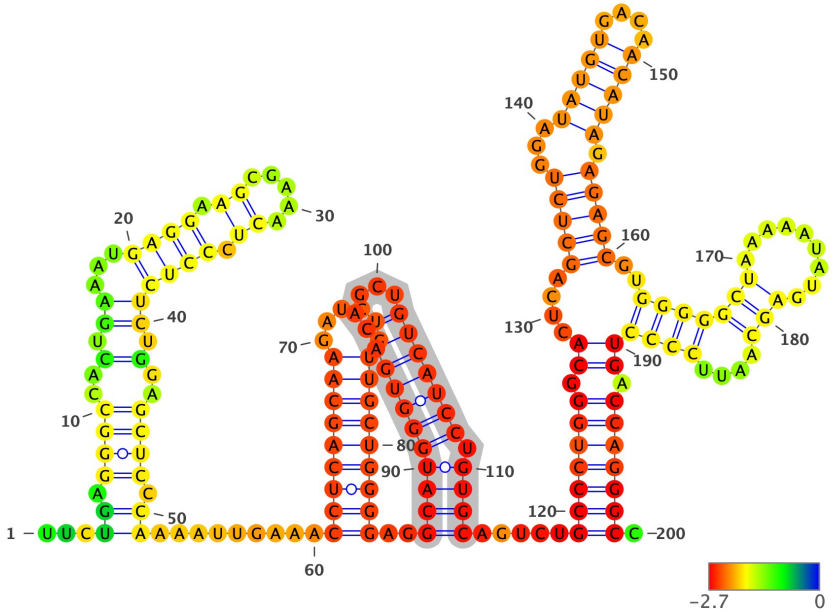
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 299 from nt 115128 to 115154 (nt 87 to 113)

```
5'-GCAUGGGUGACAGCUGUCAUCCUGUGC-3'
5'-((((((((((....)))))))).))))-3'
Motif MFE = -13.3; z-score = -3.88; 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 115042 to 115241 (motif highlighted in silver):

```
5'-UUCUGAGGGCCACUGAAAUGAGGAAGCGAAACUCCCUCUCUGGAGCUCCCAAAAUUGAAACCUCAGCAAGAUCUGUUGCUGGGGAGGCAUGGGUGACAGCUGUCAUCCUGU
GCAGUCUGCCCUGGGCACUCAGCUCUGGAUAUGUGACAACAUAGAGAGCGUGGGGGCUAAAAAUAUGAGCAAUUCCCCUGACCAGGGCC-3
5'-...((.((((..(.((...((((.((.....)).)))))).)..)))).))........(((((((((.....)))))))))..((((((((((....)))))))).))
)).....(((((((.((....((((...((((.....)))))).)))))..((((((.........)))....)))))).)))))))).-3'
MFE = -72.3; z-score = -3.25; ED = 36.58
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

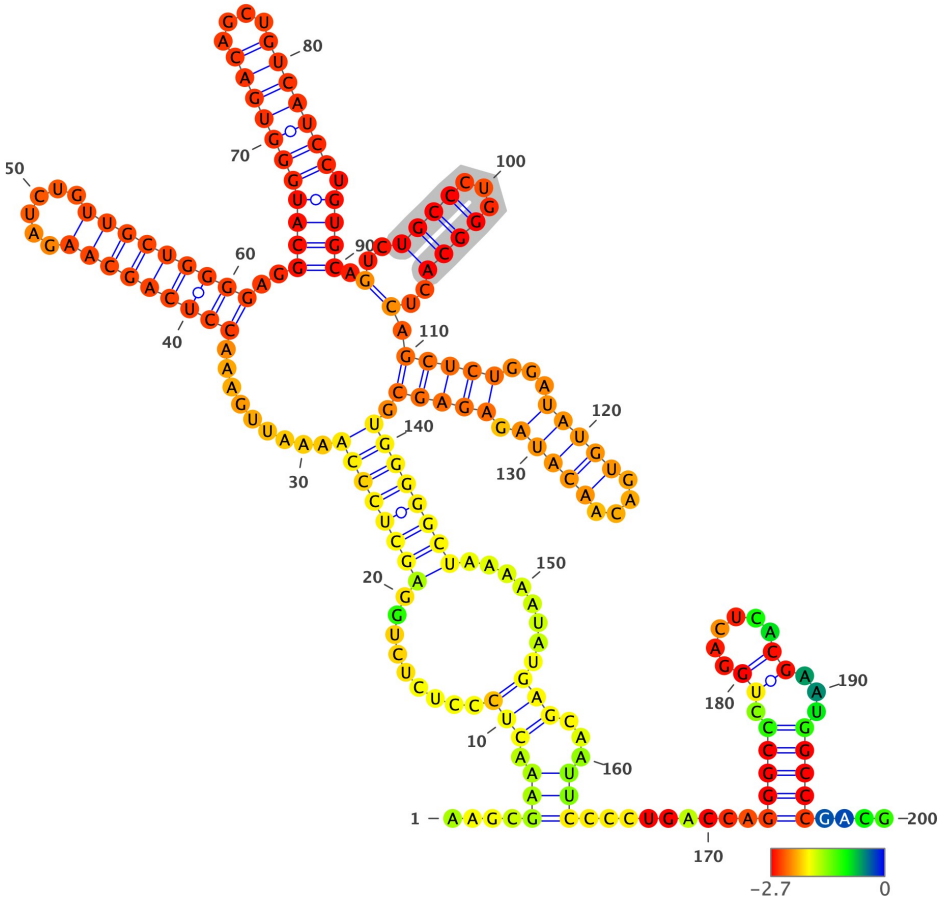
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 300 from nt 115159 to 115169 (nt 95 to 105)

```
5'-UGCCCUGGGCA-3'
5'-(((((...)))))-3'
Motif MFE = -2.9; z-score = -3.85; 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 115065 to 115264 (motif highlighted in silver):

```
5'-AAGCGAAACUCCCUCUCUGGAGCUCCCAAAAUUGAAACCUCAGCAAGAUCUGUUGCUGGGGAGGCAUGGGUGACAGCUGUCAUCCUGUGCAGUCUGCCCUGGGCACUCAGC
UCUGGAUAUGUGACAACAUAGAGAGCGUGGGGGCUAAAAAUAUGAGCAAUUCCCCUGACCAGGGCCCUGGACUCACGAAUGGCCCGACG-3
5'-....(((.(((.........(((((((.........(((((((((.....)))))))))..(((((((((((....)))))))).)))).(..(((((...)))))..).((
(((...(((((....))))).)))))).)))))))).....)))...)))).........(((((.((......))...)))))....-3'
MFE = -69.1; z-score = -2.27; ED = 27.05
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

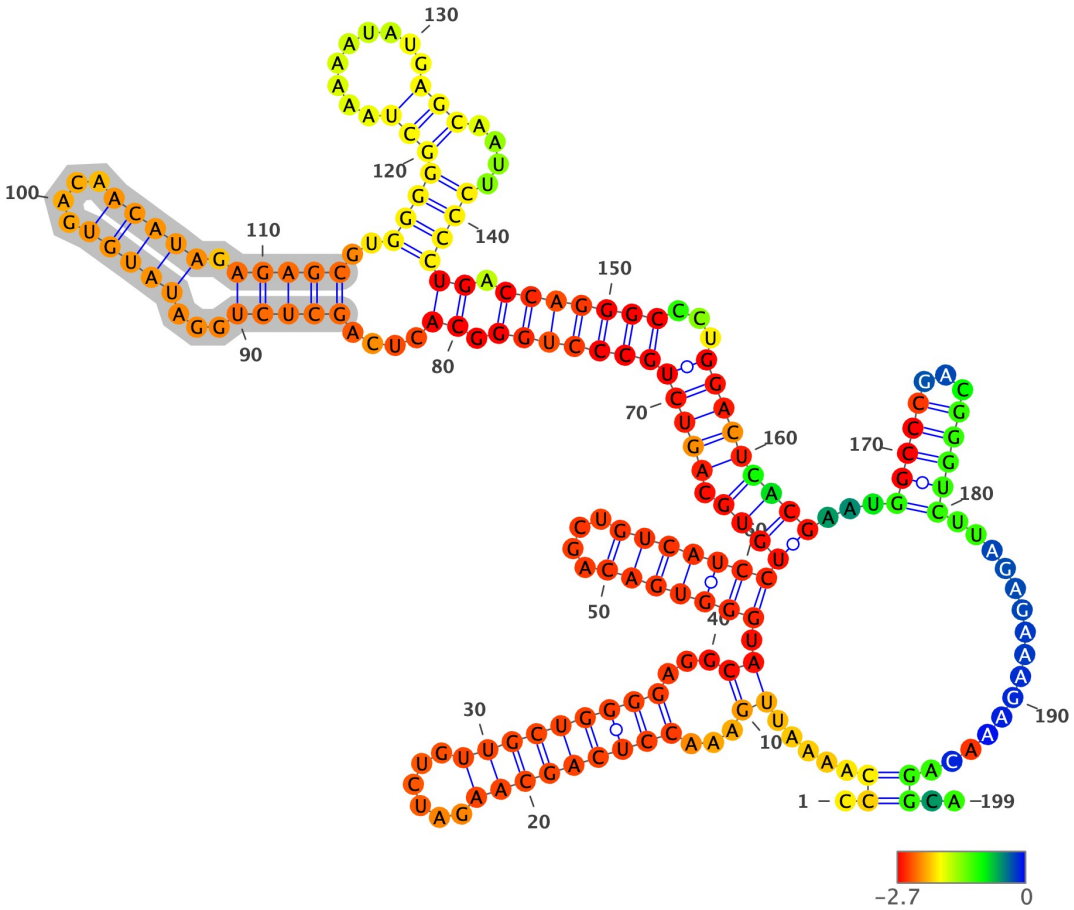
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 301 from nt 115174 to 115201 (nt 86 to 113)

```
5'-GCUCUGGAUAUGUGACAACAUAGAGAGC-3'
5'-(((((...(((((....)))))).)))))-3'
Motif MFE = -8.9; z-score = -3.19; ED = 0.59
```



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

Extracted structure model with flanking nucleotides 115089 to 115287 (motif highlighted in silver):

```
5'-CCCAAAAUUGAAACCUCAGCAAGAUCUGUUGCUGGGGAGGCAUGGGUGACAGCUGUCAUCCUGUGCAGUCUGCCCUGGGCACUCAGCUCUGGAUAUGUGACAACAUAGAGA
GCGUGGGGGCUAAAAAUAUGAGCAAUUCCCCUGACCAGGGCCCUGGACUCACGAAUGGCCCGACGGGUCUUAGAGAAAGAAACAGGCA-3
5'-.((.....((...((((((((((.....))))))))))...)).(((((((....)))))))((((.((((((((((((.((....((((((...((((((....)))))).)))
)).(((((((.........)))....)))))).)))))))...)))))))))...((((((...)))))).............)).-3'
MFE = -71.5; z-score = -2.67; ED = 22.74
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

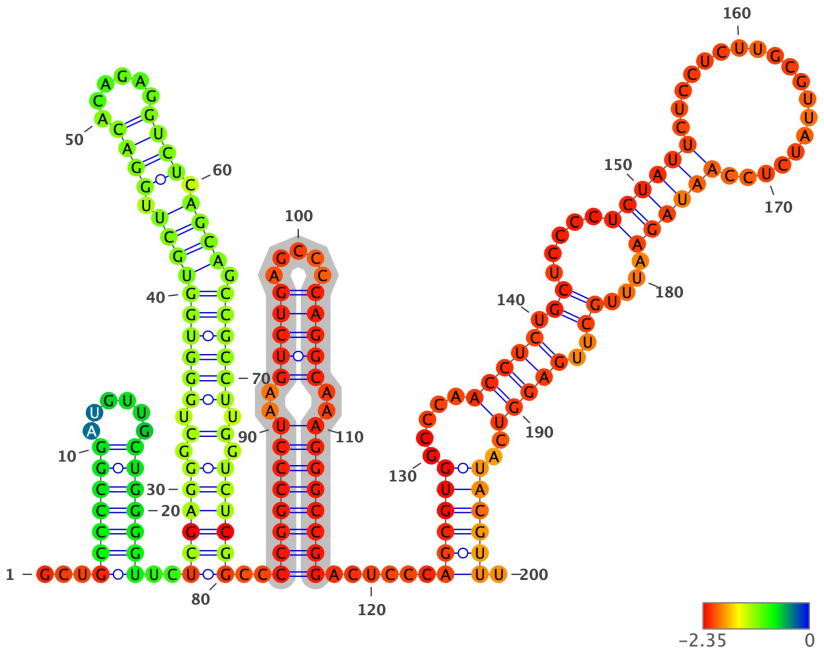
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 302 from nt 115446 to 115480 (nt 83 to 117)

```
5'-CCGGCCCUAAGUCUGAGCCCCAGGCAAAGGGCCGG-3'
5'-(((((((..(((((.....)))))..)))))))-3'
Motif MFE = -23.1; z-score = -4.63; 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 115364 to 115563 (motif highlighted in silver):

```
5'-GCUGCCCCGGAUGUUGCUGGGGUUCUCGAGGGCUGGGUGGUGCUUGGACACAGAGGUCUCAGCAGCCGCCUUGGUCUCGGCCCCGGCCCUAAGUCUGAGCCCCAGGCAAAG
GGCCGGACUCCCAGCGUGGCCCAACCUCUGCUCCCCUCUAUUCUCCUCUUGCGUUAUCUCCAAUAGAAUUUGCUUGAGGUCAUACGUUU-3
5'-...(((((((.....)))))))..(((((((.(.((((((((((.((((.....)))).)))).)))))))..)..)))))))..((((((((..(((((.....)))))..))
))))))......((((((.....(((((.((.....((((((.................))))))....)).)..)))))..)))))).-3'
MFE = -80.2; z-score = -2.05; ED = 30.67
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

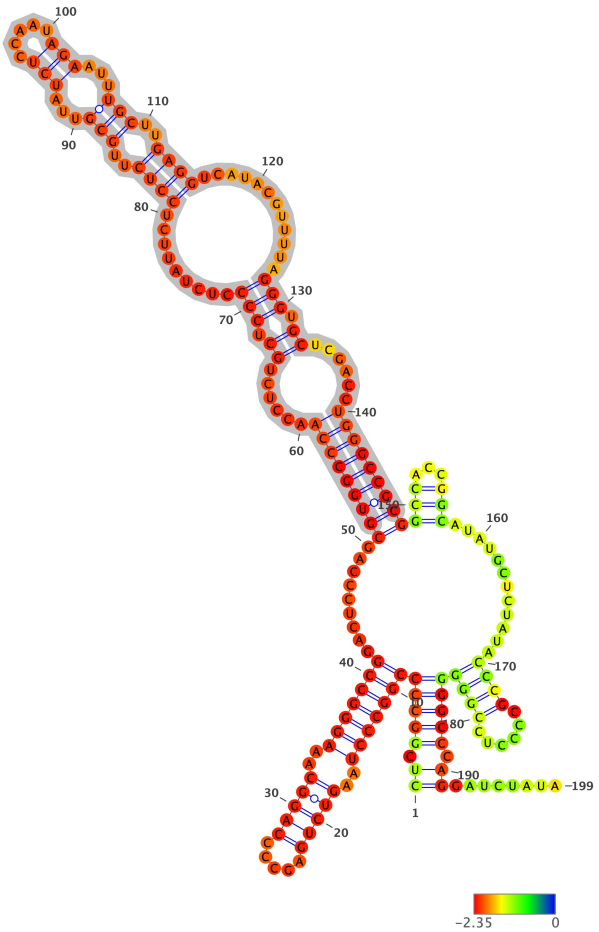
2-- nt 1 to 200--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 303 from nt 115490 to 115585 (nt 52 to 147)

5'-GUGGCCCAACCUCUGCUCCCCUCUAUUCUCCUCUUGCGUUAUCUCCAAUAGAAUUUGCUUGAGGUCAUACGUUUUAGGGUGCUCGACCUGGGCCGC-3'

5'-(((((.........((.(((.........(((((..(((...(((.....)))...)))..))))............)))).)).........)))))-3'
Motif MFE = -31.1; z-score = -3.51; ED = 7.6



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 115439 to 115637 (motif highlighted in silver):

5'-CUCGGCCCCGGCCCUAAGUCUGAGCCCCAGGCAAAGGGCCGGACUCCCAGCGUGGCCCAACCUCUGCUCCCCUCUAUUCUCCUCUUGCGUUAUCUCCAAUAGAAUUUGCUUGAGGUCAUACGUUUUAGGGUGCUCGACCUGGGCCGCGGCCACCGGCAUAUGCUCUAUACCCGCCCCUCCGGGGGGCCCAGGAUCUAUA-3
5'-((.(((((((((((..(((((.....)))))..)))))))).........((((((((.....((.(((.........((((..(((...(((.....)))...)))..))))..))))...........))).)).....)))))))))((...))).....((((.....)))))))))).)).....-3'
MFE = -76.5; z-score = -2.96; ED = 23.01

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

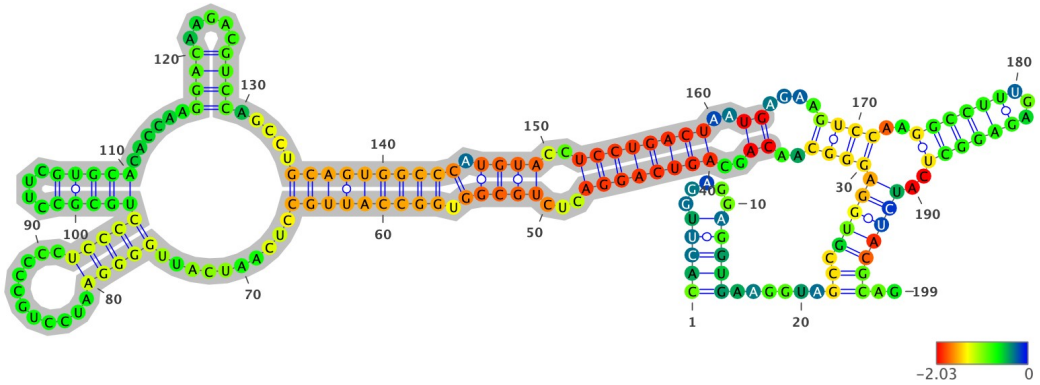
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

NC_007605.1 (forward strand): Structure number 304 from nt 117661 to 117788 (nt 36 to 163)

```
5'-CAGCAGUCAGGACUCUGCGGUGGCCAUUGCCUCAAUCAUUGGGGAAUCCUGCCCCCUCCCCUGCGCCUUCGUGCACACCAAGGACAAGACGUCCAGCCUGCAGUGGCCCAU
GUACCUCCUGACUAAUG-3'
5'-((.......................................................................................................
...............))-3'
Motif MFE = -48.3; z-score = -3.66; ED = 8.82
```



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 117626 to 117824 (motif highlighted in silver):

```
5'-CACUUGGAGGAGGUGAAGGUAGCCGUGGAGGGCAACAGCAGUCAGGACUCUGCGGUGGCCAUUGCCUCAAUCAUUGGGGAAUCCUGCCCCCUCCCCUGCGCCUUCGUGCAC
ACCAAGGACAAGACGUCCAGCCUGCAGUGGCCCAUGUACCUCCUGACUAAUGAGAAGUCCAAGGCCUUUGAGAGGCUCAUCUACGCAG-3
5'-(((((.....)))))......((.(((((((((..((..(((((((((...(((((.(((((((((.........(((((.........)))))(((((....)))))).
.....((((.....)))).....)))))))))).))))..))))))))..))....)))).(((((((...)))))))..)))))))..-3'
MFE = -69.2; z-score = -0.48; ED = 27.62
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BGRF1/BDRF1, 112650-118064(+)

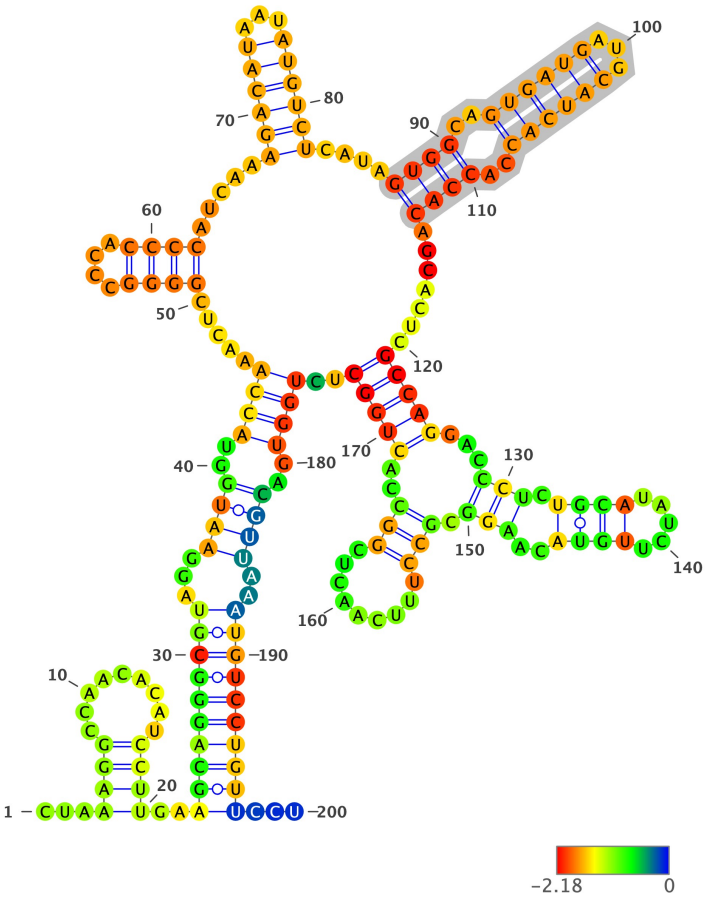
Attributes: ['ID=gene-HHV4_BGRF1/BDRF1', 'Dbxref=GeneID:3783767', 'Name=BGRF1/BDRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BGRF1/BDRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BGRF1/BDRF1']

3-- nt 1 to 199--CDS, cds-YP_401690.1, 116927-118063(+)

Attributes: ['ID=cds-YP_401690.1', 'Parent=gene-HHV4_BGRF1/BDRF1', 'Dbxref=UniProtKB/TrEMBL:Q777C9,Genbank:YP_401690.1,GeneID:3783767', 'Name=YP_401690.1', 'gbkey=CDS', 'gene=BGRF1/BDRF1', 'locus_tag=HHV4_BGRF1/BDRF1', 'product=DNA packaging terminase subunit 1', 'protein_id=YP_401690.1']

NC_007605.1 (forward strand): Structure number 305 from nt 119094 to 119120 (nt 87 to 113)

```
5'-GUGGCAGUGAUGAUGCAUCACCACCAC-3'
5'-(((((.................)))))-3'
Motif MFE = -11.1; z-score = -2.8; ED = 0.22
```



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

Extracted structure model with flanking nucleotides 119008 to 119207 (motif highlighted in silver):

```
5'-CUAAAGGCCAACACAUCCUUGAAGCAGGGCGUAGGAAUGGUACCAAACUCGGGGCCCACCCCAUCAAAGACAUAAUAUGUCUCAUAGUGGCAGUGAUGAUGCAUCACCACC
ACAGCACUCGCCAGGACCCUCUGCAUAUCUUGUACAAGGCGCCUUUCAACUCGGCCACUGGCUCUGGUGACGUUAAAUGUCCUGUUCCU-3
5'-...((((.........)))).((((((((((...(((((..((((.....((((....)))).....((((((...)))))).....((((..(((((((...)))))))..))
)).......((((((...(((.((((.....)))).)).))).(((.........)))..)))))..)))))..)))))..))))))))))...-3'
MFE = -59.3; z-score = -2.5; ED = 23.73
```

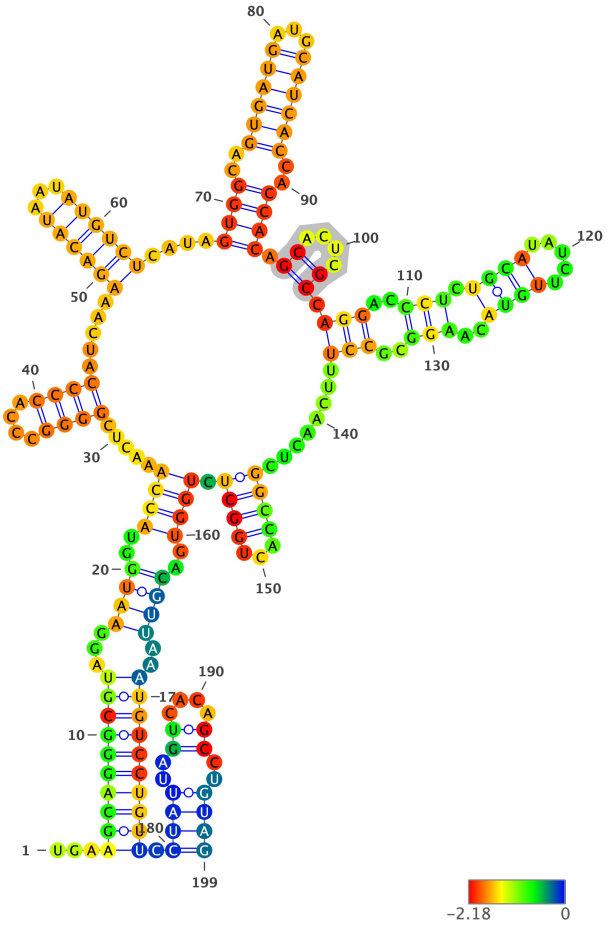
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 306 from nt 119122 to 119129 (nt 96 to 103)

```
5'-GCACUCGC-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 119027 to 119225 (motif highlighted in silver):

```
5'-UGAAGCAGGGCGUAGGAAUGGUACCAAACUCGGGGCCCACCCCAUCAAAGACAUAAUAUGUCUCAUAGUGGCAGUGAUGAUGCAUCACCACCACAGCACUCGCCAGGACCC
UCUGCAUAUCUUGUACAAGGCGCCUUUCAACUCGGCCACUGGCUCUGGUGACGUUAAAUGUCCUGUUCCUAUUAGUCACAGCCUGUAG-3
5'-...((((((((((...(((((..((((.....((((....)))).....((((((...)))))))....((((..(((((((...)))))))..)))).((....)).(((..((
(.((((.....)))).)))..)))........((((...)))).)))))..)))))..))))))))))).(((((..((....)).)))))-3'
MFE = -58.4; z-score = -1.67; ED = 30.62
```

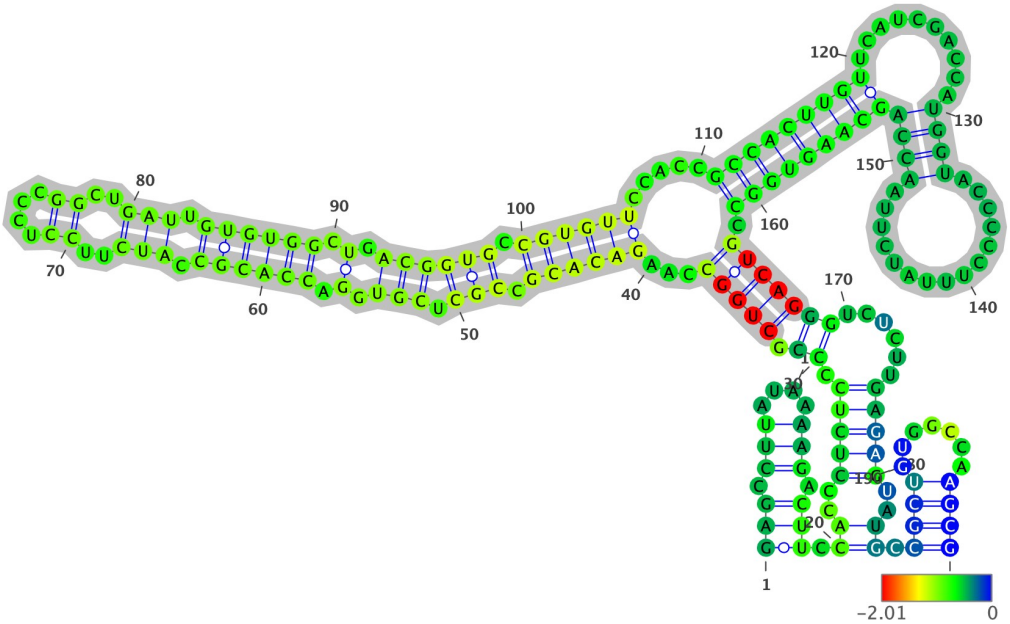
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 307 from nt 120004 to 120138 (nt 33 to 167)

```
5'-CUGGCCAAGACACGCCGCUCGUGGACCACGCCAUCUUCCUCCCGGCUGAUUGUGUGGCUGACGGUGCCGUGUUCCACCGCCACUUGUUCAUCGACCAUGGUACCCCCUUUA
UCUUAACCAGCAAGUGGCCGUCAG-3'
5'-(((((.....................................................................................................
....................))))-3'
Motif MFE = -47.7; z-score = -2.44; ED = 12.05
```



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 119972 to 120171 (motif highlighted in silver):

```
5'-GAGCCUUAUAAAAGACUUCCACCCUCUCCCCGCUGGCCAAGACACGCCGCUCGUGGACCACGCCAUCUUCCUCCCGGCUGAUUGUGUGGCUGACGGUGCCGUGUUCCACCG
CCACUUGUUCAUCGACCAUGGUACCCCCUUUAUCUUAACCAGCAAGUGGCCGUCAGGGUCUCUUGAGAGUAUGCCGCUGUGGCCAAGCG-3
5'-(((.(((....))).))).((..((((((.((.((((((...((((((.(((.(((.(.((((((.(((..((....))..))).)))))))).).)))))))..))))))).....(
(((((((.........((((..............)))))))))))))).)))))))......)))))..)).((((.......))))-3'
MFE = -59.7; z-score = -1.47; ED = 20.48
```

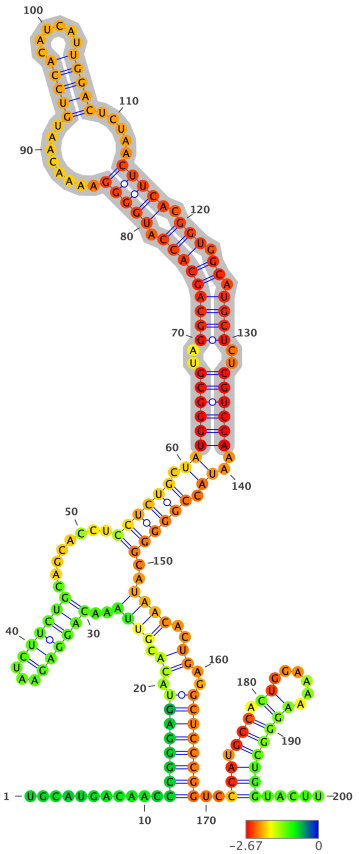
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 308 from nt 120594 to 120670 (nt 62 to 138)

```
5'-UGGGCGUAGGCAGCACCAUGGGGAAAACAAUGUCCACAUCAUUGGACUCUAACUUCACGGUGGCAUGCUCUCGUCCA-3'
5'-((((((..(((((((((.(((((.......(((((.....)))))....)))))).))).)).)))))..)))))))-3'
Motif MFE = -29.1; z-score = -3.21; ED = 9.51
```



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 120533 to 120732 (motif highlighted in silver):

```
5'-UGCAUGACAACCCGGGAGUACACGUUAAACAGGAGAAUCUUCUGCAGCACCUCCUCUGCUAUGGGCGUAGGCAGCACCAUGGGGAAAACAAUGUCCACAUCAUUGGACUCU
AACUUCACGGUGGCAUGCUCUCGUCCAAAUACCGGGGGCAUAACACUGAGGCUCCCGGUCCCAUGCCACUGGAAAAAGGGCUGGUACUU-3
5'-...........((((((((.((.((((..(((((((...)))))).......((((((.(((((((((..(((((((((.(((((........(((((.....)))))).....
..)))))).))).)).)))).)).))))))..)).)))))).))..))))).))..)))))))))..(((.(((.((.....)))))))).....-3'
MFE = -66.3; z-score = -2.45; ED = 29.38
```

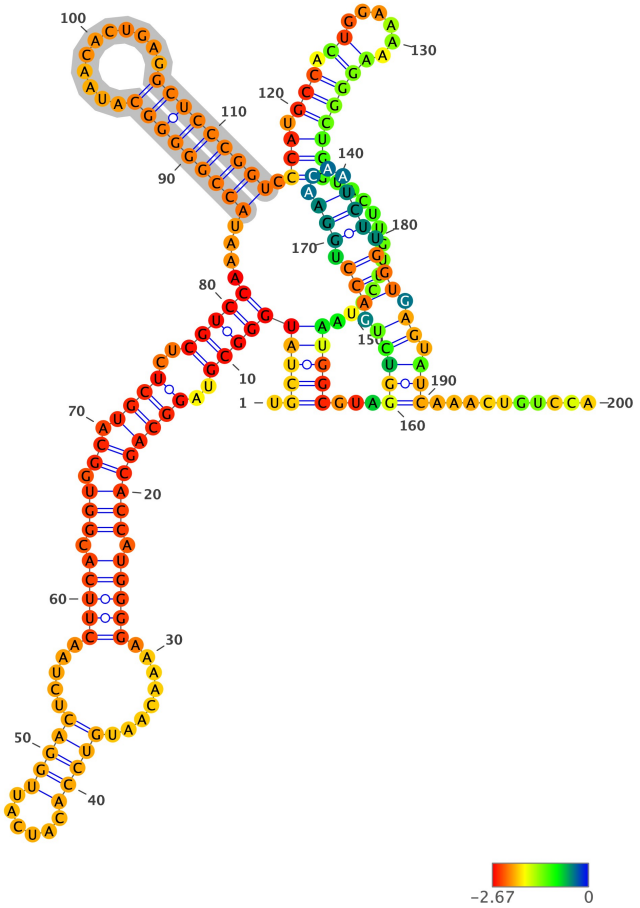
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 309 from nt 120674 to 120702 (nt 86 to 114)

```
5'-ACCGGGGGCAUAACACUGAGGCUCCCGGU-3'
5'-(((((((((..........)))))))))-3'
Motif MFE = -15.8; z-score = -3.99; 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 120589 to 120788 (motif highlighted in silver):

```
5'-UGCUAUGGGCGUAGGCAGCACCAUGGGGAAAACAAUGUCCACAUCAUUGGACUCUAACUUCACGGUGGCAUGCUCUCGUCCAAAUACCGGGGGCAUAACACUGAGGCUCCC
GGUCCCAUGCCACUGGAAAAAGGGCUGGUACUUGUUCUUAAUGGCGUAGGUCUGACCUGGAACAAUCUUGGUGAGUAUCAAACUGUCCA-3
5'-.(((((((((..((((((((((.(((((........(((((......)))))).....)))))).))).)).)))))..)))))....((((((((((.........))))))
))).(((.(((.((.....)))))))).........))))).....(((((.(((.(((....))).))).)).))).........-3'
MFE = -67.8; z-score = -2.38; ED = 35.9
```

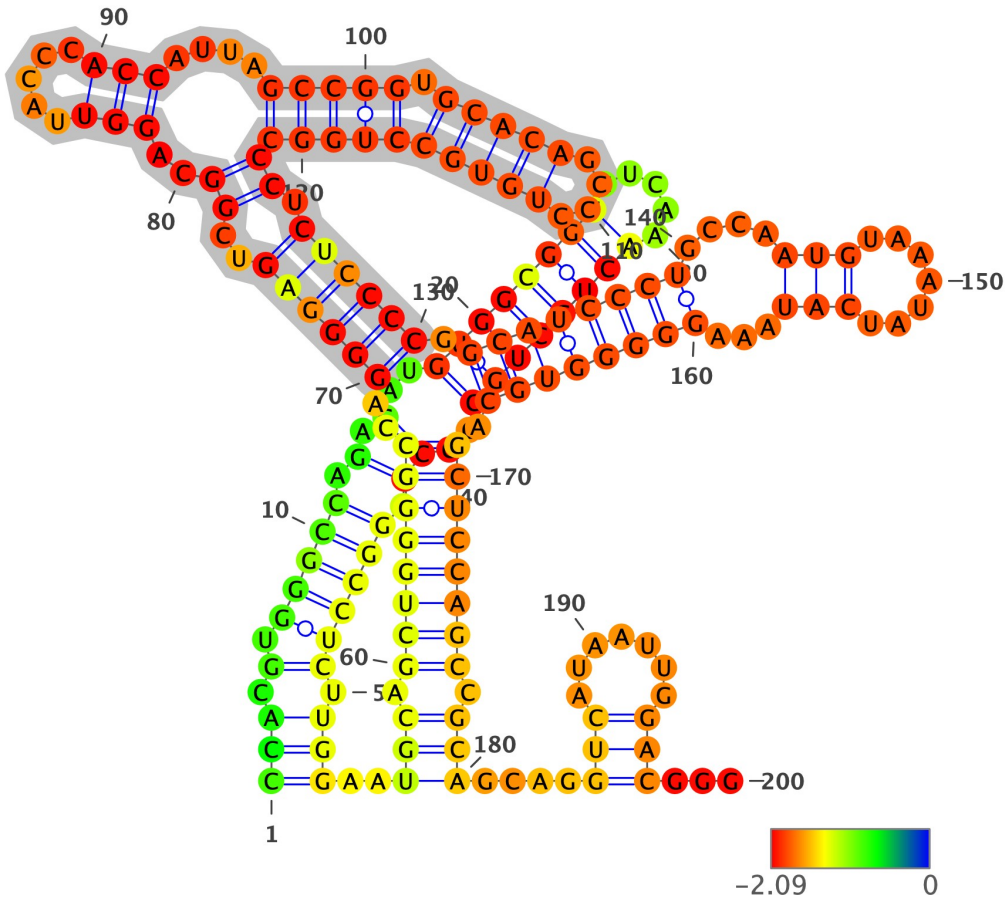
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 310 from nt 123456 to 123516 (nt 70 to 130)

```
5'-GGGGAGUCGGCAGGUUACCCACCAUUAGCCGGUGCACAGCCCUGUGCCUGGCCCUCUCCCC-3'
5'-(((..(..((..((((.....)))..............................)).)...)))-3'
Motif MFE = -26.9; z-score = -2.05; ED = 11.78
```



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 123387 to 123586 (motif highlighted in silver):

```
5'-CCACGUGGGCCAGAGAUGUGGCGGUCUCAAACUGCUGCCCCCGGGCCUCUUGGAAUGCAGCUGGGGCCAGGGGAGUCGGCAGGUUACCCACCAUUAGCCGGUGCACAGCCC
UGUGCCUGGCCCUCUCCCCGGCAUCCCUGCCAAUGUAAAUAUCAUAAAGGGGGUGCAGCUCCAGCCGCAGCAGGUCAUAAUUGGACGGG-3
5'-(((.(.(((((.(.(..(((((((((.....)))))))).)).)).)))))).)))..((((.(((((((((..((((((..((..((.....)))....(((((.(((((....
)))))))))))).)))))).((((((((....(((.......)))...)))))))).)))))))).)))....(((.......)))...-3'
MFE = -82.6; z-score = -1.38; ED = 17.07
```

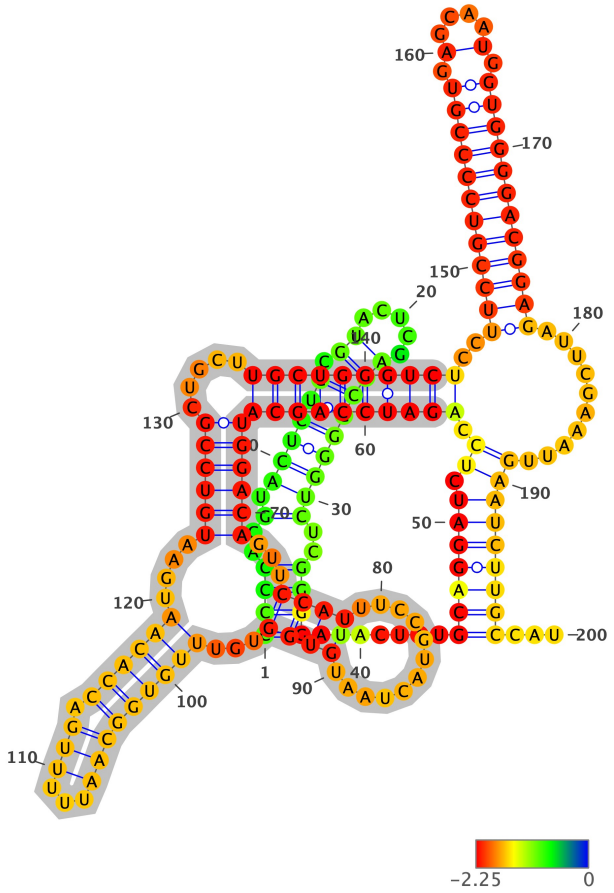
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 311 from nt 124767 to 124853 (nt 57 to 143)

```
5'-GAUCCAGCAUGGACAGUUCCAUUUCCGUACUAAUGUGGUGUUUGUGGCAAUUUUUGACCACAAUGAAUGUCCGCUGCUUGCUGGGUC-3'
5'-(((((((((((((...((((.............))))).............................)))))).....)))))))))-3'
Motif MFE = -27.7; z-score = -2.33; ED = 17.59
```



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 124711 to 124910 (motif highlighted in silver):

```
5'-CCCCACGUACUCUGCGUACUCGACCGGGGUCUCGGGGAUACUAUGCAGGAUCUCCAGAUCCAGCAUGGACAGUUCCAUUUCCGUACUAAUGUGGUGUUUGUGGCAAUUUUU
GACCACAAUGAAUGUCCGCUGCUUGCUGGGUCUCCUUCCGUCCCCGUGAGCAAUGGUGGGGACGGAGAUUCGAAAUUGAAUCUUGCCAU-3
5'-(((((..(.(((((((.((.....)))))))))..))))).....(((((((.((.(((((((((((((((...((((.............)))))...(((((((((...))
).)))))).....)))))).....)))))))))..((((((((((((.(....).)))))))))))).........))))))))...-3'
MFE = -69.9; z-score = -2.57; ED = 24.12
```

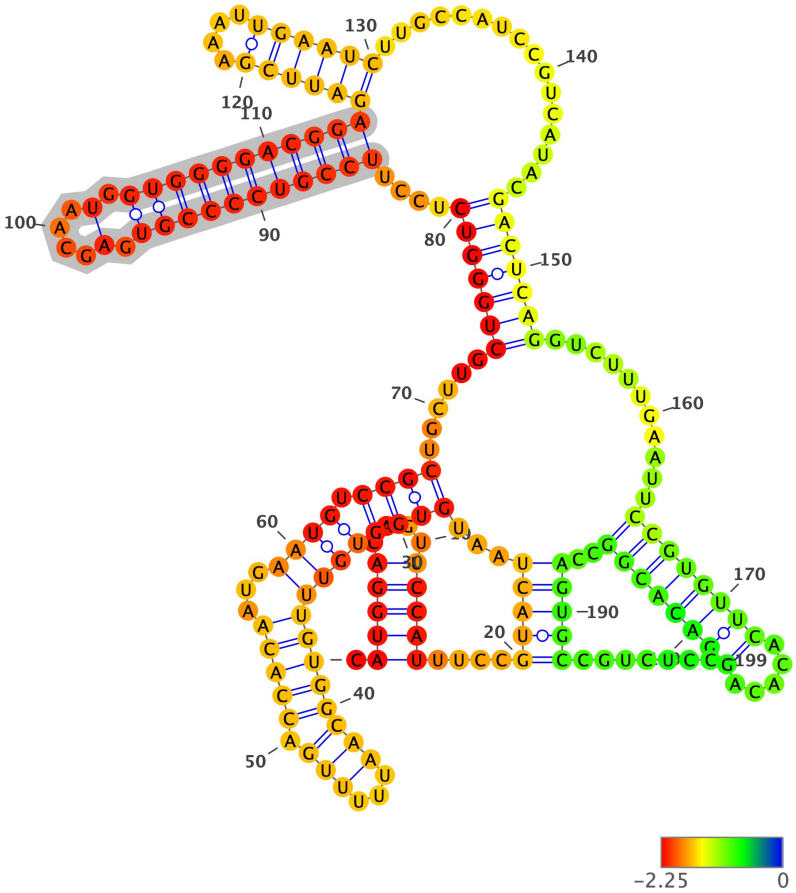
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 312 from nt 124858 to 124887 (nt 85 to 114)

```
5'-UCCGUCCCCGUGAGCAAUGGUGGGGACGGA-3'
5'-(((((((((((.(....).)))))))))))-3'
Motif MFE = -18.5; z-score = -4.74; 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 124774 to 124972 (motif highlighted in silver):

```
5'-CAUGGACAGUUCCAUUUCCGUACUAAUGUGGUGUUUGUGGCAAUUUUUGACCACAAUGAAUGUCCGCUGCUUGCUGGGUCUCCUUCCGUCCCCGUGAGCAAUGGUGGGGAC
GGAGAUUCGAAAUUGAAUCUUGCCAUCCGUCAUACGACUCAGGUCUUUGAAUUCCGUGUUCACACAGGACACGGCCAGUGCCGUCUCC-3
5'-.(((((....))))).....((((((...((((((((((((((...)))).)))))).))))).))))).....(((((((....((((((((((.(....).)))))))))
)))(((((((....)))))).................)))))))...........((((((((.....)))))))).))))).......-3'
MFE = -61.9; z-score = -1.45; ED = 45.76
```

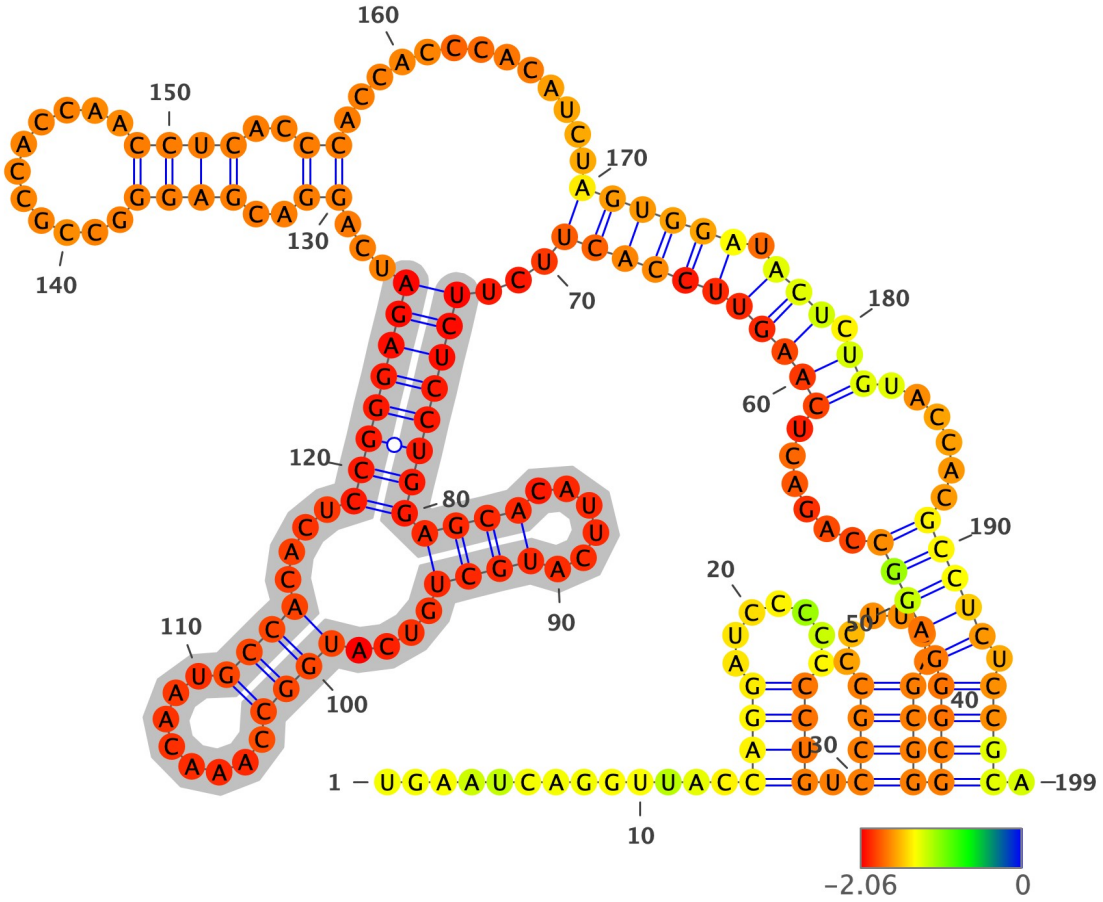
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 313 from nt 125787 to 125840 (nt 73 to 126)

```
5'-UCUCCUGGAGCACAUUCAUGCUGUCAUGGCCAAACAAUGCCACACUCCGGGAGA-3'
5'-(((.................................................)))-3'
Motif MFE = -18.6; z-score = -3.54; 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 125715 to 125913 (motif highlighted in silver):

```
5'-UGAAUCAGGUUACCAGGAUCCCCCCCUGUCCGCCCUUCAGCGGGCGGGAGGCCAGACUCAAGUUCCACUUCUUCUCCUGGAGCACAUUCAUGCUGUCAUGGCCAAACAAUG
CCACACUCCGGGAGAUCAGGACGAGGGCCGCCACCAACCUCACCCACCACCCACAUCUAGUGGAUACUCUGUACCACGCCUCUCCGCA-3
5'-.............((((.......)))).((((......))))(((((((((.....((((((((((...((((((((((((.....)))).....((((........)
)))....)))))))))...((..((((...........))))..))............)))))).))).)).....)))))).)))).-3'
MFE = -62.8; z-score = -2.95; ED = 22.95
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BcRF1.2, 125073-128686(+)

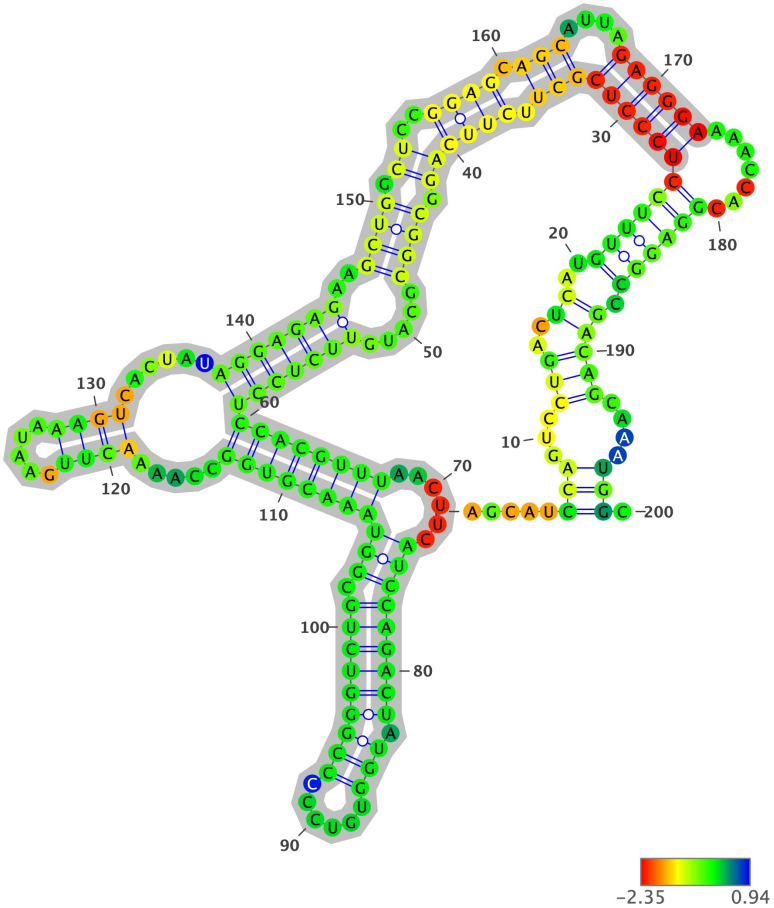
Attributes: ['ID=gene-HHV4_BcRF1.2', 'Dbxref=GeneID:3783690', 'Name=BcRF1', 'Note=betagamma gene', 'gbkey=Gene', 'gene=BcRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BcRF1.2']

3-- nt 1 to 199--CDS, cds-YP_401698.1, 125177-127429(+)

Attributes: ['ID=cds-YP_401698.1', 'Parent=gene-HHV4_BcRF1.2', 'Dbxref=UniProtKB/TrEMBL:Q8AZJ6,Genbank:YP_401698.1,GeneID:3783690', 'Name=YP_401698.1', 'gbkey=CDS', 'gene=BcRF1', 'locus_tag=HHV4_BcRF1.2', 'product=protein UL87', 'protein_id=YP_401698.1']

NC_007605.1 (forward strand): Structure number 314 from nt 131222 to 131368 (nt 27 to 173)

```
5'-UCCCUCGCUUCUUCAGGCGGCGCAUGUUCUCCUCCACGUUUAACUUCAUCCAGACUAUGGUGUCCCCCGGGUCUGCGGUAAACGUGGCCAAAACUUGAAUAAAGUCACUAU
AGGAGAGAAGCUGGCUCCGGAGCAGCAUUAGAGGGA-3'
5'-(((((((.....................................................................................................
.............................)))))))-3'
Motif MFE = -50.7; z-score = -2.6; ED = 14.69
```



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 131196 to 131395 (motif highlighted in silver):

```
5'-AGCAUCCAGUCCUGACUCAUGUUUCCUCCCUCGCUUCUUCAGGCGGCGCAUGUUCUCCUCCACGUUUAACUUCAUCCAGACUAUGGUGUCCCCCGGGUCUGCGGUAAACGU
GGCCAAAACUUGAAUAAAGUCACUAUAGGAGAGAAGCUGGCUCCGGAGCAGCAUUAGAGGGAAAACCACGGAGGCCGACAGCAAAUGGC-3
5'-.....(((...(((..((..((((((((((((((.((((((.((((.....((((((((((((((.....(((((((((.(((.....)))))))))).))))))))
)).....(((.....)))).....)))))))..)))).)).)..)))).))).....)))))).....)))))).)))))....)))).-3'
MFE = -59.9; z-score = -1.1; ED = 25.59
```

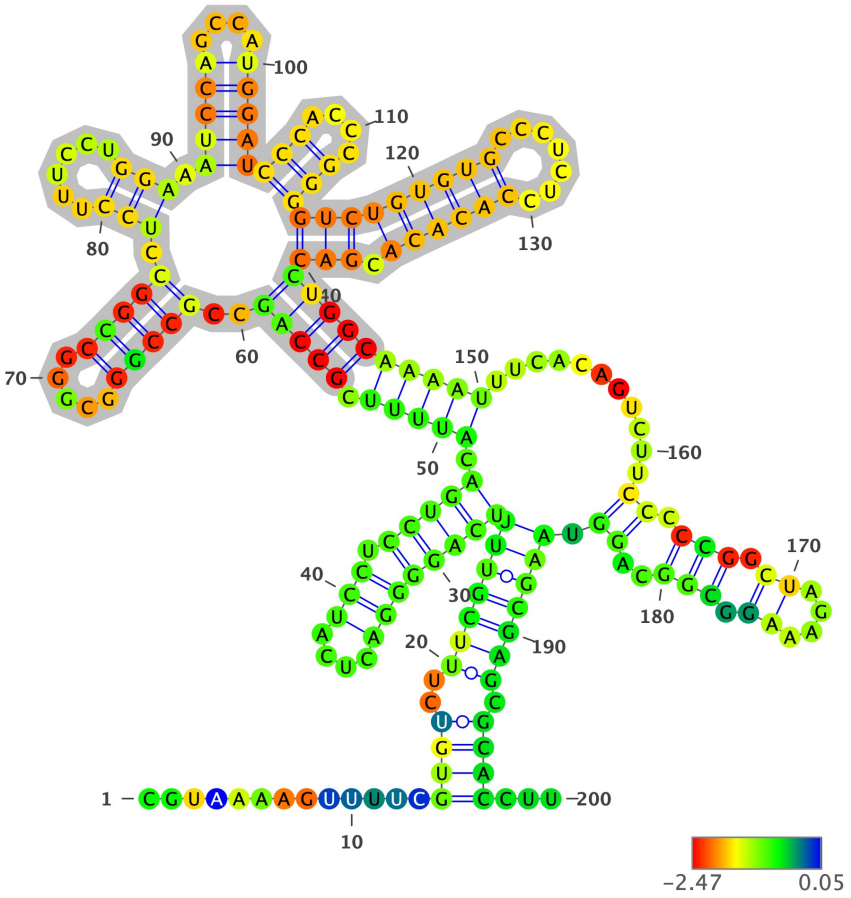
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 315 from nt 132527 to 132617 (nt 55 to 145)

```
5'-GCCAGCCGCCGGGCGGGCCGGCCUCCUUUCCUGGAAAUCCAGCCAUGGAUCCCACCCGGGGUCUGUGUGCCCUCUCCACACACGACCUGGC-3'
5'-(((.....((.(.....)).)).....(((((.................).)))..)))-3'
Motif MFE = -38.6; z-score = -1.88; ED = 24.7
```



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 132473 to 132672 (motif highlighted in silver):

```
5'-CGUAAAAGUUUUCGUGUCUUUCGUUUUCAGGGGACUCAUCCUCCUGACAUUUUCGCCAGCCGCCGGGCGGGCCGGCCUCCUUUCCUGGAAAUCCAGCCAUGGAUCCCACCC
GGGGUCUGUGUGCCCUCUCCACACACGACCUGGCAAAAUUUCACAGUCUUCCCCCGGCUAGAAAGGCGGCAGGUAAGCGAGCGCACCUU-3
5'-.............(((((..(((((((((((((((....)))).)))))).(((((.(((((..(((((.....)))))).((.......)).(((((....)))))))((....
)))(((((((((.......)))))).))))))))))))).........((.((((.((....)).)))..)).)))))))..)))))...-3'
MFE = -65.2; z-score = -2.28; ED = 29.68
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 99 to 200--gene, gene-HHV4_BXRF1, 132571-134886(+)

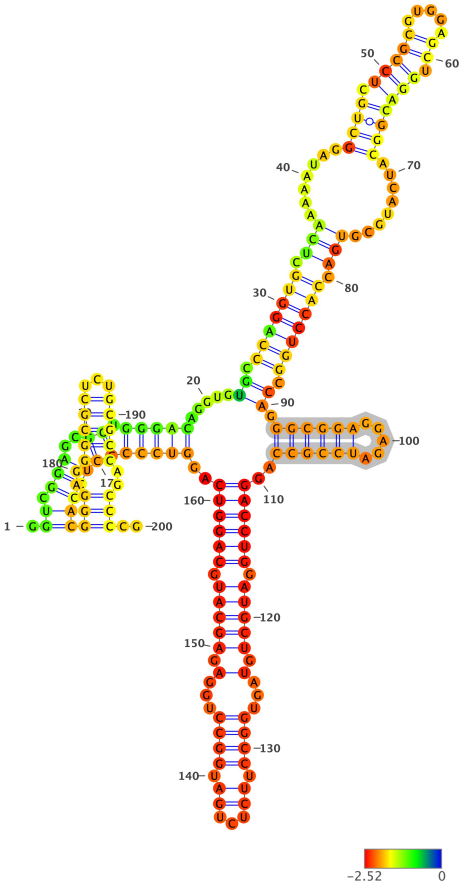
Attributes: ['ID=gene-HHV4_BXRF1', 'Dbxref=GeneID:3783743', 'Name=BXRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BXRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BXRF1']

3-- nt 99 to 200--CDS, cds-YP_401702.1, 132571-133317(+)

Attributes: ['ID=cds-YP_401702.1', 'Parent=gene-HHV4_BXRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B8,Genbank:YP_401702.1,GeneID:3783743', 'Name=YP_401702.1', 'gbkey=CDS', 'gene=BXRF1', 'locus_tag=HHV4_BXRF1', 'product=nuclear protein UL24', 'protein_id=YP_401702.1']

NC_007605.1 (forward strand): Structure number 316 from nt 133366 to 133382 (nt 92 to 108)

```
5'-GGCGGAGGAGAUCCGCC-3'
5'-((((((.....))))))-3'
Motif MFE = -10.3; z-score = -3.88; ED = 0.09
```



