



```
>NC_009964
GCUUGUUUUGCAUUUG-----CAAAGCCCAAGGUGCUAAAUCCAGCAAGCGUUUUUAGCUUGGAAGAUAGAAGAAGCGU--UAAACCCCUUCUUAUGAAGAAAGGGUUUUUA
>NC_009725
GUUJGUUUUGCCGGGAAGGCAAGGUGCAAAAGGUGCAAAUCCAGCAAGCGAUUUCACAGCUUGGAAGAUAGAAGGAAGAGA--AAAGCUCCUUCUUAUGAAGAAAGGGGCUUUUU
```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
```

```
#yxD
#The following shows an alignment in 5'-UTR of yxD and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
UUGGACUGUAGCCGAGAGAAAAACAUAAGCAGCUUGGCUUUUAGACACAGCGGUGGAUAAAGCCAGGAGUUUCUGCUCUUU--UCGAGAGCGUUCUCCU-GGGUUUUUUUUUUUGCU
>NC_014479
UUGGACUGUAGCCGAGAGAAAAACAUAAGCAGCCCGGCGUUUAUGACACAGCGGUGGAUAAAGCCAGGAGUUUCUGCUCUUU--GCGAGAGCGUACUCU--GGUUUUUUUUUGUU----
>NC_009725
UUGGUCUG-GACCGAGAGAAAAACAUAAGCAGCGUUC-CUGCUGUGACACAGCGUUGGGUAUAAAGCCCGGAGUUUCUGCUCUUUUAUAGAAGAGUGCUCUCC--GGCUUUUUUUGAU----
>NC_014551
UUGGUCUG-GACCGAGAGAAAAACAUAAGCAGCGUUC-UJGUCUGUGACACAGCGGUGGAUAAAGCCCGGAGUUUCUGCUCUUUUAUAGAAGAGUGCUCUCCCGGGCUUUUUUGAU----
>NC_006270
CUGGUCUG-GUCCGAGAGAAAAACAUAAGCGAAGUA-JCGUUUAGACACAGCGGUGGAUAAAGCCAGGAGUUUUGCUCUUAU--CAAAGAGCUUCUCUGCGGGCUUUUUUACUUUUU
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))..
..(((((((.....))))))(((((((.....)))))).....(((((((.....))))))(((((((.....))))))..
```

```
#ileS
#The following shows an alignment in 5'-UTR of ileS and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_011658
UACGUGCUAAGUGCUAUUAGUGAAGA-GCUAAUAGAA-UUAGGGUGGUUUCGCGGGUAA-CCCGUCCUUAUUUAUAGGGACGGGUUU-UUUUGUGUGCUUU-AAAACAUAUCAA
>NC_005957
UACGUGCUAAGUGCUAUUAGUGAAGA-ACUAAUAGAA-UUAGGGUGGUUUCGCGGGUAG-CCCGUCCUACUUUAUAGGGACGGUUUU-UUUUGUGUGCUUU-AAAACAUAUCAA
>NC_008600
UACGUGCUAAGUGCUAUUAGCGAAGA-GCUAAUAGAA-UUAGGGUGGUUUCGCGGGUAA-CCCGUCCUACUUCAUAGGGACGGGUUU-UUUUGUGUGCUUU-AAAACAUAUCAA
>NC_011725
UACGUGCUAAGUGCUAUUAGUAAAAUAGUAGAA-UUAGGGUGGUUUCGCGGGUAA-CCCGUCCUACUUUAUAGGGACGGGUUU-UUUUGUGUGCUUU-AAAACAUAUCAA
>NC_011772
UACGUGCUAAGCGCUAUUAGUGAAGAA-GCUAAUAGAA-UUAGGGUGGUUUCGCGGGUAA-CCCGUCCUACUUCAUAGGGACGGGUUU-UUUUGUGUGCUUU-AAAACAUAUCAA
>NC_014019
UACGUGCUGAGUCUUAUUGAUAACGGAUCAUAGAAGCCAGGUGGUACCGCGGUUAAACCCGUCUAGU-CAUAGGGACGGGUUUUCUUAUGUGUGCUUU--UAAC-UUUUAAA
```

```
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....(((((((.....))))))..-))..(((((((.....))))))..-))..(((((((.....))))))..-))..
.....(((((((.....))))))..-))..(((((((.....))))))..-))..(((((((.....))))))..-))..
.....(((((((.....))))))..-))..(((((((.....))))))..-))..(((((((.....))))))..-))..
.....(((((((.....))))))..-))..(((((((.....))))))..-))..(((((((.....))))))..-))..
.....(((((((.....))))))..-))..(((((((.....))))))..-))..(((((((.....))))))..-))..
```





```
AGUGGAACCGCGCUUAAAAGCGGUCUGUCAUUGACAGAGCGGUUUUUUUUAUCGUAACUUGGUAUAGUAUAAAUUUUUAUCGUGUAUAAAGAUUUAG
>NC_009848
AGUGGAACCGCGUUUUAACGUCUGUCAUUGACAGAGCGGUUUUUUUUUUUGUCAAACAAAGAGA-GCAAGUCCGAAAGAGAGAUUGGGGGAACGG--GGG
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.(((((((.....)))))))).(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
((((.....)))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
```

```
#yLxS
#The following shows an alignment in 5' -UTR of yLxS and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009664
CCGAGGC-AAAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGAGAAUUUUGUCUCGCAU-GUUCAUCGUUUUAGCCCCUGCUCUUUUGAAAGCAGGGUUUUUUGCAGAG
>NC_014479
CCGAGGC-AAAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGAAUUUUGUCUCGCAU-GUUCAUCGUUUUAGCCCCUGCUCUUUUGAAAGCAGGGUUUUUUGCAGAG
>NC_009725
CCGAGGC-AAAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGC-AAUUUUGCCUCGCAU-GUCCAUCGUUUUCUCAU-GCCCCUGCUCUUUUGAAAGCAGGGUUUUUUGCAGAG
>NC_014551
CCGAGGC-AAAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGC-AAUUUUGCCUCGCAU-GUCCAUCGUUUUCUCAU-GCCCCUGCUCUUUUGAAAGCAGGGUUUUUUGCAGAG
>NC_006270
CCGAGGC-GAAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGC-AAUUUUGUCUCGCAU-GUUCAUCGUUUUUCUAAAAUCCCC-UJGUUUUUGAAAGCAGGGUUUUUACG-AGGG
>NC_009848
CCGAGAC--AAGAGUGGGGAAACCCGUCUCUUUUGUAUUGAACAGGCAUUUUGUCUCGCAUUAUUCAUCCGUUUUUCGU-CCCCUGCUCACAUAAAAGCAGGGUUUUUUGCAGAA
```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....-(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
.((((.....))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
.((((.....))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
.((((.....))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
.((((.....))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
```

```
#huth
#The following shows an alignment in 5' -UTR of huth and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_011969
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUUAGGACAGAGAGUCUCUUAUAAAGAUAAAGCCCUUUUUGCCUUUUUAGGAGGAAAAA-G-AAUGAUUACAUUAAACGGGAC
>NC_014335
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUUAGGACGGGUCUCUUAUAAAGAUAAAGCCCUUUUUGCCUUUUUAGGAGGAAAAAAG-AAUGAUUACAUUAAACGGGAC
>NC_006274
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUU-AGGACAGAAAGUCUCUUAUAAAGAUAAAGGUCCCUUUUUGCCUUUUUAGGAGGAAAAAAG-AAUGAUUACGUUAAACAGGAC
>NC_003909
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUU-AGGACAGAAAGUCUCUUAUAAAGAUAAAGGUCCCUUUUUGCCUUUUUAGGAGGAAAAACA--AUGAUUACGUUAAACAGGAC
>NC_011772
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUU-AGGACAGAAAGUCUCUUAUAAAGAUAAAGGUCCCUUUUUGCCUUUUUAGGAGGAAAAAAGAAUGAUUACGUUAAACAGGAC
>NC_012659
CAUAGUCUAUUAGUAGAAAGGGGCUUACUUUUUUUAGGACAGAGUCUCUUAUAAAGAUAAAGGCCCCCUUUUUGCCUUUUUAGGAGGAAAAAGA--AUGAUUACAUUAAACAGGAC
```

```
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
.....(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..(((((((.....))))))..
```











#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.(((((((.....)))))).....(((((((.....)))))))-).....))))))
(((.....)))))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))
.(((.....)))))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))
.....)))))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))

```

```

#ilvB
#The following shows an alignment in 5'-UTR of ilvB and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_006270
A--GCCGCAGAACAGGGUGGUACCGCGGAAGAAAGCCUUUCGCCCUUUGCCUJGC--AAGGUGUGCAGCGUACAACAGUGGGCGGAAAGGCCU
>NC_009725
UG_A_CCGUAAAAAAGGUGGUACCGCGGAGAGAAAGCCUUUCGCCCUUUGGCUUAGCAUGAAAAUUCUUGGCUGAAUGUGGGUGAAAGGCCU
>NC_014551
UG_A_CCGUAAAAAAGGUGGUACCGCGGAAAGCAA--GCCUUUCGCCCUUUGGCUUAGCAUAAAAUUGCUGAAUUGUGGGUGAAAGGCCU
>NC_000964
--GG_CCGUAAAAAAGGUGGUACCGCGGAAAGAAAGCCUUUCGCCCUUUGGCUUAGCAUAGCAGUUAUCUGCGCGGCUGAUUGUGGGCGGAAAGGCCU
>NC_014479
--GGUCGUAAAAAAGGUGGUACCGCGGAAAGAAAGCCUUUCGCCCUUUGGCUUAGCAUAAAAUUGCUGAAUUGUGGGUGAAAGGCCU
>NC_016047
--GGUCGUAAAAAAGGUGGUACCGCGGAAAGAAAGCCUUUCGCCCUUUGGCUUAGCAUAAAAUUGCUGAAUUGUGGGUGAAAGGCCU

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.(((.....)))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))
.(((.....)))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))
.(((.....)))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))

```

```

#glmS
#The following shows an alignment in 5'-UTR of glmS and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_012581
GAGGAAGGUGAAAGCCUUACAAGCUUACAGGGCUGACAA-UAUGUAAUCCGUUUUUUAUAAAAUUGUUAUUGCGACUAUGUUAUUGCGAGCAGCGUAAGCA
>NC_008600
GAGGAAGGUGAAAGCCGUUAACAGGCUUACAGGGCUGACAA-UAUGUAAUCCGUUUUUUAUAAAAUUGUUAUUGCGACUAUGUUAUUGCGAGCAGCAGAAUGUAAAGCA
>NC_014479
ACCAAGGGGUAACUCCUUGAACAAAGAAAUACAUGAUCUCCAACAAA-A--CAUGUGGAGGGACGUAUGAAAGUCCCU-UGAAAUUGACUUAUCUUCUCCU-UUUACA
>NC_016047
ACCAAGGGGUGACUCCUUGAACAAAGAAAUACAUGAUCUCCAACAAA-A--CAUGUGGAGGGACGUAUGAAAGUCCCU-UGAAAUUGGACUUAUCUUCUCCU-UUUACA
>NC_000964
ACCAAGGGGUGACUCCUUGAACAAAGAAAUACAUGAUCUCCAACAAA-AA--CAUGUGGAGGGACGUAUGAAAGUCCCU-UGAAAUUGACUUAUCUUCUCCU-UUUACA
>NC_009725
ACCGAGGGGACUCUCCGAAACAAGAAAUACAUGAUCUCCAACAAA-AAACAUGUGGAGGGACGUAUGAAAGUCCCU-UGUAAUUGACUUAUCUUCUCCU-UUUUGCA

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.(((.....)))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))
.(((.....)))).....(((((((.....)))))).....(((((((.....)))))))-).....))))))

```

```

#proI
#The following shows an alignment in 5'-UTR of proI and the predicted ConSLOpt structures produced by RNAConSLOpt

```



```
>NC_014335
CUAGAGCGGUUUUAACCUAUUUC - AUUAGGUUAAAACCGUCUUUUUGCUUUUACAGGGGAAAAA - CAUGUUGACGUUAGAAACGUGGGAAGAAAAUAGUUGUUUCAUUUUUCA
>NC_003909
CUAGAGCGGUUUUAACCUAUUUC - AUUAGGUUAAAACCGUCUUUUUGCUUUUUAUAGGGGAAAAACAUGUUGACGUUAGAAACGUGGGAAGAAAAUAGUUGUUUCAUUUUUCA
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
```

```
#odhB
#The following shows an alignment in 5'-UTR of odhB and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_011725
UAACAAGAGAGGUUUUCUAGCUUGUUCUGCCCAAGCCAGGCUAA - CAAUUGGAGAUUACCGAAGACAAAAGAAAGAAAAACACACCGGUUAGGCAAAAUAAGGGG
>NC_014171
UAACAAGAGAGGUUUUCUAGCUUGUUCUGCCCAAGCCAGGCUAA - CAAUUGGAGAUUACCGAAGACAAAAGAAAGAAAAACACACCGGUUAGGCAAAAUAAGGGG
>NC_003997
UAACAAGAGAGGUUUUCUAGCUUGUUCUGCCCAAGCCAGGCUAA - CAAUUGGAGAUUACCGAAGACAAAAGAAAGAAAAACACACCGGUUAGGCAAAAUAAGGGG
>NC_003909
UAACAAGAGAGGUUUUCUAGCUUGUUCUGCCCAAGCCAGGCUAA - CAAUUGGAGAUUACCGAAGACAAAAGAAAGAAAAACACACCGGUUAGGCAAAAUAAGGGG
>NC_011772
UAACAAGAGAGGUUUUCUAGCUUGUUCUGCCCAAGCCAGGCUAA - CAAUUGGAGAUUACCGAAGACAAAAGAAAGAAAAACACACCGGUUAGGCAAAAUAAGGGG
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
```

