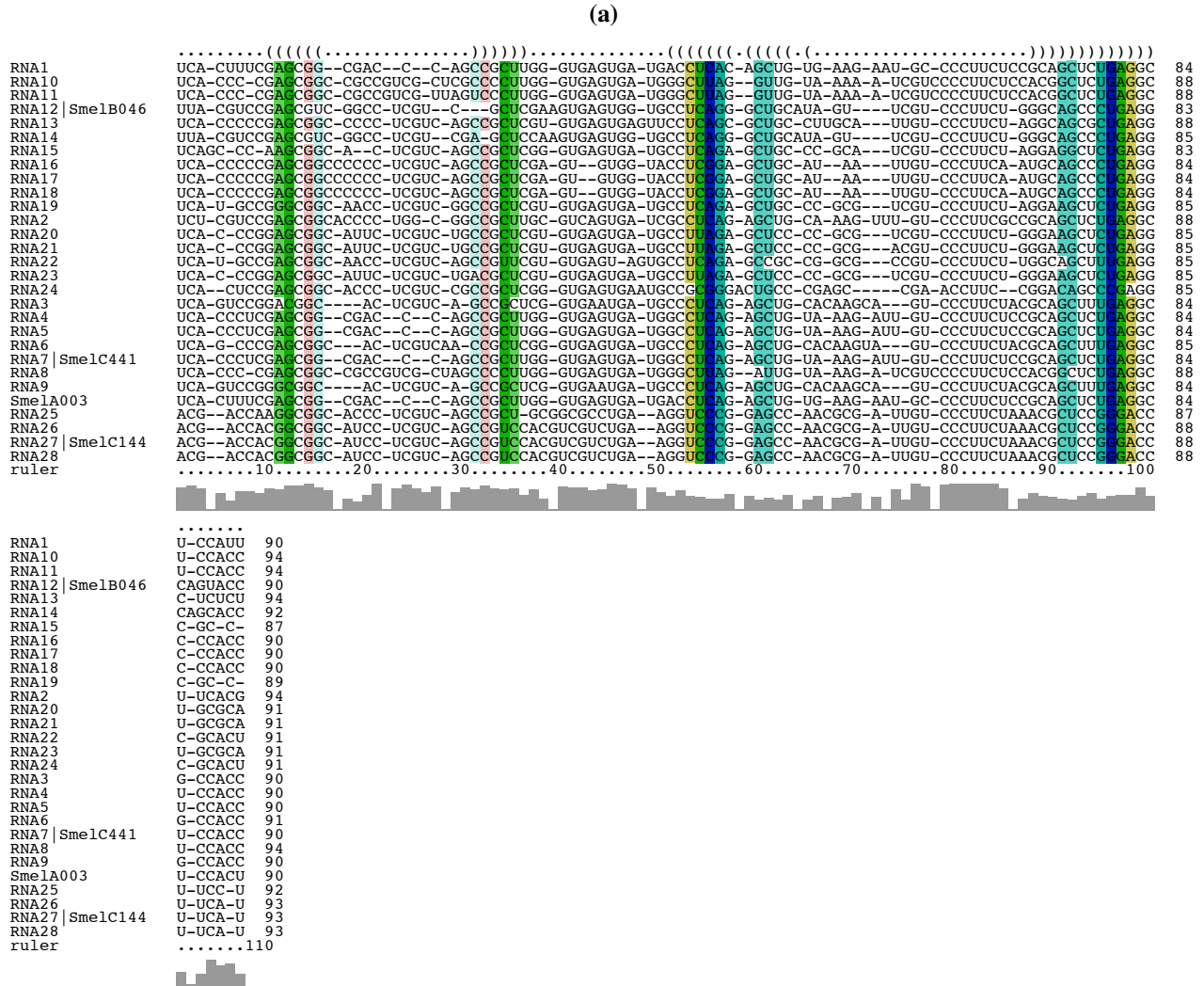
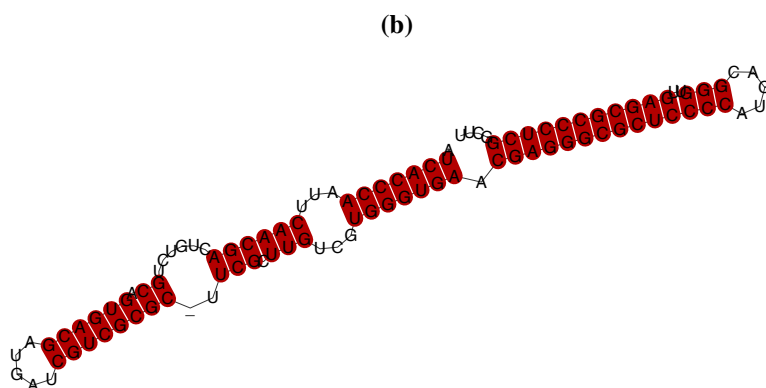
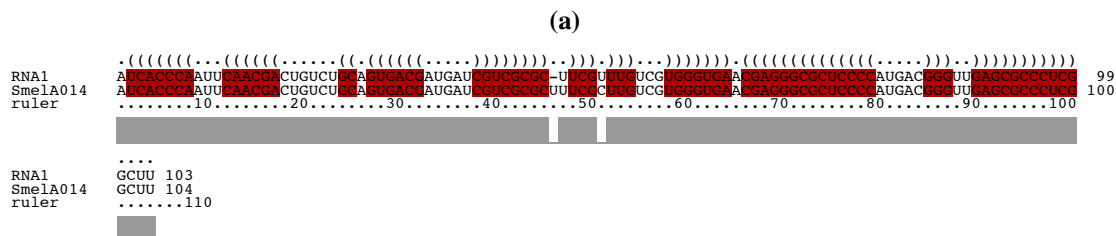


