> File PDB_00795.ct. RNA SSTRAND database. External source: RCSB Protein Data Bank 1VSA, number of molecules: 2. The secondary structure annotation was obtained with RNAview.

length 3009

kmer length: 250

GGUCAAGAUGGUAAGGGCCCACGGUGGAUGCCUCGGCACCCGAGCCGAUGAAGGACGUGGCUACCUGCGAUAAGCCAGGGGGAGCCGGU GAACUGAAACAUCUCAGUACCCAGAGGGAGAGGAAAGGGAAAUCGACUCCCUGAGUAGCGGCGGAGAGGGGACCAGCCUAAACCGUC CGGCUUGUCCGGGCGGGGUCGUGGGGCCCUCGGACACCGAAUCCCCAGCCUAGCCGAAGCUGUUGGGAAGCAGCGCCAGAGAGGGGUGAA AGCCCCGUAGGCGAAAGGUGGGGGGAUAGGUGAGGGUACCCGAGUACCCCGUGGUUCGUGGAGCCAUGGGGGAAUCUGGGCGGACCACC GCCUAAGGCUAAGUACUCCGGGUGACCGAUAGCGCACCAGUACCGUGAGGGAAAGGUGAAAAGAACCCCGGGAGGGGAGUGAAAUAGAG CCUGAAACCGUGGGCUUACAAGCAGUCACGGCCCCGCAAGGGGUUGUGGCGUGCCUAUUGAAGCAUGAGCCGGCGACUCACGGUCGUGG GCGAGCUUAAGCCGUUGAGGCGGAGGCGUAGGGAAACCGAGUCCGAACAGGGCGUCUAGUCCGCGGCCGUGGACCCGAAACCGGGCGAG CUAGCCCUGGCCAGGGUGAAGCUGGGGUGAGACCCAGUGGAGGCCCGAACCGGUGGGGGAUGCAAACCCCUCGGAUGAGCUGGGGCUAG GAGUGAAAAGCUAACCGAGCCCGGAGAUAGCUGGUUCUCCCCGAAAUGACUUUAGGGUCAGCCUCAGGCGCUGACUGGGGCCUGUAGAG CACUGAUAGGGCUAGGGGGCCCACCAGCCUACCAAACCCUGUCAAACUCCGAAGGGUCCCAGGUGGAGCCUGGGAGUGAGGGCGCGAGC GAUAACGUCCGCGUCCGAGCCGCGGAACAACCGAGACCGCCAGCUAAGGCCCCCAAGUCUGGGCUAAGUGGUAAAGGAUGUGGCCCCCC GAAGACAGCCAGGAGGUUGGCUUAGAAGCAGCCAUCCUUUAAAGAGUGCGUAAUAGCUCACUGGUCGAGUGGCGCCGCGCCGAAAAUGA UCGGGGCUCAAGCCCAGCGCCGAAGCUGCGGGUCUGGGGGAUGACCCCAGGCGGUAGGGGAGCGUUCCCGAUGCCGAUGAAGGCCGACC CGCGAGGGCGGCUGGAGGUAAGGGAAGUGCGAAUGCCGGCAUGAGUAACGAUAAAGAGGGUGAGAAUCCCUCUCGCCGUAAGCCCAAGG GUUCCUACGCAAUGGUCGUCAGCGUAGGGUUAGGCGGACCUAAGGUGAAGCCGAAAGGCCGAAGGGCAGCCGGUUAAUAUUCC GGCCCUUCCCGCAGGUGCGAUGGGGGACGCUCUAGGCUAGGGGGACCGGAGCCAUGGACCGGCCCAGAAGCCGCAGGGUGGGAGG UAGGCAAAUCCGCCUCCCAAAAGCUCUGCGUGGUGGGGAAGCCCGUACGGGUGACAACCCCCCGAAGCCAGGGAGCCAAGAAAAGCCUC UAAGCACAACCUGCGGGAACCCGUACCGCAAACCGACACAGGUGGGCGGGUGCAAGAGCACUCAGGCGCGCGGGAGAACCCUCGCCAAG GAACUCUGCAAGUUGGCCCCGUAACUUCGGGAGAAGGGGUGCUCCCUGGGGUGAUGAGCUCCGGGGAGCCGCAGUGAACAGGCUCUGGC GACUGUUUACCAAAAACACAGCUCUCUGCGAACUCGUAAGAGGGGGGUAUAGGGGAGCGCUUGCCCGGUGCCGGAAGGUCAAGGGGAG GGGUGCAAGCCCCGAACCGAAGCCCCGGUGAACGGCCGCCGUAACUAUAACGGUCCUAAGGUAGCGAAAUUCCUUGUCGGGUAAGUUCC GACCUGCACGAAAAGCGUAACGACCGGAGCGCUGUCUCGGCGAGGGACCCGGUGAAAUUGAACUGGCCGUGAAGAUGCGGCCUACCCGU GGCAGGACGAAAAGACCCCGUGGAGCUUUACUGCAGCCUGGUGUUGGCUCUUGGUCGCGCCUGCGUAGGAUAGGUGGGAGCCUGUGAAC CCCCGCCUCCGGGUGGGGGGGGGCGCCGGUGAAAUACCACCCUGGCGCGGCUGGGGGCCUAACCCUCGGAUGGGGGGACAGCGCUUGG GCAAGGGUAGAAGGGGGCCUGACUGCGAGGCCUGCAAGCCGAGCAGGGGCGAAAGCCGGGCCUAGUGAACCGGUGGUCCCGUGUGGAAG GGCCAUCGAUCAACGGAUAAAAGUUACCCCGGGGAUAACAGGCUGAUCUCCCCCGAGCGUCCACAGCGGCGGGGAGGUUUGGCACCUCG AUGUCGGCUCGCAUCCUGGGGCUGAAGAAGGUCCCAAGGGUUGGGCUGUUCGCCCAUUAAAGCGGCACGCGAGCUGGGUUCAGAAC GUCGUGAGACAGUUCGGUCUCUAUCCGCCACGGGCGCAGGAGGCUUGAGGGGGCUCUUCCUAGUACGAGAGGACCGGAAGGGACGCAC CUCUGGUUUCCCAGCUGUCCCUCCAGGGGCAUAAGCUGGGUAGCCAUGUGCGGAAGGGAUAACCGCUGAAAGCAUCUAAGCGGGAAGCC CGCCCCAAGAUGAGGCCUCCCACGGCGUCAAGCCGGUAAGGACCCGGGAAGACCCGGUGGAUGGGCCGGGGGUGUAAGCGCCGCGA GGCGUUGAGCCGACCGGUCCCAAUCGUCCGAGGUCUUGACCUCCCCCGUGCCCAUAGCGGCGUGGAACCACCCGUUCCCAUUCCGAACA CGGAAGUGAAACGCGCCAGCGCCGAUGGUACUGGGCGGCGACCGCCUGGGAGAGUAGGUCGGUGCGGGGGA