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 133275 to 133474 (motif highlighted in silver):

```
5'-GGUCGGAGCGGUGGGACAGGUGUGCCCAGGUGCUCAAAAAUAGGCUGCUCCGCGUGGAGCUGGACGGCAUCAUGCGUGACCACCUGGCCAGGGCGGAGGAGAUCCGCCAGG
ACCUGGAUGCUGUAGUGGCCUUCUCUGAUGGCCUGGAGAGCAUGCAGGUCAGGUCCCCCUCCACGGGAGGGCGCUCUGCGCCAGCCCCG-3
5'-.((.((((..((.((((((.....((.(((((((.((((.......((((.(((((.....)).)))))))........))).)))))))).)).((((((.....)))))))..(
(((((.(((((.(...((((.((...)).)))).....).)))))..)))))))..))))))))))))((..((((((...)))))..)))..-3'
MFE = -97.9; z-score = -1.89; ED = 30.1
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BXRF1, 132571-134886(+)

Attributes: ['ID=gene-HHV4_BXRF1', 'Dbxref=GeneID:3783743', 'Name=BXRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BXRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BXRF1']

3-- nt 1 to 43--CDS, cds-YP_401702.1, 132571-133317(+)

Attributes: ['ID=cds-YP_401702.1', 'Parent=gene-HHV4_BXRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B8,Genbank:YP_401702.1,GeneID:3783743', 'Name=YP_401702.1', 'gbkey=CDS', 'gene=BXRF1', 'locus_tag=HHV4_BXRF1', 'product=nuclear protein UL24', 'protein_id=YP_401702.1']

4-- nt 1 to 200--gene, gene-HHV4_BVRF1, 133013-134886(+)

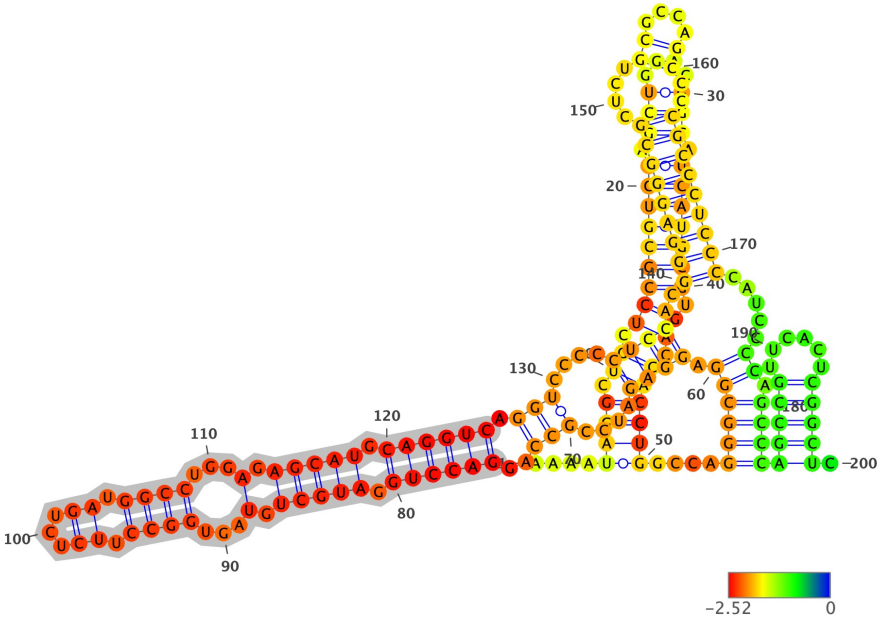
Attributes: ['ID=gene-HHV4_BVRF1', 'Dbxref=GeneID:3783732', 'Name=BVRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BVRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BVRF1']

5-- nt 1 to 200--CDS, cds-YP_401703.1, 133127-134839(+)

Attributes: ['ID=cds-YP_401703.1', 'Parent=gene-HHV4_BVRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B7,Genbank:YP_401703.1,GeneID:3783732', 'Name=YP_401703.1', 'gbkey=CDS', 'gene=BVRF1', 'locus_tag=HHV4_BVRF1', 'product=DNA packaging tegument protein UL25', 'protein_id=YP_401703.1']

NC_007605.1 (forward strand): Structure number 317 from nt 133385 to 133435 (nt 75 to 125)

```
5'-GACCUGGAUGCUGUAGUGGCCUUCUCUGAUGGCCUGGAGAGCAUGCAGGUC-3'
5'-((((((.(((((.(...(((((.((...)).)))))...).)))))).)))))))-3'
Motif MFE = -27.8; z-score = -4.11; ED = 1.41
```



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

Extracted structure model with flanking nucleotides 133311 to 133510 (motif highlighted in silver):

```
5'-AAAAUAGGCUGCUCCGCGUGGAGCUGGACGGCAUCAUGCGUGACCACCUGGCCAGGGCGGAGGAGAUCCGCCAGGACCUGGAUGCUGUAGUGGCCUUCUCUGAUGGCCUGG
AGAGCAUGCAGGUCAGGUCCCCCUCCACGGGAGGGCGCUCUGCGCCAGCCCCGCCCUCCCCAUCCCCAGCCCAGCCGUUCACUCGGCUC-3
5'-....((((.((.(((((((((.(((....))).)))))))).)).)))))).....((((((.((((....((((..((((((.(((((.(...((((.((...)).)))))...
).)))))).)))))).)))....)))))..(((((((((.....((....)).)))))))))).....)).))))((((.....)))))).-3'
MFE = -95.6; z-score = -2.62; ED = 39.47
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BXRF1, 132571-134886(+)

Attributes: ['ID=gene-HHV4_BXRF1', 'Dbxref=GeneID:3783743', 'Name=BXRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BXRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BXRF1']

3-- nt 1 to 7--CDS, cds-YP_401702.1, 132571-133317(+)

Attributes: ['ID=cds-YP_401702.1', 'Parent=gene-HHV4_BXRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B8,Genbank:YP_401702.1,GeneID:3783743', 'Name=YP_401702.1', 'gbkey=CDS', 'gene=BXRF1', 'locus_tag=HHV4_BXRF1', 'product=nuclear protein UL24', 'protein_id=YP_401702.1']

4-- nt 1 to 200--gene, gene-HHV4_BVRF1, 133013-134886(+)

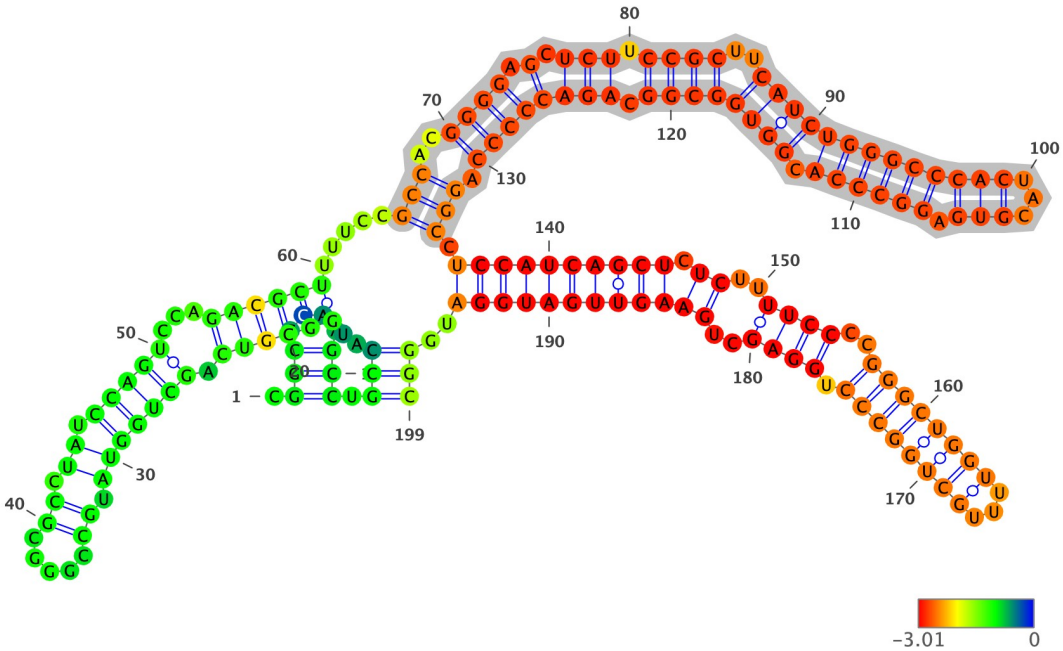
Attributes: ['ID=gene-HHV4_BVRF1', 'Dbxref=GeneID:3783732', 'Name=BVRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BVRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BVRF1']

5-- nt 1 to 200--CDS, cds-YP_401703.1, 133127-134839(+)

Attributes: ['ID=cds-YP_401703.1', 'Parent=gene-HHV4_BVRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B7,Genbank:YP_401703.1,GeneID:3783732', 'Name=YP_401703.1', 'gbkey=CDS', 'gene=BVRF1', 'locus_tag=HHV4_BVRF1', 'product=DNA packaging tegument protein UL25', 'protein_id=YP_401703.1']

NC_007605.1 (forward strand): Structure number 318 from nt 134421 to 134490 (nt 65 to 134)

```
5'-GCCACGGGGAGCUCUUCCGCUUCAUCUGGGCCCACUACGUGAGGCCCACGGUGGCGGCAGACCCCCAGGC-3'
5'-(((..((((.(.(((.((((..(((((((((((((...)))).)))))))).)))))))).)))))))).)))-3'
Motif MFE = -38.9; z-score = -3.35; ED = 5.32
```



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 134357 to 134555 (motif highlighted in silver):

```
5'-CGGCGCAAGCCUGCCAUGGCGUCAGCUGGUAUGCCGGGCGCCUAUCCAGUCCAGACGCUUUUCCGCCACGGGGAGCUCUUCCGCUUCAUCUGGGCCCACUACGUGAGGCCC
ACGGUGGCGGCAGACCCCCAGGCCUCCAUCAGCUCUCUUUUCCCCGGGCUGGUUUUGCUGGCCCUGGAGCUGAAGUUGAUGGAUGGGC-3
5'-.(((....)))).(((..(((((((.(((((((.((.....)).)).)))))...)))))).....(((..((((.(.(((.((((..((((((((((((...)))).)))))
).)))))))).)))))))).))).((((((((((.((..((((..((((((((...)))))))).)))))..)))))))))))))..)))-3'
MFE = -95.4; z-score = -3.47; ED = 21.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_BXRF1, 132571-134886(+)

Attributes: ['ID=gene-HHV4_BXRF1', 'Dbxref=GeneID:3783743', 'Name=BXRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BXRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BXRF1']

3-- nt 1 to 199--gene, gene-HHV4_BVRF1, 133013-134886(+)

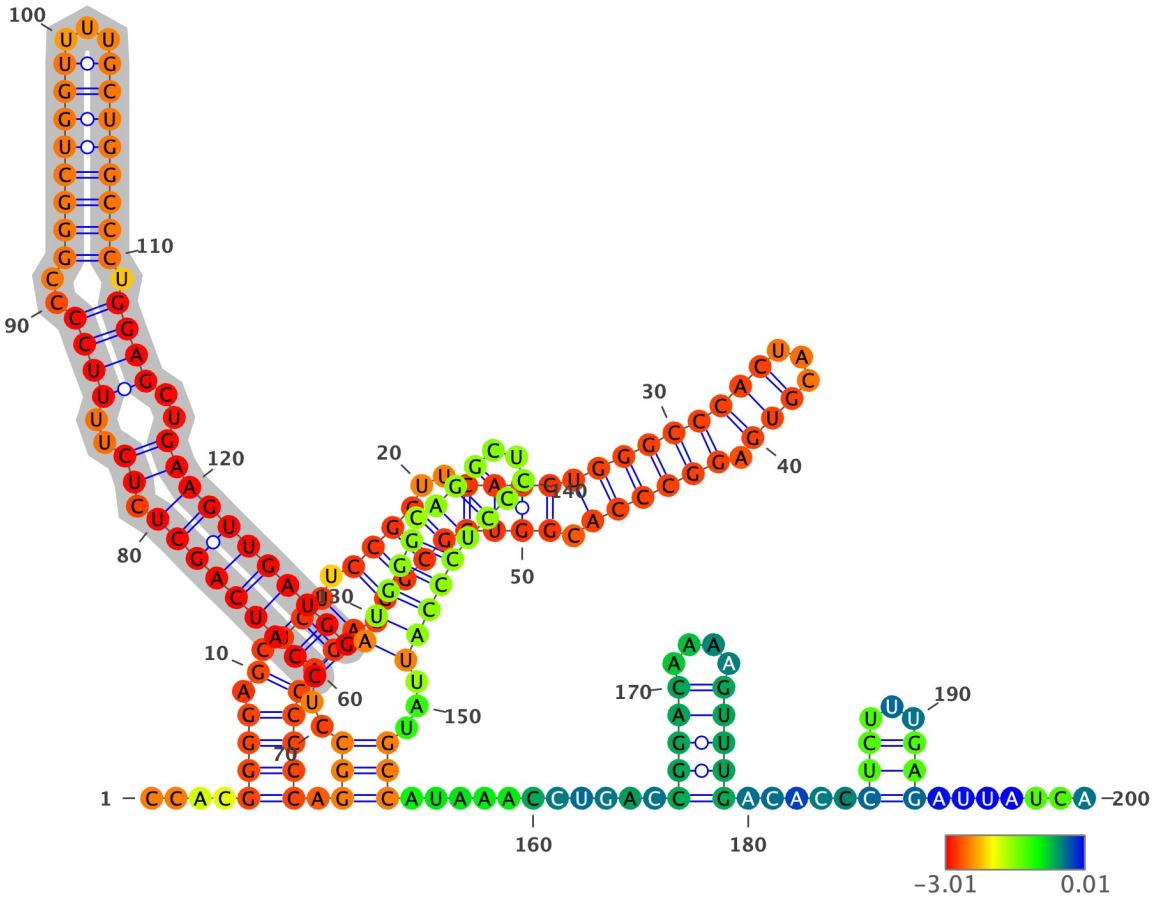
Attributes: ['ID=gene-HHV4_BVRF1', 'Dbxref=GeneID:3783732', 'Name=BVRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BVRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BVRF1']

4-- nt 1 to 199--CDS, cds-YP_401703.1, 133127-134839(+)

Attributes: ['ID=cds-YP_401703.1', 'Parent=gene-HHV4_BVRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B7,Genbank:YP_401703.1,GeneID:3783732', 'Name=YP_401703.1', 'gbkey=CDS', 'gene=BVRF1', 'locus_tag=HHV4_BVRF1', 'product=DNA packaging tegument protein UL25', 'protein_id=YP_401703.1']

NC_007605.1 (forward strand): Structure number 319 from nt 134493 to 134549 (nt 72 to 128)

```
5'-CCAUCAGCUCUCUUUUCCCCGGGCUGGUUUUGCUGGCCCUGGAGCUGAAGUUGAUGG-3'
5'-(((((((((.((..((((..(((((((((...)))))))))..))))..)))))))))))-3'
Motif MFE = -28.7; z-score = -4.25; ED = 2.06
```



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

Extracted structure model with flanking nucleotides 134422 to 134621 (motif highlighted in silver):

```
5'-CCACGGGGAGCUCUUCCGCUUCAUCUGGGCCCACUACGUGAGGCCCACGGUGGCGGCAGACCCCCAGGCCUCCAUCAGCUCUCUUUUCCCCGGGCUGGUUUUGCUGGCCCU
GGAGCUGAAGUUGAUGGAUGGGCAGGCUCCCUCCCAUUAUGCCAUAAACCUGACCGGACAAAAGUUUGACACCCUCUUUGAGAUUAUCA-3
5'-....(((((.(.(((.(((((..(((((((((((((...))).)))))).)))))))).)))))))).((((..((((((((((.((..((((..((((((((...)))))))).
))))..)))))))))))(((((.(((...)))))))...))).....((((....)))))).....(((...))).......-3'
MFE = -80.6; z-score = -3.74; ED = 18.16
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_BXRF1, 132571-134886(+)

Attributes: ['ID=gene-HHV4_BXRF1', 'Dbxref=GeneID:3783743', 'Name=BXRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BXRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BXRF1']

3-- nt 1 to 200--gene, gene-HHV4_BVRF1, 133013-134886(+)

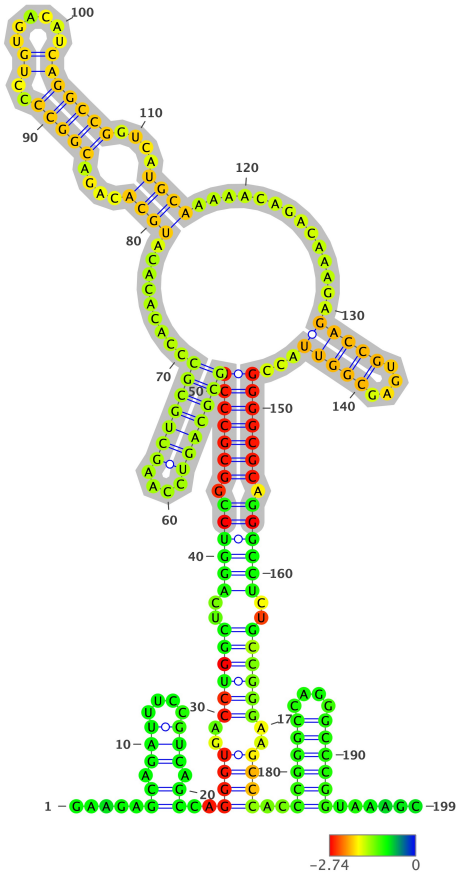
Attributes: ['ID=gene-HHV4_BVRF1', 'Dbxref=GeneID:3783732', 'Name=BVRF1', 'Note=core gene', 'gbkey=Gene', 'gene=BVRF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BVRF1']

4-- nt 1 to 200--CDS, cds-YP_401703.1, 133127-134839(+)

Attributes: ['ID=cds-YP_401703.1', 'Parent=gene-HHV4_BVRF1', 'Dbxref=UniProtKB/TrEMBL:Q777B7,Genbank:YP_401703.1,GeneID:3783732', 'Name=YP_401703.1', 'gbkey=CDS', 'gene=BVRF1', 'locus_tag=HHV4_BVRF1', 'product=DNA packaging tegument protein UL25', 'protein_id=YP_401703.1']

NC_007605.1 (forward strand): Structure number 320 from nt 135216 to 135331 (nt 42 to 157)

```
5'-CCGGCGCCCUGCGCAGUCCAAGCUGCGCCCACACACAUGCACAGACGGCCCCUGUGACAUCAGGCCGGUCAUGCAAAAACAGACAAAGAGACCGUGAGCGGUUACCGGGGC
GCAGG-3'
5'-(..(((((((.........................((((....(((((............)))))....))))..............((((((....))))))...))))))..)-3'
Motif MFE = -45.1; z-score = -2.32; ED = 13.98
```



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 135175 to 135373 (motif highlighted in silver):

```
5'-GAAGAGCAGAUUUCCGUCAGCCAGGGUGACCUGGCUCAGGUCCGGCGCCCUGCGCAGUCCAAGCUGCGCCCACACACAUGCACAGACGGCCCCUGUGACAUCAGGCCGGUC
AUGCAAAAACAGACAAAGAGACCGUGAGCGGUUACCGGGGCGCAGGGCCUCUGCCGGGAAGCCCACCCGGGCCAGGGCCCGGUAAAGC-3
5'-.....((.((.....)))).))..((((..(((((((..(((((((.(((((((((((((((....)))))))).........((((....((((((..((......)))))))).....
.))))..............((((((....)))))).....)))))))).)))))).))))))..))))..((((((....)))))).......-3'
MFE = -90.5; z-score = -3.01; ED = 7.49
```

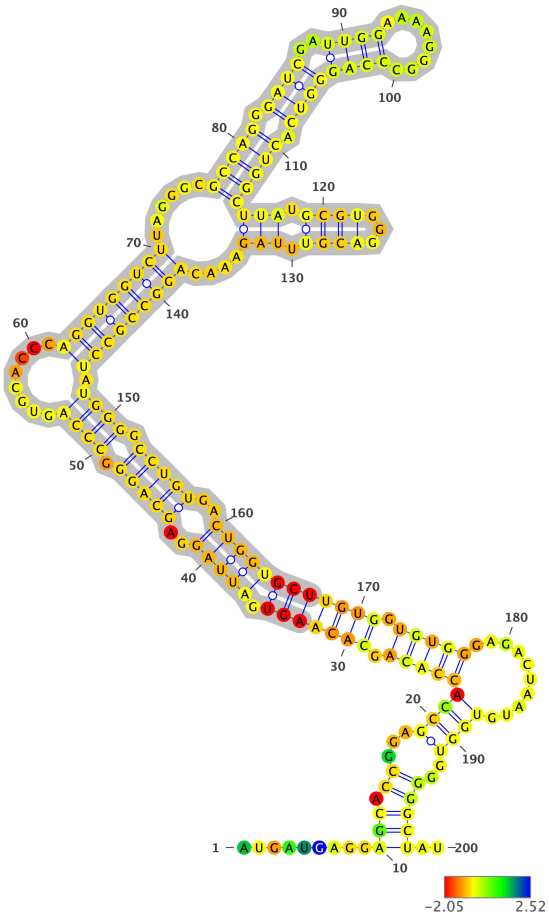
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 321 from nt 137589 to 137723 (nt 33 to 167)

```
5'-AGUGAUUAGGAGCAGGGCCCAGUGCACCCAGGUGGUCUUAGGGCGCCAGGGAUCGAUUGGAAAAGGGCCCAGGGUCACUGGCUUAUGCGUGGGACGUUUAGAAACAGGCCG
CCUAUGGGGCCUGUGACUGGUGCU-3'
5'-(((.....................................................................................................
.....................)))-3'
Motif MFE = -51.7; z-score = -1.19; ED = 38.99
```



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 137557 to 137756 (motif highlighted in silver):

```
5'-AUGAUGAGGAGCACCGGAGCCACCACAGCACAAGUGAUUAGGAGCAGGGCCCAGUGCACCCAGGUGGUCUUAGGGCGCCAGGGAUCGAUUGGAAAAGGGCCCAGGGUCACU
GGCUUAUGCGUGGGACGUUUAGAAACAGGCCGCCUAUGGGGCCUGUGACUGGUGCUUGUGGUGUGGGAGACUAAUGUGGUGGGGGCUAU-3
5'-.........(((.((...(((((((((.(((((((.(((((..(((((.(((((........(((((((((.....(((((.((((..((((........)))))))).))
)))))((.((((...)))).)))....)))))))))).)))).)))))..)))))))))))))).)))))..........))))..)))))..-3'
MFE = -80.5; z-score = -2.71; ED = 33.77
```

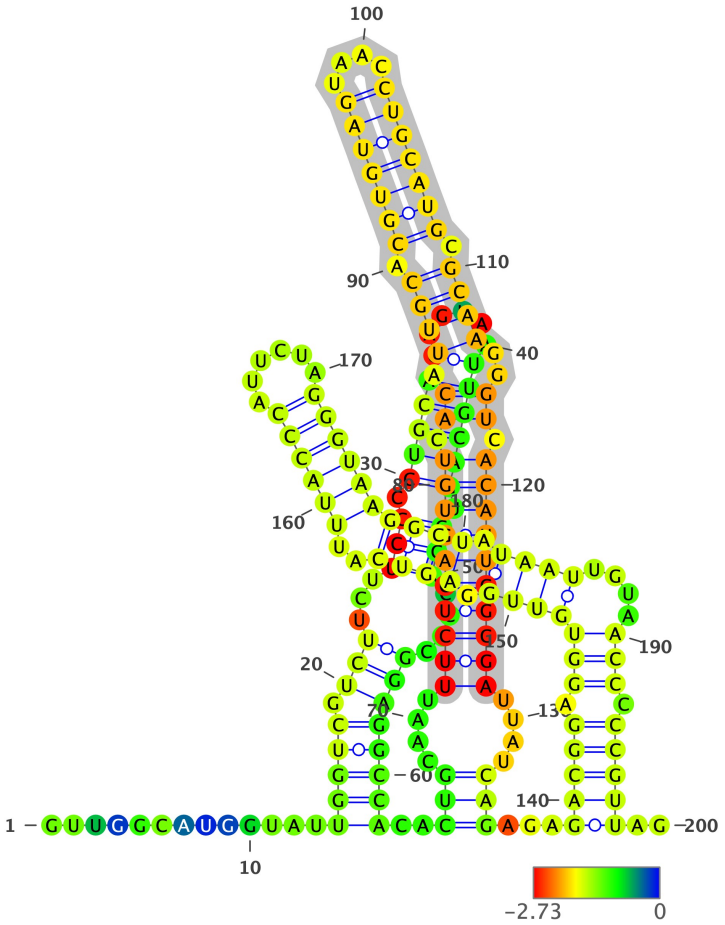
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 322 from nt 137876 to 137932 (nt 72 to 128)

```
5'-UUCUCAGUGUCACAUUGCACGUGUAGUAACCUGCAUGCGCAAGGGUCACAUUGGGGA-3'
5'-(((((((((.((.((.......................)).)).)))))))))-3'
Motif MFE = -25.4; z-score = -4.27; ED = 1.89
```



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

Extracted structure model with flanking nucleotides 137805 to 138004 (motif highlighted in silver):

```
5'-GUUGGCAUGGUAUUGGUCGUCUUCUUCCCCUGCAGAGUAAUUGCAGUGGACCCCGGAGGCCACACUGCAAUUUCUCAGUGUCACAUUGCACGUGUAGUAACCUGCAUGCGC
AAGGGUCACAUUGGGGAUUAUCAGAGAGACGGAGGUGUUGGAGUCAUUUACCCAUUCUAGGGUAAGGCUAUAAUUGUAACCCCCGUUAG-3
5'-.............(((((.(((...(((.((((((.....)))))).))).....))))))))..(((....((((((((((.((.((((.(((((((....)))))))).))
))..)).))))))))))....)))...(((((.(((((((.((((..((((((.....)))))))))))).)))).....))).)))))..-3'
MFE = -68.2; z-score = -2.26; ED = 25.23
```

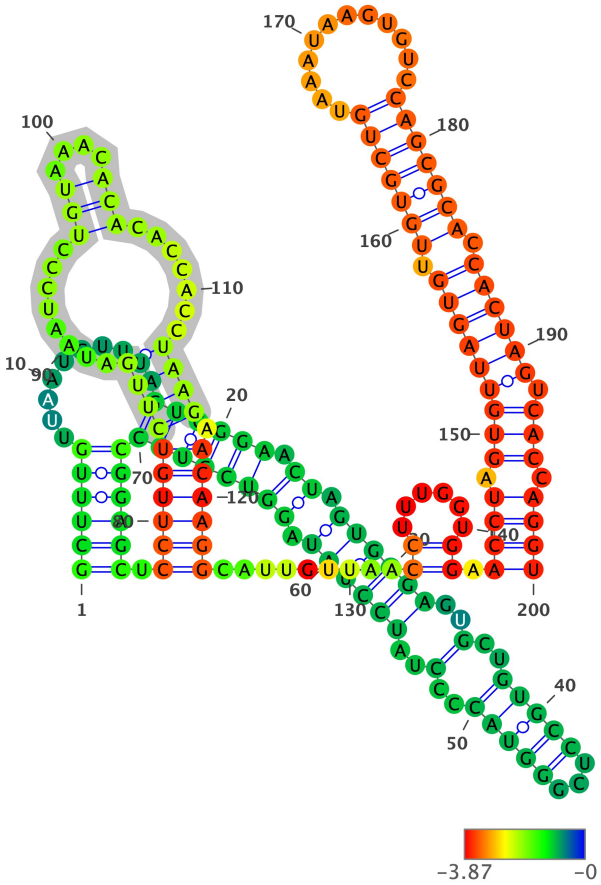
Overlapping Features #--relative location--feature type, feature_id, feature location(i,j,strand):

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

NC_007605.1 (forward strand): Structure number 323 from nt 139027 to 139059 (nt 84 to 116)

```
5'-CUUGAUAAUCCCUGUAAACACACACCACCUAAG-3'
5'-(((.........(((....)))........)))-3'
Motif MFE = 0.0; z-score = 0.67; 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 138944 to 139143 (motif highlighted in silver):

```
5'-GCUUUGUUAAUCUUUAGUGGGAACUAGUGGGAGUGCUGUGCCUCGGGUACCCCUAUCCUAUAGGUCCUACCGGAGCUCCUUGUCUUGAUAAUCCCUGUAAACACACACCAC
CUAAGAACAAGGCAUUGUUAACCUUUGGUGGAACCUAGUGUUAGUGUUGUGCUGUAAAUAAGUGUCCAGCGCACCACUAGUCACCAGGU-3
5'-(((((((..........((((((.((.(((((((..(..((((((...))))))..)..)))))))).))))))))))))))).((((((((((........(((....)))).....
.)))).)))))).........((......)).((((.(((((((((.((((((((.............)))))))).)))))))..))).)))).))))-3'
MFE = -60.3; z-score = -3.11; ED = 28.25
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 4 to 200--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 144 to 164--miRNA, rna-HHV4_RPMS1-2, 139087-139107(+)

Attributes: ['ID=rna-HHV4_RPMS1-2', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

6-- nt 144 to 164--exon, exon-HHV4_RPMS1-2-1, 139087-139107(+)

Attributes: ['ID=exon-HHV4_RPMS1-2-1', 'Parent=rna-HHV4_RPMS1-2', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

7-- nt 181 to 200--miRNA, rna-HHV4_RPMS1-3, 139124-139145(+)

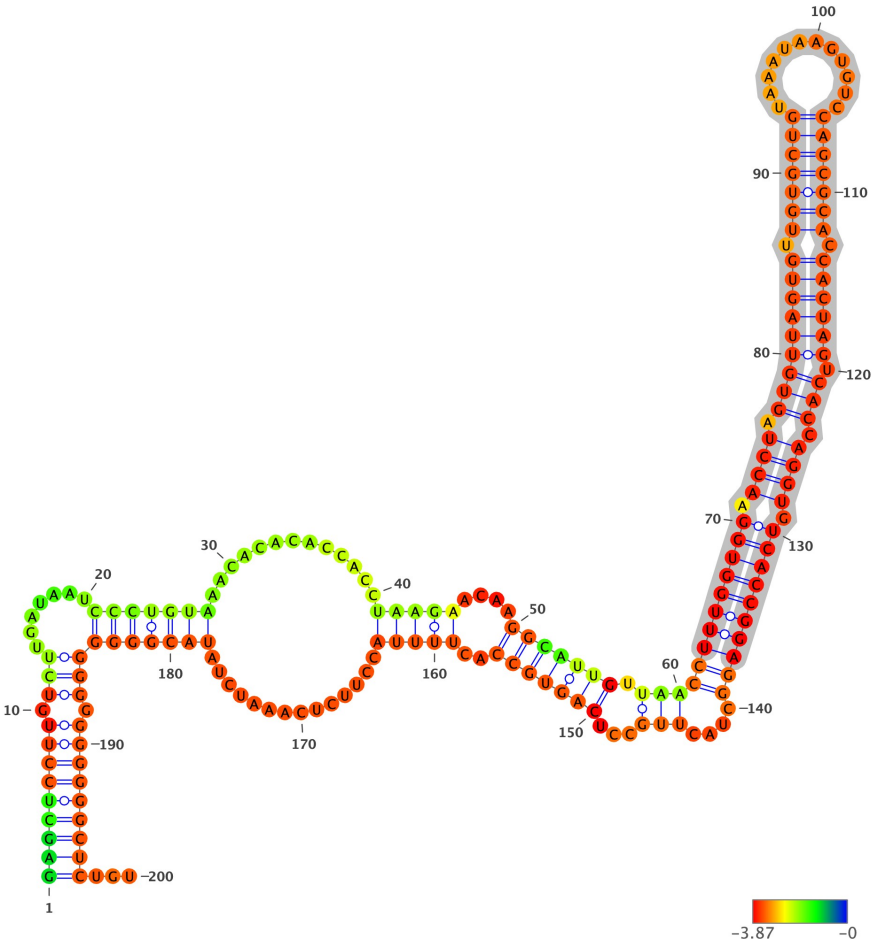
Attributes: ['ID=rna-HHV4_RPMS1-3', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

8-- nt 181 to 200--exon, exon-HHV4_RPMS1-3-1, 139124-139145(+)

Attributes: ['ID=exon-HHV4_RPMS1-3-1', 'Parent=rna-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

NC_007605.1 (forward strand): Structure number 324 from nt 139078 to 139152 (nt 63 to 137)

```
5'-UUUGGUGGAACCUAGUGUUAGUGUUGUGCUGUAAAUAAGUGUCCAGCGCACCACUAGUCACCAGGUGUCACCGGA-3'
5'-(((((((.((((.(((((((((.(((((((.........)))))))).)))))).))).)))).)))))))))-3'
Motif MFE = -34.3; z-score = -4.5; 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 139016 to 139215 (motif highlighted in silver):

```
5'-GAGCUCCUUGUCUUGAUAAUCCCUGUAAACACACACCACCUAAGAACAAGGCAUUGUUAACCUUUGGUGGAACCUAGUGUUAGUGUUGUGCUGUAAAUAAGUGUCCAGCGC
ACCACUAGUCACCAGGUGUCACCGGAGGCUACUUGCCUCAGUGCCACUUUUACCUUCUCAAAUCUAUACGGGGGGGGGGGGGGCUCUGU-3
5'-(((((((((.(((.......((((((.............(((((....(((((((.(((((((((((((.((((.(((((((((.(((((((.........)))))))
).)))))).))).)))).))))))))))....)))...)))))))..)))))).............)))))))))).)))))))))...-3'
MFE = -73.9; z-score = -4.13; ED = 19.53
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 72 to 92--miRNA, rna-HHV4_RPMS1-2, 139087-139107(+)

Attributes: ['ID=rna-HHV4_RPMS1-2', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

6-- nt 72 to 92--exon, exon-HHV4_RPMS1-2-1, 139087-139107(+)

Attributes: ['ID=exon-HHV4_RPMS1-2-1', 'Parent=rna-HHV4_RPMS1-2', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

7-- nt 109 to 130--miRNA, rna-HHV4_RPMS1-3, 139124-139145(+)

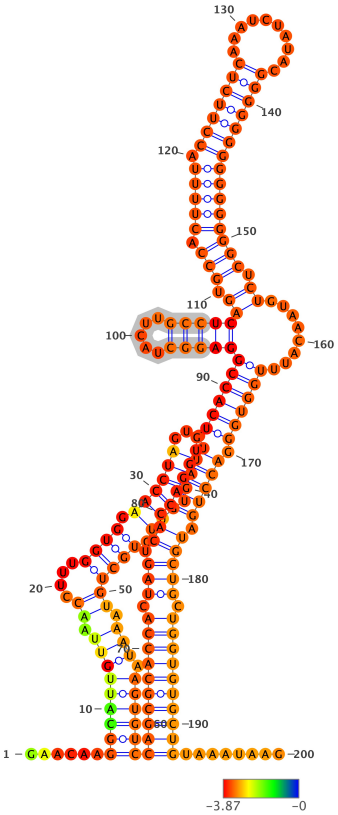
Attributes: ['ID=rna-HHV4_RPMS1-3', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

8-- nt 109 to 130--exon, exon-HHV4_RPMS1-3-1, 139124-139145(+)

Attributes: ['ID=exon-HHV4_RPMS1-3-1', 'Parent=rna-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

NC_007605.1 (forward strand): Structure number 325 from nt 139153 to 139163 (nt 95 to 105)

```
5'-GGCUACUUGCC-3'
5'-(((.....)))-3'
Motif MFE = -3.1; z-score = -4.8; ED = 0.09
```



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 139059 to 139258 (motif highlighted in silver):

```
5'-GAACAAGGCAUUGUUAACCUUUGGUGGAACCUAGUGUUAGUGUUGUGCUGUAAAUAAGUGUCCAGCGCACCACUAGUCACCAGGUGUCACCGGAGGCUACUUGCCUCAGUG
CCACUUUUACCUUCUCAAAUCUAUACGGGGGGGGGGGGGGCUCUGUAACAUUUGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAG-3
5'-......(((((((((.((....((((.((((((....))).))).)))))).))).)))))).((((((((((.(((.((.(((((.((((((((((.....)))))))(.(
((.(((((.(((((((.........)))))))))))))).))........)))))).)))))).)))))).))))))))))........-3'
MFE = -74.4; z-score = -2.95; ED = 28.57
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 29 to 49--miRNA, rna-HHV4_RPMS1-2, 139087-139107(+)

Attributes: ['ID=rna-HHV4_RPMS1-2', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

6-- nt 29 to 49--exon, exon-HHV4_RPMS1-2-1, 139087-139107(+)

Attributes: ['ID=exon-HHV4_RPMS1-2-1', 'Parent=rna-HHV4_RPMS1-2', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

7-- nt 66 to 87--miRNA, rna-HHV4_RPMS1-3, 139124-139145(+)

Attributes: ['ID=rna-HHV4_RPMS1-3', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

8-- nt 66 to 87--exon, exon-HHV4_RPMS1-3-1, 139124-139145(+)

Attributes: ['ID=exon-HHV4_RPMS1-3-1', 'Parent=rna-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

9-- nt 170 to 191--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

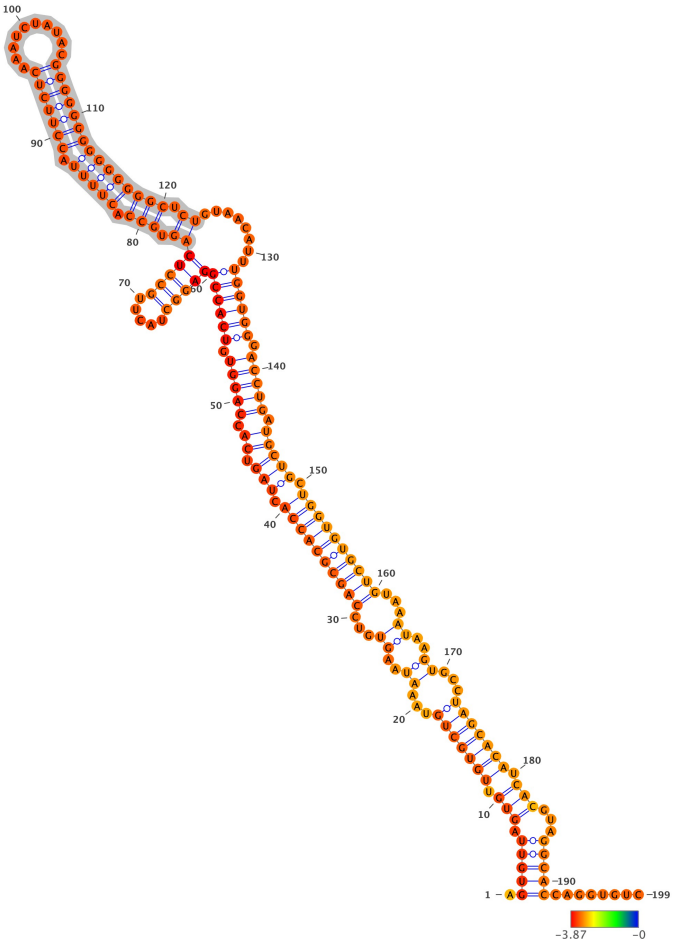
Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

10-- nt 170 to 191--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

NC_007605.1 (forward strand): Structure number 326 from nt 139166 to 139213 (nt 76 to 123)

```
5'-AGUGCCACUUUUACCUUCUCAAAUCUAUACGGGGGGGGGGGGGCUCU-3'
5'-((.((((.(((((.(((((((.........)))))))))))))))).))-3'
Motif MFE = -15.2; z-score = -0.91; ED = 8.07
```



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 139091 to 139289 (motif highlighted in silver):

```
5'-AGUGUUAGUGUUGUGCUGUAAAUAAGUGUCCAGCGCACCACUAGUCACCAGGUGUCACCGGAGGCUACUUGCCUCAGUGCCACUUUUACCUUCUCAAAUCUAUACGGGGGG
GGGGGGGGCUCUGUAACAUUUGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACAUCACGUAGGCACCAGGUGUC-3
5'-.(((((.(((.(((((((...((..((...((((((((((.(((.((.(((((.((((((((((.....)))))((.(((.(((((.(((((((.........)))))))
)))))))))).)).......))))))).)))))).)))))).))))))))))...)).)).)).....))))))).))).....)))))........-3'
MFE = -81.0; z-score = -3.59; ED = 44.22
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 17--miRNA, rna-HHV4_RPMS1-2, 139087-139107(+)

Attributes: ['ID=rna-HHV4_RPMS1-2', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

6-- nt 1 to 17--exon, exon-HHV4_RPMS1-2-1, 139087-139107(+)

Attributes: ['ID=exon-HHV4_RPMS1-2-1', 'Parent=rna-HHV4_RPMS1-2', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3*']

7-- nt 34 to 55--miRNA, rna-HHV4_RPMS1-3, 139124-139145(+)

Attributes: ['ID=rna-HHV4_RPMS1-3', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

8-- nt 34 to 55--exon, exon-HHV4_RPMS1-3-1, 139124-139145(+)

Attributes: ['ID=exon-HHV4_RPMS1-3-1', 'Parent=rna-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART3']

9-- nt 138 to 159--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

10-- nt 138 to 159--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

11-- nt 176 to 198--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

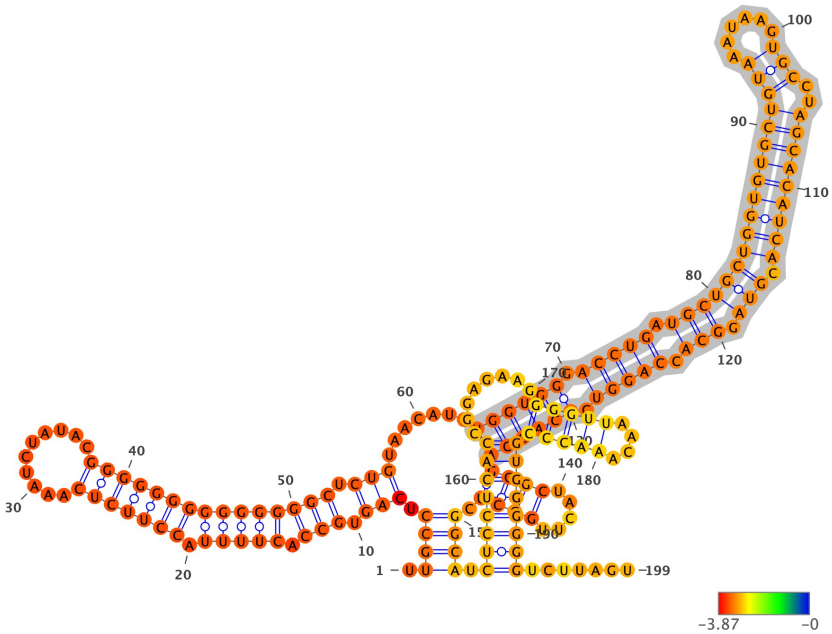
Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

12-- nt 176 to 198--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

NC_007605.1 (forward strand): Structure number 327 from nt 139222 to 139293 (nt 64 to 135)

```
5'-UGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACAUCACGUAGGCACCAGGUGUCACCA-3'
5'-((((((.(((((.(((((((((((((((((.....)))..)))))))))).)))).)))).)))))).)))))))-3'
Motif MFE = -37.5; z-score = -4.58; ED = 4.38
```



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

Extracted structure model with flanking nucleotides 139159 to 139357 (motif highlighted in silver):

```
5'-UUGCCUCAGUGCCACUUUUACCUUCUCAAAUCUAUACGGGGGGGGGGGGGGCUCUGUAACAUUUGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACA
UCACGUAGGCACCAGGUGUCACCAGGGCUACUUGCCUCGGCAUCUCCUCACCGGAGAAGGGGUUAACAAACCCGUGGGGGGUCUUAGU-3
5'-.((((.(((.(((.(((((.(((((((.........))))))))))))))).))).......((((((.(((((.((((((((((((((((.....)))).)))))))
))).))).))).)))))).))))))((((.....)))).)))).((((((((.......(((((....)))))))))))).......-3'
MFE = -82.6; z-score = -3.21; ED = 42.42
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 171--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 70 to 91--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

6-- nt 70 to 91--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

7-- nt 108 to 130--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

8-- nt 108 to 130--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

9-- nt 193 to 199--miRNA, rna-HHV4_RPMS1-6, 139351-139374(+)

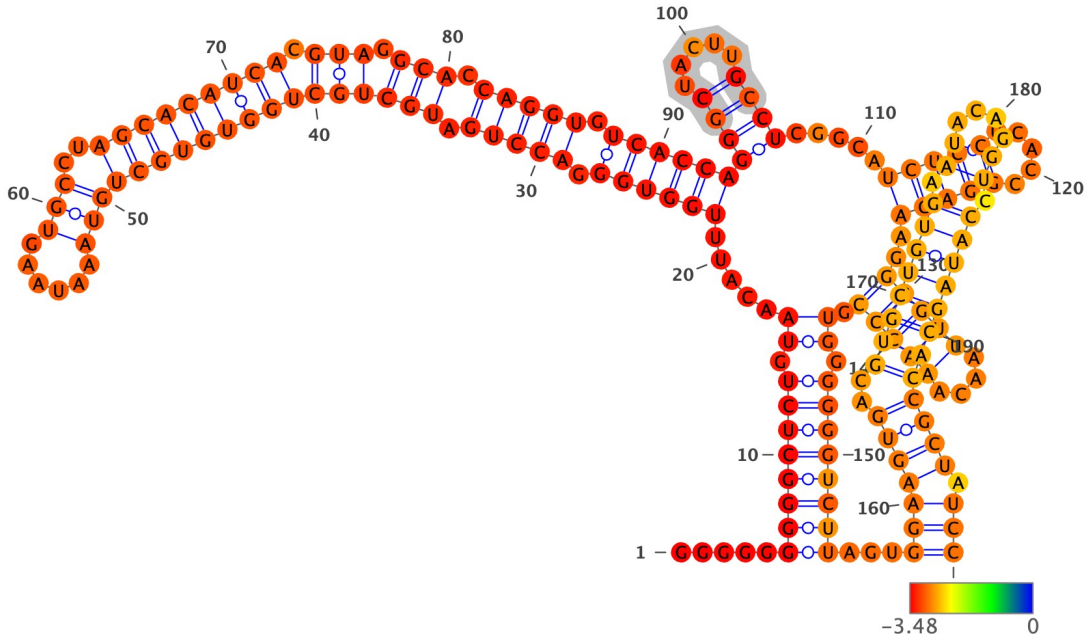
Attributes: ['ID=rna-HHV4_RPMS1-6', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

10-- nt 193 to 199--exon, exon-HHV4_RPMS1-6-1, 139351-139374(+)

Attributes: ['ID=exon-HHV4_RPMS1-6-1', 'Parent=rna-HHV4_RPMS1-6', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

NC_007605.1 (forward strand): Structure number 328 from nt 139296 to 139304 (nt 96 to 104)

```
5'-GCUACUUGC-3'
5'-(.......)-3'
Motif MFE = 0.0; z-score = #DIV/0!; ED = 0.98
```



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

Extracted structure model with flanking nucleotides 139201 to 139400 (motif highlighted in silver):

```
5'-GGGGGGGGGCUCUGUAACAUUUGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACAUCACGUAGGCACCAGGUGUCACCAGGGCUACUUGCCUCGGCA
UCUCCUCACCGGAGAAGGGGUUAACAAACCCGUGGGGGGUCUUAGUGGAAGUGACGUGCUGUGAAUACAGGUCCAUAGCACCGCUAUCC-3
5'-.....(((((((((.(((.....((((((.(((((.(((((((((((((((((((.....)))..)))))))))).))).))).)))))).))))))((((.....)))).....
(((((.....)))))..(((((.....)))))).)).))))))))...(((((((..((((((((.((....)).)))))))))))).)))-3'
MFE = -81.9; z-score = -2.86; ED = 17.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 129--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 28 to 49--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

6-- nt 28 to 49--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

7-- nt 66 to 88--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

8-- nt 66 to 88--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

9-- nt 151 to 174--miRNA, rna-HHV4_RPMS1-6, 139351-139374(+)

Attributes: ['ID=rna-HHV4_RPMS1-6', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

10-- nt 151 to 174--exon, exon-HHV4_RPMS1-6-1, 139351-139374(+)

Attributes: ['ID=exon-HHV4_RPMS1-6-1', 'Parent=rna-HHV4_RPMS1-6', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

11-- nt 187 to 200--miRNA, rna-HHV4_RPMS1-7, 139387-139408(+)

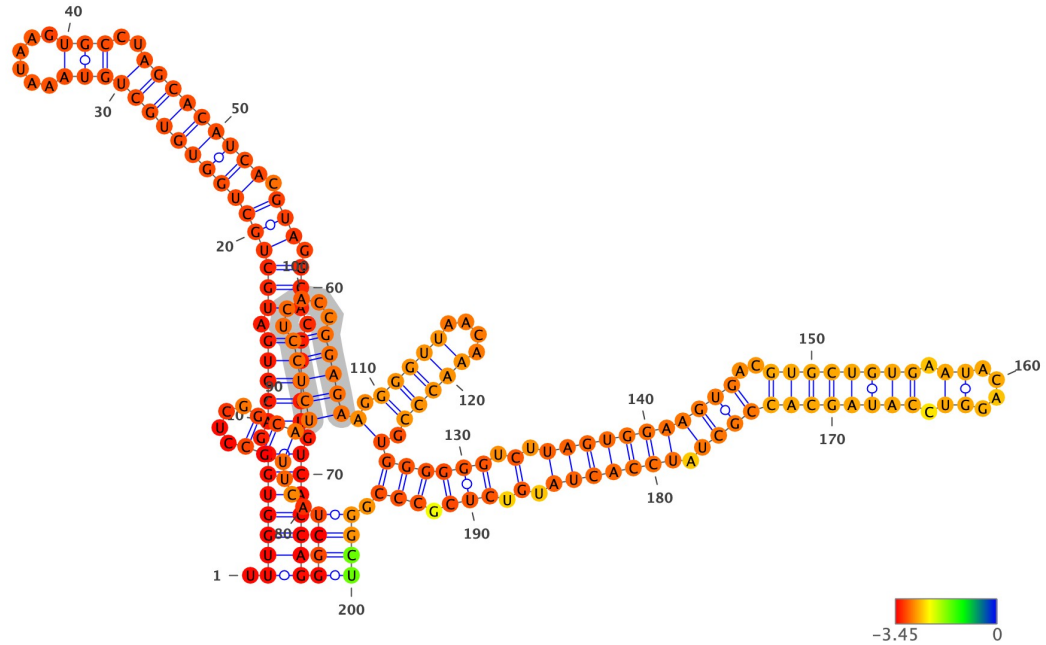
Attributes: ['ID=rna-HHV4_RPMS1-7', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

12-- nt 187 to 200--exon, exon-HHV4_RPMS1-7-1, 139387-139408(+)

Attributes: ['ID=exon-HHV4_RPMS1-7-1', 'Parent=rna-HHV4_RPMS1-7', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

NC_007605.1 (forward strand): Structure number 329 from nt 139312 to 139326 (nt 93 to 107)

```
5'-UCUCCUCACCGGAGA-3'
5'-(((((.....)))))-3'
Motif MFE = -5.4; z-score = -5.77; ED = 0.49
```



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 139220 to 139419 (motif highlighted in silver):

```
5'-UUUGGUGGGACCUGAUGCUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACAUCACGUAGGCACCAGGUGUCACCAGGGCUACUUGCCUCGGCAUCUCCUCACCGGAGAAGGG
GUUAACAAACCCGUGGGGGGUCUUAGUGGAAGUGACGUGCUGUGAAUACAGGUCCAUAGCACCGCUAUCCACUAUGUCUCGCCCGGGCU-3
5'-.(((((((.(((((.((((((((((((((((((.....)))..)))))))))).))).))).)))))).)))))))((((...((((....)))((((((.....))))))(.((
(((....))))).)((((((.(.((((((((((..(((((((.((....)).)))))))))))).))))))).).))).))).))))-3'
MFE = -92.7; z-score = -5.19; ED = 21.14
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 110--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 9 to 30--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

6-- nt 9 to 30--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

7-- nt 47 to 69--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

8-- nt 47 to 69--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

9-- nt 132 to 155--miRNA, rna-HHV4_RPMS1-6, 139351-139374(+)

Attributes: ['ID=rna-HHV4_RPMS1-6', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

10-- nt 132 to 155--exon, exon-HHV4_RPMS1-6-1, 139351-139374(+)

Attributes: ['ID=exon-HHV4_RPMS1-6-1', 'Parent=rna-HHV4_RPMS1-6', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

11-- nt 168 to 189--miRNA, rna-HHV4_RPMS1-7, 139387-139408(+)

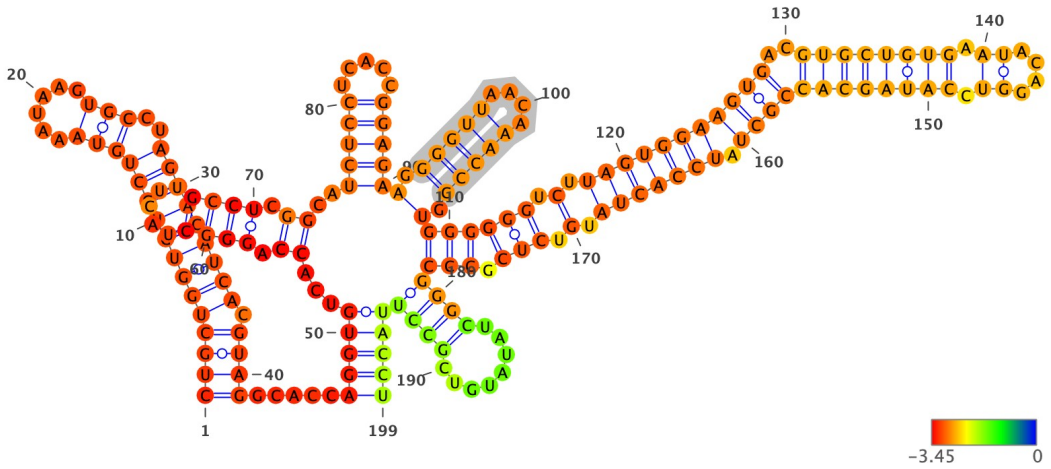
Attributes: ['ID=rna-HHV4_RPMS1-7', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

12-- nt 168 to 189--exon, exon-HHV4_RPMS1-7-1, 139387-139408(+)

Attributes: ['ID=exon-HHV4_RPMS1-7-1', 'Parent=rna-HHV4_RPMS1-7', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

NC_007605.1 (forward strand): Structure number 330 from nt 139329 to 139342 (nt 93 to 106)

```
5'-GGGUUAACAAACCC-3'
5'-(((((....)))))-3'
Motif MFE = -4.6; z-score = -5.94; 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 139237 to 139435 (motif highlighted in silver):

```
5'-CUGCUGGUGUGCUGUAAAUAAGUGCCUAGCACAUCACGUAGGCACCAGGUGUCACCAGGGCUACUUGCCUCGGCAUCUCCUCACCGGAGAAGGGGUUAACAAACCCGUGGG
GGGUCUUAGUGGAAGUGACGUGCUGUGAAUACAGGUCCAUAGCACCGCUAUCCACUAUGUCUCGCCCGGGCUAUAUGUCGCCUUACCU-3
5'-(((((((((((((((.....)))..))))))))).))))).....(((((...((.((((.....)))).)).)).(((((.....)))))(.(((((....)))))).)(((
(((.(.((((((((((..((((((((.((....)).))))))))))))).))))))).).))).)))((((.......)))))))))-3'
MFE = -81.9; z-score = -4.25; ED = 15.7
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 93--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 13--miRNA, rna-HHV4_RPMS1-4, 139228-139249(+)

Attributes: ['ID=rna-HHV4_RPMS1-4', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

6-- nt 1 to 13--exon, exon-HHV4_RPMS1-4-1, 139228-139249(+)

Attributes: ['ID=exon-HHV4_RPMS1-4-1', 'Parent=rna-HHV4_RPMS1-4', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4']

7-- nt 30 to 52--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

8-- nt 30 to 52--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

9-- nt 115 to 138--miRNA, rna-HHV4_RPMS1-6, 139351-139374(+)

Attributes: ['ID=rna-HHV4_RPMS1-6', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

10-- nt 115 to 138--exon, exon-HHV4_RPMS1-6-1, 139351-139374(+)

Attributes: ['ID=exon-HHV4_RPMS1-6-1', 'Parent=rna-HHV4_RPMS1-6', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

11-- nt 151 to 172--miRNA, rna-HHV4_RPMS1-7, 139387-139408(+)

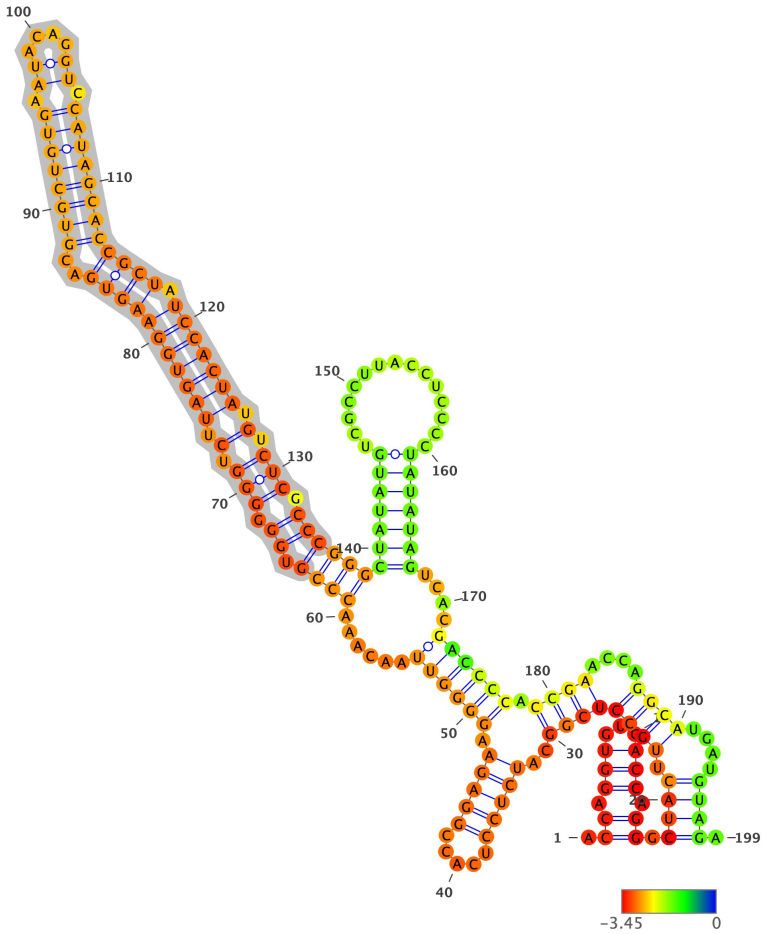
Attributes: ['ID=rna-HHV4_RPMS1-7', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

12-- nt 151 to 172--exon, exon-HHV4_RPMS1-7-1, 139387-139408(+)

Attributes: ['ID=exon-HHV4_RPMS1-7-1', 'Parent=rna-HHV4_RPMS1-7', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

NC_007605.1 (forward strand): Structure number 331 from nt 139343 to 139414 (nt 64 to 135)

```
5'-GUGGGGGGUCUUAGUGGAAGUGACGUGCUGUGAAUACAGGUCCAUAGCACCGCUAUCCACUAUGUCUCGCCC-3'
5'-(.((.(((.(.(((((((((((..(((((((((.((....)).))))))))))))).)))))))).).))).)))-3'
Motif MFE = -32.9; z-score = -3.96; 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 139280 to 139478 (motif highlighted in silver):

```
5'-ACCAGGUGUCACCAGGGCUACUUGCCUCGGCAUCUCCUCACCGGAGAAGGGGUUAACAAACCCGUGGGGGGUCUUAGUGGAAGUGACGUGCUGUGAAUACAGGUCCAUAGC
ACCGCUAUCCACUAUGUCUCGCCCGGGCUAUAUGUCGCCUUACCUCCCCUAUAUAGUCACGACCCCACCGAACCAGGCAUGAUGUAGA-3
5'-.((.((((...))).)).((((.(((((((((..(((((.....))))).((((((.....((((.((.(((.(.((((((((((..(((((((((.((....)).))))))
))))))).)))))))).).))).))))))((((((.............)))))))....)))))).))))....))))....)))).-3'
MFE = -72.2; z-score = -2.5; ED = 18.07
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 50--repeat_region, id-HHV4_RPMS1, 138947-139329(+)

Attributes: ['ID=id-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 9--miRNA, rna-HHV4_RPMS1-5, 139266-139288(+)

Attributes: ['ID=rna-HHV4_RPMS1-5', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

6-- nt 1 to 9--exon, exon-HHV4_RPMS1-5-1, 139266-139288(+)

Attributes: ['ID=exon-HHV4_RPMS1-5-1', 'Parent=rna-HHV4_RPMS1-5', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART4*']

7-- nt 72 to 95--miRNA, rna-HHV4_RPMS1-6, 139351-139374(+)

Attributes: ['ID=rna-HHV4_RPMS1-6', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

8-- nt 72 to 95--exon, exon-HHV4_RPMS1-6-1, 139351-139374(+)

Attributes: ['ID=exon-HHV4_RPMS1-6-1', 'Parent=rna-HHV4_RPMS1-6', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-5p']

9-- nt 108 to 129--miRNA, rna-HHV4_RPMS1-7, 139387-139408(+)

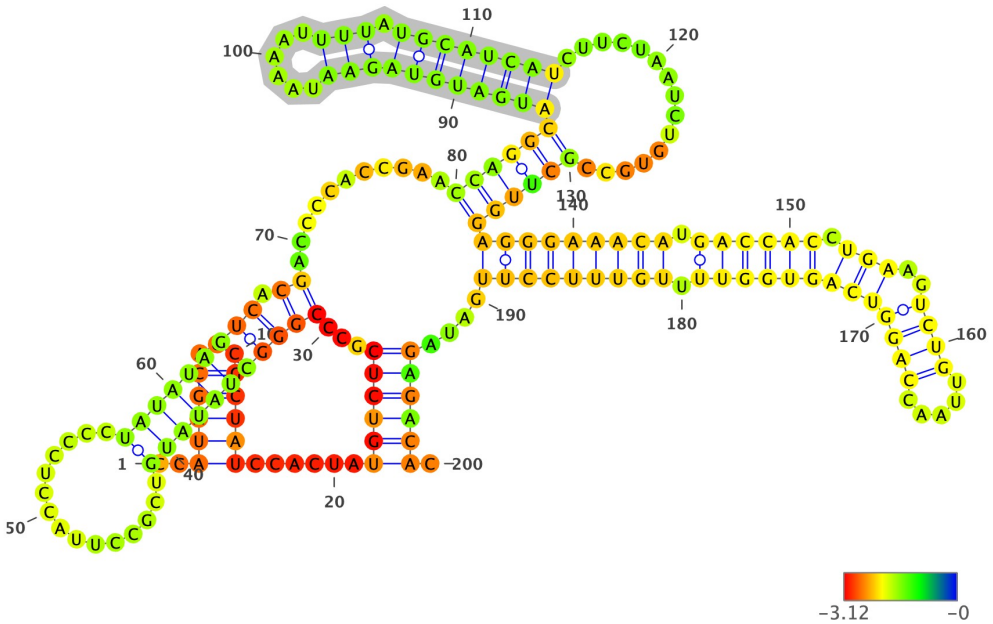
Attributes: ['ID=rna-HHV4_RPMS1-7', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

10-- nt 108 to 129--exon, exon-HHV4_RPMS1-7-1, 139387-139408(+)

Attributes: ['ID=exon-HHV4_RPMS1-7-1', 'Parent=rna-HHV4_RPMS1-7', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

NC_007605.1 (forward strand): Structure number 332 from nt 139469 to 139497 (nt 86 to 114)