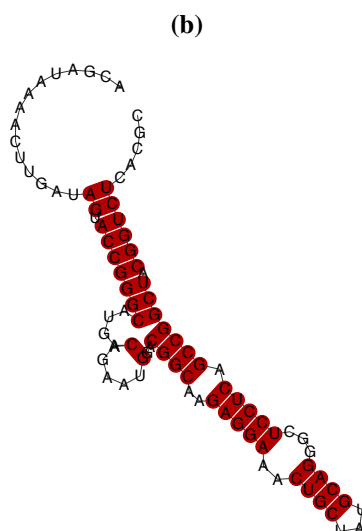
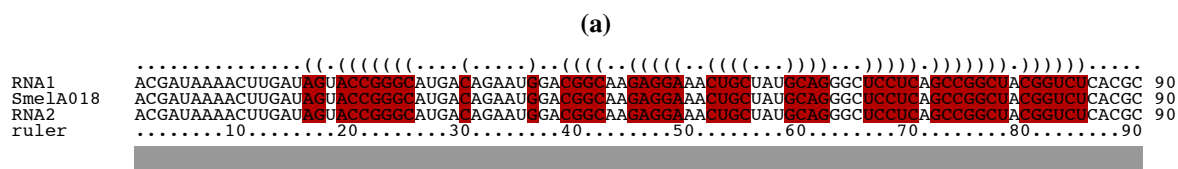
RNA Family Model of SmelA003. (a) Alignment of $RFM_{SmelA003}$ sequences (SCI = 0.73); (b) Consensus secondary structure (minimum free energy -32.39 kcal/mol) for the alignment shown in (a).



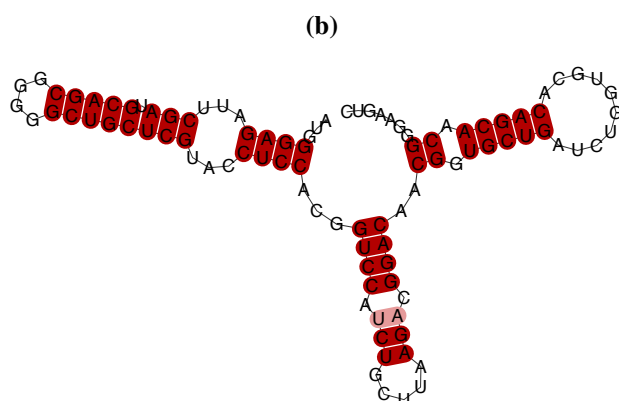
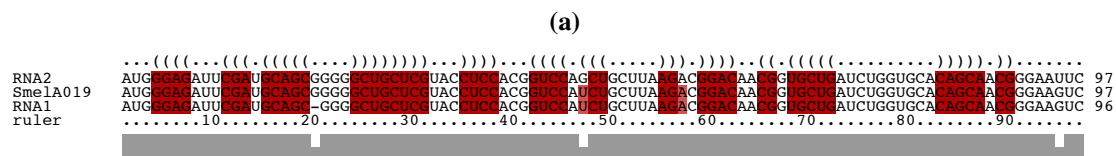
RNA Family Model of SmelA014. (a) Alignment of $RFM_{SmelA014}$ sequences (SCI = 1.01); (b) Consensus secondary structure (minimum free energy -54.90 kcal/mol) for the alignment shown in (a).



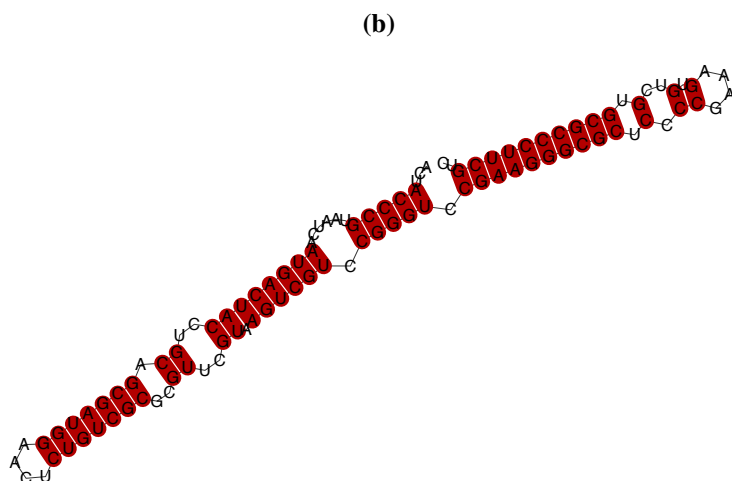
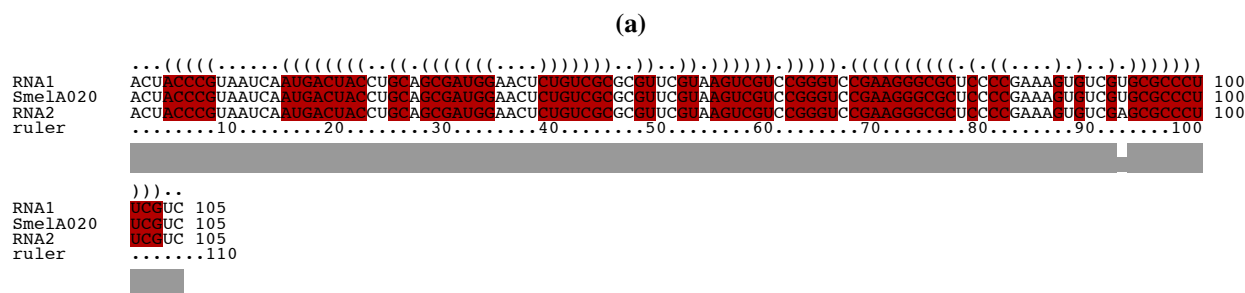
RNA Family Model of SmelA018. (a) Alignment of $RFM_{SmelA018}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -25 kcal/mol) for the alignment shown in (a).