```
#glyA
#The following shows an alignment in 5'-UTR of glyA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_006274
UGUUGUCUGACUUUUC - AUAGAAGAAAAGAACCGAUUUUCGGUUCUUUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
>NC_003909
UGUUGUCUGACUUUUC - AUAGAAGAAAAGAACCGAUUUUCGGUUCUUUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
>NC_011772
UGUUGUCUGACUUUUA - GUAGAAGAAAAGAACCGAUUUUCGGUUCUUUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
>NC_009674
-----UAU--UAU - AGGAAAGAAAAGAACCGACUUGG----UCUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
>NC_010184
UGUGUCUGACUUUUA - AUAGAAGAAAAGAACCGAUUUUUUGGUUCUUUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
>NC_012472
-UCUUUUUUUAUCUGUCUACUUGACAGGGAUAAGACC - AUUUUCGGUUCUUUUUUUUUUUAUAGAAAGUCAUGUUGAAUUAUAGAAAGUCAUGUUGAAAGGUUCGAAAAAGAAUUAUC
```

```
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
..((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
```

#The following shows an alignment in 5'-UTR of glgA and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_004722
CAGUGGGGCUUUUU-----CCUCCACUGAUAAAUUUUUAAUUGAAAAACUCGAAGGAGGAGUA-----AUAAAAACUUUUUCGGCAGUGGGACAAC
>NC_011772
CAGUGGGGCUUUUU-----CUCCCACUGAUAAAUUUUUAAUUGAAAAACUCGAAGGAGGAGUA-----AUAAAAACUUUUUCGGCAGUGGGACAAC
>NC_003909
CAGUGGGG-GUUUU-----CCUCCACUGAUAAAUUUUUAAUUGAAAAACUCGAAGGAGGAGUA-----GUAAAGCUUUUCGUCGAGUGGGACAAC
>NC_011969
CAGUGGGG-UUUUU-----CCUCCACUGAUCAAGUUUUAAUUGAAAAACUCGAAGGAGGAGUA-----GUAAAGCUUUUCGUCGAGUGGGACAAC
>NC_003997
CAGUGGGG-UCUUU-----CCUCCACUGAUAAAUUUUUAAUUGAAAAACUCGAAGGAGGAGUA-----GUAAAGCUUUUCGUCGAGUGGGACAAC
>NC_010184
UAGUGGGGGAUUUAGAAAACCCCCACAUAUUUAGGUUUUCUCUAUUGAAAAACUUGAAGGAGGAGGAGUAUGAUUAAGCGUUUUUCGUCGAGUGGAACAAC

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

((((((.....)))))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....
(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....
(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....

```

#vals

#The following shows an alignment in 5'-UTR of valS and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_012659
UUGUCGUUAUACAAGU-UAAGAGUAUA--GCAAUUCCUGAUUUUUUUUUUUUAAAUGGUAACCGCGAUGU-----GGAUGAGGGAUUUUUUUA
>NC_004722
UUGUCGUUAUACAAU-UAAGAGUAUA--GCAAUUA-UGAAUUUUUUUUUUUUUUUUUUUAAAUGGUAACCGCGAUGU-----GGAUGAGGGAUUUUUUUA
>NC_006274
UUGUCGUUAUACAAU-UAAGAGUAUA--GCAAUUCCUGAUUUUUUUUUUUUAAAUGGUAACCGCGAUGU-----GGAUGAGGGAUUUUUUUA
>NC_003909
UUGUCGUUAUACAAU-UAAGAGUAUA--ACAAUCCUGAUUUUUUUUUUUUUUUUUUAAAUGGUAACCGCGAUGU-----GGAUGAGGGAUUUUUUUA
>NC_009674
UAGACCGUAUACAAU-GAAGAGUAUA--ACAAUUU-UGCAUUUUUUUUUUUUUUUUUUAAAUGGUAACCGCGAUGU-----GGAUGAGGGAUUUUUU-A
>NC_006270
AGUCCGUUAUACAAUUAAGUGGUAUUUUUUUUUG---CAUUCAUGAAAAAUGGUAUUUUUUUAAAUGGUAACCGCGAGAGAUUCUUCGUUUUUAAACAGGAUCAAGAGGACUCUUU-

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....(((.....)))).....

```

#rtpA

#The following shows an alignment in 5'-UTR of rtpA and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_009725
CAAGAAGAGUAUUGAAA-----CCGUGU-GUUUCUGUACUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
>NC_014551
CAAGAAGAGUAUUGAAA-----CCGUGUUGUUUCUGUACUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
>NC_009964
CAAGAGAGUAUUGAAA-----C-AUAGGUUUUCUGUACUUA--GAGUGAACGGCGUAUAGCUGUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU
>NC_006270
CAAGAAGAGUAUUGAAAAGGCGUAGUUCGCGAGCGAAUUGUUU--GCCAUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUUU

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))

#gabP  
 #The following shows an alignment in 5'-UTR of gabP and the predicted ConSLOpt structures produced by RNAConSLOpt  
 >NC\_009725  
 GAC--GAGAAAAAUUGCUAUUUUCAUUAACUGCCUGUGGCAUU-UUAUAG-AAUAAUACUUGCGGAAUUAUUCAGCAUA  
 >NC\_003909  
 AUCGGCAUUUACGGGAGAGAUUCCACCUAACUUUCUUCGCCUGAAUUUGAGUGGGGCUUA-CUGCCCGUUAUUGCGGGCAA  
 >NC\_005957  
 AUCGGCAUUUACGGGCAGUAGAUUCCGCCUAACUGCUUUUUCGCUAAUUGGAGUGGGGUCUUA-CUGCCCGUUAUUGCGGGCAA  
 >NC\_006274  
 AUCGGCAUUUACGGGCAGUAGAUUCCGCCUAACUUUCUUCGCCUGAAUUUGAGUGGGGCUUA-CUGCCCGUUAUUGCGGGCAA  
 >NC\_011658  
 AUCGGCAUUUACGGGCAGUAGAUUCCGCCUAACUUUCUUCGCCUGAAUUUGAGUGGGGCUUA-CUGCCCGUUAUUGCGGGCAA  
 >NC\_012659  
 AUCGGCAUUUACGGGCAGUAGAUUCCGCCUAACUUUCUUCGCCUGAAUUUGAGUGGGGCUUA-CUGCCCGUUAUUGCGGGCAA

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))

#ribD  
 #The following shows an alignment in 5'-UTR of ribD and the predicted ConSLOpt structures produced by RNAConSLOpt  
 >NC\_009964  
 --CUAAGCCCGAA-----UUUUUUUAAUUUCGGGC-U-----UUUUUGACGGU--AAUAACA--AAAGAGGGGGGAAACAUGGAAGA  
 >NC\_003909  
 AACUUAUUUCUAGAAAAUCAGUCUCACAAACCCCAAGGAUAU-AAAAUCCUUGGGUUUUUUUAGUUAUUUUCAGGAGGUGAGAGAAUACAGAUCA  
 >NC\_006274  
 AACUUAUUUCUAGAAAAUCAGUCUCACAAACCCCAAGGAUAUAAAAUCCUUGGGUUUUUUUAGUUAUUUUCAGGAGGUGAAGAAAAUGACAGAUCA  
 >NC\_003997  
 AACUUAUUUCUAGAAAAUCAGUCUCACAAACCCCAAGGAUAUAAAAUCCUUGGGUUUUUUUAGUUAUUUUCAGGAGGUGAAGAAAAUGACAGAUCA  
 >NC\_011658  
 AACUUAUUUCUAGAAAAUCAGUCUCACAAACCCCAAGGAUAUAAAAUCCUUGGGUUUUUUUAGUUAUUUUCAGGAGGUGAAGAAAAUGACAGAUCA  
 >NC\_011772  
 AACUUAUUUCUAGAAAAUCAGUCUCACAAACCCCAAGGAUAU-AAAAUCCUUGGGUUUUUUUAGUUAUUUUCAGGAGGUGAAGAAAAUGACAGAUCA

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))  
 .....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....))))))



```

-----UAUUAAGGAGGCGUCUCAAAGAGUCGCGUAAGCU-AUAAACUUAUAAAAUAGAAAGCUAACUGUAGAAAGUUGGCUAAUUAAAAAGAAAGCUAGGAG
>NC_003909
CUCGAUUCUAUAAAAAGCGGCUCAUUCAAAAGAGCCGGUAAGCUUUAACCAUAAAAUUAAGAAAGCUAGCUCGUAAGAAAGUUGGCUAAUUAAAAAGAAAGCUAGGAG
>NC_011725
CUGGAUUCUAUAAAAAGCGGCUUUCAGGAGUCGCGUAAGCU---AAACUUAUAAAAUUAAGAAAGCUAAUCUCUGAUAGAGGCUAAUUAAAAAGAAAGCUAGGAG
>NC_011772
CUAGAUCUAUAAAAAGCGGCUUUCAAAAGAGUCGCGUAAGCU---AAACUUAUAAAAUUAAGAAAGCUAAUCUCUUAAGAAAGCUGGCUAAUUAAAAAGAAAGCUAGGAG

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....

```

#nadD

#The following shows an alignment in 5'-UTR of nadD and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_004722
GACUAGCAUGCGCUAUUUUUAUCGUUUAUGCGUAUUGAUAGAGAGCGAAACCAAUUGACUUUUAUUAUAGCAA-CUCUCUUAUUCCUAACCGGAGAGUUGCUGUU
>NC_011772
GAUJAGCAUGCGCUAUUUUUAUCGUUUAUGAUAGAGAGCGAAACCAAUUGACUUUUAUUAUAGCAA-CUCUCUUAUUCCUAACCAAGGAGAGUUGCUGUU
>NC_012581
AAUJAGCAUACGCUAUUUUUAUCACUA----GUAUUGGUGUAGAGAUUCGAAACCAAUUGACUUUUAUUAACAGUAAACUCUCUGGAUGGAAUUAAGAGAGUUGCUGUU
>NC_011658
AAUJAGCAUUAUUUUUAUCACUA---GCAUUGGUGUAGAGAUUCGAAACCAAUUGACUUUUAUUAACAGUAAACUCUCUGGAUGGAAUUAAGAGAGUUGCUGUU
>NC_003909
GAUJAGCAUGCGCUAUUUUUAUCGUUUAUGCGUAUUGAUAGAGAGCGAAACCAAUUGACUUUUAUUAUAGCAA-CUCUCUUAUUCCUAACCGGAGAGUUGCUGUU
>NC_010184
GAUUAUACGUGAGUUAUUUC-GUAUUGGAGCGUUGAU-AUGUAGAAAGCGAAACCAAUUGACUUUUAUUAACAGUUGGCGUCUCUGAAUUUGAUUGGGGAGAGUUGCUGUU

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

..((((.....)))((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....

```

#pel

#The following shows an alignment in 5'-UTR of pel and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_000964
----AGCAAGGAAAAACC-AAAAGGCCAA-UGUCGGCCUUUUGG--UUUUUUUGC--GUCUUUGCGGUGGG-AUUUUGCAGAAUCCCGCAUAGGAUAGCGGAACAUUUUCGGUUCU
>NC_0114479
----UGCAGGGUAUJAAACCCAAAAGGCCAA-CUUCGGCUUUUUGGGUUUUUUUGC--GUCUUUGCGGUGUUGUUGCAGAAUUGCCGCAUUAAGAUAGCGGAACAUUUUCGGUUCU
>NC_009725
----GCU-GAACAGAUCCCAAGGGU----UUUUGGUCUUUGGUAUUUUUUGC--GUUUCCGCAUAAA-----ACCGAAAGGCACAUU-----CUGUACAUUUUCGGUGCU
>NC_011451
----GCU-GAACAGAUCCCAAGGGU----UUUUGGUCUUUGGUAUUUUUUGC--GGUUCGCAUAAA-----ACCGAAAGACACUUU-----CAGUACAUUUUCGGUGCU
>NC_006270
UGCUAUUUUCAGAAAAAUUAAGAGUCUGUUUUUUUAUUCGUUGAUAAAAAUGAACAGCGCAUUUUGCAUAAAAUUGAAAAUUGGUGUCACAAAAAUJAGGAGGAAAAAUJAGUUGUUUU