```
5'-AUGAUGUAGAAUAAAAUUUUAUGCAUCAU-3'
5'-(.........................)-3'
Motif MFE = -6.6; z-score = -3.83; ED = 4.1
```



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 139384 to 139583 (motif highlighted in silver):

```
5'-CCAUAGCACCGCUAUCCACUAUGUCUCGCCCGGGCUAUAUGUCGCCUUACCUCCCCUAUAUAGUCACGACCCCACCGAACCAGGCAUGAUGUAGAAUAAAAUUUUAUGCAU
CAUCUUCUAAUCUGUGCCGCUUGGAGGGAAACAUGACCACCUGAAGUCUGUUAACCAGGUCAGUGGUUUUGUUUCCUUGAUAGAGACAC-3
5'-..(((((...)))))......((((((...((((((((((.............)))))))))).))..........((((((((((((((.....)))).)))))
)))).............))))))((((((((.(((((((.(((..((((.....)))))))))))))).))))))))....)))))).-3'
MFE = -56.8; z-score = -2.99; ED = 16.68
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 4 to 25--miRNA, rna-HHV4_RPMS1-7, 139387-139408(+)

Attributes: ['ID=rna-HHV4_RPMS1-7', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

5-- nt 4 to 25--exon, exon-HHV4_RPMS1-7-1, 139387-139408(+)

Attributes: ['ID=exon-HHV4_RPMS1-7-1', 'Parent=rna-HHV4_RPMS1-7', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART1-3p']

6-- nt 170 to 191--miRNA, rna-HHV4_RPMS1-8, 139553-139574(+)

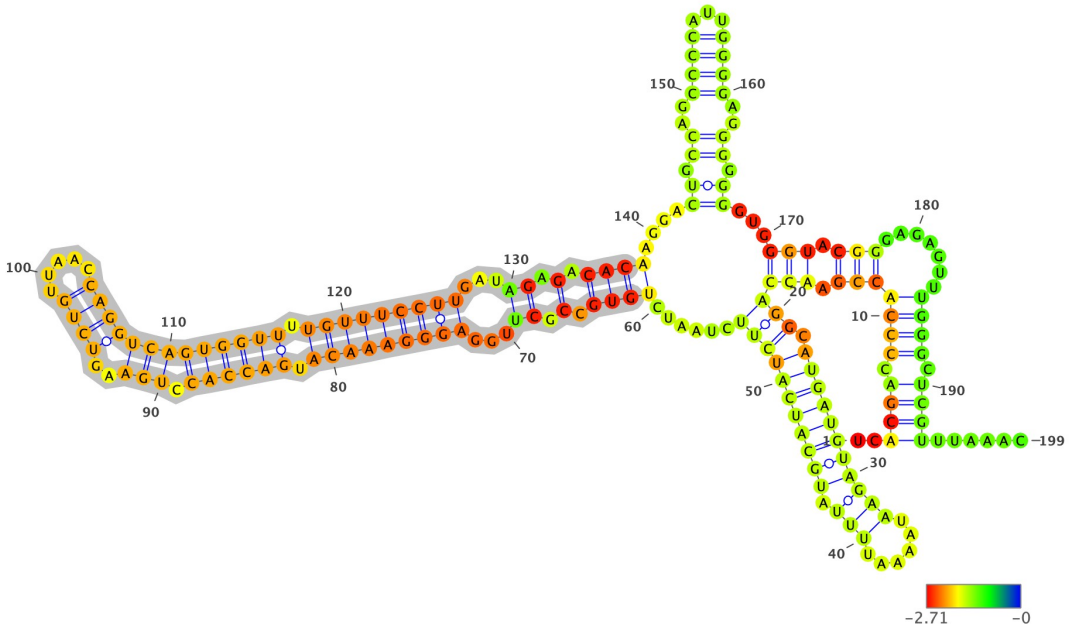
Attributes: ['ID=rna-HHV4_RPMS1-8', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART15']

7-- nt 170 to 191--exon, exon-HHV4_RPMS1-8-1, 139553-139574(+)

Attributes: ['ID=exon-HHV4_RPMS1-8-1', 'Parent=rna-HHV4_RPMS1-8', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART15']

NC_007605.1 (forward strand): Structure number 333 from nt 139508 to 139583 (nt 62 to 137)

```
5'-GUGCCGCUUGGAGGGAAACAUGACCACCUGAAGUCUGUUAACCAGGUCAGUGGUUUUGUUUCCUUGAUAGAGACAC-3'
5'-(((.(.(....(((((((((.(((((((.(((..((((.....)))))))))))))).))))))))).....).).)))-3'
Motif MFE = -28.2; z-score = -3.2; 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 139447 to 139645 (motif highlighted in silver):

```
5'-UCACGACCCCACCGAACCAGGCAUGAUGUAGAAUAAAAUUUUAUGCAUCAUCUUCUAAUCUGUGCCGCUUGGAGGGAAACAUGACCACCUGAAGUCUGUUAACCAGGUCAG
UGGUUUUGUUUCCUUGAUAGAGACACAAGGACUGCCAGCCCCAUUGGGGAGGGGGGUGGGUACGGGAGAGUUUGGGCUCGUUUAAAC-3
5'-..((((.(((((((.((((((.(((((((((((.....))).))))))))))).....((((.(.((...((((((((((.((((((.(((..((((.....)))))))))
)))))).)))))))))....)).).)))).....((.((..((((...)))))..)).)).....))).)))).....)))).)))).....-3'
MFE = -68.1; z-score = -2.5; ED = 32.56
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 107 to 128--miRNA, rna-HHV4_RPMS1-8, 139553-139574(+)

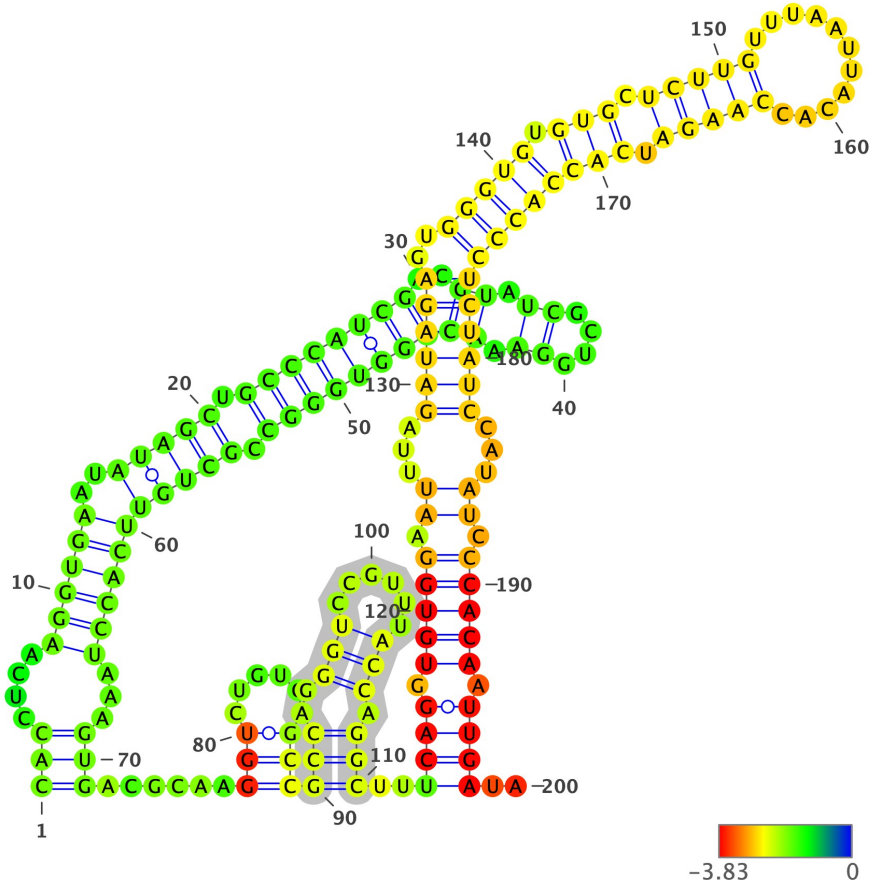
Attributes: ['ID=rna-HHV4_RPMS1-8', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART15']

5-- nt 107 to 128--exon, exon-HHV4_RPMS1-8-1, 139553-139574(+)

Attributes: ['ID=exon-HHV4_RPMS1-8-1', 'Parent=rna-HHV4_RPMS1-8', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART15']

NC_007605.1 (forward strand): Structure number 334 from nt 139759 to 139779 (nt 90 to 110)

```
5'-GCCAGGGUCCGUUUACCAGGC-3'
5'-(((..(((.....))).)))-3'
Motif MFE = -5.7; z-score = -0.87; ED = 2.17
```



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

Extracted structure model with flanking nucleotides 139670 to 139869 (motif highlighted in silver):

```
5'-CACCUCAAGGUGAAUAUAGCUGCCCAUCGACGUAUCGCUGGAAACCGGUGGGCCGCUGUUCACCUAAAGUGACGCAAGGUCUGUCAGCCGCCAGGGUCCGUUUACCAGGCU
UUCAGGUGUGGAAUUUAGAUAGAGUGGGUGUGUGCUCUUGUUUAAUUACACCAAGAUCACCACCCUCUAUCCAUAUCCCACAAUUGAUA-3
5'-((((....((((((..(((((.(((((((((..((.((....)).)))))))))).))))))))))...))).....(((.....)))(((..(((.....))).))).
.((((.(((((.((...((((((..(((((.(((.(((((..........)))))).))))))))))))...)).)))))).))))..-3'
MFE = -73.3; z-score = -4.18; ED = 16.34
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 55 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 6 to 29--miRNA, rna-HHV4_RPMS1-9, 139675-139698(+)

Attributes: ['ID=rna-HHV4_RPMS1-9', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5']

6-- nt 6 to 29--exon, exon-HHV4_RPMS1-9-1, 139675-139698(+)

Attributes: ['ID=exon-HHV4_RPMS1-9-1', 'Parent=rna-HHV4_RPMS1-9', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5']

7-- nt 48 to 65--miRNA, rna-HHV4_RPMS1-10, 139717-139734(+)

Attributes: ['ID=rna-HHV4_RPMS1-10', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5*']

8-- nt 48 to 65--exon, exon-HHV4_RPMS1-10-1, 139717-139734(+)

Attributes: ['ID=exon-HHV4_RPMS1-10-1', 'Parent=rna-HHV4_RPMS1-10', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5*']

9-- nt 126 to 149--miRNA, rna-HHV4_RPMS1-11, 139795-139818(+)

Attributes: ['ID=rna-HHV4_RPMS1-11', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

10-- nt 126 to 149--exon, exon-HHV4_RPMS1-11-1, 139795-139818(+)

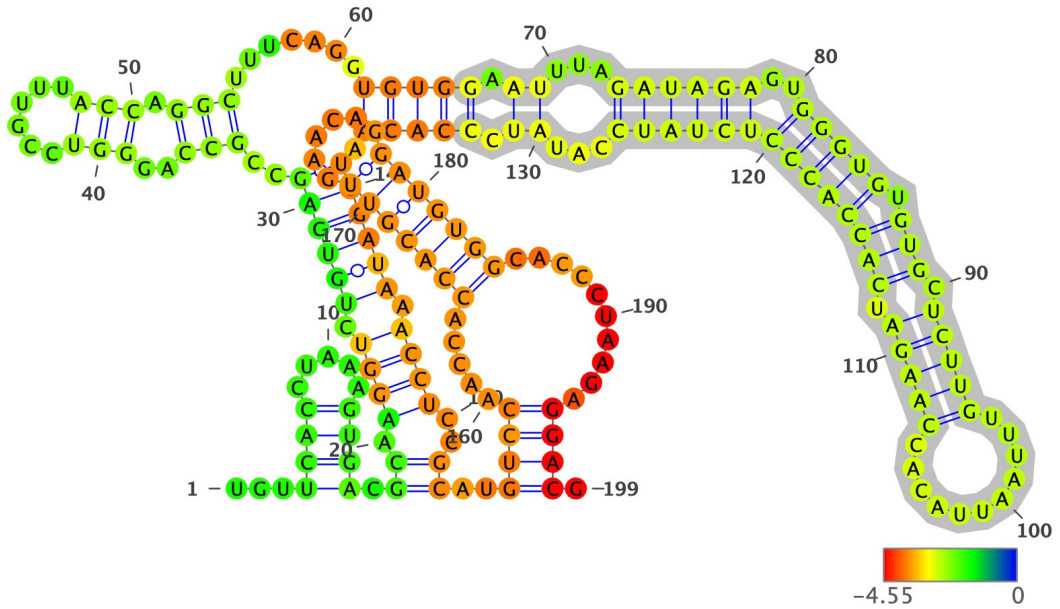
Attributes: ['ID=exon-HHV4_RPMS1-11-1', 'Parent=rna-HHV4_RPMS1-11', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

11-- nt 55 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 335 from nt 139791 to 139858 (nt 66 to 133)

```
5'-GAAUUUAGAUAGAGUGGGUGUGUGCUCUUGUUUAAUUACACCAAGAUCACCACCCUCUAUCCAUAUCC-3'
5'-(.((...(((((((..(((((.(((.(((((.........))))).))))))))))))))...)).)-3'
Motif MFE = -22.4; z-score = -4.41; ED = 3.71
```



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

Extracted structure model with flanking nucleotides 139726 to 139924 (motif highlighted in silver):

```
5'-UGUUCACCUAAAGUGACGCAAGGUCUGUCAGCCGCCAGGGUCCGUUUACCAGGCUUUCAGGUGUGGAAUUUAGAUAGAGUGGGUGUGUGCUCUUGUUUAAUUACACCAAGA
UCACCACCCUCUAUCCAUAUCCCACAAUUGAUAAACCUCCGCAUGUCCAACCACCACGUUGAACAGGAUGUGGCACCCUAAGAGGACG-3
5'-...((((.....)))).((.((((.(((((((..((((..((((.....))).))).))).....(((((.((...(((((((..(((((.(((.(((((.........))))))
.)))))))))))))...)).)))))).)))))).)))))..))..((((.....(((((((.....)))))))).........)))).-3'
MFE = -58.0; z-score = -1.76; ED = 36.17
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 9--miRNA, rna-HHV4_RPMS1-10, 139717-139734(+)

Attributes: ['ID=rna-HHV4_RPMS1-10', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5*']

6-- nt 1 to 9--exon, exon-HHV4_RPMS1-10-1, 139717-139734(+)

Attributes: ['ID=exon-HHV4_RPMS1-10-1', 'Parent=rna-HHV4_RPMS1-10', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART5*']

7-- nt 70 to 93--miRNA, rna-HHV4_RPMS1-11, 139795-139818(+)

Attributes: ['ID=rna-HHV4_RPMS1-11', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

8-- nt 70 to 93--exon, exon-HHV4_RPMS1-11-1, 139795-139818(+)

Attributes: ['ID=exon-HHV4_RPMS1-11-1', 'Parent=rna-HHV4_RPMS1-11', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

9-- nt 190 to 199--miRNA, rna-HHV4_RPMS1-12, 139915-139936(+)

Attributes: ['ID=rna-HHV4_RPMS1-12', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

10-- nt 190 to 199--exon, exon-HHV4_RPMS1-12-1, 139915-139936(+)

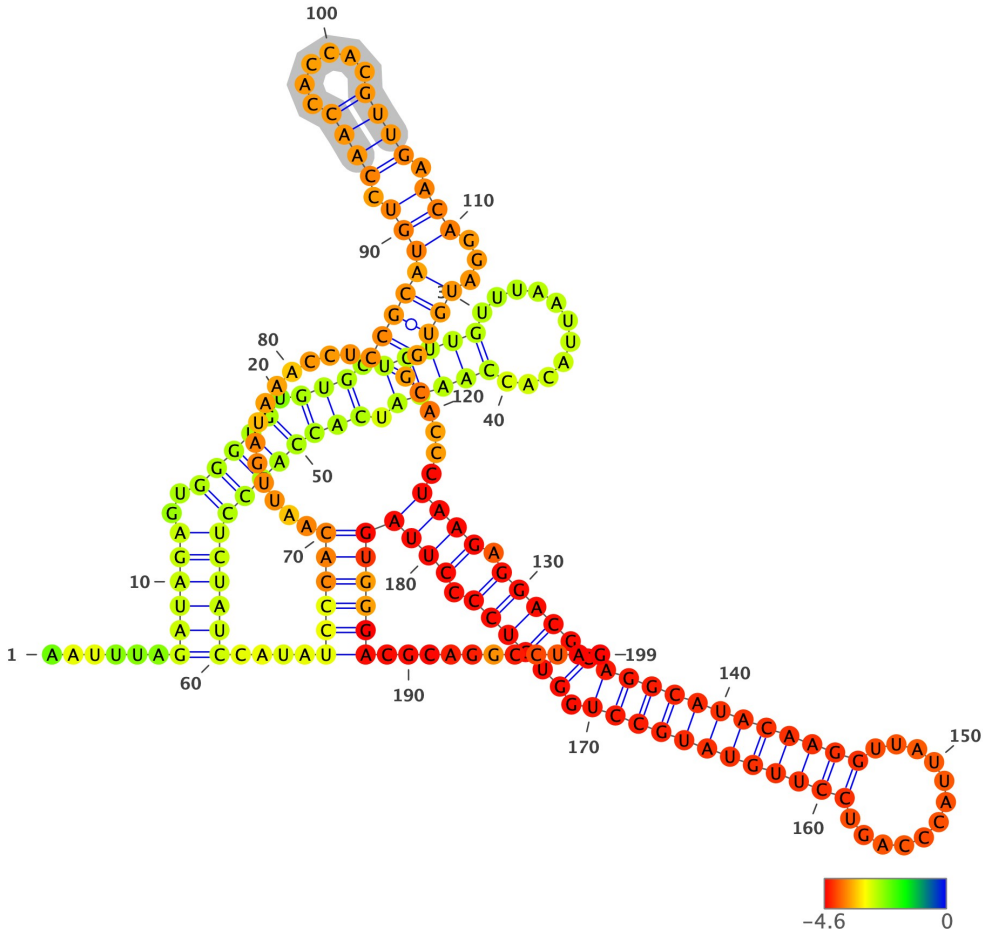
Attributes: ['ID=exon-HHV4_RPMS1-12-1', 'Parent=rna-HHV4_RPMS1-12', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

11-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 336 from nt 139885 to 139896 (nt 94 to 105)

```
5'-AACCACCACGUU-3'
5'-(((......)))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 139792 to 139990 (motif highlighted in silver):

```
5'-AAUUUAGAUAGAGUGGGUGUGUGCUCUUGUUUAAUUACACCAAGAUCACCACCCUCUAUCCAUAUCCCACAAUUGAUAAACCUCCGCAUGUCCAACCACCACGUUGAACAG
GAUGUGGCACCCUAAGAGGACGCAGGCAUACAAGGUUAUUACCCAGUCCUUGUAUGCCUGGUGUCCCCUUAGUGGGACGCAGGCCUAG-3
5'-......((((((..(((((.(((.(((((...........))))).))))))))))))))....((((((.............(((((((.((((......)))).))).
..)))))).....((((.(((((((((((((((((.........)))))))))))).)))))))).))))))..........-3'
MFE = -73.7; z-score = -5.06; ED = 23.47
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 4 to 27--miRNA, rna-HHV4_RPMS1-11, 139795-139818(+)

Attributes: ['ID=rna-HHV4_RPMS1-11', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

6-- nt 4 to 27--exon, exon-HHV4_RPMS1-11-1, 139795-139818(+)

Attributes: ['ID=exon-HHV4_RPMS1-11-1', 'Parent=rna-HHV4_RPMS1-11', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART16']

7-- nt 124 to 145--miRNA, rna-HHV4_RPMS1-12, 139915-139936(+)

Attributes: ['ID=rna-HHV4_RPMS1-12', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

8-- nt 124 to 145--exon, exon-HHV4_RPMS1-12-1, 139915-139936(+)

Attributes: ['ID=exon-HHV4_RPMS1-12-1', 'Parent=rna-HHV4_RPMS1-12', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

9-- nt 162 to 184--miRNA, rna-HHV4_RPMS1-13, 139953-139975(+)

Attributes: ['ID=rna-HHV4_RPMS1-13', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

10-- nt 162 to 184--exon, exon-HHV4_RPMS1-13-1, 139953-139975(+)

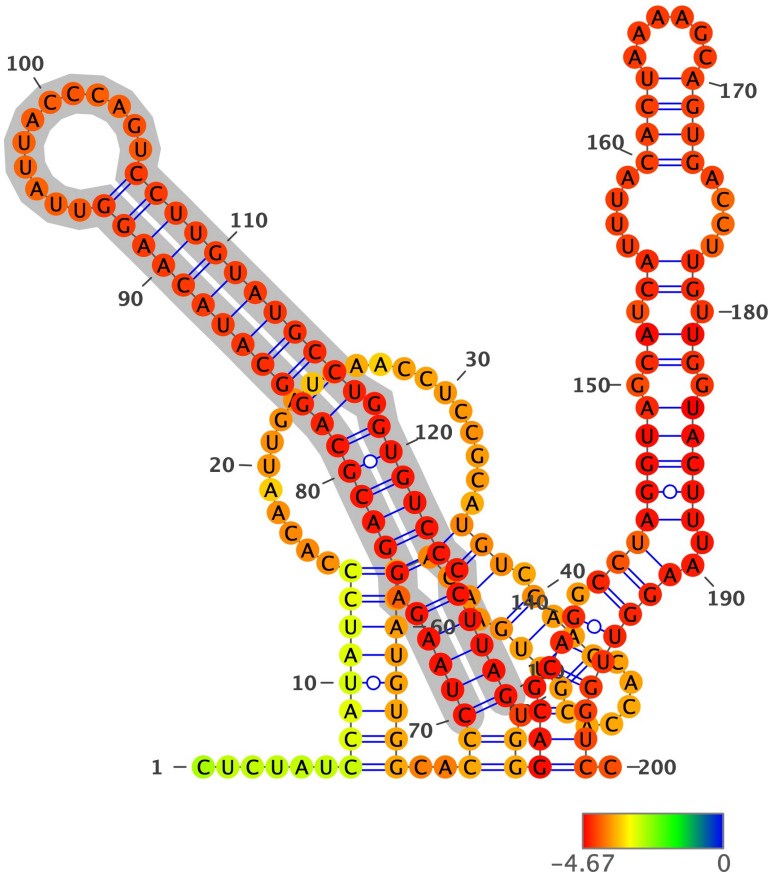
Attributes: ['ID=exon-HHV4_RPMS1-13-1', 'Parent=rna-HHV4_RPMS1-13', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

11-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 337 from nt 139914 to 139974 (nt 70 to 130)

```
5'-CUAAGAGGACGCAGGCAUACAAGGUUAUUACCCAGUCCUUGUAUGCCUGGUGUCCCCUUAG-3'
5'-(((((.(((((((((((((((((((.............)))))))))))))).)))))))..)))))-3'
Motif MFE = -35.0; z-score = -6.29; 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 139845 to 140044 (motif highlighted in silver):

```
5'-CUCUAUCCAUAUCCCACAAUUGAUAAACCUCCGCAUGUCCAACCACCACGUUGAACAGGAUGUGGCACCCUAAGAGGACGCAGGCAUACAAGGUUAUUACCCAGUCCUUGU
AUGCCUGGUGUCCCCUUAGUGGGACGCAGGCCUAGGUAGCAUCAUUUACACUAAAAGCAGUGACCUUGUUGGUACUUUAAGGUUGGUCC-3
5'-......(((((((((.....................(((.((((.....)))).)))))))))))..(((((((.(((((((((((((((((((.............)))))))
))))))).)))))).)))))).))))(((.((((.(((((((((.((.((....((((.....)))).....)).)).)))))..)))))))))).-3'
MFE = -70.3; z-score = -4.51; ED = 12.66
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 71 to 92--miRNA, rna-HHV4_RPMS1-12, 139915-139936(+)

Attributes: ['ID=rna-HHV4_RPMS1-12', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

6-- nt 71 to 92--exon, exon-HHV4_RPMS1-12-1, 139915-139936(+)

Attributes: ['ID=exon-HHV4_RPMS1-12-1', 'Parent=rna-HHV4_RPMS1-12', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

7-- nt 109 to 131--miRNA, rna-HHV4_RPMS1-13, 139953-139975(+)

Attributes: ['ID=rna-HHV4_RPMS1-13', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

8-- nt 109 to 131--exon, exon-HHV4_RPMS1-13-1, 139953-139975(+)

Attributes: ['ID=exon-HHV4_RPMS1-13-1', 'Parent=rna-HHV4_RPMS1-13', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

9-- nt 189 to 200--miRNA, rna-HHV4_RPMS1-14, 140033-140054(+)

Attributes: ['ID=rna-HHV4_RPMS1-14', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

10-- nt 189 to 200--exon, exon-HHV4_RPMS1-14-1, 140033-140054(+)

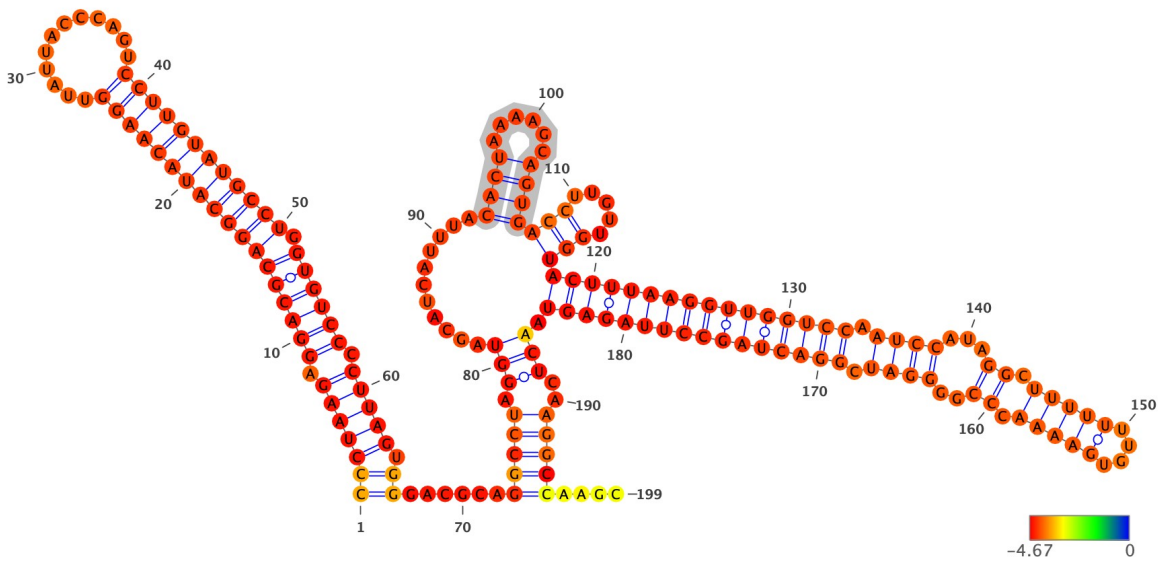
Attributes: ['ID=exon-HHV4_RPMS1-14-1', 'Parent=rna-HHV4_RPMS1-14', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

11-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 338 from nt 140004 to 140017 (nt 93 to 106)

```
5'-CACUAAAAGCAGUG-3'
5'-((((.....))))-3'
Motif MFE = -1.3; z-score = -2.37; 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 139912 to 140110 (motif highlighted in silver):

```
5'-CCCUAAGAGGACGCAGGCAUACAAGGUUAUUACCCAGUCCUUGUAUGCCUGGUGUCCCCUUAGUGGGACGCAGGCCUAGGUAGCAUCAUUUACACUAAAAGCAGUGACCUU
GUUGGUACUUUAAGGUUGGUCCAAUCCAUAGGCUUUUUUUGUGAAAACCCGGGGAUCGGACUAGCCUUAGAGUAACUCAAGGCCAAGC-3
5'-(((((((.(((((((((((((((((((.............)))))))))))))).)))))))).)))))).)).....(((((.(((...........((((......)))))))((..
...)))((((((((((((((((.((((...((.(((((....)))))).)).)..)))).)))))))))))))))).))..)))))....-3'
MFE = -87.2; z-score = -6.06; ED = 20.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 4 to 25--miRNA, rna-HHV4_RPMS1-12, 139915-139936(+)

Attributes: ['ID=rna-HHV4_RPMS1-12', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

6-- nt 4 to 25--exon, exon-HHV4_RPMS1-12-1, 139915-139936(+)

Attributes: ['ID=exon-HHV4_RPMS1-12-1', 'Parent=rna-HHV4_RPMS1-12', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-5p']

7-- nt 42 to 64--miRNA, rna-HHV4_RPMS1-13, 139953-139975(+)

Attributes: ['ID=rna-HHV4_RPMS1-13', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

8-- nt 42 to 64--exon, exon-HHV4_RPMS1-13-1, 139953-139975(+)

Attributes: ['ID=exon-HHV4_RPMS1-13-1', 'Parent=rna-HHV4_RPMS1-13', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

9-- nt 122 to 143--miRNA, rna-HHV4_RPMS1-14, 140033-140054(+)

Attributes: ['ID=rna-HHV4_RPMS1-14', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

10-- nt 122 to 143--exon, exon-HHV4_RPMS1-14-1, 140033-140054(+)

Attributes: ['ID=exon-HHV4_RPMS1-14-1', 'Parent=rna-HHV4_RPMS1-14', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

11-- nt 161 to 182--miRNA, rna-HHV4_RPMS1-15, 140072-140093(+)

Attributes: ['ID=rna-HHV4_RPMS1-15', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

12-- nt 161 to 182--exon, exon-HHV4_RPMS1-15-1, 140072-140093(+)

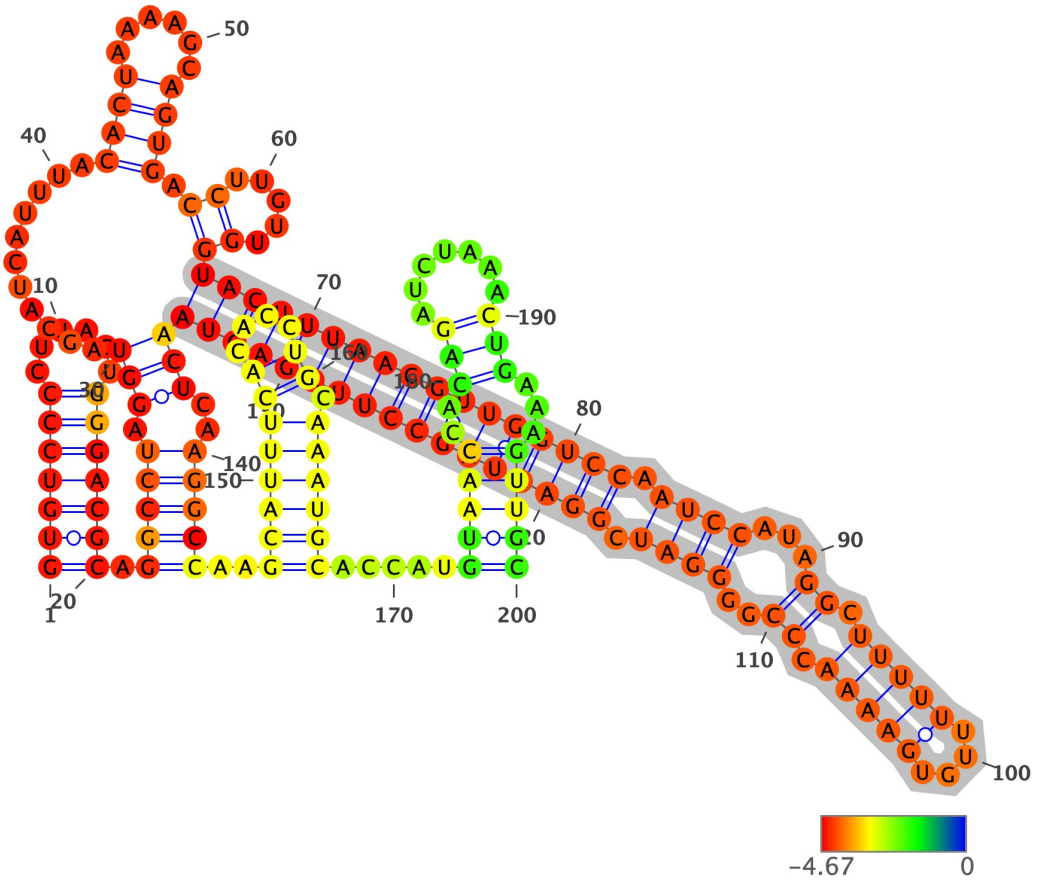
Attributes: ['ID=exon-HHV4_RPMS1-15-1', 'Parent=rna-HHV4_RPMS1-15', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

13-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 339 from nt 140028 to 140096 (nt 66 to 134)

```
5'-UACUUUAAGGUUGGUCCAAUCCAUAGGCUUUUUUUGUGAAAACCCGGGGAUCGGACUAGCCUUAGAGUA-3'
5'-(((((((((((((((((.((((...((.(((((....))))).))..)))).)))))))))))))))))-3'
Motif MFE = -34.7; z-score = -6.26; ED = 4.76
```



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 139963 to 140162 (motif highlighted in silver):

```
5'-GUGUCCCCUUAGUGGGACGCAGGCCUAGGUAGCAUCAUUUACACUAAAAGCAGUGACCUUGUUGGUACUUUAAGGUUGGUCCAAUCCAUAGGCUUUUUUUGUGAAAACCCG
GGGAUCGGACUAGCCUUAGAGUAACUCAAGGCCAAGCAUUUCACACCUGCAAAUGCACCAUGUAACCACAGAUCUAAACUGAAAGUUGC-3
5'-(((((((.....)))))))).(((((.(((..........((((......)))).((.....))((((((((((((((((.((((...((.(((((....)))))).)).
.)))).))))))))))))))))))..)))))..((((((((....)).)))))).....(((((..(((.......)))...)))))-3'
MFE = -68.4; z-score = -5.11; ED = 28.49
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 13--miRNA, rna-HHV4_RPMS1-13, 139953-139975(+)

Attributes: ['ID=rna-HHV4_RPMS1-13', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

6-- nt 1 to 13--exon, exon-HHV4_RPMS1-13-1, 139953-139975(+)

Attributes: ['ID=exon-HHV4_RPMS1-13-1', 'Parent=rna-HHV4_RPMS1-13', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART17-3p']

7-- nt 71 to 92--miRNA, rna-HHV4_RPMS1-14, 140033-140054(+)

Attributes: ['ID=rna-HHV4_RPMS1-14', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

8-- nt 71 to 92--exon, exon-HHV4_RPMS1-14-1, 140033-140054(+)

Attributes: ['ID=exon-HHV4_RPMS1-14-1', 'Parent=rna-HHV4_RPMS1-14', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

9-- nt 110 to 131--miRNA, rna-HHV4_RPMS1-15, 140072-140093(+)

Attributes: ['ID=rna-HHV4_RPMS1-15', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

10-- nt 110 to 131--exon, exon-HHV4_RPMS1-15-1, 140072-140093(+)

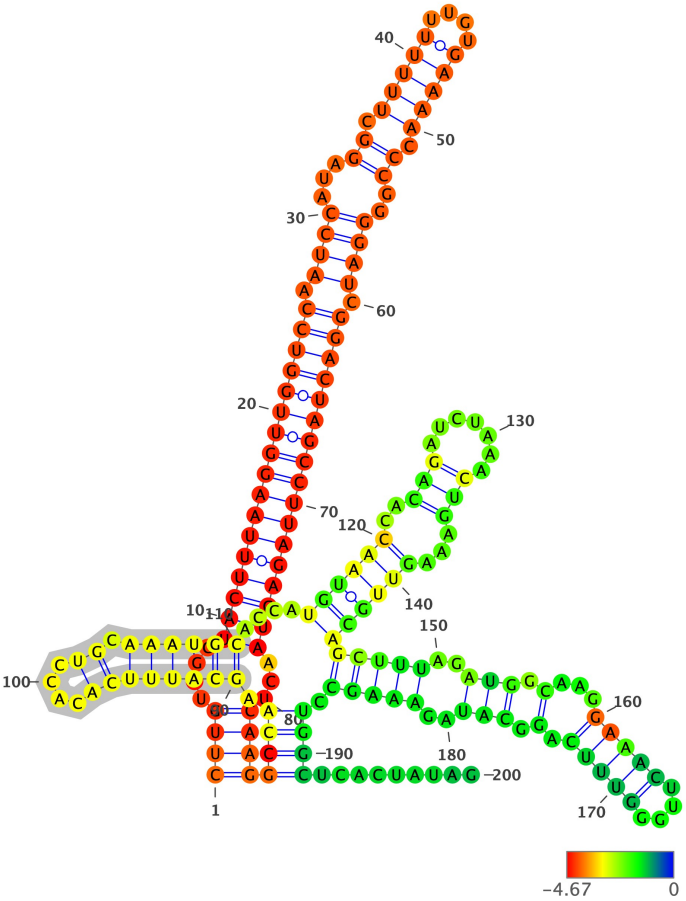
Attributes: ['ID=exon-HHV4_RPMS1-15-1', 'Parent=rna-HHV4_RPMS1-15', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

11-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 340 from nt 140109 to 140129 (nt 90 to 110)

```
5'-GCAUUUCACACCUGCAAAUGC-3'
5'-(((((((((....)).)))))))-3'
Motif MFE = -3.7; z-score = -3.63; 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 140020 to 140219 (motif highlighted in silver):

```
5'-CUUGUUGGUACUUUAAGGUUGGUCCAAUCCAUAGGCUUUUUUUGUGAAAACCCGGGGAUCGGACUAGCCUUAGAGUAACUCAAGGCCAAGCAUUUCACACCUGCAAAUGCA
CCAUGUAACCACAGAUCUAAACUGAAAGUUGCAGCUUUAGAUGGCAAGGAAACUUGGGUUUCAGGCAUAGAAAGCCUGGCUCACUAUAG-3
5'-((((....(((((((((((((((((.((((...((.((((((....))))))..))..))))).))))))))))))))))))...))))((((.((((((((....)).)))))))).
...((((((..(((.......)))...))))))((((..((((.(...((((((....))))))..).)))..)))))).))))).........-3'
MFE = -67.5; z-score = -4.35; ED = 36.73
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 14 to 35--miRNA, rna-HHV4_RPMS1-14, 140033-140054(+)

Attributes: ['ID=rna-HHV4_RPMS1-14', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

6-- nt 14 to 35--exon, exon-HHV4_RPMS1-14-1, 140033-140054(+)

Attributes: ['ID=exon-HHV4_RPMS1-14-1', 'Parent=rna-HHV4_RPMS1-14', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-5p']

7-- nt 53 to 74--miRNA, rna-HHV4_RPMS1-15, 140072-140093(+)

Attributes: ['ID=rna-HHV4_RPMS1-15', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

8-- nt 53 to 74--exon, exon-HHV4_RPMS1-15-1, 140072-140093(+)

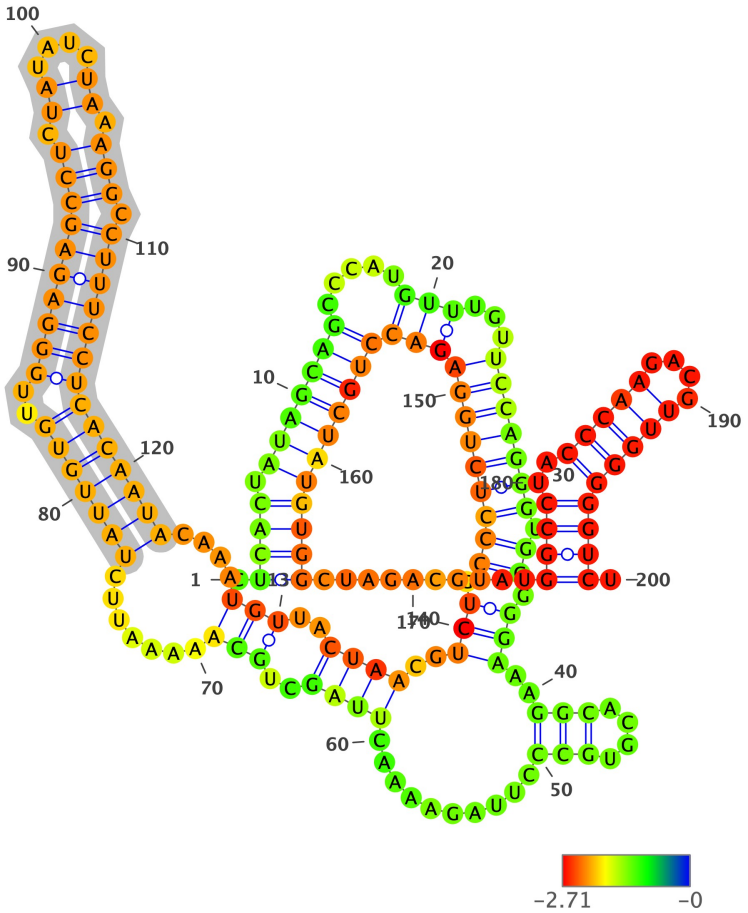
Attributes: ['ID=exon-HHV4_RPMS1-15-1', 'Parent=rna-HHV4_RPMS1-15', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART6-3p']

9-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 341 from nt 140286 to 140332 (nt 77 to 123)

```
5'-UAUUGUGUUGGGAGAGCCUCUAUAUCUAAAGGCCUUUCCUCACAAUA-3'
5'-(((((((..((((((((((.((....)).)))).)))))))))))))-3'
Motif MFE = -16.8; z-score = -4.32; ED = 8.51
```



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 140210 to 140409 (motif highlighted in silver):

```
5'-CUCACUAUAGCAGCCCAUGUUUGUUCCAGGGUGGGGGAAAGGCACGUGCCCUUAGAAAACUUAGCUGCAAAAAUUCUAUUGUGUUGGGAGAGCCUCUAUAUCUAAAGGCCU
UUCCUCACAAUACAAAUGUUACUAACGUCUGCCCUCUGGAGACCUGCUAUGUGGCUAGACGUAUGGCCUACCCAAGACGUUGGGGGUCU-3
5'-.((((.(((((((.....(((...(((((((.((.((((..(((....)))..........((((..(((.......(((((((..((((((((((.((....)).))).))
))))))))))))....)))..))))..))).))))))))))))))))))))))).........((((..(((((....)))))))))).-3'
MFE = -60.7; z-score = -1.62; ED = 41.68
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

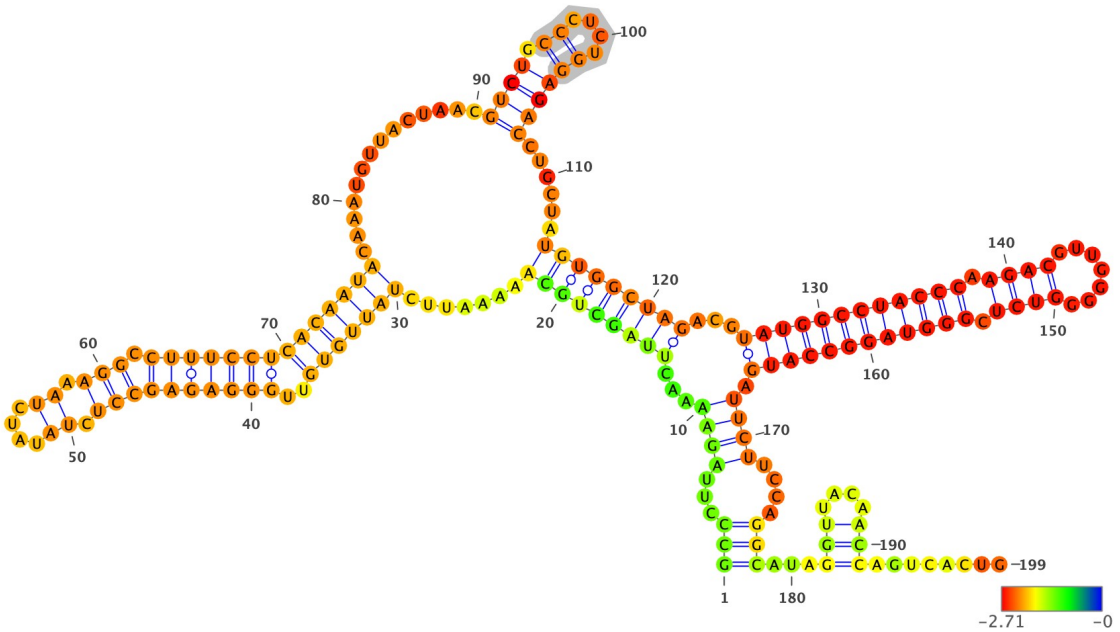
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 342 from nt 140352 to 140359 (nt 96 to 103)

```
5'-CCCUCUGG-3'
5'-((....))-3'
Motif MFE = 0.0; z-score = #DIV/0!; 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 140257 to 140455 (motif highlighted in silver):

```
5'-GCCCUUAGAAAACUUAGCUGCAAAAAUUCUAUUGUGUUGGGAGAGCCUCUAUAUCUAAAGGCCUUUCCUCACAAUACAAAUGUUACUAACGUCUGCCCUCUGGAGACCUGC
UAUGUGGCUAGACGUAUGGCCUACCCAAGACGUUGGGGGUCUCGGGUAGGCCAUGAUUCUUCCAGGCAUAGGUUACAACCAGUCACUG-3
5'-(((...((((...(((((((((.......(((((((..((((((((((.((....)).)))).))))))))))))))).............((((.((....)))))))....
..)))))))))...((((((((((((.((((.......)))).)))))))))))).))))....)))...(((....)))........-3'
MFE = -65.3; z-score = -3.15; ED = 24.37
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

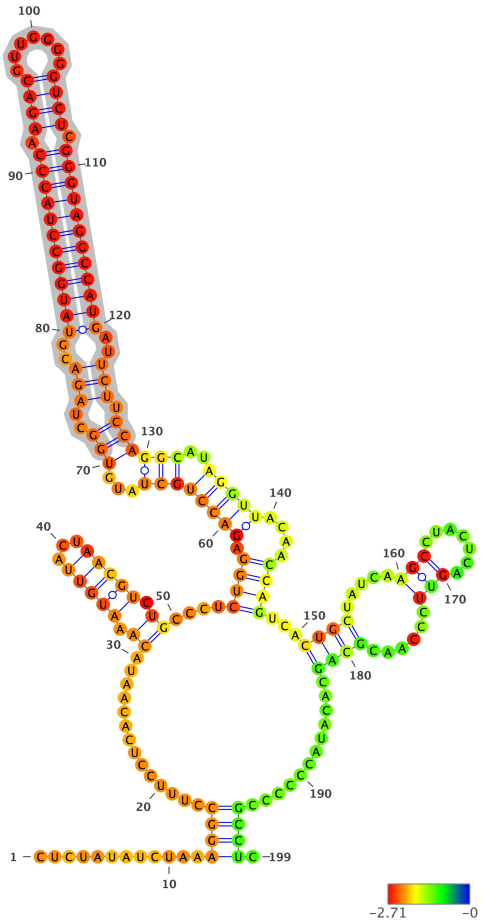
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 343 from nt 140373 to 140430 (nt 71 to 128)

```
5'-GGCUAGACGUAUGGCCUACCCAAGACGUUGGGGGUCUCGGGUAGGCCAUGAUUCUUCC-3'
5'-((..(((..(((((((((((((.((((.......)))).)))))))))))))..)))).))-3'
Motif MFE = -30.8; z-score = -4.25; ED = 2.09
```



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 140303 to 140501 (motif highlighted in silver):

```
5'-CUCUAUAUCUAAAGGCCUUUCCUCACAAUACAAAUGUUACUAACGUCUGCCCUCUGGAGACCUGCUAUGUGGCUAGACGUAUGGCCUACCCAAGACGUUGGGGGUCUCGGG
UAGGCCAUGAUUCUUCCAGGCAUAGGUUACAACCAGUCACUGCUAUCAAGCCUACUCAGUUCCCAACGCAGCACAUACCCCCCGCCUC-3
5'-............((((.............((.(((((...))))).)).....((((.(((((((((...((((..((((..(((((((((((.((((.......)))).)))
)))))))))..))).)))))).)))))....)))))...((((.....(((.......))).....)))).............)))).-3'
MFE = -52.1; z-score = -1.86; ED = 37.29
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

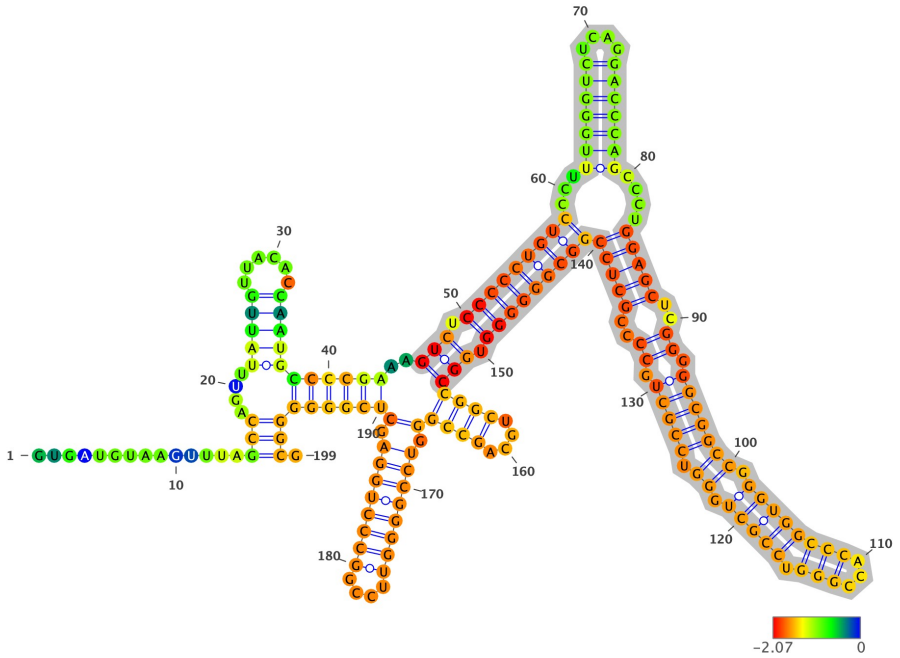
5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 344 from nt 140732 to 140839 (nt 46 to 153)

```
5'-GUCUCCCCCUGUCCCUUUGGGUCUCAGGACCCAGCCCUGGAGCUCGGGGGCGGCCGGGUGGCCCACCGGGUCCGCUGGGUCCGCUGCCCCGCUCCGGCGGGGGGUGGC-3'

5'-((..((.......................................................................................)).))-3'
Motif MFE = -71.2; z-score = -2.72; ED = 10.73
```



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 140687 to 140885 (motif highlighted in silver):

```
5'-GUGAUGUAAGUUUAGCCAGUUUAUUGUUACACCAAUGCCCCGAAAGUCUCCCCCUGUCCCUUUGGGUCUCAGGACCCAGCCCUGGAGCUCGGGGGCGGCCGGGUGGCCCAC
CGGGUCCGCUGGGUCCGCUGCCCCGCUCCGGCGGGGGGUGGCCGGCUGCAGCCGGGUCCGGGGUUCCGGCCCUGGAGCUCGGGGGGCG-3
5'-..............(((....(((((......)))))(((((((..(((.(((((((((...(((((((....)))))))....(((((..((.(((((((.(((((((..
.))).)))))).)).)))))).))..))))))))))))))).)))((((....))))(.((((((((....)))))))).))))))))).-3'
MFE = -108.2; z-score = -2.29; ED = 33.61
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 79 to 199--direct_repeat, id-HHV4_RPMS1-2, 140765-143281(+)

Attributes: ['ID=id-HHV4_RPMS1-2', 'Dbxref=GeneID:3783757', 'gbkey=repeat_region', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'rpt_family=IR4%3B PstI', 'rpt_type=direct', 'rpt_unit_range=140765..140865']

5-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

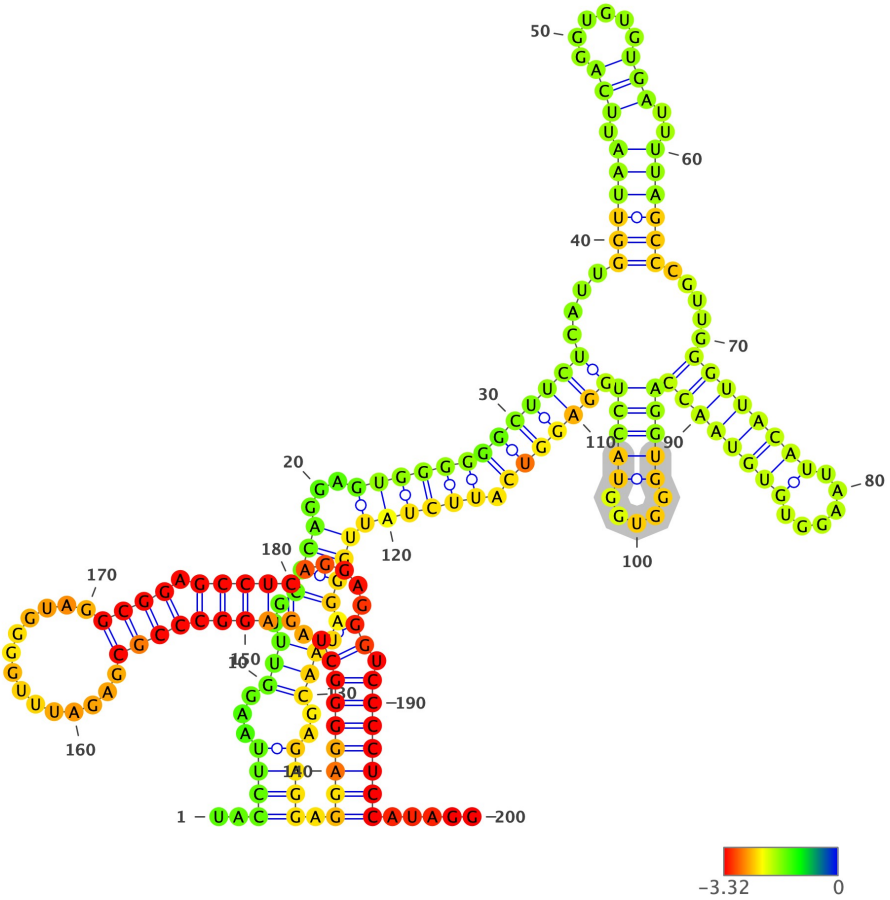
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 345 from nt 143566 to 143574 (nt 96 to 104)

```
5'-UGGGUGGUA-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 143471 to 143670 (motif highlighted in silver):

```
5'-UACCUUAAGGUUUGCUCAGGAGUGGGGGGCUUCUCAUUGGUUAAUUCAGGUGUGUGAUUUUAGCCCGUUGGGUUACAUUAAGGUGUGUAACCAGGUGGGUGGUACCUGGAG
GUCAUUCUAUUGGGAUAACGAGAGGAGGAGGGGCUAGAGGCCCGCGAGAUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGG-3
5'-..(((...(((..((((...(((((((((((((....((((((.(((......)))..)))))).....((((((((.....)))))))))((((.....)))))))))
)))).))))))))))..)))..)))).(((((((((.(((((((((.............)))).)))))).....)).)))))))).....-3'
MFE = -72.5; z-score = -2.1; ED = 22.05
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 200--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

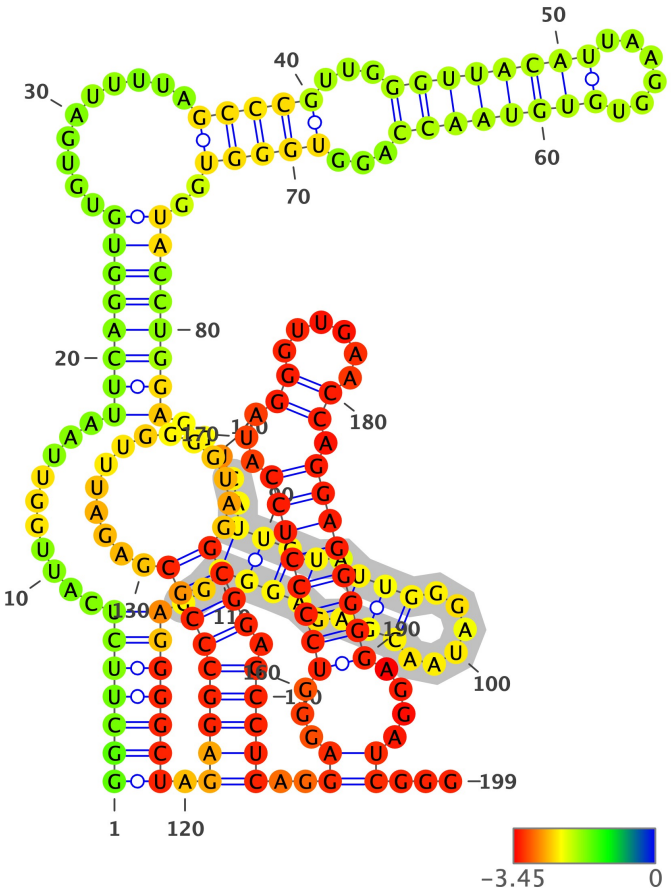
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 200--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 346 from nt 143584 to 143609 (nt 87 to 112)

```
5'-CAUUCUAUUGGGAUAACGAGAGGAGG-3'
5'-(.(((((.(.(......).).))))).)-3'
Motif MFE = -3.1; z-score = -0.64; ED = 5.82
```



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

Extracted structure model with flanking nucleotides 143498 to 143696 (motif highlighted in silver):

```
5'-GGCUUCUCAUUGGUUAAUUCAGGUGUGUGAUUUUAGCCCGUUGGGUUACAUUAAGGUGUGUAACCAGGUGGGUGGUACCUGGAGGUCAUUCUAUUGGGAUAACGAGAGGAG
GAGGGGCUAGAGGCCCGCGAGAUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAGGGGGAGGAUCGGG-3
5'-(((((((.........((((((((.........(((((...((((((((.....)))))))).....))))).)))))))).....((((.(((.....))).)))).
.)))))))..((((((((.............)))).))))))..((...((((((((...((.....)).)))))))).....))...-3'
MFE = -69.6; z-score = -3.05; ED = 49.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 199--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

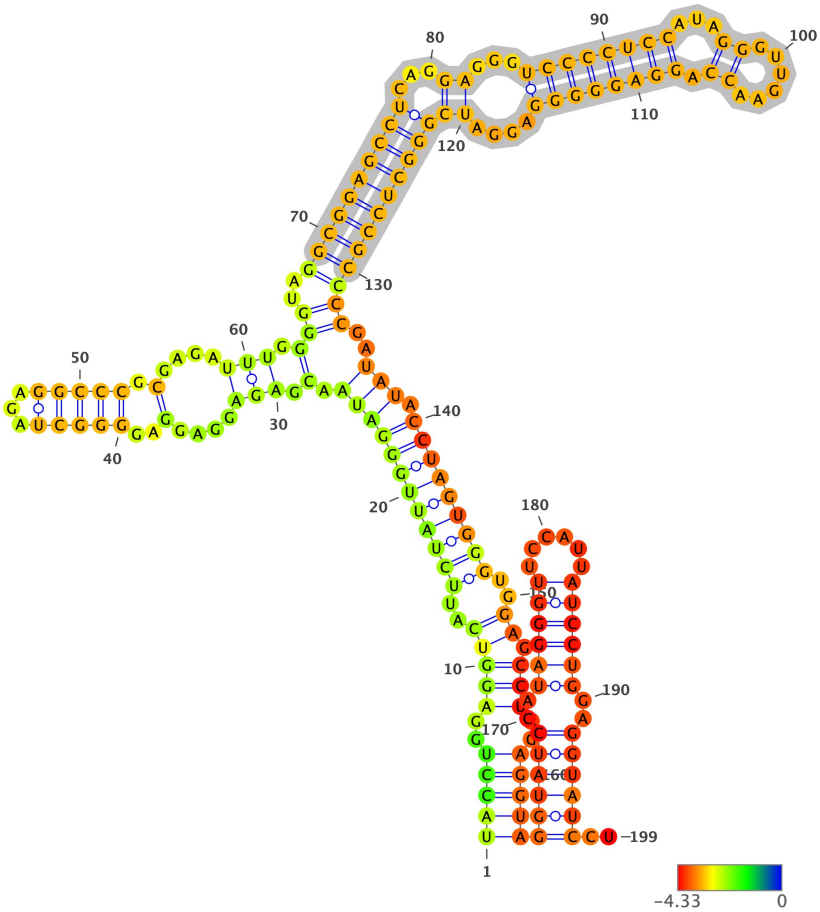
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 199--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 347 from nt 143641 to 143702 (nt 69 to 130)