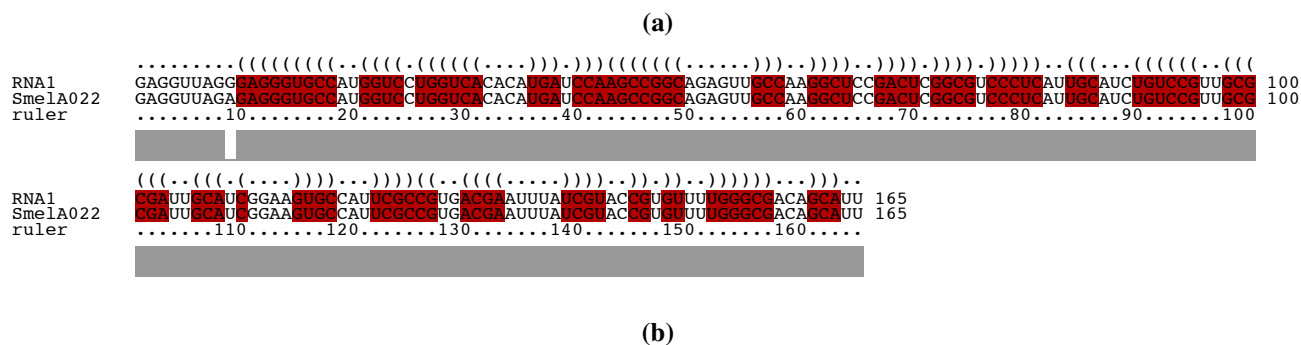
RNA Family Model of SmelA019. (a) Alignment of $RFM_{SmelA019}$ sequences (SCI = 0.98); (b) Consensus secondary structure (minimum free energy -32.80 kcal/mol) for the alignment shown in (a).



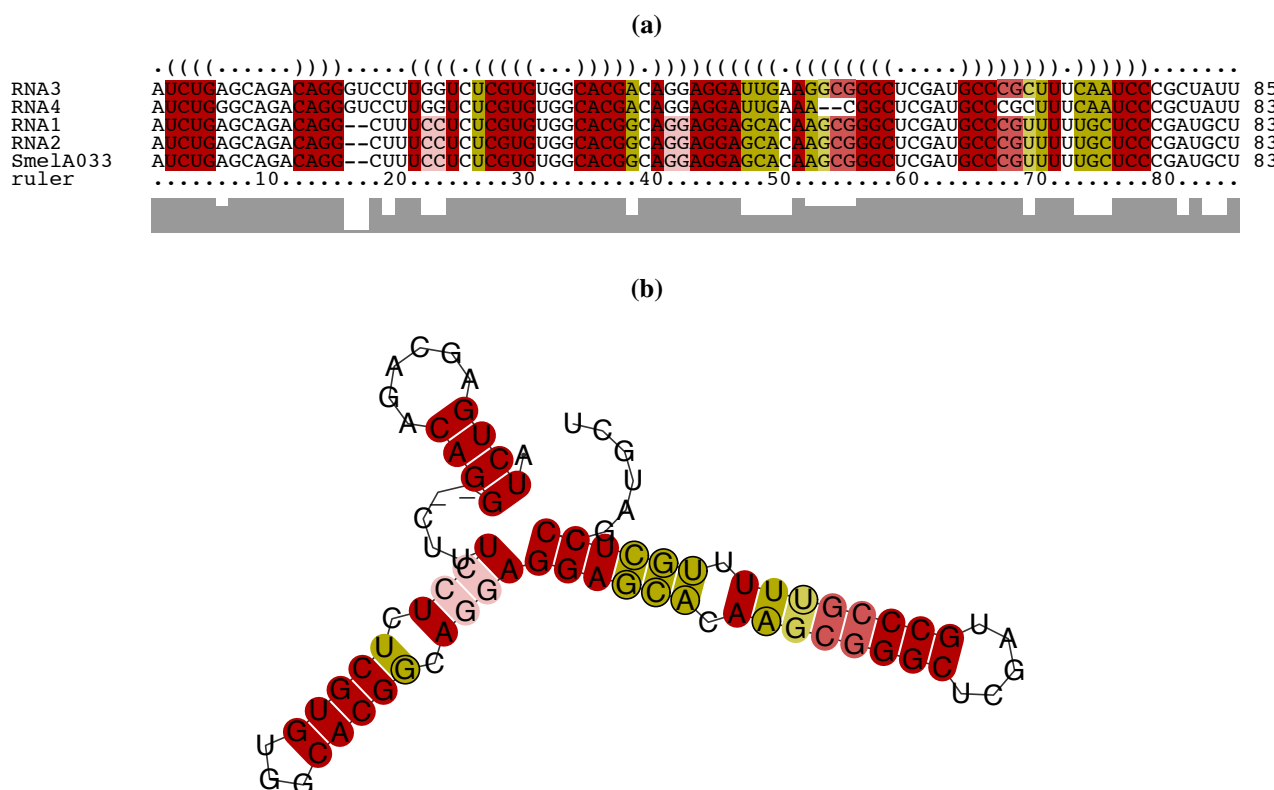
RNA Family Model of SmelA020. (a) Alignment of $RFM_{SmelA020}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -44.50 kcal/mol) for the alignment shown in (a).