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....
.....((((((((.....))))))....((((((((.....))))))....((((((((.....))))))....

```









-UAUCCGAUUUUUUGCAACACGCGCCAAUUUGGUACAUAUGUGCAUUGGUAUGACUGCGAUGAAGUGAGAGGUUGCUGACACCCGGCCGCCUUGCCAUUGGCAAGGUGA  
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).  
(((---(((....))))))(((.....))))(((.....)))(.....))))((.....)))).

#yvbw  
#The following shows an alignment in 5'-UTR of yvbw and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_009725  
UGGAUUCGGGACAUUCGGGAUCAACAAGAGUGGUACCCGGGCU-GCCU-GAGGCACGCCUCUCUUUCCCAA-----A-GAGGCGGCGUGCUUUUUUUGUGAUGAACA-CUU  
>NC\_014551  
UGGAUUCGGGAUUUCGGGAUCAACAAGAGUGGUACCCGGGCU-GCCU-GAGGCACGCCUCUCUUUUAA-----AAGAGGCGGCGUGCUUUUUUUGUGAUGAACAAUUU  
>NC\_009964  
AGAUUUCU--UCAUGAAGAUAACAACAAGAGUGGUACCCGGGCAGCGG--AAGGCUCGUCUCUUUAUUAUAGAUAGGUAGGAGAGCGGGGCUUUUUUGUUU-UGAAAA-----  
>NC\_014479  
UGGAUUUCU--UCAUGAAGAUAACAACAAGAGUGGUACCCGGGCAGCGG--AAGGCUCGUCUCUUUAUUAUAGAUAGGAGAGCGGGGCUUUUUUGUUU-UGAAAA-----  
>NC\_006270  
UGGAUUUCUUGGUA--AGGAUCAA~~AA~~AGAGUGGUACCCGGGUAAGCUUCAAGCUUCUUUAUUAUAGAUAGGAGCGGUGAGCUUUUUUAUUU---AAUA-----

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
..(((.....)))).(((.....)))-(((.....))))(((.....)))-)).....  
..(((.....)))).(((.....)))(.....))))((.....)))).

#mtnk  
#The following shows an alignment in 5'-UTR of mtnk and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_003909  
-----UGGAAAGAGUUUUUCUGUCAGAAAAACCUUGAAU  
>NC\_005957  
CCAGCAGAAAGUAAAACUUUGGCAGUAAGAGGGGAGAGAUAACUUCAAACCUUUAAGUGGAAAGGGUUUUUUAUUAACGUCAGAAAAACCUUGAAU  
>NC\_006274  
CCAGCAGAAAGUAAAACUUUGGCAGUAAGAGGGGAGAGAUAACUUCAAACCUUUAAGUGGAAAGGGUUUUUUAUUAACGUCAGAAAAACCUUGAAU  
>NC\_011658  
CCAGCAGAAAGUAAAACUUUGGCAGUAAGAGGGGAGAGAUAACUUCAAACCUUUAAGUGGAAAGGGUUUUUUAUUAAGAAAGGGUUUUUUAAGAAACCUUGAAU  
>NC\_010184  
CCAGCAGAAAGUAAA- CUUUUGGCAGUAAGAGGGGAGAGAUAACUUCAAACCUUUAAGUGGAAAGGGUUUUUUAUUAAGAAACCUUGAAU  
>NC\_009674  
CCAGCAGAAAGUAAA- UUUUUGGCAGUAAGAGGGGAGAGAUAACUUCAAACCUUUAAGUGGAAAGGGUUUUUUAUUAAGAAACCUUGAAU

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
....(((.....)))).(((.....)))(.....))))((.....)))).  
....(((.....)))).(((.....)))(.....))))((.....)))).  
....(((.....)))).(((.....)))(.....))))((.....)))).  
....(((.....)))).(((.....)))(.....))))((.....)))).  
....(((.....)))).(((.....)))(.....))))((.....)))).







```
>NC_014639
GCAAUGUCUGGUAACAGGAUCA-AAGGUGACGGG-GAAUAUAUUUUUU--CUCCGAUAUCAGGGUGGUUACCGCGAGAC---AGCUCUCGUCCUCGUGGAAACGUGUUUG
>NC_007530
GUCUUGC-CACGUUACGGCACCAUGAGGUAGUAUUUGAUUCGUAJAGCAAUAUAUAGAAUAAUUGGGUGGUUAUCGGGAGUU---AACUCUCGUCCUUUU-----
>NC_003909
GUUUUGC-CACGUUACGGCACCAUGAGGUAGUAUUUGAUUAUAUAGAAUAUAUAUAGAAUAAUUGGGUGGUUAUCGGGAGUU---AACUCUCGUCCUUUU-----
>NC_011725
GUCUUGC-CACGUUACGGCACCAUGAGGUAGUAUUUGAUUAUAUAGAAUAUAUAUUGGGUGGUUAUCGGGAGUU---AACUCUCGUCCUUUU-----
>NC_010184
GUCUUGC-CACGUUACGGCACCAUGAGGUAGUAUUUGAUUAUAUAGAAUAUAUAUUGGGUGGUUAUCGGGAGUU---AACUCUCGUCCUUUU-----

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
...((-(.....))(((((.....))))).(((.....))))...(((.....)))
...(((.....)))...(((.....)))...(((.....)))...(((.....)))...(((.....)))
...(((.....)))...(((.....)))...(((.....)))...(((.....)))

#ioli
#The following shows an alignment in 5'-UTR of ioli and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_00964
AUGGAGUUCGGCGGAUUGCGCA-CA-GCCUUUCCUGCCGAACUCC-CUUCAUAUUAACAAAGCGAGAUUCGGGAGUCUGGCAUGAAACUUAUUAUGAAAGCGACAACUUGGAAAA
>NC_014479
AUGGAGUUCGGCGGAUUGCGGAACA-GCCUUUCCUGCCGAACUCC-CUUCAUAUUAACAAAGCGAGAUUCGGGAGUCUGAUGAAACUUAUUAUUAUGAAAGCAAACAACUUGGAAAA
>NC_009725
AUGGAGUUCGGCGGAGCGGCAACAGCCUCCUGCCGGACUCC-CUUCAUAUUCGAAACGCGGAGUGGGAGGCGUGAUGAAACUUAUUAUUAUGAAAGCGACUACGCUGGAGAA
>NC_014551
AUGGAGUUCGGCGGACGGGCGAAAAAGCCUUUCAGCCGGACUCC-CUUCAUAUUAACAAAGCGAGAUUCGGGAGUCUGAUGAAACUUAUUAUUAUGAAAGCAAACAACGCUUGGAGAA
>NC_006270
-----GCCCCCCCUGAGUUCGGCGCCUCCUGCCGAACUUCUCUUCACAA-GGAUUGAGAGAAAGGAGAAUUCGAAUAUGAUCUUAUUAUGAAAGCAAACGACGCUUGGAAAA

#The top 4 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
...(((.....)))...(((.....)))...(((.....)))...(((.....)))
...(((.....)))...(((.....)))...(((.....)))...(((.....)))...(((.....)))
...(((.....)))...(((.....)))...(((.....)))...(((.....)))...(((.....)))
...(((.....)))...(((.....)))...(((.....)))...(((.....)))

#rimM
#The following shows an alignment in 5'-UTR of rimM and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_004722
AAAAAAGGGCGAGGUUAUU-CCUCUCCUUUUUAACAUAUUUAACAUAUAUAGAGAGUGCA--UGUUCCAUCUGUGAAUUGAUGAUGAUCUUAUUUAUUAUAGAAACCGGGUGACAUAUCUAU
>NC_011772
AAAAA-GGGCGAGGUUAUU-CCUCUCCUUUUUAACAUAUUUAACAUAUAUAGAGAUUGCA--UGUUCCAUCUAUUGAAUUGGAGUUAUUUAUUAUUAUAGAAACCAGGGGUGACAUAUCUAU
>NC_008600
AAAAA-GGGCGAGGUUAUU-CCUCUCCUUUUUAACAUAUUUAACAUAUAUAGAGAGAUUGCA--UGUUCCAUAUUGAAGAAUUGGGAUUGGGAUUGCUAAUUUAUUAUUAUAGAAACCCAG-----
>NC_011658
AAAAA-GGGCGAGGUUAUU-CCUCUCCUUUUUAACAUAUUUAACAUAUAUAGAGAGAUUGCA--UGUUCCAUAUUGGGAUUGGGAUUGCUAAUUUAUUAUUAUAGAAACUAGGGGUGACAUAUCUGU
>NC_010184
AAAAA-GGGCGAGGUUAUUUCCUCCUUUUUAACAUAUUUAACAUAUAUAGAGAAUUGCA--UGGUCCAUAUAUUAUUAUAGAAUUGAUAUUUAUUAUUAUAGAAACCGGGUGACAUAUCUAU
>NC_009674
```







>NC\_013791  
CUGUUAAAAGGAAGCAAGUUCAGUUUGCUUCAAUUAGGGUGGCACACGGGUUAUACUCUGUCCUGAUG--UAGAUACAUCAGAGGGGAGUUUUGUGUUU-----

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
((((--(((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....

#yda0  
#The following shows an alignment in 5'-UTR of yda0 and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_009964  
AGCGUUCGUGAGAGGAGAUAAAACUGUGUU-CGAUGUUUAGGACAGGGGCAUCGUUCCUCUGUGU-UUUUUUGUUUGUUC--AUUUUUU-GAA  
>NC\_014479  
AGCGUUCGUGAGAGGAGAUAAAACUGUGUU-CGAUGUAAUAGGACAGGGGCAUCGUUCCUCUGUGU-UUUUUUGCUUGUUC--AUUUUUUAGAA  
>NC\_009725  
AGCGUUCAGUAGAGGAGAUAAAACUGUGCA-CGA--UUUAGGCGCAGGGGCAUCGUUCCUCUGUGUUCGUUCCUCUGUGUUGCUUUAUAGGCA  
>NC\_014551  
AGCGUUCAGUAGAGGAGAUAAAACUGUGCA-CGA--UUUAGGCGCAGGGGCAUCGUUCCUCUGUGUUCGUUCCUCUGUGUUGCUUUAUAGGCA  
>NC\_006322  
AGCGUUAA-GAGAGGGGAGA--UAACUCGGAA-UAAAAUCCGAUUCGCGAGGGGCU-UUGCCUCUGCGCUUUUUUGU-----  
>NC\_009848  
AGCGUUAAAAGAGGACAAAGAC---CAACUCUGAUUAAAACAUAAGACACAGGGGCAUUUUAUUGCCUCUGUGUUCUUUUGG-----

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....

#cbi0  
#The following shows an alignment in 5'-UTR of cbi0 and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_011773  
AAGGGCAGGACAGUUUUCAAGAAACUGGUCUUGGCCUUUUUUUU---AAAUUAUUUUU-AGGCUUACUUGGCGAAGGAAAGGGUGCCUUGUUAU  
>NC\_003997  
AAGGGCAGGACAGUUUUCAAGAAACUGGUCUUGGCCUUUUUUUU---AAAUUAUUUUU-AGGCUUACUUGGCGAAGGAAAGGGUGCCUUGUUAU  
>NC\_004722  
AAGGGCAGGACAGUUUUCAAGAAACUGGUCUUGGCCUUUUUUUU---AAAUUAUUUUU-AGGCUUACUUGGCGAAGGAAAGGGUGCCUUCUUAU  
>NC\_011772  
AAGGGCAGGACAGUUUUCAAGAAACUGGUCUUGGCCUUUUUUUU---AAAUUAUUUUU-AGGCGAGCUUGGCGAAGGAAAGGGUGCCUUCUUAU  
>NC\_010184  
AAGGGCAGGACAGUUUUCAAGUAAACUGGUCUUGGCCUUUUUUUU---AAGUUAUUUUU-AGGCUUACUUGGCGAAGGAAAGGGUGCCUUGUUAU  
>NC\_009674  
AAGGGCAGGACAGUUUUCAAGUAAACUGGUCUUGGCCUUUUUUUUUUUAUUUUAUAGGAGGCUAACUCGAAAAAAGAAAGGGUGCCUUAUUAU

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....

```

#pyrR
#The following shows an alignment in 5' -UTR of pyrR and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009725
GGAUAAACGGAUAGGACAGAAGAGUAUCGCAUGUGUCUCCUGGAAAGGAAACCCUCAUGCUCUGGCAAGGAGGGUUUU- - - - -U-UUCUUCUUUAUAUACGAUUGGAGAGGUGU-
>NC_014551
GGAUAAACGGAUAGGACAGAAGAGUAUCGUGUGUCUCCUGGAAAGGAAACCCUCAUGCUCUGGCAAGGAGGGUUUU- - - - -U-UUCUUCUUUAUAUACGAUUGGAGAGGUGU-
>NC_011725
GGUAAACGGUUUGAAAUACUUAAGGGUAUGUU- GUACCCUUUUUU- -CAAAGUCCUCUGACACGCGUGAGAGGACUUUUUUU- AUACCAUUACUCUCACGCAAGAAAAA- GCUUGGA
>NC_011772
GGUAAACGGUUUGAAAUACUUAAGGGUAUGCU- GUACCCUUUUUU- -CAAAGUCCUCUGACACGCGUGAGAGGACUUUUUUU- AUACCAUUACUCUCACGCAAGAAAAAAGGCUUGGA
>NC_003909
GGUAAACGGUUUGAAAUACUUAAGGGUAUGCU- AUACCCUUUUUU- -CAAAGUCCUCUGACACGCGUGAGAGGACUUUUUUUUAUACCAUUACUCUCACGCAAGAAAAA- GCUUGGA
>NC_012659
GGUAAACGGUUUGAAAUACUUAAGGGUAUGCU- GUACCCUUUUUU- -CAAAGUCCUCUGACACGCGUGAGAGGACUUUUUUU- AUACCAUUACUCUCACGCAAGAAAAA- GCUUGGA

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....

```

```

#purM
#The following shows an alignment in 5' -UTR of purM and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_012659
AAAAAGCUUCUACUUCUUUU- GAUGVAGAAGCUAGCUUCUUUUUAUAAAUGCCCGCUGGAGGGAUUAUAAAAGACGAGGUGUAAAUA
>NC_003909
AAAAAGCUUCUACUUCUUUUUAUGVAGAAGCUAGCUUCUUUUUA- AAACGGCCCGCAGGUAUGGAGAAUUAUAAAAGACGAGGUGUAGUAUA
>NC_011969
AAAAAGCUUCUACUUCUUUU- GAUGVAGAAGCUAGCUUCUUUUUA- AAACGGCCCGCAGGUAUGGAGAAUUAUAAAAGACGAGGUGUAAAUA
>NC_006274
AAAAAGCUUCUACUUCUUUU- GAUGVAGAAGCUAGCUUCUUUUUA- AAUAGCCCGCUGGAGGGAUUAUAAAAGACGAGGUGUAAAUA
>NC_011772
AAAAAGCUUCUACUUCUUUU- GAUGVAGAAGCUAGCUUCUUUUUA- AAUAGCCCGCUGGAGGGAUUAUAAAAGACGAGGUGUAAAUA
>NC_011725
AGAAAAGCUUCUUCUUUU- GAUGVAGGAGCUAGCUUCUUUUUA- AAUAGCCCGCUGGAGGGAUUAUAAAAGACGAGGUGUAAAUA

```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....
.....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....(((((((.....)))))).....