```
5'-GCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAGGGGGAGGAUCGGGCUCCGC-3'
5'-(((((((((...((...((((((((...((......)).)))))))).....))))))))))-3'
Motif MFE = -36.1; z-score = -3.92; ED = 5.49
```



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 143573 to 143771 (motif highlighted in silver):

```
5'-UACCUGGAGGUCAUUCUAUUGGGAUAACGAGAGGAGGAGGGGCUAGAGGCCCGCGAGAUUUGGGGUAGGCGGAGCCUCAGGAGGGUCCCCUCCAUAGGGUUGAACCAGGAG
GGGGAGGAUCGGGCUCCGCCCCGAUAUACCUAGUGGGUGGAGCCUAGAGGUAGGUAUCCAUAGGGUUCCAUUAUCCUGGAGGUAUCCU-3
5'-(((((..(((((..(((((((((((((.(.((((....(..((((((...)))))).)....))).)((..((((((((((...((...((((((((...((......)).))))
))))).....))))))))))))))..))).))))))))..)).))))..)))))((((((..((((((.....))))))..))))))..-3'
MFE = -82.5; z-score = -3.17; ED = 38.81
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 199--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

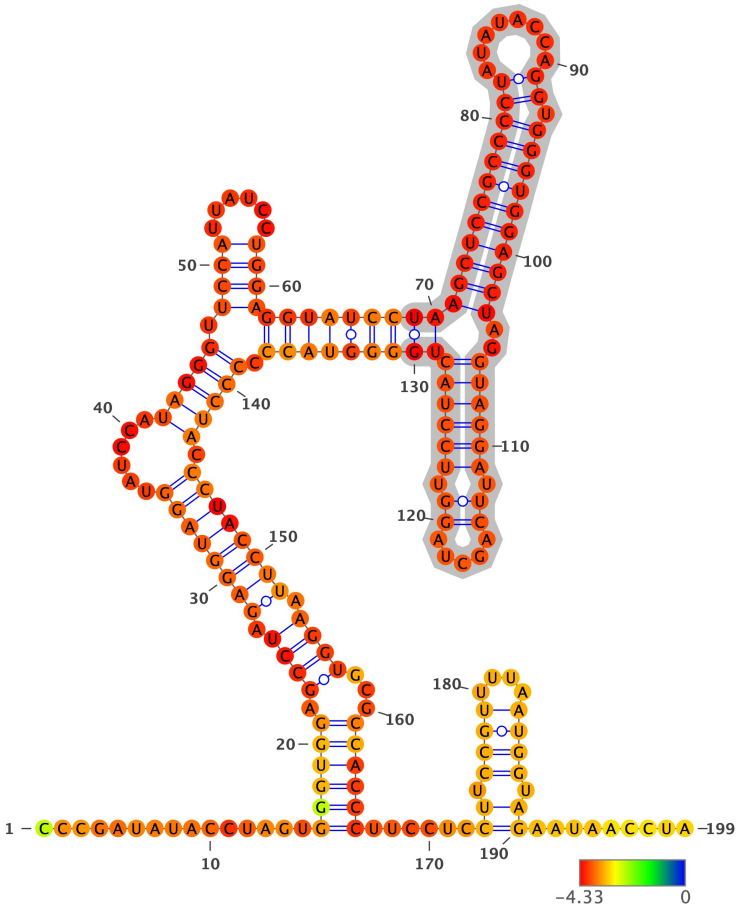
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 199--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 348 from nt 143771 to 143832 (nt 69 to 130)

```
5'-UAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUG-3'
5'-(.(((((((((((.......)).)))))))))..(((((.((.....)).))))).)-3'
Motif MFE = -30.4; z-score = -4.89; ED = 1.57
```



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

Extracted structure model with flanking nucleotides 143703 to 143901 (motif highlighted in silver):

```
5'-CCCGAUAUACCUAGUGGGUGGAGCCUAGAGGUAGGUAUCCAUAGGGUUCCAUUAUCCUGGAGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGA
UUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUA-3
5'-...............((((((.((((.(((((((((.....(((((.((((.....)))))((((((((((((((((((((.......)).)))))))))))..((((((
.((.....)).))))))))))))))).)))))).))))))))).))))...)))))).....((.((((....)))).)).........-3'
MFE = -79.2; z-score = -4.81; ED = 20.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 199--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

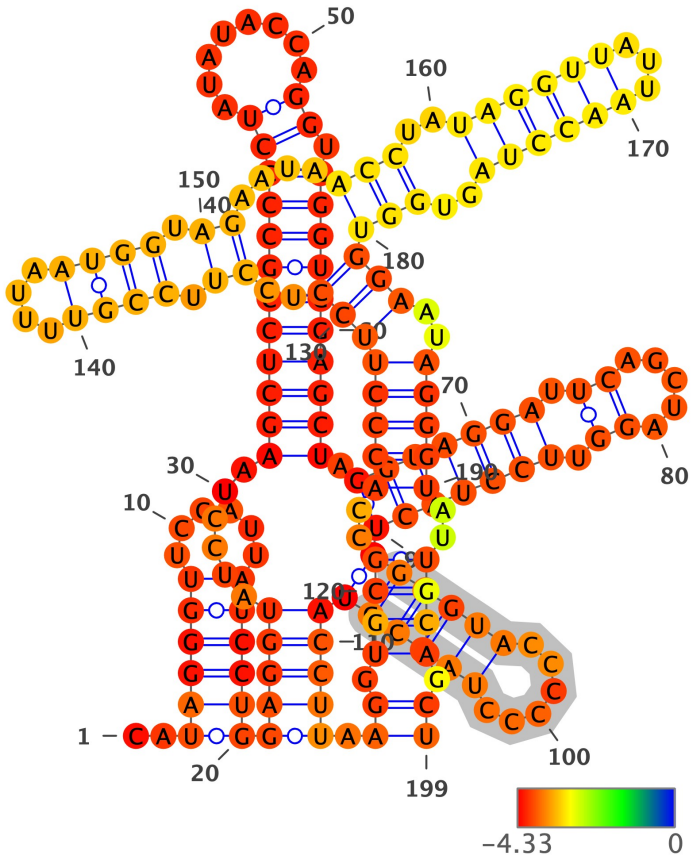
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 199--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 349 from nt 143833 to 143848 (nt 92 to 107)

```
5'-GGGUACCCCCCUACCC-3'
5'-((.((......)).))-3'
Motif MFE = -4.9; z-score = -4.46; 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 143742 to 143940 (motif highlighted in silver):

```
5'-CAUAGGGUUCCAUUAUCCUGGAGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACC
UUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCU-3
5'-..((((((.....))))))((((.....((((((((((((.......)).)))))))))).(((((((.(.....)).)))))))((((((.....)))))))))
)).((.(((((..(((((((((..((.((((....)))).)).....(((..((((((...)))))))..)))))))..)))))..)))).))-3'
MFE = -74.3; z-score = -5.05; ED = 34.44
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 199--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

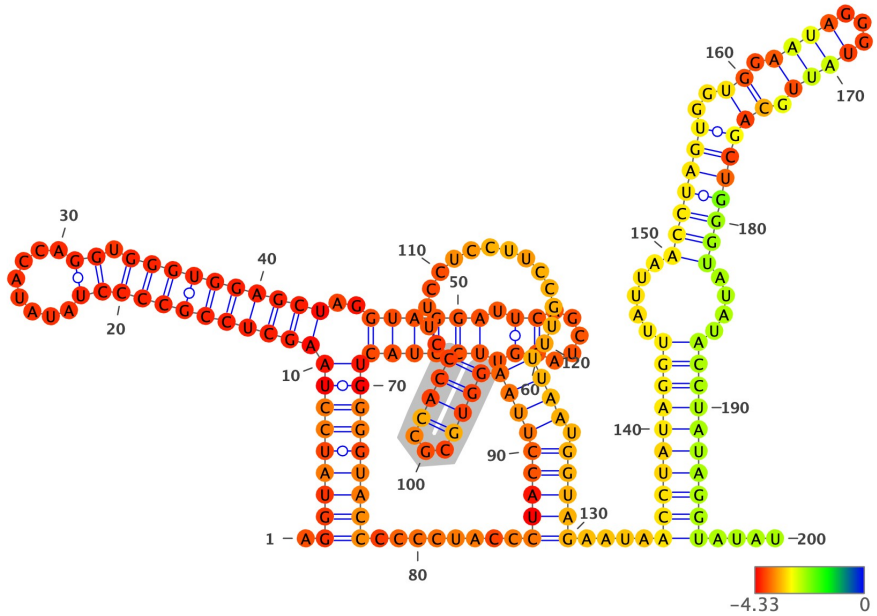
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 199--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 350 from nt 143857 to 143867 (nt 95 to 105)

```
5'-GGUGCGCCACC-3'
5'-(((.....)))-3'
Motif MFE = -2.2; z-score = -1.33; 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 143763 to 143962 (motif highlighted in silver):

```
5'-AGGUAUCCUAAGCUCCGCCCCUAUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCU
CCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAU-3
5'-.(((((((((((((((((((((.......)).)))))))))).((((((.(.....)).))))))))))))))).......((((((((((((...)))).....
.........)))).)))))....((((((((((.....(((((((..((.((((...)))).)))))))))....)))))))))).....-3'
MFE = -74.3; z-score = -4.95; ED = 40.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 200--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

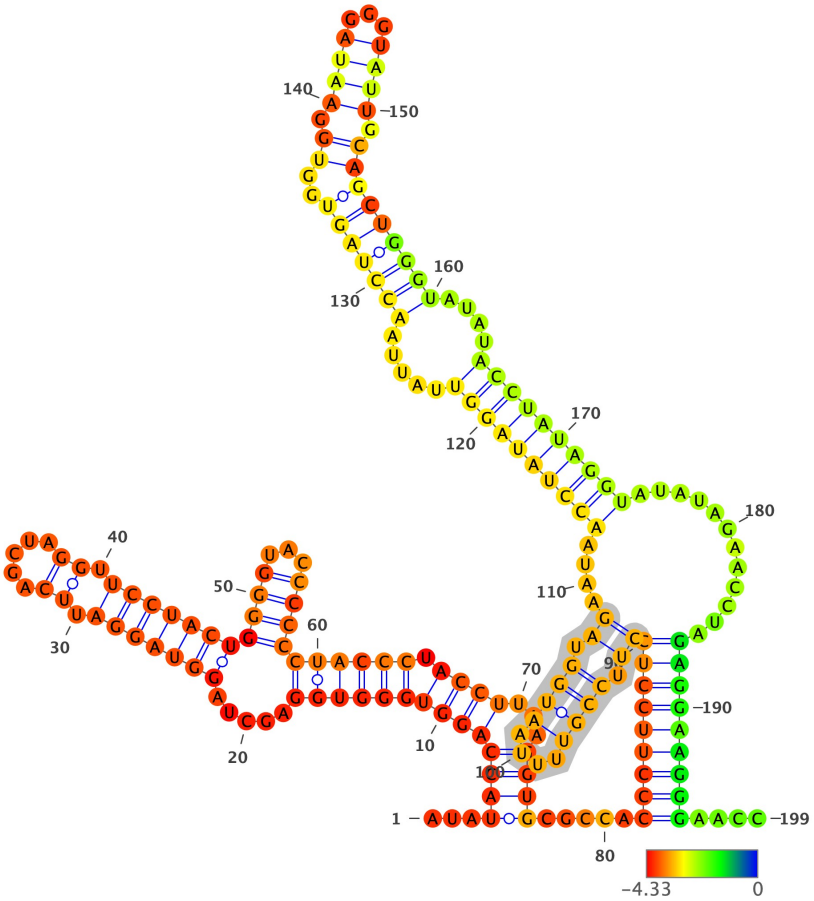
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 200--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 351 from nt 143875 to 143892 (nt 91 to 108)

```
5'-CUUCCGUUUUAAUGGUAG-3'
5'-((.((((....)))).))-3'
Motif MFE = -1.6; z-score = -1.05; ED = 1.79
```



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

Extracted structure model with flanking nucleotides 143785 to 143983 (motif highlighted in silver):

```
5'-AUAUACCAGGUGGGUGGAGCUAGGUAGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAU
AACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAACCUAGAGGAAGGGAACC-3
5'-...(((((((((((((.....(((((((.((.....)).)))))))((((...)))))))))).))))...))))).....((((((((((.((((....)))))).)).....
.((((((((((.....(((((((..((.((((...)))).)))))))))....))))))))))..............)))))))))....-3'
MFE = -74.7; z-score = -4.59; ED = 17.26
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 199--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

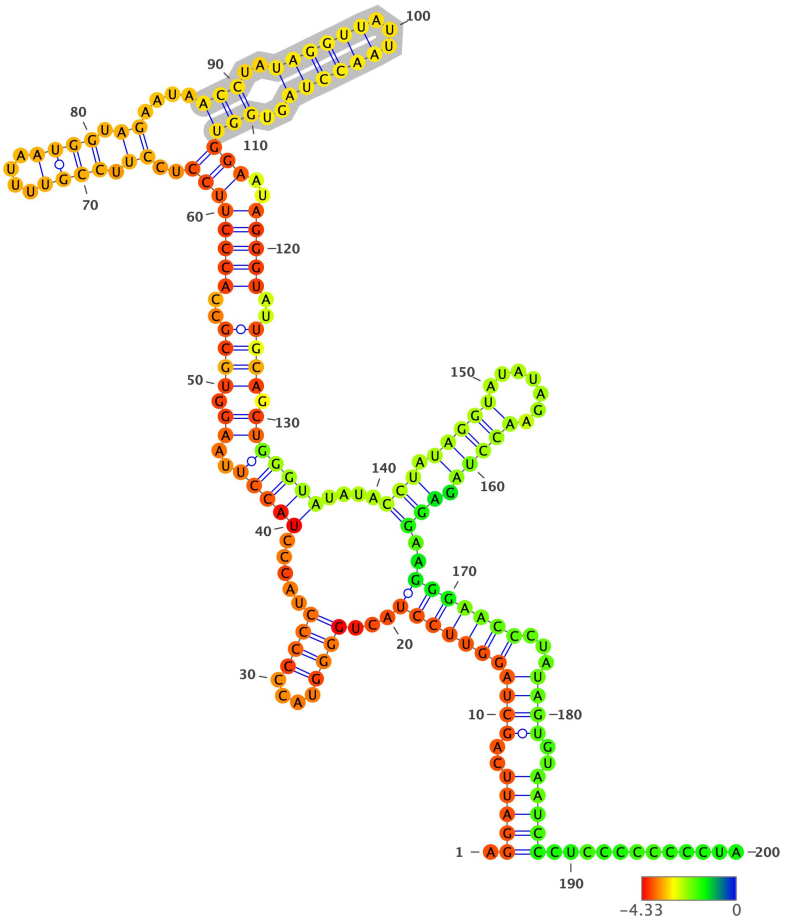
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 199--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 352 from nt 143897 to 143921 (nt 88 to 112)

```
5'-ACCUAUAGGUUAUUAACCUAGUGGU-3'
5'-(((..(((((((...)))))))..)))-3'
Motif MFE = -8.9; z-score = -4.28; 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 143810 to 144009 (motif highlighted in silver):

```
5'-AGGAUUCAGCUAGGUUCCUACUGGGGUACCCCCCUACCCUACCUUAAGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGG
UGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAACCUAGAGGAAGGGAACCCUAUAGUGUAAUCCCUCCCCCCCCUA-3
5'-.(((((..(((((((((((...((((....))))).....((((..((.((((..(((((((((..((.((((....)))).)).....(((..(((((((...)))))))..))
))))).)))))..)))).)))))))....(((.(((((.......)))))..))).)).)))))))...)))))..)))))............-3'
MFE = -65.9; z-score = -3.68; ED = 39.7
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 200--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

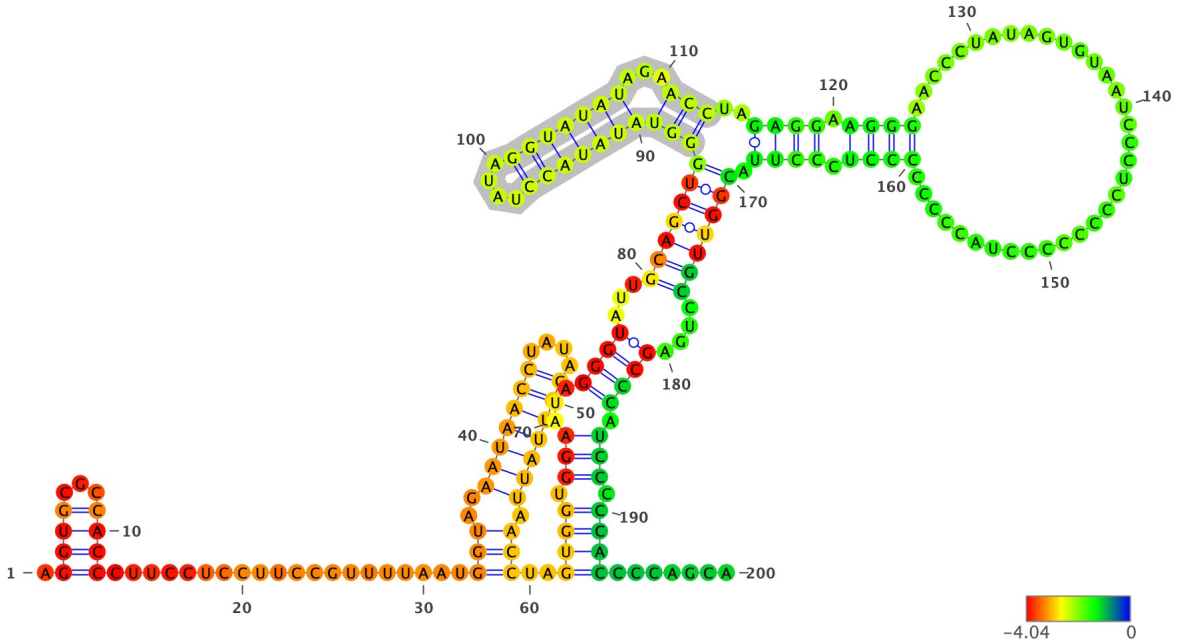
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 200--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 353 from nt 143942 to 143968 (nt 87 to 113)

```
5'-GGUAUAUACCUAUAGGUAUAUAGAACC-3'
5'-((((((((((....)))))))...)))-3'
Motif MFE = -7.3; z-score = -3.41; 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 143856 to 144055 (motif highlighted in silver):

```
5'-AGGUGCGCCACCCUUCCUCCUUCCGUUUUAAUGGUAGAAUAACCUAUAGGUUAUUAACCUAGUGGUGGAAUAGGGUAUUGCAGCUGGGUAUAUACCUAUAGGUAUAUAGAA
CCUAGAGGAAGGGAACCCUAUAGUGUAAUCCCUCCCCCCCCUACCCCCCCCUCCCUUACGGUUGCCUGAGCCCAUCCCCCACCCCAGCA-3
5'-.((((...)))).....................(((..(((((((....)))))))).))).....((((.(((...((((...((((((((((((((((....)))))))))...)
)).....((((.((((.....................................)))).)))).)))))))....)))).))).))))........-3'
MFE = -52.24; z-score = -2.6; ED = 48.07
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 200--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

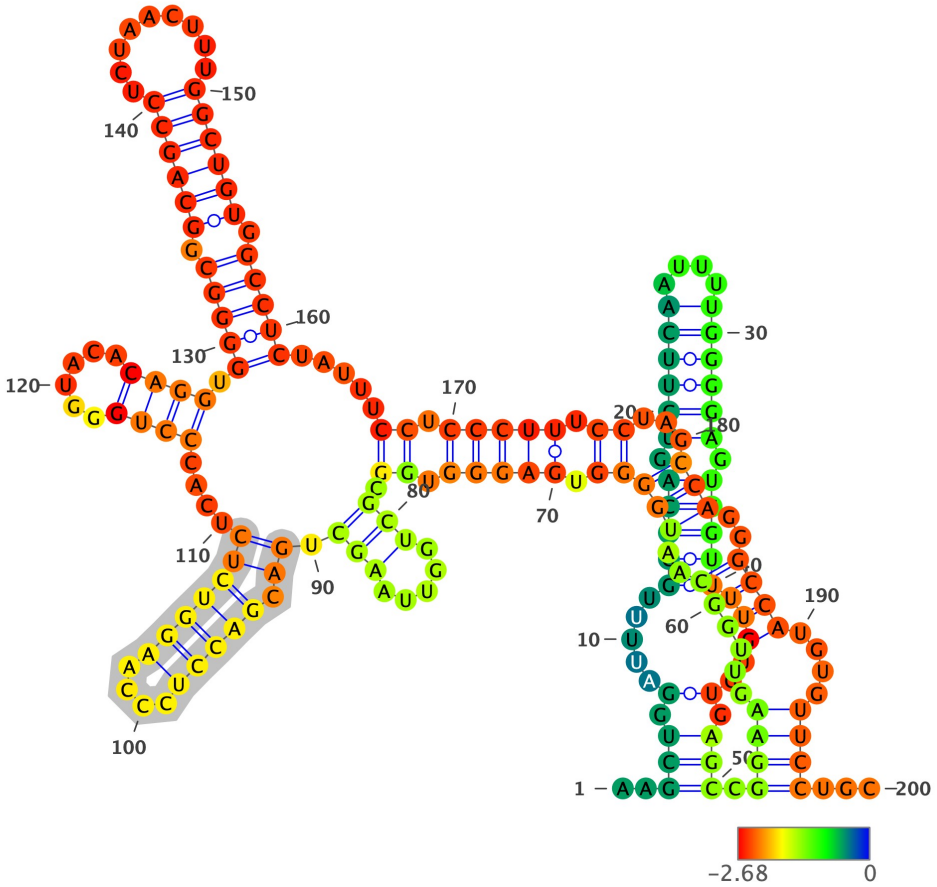
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 200--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 354 from nt 144416 to 144434 (nt 91 to 109)

```
5'-GACGACCUCCCAAGGUCUC-3'
5'-((...............))-3'
Motif MFE = -6.0; z-score = -3.26; 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 144326 to 144525 (motif highlighted in silver):

```
5'-AAGCUGGAUUUUGGCCAGUCUUCAAUUUUGGGGAGUGGUUUUGUGUGAGCCGGAAGUUGGCAAUGGGGUGAGGGUGGCGCUGGUUAAGCUGACGACCUCCCAAGGUCUCUC
ACCCUGGGUACACAGGUGGGGCGGCAGCCUCUAACUUUGGCUGUGGCCUCUAUUUCCUCCCUUUCCUAGCCAGGGCCAUGUGUUCCUGC-3
5'-..(((.(.....(((((.((((((....)))))).)))))).....).))).(((((..(((((..(((((.(((((.((.(((.....)))).((.(((((....)))))))).
..((((.....)))).(((((.((((((.........)))))).)))))).....)).)))))..)))...)))..)))).....)))).....-3'
MFE = -82.0; z-score = -2.66; ED = 10.08
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 119--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

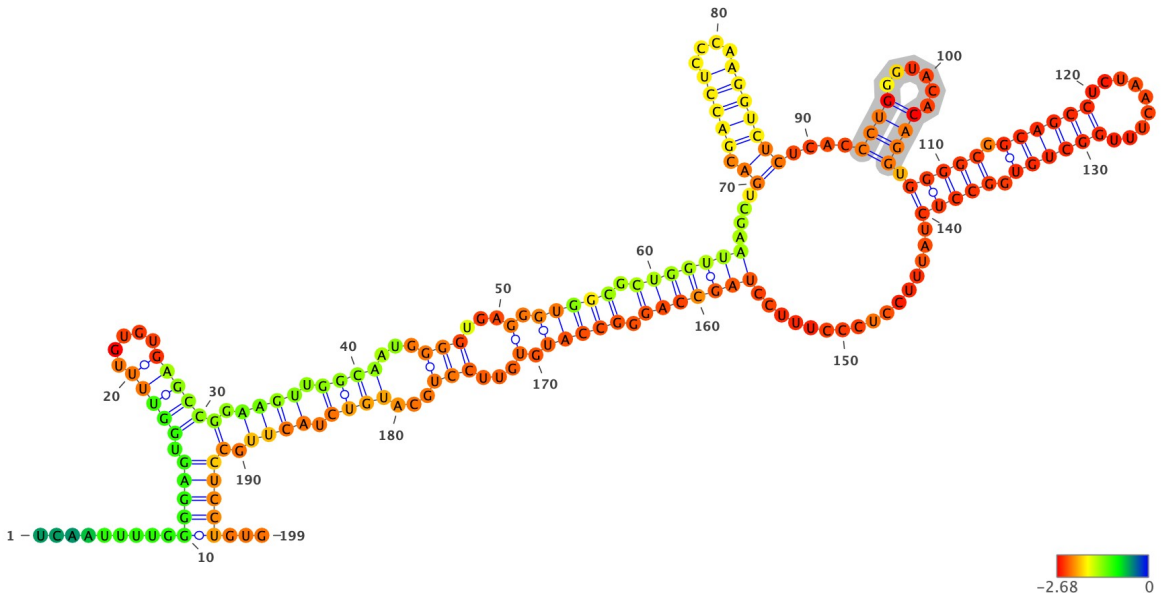
Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

7-- nt 1 to 3--direct_repeat, id-HHV4_RPMS1-6, 143272-144328(+)

Attributes: ['ID=id-HHV4_RPMS1-6', 'Note=DRright%2C similar to 40366..41409', 'gbkey=repeat_region', 'rpt_family=DR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 355 from nt 144439 to 144452 (nt 93 to 106)

```
5'-CCUGGGUACACAGG-3'
5'-(((........)))-3'
Motif MFE = -4.6; z-score = -2.38; 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 144347 to 144545 (motif highlighted in silver):

```
5'-UCAAUUUUGGGGAGUGGUUUUGUGUGAGCCGGAAGUUGGCAAUGGGGUGAGGGUGGCGCUGGUUAAGCUGACGACCUCCCAAGGUCUCUCACCCUGGGUACACAGGUGGGG
CGGCAGCCUCUAACUUUGGCUGUGGCCUCUAUUCCUCCCUUUCCUAGCCAGGGCCAUGUGUUCCUGCAUGUCUACUUGCCUCCUGUG-3
5'-.........(((((.(((((.....)))))(.(((((.((((...(((...(.(((((.(((((((....((.(((((....)))))))....((((......)))).((((
(.((((((.........)))))).)))))................)))))))).)))))..)...)))...)))).)))).)))))))...-3'
MFE = -77.4; z-score = -2.13; ED = 46.58
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

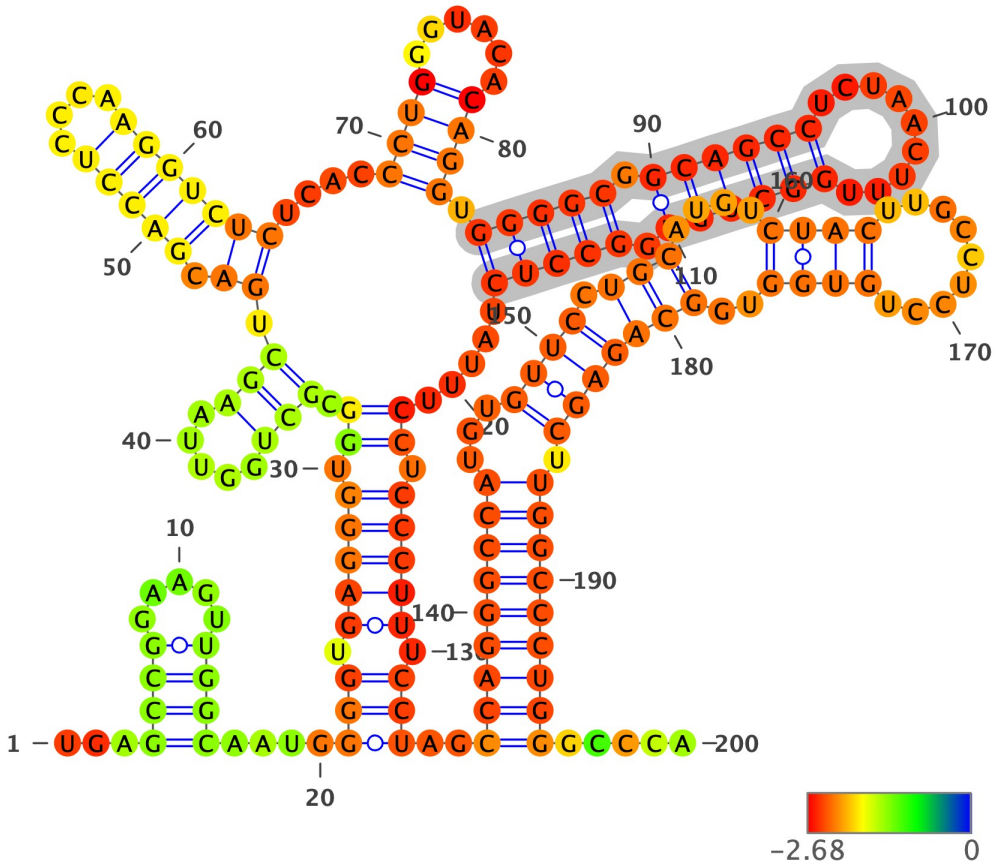
Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 98--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

NC_007605.1 (forward strand): Structure number 356 from nt 144454 to 144486 (nt 84 to 116)

```
5'-GGGGCGGCAGCCUCUAACUUUGGCUGUGGCCUC-3'
5'-(((((.((((((.........)))))).)))))-3'
Motif MFE = -20.8; z-score = -4.2; 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 144371 to 144570 (motif highlighted in silver):

```
5'-UGAGCCGGAAGUUGGCAAUGGGGUGAGGGUGGCGCUGGUUAAGCUGACGACCUCCCAAGGUCUCUCACCCUGGGUACACAGGUGGGGCGGCAGCCUCUAACUUUGGCUGUG
GCCUCUAUUCCUCCCUUUCCUAGCCAGGGCCAUGUGUUCCUGCAUGUCUACUUGCCUCCUGUGGUGGCAGAGCUUGGCCCUGGGCCCA-3
5'-...((((.....)))).....(((.(((((.((.((.....)).((.(((((....)))))))....((((......)))).(((((.(((((.........))))))).
)))))).....)).)))))..)))..(((((((((...(((((.(((....((((.........))))..)))))).))))))))).....-3'
MFE = -85.4; z-score = -2.03; ED = 27.76
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

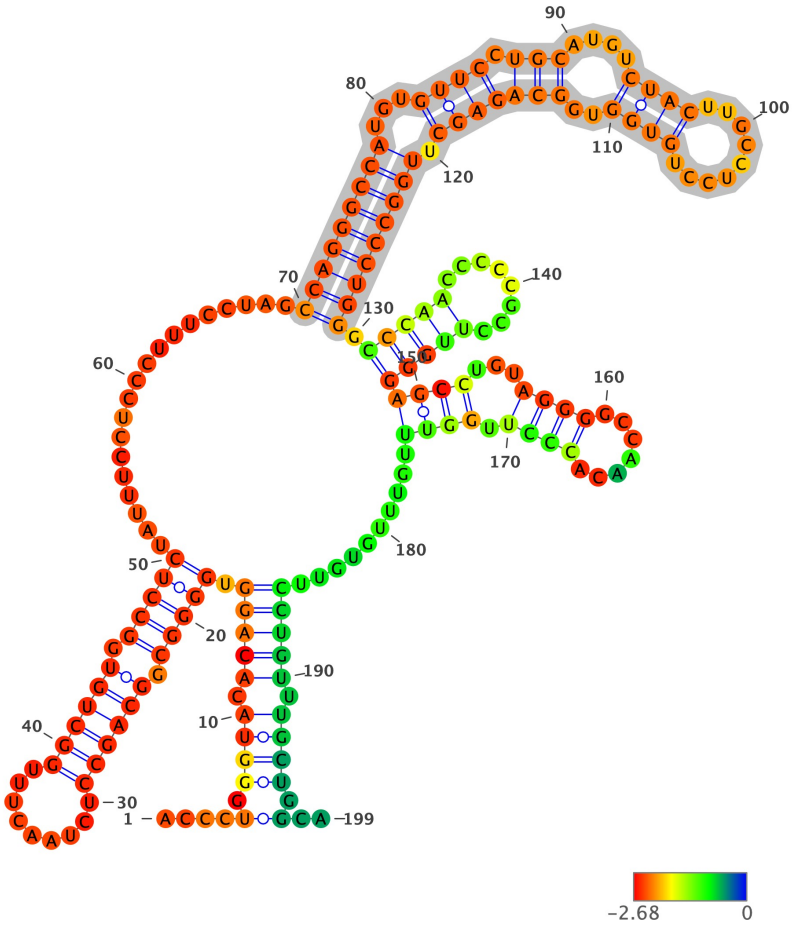
Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 74--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

NC_007605.1 (forward strand): Structure number 357 from nt 144506 to 144565 (nt 70 to 129)

```
5'-CCAGGGCCAUGUGUUCCUGCAUGUCUACUUGCCUCCUGUGGUGGCAGAGCUUGGCCCUGG-3'
5'-(((((((((...((((.(((....((((.........)))))..)))))))).)))))))))-3'
Motif MFE = -28.4; z-score = -3.19; ED = 6.21
```



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 144437 to 144635 (motif highlighted in silver):

```
5'-ACCCUGGGUACACAGGUGGGGCGGCAGCCUCUAACUUUGGCUGUGGCCUCUAUUUCCUCCCUUUCCUAGCCAGGGCCAUGUGUUCCUGCAUGUCUACUUGCCUCCUGUGGU
GGCAGAGCUUGGCCCUGGGCCCAACCCCCGCCUUGGGAGCCUGUAGGGGCCAACACCCUUGGUUUGUUUGUGUUCCUGUUUGCUGGCA-3
5'-....(.(((((.(((((.(((((.(((((.........)))))).)))))).................(((((((((...((((.(((....((((.........)))).
.)))))))).)))))))).(((((.........)))))((((...((((.......)))).)))).)))).........)))))).)))).)..-3'
MFE = -76.4; z-score = -1.81; ED = 47.15
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

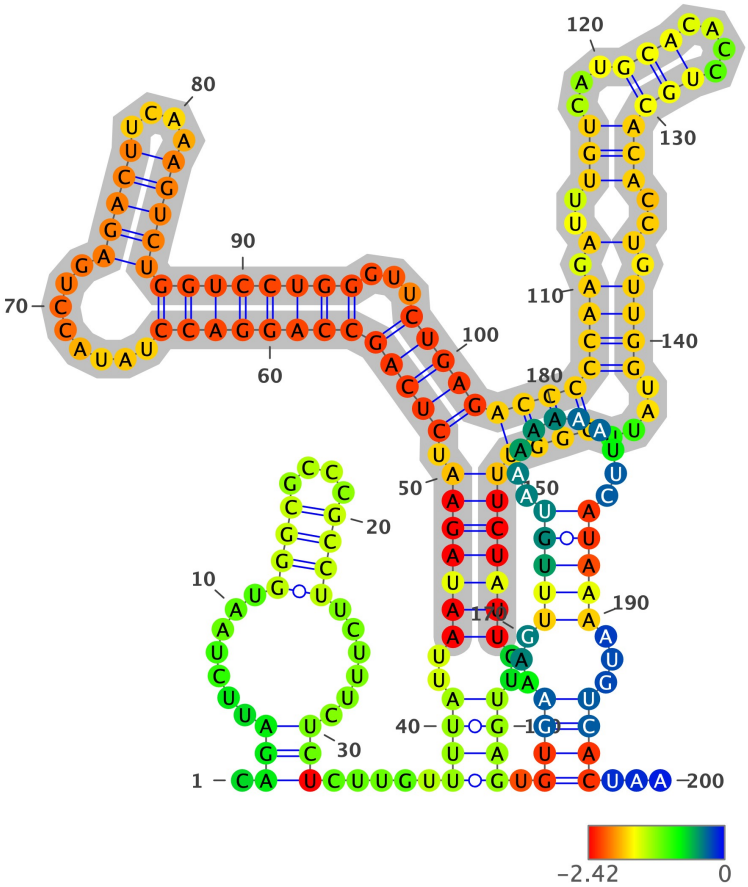
Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

6-- nt 1 to 8--origin_of_replication, id-HHV4_RPMS1-5, 143207-144444(+)

Attributes: ['ID=id-HHV4_RPMS1-5', 'Note=region containing oriLyt%2C core lytic cycle origin of DNA replication', 'gbkey=rep_origin']

NC_007605.1 (forward strand): Structure number 358 from nt 144696 to 144808 (nt 44 to 156)

```
5'-AAUAGAAUCUCAGCCAGGACCUAUACCUGAGACUUCAAAGUCUGGUCCUGGGUUCUGAGACCCCCAAGAUUUGUCAUGCACACCUGCACACCUGUUGGUAUUGGGUUUCUA
UU-3'
5'-((.((((..(((((((((((((.........((((((....)))))))))))))...)))))).............................................))).
))-3'
Motif MFE = -36.5; z-score = -3.72; ED = 15.73
```



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 144653 to 144852 (motif highlighted in silver):

```
5'-CAGAUUCUAAUGGGCGCCCGCCUUCUUUCUCUCUUGUUUUAUUAAUAGAAUCUCAGCCAGGACCUAUACCUGAGACUUCAAAGUCUGGUCCUGGGUUCUGAGACCCCCAAG
AUUUGUCAUGCACACCUGCACACCUGUUGGUAUUGGGUUUCUAUUCUUGAGUGUGAAAGUUUGUAAAAAAAUUCAUAAAAUGUCACUAA-3
5'-.(((.......((((....)))).....)))....(((((..(((((((.((((((((((((((.........(((((....)))))))))))))...)))))))))))))).
(..((((...((((....))))))..).))))....))))))))))))..)))).(((((...(((((..........)))))...)))))...-3'
MFE = -47.8; z-score = -1.54; ED = 27.08
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

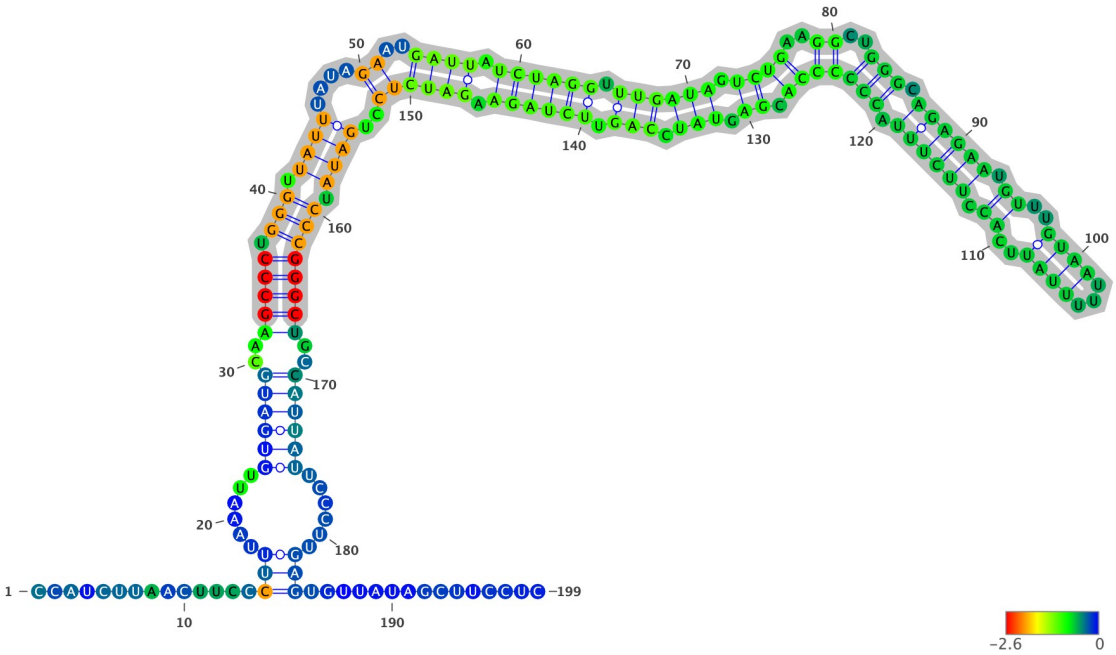
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 359 from nt 145223 to 145356 (nt 33 to 166)

```
5'-GCCCUGGGUUAUUUAUAGAAUGAUUAUCUAGGUUUGAUAGUCUGAAGGCUGGGCAGAGAAUGUUUGUAAUUUUUAUUCACCUUCUUUACCCCCCACGAGUAUCCAGUUCUA
GAAGAUCUCCUGAUAUCCCGGGC-3'
5'-((((.(((.((((....((.....................................................................................
.......))..)))).)))))))-3'
Motif MFE = -38.5; z-score = -2.78; ED = 14.53
```



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 145191 to 145389 (motif highlighted in silver):

```
5'-CCAUCUUAACUUCCCUUUAAAUUGUGAUGCAAGCCCUGGGUUAUUUAUAGAAUGAUUAUCUAGGUUUGAUAGUCUGAAGGCUGGGCAGAGAAUGUUUGUAAUUUUUAUUCA
CCUUCUUUACCCCCCACGAGUAUCCAGUUCUAGAAGAUCUCCUGAUAUCCCGGGCUGCCAUUAUUCCCUUGAGUGUUAUAGCUUCCUC-3
5'-..............(((......((((((..(((((.(((.((((....((..((((.(((((((.(((((((.((((..((..(((.((((((.((..((((...)))))..)
).)))))).)))))))..)).))).))).)))))).)))))))..))))..))))))))..)))))).....)))................-3'
MFE = -47.6; z-score = -1.96; ED = 20.62
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

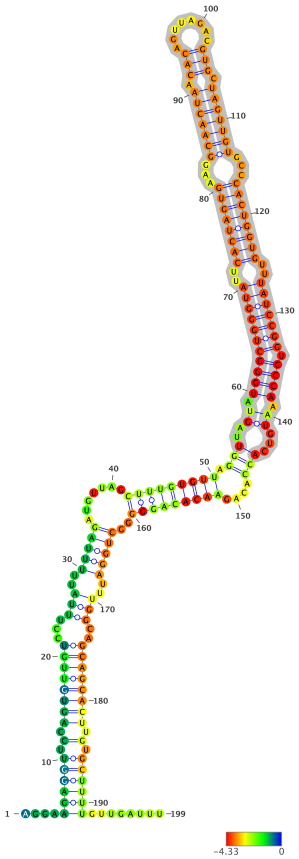
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 360 from nt 145496 to 145587 (nt 54 to 145)

```
5'-UUAGUAUGGGCUGGGUAUUCACUAGUGAAGGCAACUAACACAGUUAGACGUGCUAGUUGUGCCCACUGGUGUUUAUCCGGUCCCAAAUGUCA-3'
5'-(..(..(((((((((((..(((((((((...(((((((.(((........))).)))))))...)))))))))..)))))))).))))..)...)-3'
Motif MFE = -41.9; z-score = -5.08; ED = 5.61
```



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 145443 to 145641 (motif highlighted in silver):

```
5'-AGGAAGAGGUUCCAGUGUUGUCCUUUAUUUUUAGAUGUUAGCUUUGUGUUAGGUUAGUAUGGGCUGGGUAUUCACUAGUGAAGGCAACUAACACAGUUAGACGUGCUAGUU
GUGCCCACUGGUGUUUAUCCGGUCCCAAAUGUCACCACAGAACACAGGGGGCUGGAUUUGGCAGCAGCACUUGUGCUUUUGUUGAUUU-3
5'-....((((((.(.(((((((((...(((..(((((.......(((((((((.((..((.((((((((((..(((((((((...(((((((.(((........))).)))))
))...))))))))..)))))))).))))..))...)))....))))))))..)))))..)))..)))))))).).))))))........-3'
MFE = -70.0; z-score = -3.52; ED = 20.79
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 72 to 92--miRNA, rna-HHV4_RPMS1-16, 145514-145534(+)

Attributes: ['ID=rna-HHV4_RPMS1-16', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-5p']

6-- nt 72 to 92--exon, exon-HHV4_RPMS1-16-1, 145514-145534(+)

Attributes: ['ID=exon-HHV4_RPMS1-16-1', 'Parent=rna-HHV4_RPMS1-16', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-5p']

7-- nt 106 to 127--miRNA, rna-HHV4_RPMS1-17, 145548-145569(+)

Attributes: ['ID=rna-HHV4_RPMS1-17', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-3p']

8-- nt 106 to 127--exon, exon-HHV4_RPMS1-17-1, 145548-145569(+)

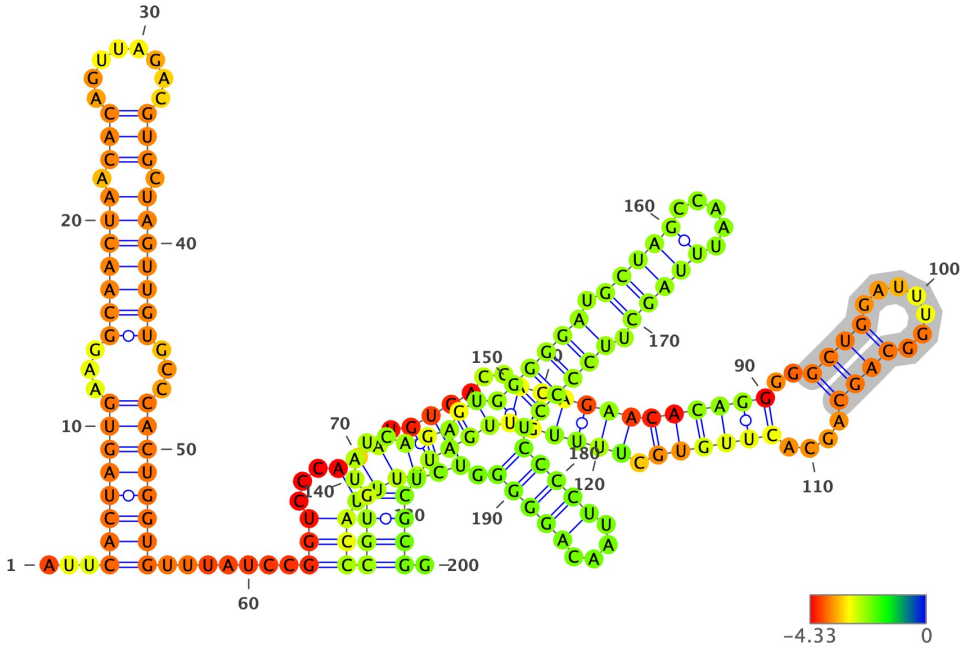
Attributes: ['ID=exon-HHV4_RPMS1-17-1', 'Parent=rna-HHV4_RPMS1-17', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-3p']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 361 from nt 145604 to 145618 (nt 93 to 107)

```
5'-GCUGGAUUUGGCAGC-3'
5'-((((.......))))-3'
Motif MFE = -3.8; z-score = -1.85; ED = 1.32
```



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 145512 to 145711 (motif highlighted in silver):

```
5'-AUUCACUAGUGAAGGCAACUAACACAGUUAGACGUGCUAGUUGUGCCCACUGGUGUUUAUCCGGUCCCAAAUGUCACCACAGAACACAGGGGGCUGGAUUUGGCAGCAGCA
CUUGUGCUUUUGUUGAUUUUUACCCGUGUAUCAGAGUGGGGGAUGCUAGCCAAUUUAGCUUCCCCUCCCCUUAACAGGGGGUCUCGCGG-3
5'-...(((((((((...(((((((.(((........))).)))))))...)))))))))).......(((...(((.((((..((((((((((((..((((.......)))))....
))))))).))))))))))..))))))((((....(((..((((((.(((((.....))))).)))))))((((....)))))..)))))))).-3'
MFE = -70.1; z-score = -3.74; ED = 23.66
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 3 to 23--miRNA, rna-HHV4_RPMS1-16, 145514-145534(+)

Attributes: ['ID=rna-HHV4_RPMS1-16', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-5p']

6-- nt 3 to 23--exon, exon-HHV4_RPMS1-16-1, 145514-145534(+)

Attributes: ['ID=exon-HHV4_RPMS1-16-1', 'Parent=rna-HHV4_RPMS1-16', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-5p']

7-- nt 37 to 58--miRNA, rna-HHV4_RPMS1-17, 145548-145569(+)

Attributes: ['ID=rna-HHV4_RPMS1-17', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-3p']

8-- nt 37 to 58--exon, exon-HHV4_RPMS1-17-1, 145548-145569(+)

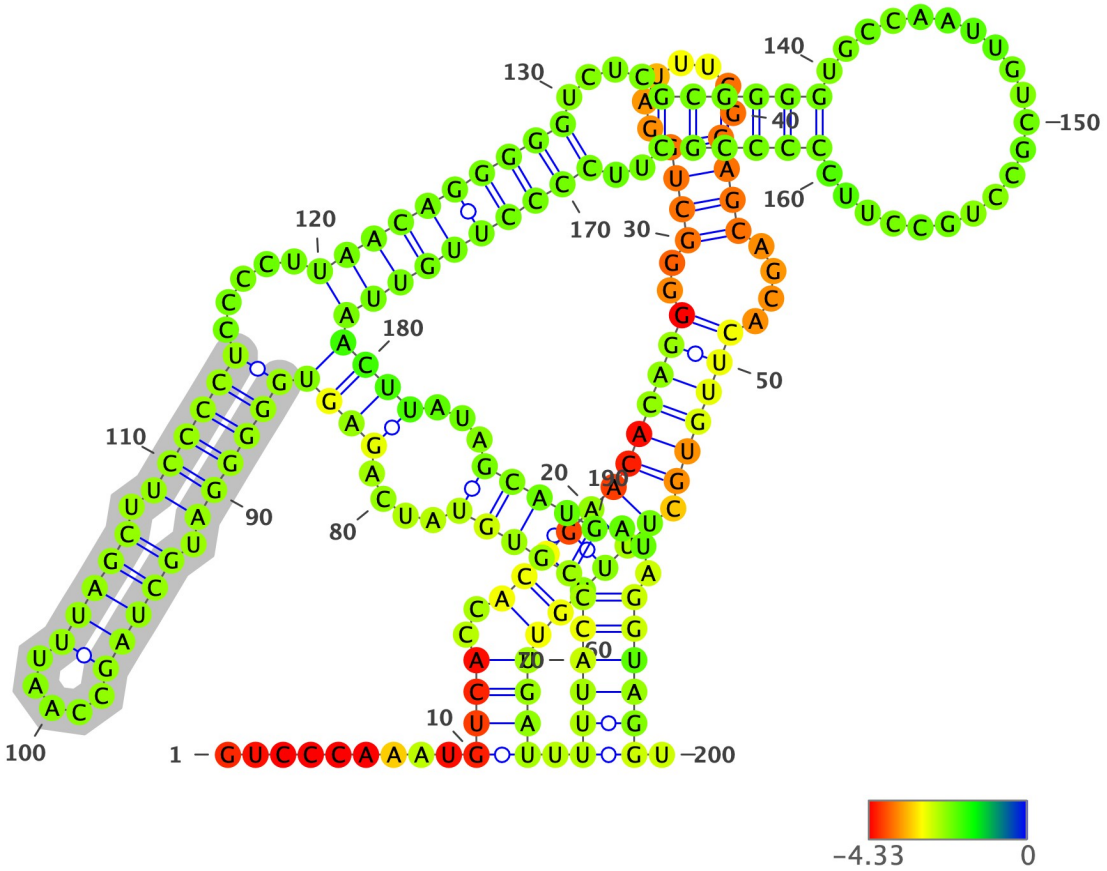
Attributes: ['ID=exon-HHV4_RPMS1-17-1', 'Parent=rna-HHV4_RPMS1-17', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART21-3p']

9-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 362 from nt 145660 to 145688 (nt 86 to 114)

```
5'-GGGGGAUGCUAGCCAAUUUAGCUUCCCCU-3'
5'-((((((.(((((.....))))).)))))))-3'
Motif MFE = -15.0; z-score = -3.95; 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 145575 to 145774 (motif highlighted in silver):

```
5'-GUCCCAAAUGUCACCACAGAACACAGGGGGCUGGAUUUGGCAGCAGCACUUGUGCUUUUGUUGAUUUUUACCCGUGUAUCAGAGUGGGGGAUGCUAGCCAAUUUAGCUUCC
CCUCCCCUUAACAGGGGGUCUCGCGGGGUGCCAAUUGUCGCCUGCCUUCCCCCGCUUCCCCUUGUUAACUUAUAGCAUGAUAGGUAGGU-3
5'-.........((((..(((((((((((..((((.......))))....)))))).))))))))))).((((((((((....((((((((((.(((((.....))))).)))
)))).....((((((((((....((((((.....................)))))).)))))))))))))...)))))...)))))).-3'
MFE = -68.7; z-score = -2.07; ED = 27.37
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

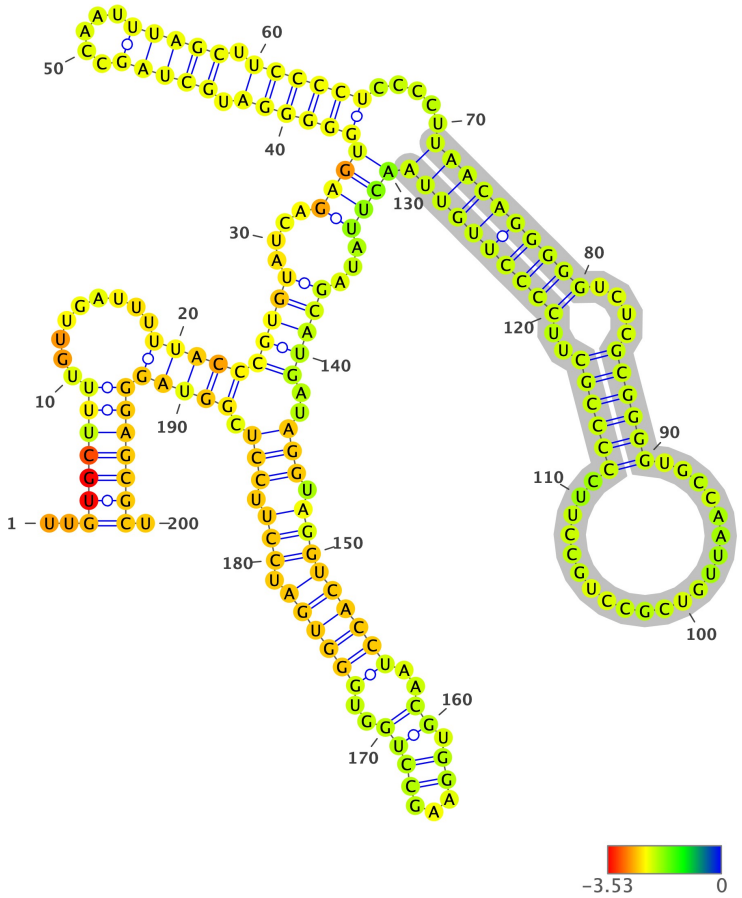
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 363 from nt 145694 to 145752 (nt 71 to 129)

```
5'-UAACAGGGGGUCUCGCGGGGUGCCAAUUGUCGCCUGCCUUCCCCCGCUUCCCCUUGUUA-3'
5'-((((((((((....((((((.....................)))))).))))))))))-3'
Motif MFE = -25.4; z-score = -3.32; ED = 5.31
```



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

Extracted structure model with flanking nucleotides 145624 to 145823 (motif highlighted in silver):

```
5'-UUGUGCUUUUGUUGAUUUUUACCCGUGUAUCAGAGUGGGGGAUGCUAGCCAAUUUAGCUUCCCCUCCCCUUAACAGGGGGUCUCGCGGGGUGCCAAUUGUCGCCUGCCUUC
CCCCGCUUCCCCUUGUUAACUUAUAGCAUGAUAGGUAGGUCACCUAACGUGGAAGCCUGGUGGGUGAUCCUUCCUCGGUAGGGAGCGCU-3
5'-..(((((((.........((((((((((....((((((((((.(((((.....))))).)))))).....((((((((((....((((((.....................
))))))..))))))))))))))...)))))..(((.((((((((((..(((.((...)))).)).)))))).))).))).)))))))))))).-3'
MFE = -72.4; z-score = -2.31; ED = 30.95
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

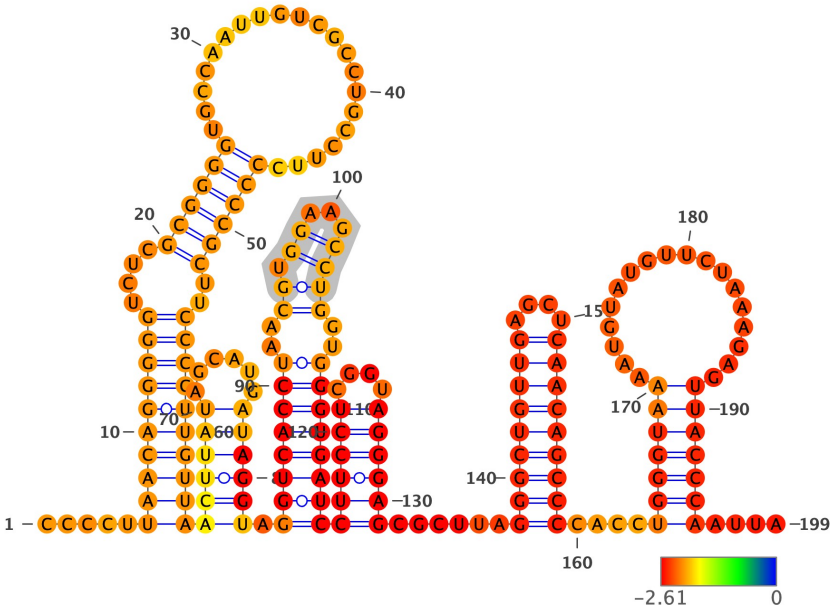
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 364 from nt 145783 to 145792 (nt 95 to 104)

```
5'-GUGGAAGCCU-3'
5'-(.((...)))-3'
Motif MFE = 0.0; z-score = 0.26; ED = 0.97
```



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

Extracted structure model with flanking nucleotides 145689 to 145887 (motif highlighted in silver):

```
5'-CCCCUUAACAGGGGGUCUCGCGGGGUGCCAAUUGUCGCCUGCCUUCCCCCGCUUCCCCUUGUUAACUUAUAGCAUGAUAGGUAGGUCACCUAACGUGGAAGCCUGGUGGGU
GAUCCUUCCUCGGUAGGGAGCGCUUAGGGCUGUUGAGCUCAACAGCCCCACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUA-3
5'-.....((((((((((....((((((.....................)))))))..))))))))))((((((......)))))).(((((((((..((.((...)))))..))))
))))((((((....)))))).....(((((((((....)))))))))....(((((((.................)))))))....-3'
MFE = -71.3; z-score = -2.32; ED = 30.03
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

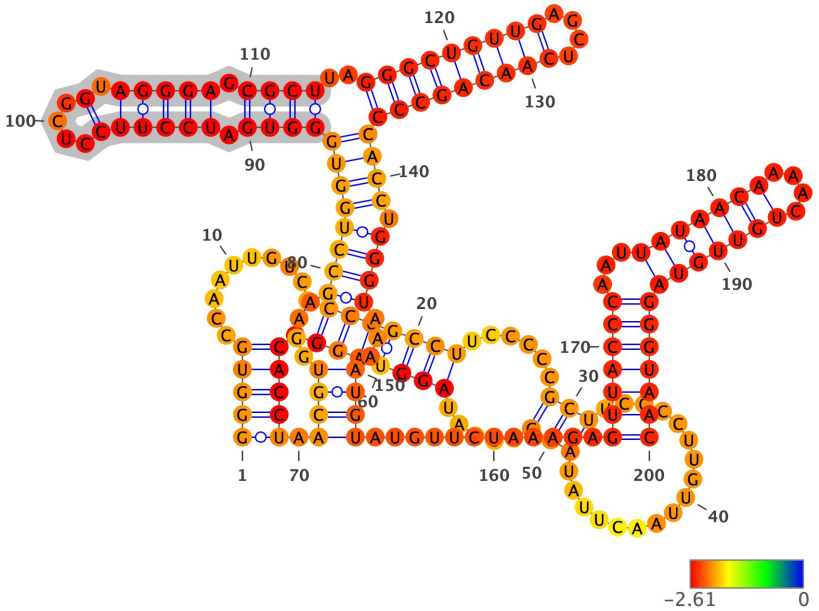
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 365 from nt 145797 to 145823 (nt 87 to 113)

```
5'-GGUGAUCCUUCCUCGGUAGGGAGCGCU-3'
5'-((((.(((((((....).)))))).))))-3'
Motif MFE = -8.8; z-score = -1.23; ED = 2.54
```



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

Extracted structure model with flanking nucleotides 145711 to 145910 (motif highlighted in silver):