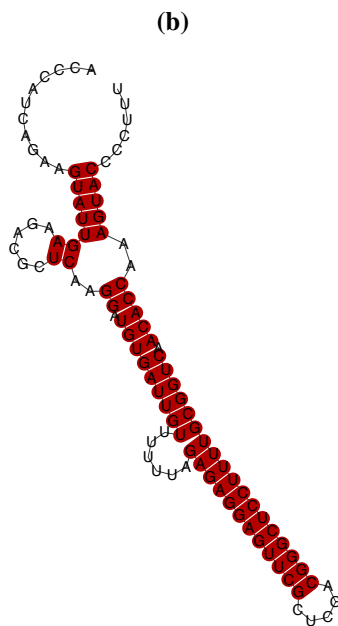
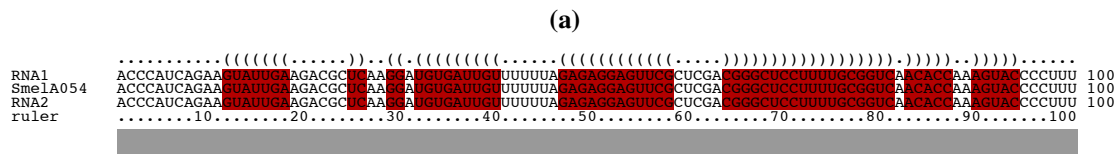
RNA Family Model of SmelA022. (a) Alignment of $RFM_{SmelA022}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -56.20 kcal/mol) for the alignment shown in (a).



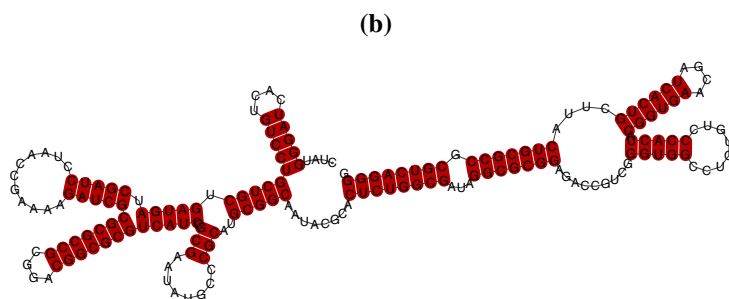
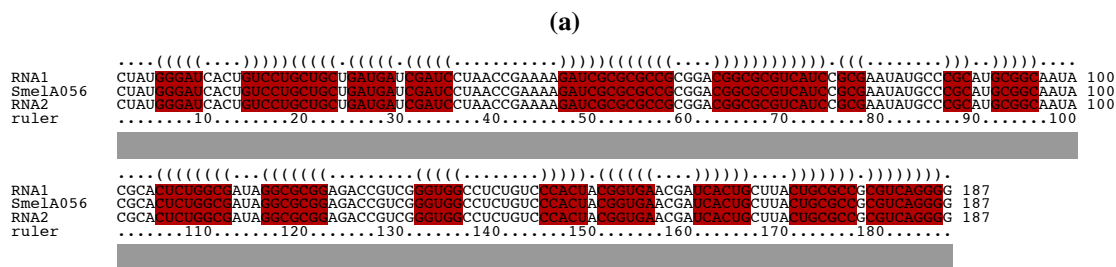
RNA Family Model of SmelA033. (a) Alignment of $RFM_{SmelA033}$ sequences (SCI = 0.92); (b) Consensus secondary structure (minimum free energy -31.88 kcal/mol) for the alignment shown in (a).



RNA Family Model of SmelA054. (a) Alignment of $RFM_{SmelA054}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -25.40 kcal/mol) for the alignment shown in (a).

