```
                                   .                                              .
dISFV-NC_024017.1  UCGCGCAUUUUGAUAGAGUUGACUAGAUAACGAAUUAUCG------AUG---------GU  45
dISFV-NC_017086.1  AUAACACGUUUGAAUAGAGUUUAUUGUGAAUCGAAAUACCG------AUG--------GC  45
dISFV-NC_016997.1  AAACAUAACGCAUUAGAAUAGGUUUGAAAGAGUUGAAUCA------AUGAGAUCAAUGGU  54
dISFV-NC_040610.1  GAACAAUUUUAAAGAAGUCAAAACUAGAAAUUUAAUUUCA------AUG---------GU  45
dISFV-NC_027999.1  GGAUUAAUUGUUGUUUGAGAGAACAGCGAGAAGUACUACU------AUG---GUUGAGAA  51
TBFV-NC_027709.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGUC  54
TBFV-NC_001672.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGUCAAGAAGGC  54
TBFV-NC_001809.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGGCAGGAAGGC  54
TBFV-NC_005062.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGG------AUGGCCGGGAAGGC  54
TBFV-NC_003690.1   GUGUUGAGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGA------AUGGCCGGGAAGGC  54
TBFV-NC_003687.1   ------AGAAAAAGACAGCUUAGGAGAACAAGAGCUGGGAGUGGUUAUG------AUGAC  48
                   .........10........20........30........40........50.......6

                                   .                                              .
dISFV-NC_024017.1  GACUAAAUCAAGAAAGCCCGCCGCAAAGCGGGCUGUUAAUAUGCUAACAC--GCAUCACC  103
dISFV-NC_017086.1  GAAUAAACCCAAGAAGC---CCGGAAGACGGGCUAUCGAUAUAGUGAGACGUGCGUUGCC  102
dISFV-NC_016997.1  CUUUCGAGCUAGGAGGC---CCGUUAAACGGGCCGUCGAUAUAAUAAAACGUAAGCUGC-  110
dISFV-NC_040610.1  UAGACAACUUGGAACCGUUGUCAUUGUCAAUAUGCGAAAGCGG--AUUACC  103
dISFV-NC_027999.1  AACUAGAGUAGGAUCUCGGGUUUAAAACCCGAGGUGUCAAUAUGAUUAGGCGUAC------  105
TBFV-NC_027709.1   CAUCCUGAAAGGUAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGACCG----C  108
TBFV-NC_001672.1   CAUCCUGAAAGGUAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGACCG----C  108
TBFV-NC_001809.1   CAUCCUGAAAGGCAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGACCG----C  108
TBFV-NC_005062.1   CAUUCUGAAAGGAAAGGGGGGCGGUCCCC--CUCGACGAGUGUCGAAAGAGACCG----C  108
TBFV-NC_003690.1   CGUUCUAAAAGGAAAGGGGGGGCGGUCCCC--CUCGACGAGCGUCGAAAGUGGCCC----C  108
TBFV-NC_003687.1   CACUUCUAAAGGAAAGGGGGGCGGUCCCC--CUAGGCGCAAGCUUAAAGUGACCG----C  102
                   0........70........80........90........100......110.......1

                                                                               ((((.
dISFV-NC_024017.1  AAGCGU-GNNNNNNNN-------CCCCACUGCUGAGAGCAAAAUAGCAUAUUUGACACUUGG  155
dISFV-NC_017086.1  UCGCGUCUNNNNNNNNAGAGGAGACCCCCCCAAAAAUGAAGGGCACUAUAUCGACACUUGG  162
dISFV-NC_016997.1  --------NNNNNNNAGGAAACCCCCCCAAAAAUGUAUAGGCUAUUAUAUCGACACCUAG  162
dISFV-NC_040610.1  ACCCG-CUNNNNNNNNA------CCCCCUCAUUAUUUAUAUAACAGCAUAUUUGACACCAGG  156
dISFV-NC_027999.1  ---UGGAANNNNNNNUGGCGAACCCCAUUGGAAAUU---UAGCUUCAUAUUGACACCAGG  159
TBFV-NC_027709.1   AA------NNNNNNNCUCUCUUCAGGAUUUUUUCCUCCUCCUAUACCAAA-UUCCCCCUCG  161
TBFV-NC_001672.1   AA------NNNNNNNCUCUCUUCAGGAUUUUUUCCUCCUCCUAUACCAAAA-UUCCCCCUCG  161
TBFV-NC_001809.1   GA------NNNNNNNN-UCUCUUCAGGGUUUUUUCCUCCUCCUAUACCAAAUUUCCCCCUCG  161
TBFV-NC_005062.1   UA------NNNNNNNCUCUCUUCAGGAAAUUUCCUCCUCCUAUACCAAA-UUCCCCCUCA  161
TBFV-NC_003690.1   AA------NNNNNNNCUCUCUUCAGGAUAUUUCCUCCUCCUAUACCAAA-UUCCCCCUCG  161
TBFV-NC_003687.1   AAAUAAGUNNNNNNNCU-UCCUCGGGAUUUUUUCCGCCUCCUAUACUAAAUUUCCCCCAGG  161
                   20.......130.......140.......150.......160.......170.......1

                   ...))))).....(((((....(((((...((.((((.((((((((((((...(((.........))