```
5'-GGGUGCCAAUUGUCGCCUGCCUUCCCCCGCUUCCCCUUGUUAACUUAUAGCAUGAUAGGUAGGUCACCUAACGUGGAAGCCUGGUGGGUGAUCCUUCCUCGGUAGGGAGCG
CUUAGGGCUGUUGAGCUCAACAGCCCCACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUAUAACAAAACUGUUGUAGGGUAAC-3
5'-(((((.........(((((((.....(((.................))).....)))))))))))).((((....((((((((((((.((((((....).)))))).))
)).(((((((((....)))))))))))))).))))...))))............(((((((...(((((((....)))))))))))))))-3'
MFE = -67.1; z-score = -2.53; ED = 21.72
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

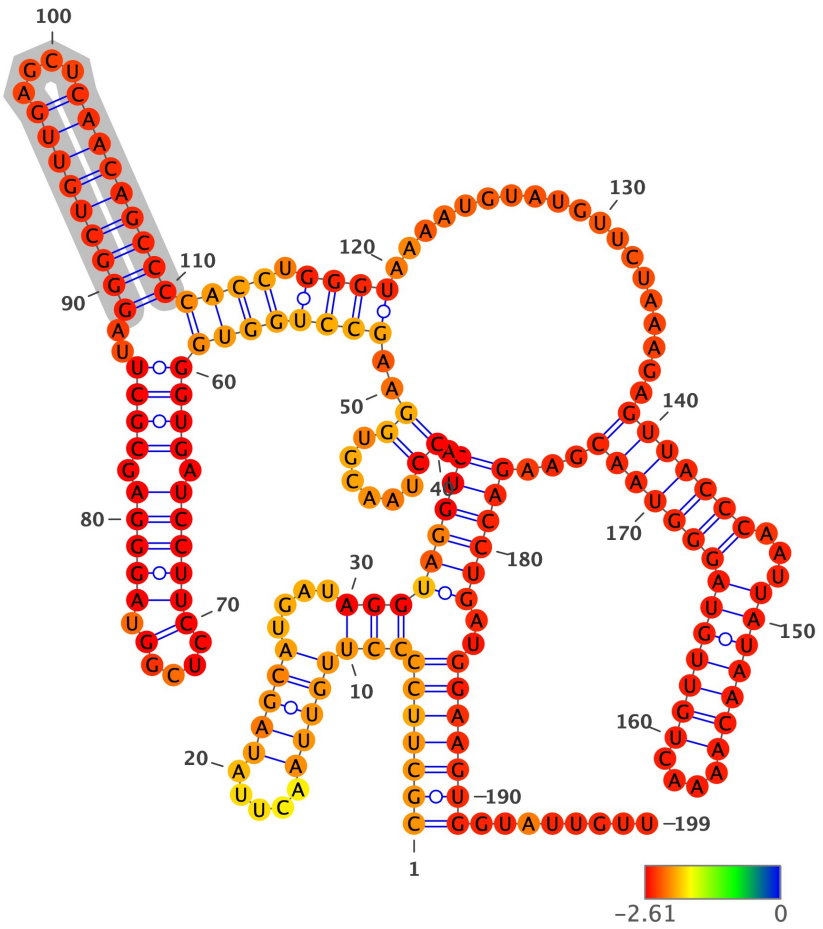
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 366 from nt 145826 to 145847 (nt 89 to 110)

```
5'-GGGCUGUUGAGCUCAACAGCCC-3'
5'-(((((((((....)))))))))-3'
Motif MFE = -15.3; z-score = -4.46; ED = 0.07
```



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 145738 to 145936 (motif highlighted in silver):

```
5'-CGCUUCCCCUUGUUAACUUAUAGCAUGAUAGGUAGGUCACCUAACGUGGAAGCCUGGUGGGUGAUCCUUCCUCGGUAGGGAGCGCUUAGGGCUGUUGAGCUCAACAGCCCC
ACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUAUAACAAAACUGUUGUAGGGUAACGAAGACCUGAUGGAAGUGGUAUUGUU-3
5'-(((((((((((((((.....)))))).....)))))))((((.(.......)).)).(((((((((((.((((((.....).)))))).))))..(((((((((....)))))))))
)))).))))..................((((((...((((((((....)))))))))))))...)))))))..)))))))........-3'
MFE = -68.2; z-score = -3.15; ED = 31.86
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

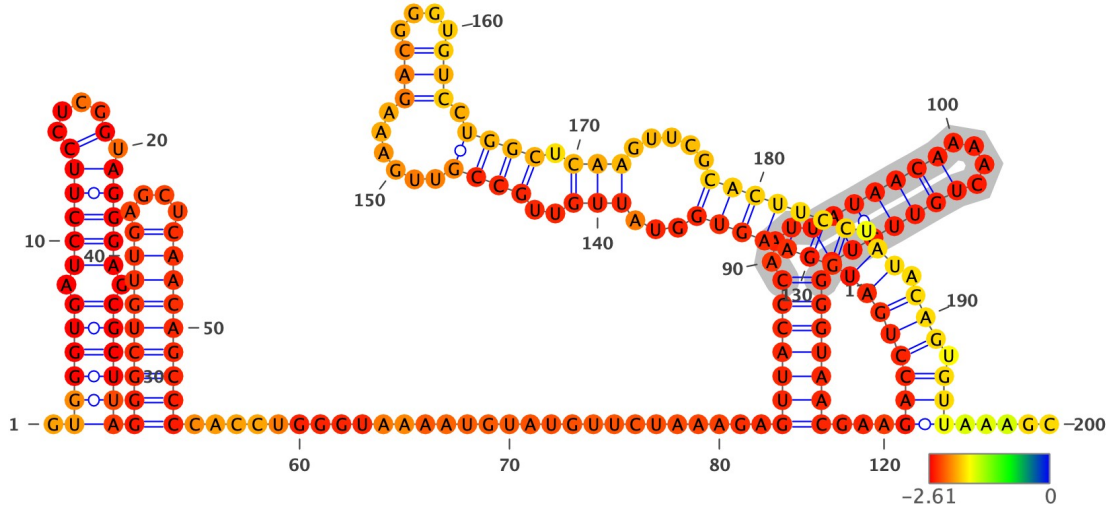
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 367 from nt 145882 to 145904 (nt 89 to 111)

```
5'-CAAUUAUAACAAAACUGUUGUAG-3'
5'-(...(((((((....)))))))-3'
Motif MFE = -4.3; z-score = -3.89; ED = 0.95
```



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 145794 to 145993 (motif highlighted in silver):

```
5'-GUGGGUGAUCCUUCCUCGGUAGGGAGCGCUUAGGGCUGUUGAGCUCAACAGCCCCACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUAUAACAAAACUGUUGUAG
GGUAACGAAGACCUGAUGGAAGUGGUAUUGUUGCCGUUGAAAGACGGGUGUCCUGGCUCAAGUUCGCACUUCCUAUACAGUGUUAAAGC-3
5'-.(((((((.(((((((....).)))))).)))))))((((((((((....))))))))))..............................(((((((...(((((((....)))))))))))))...((((((((((((((...((((..((((.....((((....)))).)))))..)))..)))))))).)).)))).)))).....-3'
MFE = -63.0; z-score = -1.95; ED = 28.66
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

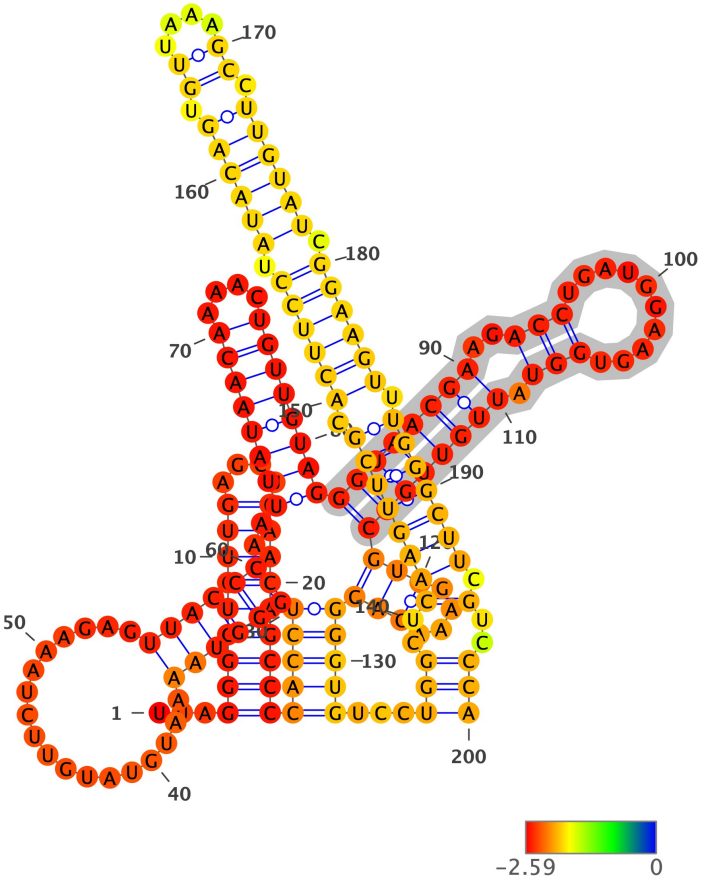
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 368 from nt 145905 to 145939 (nt 83 to 117)

```
5'-GGUAACGAAGACCUGAUGGAAGUGGUAUUGUUGCC-3'
5'-(((((((..(((.........))).)))))))-3'
Motif MFE = -11.1; z-score = -2.41; ED = 0.83
```



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

Extracted structure model with flanking nucleotides 145823 to 146022 (motif highlighted in silver):

```
5'-UUAGGGCUGUUGAGCUCAACAGCCCCACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUAUAACAAAACUGUUGUAGGGUAACGAAGACCUGAUGGAAGUGGUAUU
GUUGCCGUUGAAAGACGGGUGUCCUGGCUCAAGUUCGCACUUCCUAUACAGUGUUAAAGCCUUGUAUCGGAAGUUUGGGCUUCGUCCCA-3
5'-...(((((((((....)))))))))((((((((((.................))))))..(((((((((....)))))))))(((((((..(((..........))).))
))))))((....)))))))...((((..(((((((.((((((.((((....)).)))))).)))))).)))))))).)))..)))-3'
MFE = -68.7; z-score = -3.63; ED = 10.3
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 176 to 197--miRNA, rna-HHV4_RPMS1-18, 145998-146019(+)

Attributes: ['ID=rna-HHV4_RPMS1-18', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

6-- nt 176 to 197--exon, exon-HHV4_RPMS1-18-1, 145998-146019(+)

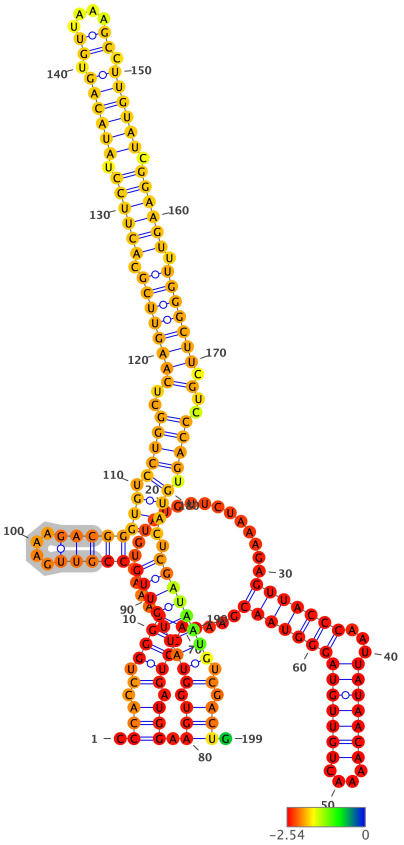
Attributes: ['ID=exon-HHV4_RPMS1-18-1', 'Parent=rna-HHV4_RPMS1-18', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

7-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 369 from nt 145940 to 145949 (nt 95 to 104)

```
5'-GUUGAAAGAC-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 145846 to 146044 (motif highlighted in silver):

```
5'-CCCACCUGGGUAAAAUGUAUGUUCUAAAGAGUUACCCAAUUAUAACAAAACUGUUGUAGGGUAACGAAGACCUGAUGGAAGUGGUAUUGUUGCCGUUGAAAGACGGGUGUC
CUGGCUCAAGUUCGCACUUCCUAUACAGUGUUAAAGCCUUGUAUCGGAAGUUUGGGCUUCGUCCCAGUGUACUCGAUAAUGUCGACUG-3
5'-.((((.(.((((.....................(((((((...(((((((....)))))))))))))).....))))).)).)).(((.((((((((((((((....)))))))((.(
((((..(((((((((.((((((.((((((.((....)).)))))).)))))).)))))))).)..)))).)))).)))))))))).).))).-3'
MFE = -59.7; z-score = -2.78; ED = 38.18
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 153 to 174--miRNA, rna-HHV4_RPMS1-18, 145998-146019(+)

Attributes: ['ID=rna-HHV4_RPMS1-18', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

6-- nt 153 to 174--exon, exon-HHV4_RPMS1-18-1, 145998-146019(+)

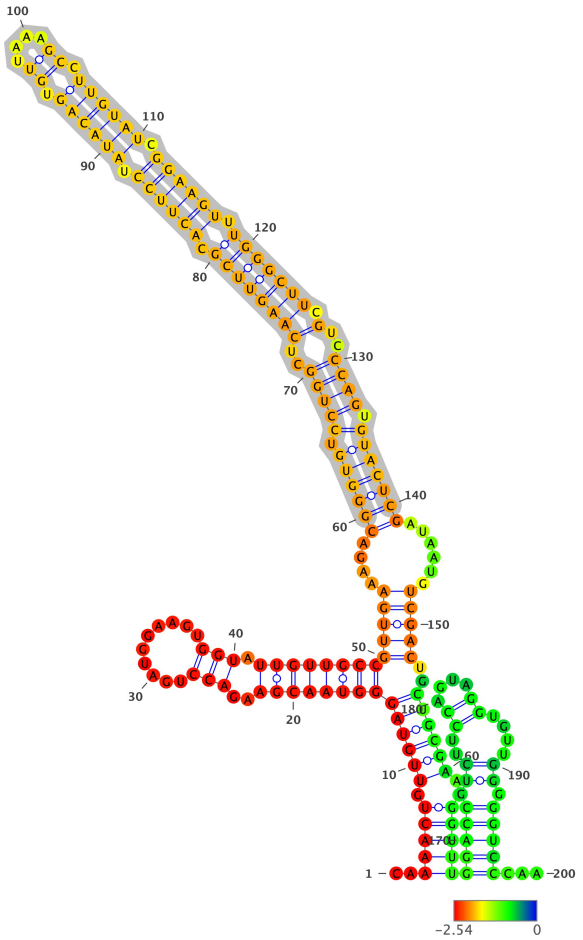
Attributes: ['ID=exon-HHV4_RPMS1-18-1', 'Parent=rna-HHV4_RPMS1-18', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

7-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 370 from nt 145950 to 146030 (nt 60 to 140)

```
5'-GGGUGUCCUGGCUCAAGUUCGCACUUCCUAUACAGUGUUAAAGCCUUGUAUCGGAAGUUUGGGCUUCGUCCCAGUGUACUC-3'
5'-((.....((.....(.................................................).....)).....))-3'
Motif MFE = -30.5; z-score = -3.42; ED = 3.29
```



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 145891 to 146090 (motif highlighted in silver):

```
5'-CAAAACUGUUGUAGGGUAACGAAGACCUGAUGGAAGUGGUAUUGUUGCCGUUGAAAGACGGGUGUCCUGGCUCAAGUUCGCACUUCCUAUACAGUGUUAAAGCCUUGUAUC
GGAAGUUUGGGCUUCGUCCCAGUGUACUCGAUAAUGUCGACUGCUGCGAAAGGUUUGGACCGUCUUCCAGUAGGUGUUGGGGGUCCCAA-3
5'-..(((((.(((((((((((((..(((.........))).)))))))))(((((....((((((.(((((..(((((((((.((((((.((((((.((....)).)))))))).
))))))).)))))))..)..)))).)))))))).....)))))..)))))).)))))((((((.((..((....)).....)).)))))...-3'
MFE = -70.0; z-score = -2.36; ED = 33.31
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 108 to 129--miRNA, rna-HHV4_RPMS1-18, 145998-146019(+)

Attributes: ['ID=rna-HHV4_RPMS1-18', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

6-- nt 108 to 129--exon, exon-HHV4_RPMS1-18-1, 145998-146019(+)

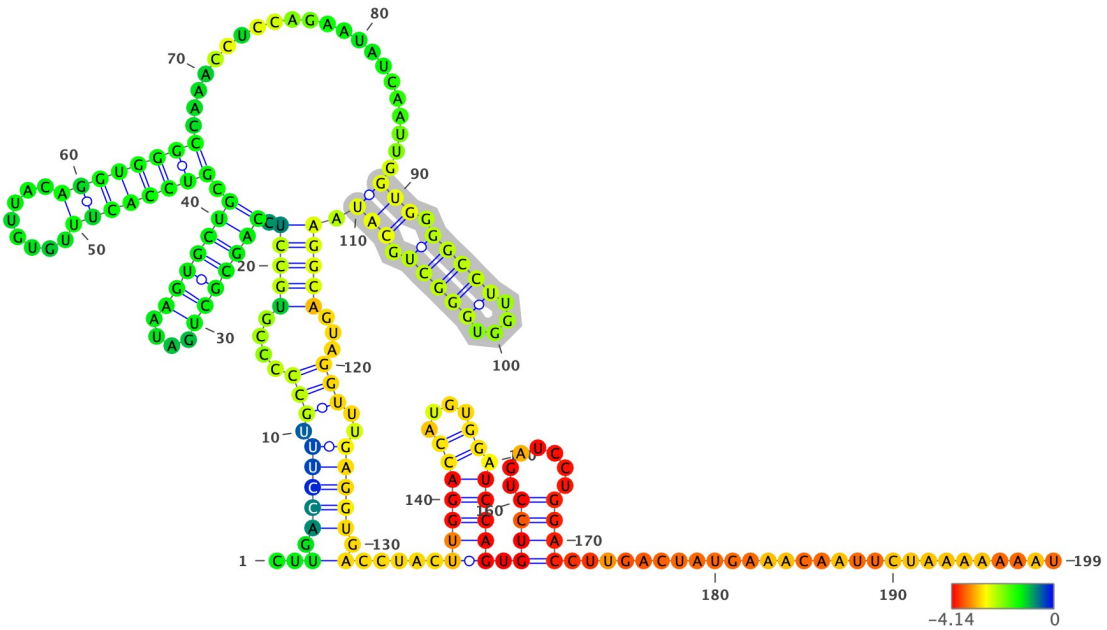
Attributes: ['ID=exon-HHV4_RPMS1-18-1', 'Parent=rna-HHV4_RPMS1-18', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART18-3p']

7-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 371 from nt 146363 to 146384 (nt 89 to 110)

```
5'-GUGGGGCCUUGGUGGGCUGCAU-3'
5'-(((.(((((....))))).)))-3'
Motif MFE = -10.6; z-score = -3.61; 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 146275 to 146473 (motif highlighted in silver):

```
5'-CUUGACCUUUGCCCCCGUGCCUCCAGCGCUGAUAAGUGCUGCGUCCACUUUGUGUUACAGGUGGGCCAAACCUCCAGAAUAUCAAUUGGUGGGGCCUUGGUGGGCUGCAUA
AGGCAGUAGGUUUGAGGUGACCUACUUGGACCAUGUGGAUCCAGUGUCCUGAUCCUGGACCUUGACUAUGAAACAAUUCUAAAAAAAU-3
5'-..(.(((((.(((....(((((.(((((((....)))))))).(((((((.......)))))))).....................(((.(((((....))))).))).
)))))...)))..)))))).).....(((((((....)).)))))..((((.......))))..........................-3'
MFE = -58.6; z-score = -1.15; ED = 44.61
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 165 to 186--miRNA, rna-HHV4_RPMS1-19, 146439-146460(+)

Attributes: ['ID=rna-HHV4_RPMS1-19', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

6-- nt 165 to 186--exon, exon-HHV4_RPMS1-19-1, 146439-146460(+)

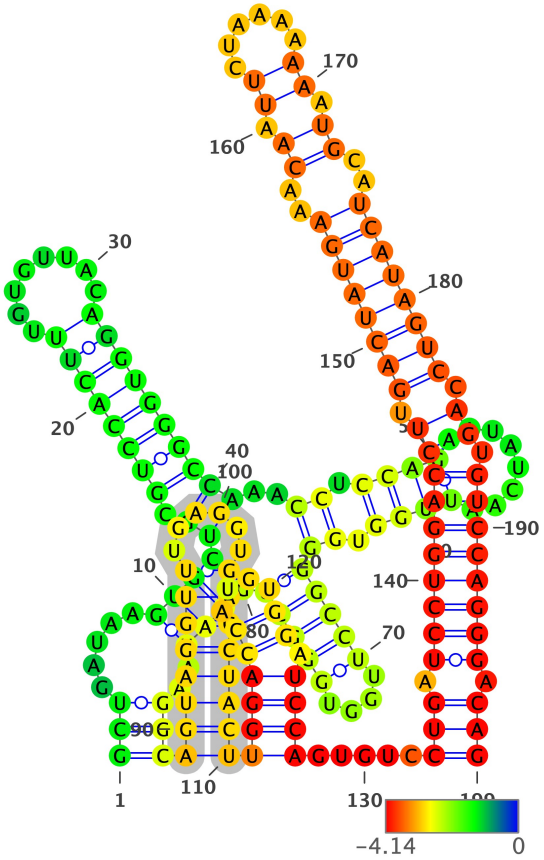
Attributes: ['ID=exon-HHV4_RPMS1-19-1', 'Parent=rna-HHV4_RPMS1-19', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

7-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 372 from nt 146390 to 146411 (nt 89 to 110)

```
5'-AGUAGGUUUGAGGUGACCUACU-3'
5'-(((((((.....)))))))-3'
Motif MFE = -9.5; z-score = -3.83; 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 146302 to 146500 (motif highlighted in silver):

```
5'-GCUGAUAAGUGCUGCGUCCACUUUGUGUUACAGGUGGGCCAAACCUCCAGAAUAUCAAUUGGUGGGGCCUUGGUGGGCUGCAUAAGGCAGUAGGUUUGAGGUGACCUACUU
GGACCAUGUGGAUCCAGUGUCCUGAUCCUGGACCUUGACUAUGAAACAAUUCUAAAAAAAUGCAUCAUAGUCCAGUGUCCAGGGACAG-3
5'-(((.....((((((.(((((((((.......)))))))))..((.((((.......)))).))((((((....)))))))))..)))((((((((.....)))))))))(
(((((....)).))))....(((.((((((((((.(((((((..((.((......)).)).)..)))))))).)).)))))))).)))-3'
MFE = -71.6; z-score = -4.29; ED = 45.63
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 138 to 159--miRNA, rna-HHV4_RPMS1-19, 146439-146460(+)

Attributes: ['ID=rna-HHV4_RPMS1-19', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

6-- nt 138 to 159--exon, exon-HHV4_RPMS1-19-1, 146439-146460(+)

Attributes: ['ID=exon-HHV4_RPMS1-19-1', 'Parent=rna-HHV4_RPMS1-19', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

7-- nt 174 to 195--miRNA, rna-HHV4_RPMS1-20, 146475-146496(+)

Attributes: ['ID=rna-HHV4_RPMS1-20', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

8-- nt 174 to 195--exon, exon-HHV4_RPMS1-20-1, 146475-146496(+)

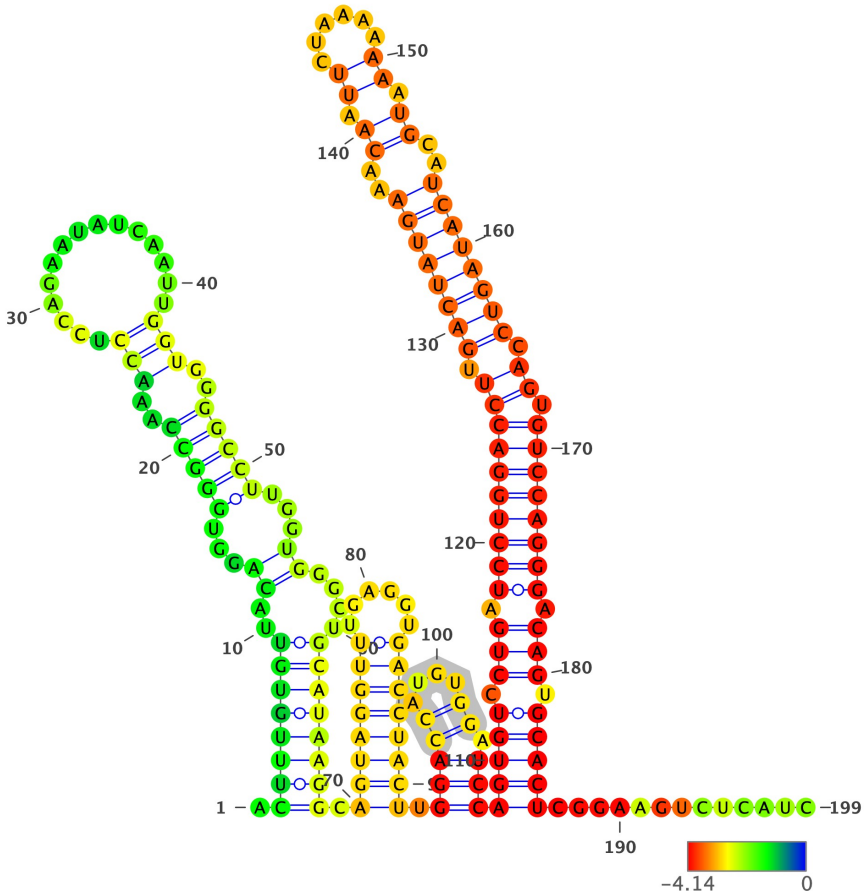
Attributes: ['ID=exon-HHV4_RPMS1-20-1', 'Parent=rna-HHV4_RPMS1-20', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 373 from nt 146416 to 146423 (nt 96 to 103)

```
5'-CCAUGUGG-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 146321 to 146519 (motif highlighted in silver):

```
5'-ACUUUGUGUUACAGGUGGGCCAAACCUCCAGAAUAUCAAUUGGUGGGGCCUUGGUGGGCUGCAUAAGGCAGUAGGUUUGAGGUGACCUACUUGGACCAUGUGGAUCCAGUG
UCCUGAUCCUGGACCUUGACUAUGAAACAAUUCUAAAAAAAUGCAUCAUAGUCCAGUGUCCAGGGACAGUGCACUCGGAAGUCUCAUC-3
5'-.(((((((((..((...((((((..(((.............)))..)))))...)).....)))))))).((((((((......)))))))).(((((....)).)))((((
(.((((.(((((((((((.((((((((..((.((......)).)).)).)))))))).)).)))))))).)))).)))))..............-3'
MFE = -72.4; z-score = -4.48; ED = 32.55
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 119 to 140--miRNA, rna-HHV4_RPMS1-19, 146439-146460(+)

Attributes: ['ID=rna-HHV4_RPMS1-19', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

6-- nt 119 to 140--exon, exon-HHV4_RPMS1-19-1, 146439-146460(+)

Attributes: ['ID=exon-HHV4_RPMS1-19-1', 'Parent=rna-HHV4_RPMS1-19', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

7-- nt 155 to 176--miRNA, rna-HHV4_RPMS1-20, 146475-146496(+)

Attributes: ['ID=rna-HHV4_RPMS1-20', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

8-- nt 155 to 176--exon, exon-HHV4_RPMS1-20-1, 146475-146496(+)

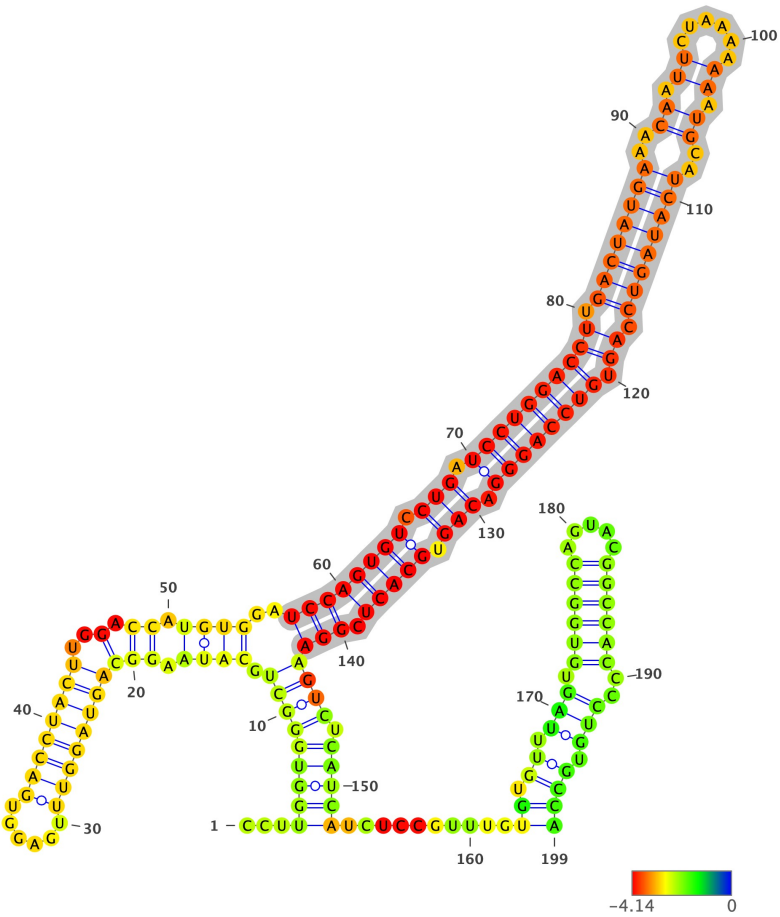
Attributes: ['ID=exon-HHV4_RPMS1-20-1', 'Parent=rna-HHV4_RPMS1-20', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 374 from nt 146425 to 146510 (nt 57 to 142)

```
5'-UCCAGUGUCCUGAUCCUGGACCUUGACUAUGAAACAAUUCUAAAAAAAUGCAUCAUAGUCCAGUGUCCAGGGACAGUGCACUCGGA-3'
5'-(((((((.(((.((((((((((.(((((((((..((.((......)).))..)))))))).)).)))))))).))).)))))).)))-3'
Motif MFE = -38.4; z-score = -5.67; ED = 4.39
```



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

Extracted structure model with flanking nucleotides 146369 to 146567 (motif highlighted in silver):

```
5'-CCUUGGUGGGCUGCAUAAGGCAGUAGGUUUGAGGUGACCUACUUGGACCAUGUGGAUCCAGUGUCCUGAUCCUGGACCUUGACUAUGAAACAAUUCUAAAAAAAUGCAUCA
UAGUCCAGUGUCCAGGGACAGUGCACUCGGAAGUCUCAUCAUCUCCGUUUGUGUGUUUAGUGUGGCCAGUACGGCCACCCCUGUGCCA-3
5'-...(((((((((.((((.((((((((((.....)))))))).)).)).)))).)).(((((((((.(((.((((((((((.((((((((..((.((......)).)).)..)))
)))))).)).)))))))).))).)))))).))))))).))))).....((.((.(((.((((((.....)))))))..))).))))-3'
MFE = -73.6; z-score = -3.7; ED = 38.49
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 71 to 92--miRNA, rna-HHV4_RPMS1-19, 146439-146460(+)

Attributes: ['ID=rna-HHV4_RPMS1-19', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

6-- nt 71 to 92--exon, exon-HHV4_RPMS1-19-1, 146439-146460(+)

Attributes: ['ID=exon-HHV4_RPMS1-19-1', 'Parent=rna-HHV4_RPMS1-19', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

7-- nt 107 to 128--miRNA, rna-HHV4_RPMS1-20, 146475-146496(+)

Attributes: ['ID=rna-HHV4_RPMS1-20', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

8-- nt 107 to 128--exon, exon-HHV4_RPMS1-20-1, 146475-146496(+)

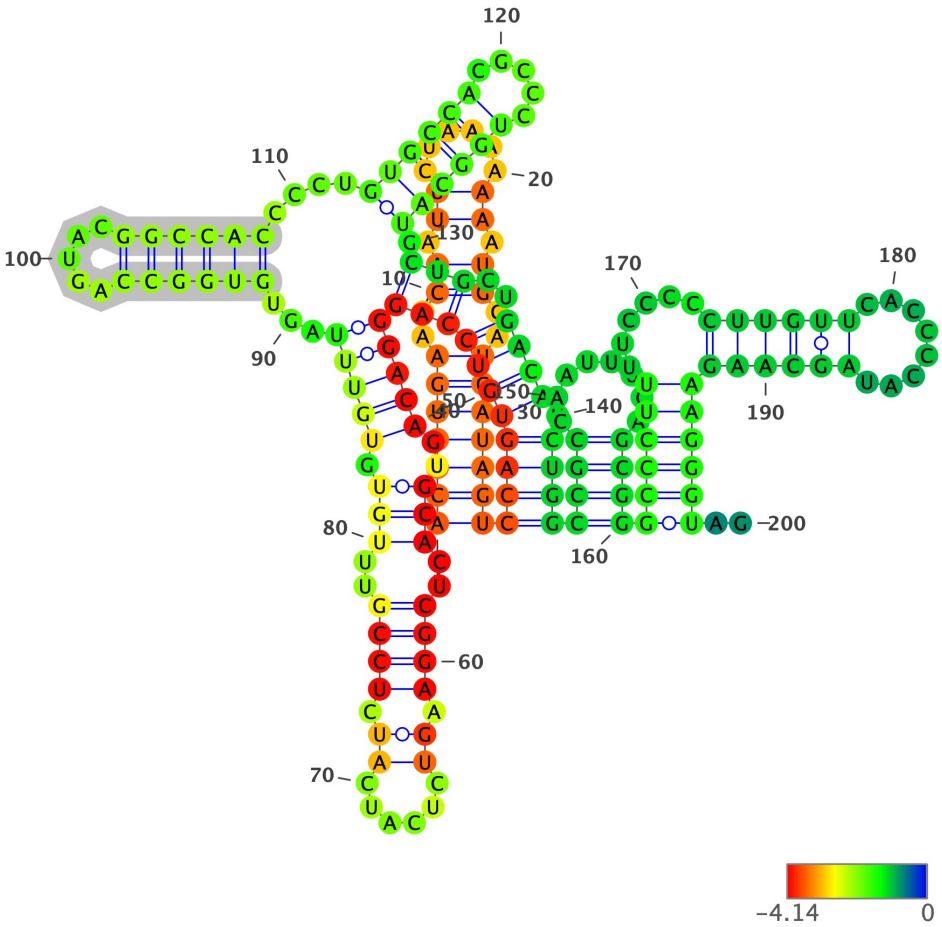
Attributes: ['ID=exon-HHV4_RPMS1-20-1', 'Parent=rna-HHV4_RPMS1-20', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 375 from nt 146541 to 146557 (nt 92 to 108)

```
5'-GUGGCCAGUACGGCCAC-3'
5'-((((((.....))))))-3'
Motif MFE = -10.1; z-score = -4.06; ED = 0.1
```



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 146450 to 146649 (motif highlighted in silver):

```
5'-ACUAUGAAACAAUUCUAAAAAAAUGCAUCAUAGUCCAGUGUCCAGGGACAGUGCACUCGGAAGUCUCAUCAUCUCCGUUUGUGUGUUUAGUGUGGCCAGUACGGCCACCCC
UGUGCCACGCCCUGGCAUGCUGCUGACAUCUGGCCGCCAAUUUCAGCGGGCCCUUUUCCCCCUUGUUCACCCCAUAGCAAGAAGGGUAG-3
5'-(((((((..((.((......)).)).)).))))))((((((((((((((((..(((..(((((.((......)).)))))..))).)))))...((((((.....)))))))...
.((((((.....)))))).))).)).)))).))))((((.......)))))))((((.....(((((.......)))))))))))))..-3'
MFE = -59.6; z-score = -1.39; ED = 47.13
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 11--miRNA, rna-HHV4_RPMS1-19, 146439-146460(+)

Attributes: ['ID=rna-HHV4_RPMS1-19', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

6-- nt 1 to 11--exon, exon-HHV4_RPMS1-19-1, 146439-146460(+)

Attributes: ['ID=exon-HHV4_RPMS1-19-1', 'Parent=rna-HHV4_RPMS1-19', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7*']

7-- nt 26 to 47--miRNA, rna-HHV4_RPMS1-20, 146475-146496(+)

Attributes: ['ID=rna-HHV4_RPMS1-20', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

8-- nt 26 to 47--exon, exon-HHV4_RPMS1-20-1, 146475-146496(+)

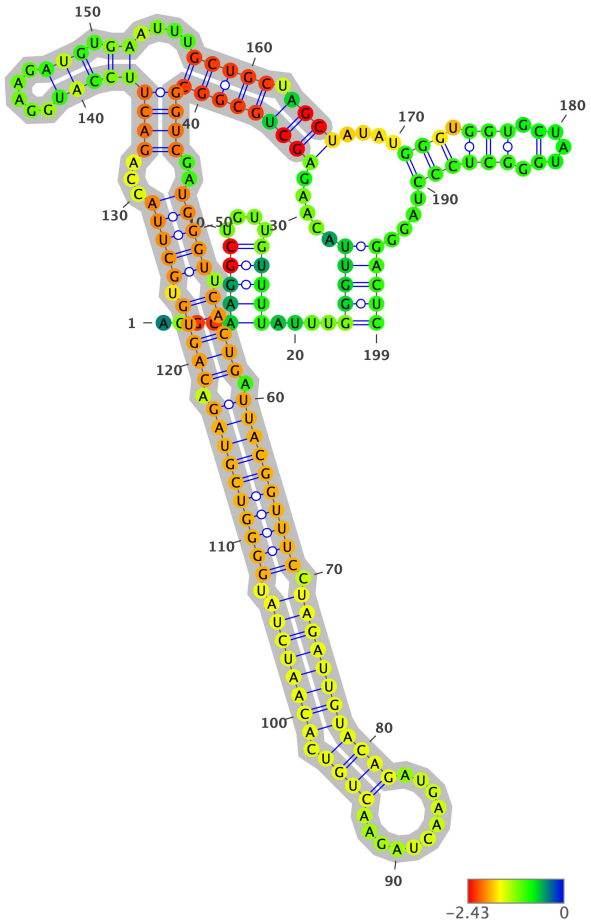
Attributes: ['ID=exon-HHV4_RPMS1-20-1', 'Parent=rna-HHV4_RPMS1-20', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART7']

9-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 376 from nt 146745 to 146876 (nt 34 to 165)

```
5'-GCUGCGGCGGUCGAUGGGUUCACUGAUUACGGUUUCCUAGAUUGUACAGAUGAACUAGAACUGUCACAAUCUAUGGGGUCGUAGACAGUGUGCUUACCAGACUUCCAUGGA
AGAUGUGAAUUUGCUGCUAGC-3'
5'-((.(((((((((..(.....................................................................................)...)))).......
............)))))..))-3'
Motif MFE = -45.5; z-score = -3.02; ED = 13.01
```



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 146712 to 146910 (motif highlighted in silver):

```
5'-ACGCAAGGCUGUUGUUUUAUUUGGGUUACAAGAGCUGCGGCGGUCGAUGGGUUCACUGAUUACGGUUUCCUAGAUUGUACAGAUGAACUAGAACUGUCACAAUCUAUGGGG
UCGUAGACAGUGUGCUUACCAGACUUCCAUGGAAGAUGUGAAUUUGCUGCUAGCUAUAUGGGUGGUGCUAUGGGCUCCCUAGGGACUC-3
5'-....(((((....)))))....(((((.....(((((((((((((..(((((.(((((.((((((((((.(((((((((((.....)))).)))))))).))))
))))))).)))))).)))))...))))((((.....)))).)).....)))))).))))....(((.(((.(...).)))))).....)))))-3'
MFE = -56.7; z-score = -0.62; ED = 33.89
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 61 to 82--miRNA, rna-HHV4_RPMS1-21, 146772-146793(+)

Attributes: ['ID=rna-HHV4_RPMS1-21', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART8']

6-- nt 61 to 82--exon, exon-HHV4_RPMS1-21-1, 146772-146793(+)

Attributes: ['ID=exon-HHV4_RPMS1-21-1', 'Parent=rna-HHV4_RPMS1-21', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART8']

7-- nt 96 to 118--miRNA, rna-HHV4_RPMS1-22, 146807-146829(+)

Attributes: ['ID=rna-HHV4_RPMS1-22', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART8*']

8-- nt 96 to 118--exon, exon-HHV4_RPMS1-22-1, 146807-146829(+)

Attributes: ['ID=exon-HHV4_RPMS1-22-1', 'Parent=rna-HHV4_RPMS1-22', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART8*']

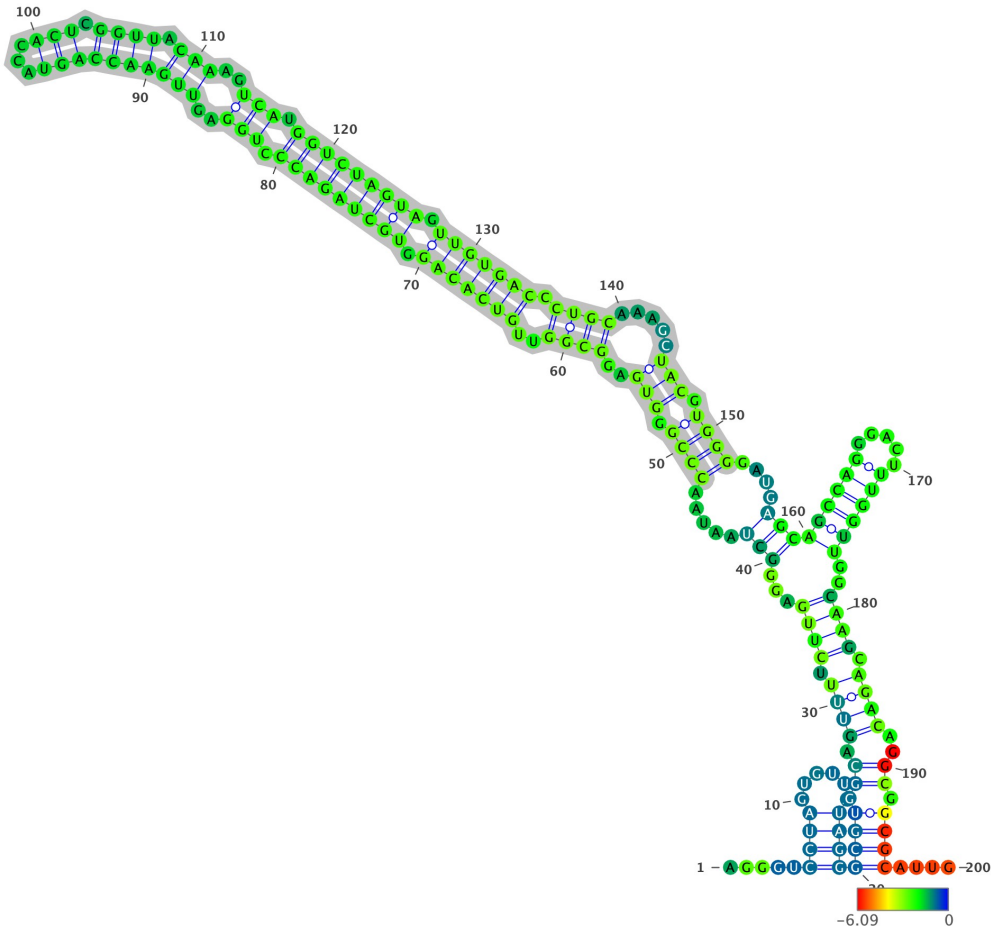
9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 377 from nt 147145 to 147249 (nt 48 to 152)

5'-CCCGGGUGAGGCGGUUGUCACAGGUGCUAGACCCUGGAGUUGAACCAGUACCACUCGGUUACAAAGUCAUGGUCUAGUAGUUGUGACCCUGCAAAGCUACGUGGG-3'

5'-((((.(((..(((((..(((((((.(((((((((.(((.....))).))))))))).)))))))).)))).....))).))))-3'
Motif MFE = -47.6; z-score = -4.06; ED = 6.89



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 147098 to 147297 (motif highlighted in silver):

5'-AGGGUCCUAGUGUUAUAGGGCGUGGCAGUUUUCUUGAGGGCUAAUAACCCGGGUGAGGCGGUUGUCACAGGUGCUAGACCCUGGAGUUGAACCAGUACCACUCGGUUACAA
AGUCAUGGUCUAGUAGUUGUGACCCUGCAAAGCUACGUGGGGAUGAGCAGCCAGGGACUUUGGUUGGCAAGCAGACAGGCGGCGCAUUG-3
5'-.....((((.....)))))((((.((.((((.((((...((((.....((((.((((..((((..(((((((.(((((((((.(((..((((((((((...)))).)))))..)))
..))).)))))))))).)))))))).)))).....))).)))).....)))((((((.....)))))).))))).))))..)).)))).....-3'
MFE = -76.9; z-score = -3.06; ED = 7.79

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 106 to 128--miRNA, rna-HHV4_RPMS1-25, 147203-147225(+)

Attributes: ['ID=rna-HHV4_RPMS1-25', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 106 to 128--exon, exon-HHV4_RPMS1-25-1, 147203-147225(+)

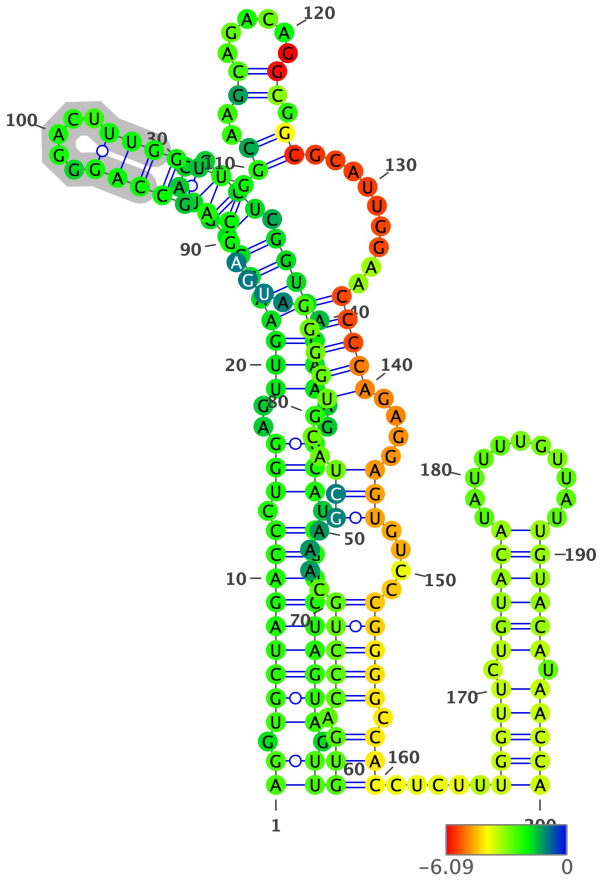
Attributes: ['ID=exon-HHV4_RPMS1-25-1', 'Parent=rna-HHV4_RPMS1-25', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

7-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 378 from nt 147260 to 147270 (nt 95 to 105)

```
5'-CAGGGACUUUG-3'
5'-(((.....)))-3'
Motif MFE = 0.0; z-score = 0.29; ED = 0.25
```



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

Extracted structure model with flanking nucleotides 147166 to 147365 (motif highlighted in silver):

```
5'-AGGUGCUAGACCCUGGAGUUGAACCAGUACCACUCGGUUACAAAGUCAUGGUCUAGUAGUUGUGACCCUGCAAAGCUACGUGGGGAUGAGCAGCCAGGGACUUUGGUUGGC
AAGCAGACAGGCGGCGCAUUGGAACCCCAGAGGAGUGUCCCGGGGCCACCUCUUUGGUUCUGUACAUAUUUUGUUAUUGUACAUAACCA-3
5'-((.(((((((((.((((..((((((((((...)))).)))))..)))).))..))).)))))))))..))((((.(((((.....((((...((((((.....(((((((.....)))))))))((
..((......)).))........)))))....)))....)))))..)))).....(((((.((((((.....)))))).))))).))))-3'
MFE = -66.4; z-score = -1.2; ED = 36.52
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 38 to 60--miRNA, rna-HHV4_RPMS1-25, 147203-147225(+)

Attributes: ['ID=rna-HHV4_RPMS1-25', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 38 to 60--exon, exon-HHV4_RPMS1-25-1, 147203-147225(+)

Attributes: ['ID=exon-HHV4_RPMS1-25-1', 'Parent=rna-HHV4_RPMS1-25', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

7-- nt 156 to 177--miRNA, rna-HHV4_RPMS1-26, 147321-147342(+)

Attributes: ['ID=rna-HHV4_RPMS1-26', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10*']

8-- nt 156 to 177--exon, exon-HHV4_RPMS1-26-1, 147321-147342(+)

Attributes: ['ID=exon-HHV4_RPMS1-26-1', 'Parent=rna-HHV4_RPMS1-26', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10*']

9-- nt 191 to 200--miRNA, rna-HHV4_RPMS1-27, 147356-147378(+)

Attributes: ['ID=rna-HHV4_RPMS1-27', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10']

10-- nt 191 to 200--exon, exon-HHV4_RPMS1-27-1, 147356-147378(+)

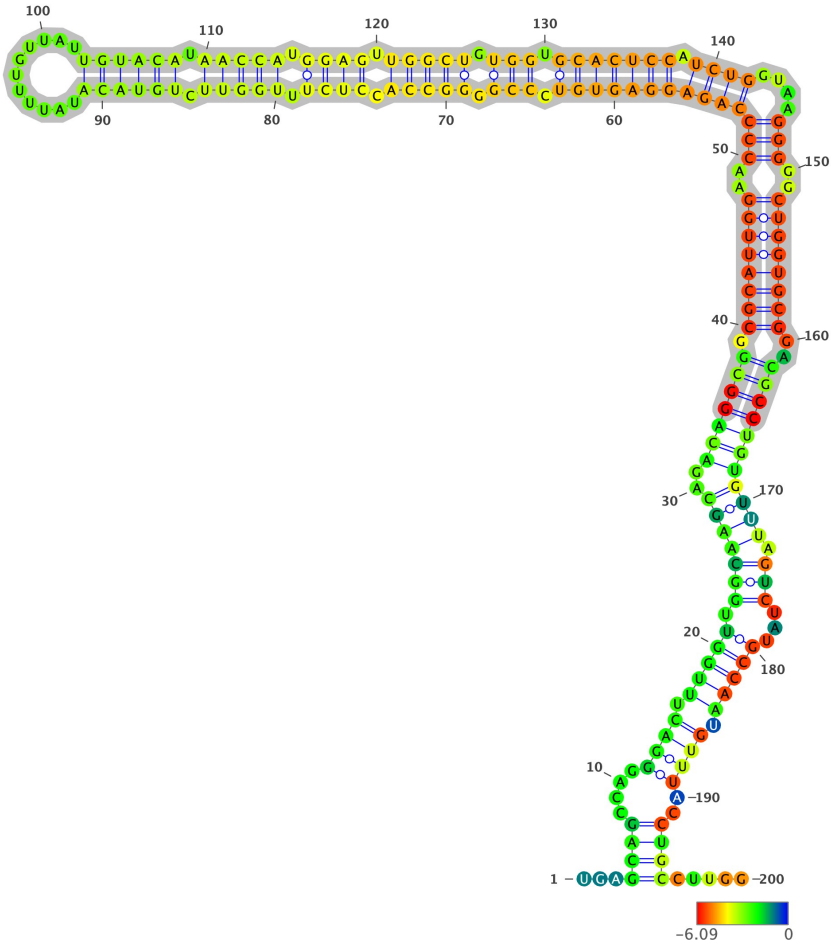
Attributes: ['ID=exon-HHV4_RPMS1-27-1', 'Parent=rna-HHV4_RPMS1-27', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10']

11-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 379 from nt 147286 to 147416 (nt 35 to 165)

```
5'-GGCGGCGCAUUGGAACCCCAGAGGAGUGUCCCGGGGCCACCUCUUUGGUUCUGUACAUAUUUUGUUAUUGUACAUAACCAUGGAGUUGGCUGUGGUGCACUCCAUCUGGUA
AGGGGGCUGGUGCGGACGCC-3'
5'-((...(((((((((..(((((((((((((((.(((.(((((.((((.(((((.((((((.........)))))).)))))).)))).)))))).))).)))))))).)))).....
.)))..)))))))))....))-3'
Motif MFE = -74.0; z-score = -5.85; ED = 4.32
```



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

Extracted structure model with flanking nucleotides 147252 to 147451 (motif highlighted in silver):

```
5'-UGAGCAGCCAGGGACUUUGGUUGGCAAGCAGACAGGCGGCGCAUUGGAACCCCAGAGGAGUGUCCCGGGGCCACCUCUUUGGUUCUGUACAUAUUUUGUUAUUGUACAUAA
CCAUGGAGUUGGCUGUGGUGCACUCCAUCUGGUAAGGGGGCUGGUGCGGACGCCUGUGUUUAGUCUAUGCCAAUGUUUACCUGCCUUGG-3
5'-...((((....((((.(((((.(((((((..(((((((.((((((((..(((((((((((((((.(((.(((((.((((.(((((.((((((.........)))))).))
)))).)))).)))))).))).)))))))).))))....)))..)))))))..))))))))))))).)))...)))))).))))..)))).....-3'
MFE = -97.9; z-score = -5.87; ED = 20.77
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 70 to 91--miRNA, rna-HHV4_RPMS1-26, 147321-147342(+)

Attributes: ['ID=rna-HHV4_RPMS1-26', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10*']

6-- nt 70 to 91--exon, exon-HHV4_RPMS1-26-1, 147321-147342(+)

Attributes: ['ID=exon-HHV4_RPMS1-26-1', 'Parent=rna-HHV4_RPMS1-26', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10*']

7-- nt 105 to 127--miRNA, rna-HHV4_RPMS1-27, 147356-147378(+)

Attributes: ['ID=rna-HHV4_RPMS1-27', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10']

8-- nt 105 to 127--exon, exon-HHV4_RPMS1-27-1, 147356-147378(+)

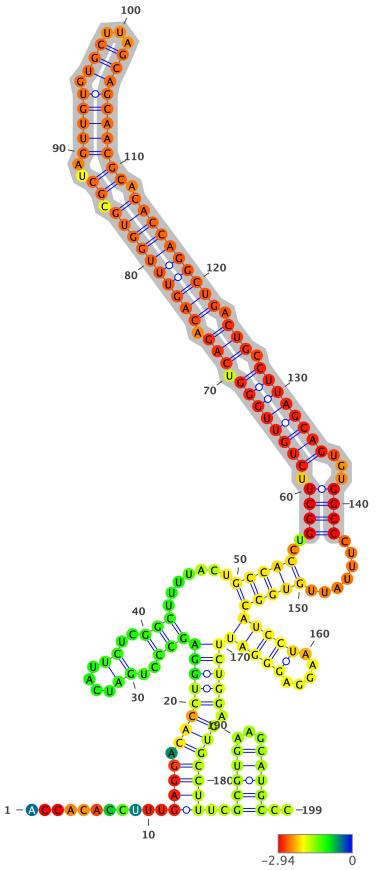
Attributes: ['ID=exon-HHV4_RPMS1-27-1', 'Parent=rna-HHV4_RPMS1-27', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART10']

9-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 380 from nt 147524 to 147609 (nt 57 to 142)

```
5'-GGCUUCUGUUGGGUCAGACAGUUUGGUGCGCUAGUUGUGUGCUUAGCAGCAACGCACACCAGGCUGACUGCCUUAGCAGUGUGGCC-3'
5'-((((.(((((((((.(((.(((((((((((.((..((((((.(((...)))))))))))).)))))))))))).))).)))))))))...))))-3'
Motif MFE = -42.7; z-score = -4.28; 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 147468 to 147666 (motif highlighted in silver):

```
5'-ACCACACCUUUGAGGACACCUGGAGCCCUGAUCAUUCUCGGCUUUUACUGCCACCUGGCUUCUGUUGGGUCAGACAGUUUGGUGCGCUAGUUGUGUGCUUAGCAGCAACGC
ACACCAGGCUGACUGCCUUAGCAGUGUGGCCCUUUAUUGUGGCAUCCUAAGGAGGGAUUCUGGAGUGCCUUUCGCGUGAAGCAUGCCC-3
5'-...........((((.(((((((((((..((....))..)))).......((((..((((.(((((((((.(((.((((((((((.((..(((((.(((...)))))))))))
.)))))))))).)))).)))))))...)))).......)))))((((.....)))))))))).)))))))..(((((...)))))..-3'
MFE = -73.9; z-score = -2.54; ED = 23.83
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 70 to 93--miRNA, rna-HHV4_RPMS1-28, 147537-147560(+)

Attributes: ['ID=rna-HHV4_RPMS1-28', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-5p']

6-- nt 70 to 93--exon, exon-HHV4_RPMS1-28-1, 147537-147560(+)

Attributes: ['ID=exon-HHV4_RPMS1-28-1', 'Parent=rna-HHV4_RPMS1-28', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-5p']

7-- nt 108 to 128--miRNA, rna-HHV4_RPMS1-29, 147575-147595(+)

Attributes: ['ID=rna-HHV4_RPMS1-29', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-3p']

8-- nt 108 to 128--exon, exon-HHV4_RPMS1-29-1, 147575-147595(+)

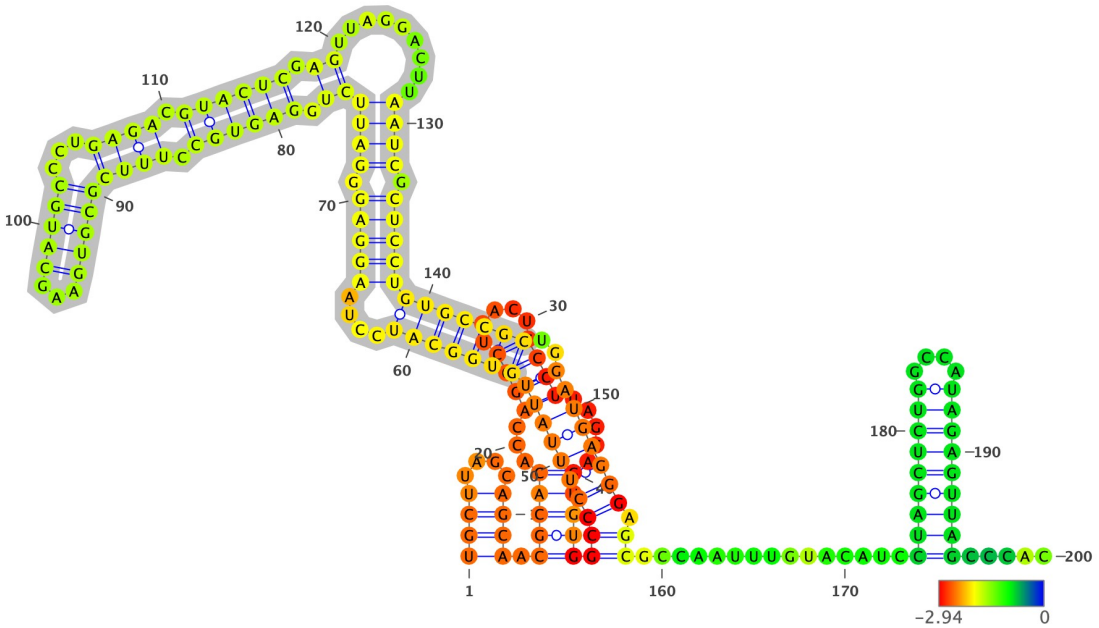
Attributes: ['ID=exon-HHV4_RPMS1-29-1', 'Parent=rna-HHV4_RPMS1-29', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-3p']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 381 from nt 147617 to 147707 (nt 55 to 145)

```
5'-GUGGCAUCCUAAGGAGGGAUUCUGGAGUGCCUUUCGCGUGAAGCAUGCCCUGAGACGUACUCGAGUUAGGACUUAAUCGCUCCUGUGCCGC-3'
5'-(((((((.......................................................................)))))))-3'
Motif MFE = -37.2; z-score = -2.91; 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 147563 to 147762 (motif highlighted in silver):

```
5'-UGCUUAGCAGCAACGCACACCAGGCUGACUGCCUUAGCAGUGUGGCCCUUUAUUGUGGCAUCCUAAGGAGGGAUUCUGGAGUGCCUUUCGCGUGAAGCAUGCCCUGAGACG
UACUCGAGUUAGGACUUAAUCGCUCCUGUGCCGCUGGAUGAGGGAGCGCCAAUUUGUACAUCCUAGCUCUGGCCAUAGAGUUAGCCCAC-3
5'-((((....)))).(((((...((((.....)))).....)))))((((((((((((((((....(((((.(((((.(((((.(((((((((...)))))...)))))..)
)))))).))........)))).))))))))))))..)))))))).))...............(((((((((....)))))))))).....-3'
MFE = -72.5; z-score = -2.12; ED = 28.91
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 13 to 33--miRNA, rna-HHV4_RPMS1-29, 147575-147595(+)

Attributes: ['ID=rna-HHV4_RPMS1-29', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-3p']

6-- nt 13 to 33--exon, exon-HHV4_RPMS1-29-1, 147575-147595(+)

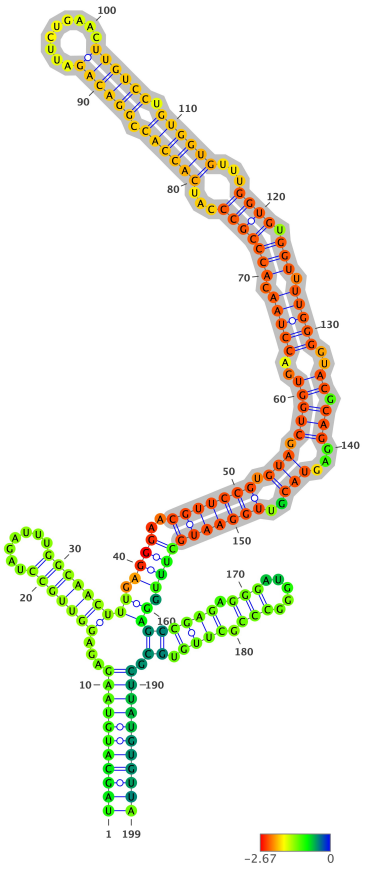
Attributes: ['ID=exon-HHV4_RPMS1-29-1', 'Parent=rna-HHV4_RPMS1-29', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART11-3p']

7-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 382 from nt 147876 to 147985 (nt 45 to 154)