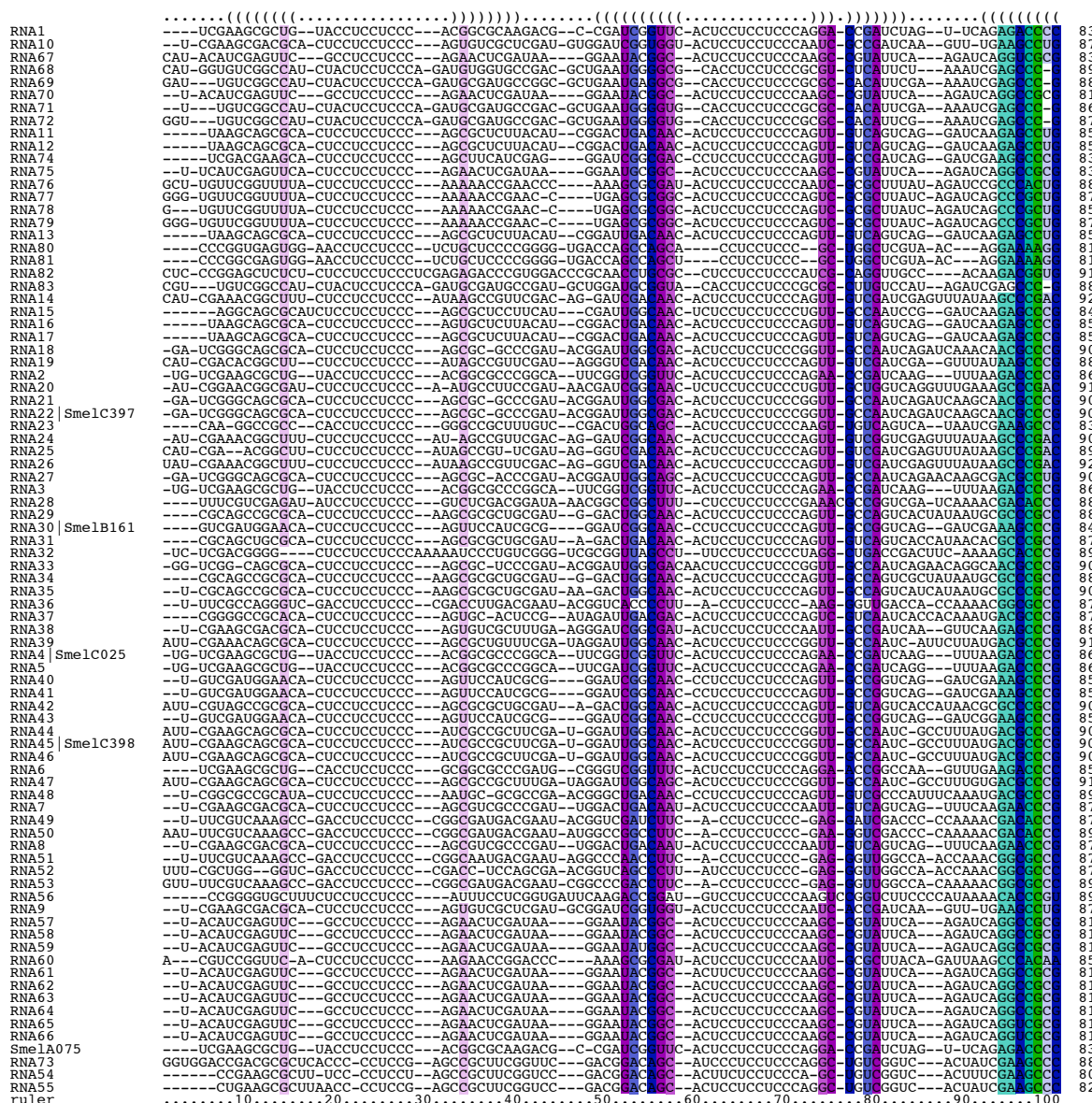


RNA Family Model of SmelA056. (a) Alignment of $RFM_{SmelA056}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -74.30 kcal/mol) for the alignment shown in (a).



RNA Family Model of SmelA075. (a) Alignment of $RFM_{SmelA075}$ sequences (SCI = 0.99); (b) Consensus secondary structure (minimum free energy -52.38 kcal/mol) for the alignment shown in (a).

(a)



RNA Family Model of SmelA075. Cont.