dISFV-NC_024017.1  GAAGAGACCAGAAGAUAUGAUGUUGUUUGUCAAUGCUGACAACAGCCAUGGCACAGAGCGC  215
dISFV-NC_017086.1  GAA-AGACCAGAGGGUACUCGCUGAUUCACCGCC---ACCAGACUACACGGGCACAGCGCCGC  218
dISFV-NC_016997.1  GAA-AGACUGGAGAUACCUUUGAUUGUUCUUCGA---CACUAACUCCUAAUGGCACAGAGCGC  218
dISFV-NC_040610.1  G-AUAGACCUGAGAGAAAUACACAAUUUCUGGGCACUAAAACAACUAC--AAGCACAGAGCGC  213
dISFV-NC_027999.1  GAAAAGACCGGACGAAACUUCUUGCUUACUGGGCAGCAACCACCGA--AGGCACAGUAUGC  217
TBFV-NC_027709.1   ACAGAGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCC---AGACACAGAUAGU  218
TBFV-NC_001672.1   GUAGAGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCC---AGACACAGGUAGU  218
TBFV-NC_001809.1   ACAGAGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCC---AGACACAGAUAGU  218
TBFV-NC_005062.1   UCUGAGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCC---AGACACAGGCAGU  218
TBFV-NC_003690.1   UCAGAGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCAUCACCU--AGACACAGAUAGU  218
TBFV-NC_003687.1   AAACUGG-GGGGGCGGUUCUUGUUCUCCCCUGAGCCACCACCAUCC--AGGCACAGAUAGC  218
                   80.......190.......200.......210.......220.......230.......2

                   ))........)))))))))).)))).))).)).)...))))....)))))...
dISFV-NC_024017.1  CUGAAGAGAGCUGUUGU-UAUAAUUUACAAAAAAUAACAUAUCU---  258
dISFV-NC_017086.1  CGGAAAAGGUAGUUUGG----AGGUUGUAAAACAACAAGUAUCU---  258
dISFV-NC_016997.1  CAUAAGAAACGGAGUUA-GU---AUGGAAAAAACAUAAGUAUCU---  258
dISFV-NC_040610.1  UUCGAGA-AGUAGUUGU-UUCUUGACGAGAGAAUAUGUAUAUCUUGG  258
dISFV-NC_027999.1  CUGAA-ACAUUCUGUGU-UUGAUGU-AGUAAACAACCAGUUUCU---  258
TBFV-NC_027709.1   CUGACAAGGAGGUGAUGCGUGACUC-GGAAAAACAC---CCGCU---  258
TBFV-NC_001672.1   CUGACAAGGAGGUGAUGUGUGACUC-GGAAAAACAC---CCGCU---  258
TBFV-NC_001809.1   CUGACAAGGAGGUGAUGUGUGACUC-GGAAAAACAC---CCGCU---  258
TBFV-NC_005062.1   CUAACAAGGAGGUGAUGUGUGACUC-GGAACAACAC---CCGCU---  258
TBFV-NC_003690.1   CUGACAAGGAGGUGAUGCGUGUCUC-GGAAAAACAC---CCGCU---  258
TBFV-NC_003687.1   CUGACAAGGAGAUGGUGUGUGACUC-GGAAAAACAC---CCGCU---  258
                   40.......250.......260.......270.......280.....
```