```
5'-CGUUCCGUGUAGCUGGUGACCUAACACCCGCCCAUCACCACCGGACAGAUUCUGAACUUGUCCUGUGGUGUUUGGUGUGGUUUUGGGGUACGCAGGAGUACGUUGGAAUG-
3'
5'-(((((((.(((.(((((..(((((.(((((((...(((.............................)))...)))).)))).)))))..)).)))...)))..)))))))-
3'
Motif MFE = -47.2; z-score = -3.37; ED = 10.41
```



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 147832 to 148030 (motif highlighted in silver):

```
5'-UAGCAUGUAAGAGAGGUUGCCUAGAUUUGGCAACUUUGAGGGAACGUUCCGUGUAGCUGGUGACCUAACACCCGCCCAUCACCACCGGACAGAUUCUGAACUUGUCCUGUG
GUGUUUGGUGUGGUUUUGGGGUACGCAGGAGUACGUUGGAAUGCUUUGGAGCCGAGAGGGAUGGGCCCGCUUGUGCGCUUAUGUGUUA-3
5'-(((((((((((...(((((((.......)))))))(((.((((..(((((((.(((.(((((..(((((.(((((((...((((((.(((((.........)))))).)))
)))...)))).))).)))))..)).)))...)))..))))))))))).))(((((((.(((.....))).)))).)).)))))))))))-3'
MFE = -80.2; z-score = -3.7; ED = 16.3
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 105 to 126--miRNA, rna-HHV4_RPMS1-30, 147936-147957(+)

Attributes: ['ID=rna-HHV4_RPMS1-30', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART12']

6-- nt 105 to 126--exon, exon-HHV4_RPMS1-30-1, 147936-147957(+)

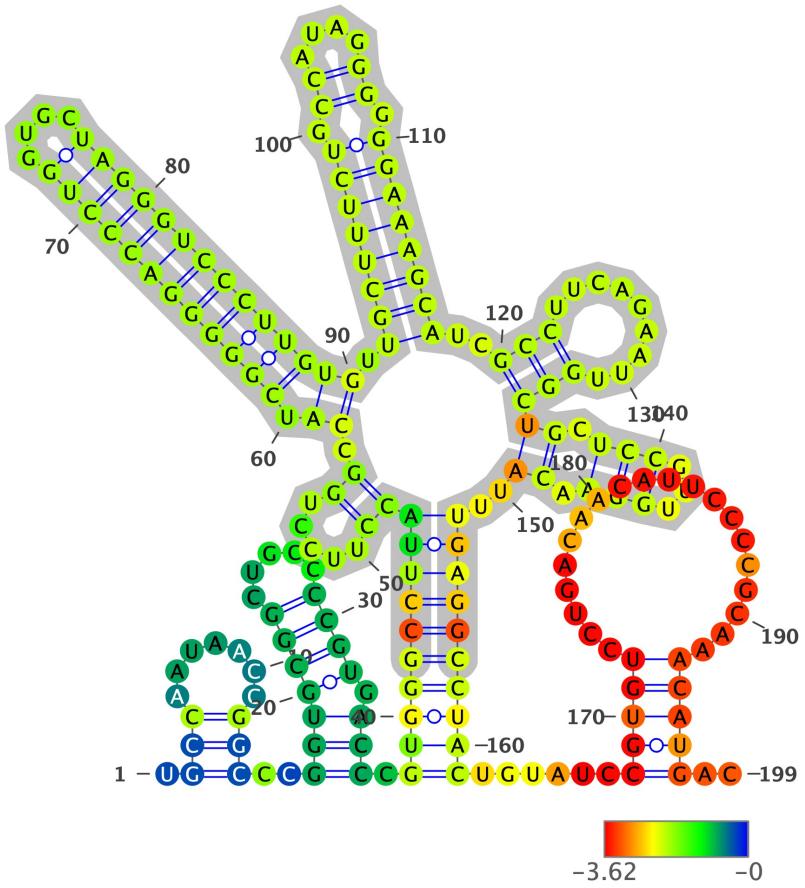
Attributes: ['ID=exon-HHV4_RPMS1-30-1', 'Parent=rna-HHV4_RPMS1-30', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART12']

7-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 383 from nt 148077 to 148192 (nt 42 to 157)

```
5'-GCCUUACCUUCCUGGCCAUCGGGGGACCCUGGUGCUAGGGUCCCUUGUGUUGCUUUCUGCCAUAGGGGGGAAAGCAUCGCCUUCAGAAUUGGCUGCUCCGUUGGAACAUUU
GAGGC-3'
5'-(.................................................((((((((.((....)).)))))))).((((.........))).(.(((...))).).....
....)-3'
Motif MFE = -49.5; z-score = -3.29; ED = 16.64
```



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 148036 to 148234 (motif highlighted in silver):

```
5'-UGCCAAUAACCGGCCCGGUGCGGCUGCCCCGUGACCCGUGGGCCUUACCUUCCUGGCCAUCGGGGGACCCUGGUGCUAGGGUCCCUUGUGUUGCUUUCUGCCAUAGGGGGG
AAAGCAUCGCCUUCAGAAUUGGCUGCUCCGUUGGAACAUUUGAGGCCUACUGUAUCCGUGUCCUGACAACAUUCCCCGCAAACAUGAC-3
5'-.(((.......)))..(((((((.....)))).))).((((((((((((.....)).((.(((((((((((((....)))))))))))))).((((((((.((....)).))
))))))..(((.........)))((.(((...))).)).)..))))))))))......(((((.....................)))))..-3'
MFE = -71.1; z-score = -0.6; ED = 20.03
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 180 to 199--piRNA, rna-HHV4_RPMS1-31, 148215-148237(+)

Attributes: ['ID=rna-HHV4_RPMS1-31', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

6-- nt 180 to 199--exon, exon-HHV4_RPMS1-31-1, 148215-148237(+)

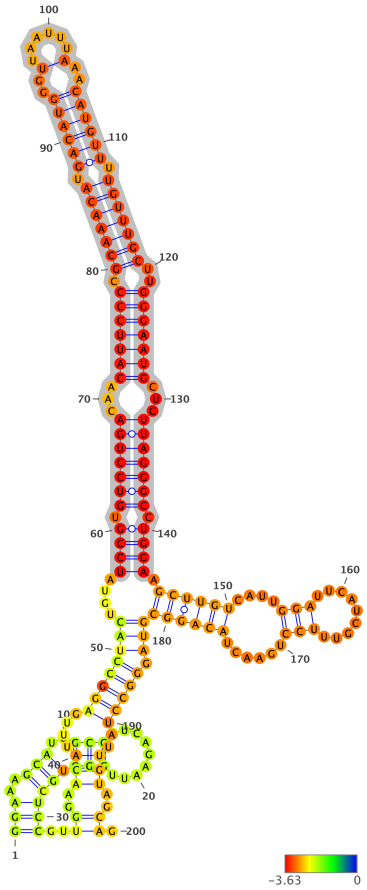
Attributes: ['ID=exon-HHV4_RPMS1-31-1', 'Parent=rna-HHV4_RPMS1-31', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

7-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 384 from nt 148201 to 148287 (nt 57 to 143)

```
5'-UCCGUGUCCUGACAACAUUCCCCGCAAACAUGACAUGGGUUAAUUUAAACAUGUUUUGUUUGCUUGGGAAUGCUCUUAGGGCCUGGA-3'
5'-((((.(((((((...(((((((.(((((((.(((((..(......)..)))))).)))))))..)))))))...)))))))).))))-3'
Motif MFE = -39.9; z-score = -6.01; 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 148145 to 148344 (motif highlighted in silver):

```
5'-GGAAAGCAUCGCCUUCAGAAUUGGCUGCUCCGUUGGAACAUUUGAGGCCUACUGUAUCCGUGUCCUGACAACAUUCCCCGCAAACAUGACAUGGGUUAAUUUAAACAUGUU
UUGUUUGCUUGGGAAUGCUCUUAGGGCCUGGAAGCUUGUCAUUGGAUUCAUCGUUUCCUGAACUACAGGCGUAGGGCCUAUUGUAGCAG-3
5'-((((..((((..(((.........)))))))))..((..((((....(((((((((....((((.(((((((...(((((((.(((((((.((((((..(......)..)))))))
.)))))))..)))))))...)))))))).)))).((((((....(((.........)))).....)))))))))..)))))..)))..)).-3'
MFE = -69.8; z-score = -3.12; ED = 14.27
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 71 to 93--piRNA, rna-HHV4_RPMS1-31, 148215-148237(+)

Attributes: ['ID=rna-HHV4_RPMS1-31', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

6-- nt 71 to 93--exon, exon-HHV4_RPMS1-31-1, 148215-148237(+)

Attributes: ['ID=exon-HHV4_RPMS1-31-1', 'Parent=rna-HHV4_RPMS1-31', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

7-- nt 110 to 130--miRNA, rna-HHV4_RPMS1-32, 148254-148274(+)

Attributes: ['ID=rna-HHV4_RPMS1-32', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

8-- nt 110 to 130--exon, exon-HHV4_RPMS1-32-1, 148254-148274(+)

Attributes: ['ID=exon-HHV4_RPMS1-32-1', 'Parent=rna-HHV4_RPMS1-32', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

9-- nt 195 to 200--miRNA, rna-HHV4_RPMS1-33, 148339-148359(+)

Attributes: ['ID=rna-HHV4_RPMS1-33', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

10-- nt 195 to 200--exon, exon-HHV4_RPMS1-33-1, 148339-148359(+)

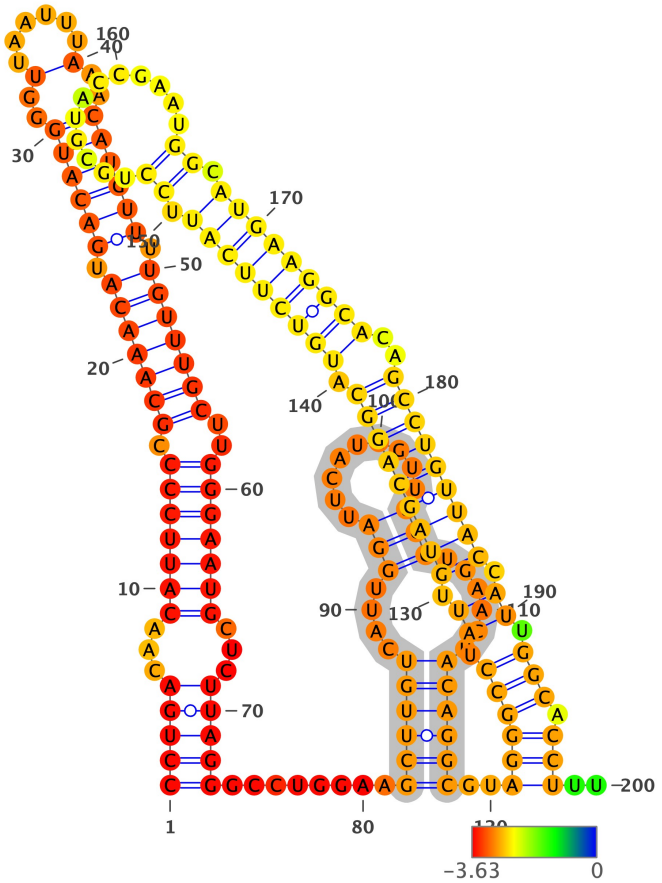
Attributes: ['ID=exon-HHV4_RPMS1-33-1', 'Parent=rna-HHV4_RPMS1-33', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

11-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 385 from nt 148289 to 148325 (nt 82 to 118)

```
5'-GCUUGUCAUUGGAUUCAUCGUUUCCUGAACUACAGGC-3'
5'-((((((....(((.........)))......)))))))-3'
Motif MFE = -7.1; z-score = -1.19; ED = 4.61
```



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

Extracted structure model with flanking nucleotides 148208 to 148407 (motif highlighted in silver):

```
5'-CCUGACAACAUUCCCCGCAAACAUGACAUGGGUUAAUUUAAACAUGUUUUGUUUGCUUGGGAAUGCUCUUAGGGCCUGGAAGCUUGUCAUUGGAUUCAUCGUUUCCUGAAC
UACAGGCGUAGGGCCUAUUGUAGCAGGCAUGUCUUCAUUCCUGCGUACCGAAUGGCAUGAAGGCACAGCCUGUUACCAUUGGCACCUUU-3
5'-(((((...(((((((.(((((((.(((((((..(......)..)))))))..))))))).))))))).))))))...)))))).......((((((....(((.........)))).....
.)))))).((((((.((.(((((((((.(((((((((.(((.........)).))))))))).))))))))).)).)).)).)))..-3'
MFE = -77.3; z-score = -5.34; ED = 11.5
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 8 to 30--piRNA, rna-HHV4_RPMS1-31, 148215-148237(+)

Attributes: ['ID=rna-HHV4_RPMS1-31', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

6-- nt 8 to 30--exon, exon-HHV4_RPMS1-31-1, 148215-148237(+)

Attributes: ['ID=exon-HHV4_RPMS1-31-1', 'Parent=rna-HHV4_RPMS1-31', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-5p']

7-- nt 47 to 67--miRNA, rna-HHV4_RPMS1-32, 148254-148274(+)

Attributes: ['ID=rna-HHV4_RPMS1-32', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

8-- nt 47 to 67--exon, exon-HHV4_RPMS1-32-1, 148254-148274(+)

Attributes: ['ID=exon-HHV4_RPMS1-32-1', 'Parent=rna-HHV4_RPMS1-32', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

9-- nt 132 to 152--miRNA, rna-HHV4_RPMS1-33, 148339-148359(+)

Attributes: ['ID=rna-HHV4_RPMS1-33', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

10-- nt 132 to 152--exon, exon-HHV4_RPMS1-33-1, 148339-148359(+)

Attributes: ['ID=exon-HHV4_RPMS1-33-1', 'Parent=rna-HHV4_RPMS1-33', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

11-- nt 167 to 188--miRNA, rna-HHV4_RPMS1-34, 148374-148395(+)

Attributes: ['ID=rna-HHV4_RPMS1-34', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-3p']

12-- nt 167 to 188--exon, exon-HHV4_RPMS1-34-1, 148374-148395(+)

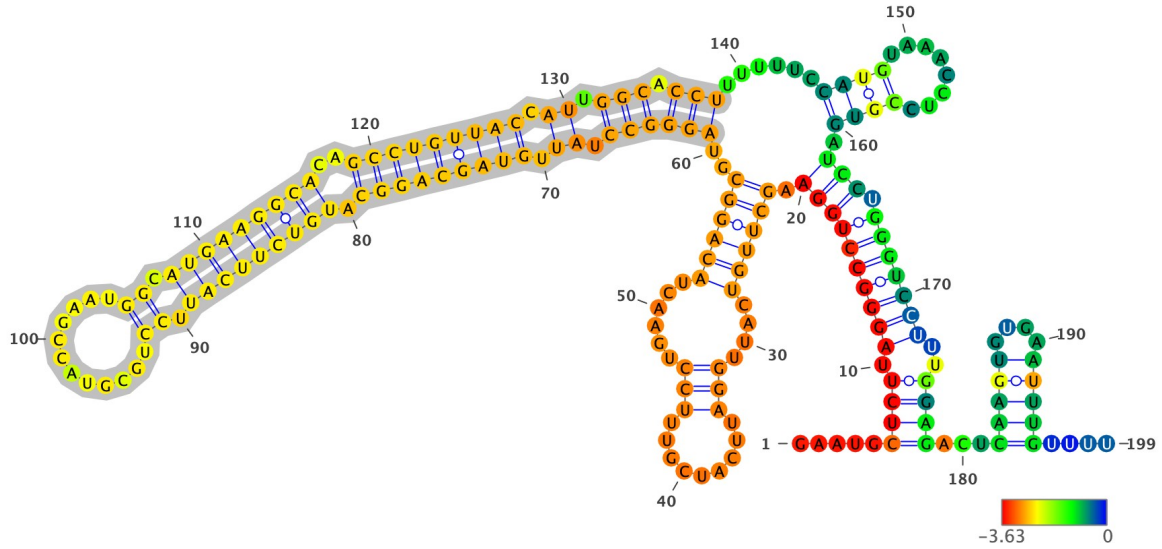
Attributes: ['ID=exon-HHV4_RPMS1-34-1', 'Parent=rna-HHV4_RPMS1-34', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-3p']

13-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 386 from nt 148328 to 148405 (nt 61 to 138)

```
5'-AGGGCCUAUUGUAGCAGGCAUGUCUUCAUUCCUGCGUACCGAAUGGCAUGAAGGCACAGCCUGUUACCAUUGGCACCU-3'
5'-((((((..(.(((((((((.(((((((((.((...........)).))))))))).))))))))).)..))).)))-3'
Motif MFE = -36.5; z-score = -5.02; ED = 3.56
```



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

Extracted structure model with flanking nucleotides 148268 to 148466 (motif highlighted in silver):

```
5'-GAAUGCUCUUAGGGCCUGGAAGCUUGUCAUUGGAUUCAUCGUUUCCUGAACUACAGGCGUAGGGCCUAUUGUAGCAGGCAUGUCUUCAUUCCUGCGUACCGAAUGGCAUGA
AGGCACAGCCUGUUACCAUUGGCACCUUUUUUCCAUGUAAACCUCCGUGAUCCUGGGUCCUUUGGAGACUCAAGUGUGAAUUUGUUUU-3
5'-.....((((.((((((((((.((((((....(((.........)))......)))))).((((((.((.((((((((((.((((((((((.(((.............)).))))
)))))..))))))))).)).))).))).)).....(((.........)))).))).)))))))..)))).....((((.....)))))....-3'
MFE = -66.6; z-score = -3.37; ED = 15.03
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 7--miRNA, rna-HHV4_RPMS1-32, 148254-148274(+)

Attributes: ['ID=rna-HHV4_RPMS1-32', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

6-- nt 1 to 7--exon, exon-HHV4_RPMS1-32-1, 148254-148274(+)

Attributes: ['ID=exon-HHV4_RPMS1-32-1', 'Parent=rna-HHV4_RPMS1-32', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART19-3p']

7-- nt 72 to 92--miRNA, rna-HHV4_RPMS1-33, 148339-148359(+)

Attributes: ['ID=rna-HHV4_RPMS1-33', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

8-- nt 72 to 92--exon, exon-HHV4_RPMS1-33-1, 148339-148359(+)

Attributes: ['ID=exon-HHV4_RPMS1-33-1', 'Parent=rna-HHV4_RPMS1-33', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-5p']

9-- nt 107 to 128--miRNA, rna-HHV4_RPMS1-34, 148374-148395(+)

Attributes: ['ID=rna-HHV4_RPMS1-34', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-3p']

10-- nt 107 to 128--exon, exon-HHV4_RPMS1-34-1, 148374-148395(+)

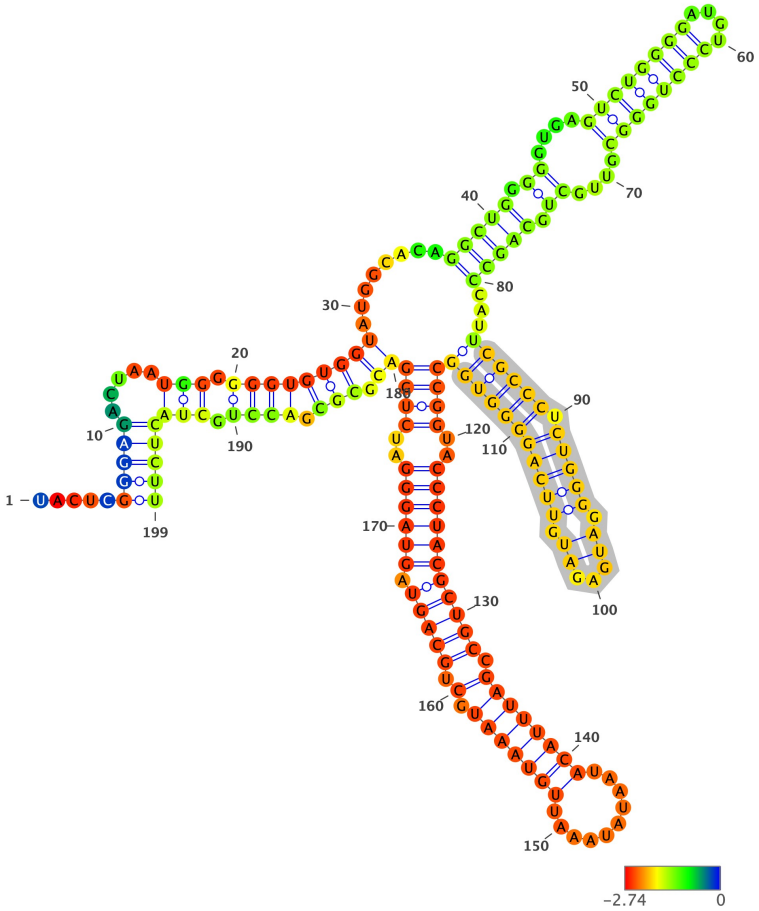
Attributes: ['ID=exon-HHV4_RPMS1-34-1', 'Parent=rna-HHV4_RPMS1-34', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART20-3p']

11-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 387 from nt 148709 to 148738 (nt 85 to 114)

```
5'-CGCCCUCUGGGGAUGAGAUGUUCAGGGGUG-3'
5'-(((((.....................)))))-3'
Motif MFE = -12.1; z-score = -2.25; ED = 1.71
```



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

Extracted structure model with flanking nucleotides 148625 to 148823 (motif highlighted in silver):

```
5'-UACUCGGGAGACUAAUGGGGGGUGUGGUAUGGCACAGGCUGGGGGUGAGUCUGGGGAUGUCCCUGGGCGUUGCUGCAGCCCAUUCGCCCUCUGGGGAUGAGAUGUUCAGGG
GUGGCCGGUACCCUACGCUGCCGAUUUACAUAAUAUAAAUUGUAAAUGCUGCAGUAGUAGGGAUCUGGACGCGCGACCUGCUACUCUU-3
5'-.....(((((.....(((.(((((((((.......(((((.((....(((((((((....)))))))))....)).))))).....((((((.(((((.((...)).)))))))
))))))((((..(((((((((((.(((((((((.........)))))))).).))))).)))))).).))))))..))))))).))).)))).)))))))))-3'
MFE = -80.8; z-score = -2.84; ED = 23.75
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 120 to 141--miRNA, rna-HHV4_RPMS1-37, 148744-148765(+)

Attributes: ['ID=rna-HHV4_RPMS1-37', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14*']

6-- nt 120 to 141--exon, exon-HHV4_RPMS1-37-1, 148744-148765(+)

Attributes: ['ID=exon-HHV4_RPMS1-37-1', 'Parent=rna-HHV4_RPMS1-37', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14*']

7-- nt 154 to 175--miRNA, rna-HHV4_RPMS1-38, 148778-148799(+)

Attributes: ['ID=rna-HHV4_RPMS1-38', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14']

8-- nt 154 to 175--exon, exon-HHV4_RPMS1-38-1, 148778-148799(+)

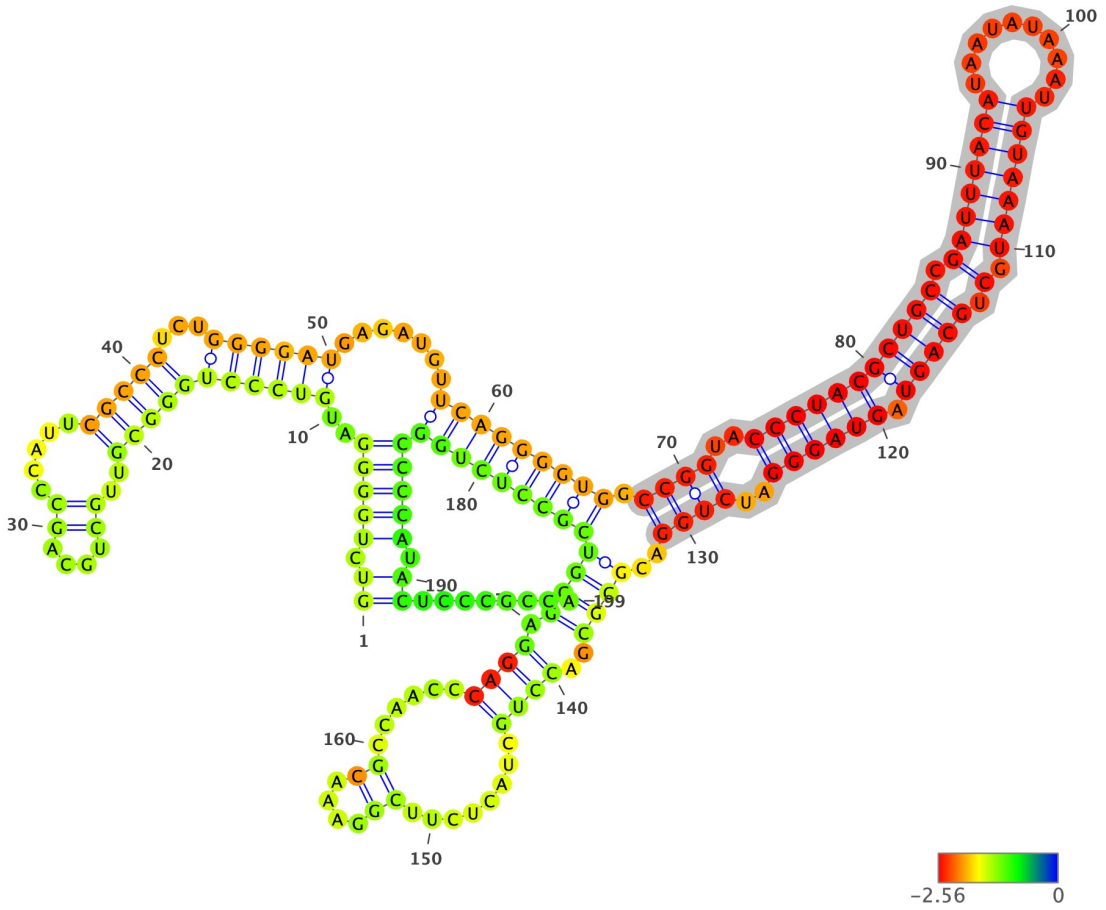
Attributes: ['ID=exon-HHV4_RPMS1-38-1', 'Parent=rna-HHV4_RPMS1-38', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 388 from nt 148740 to 148803 (nt 68 to 131)

```
5'-CCGGUACCCUACGCUGCCGAUUUACAUAAUAUAAAUUGUAAAUGCUGCAGUAGUAGGGAUCUGG-3'
5'-((((..(((((((((((.((((((((.........)))))))).).)))))).)))))))..))))-3'
Motif MFE = -26.9; z-score = -5.22; 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 148673 to 148871 (motif highlighted in silver):

```
5'-GUCUGGGGAUGUCCCUGGGCGUUGCUGCAGCCCAUUCGCCCUCUGGGGAUGAGAUGUUCAGGGGUGGCCGGUACCCUACGCUGCCGAUUUACAUAAUAUAAAUUGUAAAUG
CUGCAGUAGUAGGGAUCUGGACGCGCGACCUGCUACUCUUCGGAAACGCCAACCCAGGAGCGUCGCCUCUGGCCCCAUACUCCCGCCA-3
5'-((.(((((..(((((((((((..((....)).....)))))...)))))).....(((((((((.((((..(((((((((((.(((((((((.........)))))))).
).)))))).)))))))..)))))..((((..((((........((....)).....)))).)))))))))))))))))).))........-3'
MFE = -74.9; z-score = -1.5; ED = 57.71
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 72 to 93--miRNA, rna-HHV4_RPMS1-37, 148744-148765(+)

Attributes: ['ID=rna-HHV4_RPMS1-37', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14*']

6-- nt 72 to 93--exon, exon-HHV4_RPMS1-37-1, 148744-148765(+)

Attributes: ['ID=exon-HHV4_RPMS1-37-1', 'Parent=rna-HHV4_RPMS1-37', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14*']

7-- nt 106 to 127--miRNA, rna-HHV4_RPMS1-38, 148778-148799(+)

Attributes: ['ID=rna-HHV4_RPMS1-38', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14']

8-- nt 106 to 127--exon, exon-HHV4_RPMS1-38-1, 148778-148799(+)

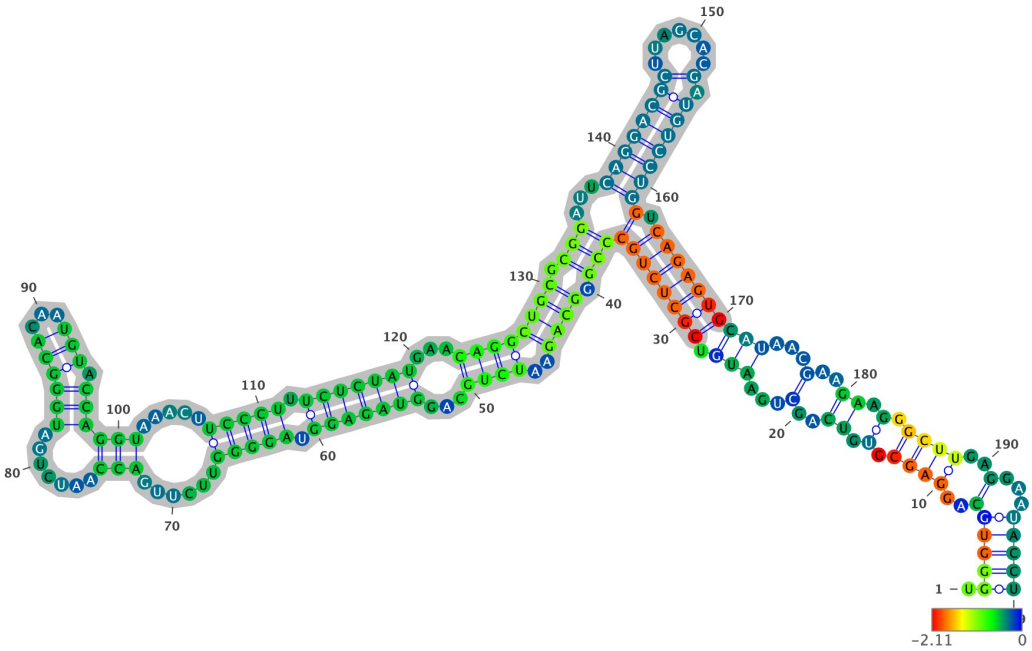
Attributes: ['ID=exon-HHV4_RPMS1-38-1', 'Parent=rna-HHV4_RPMS1-38', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART14']

9-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 389 from nt 149826 to 149967 (nt 29 to 170)

```
5'-CGCUCUGCCCGGGCAGAAUCUGCAGGUAGAGGUAGGGGUUCUUGACCAAUCUGAUGGGCACAAUGUACCAGGUAAACUUCCCUUUCUCUAUGAACAGGCUGCGCGGAUUCA
GGACGCUUAGCACGAUGUCCUGGUCAGAGUG-3'
5'-((.......................................................................................................
.............................))-3'
Motif MFE = -51.8; z-score = -1.9; ED = 12.71
```



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 149798 to 149996 (motif highlighted in silver):

```
5'-UGGGUGCAGGAGCGUGUCAGCUGAAUGUCGCUCUGCCCGGGCAGAAUCUGCAGGUAGAGGUAGGGGUUCUUGACCAAUCUGAUGGGCACAAUGUACCAGGUAAACUUCCCU
UUCUCUAUGAACAGGCUGCGCGGAUUCAGGACGCUUAGCACGAUGUCCUGGUCAGAGUGCAUAACGAAGAAGGGCUUGAGGAAUACCU-3
5'-.(((((((..((((.(.((..(...(((.(((((((((((.((((..((((...(((((((.(((((.......(((.......((((((...)))).)))))).....))))))
.)))))))...)))))))).)))...((((((((.......).)))))))).))))))))))...)..)).).)))))..)...)))))-3'
MFE = -64.1; z-score = -0.48; ED = 17.56
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 126 to 199--exon, exon-HHV4_RPMS1-3, 149923-150077(+)

Attributes: ['ID=exon-HHV4_RPMS1-3', 'Parent=rna-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 199--region, id-HHV4_RPMS1-3, 139724-151554(+)

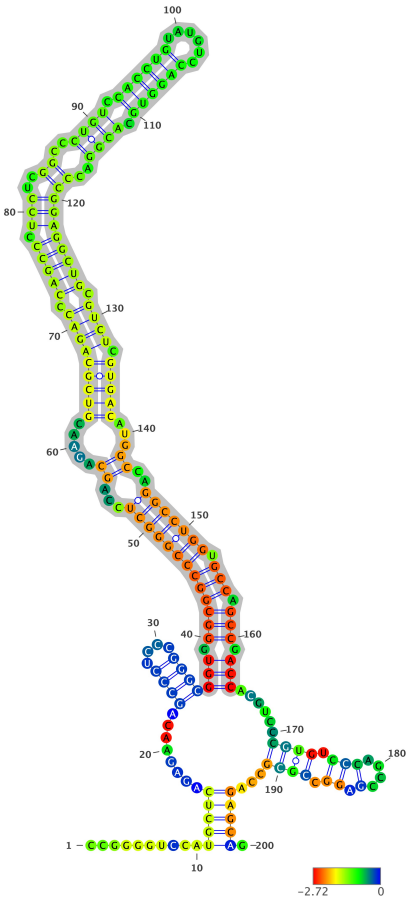
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 1 to 199--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 390 from nt 150771 to 150899 (nt 36 to 164)

```
5'-GGUGGGCGGCCCGGGCUCCAGCAGAACGUCGCAGACCCAGCCCUCCUCGGCCCUGUCCACCUGUAUGUCCAGGUGCACGGACCCGGAGGCUGCGUCUCGUGACAUGGCCAG
GCCUGGUGCCAGCCGACC-3'
5'-(((.(((((((((((...((.....................................................................................)).)
))))))).))).))).))-3'
Motif MFE = -70.8; z-score = -3.73; ED = 8.4
```



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 150736 to 150935 (motif highlighted in silver):

```
5'-CCGGGGUCCAUGCUCAGAGAACAGCCCUCCCGGGCGGUGGGCGGCCCGGGCUCCAGCAGAACGUCGCAGACCCAGCCCUCCUCGGCCCUGUCCACCUGUAUGUCCAGGUGC
ACGGACCCGGAGGCUGCGUCUCGUGACAUGGCCAGGCCUGGUGCCAGCCGACCACGUCCCGUGUCCCAGCCGAGGCCGCGCCAGAGCAG-3
5'-..........(((((........((((....)))))((.(((((((((((...((.....(((((((((.(((((.(((..((..((((.(((((((.....)))))))).
))))..))))))))))).))))).))))))...))..)))))))).))).))).))).....((((.((((....)).)).)))).....)))))).-3'
MFE = -90.8; z-score = -0.51; ED = 28.56
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

3-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--region, id-HHV4_RPMS1-3, 139724-151554(+)

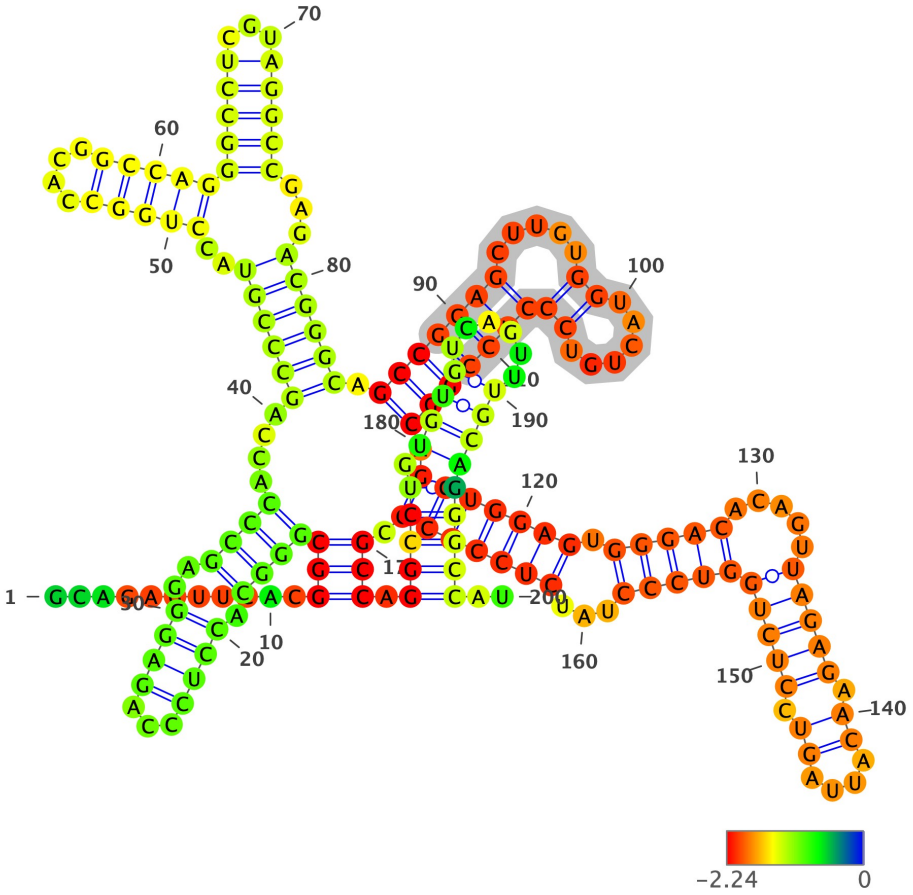
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 391 from nt 151583 to 151605 (nt 89 to 111)

```
5'-GGAGCUUGUGGUACUGUCCCUCC-3'
5'-(((((.....((.....)))))))-3'
Motif MFE = -3.3; z-score = 0.21; 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 151495 to 151694 (motif highlighted in silver):

```
5'-GCAGAGUUCACGGCGGGCACCUCCCAGAGGGAGCCCACCAGCCCGUACCUGGCCACGGCCAGGGCCUCGUAGGCCGAGACGGGCAGCCGGAGCUUGUGGUACUGUCCCUCC
GGCAGGUGGAGUGGGACACAGUUAGAGAACAUUAGUCCUCUGGUCCCUAUCUCCACCCGCCAGGCCUGUGUGUCAGUUUGCAGGGCCAU-3
5'-...........(((((((.((((...)))).)))).....((((((..((((((....)))))((((((...)))))).....)))))))..((((((.....((.....)))))))
))).(((((((.(((((.....(((((.((....)).)))))))))...)))))))..))).(((((.((((.....)))))))))..-3'
MFE = -94.1; z-score = -3.42; ED = 25.38
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 61 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 60--region, id-HHV4_RPMS1-3, 139724-151554(+)

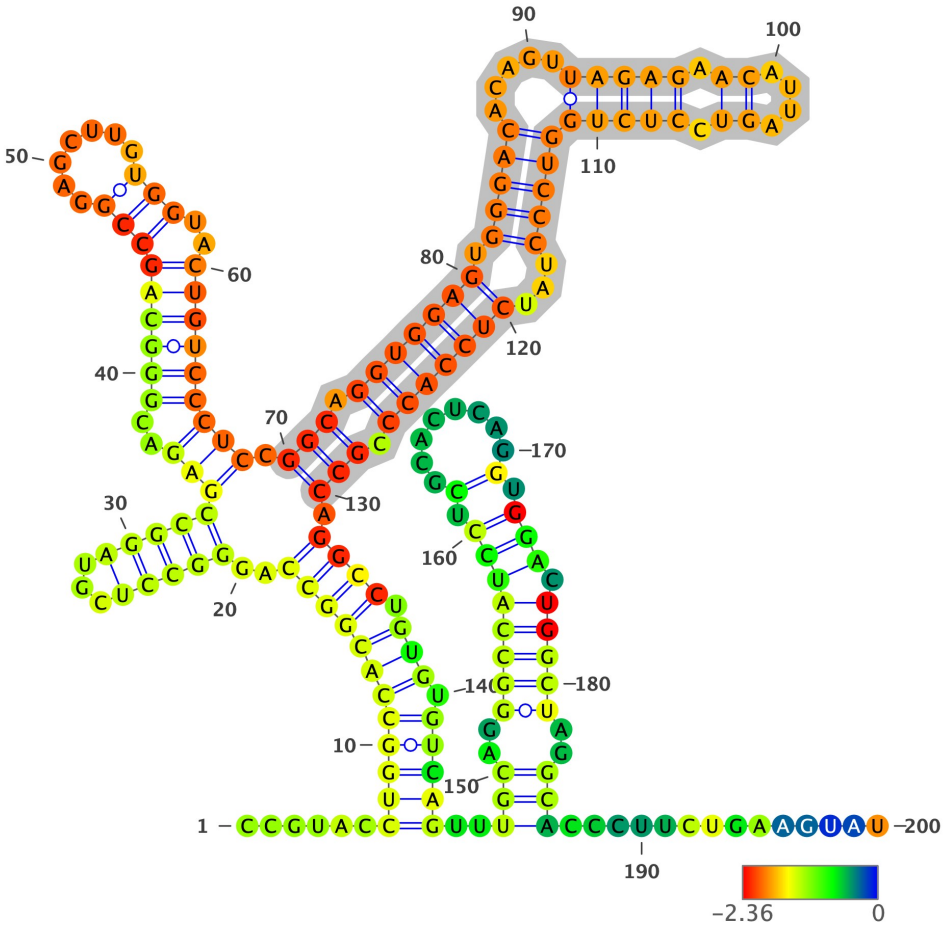
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 1 to 60--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 392 from nt 151606 to 151666 (nt 70 to 130)

```
5'-GGCAGGUGGAGUGGGACACAGUUAGAGAACAUUAGUCCUCUGGUCCCUAUCUCCACCCGCC-3'
5'-(((.(((((((.(.................................)...)))))))).)))-3'
Motif MFE = -30.5; z-score = -4.49; ED = 6.41
```



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 151537 to 151736 (motif highlighted in silver):

```
5'-CCGUACCUGGCCACGGCCAGGGCCUCGUAGGCCGAGACGGGCAGCCGGAGCUUGUGGUACUGUCCCUCCGGCAGGUGGAGUGGGACACAGUUAGAGAACAUUAGUCCUCUG
GUCCCUAUCUCCACCCGCCAGGCCUGUGUGUCAGUUUGCAGGGCCAUCCUCGCACUCAGGUGGACUGGCUAGGCACCCUUCUGAAGUAU-3
5'-......(((((((((((..(((((...)))))))((..(((((((((.......)))..)))))))))).(((.(((((((.(((((.....(((((.((....)).)))))
)))))...)))))))).))).)))).))).)))))..((((..(((((((.(........).))).)))))..)))..............-3'
MFE = -83.8; z-score = -1.79; ED = 49.63
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 19 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 18--region, id-HHV4_RPMS1-3, 139724-151554(+)

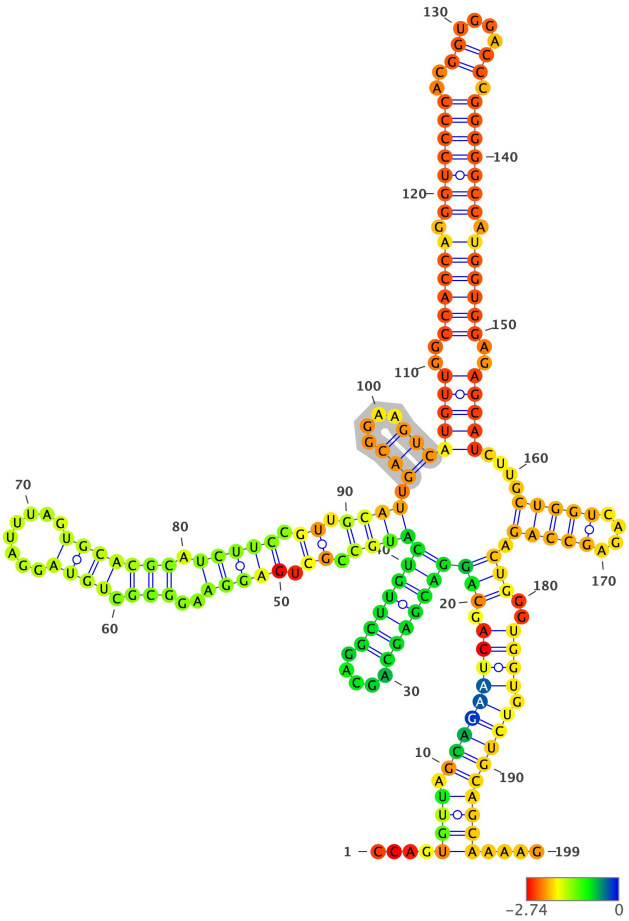
Attributes: ['ID=id-HHV4_RPMS1-3', 'Dbxref=GeneID:3783757', 'gbkey=Src', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 1 to 18--sequence_feature, id-HHV4_RPMS1-4, 139724-151554(+)

Attributes: ['ID=id-HHV4_RPMS1-4', 'Note=B95-8 deletion restored from Raji', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 393 from nt 152579 to 152588 (nt 95 to 104)

```
5'-GACGGAAGUC-3'
5'-(((....)))-3'
Motif MFE = -1.3; z-score = -4.97; 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 152485 to 152683 (motif highlighted in silver):

```
5'-CCAGUGUUAGCAGAAUCAGCAGGACGAGCAGCAGGCUUGUCAUGCCGCUGAGGAAGGCGCUGUAGGAUUUAGUGCACGCAUCUUCCGUUGCAUUGACGGAAGUCAUGUUGG
CCACCAGGGUCCCCACGGUGGACCCGGGGGCCAUGGUGGAGAGCAUCUUGCUGGUCAGAGCCAGACUGGGUGGUGUCUGCAGCAAAAG-3
5'-....((((.(((((((((.((((((((((.....)))))))))((((.((.((((((..((((.(((((........)))))))).)))))).)).)))).(((....)))(((((..
((((((.(((((((..((....)).)))))))..)))))).)))))....((((((....)))))).))))..)))).)))))))))....-3'
MFE = -84.4; z-score = -3.0; ED = 40.66
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

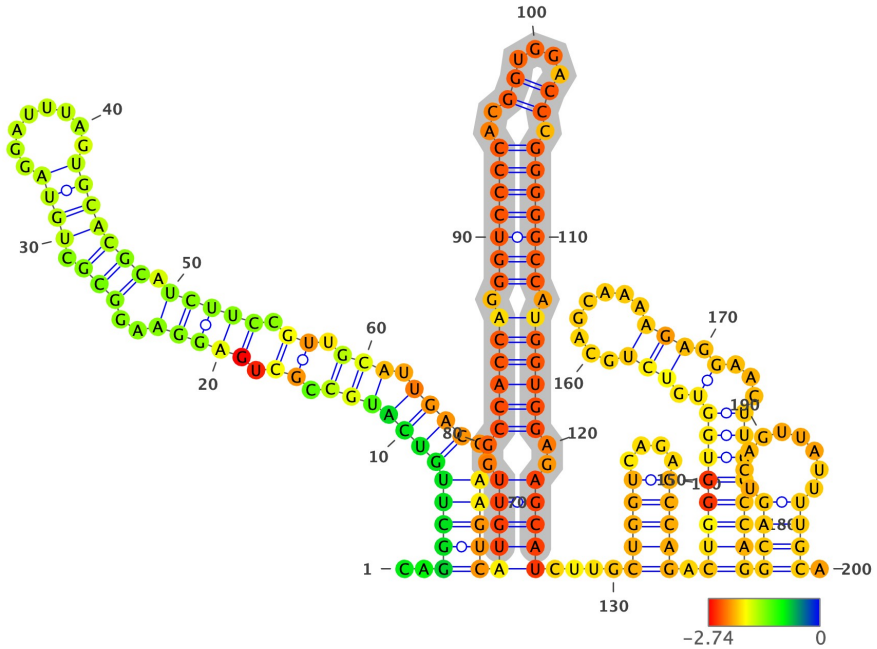
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 394 from nt 152590 to 152640 (nt 75 to 125)

```
5'-UGUUGGCCACCAGGGUCCCCACGGUGGACCCGGGGGCCAUGGUGGAGAGCA-3'
5'-(((((..((((((..(((((((..((....)).)))))))..))))))..)))))-3'
Motif MFE = -29.7; z-score = -4.07; ED = 6.8
```



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

Extracted structure model with flanking nucleotides 152516 to 152715 (motif highlighted in silver):

```
5'-CAGGCUUGUCAUGCCGCUGAGGAAGGCGCUGUAGGAUUUAGUGCACGCAUCUUCCGUUGCAUUGACGGAAGUCAUGUUGGCCACCAGGGUCCCCACGGUGGACCCGGGGGC
CAUGGUGGAGAGCAUCUUGCUGGUCAGAGCCAGACUGGGUGGUGUCUGCAGCAAAAGAGGAACUUGCCCAGGCAGUCAGUUAUUUUGCA-3
5'-..(((((((((((.((.((((((..(((.((((.......)))))))).)))))).)).)))).)))))..))))))((((((..((((((.(((((((..((....)).)))))))
).)))))))..)))))....((((((....)))))).(((((((((.(((.......))).)...)))))))))((((.........)))).-3'
MFE = -78.0; z-score = -2.17; ED = 53.2
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

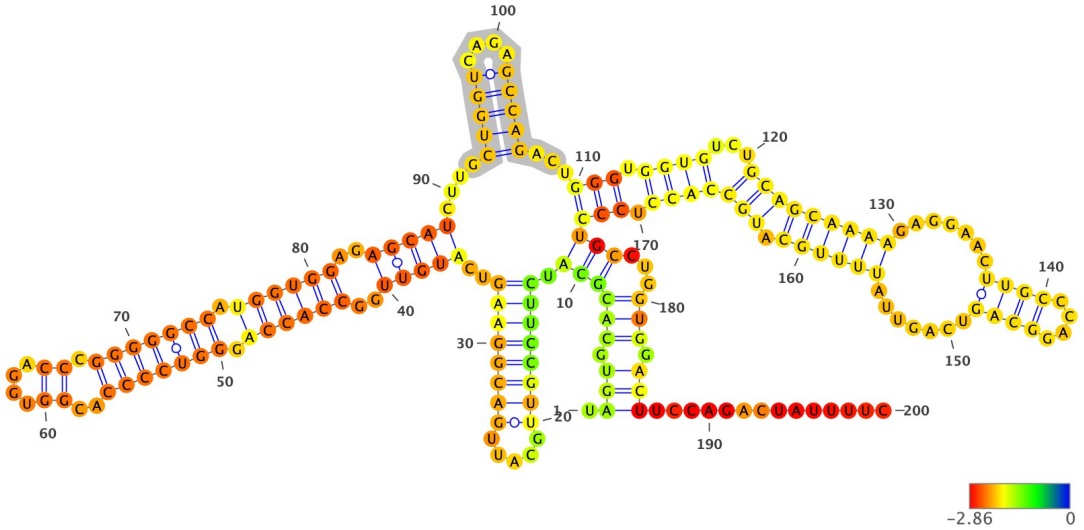
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 395 from nt 152645 to 152661 (nt 92 to 108)

```
5'-GCUGGUCAGAGCCAGAC-3'
5'-((((((....)))))).)-3'
Motif MFE = -5.9; z-score = -1.74; ED = 0.38
```



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

Extracted structure model with flanking nucleotides 152554 to 152753 (motif highlighted in silver):

```
5'-UAGUGCACGCAUCUUCCGUUGCAUUGACGGAAGUCAUGUUGGCCACCAGGGUCCCCACGGUGGACCCGGGGGCCAUGGUGGAGAGCAUCUUGCUGGUCAGAGCCAGACUGG
GUGGUGUCUGCAGCAAAAGAGGAACUUGCCCAGGCAGUCAGUUAUUUUGCAUGCCACCUCCCUGCCUGGUGGACUUCCAGACUAUUUUC-3
5'-.(((.(((((((.(((((((.....)))))))).(((((..(((((((.(((((((..((....)).)))))))).)))))).))))).....((((.....)))))).....((
(.((((...(((((((((.......((((....)))).......)))))).)))))))..)))))).)))).....................-3'
MFE = -78.7; z-score = -2.28; ED = 60.43
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 194 to 200--miRNA, rna-HHV4_RPMS1-39, 152747-152768(+)

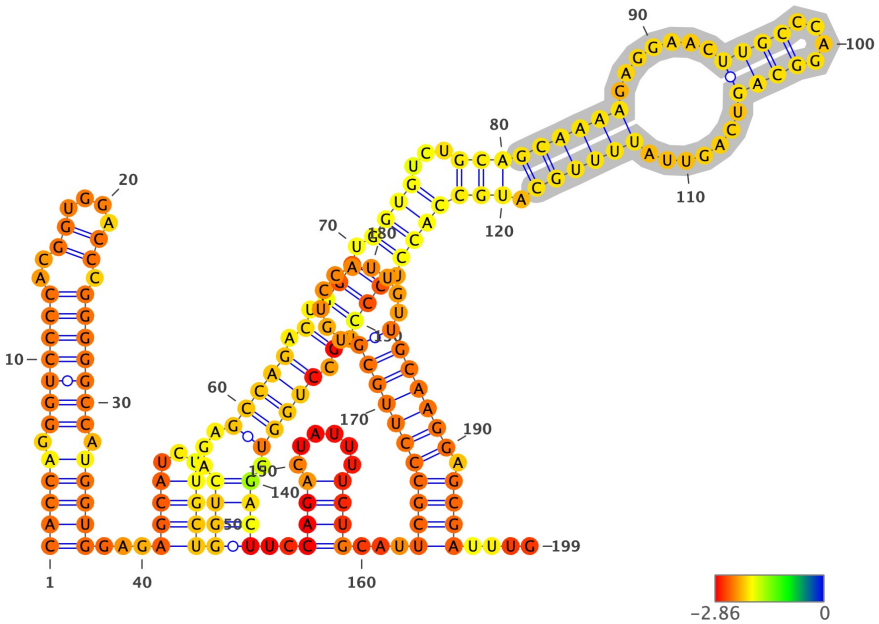
Attributes: ['ID=rna-HHV4_RPMS1-39', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

6-- nt 194 to 200--exon, exon-HHV4_RPMS1-39-1, 152747-152768(+)

Attributes: ['ID=exon-HHV4_RPMS1-39-1', 'Parent=rna-HHV4_RPMS1-39', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

NC_007605.1 (forward strand): Structure number 396 from nt 152677 to 152714 (nt 81 to 118)

```
5'-GCAAAAGAGGAACUUGCCCAGGCAGUCAGUUAUUUUGC-3'
5'-((((((.......((((....))))).......))))))-3'
Motif MFE = -7.6; z-score = -0.88; ED = 4.81
```



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

Extracted structure model with flanking nucleotides 152597 to 152795 (motif highlighted in silver):

```
5'-CACCAGGGUCCCCACGGUGGACCCGGGGGCCAUGGUGGAGAGCAUCUUGCUGGUCAGAGCCAGACUGGGUGGUGUCUGCAGCAAAAGAGGAACUUGCCCAGGCAGUCAGUU
AUUUUGCAUGCCACCUCCCUGCCUGGUGGACUUCCAGACUAUUUUCUGCAUUCGCCCUUGCGUGUCCAUUGUUGCAAGGAGCGAUUUG-3
5'-(((((.(((((((..((....)).)))))))..)))))...((((...))))((((...((((((.(.(((.((((...(((((((((.......((((....)))).....
.)))))).)))))))..))).).)))))..))))..((((......)))).....((((((((((.........)))))))).)))).....-3'
MFE = -79.0; z-score = -1.83; ED = 25.35
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 151 to 172--miRNA, rna-HHV4_RPMS1-39, 152747-152768(+)

Attributes: ['ID=rna-HHV4_RPMS1-39', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

6-- nt 151 to 172--exon, exon-HHV4_RPMS1-39-1, 152747-152768(+)

Attributes: ['ID=exon-HHV4_RPMS1-39-1', 'Parent=rna-HHV4_RPMS1-39', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

7-- nt 187 to 199--miRNA, rna-HHV4_RPMS1-40, 152783-152806(+)

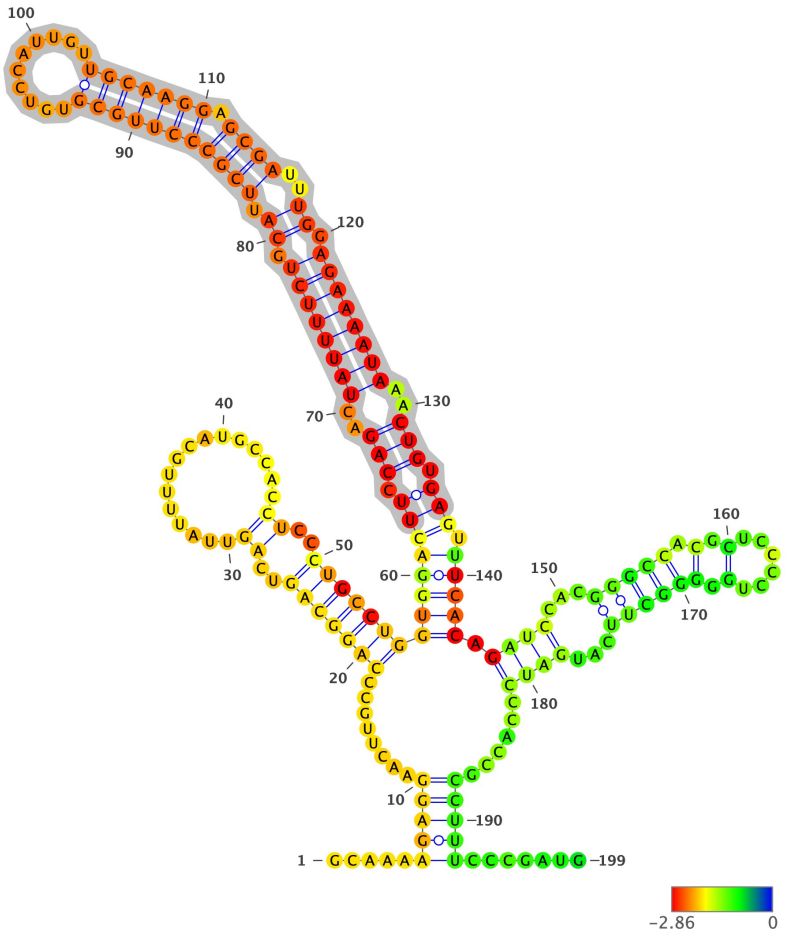
Attributes: ['ID=rna-HHV4_RPMS1-40', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-3p']

8-- nt 187 to 199--exon, exon-HHV4_RPMS1-40-1, 152783-152806(+)

Attributes: ['ID=exon-HHV4_RPMS1-40-1', 'Parent=rna-HHV4_RPMS1-40', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-3p']

NC_007605.1 (forward strand): Structure number 397 from nt 152739 to 152812 (nt 63 to 136)

```
5'-UUCCAGACUAUUUUCUGCAUUCGCCCUUGCGUGUCCAUUGUUGCAAGGAGCGAUUUGGAGAAAAUAAACUGUGA-3'
5'-((.(((..(((((((((.((.((((((((((((.........)))))))).)))))..)).)))))))))..))).))-3'
Motif MFE = -29.3; z-score = -4.29; 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 152677 to 152875 (motif highlighted in silver):

```
5'-GCAAAAGAGGAACUUGCCCAGGCAGUCAGUUAUUUUGCAUGCCACCUCCCUGCCUGGUGGACUUCCAGACUAUUUUCUGCAUUCGCCCUUGCGUGUCCAUUGUUGCAAGGA
GCGAUUUGGAGAAAAUAAACUGUGAGUUUCACAGAUCCACGGGCCACGCUCCCCUGGGGGCUUCAUGAUCCCACCGCCUUUCCCGAUG-3
5'-.....(((((.......(((((((..((.............)).))))))))))))))))).((((..(((((((((.((.((((((((((.........)))))))).
))))..)).))))))))..)))).)))).)))))).((((...((((((.(.(......).)))))))...)))).....)))))).......-3'
MFE = -62.6; z-score = -2.0; ED = 36.9
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 71 to 92--miRNA, rna-HHV4_RPMS1-39, 152747-152768(+)

Attributes: ['ID=rna-HHV4_RPMS1-39', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

6-- nt 71 to 92--exon, exon-HHV4_RPMS1-39-1, 152747-152768(+)