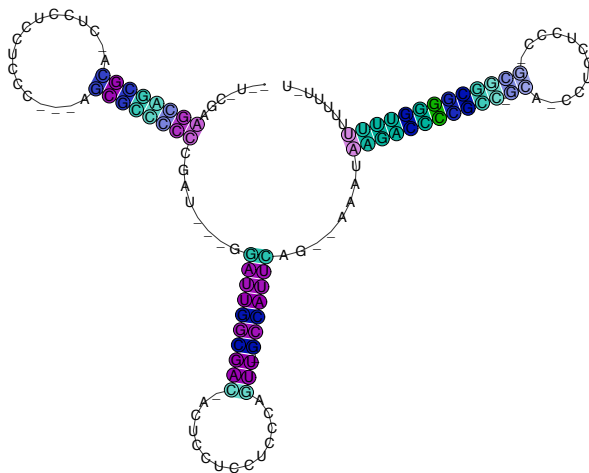
(a)

```

((.....)).....
RNA1      GA-UGCACCUCUCCGCAUCGAGCUUUUCUGUA-U 118
RNA10     CC-GCA-CCUCCUCCGCGGAGUUUUUCUU-U 120
RNA67     C----AUCUCCUCCGCGGAGUUUUUCUU-U 109
RNA68     CU-GCCACCUCUCCGCGGAGCUUUUUUCU-U 122
RNA69     CU-GCCACCUCUCCGCGGAGCUUUUUUU-U 120
RNA70     C----AUCUCCUCCGCGGAGCUUUUUUCUUU 110
RNA71     CU-GCCACCUCUCCGCGGAGCUUUUUUGUU 121
RNA72     CU-GCCACCUCUCCGCGGAGCUUUUUUCU-G 120
RNA11     GC-GCA-CCUCCUCCGCGGAGUUUUUUUCUU-U 118
RNA12     GC-GCA-CCUCCUCCGCGGAGUUUUUUUCUU-U 118
RNA74     GC-GCA-CCUCCUCCGCGGAGUUUCUCUUU-U 116
RNA75     C----AUCUCCUCCGCGGAGCUUUUUUCUUU 112
RNA76     CA-CAUCCUCCUCCGCGGAGUUUCUCUUU-U 121
RNA77     CA-CAUCCUCCUCCGCGGAGUUUCUCUUU-U 120
RNA78     CA-CAUCCUCCUCCGCGGAGUUUCUCUUU 120
RNA79     CA-CAUCCUCCUCCGCGGAGUUUCUCUUU-U 120
RNA13     GC-GCA-CCUCCUCCGCGGAGUUUUUUUCUU-U 118
RNA80     CC-GGCACCUCUCCGCGGAGUUUUUUU----- 112
RNA81     CC-GGCACCUCUCCGCGGAGUUUUUUU----- 112
RNA82     GC-GUACUCCUCCGCGGAGUUUCUUU----- 123
RNA83     CU-GGCACCUCUCCGCGGAGUUUUUUUUUCC 124
RNA14     GGAUCU-CCUCC-CCC-----UUUGUUUCUA-U 121
RNA15     AU-GCAUCCUCCUCCGCGGAGUUUUUUUUU 118
RNA16     GC-GCA-CCUCCUCCGCGGAGUUUUUUUCUU-U 118
RNA17     GC-GCA-CCUCCUCCGCGGAGUUUUUUUCUU-U 118
RNA18     CU-GGA-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA19     AC-GGA-UCUCCUCCGCGGAGUUUUUUU-U 119
RNA2      AG-CCA-CCUCCUCCGCGGAGUUUUUUU-CUG-U 118
RNA20     GGAUCU-CCUCC-CCC-----UUUGUUUUCAU-U 120
RNA21     CU-GGA-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA22     CU-GGA-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA23     GG-UGCACCUCUCCGCGGAGUUUUUUU-U 117
RNA24     GGAUCU-CCUCC-CCC-----UUUGUUUCUG-U 119
RNA25     GGA--U-CCUCC-CCC-----UUUGUUUCUG-U 116
RNA26     GGA--U-CCUCC-CCC-----UUUGUUUCUG-U 119
RNA27     CU-GGA-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA3      AG-CCA-CCUCCUCCGCGGAGUUUUUUU-CUG-U 118
RNA28     GC-GGCACCUCUCCGCGGAGUUUUUUUUU-U 122
RNA29     GGA--U-CCUCC-CCC-----UUUGUUUUUU-U 115
RNA30     GC-GCA-CCUCCUCCGCGGAGUUUCUCUU-U 116
RNA31     GGA--U-CCUCC-CCC-----UUUGUUUUUUU-U 114
RNA32     GGA-CCUCCUCCGCGGAGUUUUUUU-U 120
RNA33     CU-GGA-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA34     GGA--U-CCUCC-CCC-----UUUGUUUUUUU-G 115
RNA35     GGA--U-CCUCC-CCC-----UUUGUUUUUUU-U 117
RNA36     GC-GGCACCUCUCCGCGGAGUUUUUUU-U 119
RNA37     CC-GCAUCCUCCUCCGCGGAGUUUUUUU-U 119
RNA38     AC-GCAUCCUCCUCCGCGGAGUUUUUUUGU-U 122
RNA39     CC-GGA-UCUCCUCCGCGGAGUUUUUUU-U 122
RNA40     AG-CCA-CCUCCUCCGCGGAGUUUUUUU-CUG-U 118
RNA41     GC-GCA-CCUCCUCCGCGGAGUUUCUCUU-U 116
RNA42     GGA--U-CCUCC-CCC-----UUUGUUUUUUU-U 117
RNA43     GC-GCA-CCUCCUCCGCGGAGUUUCUCUU-U 116
RNA44     CC-GGU-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA45     CC-GGU-CCUCCUCCGCGGAGUUUUUUU-U 121
RNA46     GAGCACCUCUCCGCGGAGUUUUUUU-U 121
RNA47     CC-GGU-CCUCC-CCC-----UUUGUUUCUU-U 119
RNA48     CC-GGA-UCUCCUCCGCGGAGUUUUUUUUU-U 122
RNA7      GC-GCA-CCUCCUCCGCGGAGUUUUUUU-U 120
RNA49     GC-CGGACCUCUCCGCGGAGUUUUUUUUU-U 121
RNA50     GC-CGGACCUCUCCGCGGAGUUUUUUUUU-U 121
RNA8      GC-GCA-CCUCCUCCGCGGAGUUUUUUU-U 120
RNA51     GC-CGCACCUCUCCGCGGAGUUUUUUU-U 121
RNA52     GC-CGCACCUCUCCGCGGAGUUUUUUU-U 121
RNA53     GC-CGCACCUCUCCGCGGAGUUUUUUU-U 121
RNA54     CG-----UUUUUUUUUUUUUUUUUUUU 119
RNA9      CC-GCA-CCUCCUCCGCGGAGUUUUUUUUU-U 120
RNA57     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA58     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA59     CG-UUCUCCUCCUCCGAGGCUUUUUUUUUU 121
RNA61     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA62     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA63     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA64     C----AUCUCCUCCGCGGAGUUUUUUUUU 110
RNA65     C----AUCUCCUCCGCGGAGUUUUUUUUU 109
RNA66     C----AUCUCCUCCGCGGAGUUUUUUUUU 109
SmelA075 GA-UGCACCUCUCCGCAUCGCUUUUCUGUA-- 117
RNA73     GG-CGC-CCU-CCUCCGCGGAGUUUUUUU-U 118
RNA54     GG-CGCACU-CCUCCGCGGAGUUUUUUU-U 113
RNA55     GG-CGCACU-CCUCCGCGGAGUUUUUUU-U 115
ruler     .....110.....120.....130.....