```

```

#lepA
#The following shows an alignment in 5' -UTR of lepA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_014479
-----GUGCGUGAAAGAGAAAAG--CAGCCAGGUUAGACAGGGAACUUUUCUCUUU
>NC_012581
AAACGGAGCGGUUGUUUACAGAUUUUAAGACGACCGGUUUUUUAUUUUAUUUAAAAGGUUGUCUUCUUUUGUUUUCGCAUAAGAUUAGAUUUUGUAUUUGUAAGCAGC

```















```

>NC_014335
UAUUGAUAUGAAAACGAGCAUAGUUUAGUUUAUUAUUUUUUAUUUUGGGAUUAUUGGGGAUUAUUGGGGAUUAUUGAAUAUUAUGAAUAUUGAAUUAUUGUUCGGGGGUGAGCAUUGUUAGCU
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....

```

```

#comFA
#The following shows an alignment in 5'-UTR of comFA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_012581
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUGCUGAUCUCGCGUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC
>NC_008600
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUACUGAUGGUUGCUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC
>NC_006274
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUGCUGAUCUCGCGUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC
>NC_014335
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUGCUGAUCUCGCGUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC
>NC_011658
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUUAUUAUGUAUUGCUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC
>NC_003909
GGUUAUCGGCUUUUUGAGUUUACGAGAUUAUAAGAAAGGUUUUAUUAUUAUGUAUUGCUUGGGGUGGUUUAUUAUGUAUUGCUUGGAAAGCAGUUAUAUUAGAAGAACUCCCUUCAGAUUUAC

```

```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....
.....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....((((((((((((((((.....)))))))))))).....

```

```

#upps
#The following shows an alignment in 5'-UTR of upps and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_00964
ACUUAUGUACAAUAGUUAUAGUG-AAAAACCCUCUAUGUUUACAGGGGGUUUUUU-UGUUAAUACU--GUU-GAUUACAUUGAUUUU-AAGCAGGGGAAUGUA
>NC_012581
-----UAGCGAUACCUUCGCAAUAUAGACCCUCU--UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUGGAGGUAUGAAUGAUUUUAAA
>NC_003909
-----UAGCGAUACUUUCGCAAUAUAGACCCUCU-UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUUGGGGUAUGAAUGAUUUUAAA
>NC_014335
-----UAGCGAUACUUUCGCAAUAUAGACCCUCU--UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUGGAGGUAUGAAUGAUUUUAAA
>NC_011725
-----UAGCGAUACUUUCGCAAUAUAGACCCUCU-UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUUGGGGUAUGAAUGAUUUUAAA
>NC_011772
-----UAGCGAUACUUUCGCAAUAUAGACCCUCU--UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUUGGGGUAUGAAUGAUUUUAAA
-----UAGCGAUACUUUCGCAAUAUAGACCCUCU-UCUUAAGGGGUCUUUUUACUUUUUAGGCAUACGUCUUGCGUUGGGGUAUGAAUGAUUUUAAA

```

```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)

```
#ldh
#The following shows an alignment in 5' -UTR of ldh and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_012581
ACUJACUCCUAUUGCAAGAAUUGCACGGGAUACAUUUUCAAUUACUUUGAAUUUAAUAAAUUGAAUUAAGAAUUAUAGAAUAAGACGUAUUA
>NC_008600
ACUJACUCCUAUUGCAAGAAUUGCACGAGAUACAUUUUCAAUUACUUUGAAUUUAAUAAAUUGAAUUAAGAAUUAUAGAAUAAGACGUAUUA
>NC_012472
ACUJACUCCUAUUGCAAGAAUUGCACGGGAUACAUUUUCAAUUACUUUGAAUUUAAUAAAUUGAAUUAAGAAUUAUAGAAUAAGACGUAUUA
>NC_003909
ACUJACUCCUAUUGCAAGAAUUGCACGGGAUACAUUUUCAAUUACUUUGAAUUUAAUAAAUUGAAUUAAGAAUUAUAGAAUAAGACGUAUUA
>NC_005957
ACUGAAUCCUAUUGCAAGAAUUGCACGGGAUACAUUUUCAAUUACUUUGAAUUUAAUAAAUUGAAUUAAGAAUUAUAGAAUAAGACGUAUUA
>NC_010184
ACAGAAUCCUAUUGCAAGAAUUGGAGUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUAUUGAAUUA
```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)

```
#gatc
#The following shows an alignment in 5' -UTR of gatc and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_000964
-AGUUAUAAAUUUAUJAGGGUAUUUGGAAAACACAGGCCUGUCUCAAGGGUUUUG-UUGCUIUUAAGGGUUUUUUGAUUAUAGAUACAGUAUUU- AUGACUU
>NC_005945
AAAGAAAGGGUUUGCCUUUUUUUUAUGUAAAAUUGCUGUAAAGUCCUGUGUUGAAUUGCUUGAAAACUGAACUUUUGGUAUUAUUGAAUUAUUGAAUUA
>NC_010184
AAAGAAAGGCACUUGCCUUUUUUUUAUGUAAAAUUGCUGUAAAGUCCUGUGUUGAAUUGCUUGAAAGUACUGGAAUUUUGGUAUUAUUGAAUUAUUGAAUUA
>NC_011772
AAAGAAAGGCACUUGCCUUUUUUUUAUGUAAAAUUGCUGUAAAGUCCUGUGUUGAAUUGCUUGAAAACUGAACUUUUGGUAUUAUUGAAUUAUUGAAUUA
>NC_011725
AAAGAAAGGCACUUGCCUUUUUUUUAUGUAAAAUUGGUAAGUAUCUGUGUUGAAUUGCUUGAAAGUACUGGAAUUUUGGUAUUAUUGAAUUAUUGAAUUA
>NC_009674
CGAGAAAGGCACUUGCCUUUUUUUUAUGUAAAAUUGCUGUAAAGUCCUGUGUUGAAUUGCUUGAAAACUGAACUUUUGGUAUUAUUGAAUUAUUGAAUUA
```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)  
.....(((.....)))(.....(((---(...)))))(.....(((.....))))(.....(((.....))))(.....)



```

AUAG--UAGUAUUGUUUAUAAAAAGAGUAAGGUACCUUCAACAGAGUGGUUAACGAAAAUAAAGUUUCAUCUUUUUUUUUCAAA
>NC_006274
AUAGAGUAUCAUUGUUAGAAAAAGAGUAUAAGUAGACUACCUUCAACAGAGUGGUUUUACGAGAAUAAAAGUUUCAUCUUUUUUUCAAA
>NC_011658
AUAGAGUAUAUUGUUAGAAAAAGAGUAUAAGUAGACUACCUUCAACAGAGUGGUUUUAAAGAGAAUAAAAGGUUUUAGCUUUUUUUUCAAA
>NC_003909
AUAGAGUAUAUUGUUAGAAAAAGAGUAUAAGUAGACUACCUUCAACAGAGUGGUUUUAAAAGUAUAAAAGGUUUUAGCUUUUUUUUCAAA

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
.....((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((

#rbsR
#The following shows an alignment in 5' -UTR of rbsR and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_006270
CAUUGUUAUCUGUAUUCGCCCAUUAACGCCCCUUAUAUAUGUCUGAUUACCCAGCCCGGUUAAAAUUUCAGUGUUCAUC-CAUUUUUUUUUAUUGUGAUUUAAAUGGAUCGUGAUAAUC
>NC_007530
UCGJAAUUGAAAAAGCAUCGCCUUAUUGGCCAUUUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUCUAGAAAUACGGUUUAUUUA
>NC_012581
-----UGAAAAAGCAUCGCCUUAUUGGCCAUUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUCUAGAAAUACGGUUUAUUUA
>NC_006274
-----UGAAAAAGCAUCGCCUUAUUGGCCAUUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUCUAGAAAUACGGUUUAUUUA
>NC_011772
-----UGAAGAGCAUCGCCUUAUUGGCCGUGUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUUUAGAAAUACGGUUUAUUUA
>NC_011725
-----UGAAGGAGCAUCGUUUUUGGCCGUGUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUUUAGAAAUACGGUUUAUUUA
-----UGAAGGAGCAUCGUUUUUGGCCGUGUUUUUU-----GAGUAUAACUUAAAAGCUUUUUUCUUGA-GAAAUUGAUUGAC--GUAUUUUUAGAAAUACGGUUUAUUUA

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((

#panB
#The following shows an alignment in 5' -UTR of panB and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_00964
CUUUAGA--AAGUGAAGAAUCCUUCUGUUAACGGAAGGUUUUUUUGCCUUGCAGAAAAACGGCAGAUCAUCUCCUCUA-AACAUGAGGGAGGAGAAAAACAACAAACUG
>NC_012581
UAACACACA--ACCCUUCUGCCUUUUUAUGGC--CAGAGGGGUUUUU--UAUAUGAUUCG---GCCAUCUCCUCUCUCUGUAU-AAAGGAGGAGUUUUUUGAAAAACAACAAACA
>NC_014335
UAACACACA--ACCCUUCUGCCUUUUUAUGGC--CAGAGGGGUUUUU--UAUAUGAUUCG---GCCAUCUCCUCUCUCUGAUUAAAAGGAGGAGUUUUUUGAAAAACAACAAACA
>NC_004722
-----CCUUUCUGCCUUUUUAUGGU--CAGAGGGGUUUUU--UAUAUGAUUCG---GCCAUCUCCUCUCUCUGAU-AAAAGGAGGAGUUUUUUGAAAAACAACAAACA
>NC_014171
UAACACACA--ACCCUUCUGCCUUUUUAUGGU--CAGAGGGGUUUUU--UAUAUGAUUCG---GCCAUCUCCUCUCUCUGAU-AAAAGGAGGAGUUUUUUGAAAAACAACAAACA
>NC_009674
UUACAAACACUACCCUUCUGCCUUUUUAUGGU--CAGAGGGGUUUUU--UAUAUGAUUCG---GCCAUCGCCUCUCUCUCAAUU-AAAAGGAGGAGUAAUUUUUGAAAAACGAAACA

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```



```

>NC_009964
AUGUCAUACC - -UUUUUGACAUUUGUCUCCUAGAAUGAAUAAUAAACCAAGGUGCUCCGAAUAAA - CCUGU - UACUUUUGGAGGAUUAUGUUUAUGUCUUIUAUGAUAAAGUAUACACAGGCCA
>NC_009725
AUGUCAUACG - -UUUUUGACAUUCCGUGUCAGAGUAAUUAUUAAACCAAGGUGCUCGAAUAAACCCUGU - UACUUUUGGAGGAUUAUGUUUAUGUCUUIUAUGAUAAAGUAUACACAGGCCA
>NC_006270
UUUGUCAU - -AUGUUUGACAUUCCUUCUUCAGGAUAAUUAACCAAGGUGCUCAAUUAAA - CCUGU - UACUUUUGGAGGAUUAU - AUGAUGUCUUIUAUGAUAAAGUAUACACAGGCCUC
>NC_009848
CUGUCAUUG - -AUUUUGACAUUCCUUGCCAUUAUUAUAAUAAACCAAGGUGCUCAAUAAACCCUGU - UACUUUUGGAGGAUUAU - UJCGAUGUCUUIUAUGAUAAAGUAUACACAGGCCUC
>NC_013791
UAUUAAUAAG - -UGGUUGACACACAUUAUCAGGGUGUAAGAUA - UCAAAGUGUGC - -UCAGAACCUGU - UGCUUUUGGAGGAUGA - ACAUUGUCUUIUAUGAAAAAGUAAAAGCAGGCCUA
>NC_015634
UUUUUACACGGGCUUUGACUUUAGUUUCAAAGUGAAUUAUUUUAUUAAGGUGCUCCUUGAAUACCUUGUAUUAUGGAGGAUUUGGGAUGUCUUIUAUGAAAAGUAAAUACAGGCCGA

```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
```

```

.....(((.....))).....(((.....))).....(((.....))).....(((.....))).....
.(((.....))).....(((.....))).....(((.....))).....(((.....))).....
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.(((.....))).....(((.....))).....(((.....))).....(((.....))).....

```

```
#thrZ
```

```
#The following shows an alignment in 5'-UTR of thrZ and the predicted ConSLOpt structures produced by RMAConSLOpt
```

```

>NC_009964
UGCUGGUUAACAGCACCGGCCGACAA - CAUAGUAAUUUGUC - - -GGGAACUUUGGGUGACCACGGGUUAUACACACACUCGUCCUUCUGCGGG - ACGGGUGUGUUUUUUAUUAUUA
>NC_014479
UGCUGGUUAACAGCACCGGCCGACAA - CAUAGUAAUUUGUC - - -GGGAUUUUUGGGUGACCACGGGUUAUACACACACUCGUCCUUCUGCGGG - ACGGGUGUGUUUUUUAUUAUUAUUAUUA
>NC_009848
UGCCACGUUAACGGCACCGAGCCAUAAAGCGGAGUAGCAUUUAU - -GGGAUUUUUGGGUGACCACCGG - - -AUUACACAUUCGUCCUUCACACGGG - AUGGGGUGUGUUUUUUAUUAUUU
>NC_014551
-GCCGGUUAACGGCAA - AAUAGAGCCGUCACUUUAGGAGUAC - - -GGGAUUUUUGGGUGACCACCGG - - -AUUACACAUUCGUCCUUCUGCGGG - AUGGAGUGUGUUUUUUAUUAUUU
>NC_006270
UGCAACGUUAACAGCACAGGCCAUUAAGUUGUCCAUUUUAACUUUAGGGAAAAUUUGGGUGACCACCGG - - -GUAAUGCACUCGUCCUUCUUGGGGUAUAGUGCAUUUUUUUUAUUAUUU

```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
```

```

(((.....))).....(((.....))).....(((.....))).....(((.....))).....
(((.....))).....(((.....))).....(((.....))).....(((.....))).....