Assembly result: Wrong sequence highlited

GGUCAAGAUGGUAAGGGCCCACGGUGGAUGCCUCGGCACCCGAGCCGAUGAAGGACGUGGCUACCUGCGAUAAGCCAGGGGGAGCCGGU CGGCUUGUCCGGGCGGGGUCGUGGGGCCCUCG<mark>GACCAGCCUAAACCGUCCGGCUUGUCCGGGCGGGGUCGUGGGGCCCUCG</mark>GACACCGA AUCCCCAGCCUAGCCGAAGCUGUUGGGAAGCAGCGCCAGAGAGGGGGGAAAGCCCCGUAGGCGAAAGGUGGGGGGAUAGGUGAGGGUACC CGAGUACCCCGUGGUUCGUGGAGCCAUGGGGGAAUCUGGGCGGACCACCGCCUAAGGCUAAGUACUCCGGGUGACCGAUAGCGCACCAG GGGUUGUGGCGUGCCUAUUGAAGCAUGAGCCGGCGACUCACGGUCGUGGGCGAGCUUAAGCCGUUGAGGCGGAGGCGUAGGGAAACCGA GUCCGAACAGGGCGUCUAGUCCGCGGCCGUGGACCCGAAACCGGGCGAGCUAGCCCUGGCCAGGGUGAAGCUGGGGUGAGACCCAGUGG AGGCCCGAACCGGUGGGGGAUGCAAACCCCUCGGAUGAGCUGGGGCUAGGAGUGAAAAGCUAACCGAGCCCGGAGAUAGCUGGUUCUCC CCGAAAUGACUUUAGGGUCAGCCUCAGGCGCUGACUGGGGCCUGUAGAGCACUGAUAGGGCUAGGGGGCCCACCAGCCUACCAAACCCU CAGCUAAGGCCCCAAGUCUGGGCUAAGUGGUAAAGGAUGUGGCGCCGCGAAGACAGCCAGGAGGUUGGCUUAGAAGCAGCCAUCCUUU AAAGAGUGCGUAAUAGCUCACUGGUCGAGUGGCGCCGCCGAAAAUGAUCGGGGCUCAAGCCCAGCGCCGAAGCUGCGGGUCUGGGGG AUGACCCCAGGCGGUAGGGGAGCGUUCCCGAUGCCGAUGAAGGCCGACCCGCGAGGCGGCUGGAGGUAAGGGAAGUGCGAAUGCCGGC AUGAGUAACGAUAAAGAGGGUGAGAAUCCCUCUCGCCGUAAGCCCAAGGGUUCCUACGCAAUGGUCGUCAGCGUAGGGUUAGGCGGGAC CUAAGGUGAAGCCGAAAGGCGUAGCCGAAGGGCAGCCGGUUAAUAUUCCGGCCCUUCCCGCAGGUGCGAUGGGGGGACGCUCUAGGCUA GGGGGACCGGAGCCAUGGACGAGCCCGGCCAGAAGCGCAGGGUGGGAGGUAGGCAAAUCCGCCUCCCAAAAGCUCUGCGUGGUGGGGAA GCCCGUACGGGUGACAACCCCCCGAAGCCAGGGAGCCAAGAAAAGCCUCUAAGCACAACCUGCGGGAACCCGUACCGCAAACCGACACA GGUGGGCGGGUGCAAGAGCACUCAGGCGCGGGAGAACCCUCGCCAAGGAACUCUGCAAGUUGGCCCCGUAACUUCGGGAGAAGGGGU GCUCCCUGGGGUGAUGAGCUCCGGGGAGCCGCAGUGAACAGGCUCUGGCGACUGUUUACCAAAAACACAGCUCUCUGCGAACUCGUAAG AGGAGGUAUAGGGAGCGACGCUUGCCCGGUGCCGGAAGGUCAAGGGGGAGGGGUGCAAGCCCCGAAGCCCCGGUGAACGGCGGCC GUAACUAUAACGGUCCUAAGGUAGCGAAAUUCCUUGUCGGGUAAGUUCCGACCUGCACGAAAAGCGUAACGACCGGAGCGCUGUCUCGG CGAGGGACCCGGUGAAAUUGAACUGGCCGUGAAGAUGCGGCCUACCCGUGGCAGGACGAAAAGACCCCGUGGAGCUUUACUGCAGCCUG CCCUGGCGCGGCUGGGGGCCUAACCCUCGGAUGGGGGGACAGCGCUUGGCGGGCAGUUUGACUGGGGCGGUCGCCUCCUAAAAGGUAAC