```

(b)



RNA Family Model of SmelA099. (a) Alignment of $RFM_{SmelA099}$ sequences (SCI = 0.87); (b) Consensus secondary structure (minimum free energy -60.52 kcal/mol) for the alignment shown in (a).

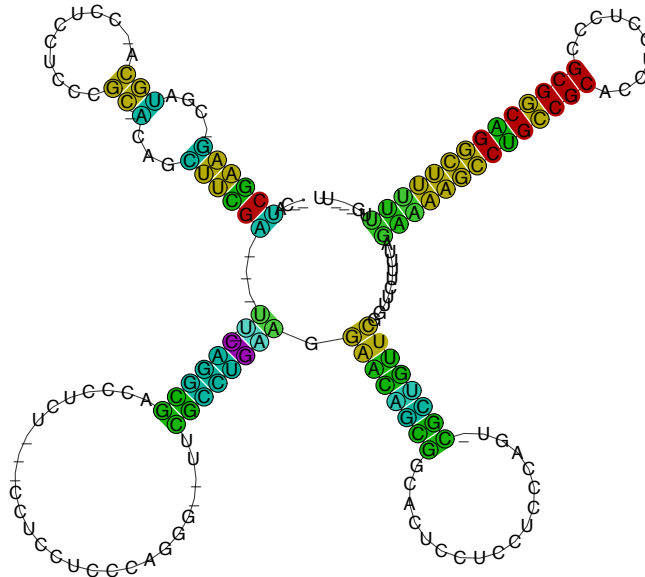
(a)

Phylogenetic tree showing the relationship between various RNA sequences. The tree is rooted at the bottom left and branches out to the right. Bootstrap values are indicated at the nodes. The sequences are color-coded: green for conserved regions, red for variable regions, and blue for regions with specific mutations.

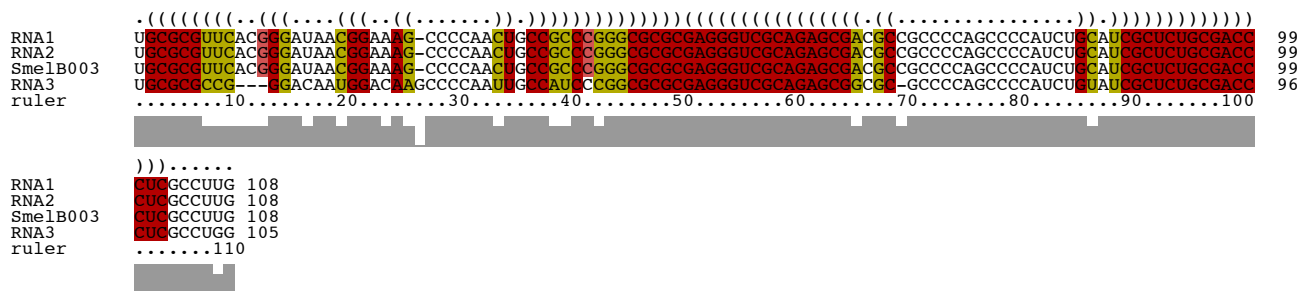
Sequence alignment of the 5' UTR region (nucleotides 10-100) for various RNA sequences. The sequences are color-coded: green for conserved regions, red for variable regions, and blue for regions with specific mutations.

Sequence alignment of the 5' UTR region (nucleotides 110-170) for various RNA sequences. The sequences are color-coded: green for conserved regions, red for variable regions, and blue for regions with specific mutations.