```

```
#ypbR
```

```
#The following shows an alignment in 5'-UTR of ypbR and the predicted ConSLOpt structures produced by RMAConSLOpt
```

```

>NC_009964
UAAAUUCUGU - - - -UUUGAUGAAUUCUGGAAACUUGUA AAAAGUUGCAGAUUUUCUUU - -UUAUGAAGCUGCCG - UAAUGGGCGUUUUUUUAUUCUCCUAAAAGAAAUUUGUUUUUAUUCUUG
>NC_014479
UAAAUUCUGU - - - -UUAA - AAUUCUGGAACUUGUCAAAAGUUGCAGAUUUUCUUU - -UUAUGAAGCUGCCG - UAAUGGGCGUUUUUUUAUUCUCCUAAAAGAAAUUUGGUUUAUUCUUG
>NC_009725
UAAAUUCAGUUCUUAUAACAUCUGCGGUUUUUCU - -GCCC GGUGUUUUUCU - -UUUUUACGUCGCCGCUUUUUUUCUUAUUCUCCUAAAAGAAAUUUGGCUCAUUCUUG
>NC_014551
UAAAUUCAGUUCUUAUAACAUCUGCGGUUUUUCU - -GCCC GGUGUUUUUCU - -GCCC GGUGUUUUUCUUAUUCUCCGCUUUUUCUUAUUCGCGCUUUUUCGAAAGAAAAGUACCAUUCUUG
>NC_006270

```



```
-----AUAGAUACA - CGUGCUGAAGCUGCCGA-----AACGGCAGCUUUUUCUGUUUUUCUGAUUGUGAAGAAAAUUACAGCAAGGUUG
>NC_006322
AGCGAAUCCGCAAAAUAAUAGAUACA - CGUGCUGAAGCUGCCGA-----AACGGCAGCUUUUUCUGUUUUUCUGAUUGUGAAGAAAAUUACAGCAAGGUUG
```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....  
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....

#gabR  
#The following shows an alignment in 5' -UTR of gabR and the predicted ConSLOpt structures produced by RNAConSLOpt

```
>NC_009964
AUUUUCUUAUCAUUCUGACUUCUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUAUCAGAGGAGAAACUACAAAUGGAUAUC - ACGAUUACACUC
>NC_014479
AUUUUCUUAUCAUUCUGACUUCUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUACCAAGGAGAAUCUGCAA - UGGACAUC - ACAUUACACACUC
>NC_009725
GUUUUCUUAUCAUUCUGACUUCUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUAUCAGAGGAGAAAGGGG---CAGGGUCUGGAUCGACGAAUUCCAUU
>NC_014551
GUUUUCUUAUCAUUCUGACUUCUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUAUCAGAGGAGAAAGGGGU--CAGGGUCUGUAUGCACAUAUUUCCAUU
>NC_006270
UAAUUUCUUAUAAUUCUGAAUUAUUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUACCAAGGAGGGGCUAUGAUC-----ACAAUACCGAUU
>NC_009848
UCUUUUUUAUUAUUCUGAAUUAUUUGGUUAUGAUGAAAAGUACCAAUUAUAAUCUUUUUUGGUUACCAAGGAGAAAGG- -AAUGACGCAUCGACAAUUCAACUA
```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....  
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....  
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....

#ydbJ  
#The following shows an alignment in 5' -UTR of ydbJ and the predicted ConSLOpt structures produced by RNAConSLOpt

```
>NC_009964
UAUAAUA - -CAAACAGUGCCUAAUGUU - GGGCACUGUUUAUUUUUUUGUCGA - -AAAAGGGGAAG - GCUUUUUGGCUGAGCCGAUUUAUAUUUGAAGGCCUCGAUAAAAAAUUUGGG
>NC_014479
UAUAAUA - -CUAACAGUGCCUAAUUUUUGGCACUGUUUAUUUUUUUGUCGA - -AAAAGGGGAAG - GCUUUUUGGCUGAGCCGAUUUAUAUUUGAAGGCCUCGAUAAAAAAGAUUUGGG
>NC_006270
UAUAAU - - -CAAACAGUGCCU - - -UUUCGGCACUGUUUAUUUUUUUUG - GA - -AAGAGGGGGGG - CUAUGACAAAAGCAGCCUGUUUAUAUUUAGAAAAUUUGUAUUAAUUAUAGA -
>NC_009725
UAUAAUG - - CAGACAGUGCCU - AUGUACGGGCACUGUUUAUUUUUUUGU - GA - -AAAAGGGGAAG - GCUUGAUGACUGAGCCGAUUUAUAUUUGAAGGCCUUGACAAAACAAUAGGC
>NC_014551
UAUAAUG - - CAGACAGUGCCUUAUGUACGGGCACUUAUUUAUUUUUUUGU - GA - -AAAAGGGGAAG - GCUUGAUGACUGAGCCGAUUUAUAUUUGAAGGCCUUGACAAAACAAUAGGC
>NC_014019
UAUAAUGUAGACAAUUAUUAAAAAGAAACAUAUAGAAGGGUUAUUGCUAUAUUAAAGAAAGGAUGAUGACAGAAAACAGUACAGUACAAAGAUCAUAGUAGUACAGUAAAAAGUAAUUUGGG
```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....-((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....  
.....-((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....









```
>NC_014551
UAGGCCUCGGGAUACUUUUAUAGCCAUAGUUGCCACAGUUGGUAUAGGCGUGUUUCCUGUCUUUUUACAACUUUCCACAAAUCCA
>NC_006270
-----GUGAUGAGC--GGGAA-AGUGUGAAUAACUUGAACAUUGGCCUUACACAGUUGUCCACAGUUGGUAUAGGCGUGUUUCCGUUUUUUUAACA-CUUUCCACAAAUCCA
>NC_014019
-----GCUUUUUUAUCUUGUAUUUUGGUAUAAGAGUAGUAACACAGUUGUCCACAGUUGGUAUAGGCGUGUUUCACGUUUU-U-AGGGGUUAUCCACAUUUUCCA
```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
-.....(((.....(((.....(((.....(((.....))))))))......)))))).....
```

```
#yrhE
#The following shows an alignment in 5'-UTR of yrhE and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
UAUAGUCUAUCGUUUUAUAAAAUAAGGUAUCU-GUUAGUA--AGACUUGCUAGGAACUAUUCGCCAUUGUGUUUACACC--UUCUUAGAAUUAAGGCGGUGUAUCUAU
>NC_014479
UAUAGUCUAUCGGUUUAUAAAAUAAGGUAUCU-GUUAGUA--AGACUUGCUAGGAACUAUUCGCCAUUGUGUUUACACC--UUCUUAGAAUUAAGGCGGUGUAUCUAU
>NC_009725
UAUAGUCUAUCGUUUUAUACAAU--AGGAUUGGUCU-GUUAGUA--AGACUUGCUAGGAACUAUUCGCCAUUGGUUUUAUACCG-UUCUCCGUJACAGGAGGCCGGUAUCUAUGU
>NC_014551
UACGAGUCUAUCGUUUUAUACAAU--AGGAUUGGUCU-GUUAGUA--AGACUUGCUAGGAACUAUUCGCCAUUGGUUUUAUACCG-UUCUCCGUJACAGGAGGCCGGUAUCUAUGU
>NC_006270
UAUGAAUCUAUCGAAUC-UGACAAUAAGGAUUGGUCU-GUUAGUA--AGCUUUGCUAGAAACUAUUCGCCAUUGGUUUUAUACCGAUUUCGCCGCGGAAAUCCGGUAUUAUGU
>NC_015634
GGUUUGUUCAUUUUGCAUCAGAUUCAGAAUAAAAAGAGAAUAGUAGUUUUUUUUGCAAAGGUUUGGUUAAGUA---ACAGAG-UUGCCGGUUUUUUUGUAUUCUUUUUCUGAAG
```

```
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
.....(((.....)))).....(((.....)))).....(((.....)))).....
```

```
#rpsL
#The following shows an alignment in 5'-UTR of rpsL and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_012581
UUUGAGGAGAGGAGCAUUUGCUCUCCUUGCAAAAACUUUUUUUAACAAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
>NC_011969
UUUGAGGAGGAGGAGCAUUUGCUCUCCUUGCAAAAACUUUUUUUAACAAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
>NC_011772
UUUGAGGAGGAGGAGCAUUUGCUCUCCUUGCAAAAACUUUUUUUAACAAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
>NC_009674
UUUGAGGAGGAGGAGGAGCAUUUGCUCUCCUUGCAAAAACUUUUUUUAACAAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
>NC_009725
U--GUUUUUUAUUAAGAUACAUCUUUGUUAAGACAUUUUUUUUGCCUUAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
>NC_014551
U--GUUUUUUAUUAAGAUACAUCUUUGUUAAGACAUUUUUUUUGCCUUAUUAUAGACCACCUUGGUAUUGGUAUACAAAACAUGC----GA
```



#The following shows an alignment in 5'-UTR of ydeB and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_009725  
AU-ĀUCUCAC - UCCAUUAUGGUAACCUUAAGUUCCCAUUAUUGGAGGUGGAUUUAUGUUUCAAUUUGCGGAUAACAUAUUUUUUAUCCAAUGCA  
>NC\_014479  
AU-ĀUJACACCUACGUUAUGGUAACUUUAAG - -AAGGUACAA - AUJUGGAGGUGGAUUAUGUUUCAAUUUGCGGAUAACAUAUUUUUUAUCCAAU - - -  
>NC\_009848  
AUUĀUUUUUUUUAUCCAAAGUGGUACCCUUAAAG - UAGAUJACAUJAUJUGGAGGCGGAUUAUGUUUCAAUUUGGUGAUACAUAUUUUUUAUCCAAUGCA  
>NC\_009964  
AU-ĀUJACACCUCAUUAUGGUAACUUUAAGA - AGGAUJACCAUUAUJUGGAGGUGGAUUAUGUUUCAAUUUGCGGAUAACAUAUUUUUUAUCCAAUGCA

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
((-((((((.....)))))).....)))).....(((.....)))).....  
-.....(((.....)))).....(((.....)))).....(((.....)))).....  
-.....(((.....)))).....(((.....)))).....(((.....)))).....

#cotG  
#The following shows an alignment in 5'-UTR of cotG and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_014479  
GGUĀUAAGGAUUCGUCCUUAUUUAAAAGGAGGAUUUCAAUUUGGCGCAUUAUCCCAUUCUGACAUCAAAAGAGCGGUAUUCCGCA  
>NC\_016047  
GGUĀGUAAGGAUUCUUAUCCUUAACAUAUUUCAAAGGAGGAUUUCAAUUUGGCGCAUUAUCCCAUUCUGACAUCAAAAGAGCGGUAUUCCGCA  
>NC\_009964  
GGUĀGUAAGGAUUCUUAUCCUUAACAUAUUUAAAAGGAGGAUUUCAAUUUGGCGCAUUAUCCCAUUCUGACAUCGAAGAGCGGUAUUCCGCA  
>NC\_009725  
G-UĀGUAAGGGAUG - CAUCCUUAACAUAUUAUGAGGAGG - UUUCAAUUUGGCGCAUUAUCCCAUUCUGAUUCGAAGAGCAGUAAGUCCGCA

#The top 4 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....(((.....)))).....(((.....)))).....(((.....)))).....  
.....(((.....)))).....(((.....)))).....(((.....)))).....  
.....(((.....)))).....(((.....)))).....(((.....)))).....  
.....(((.....)))).....(((.....)))).....(((.....)))).....

#yunB  
#The following shows an alignment in 5'-UTR of yunB and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_009964  
CUĀUUAUAUGUCCCCUUAACAAGCAUAUUGAUUAGUAAAGGGGGAUUUU - CUUCCAAGAUJUGCGGCCUUAUUCGC - AAGAGAGGAC  
>NC\_016047  
CUĀUUAUAUGUCCCCUUAACAAGCAUAUUGAUUAGUAAAGGGGGAUUUU - CUUCCAAGAUJUGCGGCCUUAUUCGC - AAGAGAGGAC  
>NC\_014479  
CUĀUUAUAUGUCCCCUUAACAAGCAUAUUGAUUAGUAAAGGGGGAUUUU - CUUCCAAGAUJUGCGGCCUUAUUCGC - AAGAGAGGAC  
>NC\_006270  
UGĀĀUCGUĀUAUCCCUUAACAAGCAUACACU - UGUAGUAUAGGAGGGAUUUJUGCUUGAAGACUUCGCGGCCUUAUUC - AAAAGAGGAC  
>NC\_009725  
AAAĀUAUAUGUCCCCUUAACAAGCAUAUUGAUUAGUAAAGGGGGAUUUUUUAUCCUAGAUJUGCGGAGCGGUUAUCGC - AAGAGAGGGC  
>NC\_014019  
AGAĀGCGUĀAACCUUAACAUGCAUACA - UAJUGCUUAGGAGGGAUUUUUUUUAUUAACUUCGUCGGAUUUAACA - GAAAAAGGCC

#The top 4 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):



```
.....((((((((((((((((.....((((((((((((.....
.....((((((((((((((((.....((((((((((((.....
.....((((((((((((((((.....((((((((((((.....
.....((((((((((((((((.....((((((((((((.....
.....((((((((((((((((.....((((((((((((.....
```