Attributes: ['ID=exon-HHV4_RPMS1-39-1', 'Parent=rna-HHV4_RPMS1-39', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-5p']

7-- nt 107 to 130--miRNA, rna-HHV4_RPMS1-40, 152783-152806(+)

Attributes: ['ID=rna-HHV4_RPMS1-40', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-3p']

8-- nt 192 to 199--transcript, rna-NC_007605.1:152868..152932, 152868-152932(+)

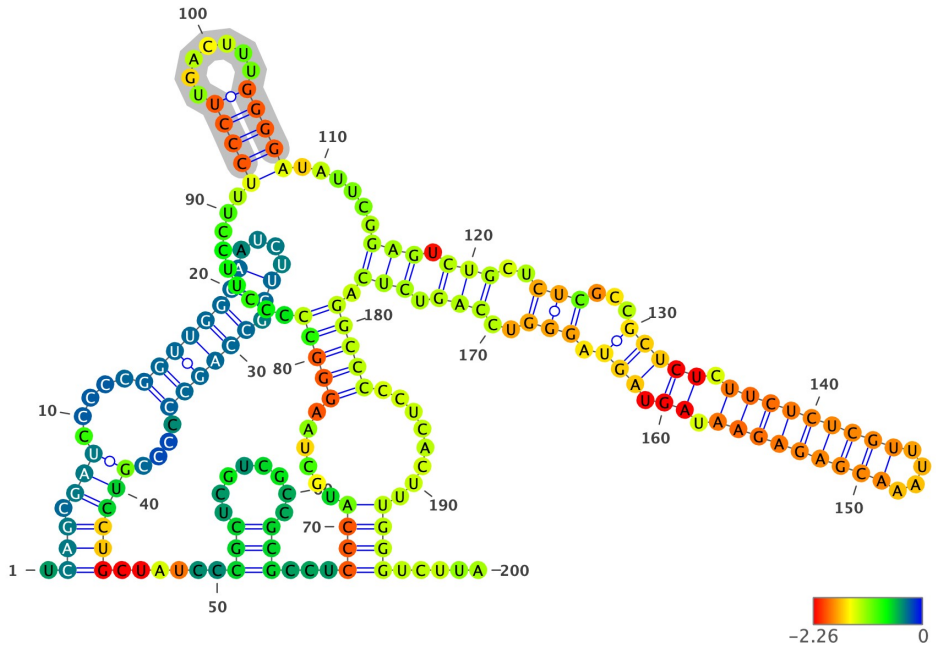
Attributes: ['ID=rna-NC_007605.1:152868..152932', 'gbkey=misc_RNA', 'product=v-snoRNA1 (viral small nucleolar RNA)']

9-- nt 107 to 130--exon, exon-HHV4_RPMS1-40-1, 152783-152806(+)

Attributes: ['ID=exon-HHV4_RPMS1-40-1', 'Parent=rna-HHV4_RPMS1-40', 'Dbxref=GeneID:3783757', 'gbkey=ncRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1', 'product=ebv-miR-BART2-3p']

NC_007605.1 (forward strand): Structure number 398 from nt 153136 to 153150 (nt 93 to 107)

```
5'-CCCUUGACUUUGGGG-3'
5'-((((.......))))-3'
Motif MFE = -4.5; z-score = -2.69; ED = 2.32
```



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

Extracted structure model with flanking nucleotides 153044 to 153243 (motif highlighted in silver):

```
5'-UCAGCGAUCCCCCGGUUGGGAAUCUUCGCCAGCCCCCCGUCCUGCUAUCCCGCUCGUCGCCGCGCCUCCCAUGCUAAGGGCCCCCUUCCUUUCCCUUGACUUUGGGGAUAU
UCGGAGUCUGCUCUCGCCGCUCUCUUCUCUCGUUUAAACGAGAGAAUAGUAGUAGGGUCCAGUCUCAGGCCCCCUCACUUUGGGUCUUA-3
5'-.(((.(((.....(((((((.....)).)))))).....)))))).....(((........))).....((((.....(((((.........(((((.......)))))).....
...(((.((((..((((...(((((.(((((((((.....)))))))))).)).))).))).))..))).))).))))).....)))).....-3'
MFE = -60.5; z-score = -1.82; ED = 41.23
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

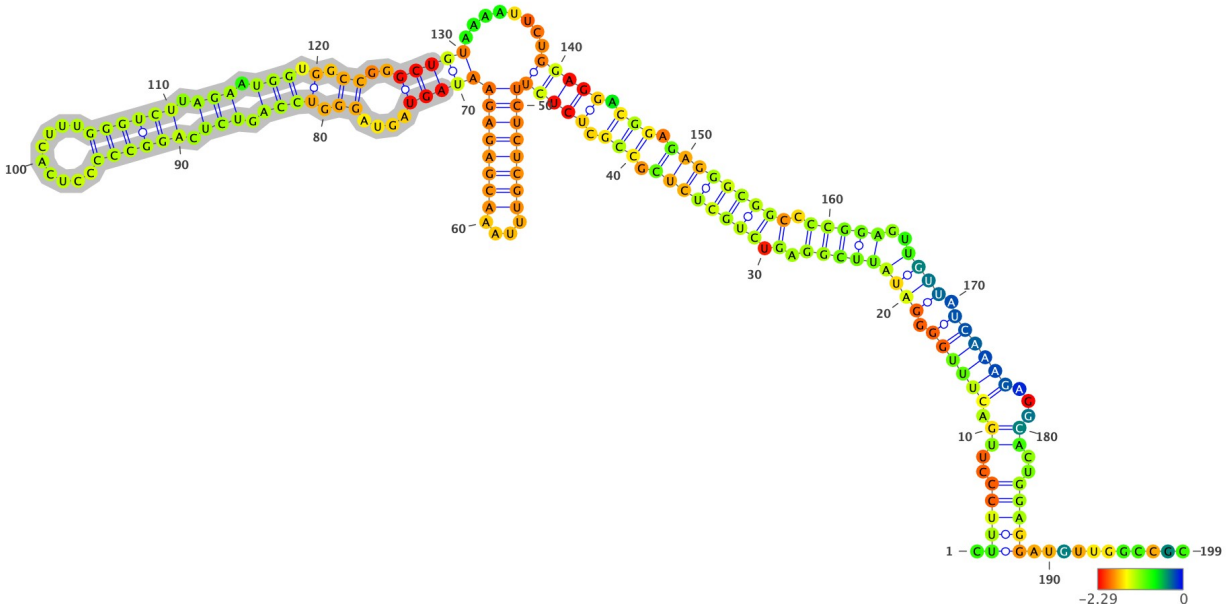
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 399 from nt 153202 to 153259 (nt 71 to 128)

```
5'-AGUAGUAGGGUCCAGUCUCAGGCCCCCUCACUUUGGGUCUUAGAAUGGUGGCCGGGCU-3'
5'-(((.....)))-3'
Motif MFE = -18.0; z-score = -0.23; ED = 7.11
```



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 153132 to 153330 (motif highlighted in silver):

```
5'-CUUUCCCUUGACUUUGGGGAUAUUCGGAGUCUGCUCUCGCCGCUCUCUUCUCUCGUUUAAACGAGAGAAUAGUAGUAGGGUCCAGUCUCAGGCCCCCUCACUUUGGGUCUU
AGAAUGGUGGCCGGGCUGUAAAAUUCUGGAGGACGGAGAGGGCGGCCCCGGAGUUGUUAUCAAAGAGGCACUGGAGGAUGUUGGCCGC-3
5'-.(((((..((.((((((.(((((((((.(.((((((((.(((.(((((((((((((....)))))))))(((((....((.((((.(((.((((((.........)))))).
))).))).).))..)))))........)))))..))).)))))))))..)))))..))))..))))))...))..)))))...........-3'
MFE = -71.7; z-score = -1.04; ED = 32.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

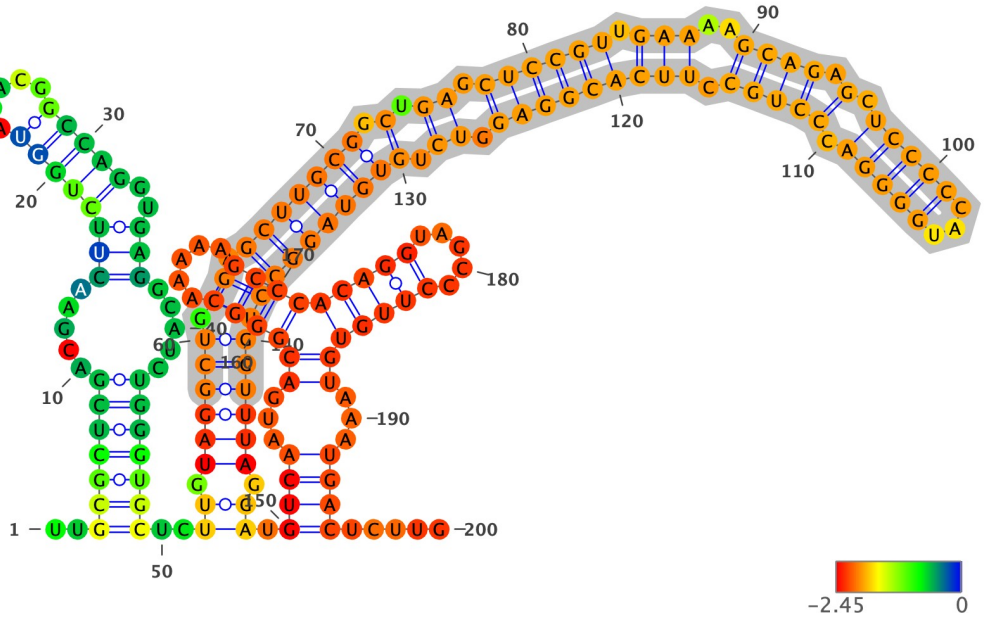
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 400 from nt 153554 to 153638 (nt 58 to 142)

```
5'-GCUGAGAGCUUGCGGCUGAGCUCCGUUGAAAAGCAGAGCUCCCCCAUGGGGACCCUGCCUUCACGGAGGUCUGUGUAGGCCUGGU-3'
5'-(((.((.(((((((.....................................................................))))))))))))-3'
Motif MFE = -39.8; z-score = -3.25; ED = 6.54
```



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 153497 to 153696 (motif highlighted in silver):

```
5'-UUGCGCUCGACGAACUUCUGGUAGACGGCCAGGUGAGGCAUCUGGGUGCUCUUGUAGGCUGAGAGCUUGCGGCUGAGCUCCGUUGAAAAGCAGAGCUCCCCCAUGGGGACC
CUGCCUUCACGGAGGUCUGUGUAGGCCUGGUUUAGGAUGUCAAUGACGGGCAAAAAGCCCACAGGUAGCCCUUGUGUAAAUGACUCUUG-3
5'-..(((((((.....(((((((.....)))))..)))).....)))))))..((.(((((((.((.(((((((.(.((.(((((((.(((..((((.(.(((((...)))))).)
)))).)))))))))).)).)))))))))))))))).)).((((...((((((.....)))))((((.....)))))))...)))).....-3'
MFE = -73.6; z-score = -1.08; ED = 29.74
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

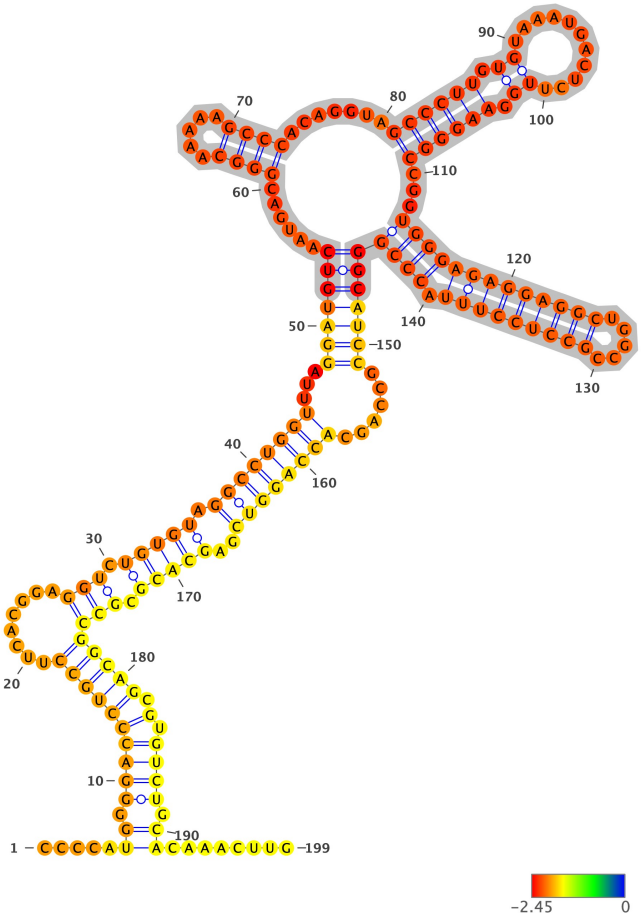
4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 401 from nt 153646 to 153741 (nt 52 to 147)

```
5'-GUCAAUGACGGGCAAAAAGCCCACAGGUAGCCCUUGUGUAAAUGACUCUUGGAAGGGCCGGUGGGAGAGGAGGCUGGCCGCCUCCUUUACCCGGGC-3'

5'-(((......((((.....))))).......((((((.((...........)).)))))).....((((((((((((.....)))))))))).)))))))-3'
Motif MFE = -38.1; z-score = -1.98; ED = 13.91
```



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 153595 to 153793 (motif highlighted in silver):

```
5'-CCCCAUGGGGACCCUGCCUUCACGGAGGUCUGUGUAGGCCUGGUUUAGGAUGUCAAUGACGGGCAAAAAGCCCACAGGUAGCCCUUGUGUAAAUGACUCUUGGAAGGGCCG
GUGGGAGAGGAGGCUGGCCGCCUCCUUUACCCGGGCAUCCGCCAGCACCAGGUCGAGCACGCGCCGGCAGCGUGUCUGCACAAACUUG-3
5'-.....((.(((((((((.......(((.(((((.(((((((...(((((((.....((((.....)))).....((((((.((...........)).)))))).
.((((((((((((.....)))))))))).))))))))))).....)))))))..)))))).)))))))).).)))).)).......-3'
MFE = -84.6; z-score = -1.77; ED = 28.92
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

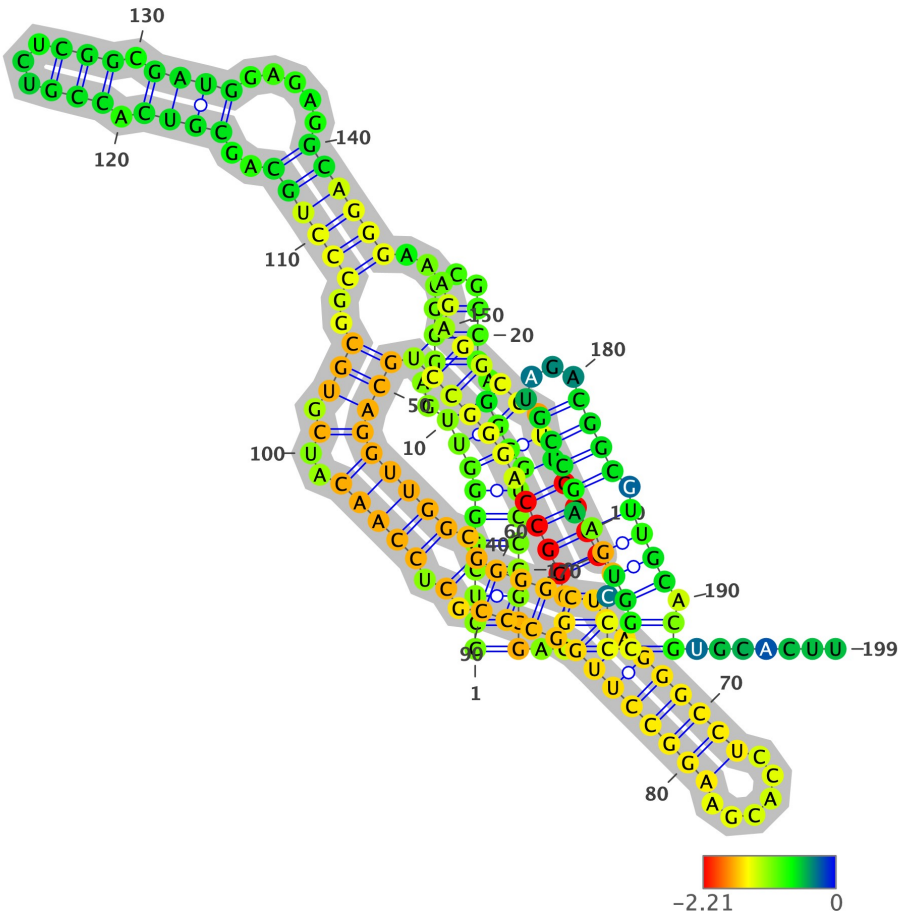
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 402 from nt 154087 to 154210 (nt 38 to 161)

```
5'-GGCCAGGGCCUGCAGGUUGGCGGGGCUCAGGGCCUCCACGAAGGCCUUGGCCCGCUCCAACAUCGUGCGGCCCUGCAGCGUCACCGUCUCGGCGAUGGAGAGGCAGGGAAA
GAGGCCGUUGGCC-3'
5'-((((.......................................................................................................
.........))))-3'
Motif MFE = -68.2; z-score = -2.81; ED = 11.2
```



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 154050 to 154248 (motif highlighted in silver):

```
5'-CCUCGGGGUUGAGGGGCGCCCAGGCGUCCGGGGAGGGGGCCAGGGCCUGCAGGUUGGCGGGGCUCAGGGCCUCCACGAAGGCCUUGGCCCGCUCCAACAUCGUGCGGCCCU
GCAGCGUCACCGUCUCGGCGAUGGAGAGGCAGGGAAAGAGGCCGUUGGCCACCCCGGUGAAGCCGUAGACGGCGUUGCACGUGCACUU-3
5'-((((((((((..(((...))).))).)))))))).((((((((((((((((((((((((.(((((.(((((((((.....)))))))))))))).).)))))..).))).)).((((
((..((((.(((...))).)))).....)))))).....)))))).)))))).))).((((((.((((....)))).)))).)).......-3'
MFE = -100.9; z-score = -0.98; ED = 35.66
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_RPMS1, 138352-160531(+)

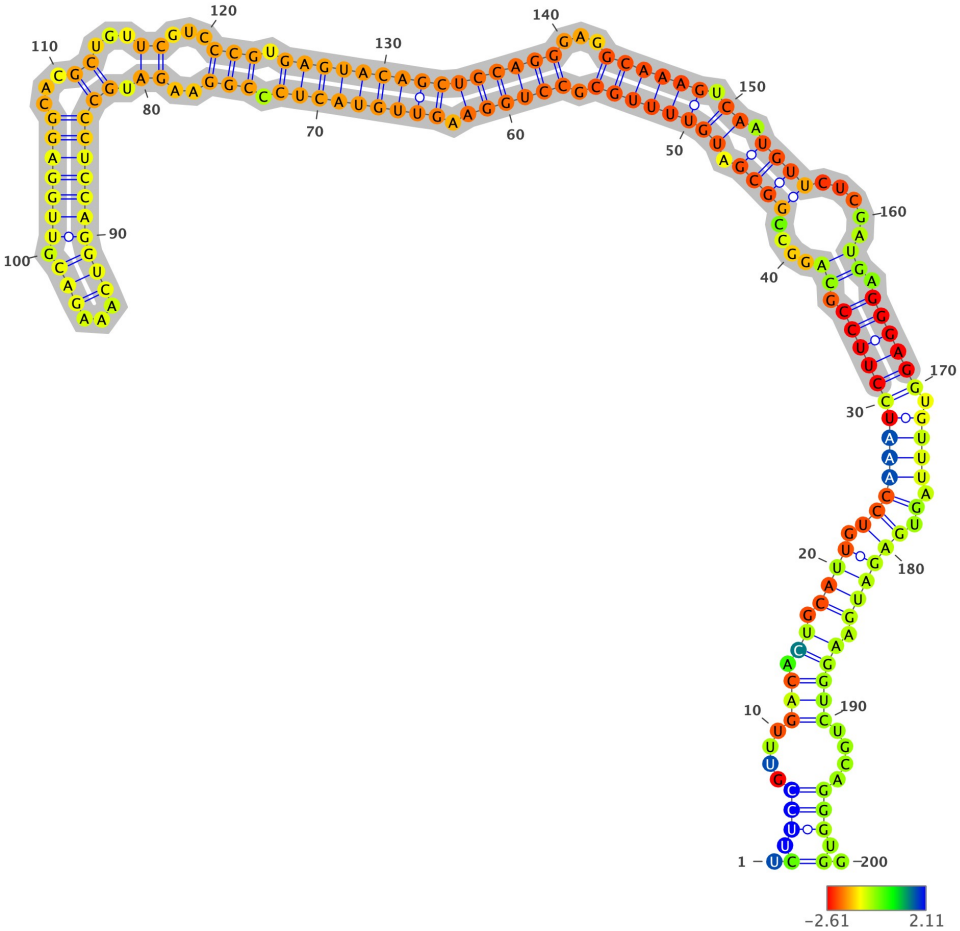
Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 199--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

NC_007605.1 (forward strand): Structure number 403 from nt 156837 to 156975 (nt 31 to 169)

```
5'-CUUCCGCAGGCCGGCGAUGUUUUGCGCCUGGAAGUUGUACUCCCGGAAGAUGCCCUCCAGGUCAAAGACGUUGGAGGCACGCUGUUCGUCCCGUGAGUACAGCUCCAGGGA
GGCAAAGUCAAUGUUCUCGAUGAGGGAG-3'
5'-(((((........(((.(((((((((.((.....................................................................................)).
.)))))).)).)))........)))))-3'
Motif MFE = -57.3; z-score = -2.81; ED = 15.85
```



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 156807 to 157006 (motif highlighted in silver):

```
5'-UCUUCCGUUUGACACUGCAUUGUCCAAAUCCUUCCGCAGGCCGGCGAUGUUUUGCGCCUGGAAGUUGUACUCCCGGAAGAUGCCCUCCAGGUCAAAGACGUUGGAGGCACG
CUGUUCGUCCCGUGAGUACAGCUCCAGGGAGGCAAAGUCAAUGUUCUCGAUGAGGGAGGUGUUUAGUGAGAUGAAGGUCUGCAGGGUGG-3
5'-.(.(((....(((.((.(((((.(((((((((((((.((....((((.(((((((((.((((((.(((((((((.((..((.(((((((((((...)))).)))))))...)
)...))...))).))))))))))))))...)))))).)).))))).....)).)))))).)))).).)))))).)))))....))).).-3'
MFE = -72.5; z-score = -1.36; ED = 20.6
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 40 to 122--exon, exon-HHV4_RPMS1-6, 156846-156928(+)

Attributes: ['ID=exon-HHV4_RPMS1-6', 'Parent=rna-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

6-- nt 1 to 200--gene, gene-HHV4_A73, 155549-160531(+)

Attributes: ['ID=gene-HHV4_A73', 'Dbxref=GeneID:3783676', 'Name=A73', 'gbkey=Gene', 'gene=A73', 'gene_biotype=protein_coding', 'locus_tag=HHV4_A73', 'partial=true', 'start_range=.,155549']

7-- nt 1 to 200--mRNA, rna-HHV4_A73, 155549-160531(+)

Attributes: ['ID=rna-HHV4_A73', 'Parent=gene-HHV4_A73', 'Dbxref=GeneID:3783676', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=A73', 'locus_tag=HHV4_A73', 'partial=true', 'start_range=.,155549']

8-- nt 40 to 122--exon, exon-HHV4_A73-2, 156846-156928(+)

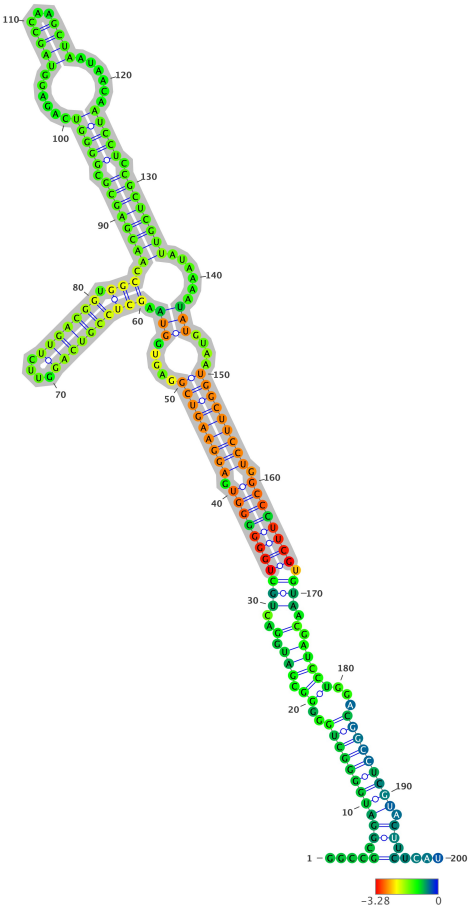
Attributes: ['ID=exon-HHV4_A73-2', 'Parent=rna-HHV4_A73', 'Dbxref=GeneID:3783676', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=A73', 'locus_tag=HHV4_A73', 'partial=true']

9-- nt 40 to 122--CDS, cds-YP_401714.1, 156846-156928(+)

Attributes: ['ID=cds-YP_401714.1', 'Parent=rna-HHV4_A73', 'Dbxref=UniProtKB/TrEMBL:Q9Q2P1,Genbank:YP_401714.1,GeneID:3783676', 'Name=YP_401714.1', 'Note=questionable whether a protein function is encoded', 'gbkey=CDS', 'gene=A73', 'locus_tag=HHV4_A73', 'product=protein A73', 'protein_id=YP_401714.1']

NC_007605.1 (forward strand): Structure number 404 from nt 157643 to 157777 (nt 33 to 167)

```
5'-UGGGGGGUGAGGAAGUCGGAGUGGUAAGCUCCGUCAGGUUCUUGACGGUGGCCAACGAGCGCGGGGUCAGAGGUAGCCAAGCUAAUAACAAUCCUCCGCUCGUUAUAAAAU
AUGUAAUGGCUUCCUGGCCCUUCG-3'
5'-((((.((((.(((((((((.....((..((((.................).)))..............................................................
))....)))))))))).))).))))-3'
Motif MFE = -59.0; z-score = -3.88; ED = 15.99
```



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 157611 to 157810 (motif highlighted in silver):

```
5'-GGCCGCGGAUGGGGCUGGGGGCGAUGGACUGCUGGGGGGUGAGGAAGUCGGAGUGGUAAGCUCCGUCAGGUUCUUGACGGUGGCCAACGAGCGCGGGGUCAGAGGUAGCCA
AGCUAAUAACAAUCCUCCGCUCGUUAUAAAAUAUGUAAUGGCUUCCUGGCCCUUCGUGUAACGAUCCUGGACGGCCUCGUACUUCUCAU-3
5'-....(.(((((((((((..(((.(((.(..((((((((((.(((((((((.....(((.((((((((((....)))))))).))).((((((((.(((((.....((((..
.))))......)))))).))))))))......)))....)))))))))).))))))))..))).).))))))...))))))))))..)).).....-3'
MFE = -80.3; z-score = -2.08; ED = 17.46
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--gene, gene-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Name=RPMS1', 'gbkey=Gene', 'gene=RPMS1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_RPMS1']

4-- nt 1 to 200--mRNA, rna-HHV4_RPMS1, 138352-160531(+)

Attributes: ['ID=rna-HHV4_RPMS1', 'Parent=gene-HHV4_RPMS1', 'Dbxref=GeneID:3783757', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=RPMS1', 'locus_tag=HHV4_RPMS1']

5-- nt 1 to 200--gene, gene-HHV4_A73, 155549-160531(+)

Attributes: ['ID=gene-HHV4_A73', 'Dbxref=GeneID:3783676', 'Name=A73', 'gbkey=Gene', 'gene=A73', 'gene_biotype=protein_coding', 'locus_tag=HHV4_A73', 'partial=true', 'start_range=.,155549']

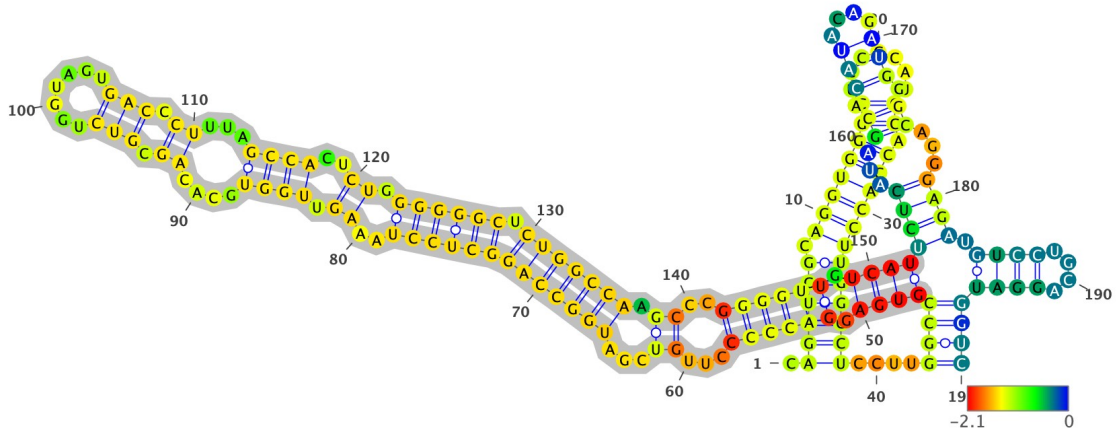
6-- nt 1 to 200--mRNA, rna-HHV4_A73, 155549-160531(+)

Attributes: ['ID=rna-HHV4_A73', 'Parent=gene-HHV4_A73', 'Dbxref=GeneID:3783676', 'Note=BART mRNAS%2C of which RMPS1 and part of A73 are included as representatives%2C are complex spliced transcripts', 'gbkey=mRNA', 'gene=A73', 'locus_tag=HHV4_A73', 'partial=true', 'start_range=.,155549']

NC_007605.1 (forward strand): Structure number 405 from nt 162292 to 162397 (nt 47 to 152)

5'-GUGAGGACCCCCUUGUCGAUGGCCAGGCUCCUAAAGUUGGUGCACAGCGUCUGGUAGUGACCCUUUAGCCACUCUGGGGGGCUCUGGCCAAGCCCGGGGUUGUCAU-3'

5'-((((.....))))-3'
Motif MFE = -48.3; z-score = -2.76; ED = 10.28



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 162246 to 162444 (motif highlighted in silver):

5'-CAGGUCGCAGGUGGGCUCCCCAUGCACCACCUUGGCCUCCUUGGCCGUGAGGACCCCCUUGUCGAUGGCCAGGCUCCUAAAGUUGGUGCACAGCGUCUGGUAGUGACCCUU
UAGCCACUCUGGGGGGCUCUGGCCAAGCCCGGGGUUGUCAUUCUCAUAGCACAUACAGAUGGGCAGGGAGAUGUCCUGCAGGAUGGUC-3
5'-.(((((((.(((((((((.....)).))))))))))))....((((((((.((((((...((...((((((((((((((..((.((((....((.(((.....)))).)).
..))))..)).)))))).)))))))..)).....)))))).))))((((...((.(((....))).)).)...)))).((((....)))))))-3'
MFE = -82.2; z-score = -1.42; ED = 37.46

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

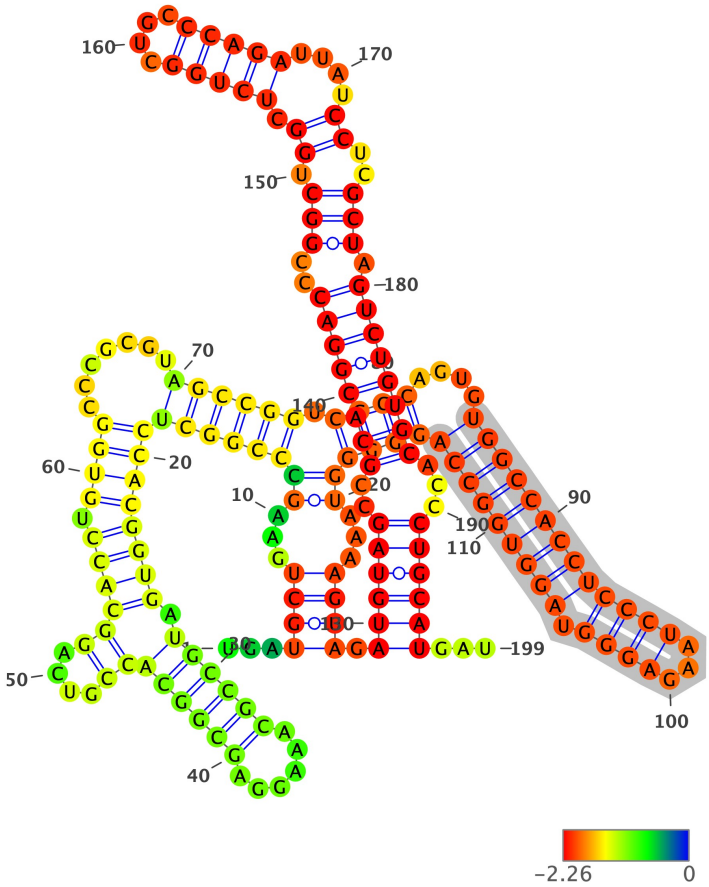
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

NC_007605.1 (forward strand): Structure number 406 from nt 164201 to 164230 (nt 85 to 114)

```
5'-UGGCCACCUCCCUAAGAGGGUAGGUGGCCA-3'
5'-(((((((((((((...)))))).)))))))))-3'
Motif MFE = -22.7; z-score = -6.21; ED = 1.13
```



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 164117 to 164315 (motif highlighted in silver):

```
5'-UGAUGCUGAAGCCCGGCUCCACGGUGAUGCCGCAAAGGAGCGGCACCGUCAGGCACCUGUGGCCCGCGUAGCCGGUCCCCAGUGUGGCCACCUCCCUAAGAGGGUAGGUGG
CCAGGGGGUAAAAGUAGAUGUAGCCGCACGGACCCGGCUGGCUCUGGCUGCCCAGAUUAUCCUCGCUAGUCUGUGCACCCUGCAUGAU-3
5'-...((((...(((((((((((((((.((((((.....)))))))((....)))))).))))).......)))))).((((....((((((((((((...)))))).))))))
)))))))))...)))).((((((..(((((((..(((.((.(((((....)))))....)).)).)))).)))))))...)))))))...-3'
MFE = -89.2; z-score = -2.28; ED = 44.05
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

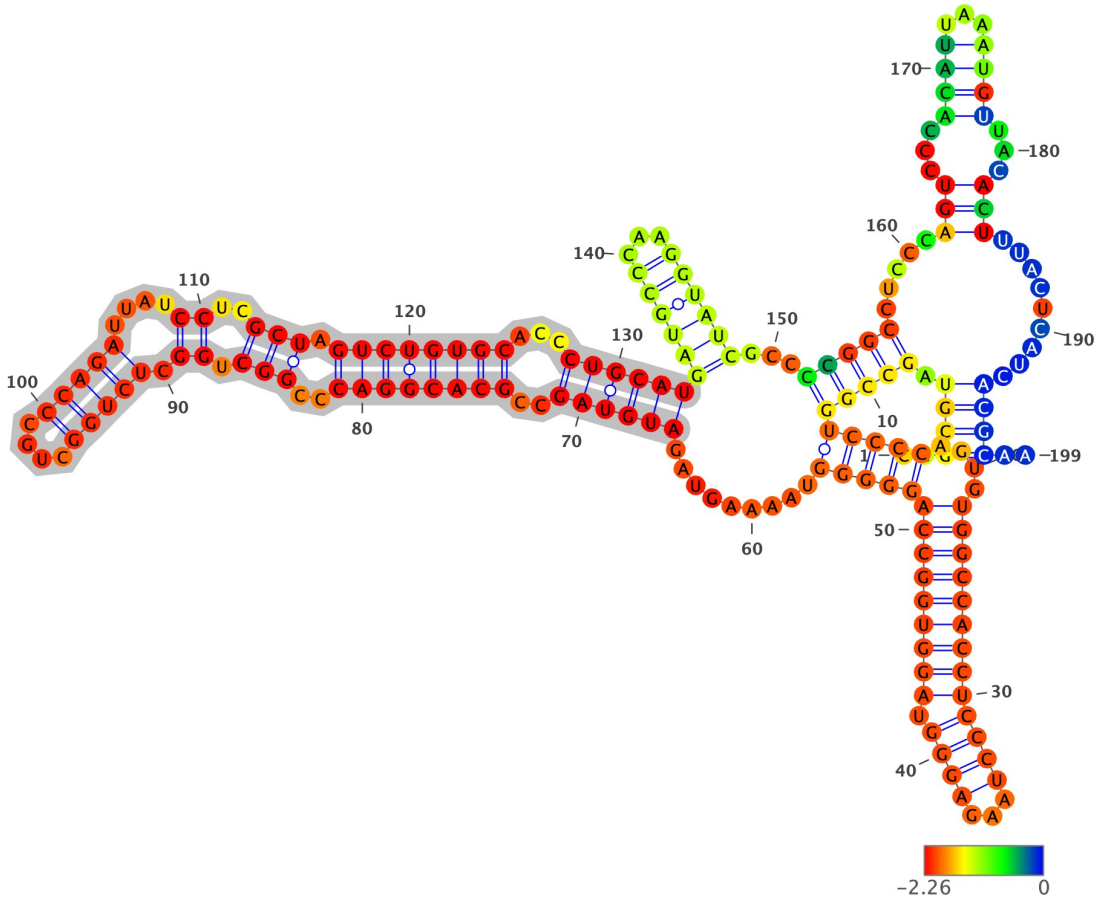
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

NC_007605.1 (forward strand): Structure number 407 from nt 164245 to 164312 (nt 66 to 133)

```
5'-AUGUAGCCGCACGGACCCGGCUGGCUCUGGCUGCCCAGAUUAUCCUCGCUAGUCUGUGCACCCUGCAU-3'
5'-((((((..(((((((((..(((.((.(((((....)))))....)).)))).)))))))))...)))))))-3'
Motif MFE = -26.3; z-score = -2.44; 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 164180 to 164378 (motif highlighted in silver):

```
5'-CCGCGUAGCCGGUCCCCAGUGUGGCCACCUCCCUAAGAGGGUAGGUGGCCAGGGGGUAAAAGUAGAUGUAGCCGCACGGACCCGGCUGGCUCUGGCUGCCCAGAUUAUCCU
CGCUAGUCUGUGCACCCUGCAUGAUGCCCAAGGUAUCGCCCCGGCCUCCCAGUCCCACAUUAAAUGUUACACUUUACUCAUCACGCAA-3
5'-..(((((.((((((((((....((((((((((((...)))).)))))))))))))).........((((((..(((((((((..(((.((.((((((....)))))).....)).
.))).)))))))).....))))))((((((...)))))))...)))))).....(((...((((...))))...)))).........)))))..-3'
MFE = -76.9; z-score = -2.81; ED = 9.64
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

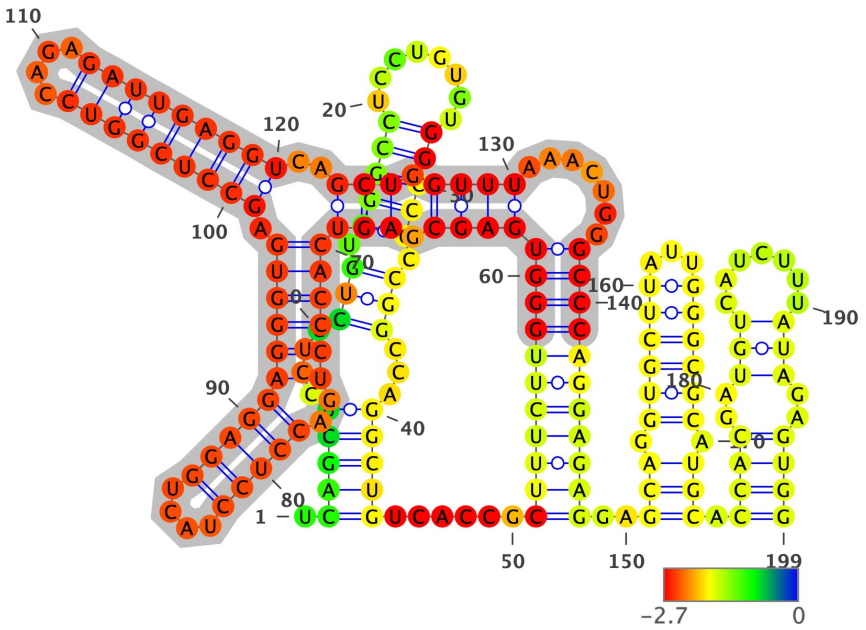
Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

NC_007605.1 (forward strand): Structure number 408 from nt 165120 to 165203 (nt 58 to 141)

```
5'-GGGUGAGCGAGUCACCCUGACCUCCUACUGGAGGAGGGUGAGCCUCGGUCCAGAGAUUGAGGUCAGCUGGUUUAAACUGGGCCC-3'
5'-(((((((.((.((((((..(((((....)))))))))).((((((((....)))))))))...)).)))).......))))-3'
Motif MFE = -37.9; z-score = -2.8; ED = 30.86
```



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 165063 to 165261 (motif highlighted in silver):

```
5'-UCAGCUCCUCCUGUUGGCCUCCUGUGUGGCCGCCGGCCAGGCUGUCACCGCUUUCUUGGGUGAGCGAGUCACCCUGACCUCCUACUGGAGGAGGGUGAGCCUCGGUCCAGA
GAUUGAGGUCAGCUGGUUUAAACUGGGCCCAGGAGAGGAGCAGGUGCUUAUUGGGCGCAUGCACCACGAUGUCAUCUUUAUAGAGUGG-3
5'-.(((((....(((.(((((........)))))..)))...)))))......(((((((((((((((.(((((((((..(((((....)))))))))))).(((((((((....
))))))))).))).)))).......))))))))))..(((.((((((...)))))).))).((((..(((.......)))..))))-3'
MFE = -82.3; z-score = -2.03; ED = 23.89
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--gene, gene-HHV4_BARF1.2, 165008-165712(+)

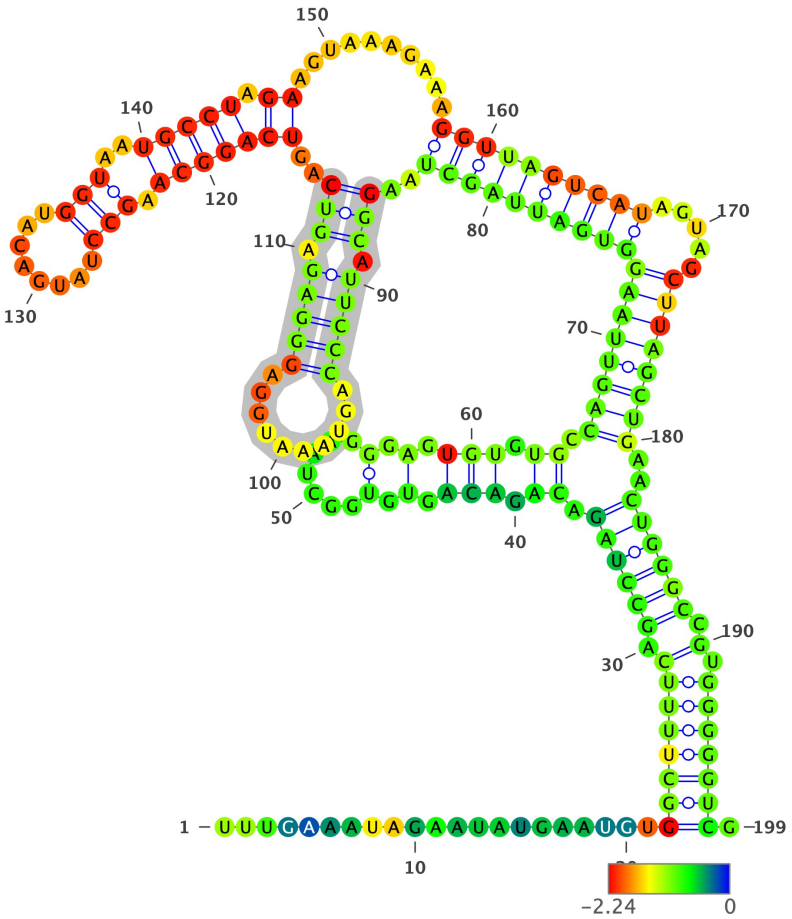
Attributes: ['ID=gene-HHV4_BARF1.2', 'Dbxref=GeneID:3783772', 'Name=BARF1', 'gbkey=Gene', 'gene=BARF1', 'gene_biotype=protein_coding', 'locus_tag=HHV4_BARF1.2']

4-- nt 1 to 199--CDS, cds-YP_401719.1, 165046-165711(+)

Attributes: ['ID=cds-YP_401719.1', 'Parent=gene-HHV4_BARF1.2', 'Dbxref=UniProtKB/TrEMBL:Q777A5,Genbank:YP_401719.1,GeneID:3783772', 'Name=YP_401719.1', 'gbkey=CDS', 'gene=BARF1', 'locus_tag=HHV4_BARF1.2', 'product=protein BARF1', 'protein_id=YP_401719.1']

NC_007605.1 (forward strand): Structure number 409 from nt 167628 to 167655 (nt 86 to 113)

```
5'-GGCAUUCCCAGUAAAUGGAGGGAGAGUC-3'
5'-(.........................)-3'
Motif MFE = -8.0; z-score = -2.07; 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 167543 to 167741 (motif highlighted in silver):

```
5'-UUUGAAAUAGAAUAUGAAUGUGGCUUUUCAGCCUAGACAGACAGUGUGGCUAAGGGAGUGUGUGCCAGUUAAGGUGAUUAGCUAAGGCAUUCCCAGUAAAUGGAGGGAGAG
UCAGUCAGGCAAGCCUAUGACAUGGUAAUGCCUAGAAGUAAAGAAAGGUUAGUCAUAGUAGCUUAGCUGAACUGGGCCGUGGGGGUCG-3
5'-.....................(((((((.((((((.((.((((.(.(.......).).))).)).((((((((((((((((..(((.(((((..........))))).)
)).(((((((.(((........))).)))))).))..........))))))))).....))))))))..)))))).).))))))).-3'
MFE = -54.4; z-score = -1.67; ED = 42.0
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

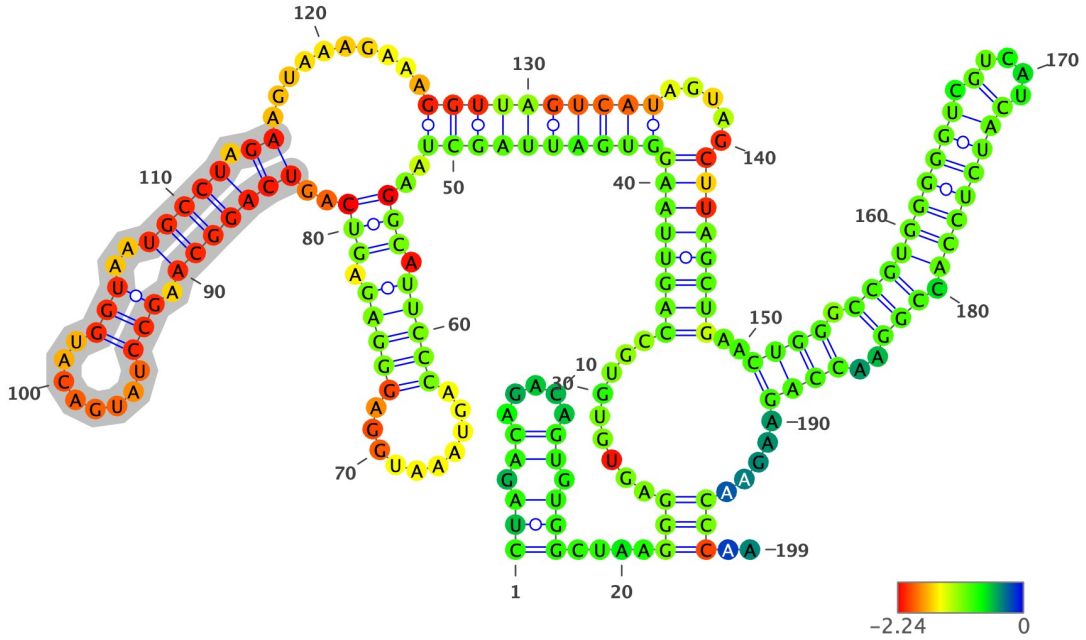
Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

NC_007605.1 (forward strand): Structure number 410 from nt 167658 to 167689 (nt 84 to 115)

```
5'-UCAGGCAAGCCUAUGACAUGGUAAUGCCUAGA-3'
5'-(((((((.(((........)))..)))))).))-3'
Motif MFE = -9.9; z-score = -2.86; ED = 1.44
```



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

Extracted structure model with flanking nucleotides 167575 to 167773 (motif highlighted in silver):

```
5'-CUAGACAGACAGUGUGGCUAAGGGAGUGUGUGCCAGUUAAGGUGAUUAGCUAAGGCAUUCCCAGUAAAUGGAGGGAGAGUCAGUCAGGCAAGCCUAUGACAUGGUAAUGCC
UAGAAGUAAAGAAAGGUUAGUCAUAGUAGCUUAGCUGAACUGGGCCGUGGGGGUCGUCAUCAUCUCCACCGGAACCAGAAGAACCCAA-3
5'-(((.((.....)).))).....(((.........((((((((((((((((((..(((.(((((.........)))))).))).)).(((((((.(((........))).)))
).)).........))))))))).....)))))))..((((.((((((((((.(....)))))))).))).))))).....))).)-3'
MFE = -59.6; z-score = -2.38; ED = 16.38
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

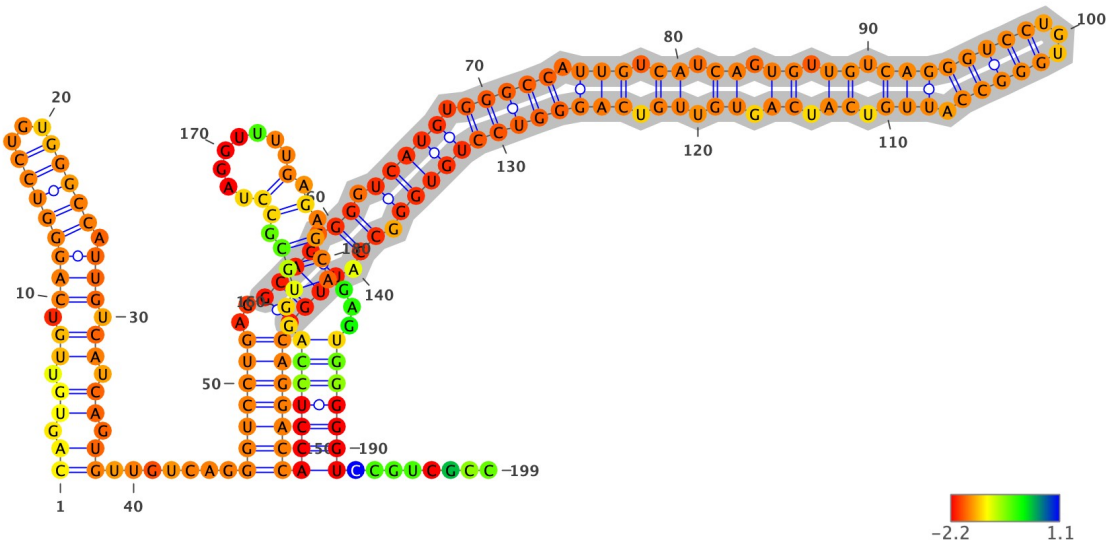
Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

NC_007605.1 (forward strand): Structure number 411 from nt 168025 to 168114 (nt 55 to 144)

```
5'-GCAGCGGGUCAUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGU-3'
5'-(((((.((.(((((.......................................................................)))))).)).)))))-3'
Motif MFE = -38.4; z-score = -2.99; 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 167971 to 168169 (motif highlighted in silver):

```
5'-CAGUGUUGUCAGGGUCCUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGAGGCAGCGGGUCAUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGU
CAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGUCAGGACCACCUCCAGGUGCGCCUAGGUUUUGAGAGCAGAGUGGGGGUCCGUCGCC-3
5'-((.((.((.(((((((...)))))).))).)).)).).....(((((((..((((.((.(((((.(((((.(((.((.((.((.((.(((((((...)))))).))).
)).)).)).)).))))))))))))).)).))))))))))(((((((..(((.((........).).)))...)))))))........-3'
MFE = -79.7; z-score = -1.42; ED = 29.9
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

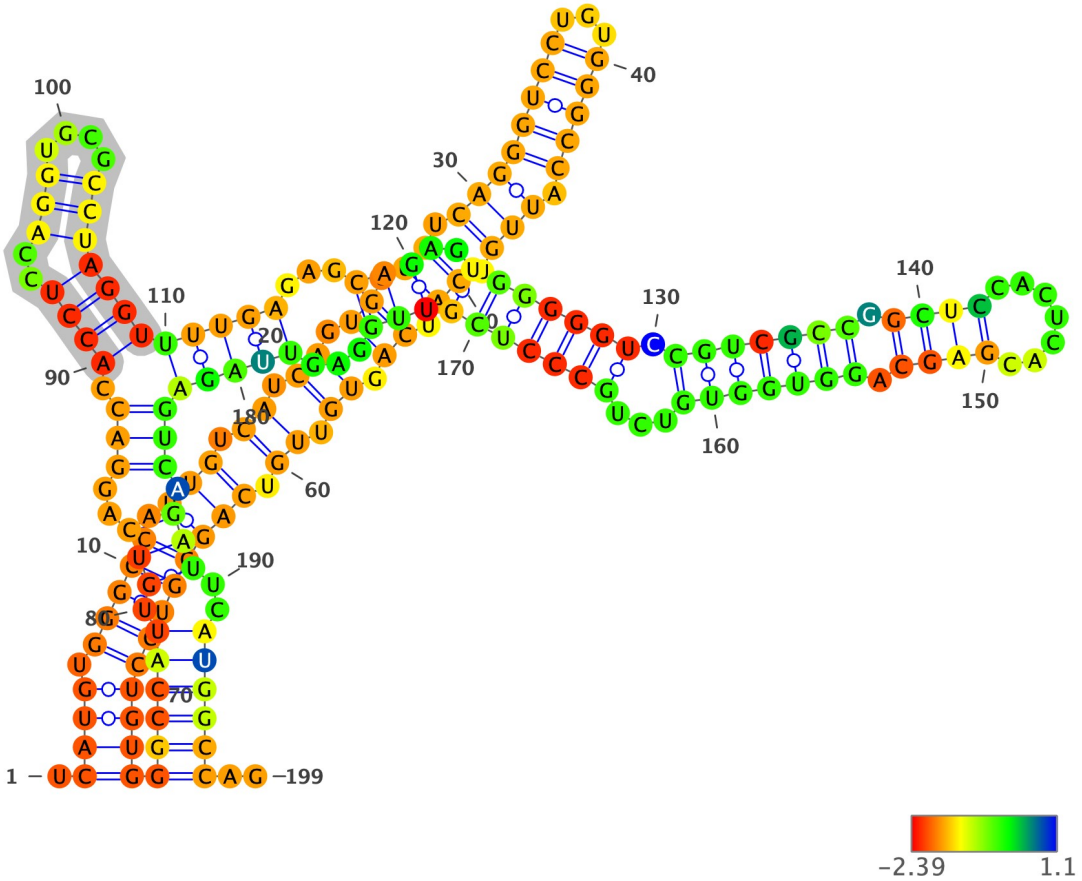
Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

5-- nt 1 to 146--repeat_region, id-HHV4_LMP-2A-2, 167941-168116(+)

Attributes: ['ID=id-HHV4_LMP-2A-2', 'Dbxref=GeneID:3783751', 'gbkey=repeat_region', 'gene=LMP-2A', 'locus_tag=HHV4_LMP-2A', 'rpt_unit_range=167941..167973']

NC_007605.1 (forward strand): Structure number 412 from nt 168122 to 168141 (nt 90 to 109)

```
5'-ACCUCCAGGUGCGCCUAGGU-3'
5'-((((............))))-3'
Motif MFE = -4.2; z-score = -0.47; 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 168033 to 168231 (motif highlighted in silver):

```
5'-UCAUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGUCAUCAGUGUUGUCAGGGUCCUGUGGGCCAUUGUCAGGACCACCUCCAGGUGCGCCUAGGUUU
UGAGAGCAGAGUGGGGGUCCGUCGCCGGCUCCACUCACGAGCAGGUGGUGUCUGCCCUCGUUGGAGUUAGAGUCAGAUUCAUGGCCAG-3
5'-.((((.(((((.(((.((.((.((.((.((((((((...)))))).))).)).)).)).)).))))))))))))(((((.(((..(((.((((..(((....)))))))(
(((...(((..(((((((.(((((((.((((.......)))).)))))))...)))))))))...)))))))).)))..)))))).-3'
MFE = -72.9; z-score = -0.77; ED = 44.65
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

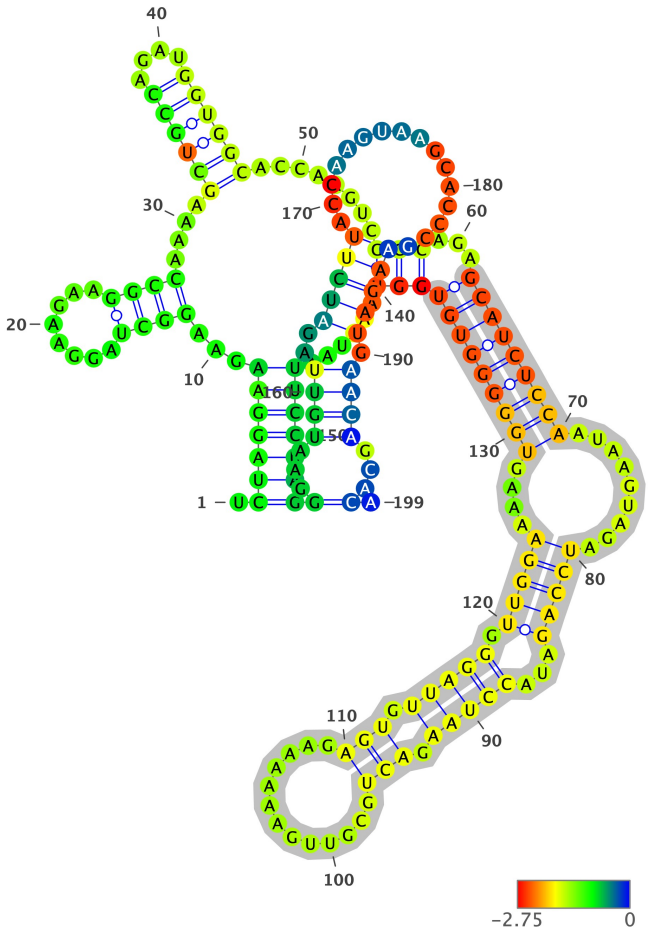
Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

5-- nt 1 to 84--repeat_region, id-HHV4_LMP-2A-2, 167941-168116(+)

Attributes: ['ID=id-HHV4_LMP-2A-2', 'Dbxref=GeneID:3783751', 'gbkey=repeat_region', 'gene=LMP-2A', 'locus_tag=HHV4_LMP-2A', 'rpt_unit_range=167941..167973']

NC_007605.1 (forward strand): Structure number 413 from nt 168475 to 168550 (nt 62 to 137)

```
5'-GCAUCUCCAAUAAGUAGAUCCAGAUACCUAAGACUGCGUUGAAAAAAGAGUGUUAGGGUUGGAAAAGUGGGGGUGU-3'
5'-(((((((((.............................................................)))))))))-3'
Motif MFE = -22.3; z-score = -3.24; ED = 4.76
```