```
#groES
#The following shows an alignment in 5'-UTR of groES and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009674
GAAUGAU- - - - -GUAAGC- GUGAAAAUUUUUAUCUUAUCACUUGAAAAUUGGAAUUGGAAUUAUAUUAAGAAUUGUUGUAGCUCUUUAGUGUGAGUGCUAA- AAUUACA-
>NC_014479
GAAUCAU- - - - -GUAAGC- GUGAAAAUUUUUAUCUUAUCACUUGAAAAUUGGAAUUAUAUUAAGAAUUGUUGUAGCUCUUUAGUGUGAGUGCUAA- AAUUACA-
>NC_009725
GAAUCAU- - - - -GUAAGC- GUGAAAAUUUUUAUCUUAUCACUUGAAAAUUGGAAUUAUAUUAAGAAUUAUAUUAACUGUGUUAAGCUCUUUAGAGCUGUGUUA- AAUUACA-
>NC_014639
GAAJAAU- - - - -GUAAGC- GUGAAAAUUUUUAUCUUAUCACUUGAAAAUUGGAAUUAUAUUAAGAAUUAUAUUAAGAAUUAUAUUAAGCUCUUUAGAGCUGUGCUAA- AAUUACA-
>NC_010184
AAAGUGCAUAAAGUAUUUUGGAAAAUUUAUGAUUUUUUAUCUUGCAAAGAAUUUAUUUAAGAAUUAUAUUAAGUUGUUAAGCUCUGGAGACUUGAGUGCUAAUAAA- AGAA
>NC_009674
AAAGUUUAUUAUCGUAUUUGAGAAAAUUUAUGAUUUUUUAUCUUGCAAAGAAUUUAUUUAAGAAUUAUAUUAAGUUGUUAAGCUCUGGAGACUUGAGUGCUAAUAAA- AGAA
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..(((-----(-.....)).....((((((((((((((((((((((((((((((((((((.....((((((((((((((((.....
.....((((((((((((((((((((((((((((((((((((.....((((((((((((((((.....
```

```
#gabT
#The following shows an alignment in 5'-UTR of gabT and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_011773
GUCUUAUAAAGACUCUUAAUGAGUCUUUAUAGACUUUAUUUUU- AUGGCGAAAUAGAGGUUGUAGGAUUAUUUGGAAAAAGAAUUGUUGGCAUACAUUUUUGCA
>NC_008600
GUCUUAUAAAGACUCUUAUAAUGAGUCUUUAUAGACUUUUUUUUUUAUGGCGAAAUAGAGGUUGUAGGAUUAUUUGGAAAAAGAAUUGUUGGCAUACAUUUUUGCA
>NC_003909
GUCUUAUAAAGACUCUGAAUGAGUCUUUAUAGACUUUAUUUUUUUUAUGGCGAAAUAGAGGUUGUAGGAUUAUCUGAAAAAGAAUUAUUUGGCAUACAUUUUUGCA
>NC_006274
GUCUUAUAGAGACUCUUAACGAGUCUUAUAGACUUUUUUUUUUAUGGCGAAAUAGAGGUUGUAGGAUUAUCUGAAAGAAUUAUUUGGCAUACAUUUUUGCA
>NC_011658
GUCUUAUAAAGACUCUUAUAAUGAGUCUUUAUAGACUUUUUUUUUUAUGGCGAAAUAGAGGUUGUAGGAUUAUUUGGCAUACAUUUUUGCA
>NC_011725
GUCUUAUAAAGACUCUUAUAAUGAGUCUUUAUAGACUUUUUUUUUUAUGGCGAAAUAGA-----UGAAUACUAGAAAAAGAAUUAUUUGGCAUACAUUUUUGCA
```

```
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
((((((((((((((((((((((((((((((((((((.....((((((((((((((((.....
((((((((((((((((((((((((((((((((((((.....
.....((((((((((((((((((((((((((((((((((((.....
```

```
#secA
#The following shows an alignment in 5'-UTR of secA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_014479
```

```
-----UGAAGAGCAACCUGUGAUUUUCGGGAAGG- UUUUUGUUUUUUCUUAUUUGCAAAUUCUUUGAAUUAGAAAGUAUUAUGAUAAUGAGAGGUUU
>NC_016047
-----AGAAACAAAAGCCUUCGUGAUGACCGGGAAGG- UUUUUGUUUUU - CUUAUUUGCAAAUUCUUUGGAAUAACAACAAAGUAUUAUGAUAAUGAGAGGUUU
>NC_000964
-----UGAAGAGAAGCCUUCGUGAUGCCGGGAAGG- UUUUUGUUUUU - CUUAUUUGCAAAUUCUUUGGAAUAACAACAAAGUAUUAUGAUAAUGAGAGGUUU
>NC_009725
-----ACCCAUCCAGCCUUCGUGA- ACCGCGGGAAGG- UUUUUCUCUACUUUACCUUUCGCAAAUUCUUUGGAAUAAGCAAAAAGGUUUUUAUGAUAAUGAGAGGUUU
>NC_014551
-----ACCCAUCCAGCCUUCGUGA- ACCGCGGGAAGG- UUUUUCUCUACUUUACCUUUCGCAAAUUCUUUGGAAUAACAACAAAGUAUUAUGAUAAUGAGAGGUUU
>NC_005945
UUUUGUCAUAGUAAGAACAAGUUAACAUAUUAAGGUUAUUAUUAUUUUUUUAAGGAGAAUUUUGCAUAUAUAUUUUUUAUAUUAUUUUUUUAACGACGUCUGAUUG
```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
-----((((((.....))))))--(((.....(((.....)))))).....(((.....))))).((.....))))).((.....))))).  
-----(((.....))))))--(((.....))))).((.....))))).((.....))))).((.....))))).((.....))))).

#murC  
#The following shows an alignment in 5' -UTR of murC and the predicted ConSLOpt structures produced by RNAConSLOpt

```
>NC_000964
AAUGAGCGUCAUAUACUGGGGAACAGAUAGACGUUUGUUGGGGUACA - AUUAUGACUUUAUCAUUUUUGGAAUAACAAGGGACCGGUUAUGAGUCCG
>NC_014639
AAUGAACGUCAUAUACUGGGGAACAGAUAGACGUUUGUUGGGGUACA - AUUAUGACUUUAUCAUUUUUGGAAUAACAAGGGACAGGUUAUGAGUCCG
>NC_009725
AAUGAGCGUCAUAUACUGGGGAACAGAUAGACGUUUGUUGGGGUACG - AUUAUGACUUUAUCAUUUUUGGAAUAACAAGGGACAGGUUAUGAGUCCG
>NC_006270
AAUGAACGUCAUAUACUGGGGAACAGAUAGACGUUUGUUGGGGUACU - AUUAUGACUUUAUCAUUUUUGGAAUAACAAGGGACAGGUUAUGAGUCCG
>NC_009848
AAUGAGCGUCAUAUACUGUAAGUCAGAUAGACGUUUGUUGGGGUACA - AUUAUGACUUUAUCAUUUUUGGAAUAACAAGGGACAGGUUAUGAGUCCG
>NC_014019
GAUAAACCGUCAUAUACUGUCAAGACAGAAUGUUGGGGUUCUUUAU - AUGACAUUUUACAUUUUUUGAAGGUUAUAACAAGGAAACAGGAUAUGAGUCCG
```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
-----(((.....)))))).....(((.....))))).((.....))))).((.....))))).  
-----(((.....)))))).....(((.....))))).((.....))))).((.....))))).  
-----(((.....)))))).....(((.....))))).((.....))))).((.....))))).  
-----(((.....))))).((.....))))).((.....))))).((.....))))).  
-----(((.....))))).((.....))))).((.....))))).((.....))))).  
-----(((.....))))).((.....))))).((.....))))).((.....))))).  
-----(((.....))))).((.....))))).((.....))))).((.....))))).

```
#cspB
#The following shows an alignment in 5' -UTR of cspB and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_000964
UCUGAAGAUUACUGGUAGAGUAAGUAUUUUUUGUUCGAACUAUUUUUUAAGAAAGUUUUUUAAGAGUUUUUGUAAGAGUUUUGCUUGAAAGUUUUG - UAAGAGCAAGAAUUAAG
>NC_014479
UUUGAGGAUUUACUGGUAGAGUAAAGUAAUUUUUUUUGUUCGAACUAUUUUUUAAGAAAGUUUUUUAAGAGUUUUUUGCUUGAAAGUUUUGU - UAAGAGCAAGAAUUAAG
>NC_006270
UCGUUAACACACUGGUAAAGUAUUUUUUGUUCGAACUAUUUUUUAAGAAAGUUUUUUGAAGAGUUUUUGCUUGAAAGUUUUGUUGAAAGUUUUGAAUUAAG
>NC_009848
UCCGCAACACACUGGUAAAGUAUUUUUUGUUCGUAUCUUUUUUAAGAAAGUUUUUUAAGAGUUUUUUGCUUGAAAGUUUUGUUAAGAGCAAGAAUUAAG
```



```
#arfM
#The following shows an alignment in 5' -UTR of arfM and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
UUACCCUUCUGAU-AGUGACAUUACAUACAGGC-UGUGAAAUACAUCACUGUGCAGGCUCAGUCGAGCUACACUAAAGCUAUCCUUGACACAGGAGUUUUCUUAUGAAUUA
>NC_014479
GUCAUCUCCCGAU-AGUGACAUUACAUACAGGC-UGUGAAAUACAUCACUGUGCAGGCUCAAUCGAGCUACACUAAAGCUAUCCUUGACACAGGAGUUUUCUUAUGAAUUA
>NC_009725
UACACUUCUUCUGAU-AGUGACUUUUUAUACAAGC-UGUGAAAUACAUCACUGCCGUCAGGCUCAAUCGGGCUACACUAAAGCUAUCCUUGACACAGGAGUUUUCUUAUGAAUUA
>NC_006270
UUCGUUUUUUACACAGUACAUUUGCAUACAGUCGUGUGAAUUAAAUAUCACUGCCGUCAGCCGGCGUUUAUACUAAAAGCCAAUAUAGAGAGGAGGAUAUACCAUGGACCCG
```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....(((((((.....((((.....)))))).....((((.....))))).((((.....))))).((((.....))))).((((.....))))).((((.....))))).
.((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....
.....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....
.....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....
```

```
#csbX
#The following shows an alignment in 5' -UTR of csbX and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_006274
UCGUUAUGUAAGCGUAUACUUUUUUUUAUCAAAGAAUUAAAGCGCUAAACCAAAAAUACUUA--UCGGUGGUGG-GAGAAUGAACGCUAUUAGUUAACAAACAACAAUUAUUGGACAG
>NC_014335
UCAUUAUGUAAGCGUAUACUUUUUUU--AUCAAAAAGAAUUAAAGCGCUUAAACCAAAAAUACUUA--UCGGUGGUGG-GAGAAUGAACGCUAUUAGUUAACAAACAACAAUUAUUGGACAG
>NC_005957
UCAJAAUUAAGCGUAUACUUUUUUUAUCAAAGAAUUAAAGCGCUUAAACCAAAAAUACUUA--UCGGUGGUGG-GAGAAUGAACGCUAUUAGUUAACAAACAACAAUUAUUGGACAG
>NC_012472
UUUAUAUGUAAGCGUAUACUUUUUUUAUCAAAGAAUUAAAGCGCUUAAACCAAAAAUACUUA--UACUUA--UCGGUGGUGG-GAGAAUGAACGCUAUUAGUUAACAAACAACAAUUAUUGGACAG
>NC_012581
UCAJAAUUAAGCGCAUACUUUUUU--AUCAAAAAGAAUUAAAGCGCUUAAACCAAAAAUACUUA--UCGGUGGUGG-GAGAAUGAACGCUAUUAGUUAACAAACAACAAUUAUUGGACAG
>NC_009964
-----UCUAACAGGAUUACAACAGCAGCUUGGGUUAUAUCUCCAUAUUUAAUAGGCGGGGAGAAUUAACAGUACAUAGGAAUUAAGGAAUUAAGUUAUGAAUUAUGAAACA
```

```
#The top 4 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....(((((((.....((((.....)))))).....((((.....))))).((((.....))))).((((.....))))).((((.....))))).((((.....))))).
.....((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....((((.....))).....
.....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....
.....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....((((.....-)))).....
```

```
#ycsF
#The following shows an alignment in 5' -UTR of ycsF and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
UUUAUAUGAAUAAAGUUCAAAAAGUUUCGGAAUAGUCGUUCCGAAUUUCGGACAAUAAAGACAUAAAGCAUAUC-----GUUUGCUUUGG-----CAGGAGGGAUUCUGUGUUUUA
>NC_014479
UUUAUAUGAAGCAAAGUUCAAAAAGUUUCGGAAUAGUCAUUCCGAAUUUCGGAAACAUAUAA--ACAUAAAGCAUAUC-----GUUUGCUUUGG-----CAGGAGGGAUUCUGUGUUUUA
>NC_009725
AAUAUAUGAAGAAAUCCAACAACUUCGGAAUAGUCAUUCCGAAUAGCGGAUAUAAU-----AUUAUAAAC-----GUUUAACAUA-----CAGGAGGGAUUCUUAUGUUUUA
```



```
#The following shows an alignment in 5'-UTR of zur and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_014479
UGGUAUAUUUUAUCUCAGUAGAGAAAAGCCUUGCUGGUCAGACAGCUGCCAUUUUUUUUCAUAUGUAUCGUUUUAAAGCAAAAGCGAAAGGGGAAACCUUCAUGAACCGU
>NC_009964
UGGUAUAUUUUAUCUCAGUAAAGAAAGCCUUGCUGGACAGACAGCUGCCAUUUUUUUUCAUAUGUAUCGUUUUAAAGCAAAAGCGAAAGGGGACCCUUCAUGAACCGU
>NC_009725
UAGGUAUAUUUUAUCUCAGUAAAGAAAGCCUUGCUGGACAGACAGCUGCCAUUUUUUUUCAUAUGUAUCGUUUUAAAGCAAAAGCGAAAGGGGAGGUCUUGAACCGU
>NC_014551
UAGGUAUAUUUUAUCACAGCAUA - GGAAAAGGCCUGCUGUUCAGACAGCUGCCAUUUUUUUUGGA --- GCGAUAC - - - - - CGUJUUGUAAAAGGGGAGGUCUUGAACCGU
UAGGUAUAUUUUAUCACAGCAUA - GGAAAAGGCCUGCUGUUCAGACAGCUGCCAUUUUUUUUGGA --- GCGAUAC - - - - - CGUGAUGUAAAAGGGGAGGUCUUGAACCGU
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
..(((.....(((.....)))))).....(((.....)))).....
.(((.....))).....(((.....))).....(((.....))).....
```

```
#yaaH
#The following shows an alignment in 5'-UTR of yaaH and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
AUCAGCCUUUUUCAUAUAU - GAUAGCG - AUAUGAAA - GGAGGCGUUUU - UCAUUAAAUAUUUUAUGUGUA AAAACAAGGGGACACUCUUUCUGCUAUCGUUCACAAUACAGAAC -
>NC_014479
AUCAGCCUUUUUCAUAUAU - GAUAGCG - AUAUGAAA - GGAGGCGUUUU - UCAUUAAAUAUUUUAUGUGUGUA AAAACAAGGGGACACUCUCUGCUAUCGUUCACAAUACAGAAC -
>NC_009725
AUCAGCCUUUUUCAUAUAUUUUAUGAGCGGAUAUGAAA - GGAGGCGUUUU - UCAUUAGAUCUAUAUAGUAAAACGGGGGACACCGUUUCCGUUUGCGGCGCUACCCGGACU
>NC_014551
AUCAGCCUUUUUCAUAUAUUAUGAGCGGAUAUGAAA - GGAGGCGUUUU - UCAUUAGAUAUUUAUGUAUGUAAAACGGGGGACACACUUUCUGCUAUCGUUCGCGCUACCCGGAAU
>NC_014019
AAAAGCCUUUCAUAUGAUGGA --- AGUAAGUCAUAUGAAAAGGAGGCGUUUUUAUUUUAUGAAAUAUCACUGUUAAAAGCAGGUGACAGUAUAUAGUAUUGCAA - - - - -
```

```
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
...(((.....))).....(((.....))).....(((.....))).....
..(((.....))).....(((.....))).....(((.....))).....
.(((.....))).....(((.....))).....(((.....))).....
.(((.....))).....(((.....))).....(((.....))).....
.(((.....))).....(((.....))).....(((.....))).....
```

```
#trpS
#The following shows an alignment in 5'-UTR of trpS and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009964
GUCUCGUAACAACGUA - GAGUGAUUCCAUIU - - - - - UAAUGGAAUAUACAGGGUGUACACCGGUUAUCUGCCUUUUUUAACA - - - GGGGAAGAAUGA
>NC_016047
GUCUCGUAACAACGUA - GAGUGAUUCCAUIU - - - - - UAAUGGAAUAUACAGGGUGUACACCGGUUAUCUGCCUUUUUUAUA - - - GGGGAAGAAUGG
>NC_009725
GCCUCGUAACAACGUA - GAGUGAUUCCAUIU - - - - - UAAUGGAAUAUACAGGGUGUACACCGGUUAUCUGCCUUUUUUAUA - - - GGGGAAGAAUGG
>NC_014551
GCCUCGUAACAACGUA - GAGUGAUUCCAUIU - - - - - UAAUGGAAUAUACAGGGUGUACACCGGUUAUCUGCCUUUUUUAUA - - - GGGGAAGAAUGG
>NC_006270
GACUCGUAACAACGUA - GAGUGAUUCCAUIUUAUGACCAUAUUAUACAGGGUGUACACCGGUUAUCUGCCUUUUUUAUA - - - AAGGGGAAGAAUGG
>NC_011772
CCAGACUUAUGGUAUAGAGAUUACAGUA - - - - - GUGA - - - - - AAUAUUAGGGUGUACCGGGUCCAUUCGUUCUUAUAGUUUUUU - - - GGGGAAGAAUGG
```

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.....((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.....((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.....((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))

#ydcC  
#The following shows an alignment in 5'-UTR of ydcC and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_000964  
GA\_CAAAGUUUUU-GAGGCUUUUUAUGGUACGCAUCU--GUUCUGCCUAAA-CGUGUACCAGCGUACCGUUAAAAGUCAAAACAAAGCGAUUUCUCCUUUU  
>NC\_014479  
GA\_CAAAGUUUUU-GAGGCUUUUUAUGGUACGCAUC--GUUCUGCCUAA--CGUGUACCAGCGUACCGUUAAAAGUCAAAACAAAGCGAUUUCUCCUUUU  
>NC\_006270  
GA\_CGAGUCGUUG-CAGGCUUUUUAUGGUACGCACGCCGCAUACAGCCGCCCCUGUUUUAAGCGGUACCGUUAAAAGUCGAAACAAGCGGUUUCUCCUUUU  
>NC\_009848  
GGG\_CGAGUUUCUAAACAGGCUUUUGAUUGUCGGU---ACGCAGUUAAAC-----UCUUGGGCGUACUGUUAAAAGUCAAAACAAAGCGGUUUCUCCUUUU  
>NC\_009725  
GA\_CAAAGUUUUU-GAGGCUUUUUAUGGUACGGUC-----CGUCCG-----UUCAGGGCGUACCGUUAAAAGUCAAAACAAGCGAUUUCUCCUUUU  
>NC\_014551  
GA\_CAAAGUUUUU-GAGGCUUUUUAUGGUACGGUC-----CGGCCG-----UUCAGGGCGUACCGUUAAAAGUCAAAACAAGCGAUUUCUCCUUUU

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
..-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
(-((.....)))-((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))

#pheS  
#The following shows an alignment in 5'-UTR of pheS and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC\_012659  
GG\_CGACACUUGUUCUCAAU---UUAGGGUGGUJACCGCGAAUUUACCUCGUCCUUU-UUGGGAGCGAGG--UUUUUUUUUUUUUUUUUUUUUAGGGGUUCCAAA  
>NC\_011725  
GG\_CGACACUUGUUCUCAAU---UUAGGGUGGUJACCGCGAAUUUACCUCGUCCUUU-UUGGGAGCGAGG--UUUUUUUUUUUUUUUUUUUUUAGGGGUUCCAAA  
>NC\_009674  
GG\_ACAGACUUGUUCUCAAU---UUAGGGUGGUJACCGCGAAUUUACCUCGUCCUUU-UUGGGAGCGAGG--UUUUUUUUUUUUUUUUUUUUUAGGGGUUCCAAA  
>NC\_010184  
GG\_CGACACUUGUUCUCAAU---UUAGGGUGGUJACCGCGAAUUUACCUCGUCCUUU-UUGGGAGCGGGG--UUUUUUUUUUUUUUUUUUUUUAGGGGUUCCAAA  
>NC\_002570  
GG\_AUGCACUCAGUUUGUCAUCAAUAGGGUGGUJAUJCGCGAAAC--CUUCGUCCUUUGUUGGGAAACGAAAGUUUUUUGCACUUGCAGAAAAGUUUAAUUUCUAUA  
>NC\_009725  
-GU\_CGACAGUAGUUCUCAAUAAAAGGGUGGUJACCGCGGCCACAAACUCGUCCUUUCUC-AAGGGCGGGUUUUUUUGUUUUUCUGAAAAGCGUAAGAAACG-GU

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
..-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))  
.-((((.....))))).....((((.....))))).....((((.....))))).....((((.....))))).....((((.....)))))

```

#adk
#The following shows an alignment in 5'-UTR of adk and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_000964
-----AGGAAUJGGAUU-UAUCCAUUCCCUUUAUAAGAGAGGACGGGGAAUJCGAA--UGAACUUAGUCUUAUUGGGGUUCCUGGUGCCGGUAAAGGCACACAG
>NC_004722
GUGAGUAAGUGGGGAAGAA--UUGUCUUCUCCUACAUJGCUAUG-UACUCUGAGGGGGAA-AAGGA-UGAACUUUAUUUAUUGGGGUUCCUGGUGUAAAGGUJACACAA
>NC_009674
GUAAGUAUGGGGAAGAGA--AUGUUCUUCUCCUACAUJGCUAUG--UA---UGAGGGGAA-AAAGA-UGAACUUUAUUUAUUGGGGUUCCUGGUGUAAAGGUJACACAA
>NC_010184
>--GUAAGUGGGGAAGAA--CUGUCUUCUCCUACAUJGCUAUG-UAC--UGAGGGGAA--AAGGA-UGAACUUUAUUUAUUGGGGUUCCUGGUGUAAAGGUJACACAA
>NC_011772
>--GUAAGUGGGGAAGAA--CUAUUCUUCUCCUACAUJGCUAUG-UAC--UGAGGGGAA--AAGGA-UGAACUUUAUUUAUUGGGGUUCCUGGUGUAAAGGUJACACAA
>NC_014019
GCUGUUUJAGUGGGGAAGCAAGCUGCUUUAACGGUAUAGAUACUGAGGGGGGAAGAAUUAUGUUUAUGUUUAUGGGGUUCCUGGUGUAAAGGUJACUCUCAA

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....

#glpX
#The following shows an alignment in 5'-UTR of glpX and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_004722
-----GUGAUACUUCGCAAGGGGGAAGCGAAGCAUCUACUUGCGGAGUACACUUUAUJAGAAAAA--CACGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA
>NC_012581
-----GUGAUACUUCGCAAGGGGGAAGCAUCUACUUCGCGGAGUACACUUUAUJAGAAAAA--CACGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA
>NC_011658
-----GUGAUACUUCGCGAGGGGGAAGCGAAGCAUCUACUUCGCGGAGUACACUUUAUJAGAAAAA--CACGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA
>NC_003909
-----GUGAUACUUCGCGAGGGGGAAG---UAUCACUACUUCGCGGAGUACACUUUAUJAGAAAAA--CACGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA
>NC_011772
-----GUGAUACUUCGCAAGGGGGAAGCGAAGCAUCUACUUCGCGGAGUACACUUUAUJAGAAAAA--CACGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA
>NC_010184
AAUCGGGAUAAGGUGUACUUCGUAUUGGGGAGCGAAGAAUACUAACUACUACCGGAGUACACUUUAUJAGAAAAA--UAAGGUUCACAAAUAUACGGCAGAAAUAUAAAAGGCUUAAAA

#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....
.....((((((((.....)))))).....((((((((.....)))))).....((((((((.....)))))).....

#ywcI
#The following shows an alignment in 5'-UTR of ywcI and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009725
AAACAUAUUCGCCCGGACCGGUCUAUCAUJAGAGUCAUJAGGGUU--GCUJAGACCCCGCUAGUUUUAGCGGAGAAAGGAUUGGGCCUUUUCCGUUAAA--GCGGAGAGAAAAACAGGCCUCG
>NC_014551
AAACAUAUUCGCCCGGCGUCUAUCAUJAGAGUCAUJAGGGUU--GCUJAGACCCCGCUAGUUUUAGCGGAGAAAGGAUUGGGCCUUUUCCGUUAAA--GCGGAGAGAAAA--CAGGCCUCG
>NC_000964
AAAGAAUUCUUCUCCACGGGUCUAUCAUJAGAGUCAUJAGUUUUGCUJAGAGCCGCUAGUJGCGA--GAAAAAGAAUUGGGCCUUCUUUUCUGGGCCUGGAGAAAAACAGGCCUCG

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```

>NC_014479
AAAGAAUUCUUCCGCAGUCUUAUAGAGUCAUGAGUUUCUAGAGCGGCUAGUUGCGA - GAAAGAAAUUCGGCCGUCUUUCGCGGUCGAGAAACGGGCGUCG
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
#yfq
#The following shows an alignment in 5' -UTR of yfq0 and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_009725
AAAAACAUGAAGGAACCCGGCGCAUGUUUAUCUGAAAAGAUGUAUUUCAAUUCGCGUUUUC - CAGGAGGAAAGCGUUUUC - AUAGAAACGGAGAGAAAAACCGUGAAUCA
>NC_014551
AAAAACAUGAAGGAACCCGGCGCAUGUUUAUCUGAAAAGAUGUAUUUCAAUUCGCGUUUUC - CAUGAGGGAUGGCUUUUAUAGAAAACGGAGAGAAUAAAACCGUGAAUCA
>NC_000964
ACAA---UGAAGGAAAUCCUGCAAACGUGUUUAUCUAGAAAAGUGAGAAAACCAAUUUCUGCCAGAAAGCUUCAU- AUAGAAACGGAGAGAACAA--CGUGAAACCA
>NC_014479
AAAAUAUGAAGGAUUCJAGGCAAGCGUGUUUAUCUAGAAAAGAUGUAUUUCAAUUCGCGUUUUC - AUAGAAACGGAGAGAACAA--CGUGAAACCA
#The top 3 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
.....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....
#ddl
#The following shows an alignment in 5' -UTR of ddl and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_004722
CUAGAUUAGAUUCCAUUUUAU-UUUG-----UGUAGCUAUUA-----AUGAAA-----UGAAAAACAUAAGUGAUGUUUAUUUAUUUUUA
>NC_003909
CUAGAUUAGAUUCCAUUUUA-----UAUAUCUAUGAA-----GAA-AUUUAAGUGGAAAAAGUAAGAAAAACAUAAGUGGUGUCAUUUAUUUAUUUUG
>NC_008600
UCAGUAGGGGGAUGAAGCCCCC-ACUGAUUAAAGUUUCACUUUAUAUUUA-----GAAGAAAGUUAGUGGAAAAGUAAGAACCAUAAGUGGUGUCAUUUAUUUAUUUUG
>NC_011773
UCAGUAGGGGAUGAAGCCCCCUCACUUUAUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUA
>NC_011658
UCAGUAGGGGAUGAAGCCCCC-ACUGAUUAAAGUUUCACUUUAUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUA
>NC_011969
UCAGUAGGGGAUGAAGCCCCC-ACUGAUUAAAGUUUCACUUUAUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUAUUUA
#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
((((((((.....))))))....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....)
((((((((.....))))))....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....)
((((((((.....))))))....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....)
((((((((.....))))))....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....)
((((((((.....))))))....((((((((.....))))))....((((.....)))).....((((.....)))).....((((.....)))).....)
#bioA