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 168414 to 168612 (motif highlighted in silver):

```
5'-UCUAGGAAGAAGGCUAGGAAGAAGGCCAAAAGCUGCCAGAUGGUGGCACCAAGUCGCCAGAGCAUCUCCAAUAAGUAGAUCCAGAUACCUAAGACUGCGUUGAAAAAAGAG
UGUUAGGGUUGGAAAAGUGGGGGUGUGGUAAAUAAUUCCUAGGGAAUGUUAGAUCUUACCAAGUAAGCACCCGAAGAUGAACAGCACA-3
5'-.(((((((...((((........))))....((((((....)))))).........(((...(((((((((.........(((((...(((((.(((.............))
).)))))).)))))....))))))))))).....)))))))(...(((((..(((((.................)))))).))))...).-3'
MFE = -50.4; z-score = -1.99; ED = 25.03
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

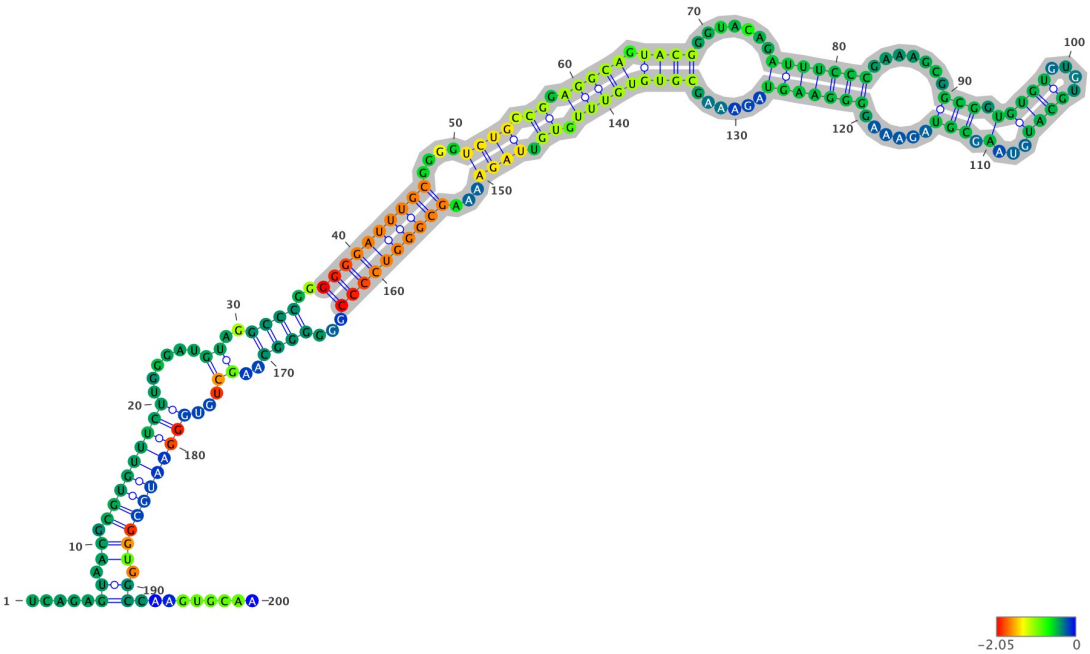
Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

NC_007605.1 (forward strand): Structure number 414 from nt 169136 to 169262 (nt 37 to 163)

```
5'-GGGGAUUUGCGGGGUCUGCCGGAGGCAGUACGGGUACAGAUUUCCCGAAAGCGGCGGUGUGUGUGUGCAUGUAAGCGUAGAAAGGGGAAGUAGAAAGCGUGUGUUUGUGUU
AGAAAAGCGGGUCCCC-3'
5'-(.....)-3'
Motif MFE = -43.3; z-score = -2.54; ED = 17.06
```



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 169100 to 169299 (motif highlighted in silver):

```
5'-UCAGAGUAACGCGUGUUUCUUGGGAUGUAGGCCCGGGGGGAUUUGCGGGGUCUGCCGGAGGCAGUACGGGUACAGAUUUCCCGAAAGCGGCGGUGUGUGUGUGCAUGUAAG
CGUAGAAAGGGGAAGUAGAAAGCGUGUGUUUGUGUUAGAAAAGCGGGUCCCCGGGGGGCAAGCUGUGGGAAUGCGGUGGCCAAGUGCAA-3
5'-.....((.((.(((((((((.....((..(((((..((((((((((....((((.((.(((((.((((.......(((((((.......(((.(((((....)))).)).
)))......)))))))).....)))))))))).)).)))).....))))))))))...))))..)).....))))))))))).))..........-3'
MFE = -65.3; z-score = -1.18; ED = 30.56
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 195 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 195 to 200--exon, exon-NC_007605.1:58..169448-1, 169294-169448(+)

Attributes: ['ID=exon-NC_007605.1:58..169448-1', 'Parent=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

7-- nt 195 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

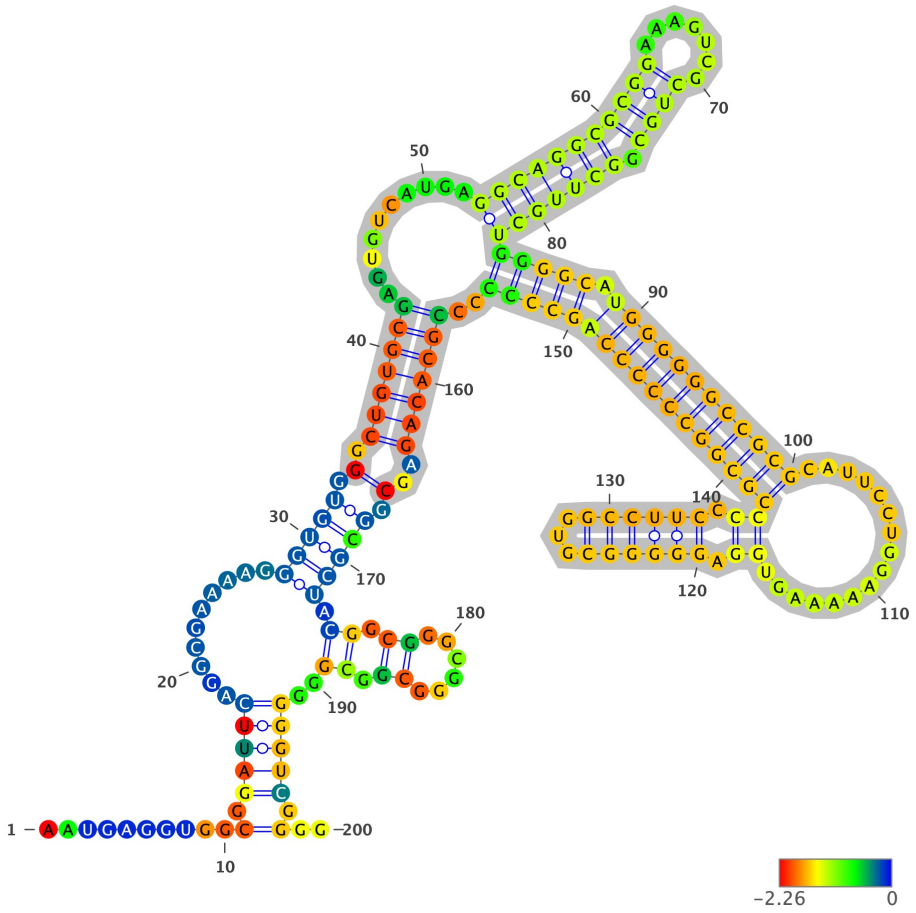
Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

8-- nt 195 to 200--exon, id-HHV4_LMP-2B, 169294-169448(+)

Attributes: ['ID=id-HHV4_LMP-2B', 'Parent=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Note=LMP-2B first exon', 'gbkey=exon', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B']

NC_007605.1 (forward strand): Structure number 415 from nt 169588 to 169720 (nt 34 to 166)

```
5'-GGCUGUGCGAGUGUCAUGAGGCAGGCGCGGAAAGUCGCUGCGGCUUGCUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCC
CCCCAGCCCCCCCGCACAGAGC-3'
5'-(.(((.......................................................................................................
................)))..)-3'
Motif MFE = -73.9; z-score = -2.56; ED = 17.2
```



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 169555 to 169754 (motif highlighted in silver):

```
5'-AAUGAGGUGGCGGAUUCAGGCGAAAAGGGUGUGGGCUGUGCGAGUGUCAUGAGGCAGGCGCGGAAAGUCGCUGCGGCUUGCUGGGGCAUGGGGGGCCGCGCAUUCCUGGAA
AAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGGGCGGCGGGGGGUCGGGG-3
5'-..........(.(((((.........(((((.(.(((((((.........((((((((((.......)))).)))))))((((.(((((((((((.........
.....((.((((((...)))))).))))))))))))))))))..)))))))..).)))))).((.(((.....)).)).)..)))))).)..-3'
MFE = -90.9; z-score = -2.29; ED = 34.94
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 82 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 82 to 200--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

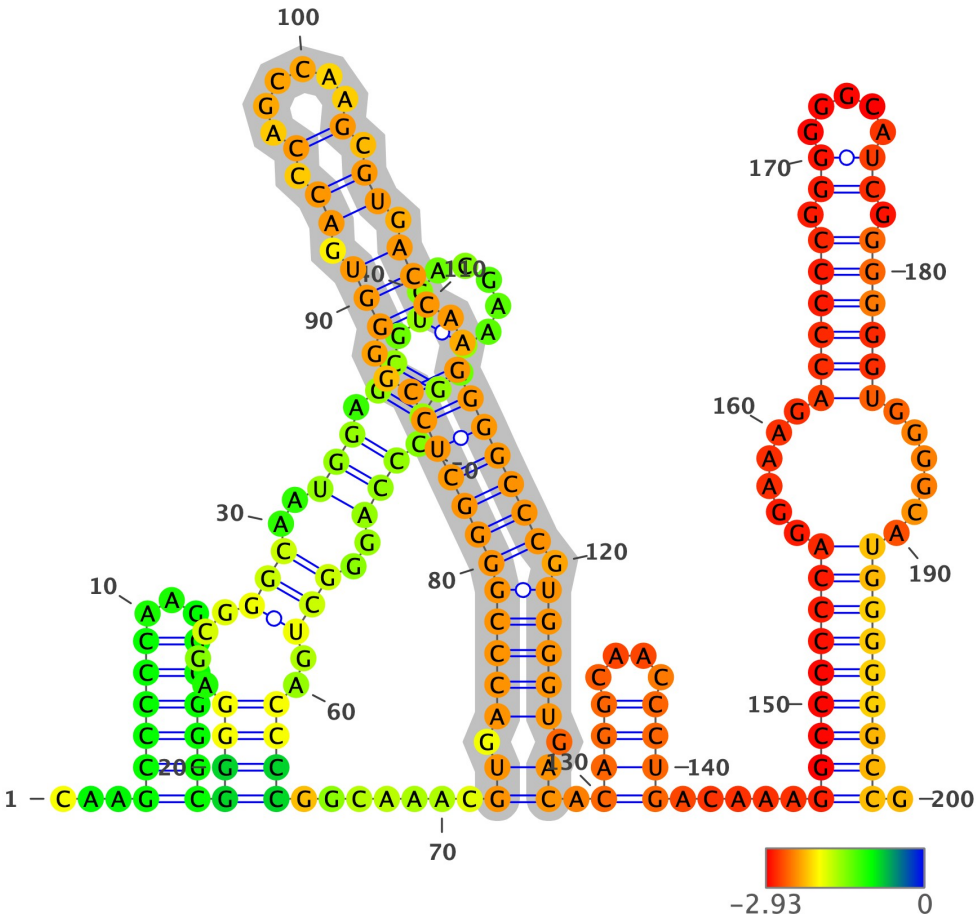
Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 164 to 183--sequence_feature, id-NC_007605.1:169718..169737, 169718-169737(+)

Attributes: ['ID=id-NC_007605.1:169718..169737', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 416 from nt 170062 to 170118 (nt 72 to 128)

```
5'-GUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGAC-3'
5'-((.(((((((((((..(((.((.(......).)).)))..)))))))).)))))).))-3'
Motif MFE = -33.0; z-score = -2.9; ED = 1.86
```



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 169991 to 170190 (motif highlighted in silver):

```
5'-CAAGCCCCCAAGGGGGGCGGGGAGCGGGCAAUGGAGCGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCA
AGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCG-3
5'-...((((((...))))))((((....((((..((((.((.(......).)).)))..)))).))))).....((.((((((((((((..(((.((.(......).)).))).
.)))))))).)))))).)).((((....)))).....(((((((((.....((((((.((.....)).)))))).....)))))))).-3'
MFE = -108.6; z-score = -3.75; ED = 17.55
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 183--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

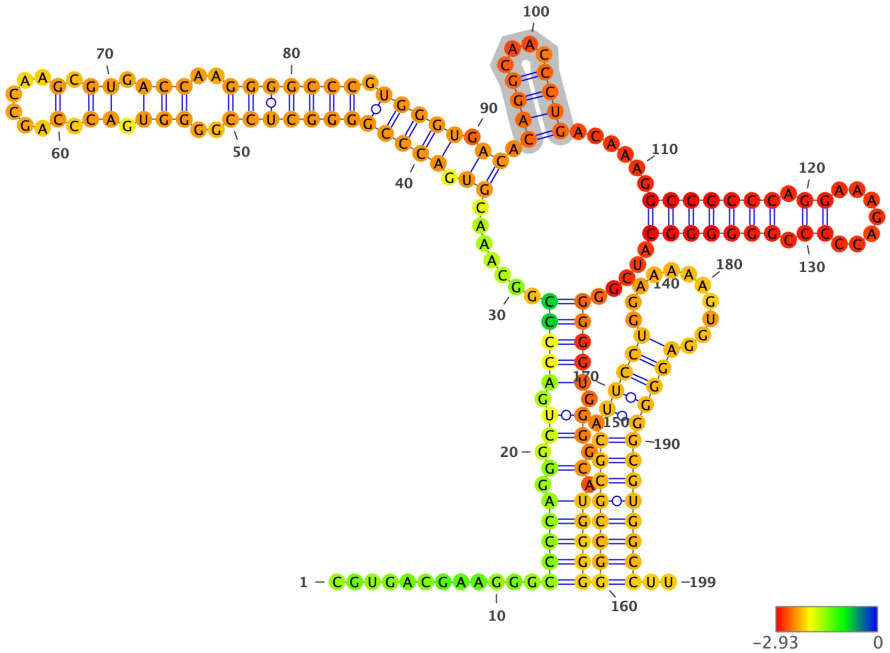
Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 184 to 200--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 417 from nt 170120 to 170131 (nt 94 to 105)

```
5'-CAGGCAACCCUG-3'
5'-((((....))))-3'
Motif MFE = -2.6; z-score = -3.01; 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 170027 to 170225 (motif highlighted in silver):

```
5'-CGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAG
GCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUU-3
5'-............(((((.(.((.(((((.......((.(((((((((((((..((((.((.(.......).)).)))..)))))))).)))))).)).((((....)))).....
(((((((.(.......)).)))))))....)))))).)).).)))))((((((((.(((((.........)))))))))))))..-3'
MFE = -104.4; z-score = -3.19; ED = 10.9
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 147--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

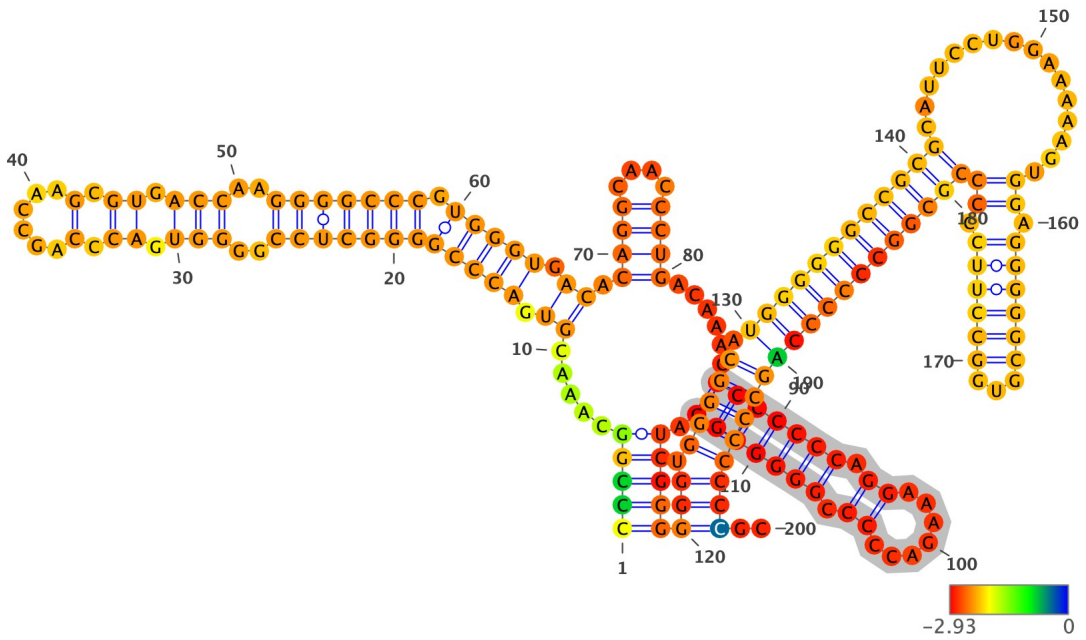
Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 148 to 199--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 418 from nt 170138 to 170164 (nt 87 to 113)

```
5'-GCCCCCCAGGAAAGACCCCCGGGGGGC-3'
5'-(((((((.((.......)).)))))))-3'
Motif MFE = -18.2; z-score = -3.71; ED = 2.29
```



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

Extracted structure model with flanking nucleotides 170052 to 170251 (motif highlighted in silver):

```
5'-CCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGG
GCAUCGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGC-3
5'-(((((.....((.(((((((((((..(((.((.(......).)).)))..)))))))).)))))).)).((((....)))).....(((((((.((.......)).)))))
)).)))))((.(((((.((((((((((((.................((.(((((...))))))).))))))))))))))))))))..-3'
MFE = -119.8; z-score = -4.21; ED = 16.26
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 122--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

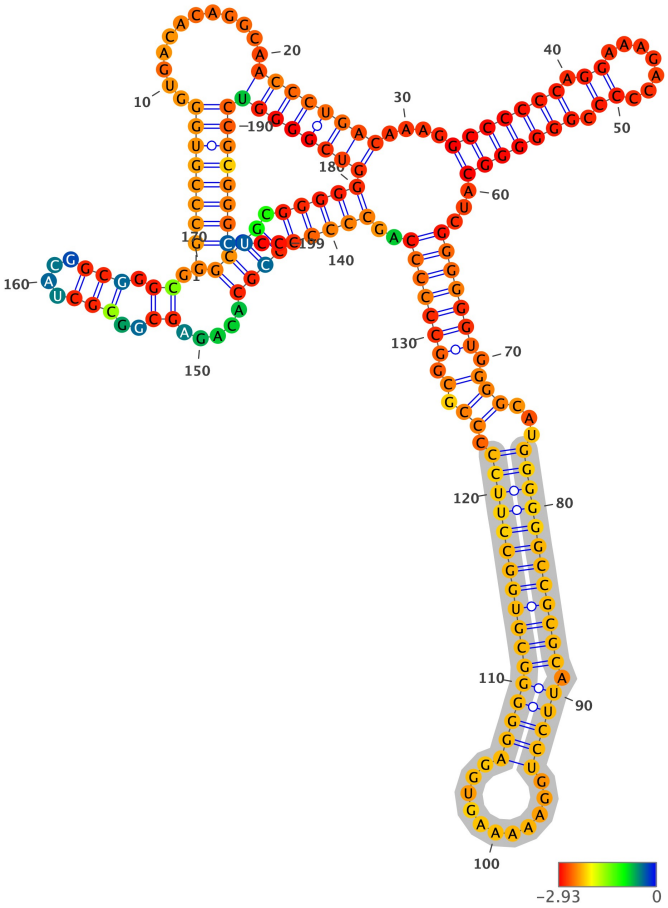
Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 123 to 200--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 419 from nt 170182 to 170227 (nt 77 to 122)

```
5'-GGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCC-3'
5'-(((((((((((.(((((.........)))))))))))))))))-3'
Motif MFE = -27.7; z-score = -4.59; 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 170106 to 170304 (motif highlighted in silver):

```
5'-GCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGG
CGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGGCUCC-3
5'-(((((((((.........((((((((....(((((((.((.......)).)))))))...(((((((.(((...((((((((((((.(((((.........))))))
))))))))))).)).).))))))).((((((((.....((..((((....)))).)).)).)))).))))))))))))))))))))...-3'
MFE = -123.9; z-score = -3.4; ED = 34.07
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 68--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 69 to 199--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

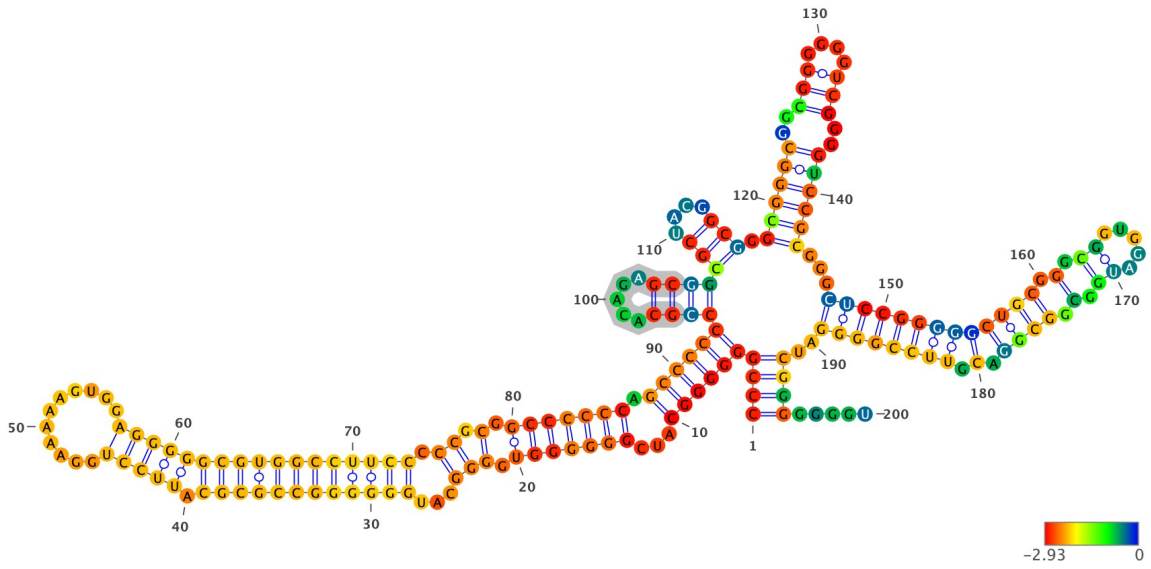
Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 151 to 170--sequence_feature, id-NC_007605.1:170256..170275, 170256-170275(+)

Attributes: ['ID=id-NC_007605.1:170256..170275', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 420 from nt 170250 to 170258 (nt 96 to 104)

```
5'-GCACAGAGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.21; 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 170155 to 170354 (motif highlighted in silver):

```
5'-CCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUA
CGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGGCUCCGGGGGCUGCGGGCGGUGGAUGGCGGCGGACGUUCCGGGGAUCGGGGGGGU-3
5'-(((((((((...(((((((.(((...((((((((((((.(((((.........))))))))))))))))))).)).).)))))))).))))))((((.....)))))((..
..))).((((((..(((....))).)).))))))...((((((((((((.(.(((.....)).).)))).).)))))))).))))).....-3'
MFE = -116.2; z-score = -0.07; ED = 33.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 19--direct_repeat, id-HHV4_LMP-2B-3, 169636-170173(+)

Attributes: ['ID=id-HHV4_LMP-2B-3', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 20 to 200--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 102 to 121--sequence_feature, id-NC_007605.1:170256..170275, 170256-170275(+)

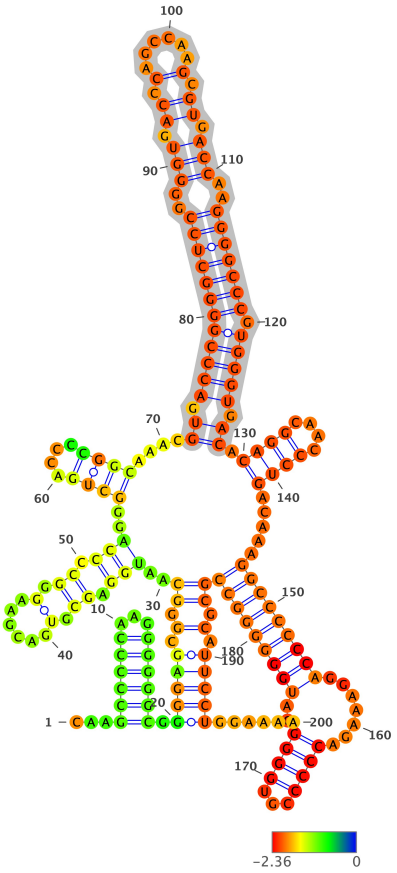
Attributes: ['ID=id-NC_007605.1:170256..170275', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

11-- nt 197 to 200--sequence_feature, id-NC_007605.1:170351..170367, 170351-170367(+)

Attributes: ['ID=id-NC_007605.1:170351..170367', 'Note=EBER2 interaction site B on nascent TR transcript', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 421 from nt 170600 to 170656 (nt 72 to 128)

```
5'-GUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGAC-3'
5'-((.(((((((((((..(((.((.(.......).)).)))..)))))))).)))))).))-3'
Motif MFE = -33.0; z-score = -2.96; ED = 1.86
```



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 170529 to 170728 (motif highlighted in silver):

```
5'-CAAGCCCCCAAGGGGGGCGGGGAGCGGGCAAUGGAGCGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCA
AGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAA-3
5'-...((((((...)))))).(((((.(((..(((.((.(.......).)).)))..((((....)))).....((.((((((((((((..(((.((.(.......).)).))).
.)))))))).)))))).)).((((....)))).....((((((((.......((((...)))).)).))))))))))).).)))))).......-3'
MFE = -98.2; z-score = -2.92; ED = 24.29
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 168--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 169 to 200--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 170697 to 170697--sequence_feature, id-NC_007605.1:170697..170697, 170697-170697(+)

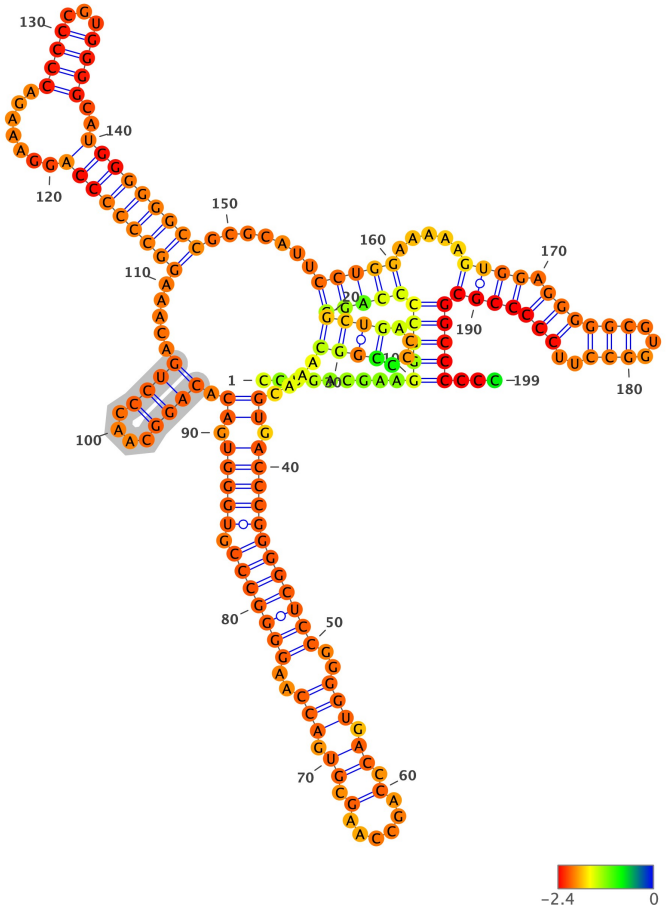
Attributes: ['ID=id-NC_007605.1:170697..170697', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

11-- nt 170705 to 170705--sequence_feature, id-NC_007605.1:170705..170705, 170705-170705(+)

Attributes: ['ID=id-NC_007605.1:170705..170705', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

NC_007605.1 (forward strand): Structure number 422 from nt 170658 to 170669 (nt 94 to 105)

```
5'-CAGGCAACCCUG-3'
5'-((((....))))-3'
Motif MFE = -2.6; z-score = -3.64; 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 170565 to 170763 (motif highlighted in silver):

```
5'-CGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAG
GCCCCCCAGGAAAGACCCCCGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCC-3
5'-.........((((((((((((((....)))).....((.((((((((((((..((((.((.(.(......).)).)))..)))))))).)))))).)).((((....)))).....(
((((((((.......((((...)))))..)))))))))).......)))))).....((((.((((((...)))).)).)))))))))))))...-3'
MFE = -99.5; z-score = -1.92; ED = 43.08
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 132--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 133 to 199--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 170697 to 170697--sequence_feature, id-NC_007605.1:170697..170697, 170697-170697(+)

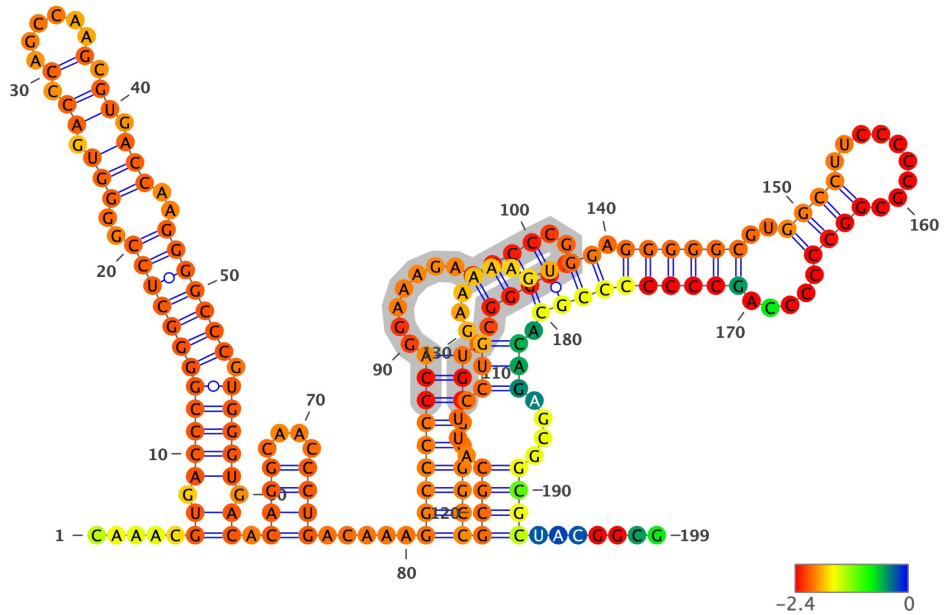
Attributes: ['ID=id-NC_007605.1:170697..170697', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

11-- nt 170705 to 170705--sequence_feature, id-NC_007605.1:170705..170705, 170705-170705(+)

Attributes: ['ID=id-NC_007605.1:170705..170705', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

NC_007605.1 (forward strand): Structure number 423 from nt 170681 to 170706 (nt 87 to 112)

```
5'-CCAGGAAAGACCCCCGUGGGGCAUGG-3'
5'-((........((((...))))...))-3'
Motif MFE = -5.6; z-score = -0.02; 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 170595 to 170793 (motif highlighted in silver):

```
5'-CAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGUGGGGCAUG
GGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCG-3
5'-.....((.(((((((((((..(((.((.(.......)).))).))..)))))))).)))))).))..((((....)))).....(((((((((.......((((...)))))..))
)))))))((((....(((.....((((.(((((((..((((.........)))).....)))))))))).))).....)))).......-3'
MFE = -97.9; z-score = -1.96; ED = 16.39
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 102--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 103 to 199--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 185 to 199--sequence_feature, id-NC_007605.1:170779..170798, 170779-170798(+)

Attributes: ['ID=id-NC_007605.1:170779..170798', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

11-- nt 170697 to 170697--sequence_feature, id-NC_007605.1:170697..170697, 170697-170697(+)

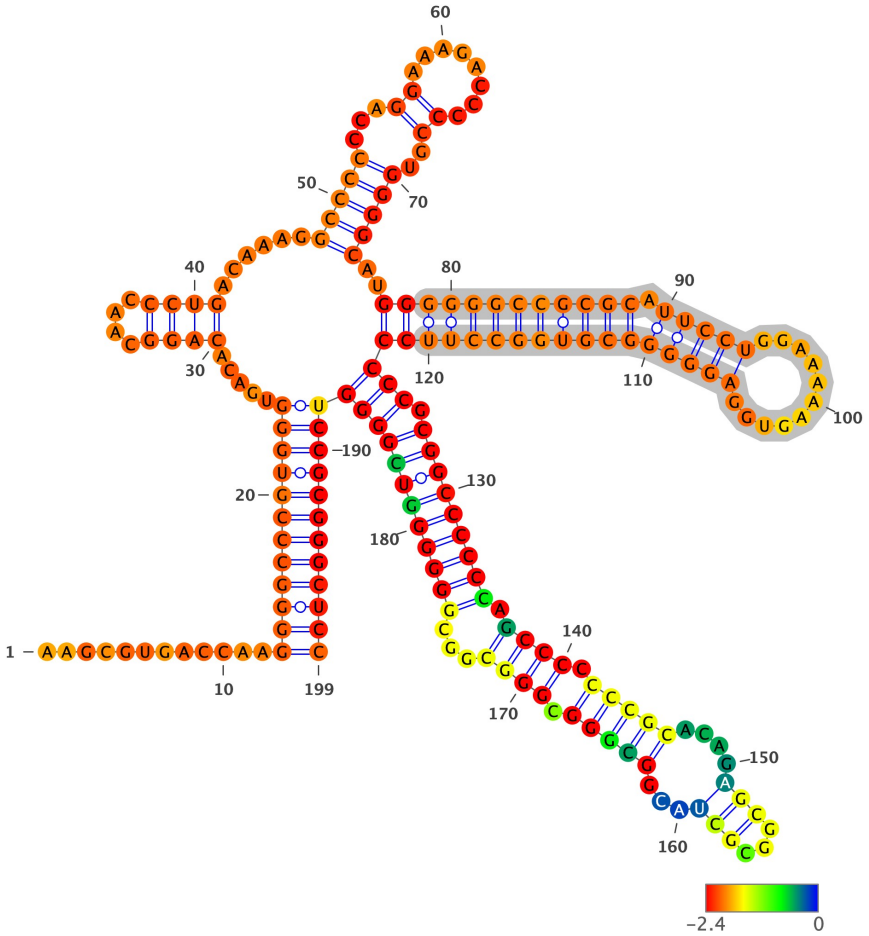
Attributes: ['ID=id-NC_007605.1:170697..170697', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

12-- nt 170705 to 170705--sequence_feature, id-NC_007605.1:170705..170705, 170705-170705(+)

Attributes: ['ID=id-NC_007605.1:170705..170705', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

NC_007605.1 (forward strand): Structure number 424 from nt 170707 to 170748 (nt 79 to 120)

```
5'-GGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUU-3'
5'-(((((.((((.(((((..........)))))))))).)))))-3'
Motif MFE = -22.6; z-score = -4.01; 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 170629 to 170827 (motif highlighted in silver):

```
5'-AAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGG
CGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGGCUCC-3
5'-............((((((((((((.....((((....))))......((((...((........))..)))))..((((((((((((.(((((..........))))))
))))))))))))((((.(((((((((.((((.(((((....((((...)))).....)))))).)))))...))))))))))))))))))))))))))))))))-3'
MFE = -116.1; z-score = -2.96; ED = 15.88
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 68--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 69 to 199--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 151 to 170--sequence_feature, id-NC_007605.1:170779..170798, 170779-170798(+)

Attributes: ['ID=id-NC_007605.1:170779..170798', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

11-- nt 170697 to 170697--sequence_feature, id-NC_007605.1:170697..170697, 170697-170697(+)

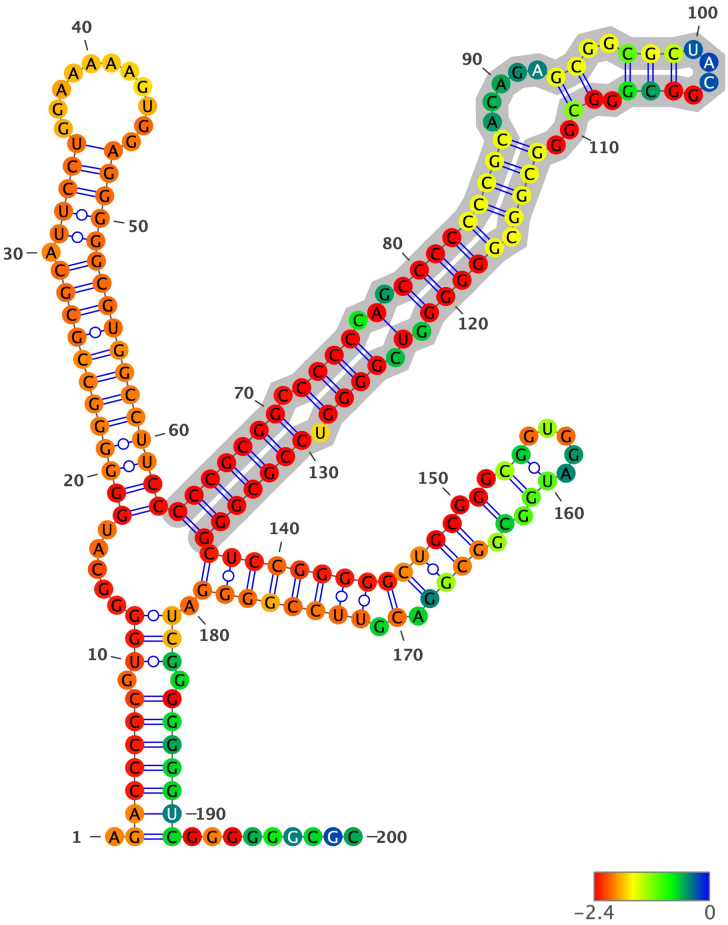
Attributes: ['ID=id-NC_007605.1:170697..170697', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

12-- nt 170705 to 170705--sequence_feature, id-NC_007605.1:170705..170705, 170705-170705(+)

Attributes: ['ID=id-NC_007605.1:170705..170705', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

NC_007605.1 (forward strand): Structure number 425 from nt 170751 to 170823 (nt 64 to 136)

```
5'-CCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGG-3'
5'-(((((((.(((((.(.((((.....................................)))))..).)))).)))))))-3'
Motif MFE = -52.7; z-score = -1.88; ED = 14.67
```



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 170688 to 170887 (motif highlighted in silver):

```
5'-AGACCCCCGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGG
GCGGCGGGGGGUCGGGGUCCGCGGGCUCCGGGGGCUGCGGGCGGUGGAUGGCGGCGGACGUUCCGGGGAUCGGGGGGGUCGGGGGGCGC-3
5'-.(((((((.(((.....((((((((((((.(((((.........))))))))))))))))))))((((((.((((.(.(((((((((.....((..(((....)))).)).)).
))))).)))))).).)))).)))))))((((((((((((((.(.((.....)).).)))).).)).)))))))).))).))))))).........-3'
MFE = -120.9; z-score = -0.66; ED = 9.01
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 9--direct_repeat, id-HHV4_LMP-2B-4, 170174-170696(+)

Attributes: ['ID=id-HHV4_LMP-2B-4', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 10 to 200--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 92 to 111--sequence_feature, id-NC_007605.1:170779..170798, 170779-170798(+)

Attributes: ['ID=id-NC_007605.1:170779..170798', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

11-- nt 187 to 200--sequence_feature, id-NC_007605.1:170874..170890, 170874-170890(+)

Attributes: ['ID=id-NC_007605.1:170874..170890', 'Note=EBER2 interaction site B on nascent TR transcript', 'gbkey=misc_feature']

12-- nt 170697 to 170697--sequence_feature, id-NC_007605.1:170697..170697, 170697-170697(+)

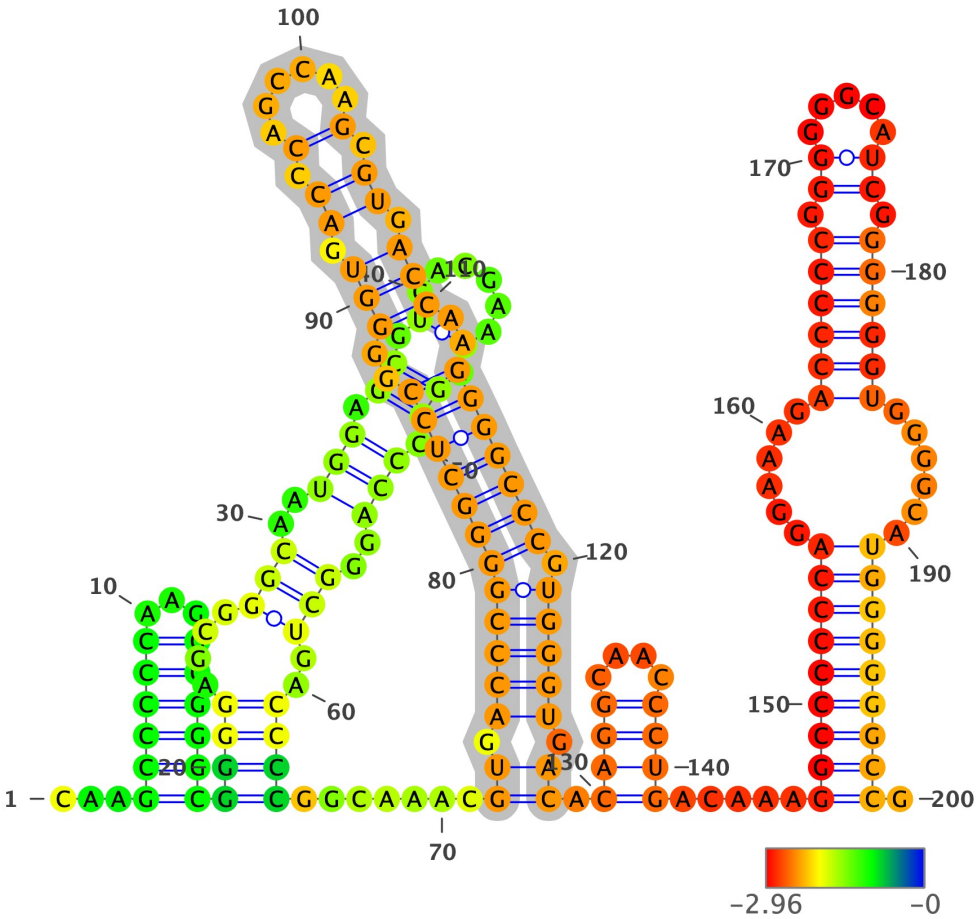
Attributes: ['ID=id-NC_007605.1:170697..170697', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

13-- nt 170705 to 170705--sequence_feature, id-NC_007605.1:170705..170705, 170705-170705(+)

Attributes: ['ID=id-NC_007605.1:170705..170705', 'Note=inter-repeat polymorphism', 'gbkey=misc_feature', 'color=#eb0c0c']

NC_007605.1 (forward strand): Structure number 426 from nt 171123 to 171179 (nt 72 to 128)

```
5'-GUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGAC-3'
5'-((.(((((((((((..(((.((.(.....).)).)))..)))))))).)))))).))-3'
Motif MFE = -33.0; z-score = -3.17; ED = 1.86
```



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 171052 to 171251 (motif highlighted in silver):

```
5'-CAAGCCCCCAAGGGGGGCGGGGAGCGGGCAAUGGAGCGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCA
AGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCG-3
5'-...((((((...))))))((((....((((..((((.((.(.....).)).)))..)))).)))).....((.((((((((((((..(((.((.(.....).)).))).
.)))))))).)))))).)).((((....)))).....(((((((((.....((((((.((.....)).)))))).....)))))))).-3'
MFE = -108.6; z-score = -4.17; ED = 17.55
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 183--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

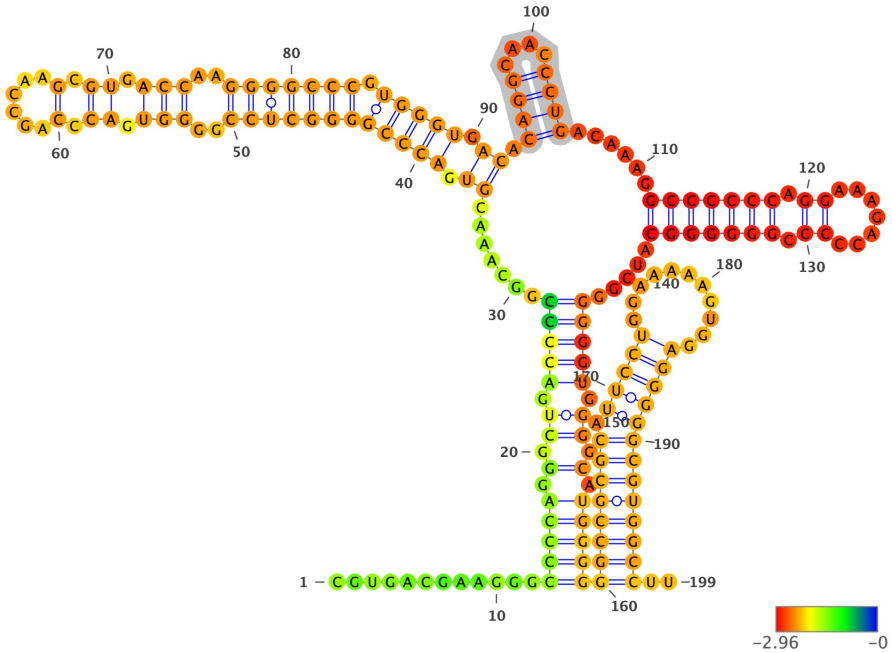
Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 184 to 200--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 427 from nt 171181 to 171192 (nt 94 to 105)

```
5'-CAGGCAACCCUG-3'
5'-((((....))))-3'
Motif MFE = -2.6; z-score = -4.62; 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 171088 to 171286 (motif highlighted in silver):

```
5'-CGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAG
GCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUU-3
5'-............(((((.(.((.(((((.......((.(((((((((((((..((((.((.(.......).)).)))..)))))))).)))))).)).((((....)))).....
(((((((.(.......)).)))))))....)))))).)).).)))))((((((((.((((((..........)))))))))))))..-3'
MFE = -104.4; z-score = -3.71; ED = 10.9
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 147--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

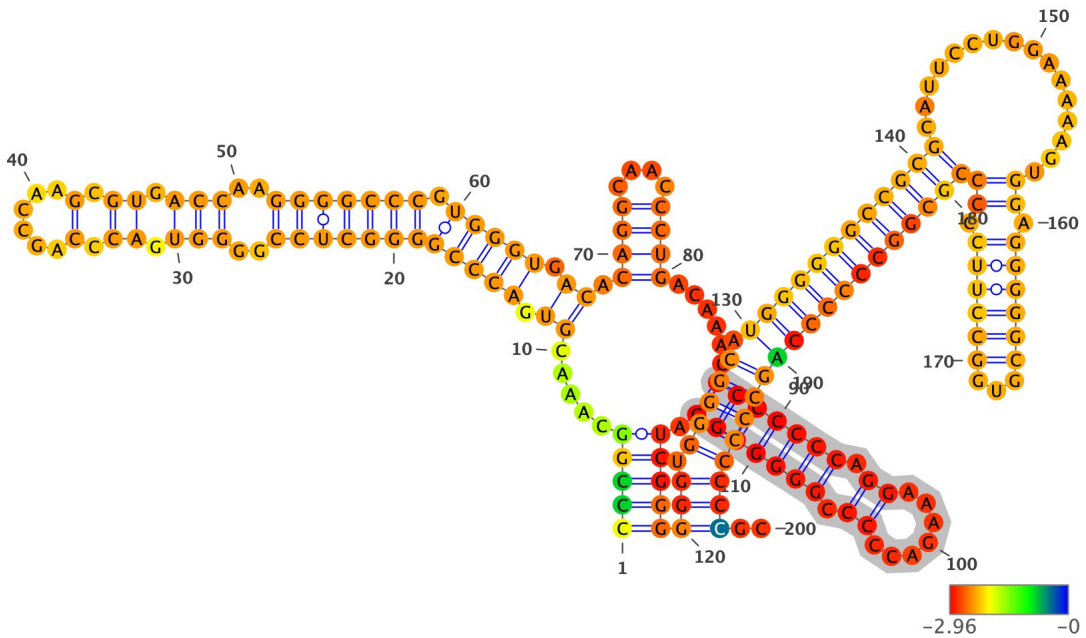
Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 148 to 199--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 428 from nt 171199 to 171225 (nt 87 to 113)

```
5'-GCCCCCCAGGAAAGACCCCCGGGGGGC-3'
5'-(((((((.((.......)).)))))))-3'
Motif MFE = -18.2; z-score = -3.68; ED = 2.29
```



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

Extracted structure model with flanking nucleotides 171113 to 171312 (motif highlighted in silver):

```
5'-CCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGG
GCAUCGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGC-3
5'-(((((.....((.(((((((((((..(((.((.(......).)).)))..)))))))).)))))).)).((((....)))).....(((((((.((.......)).)))))
)).)))))((.(((((.((((((((((((.................((.(((((...))))))).))))))))))))))))))))..-3'
MFE = -119.8; z-score = -4.07; ED = 16.26
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 122--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

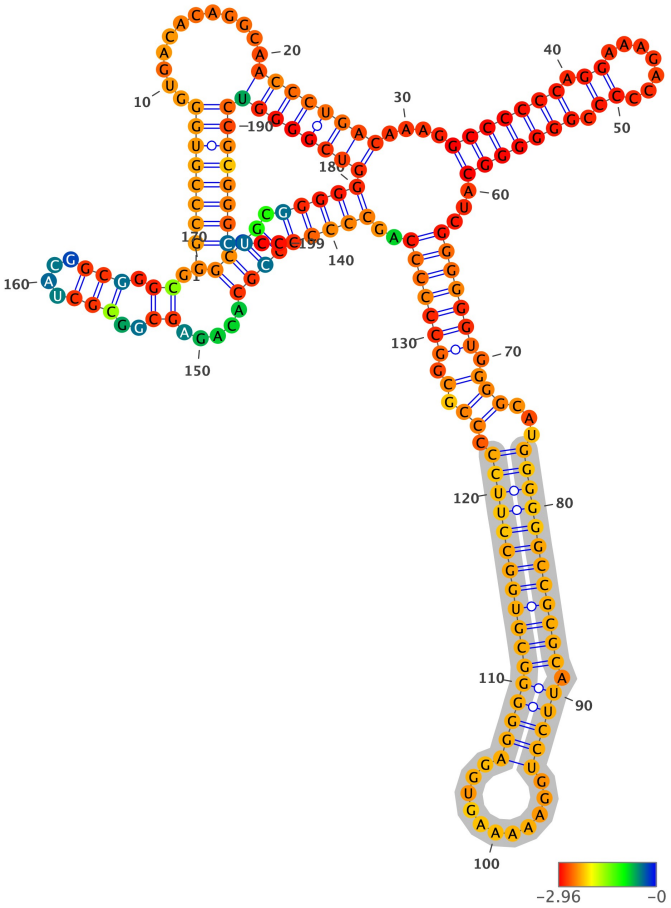
Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 123 to 200--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

NC_007605.1 (forward strand): Structure number 429 from nt 171243 to 171288 (nt 77 to 122)

```
5'-GGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCC-3'
5'-(((((((((((.(((((.........)))))))))))))))))-3'
Motif MFE = -27.7; z-score = -4.41; 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 171167 to 171365 (motif highlighted in silver):

```
5'-GCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGG
CGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUACGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGGCUCC-3
5'-(((((((((.........((((((((....(((((((.((.......)).)))))))...(((((((.(((...((((((((((((.(((((.........))))))
))))))))))).)).).))))))).((((((((.....((..((((....)))).)).)).)))).))))))))))))))))))))...-3'
MFE = -123.9; z-score = -3.49; ED = 34.07
```

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

1-- nt 1 to 199--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 199--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 199--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 199--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 199--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 199--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 199--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct',

'rpt_unit_range=169636..170173']

8-- nt 1 to 68--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 69 to 199--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

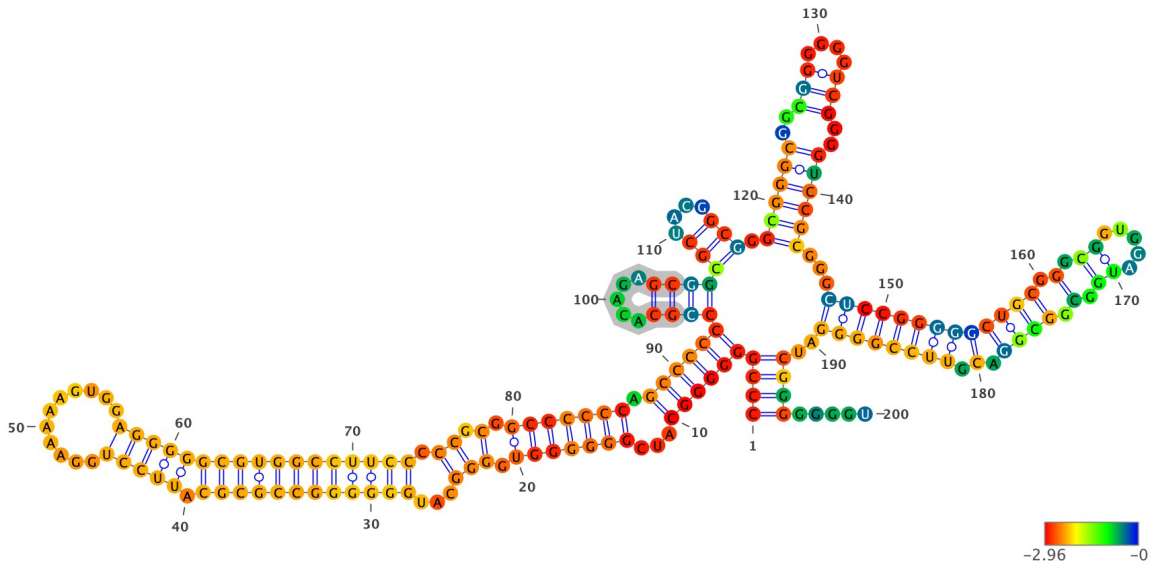
Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 151 to 170--sequence_feature, id-NC_007605.1:171317..171336, 171317-171336(+)

Attributes: ['ID=id-NC_007605.1:171317..171336', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 430 from nt 171311 to 171319 (nt 96 to 104)

```
5'-GCACAGAGC-3'
5'-((.....))-3'
Motif MFE = 0.0; z-score = 0.22; 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 171216 to 171415 (motif highlighted in silver):

```
5'-CCCGGGGGGCAUCGGGGGGUGGGGCAUGGGGGGCCGCGCAUUCCUGGAAAAAGUGGAGGGGGCGUGGCCUUCCCCCGCGGCCCCCCAGCCCCCCCGCACAGAGCGGCGCUA
CGGCGGGCGGGCGGCGGGGGGUCGGGGUCCGCGGGCUCCGGGGGCUGCGGGCGGUGGAUGGCGGCGGACGUUCCGGGGAUCGGGGGGGU-3
5'-(((((((((...(((((((.(((...((((((((((((.(((((.........))))))))))))))))))).)).).)))))))).))))))((((.....)))))((..
..))).((((((..(((....))).)).))))))...((((((((((((.(.(((.....)).).)))).).)))))))).))))).....-3'
MFE = -116.2; z-score = -0.23; ED = 33.48
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 200--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 19--direct_repeat, id-HHV4_LMP-2B-5, 170697-171234(+)

Attributes: ['ID=id-HHV4_LMP-2B-5', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

9-- nt 20 to 200--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']

10-- nt 102 to 121--sequence_feature, id-NC_007605.1:171317..171336, 171317-171336(+)

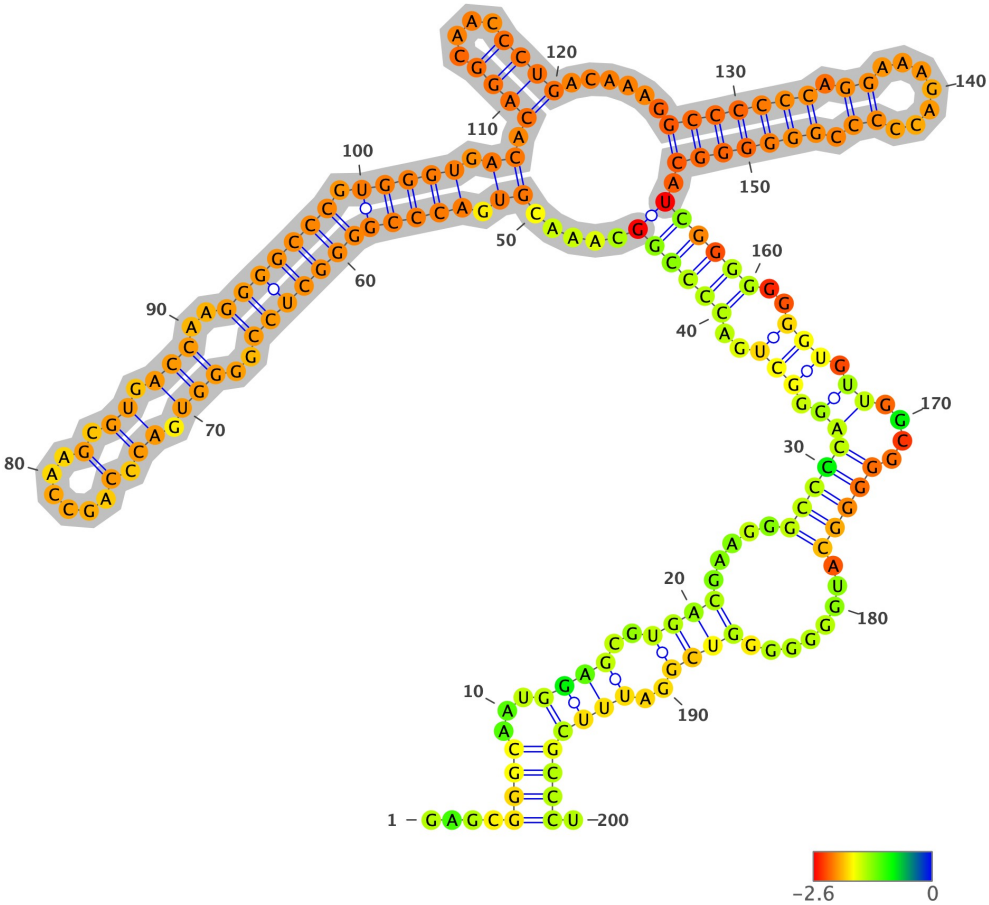
Attributes: ['ID=id-NC_007605.1:171317..171336', 'Note=EBER2 interaction site A on nascent TR transcript', 'gbkey=misc_feature']

11-- nt 197 to 200--sequence_feature, id-NC_007605.1:171412..171428, 171412-171428(+)

Attributes: ['ID=id-NC_007605.1:171412..171428', 'Note=EBER2 interaction site B on nascent TR transcript', 'gbkey=misc_feature']

NC_007605.1 (forward strand): Structure number 431 from nt 171655 to 171765 (nt 45 to 155)

```
5'-GCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAGGCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAU
-3'
5'-(.....((.(((((((((((..(((.((.(.....).)).)))..)))))))).)))))).)).((((....)))).....(((((((.(.....)).)))))))).)
-3'
Motif MFE = -57.8; z-score = -4.13; 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 171611 to 171810 (motif highlighted in silver):

```
5'-GAGCGGGCAAUGGAGCGUGACGAAGGGCCCCAGGGCUGACCCCGGCAAACGUGACCCGGGGCUCCGGGGUGACCCAGCCAAGCGUGACCAAGGGGCCCGUGGGUGACACAG
GCAACCCUGACAAAGGCCCCCCAGGAAAGACCCCCGGGGGGCAUCGGGGGGGGUGUUGGCGGGGGCAUGGGGGGGUCGGAUUUCGCCCU-3
5'-....((((...((((..((((.....(((((((.(((..((((((.....((.((((((((((((..(((.((.(.....).)).)))..)))))))).)))))).)).(((
(....))))......(((((((.(.....)).)))))))).)))))).))...)).)....)))))........))))..)))))))).-3'
MFE = -93.7; z-score = -1.45; ED = 24.82
```

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

1-- nt 1 to 200--region, NC_007605.1:1..171823, 1-171823(+)

Attributes: ['ID=NC_007605.1:1..171823', 'Dbxref=taxon:10376', 'Is_circular=true', 'acronym=HHV-4', 'common=Epstein-Barr virus', 'gbkey=Src', 'mol_type=genomic DNA', 'nat-host=Homo sapiens', 'strain=Raji', 'type=1']

2-- nt 1 to 200--region, id-NC_007605.1:1..171823, 151555-311546(+)

Attributes: ['ID=id-NC_007605.1:1..171823', 'gbkey=Src']

3-- nt 1 to 200--mRNA, rna-NC_007605.1:58..166458, 166040-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..166458', 'gbkey=mRNA']

4-- nt 1 to 200--mRNA, rna-NC_007605.1:58..169448, 169294-177679(+)

Attributes: ['ID=rna-NC_007605.1:58..169448', 'gbkey=mRNA']

5-- nt 1 to 200--gene, gene-HHV4_LMP-2A, 166011-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2A', 'Dbxref=GeneID:3783751', 'Name=LMP-2A', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2A', 'gene_biotype=other', 'locus_tag=HHV4_LMP-2A']

6-- nt 1 to 200--gene, gene-HHV4_LMP-2B, 169294-177679(+)

Attributes: ['ID=gene-HHV4_LMP-2B', 'Dbxref=GeneID:3783760', 'Name=LMP-2B', 'Note=LMP-2 family', 'gbkey=Gene', 'gene=LMP-2B', 'gene_biotype=protein_coding', 'locus_tag=HHV4_LMP-2B']

7-- nt 1 to 162--direct_repeat, id-HHV4_LMP-2B-2, 169636-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-2', 'Dbxref=GeneID:3783760', 'gbkey=repeat_region', 'gene=LMP-2B', 'locus_tag=HHV4_LMP-2B', 'rpt_family=TR', 'rpt_type=direct', 'rpt_unit_range=169636..170173']

8-- nt 1 to 162--direct_repeat, id-HHV4_LMP-2B-6, 171235-171772(+)

Attributes: ['ID=id-HHV4_LMP-2B-6', 'gbkey=repeat_region', 'rpt_family=TR', 'rpt_type=direct']