```



```

>NC_011725                      UAAAAAAAAAAGGCAAGUGUAUUCGUUUGCUUUUUUUGCGAAAAAUUAUUAACCCUACUUUUAAACUGAAAAAGUAUGAAAAG
>NC_014171
GAAAUACGGUCUUAAGUAAUAAAAAAAAACAGGCAAGUGUAUUCGUUUGCUUUUUUUUUGCGAAAAAUUAUUAACCCUACUUUUAAACUGAAAAAGUAUGAAAAG
>NC_011772
-----UAAAAAAAAAAGGCAAGUGUAUUCGUUUGCUUUUUUUGCGAAAAAUUAUUAACCCUACUUUUAAACUGAAAAAGUAUGAAAAG
-----

```

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
-----

```

```

#The following shows an alignment in 5'-UTR of mals and the predicted ConSLOpt structures produced by RNAConSLOpt

```

```

>NC_011658
--AAGAAGAGGGGGACAGCCCCUUUUUUUGUUUACAAUUAUAGAAAUCUAUUAUAAUAGAGGUAUGGAUUAUUAUGAGCAAGUUUAUCAGUAGGU
>NC_012472
---AAGAAGAGGGGG--ACAAGCCCCUUUUUUUGUUUACAAUUAUAGAAAUCUAUUAUAAUAGAGGUAUGGAUUAUUAUGAGCAAGUUUAUCAGUAGGU
>NC_012581
--AAAAAGAGGGGGACAGCCCCUUUUUUUGUUUACAAUUAUAGAAAUCUAUUAUAAUAGAGGUAUGGAUUAUUAUGAGCAAGUUUAUCAGUAGGU
>NC_011725
---AAGAAGAGGGGG--ACAAGCCCCUUUUUUUGUUUACAAUUAUAGAAAUCUAUUAUAAUAGAGGUAUGGAUUAUUAUGAGCAAGUUUAUCAGUAGGU
>NC_011772
--AAGAAGAGGGGGACAAUCCCCUUUUUUUGUUUACAAUUAUAGAAAUCUAUUAUAAUAGAGGUAUGGAUUAUUAUGAGUAAGUUUAUCAGUAGGU
>NC_014479
UUUUUAUGUUUUAUCCCUUGCAUUUUUCCGGCUUUUAUAGCAAAACCUAGUUAUUUUUUGCCAGAAAGGAAGAGGCGGGUUAUUAUUAUUAUUAUUAUUA

```

```

#The top 4 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((((
----

```

```

#hprk
#The following shows an alignment in 5'-UTR of hprK and the predicted ConSLOpt structures produced by RNAConSLOpt

```

```

>NC_012472
CAAAAAGAAAAACAUUUCAUGAUGUGUAUGAAAUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU
>NC_006274
CAAAAAGAAAAACAUUUCAUGAUGUGUAUGAAAUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU
>NC_003909
CAAAAAGAAAAACAUUUCAUGAUGUGUAUGAAAUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU
>NC_011725
CAAAAAGAAAAACAUUUCAUGAUGAAAUUUUUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU
>NC_014171
CAAAAAGAAAAACAUUUCAUUUCUGUAUGAAAUUUUUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU
>NC_011772
CAAAAAGAAAAACAUUUCAUUUCUGUAUGAAAUUUUUUUUUUUUUUUUUUUUUUUAUUUUAUAGAAAACCGAUUUUCUGUUUCCAGAAAAAAUUGGUACAUAU

```

```

#The top 5 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```







```

>NC_009964
UUUCAUGGAUUG---UAUCCAUCGGGUU-----
>NC_014479
UUUCAUGGAUUUGGAUAUCCAUCGG-----
>NC_006270
GUUCAUGGAUCUUC--AUCCAUCGGGUUGGCAUUUAUAAGUAACCAUGCUAGCAAGACCUUUGCCUUAUUGGCGAGAGGUCUUUUUUUCUGAAAAUACCCUG
>NC_009725
AUUCAUGGAUCAU---AUCCAUCGGGUUGGCAUUGCC-----AAUCAU--UCAUGCUAGCAAGACCUUUGCCUUAUUAUCGGCAAAGGUCUUUUUUUGCGU- ---AAAAA-CCGC
>NC_014551
AUUCAUGGAUCAU---AUCCAUCGGGUUGGCAUUGCC-----AAUGAU--UCAUGCUAGCAAGACCUUUGCCUUAUUAUCGGCAAAGGUCUUUUUUUGCGU- ---AAAAAACCGC
>NC_009848
UUAACAUGGACUUA- GUUCAUCGGGUUGGCAUGAUUCACAUUA- ---CAUGCUAGCAAGACCUUUGCCAU- UACAGGCAAAGGUCUUUUUUUGCAUUC-----AUAAAGCCU

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....
.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....
.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....

```

#oppB

#The following shows an alignment in 5'-UTR of oppB and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_014479
-GUCU-AUGUGAAAAACAAAACCUCAAGG--UAUAUGGG-ACCUA-----UUUCCAAUAUACUUUACUGA-----UAAUGUAAAAACAUAUGGAGGUGUUUCCCCCUUGC
>NC_016047
-GUCUUUUUUUGAAAAACAAAACCUCAAGG--UAUAUGGGACCUA- ---UUUCCAAUACUUUACUGAAAGAUAAAAAUUAAAAUUAUGGAGGUGUUUCCCCCUUGC
>NC_009964
-GGCUACGUCUGAAAAUAAAGACCUCUAGG--UAUAUGGGGAGAA- ---AGCCCCAAUACUUUACUGAUGGAGAUAAAAUUAUGAAGGAGGUGUUUCCCCCUUGC
>NC_009725
AAGACGGUUCUGAAAAACAAAAGACC- CAAGG--UAUAUGGGGAGAU- ---GUCCCCAAUACUUUACUGAUUAAGAUAAAAUUAUGAAGGAGGUGUU- CACCUUUGC
>NC_006270
-----AAUUGCAUGAAAG--UAUAUGGGGCUUAGACUUUCCCCCAUAUUAUUGAAAAAGAUUAUAGACUGAAUUAUUCGGAGGUGUAAAAAUUGA
>NC_014019
-----GUAACAUAUUUGACAAAAGGUUAUUGGGCCUUG- ---UGCUCCAAUACUUUACUUUUGUGCG- --CGAAUUUUUUAUAAAAUUAUGGAGGUGUUCAGGGGUGU

```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):

```

.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....
.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....
.....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....((((((-.....)))))).....

```

#nagA

#The following shows an alignment in 5'-UTR of nagA and the predicted ConSLOpt structures produced by RNAConSLOpt

```

>NC_012581
AACAGACGUACUAAGUUUCCUUUU- UGUUAAACAAAGAGGAAUUUCAUUAGAUAUGACAAUCUACUCGCGCAUAUUAUUAAGAUUGGAAUUAUGGCGAAUAAAGGUAUAUAUA
>NC_012472
--AGACGUACUAAGUUUCCUUUU- UGUUAAACAAAGAGGAAUUUCAUUAGAUAUGACAAUCUACUCGUGCAUAUUAUUAAGAUUGGAAUUAUGGCGAAUAAAGGUAUAUAUA
>NC_005957
GAGAGACGUACGAAACUUCUUUUU- UGUUAAACAAAGAGGAAUUUCAUUAGAUAUGACAAUCUACUCGUGCAUAUUAUUAAGAUUGGAAUUAUGGCGAAUAAAGGUAUAUAUA
>NC_011725
AAGAGACGUAAAGAAUUUCCUUUUUGAAUAAAAAGGAAUUUUAUUAAGAUAUGACAAUCUACUCGUGUUAUUAUUAAGAUUGGAAUUAUGGCGAAUAAAGGUAUAUAUA
>NC_014171
AAGAGACGUAAAGAAUUUCCUUUUUGAAUAAAAAGGAAUUUCAUUAGAUAUGACAAUCUACUCGUGCGUUAUUAUUAAGAUUGGAAUUAUGGCGAAUAAAGGUAUAUAUA

```





.....((((((((((((((((.....)))))))).)))))).....

```
#acoA
#The following shows an alignment in 5'-UTR of acoA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_014479
GGUGAUGCCCGGUCUUAUUUGCAUAAAA---CGAGACAAAUGGUUCAGAUCGAAACAAAUAUGAGACACCUGUCUCAAACUGUCUC-CAGUG
>NC_011773
-----GAUAAUAUUUUCAAAUAUUAGGUGAAACAAAAGUGACAAAAGUGACAAAACGAGACAGGUGUCUCAUUUUGUCCACCUUUUU
>NC_003909
-----AAUAUAUGAUUCUCAAUUUAGGUGAAACAAAAGUGACAAAACGAGACAGAUUGUCUCAAAUUUGUCCACCUUUUU
>NC_011772
-----GAUAAUAUGUUCUCAAUUUAGGUGAAACAAAAGUGACAAAACGAGACCAUCUCUGUCUCAUUUUGUCCACCUUUUU
>NC_005957
-----GAUAAUAUUUUCAAAUAUUAGGUGAAACAAAAGUGACAAAACGAGACUAUAUGUCUCAUUUUGUCCACCUUUUU
>NC_006274
-----GAUAAUAUUUUCAAAUAUCAGGUGAAACAAAAGUGACAAAACGAGACUAAUUGUCUCAUUUUGUCCACCUUUUU
```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....((((((((((((((((.....)))))))).)))))).....

```
#rpsB
#The following shows an alignment in 5'-UTR of rpsB and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_014479
AAA-----UACACACCCUUAACGAUUUUGCAGGGGUGCUGCAGG-CG--GCAGUUCGCACAAAAUAGACCUAAGCGGAGGAAAAAACCA
>NC_009674
AGUACAAAAGUACACACGUUUGCUGAUUUUAGU-GUUGGUGCUACUUU-U-GU--AGUUUACUUAAGAUAGUAGCGGAGGAGGAUAUCAAAAA
>NC_014019
AUU-----ACACACCCUUGUUGAUUC-GGUUGAUGGUGCUACUUUU---UGUAGUUUGGCUGAAGAUAGAAUAGCGGAGGAGACUUAAAA
>NC_011773
AGUACAAAAGUACACACGUUUACUGAUUUUAGU-GUUGGUGCUACGUU----UGUAGUUUGCUUAGAGAUAGAAUAAACGGAGGAUAUCAAAAA
>NC_003997
AGUACAAAAGUACACACGUUUGCUGAUUUUAGU-GUUGGUGCUACGUU----UGUAGUUUGCUUAGAGAUAGAAUAAACGGAGGAUAUCAAAAA
>NC_010184
AGUACAAAAGUACACACGUUUACUGAUUUUAGU-GUUGGUGCUACGUU----CGUAGUUUGCUUAGAGAUAGAAUAAACGGAGGGAUAUCAAAAA
```

#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
.....((((((((((((((((.....)))))))).)))))).....

```
#ymdA
#The following shows an alignment in 5'-UTR of ymdA and the predicted ConSLOpt structures produced by RNAConSLOpt
>NC_000964
ACUUGACAAGGGCGGAUAAACACACU-CAUUCUCCUGAAGGUUCUGUAUGUUGAGAAAAUAGACAAUUAUGACUCCGACACUU--UUUAAGCAACAAC
>NC_014479
ACUUGACAAGGGCGGAUAAAUAUCU-CAUUCUCCUGAAGGUUCUGUAUGUUGAGAAAAUAGACAAUUAUGACUCCGACACUUU-UUUUAAGCAACAAC
>NC_009725
```



```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
(((.....(((.....)))))).....(((.....)))).....  
.....(((.....))).....(((.....)))).....(((.....)))).....
```

```
#exoA  
#The following shows an alignment in 5' -UTR of exoA and the predicted ConSLOpt structures produced by RNAConSLOpt  
>NC_003997  
--UUUGUAUAGCAUGAAAUUUGGAAAGAAACAUCACAGAGGAGGAGGCUAAAAGUGAAGUUUUCAUGGAAUGUAAAUGGUUUUGCGAGCGUUUAUCGCAA  
>NC_011725  
--UUUGUAUAGCAUGAAAUUUGGAAAGAAACAUCACAGAGGAGGAGGCUAAAAGUGAAGUUUUCAUGGAAUGUAAAUGGUUUUGCGAGCGUUUAUCGCAA  
>NC_014171  
--UUUGUAUAGCAUGAAAUUUGGAAAGAAACAUCACAGAGGAGGAGGCUAAAAGUGAAGUUUUCAUGGAAUGUAAAUGGUUUUGCGAGCGUUUAUCGCAA  
>NC_011772  
--UUUGUAUAGCAUGAACUUUGAAAUGUAACAUCACAGAGGAGGAGGCUAAAAGUGAAGUUUUCAUGGAAUGUAAAUGGUUUUCGUGCGUUUAUCGCAA  
>NC_006274  
--UUUGUAUAGCAUGAAAUUUGGAAAGAAACAUCACAGAGGAGGAGGCUAAAAGUGAAGUUUUCAUGGAAUGUAAAUGGUUUUCGUGCGUUUAUCGCAA  
>NC_006582  
AUCUAUGCACACUCUGGCACUGGAUAAAAGAGAGGAGGAGUACGACAACUA-UGAAAUUUCUAUCGUGGAAUGUCAAUUGCCUGCGCGCAUGUGUAAAAAA
```

```
#The top 2 predicted ConSLOpt structures ranked by RankB (structures' associated minimal energy barriers):  
--(((.....(((.....)))))).....(((.....)))).....  
--(((.....(((.....)))))).....(((.....)))).....
```