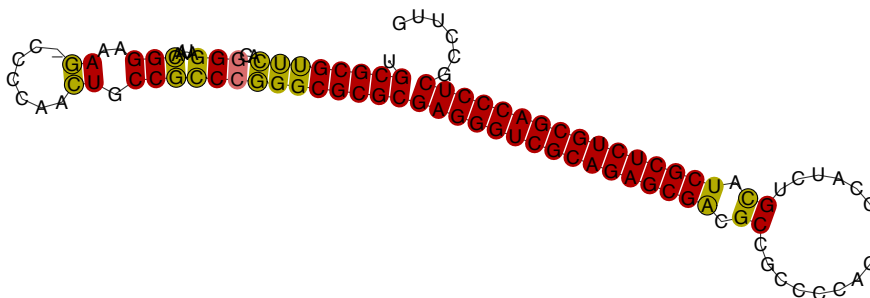
(b)



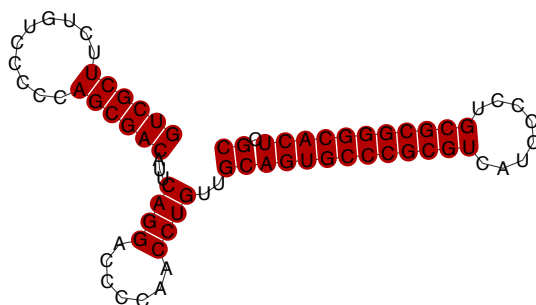
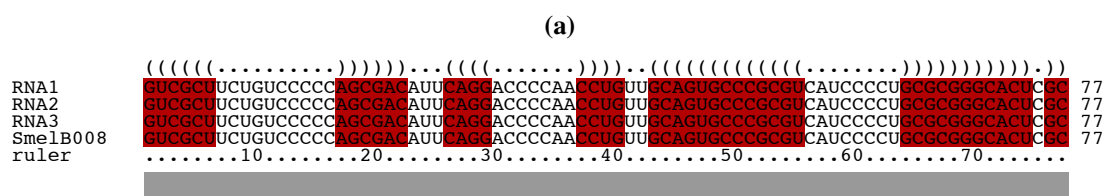
(a)



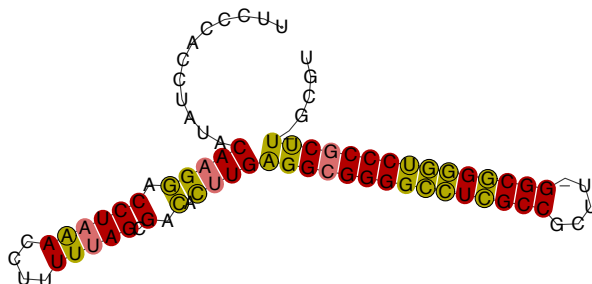
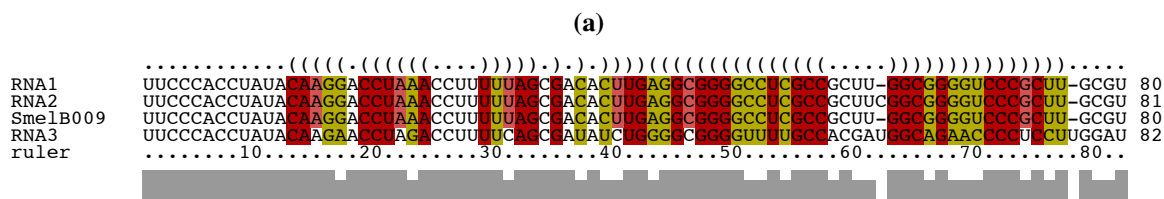
(b)



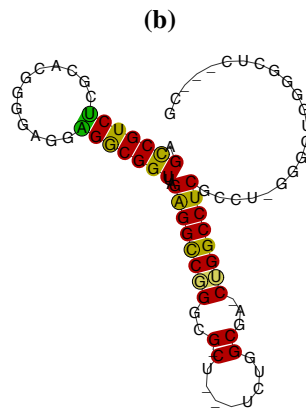
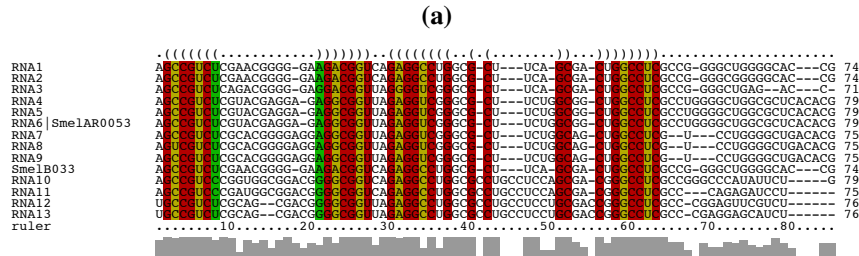
RNA Family Model of SmelB008. (a) Alignment of $RFM_{SmelB008}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -34.40 kcal/mol) for the alignment shown in (a).



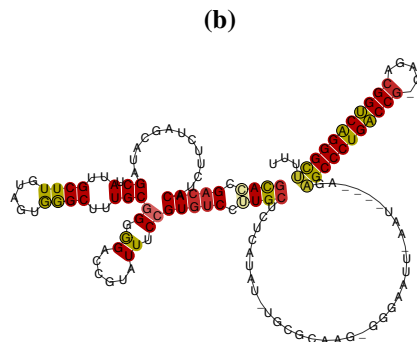
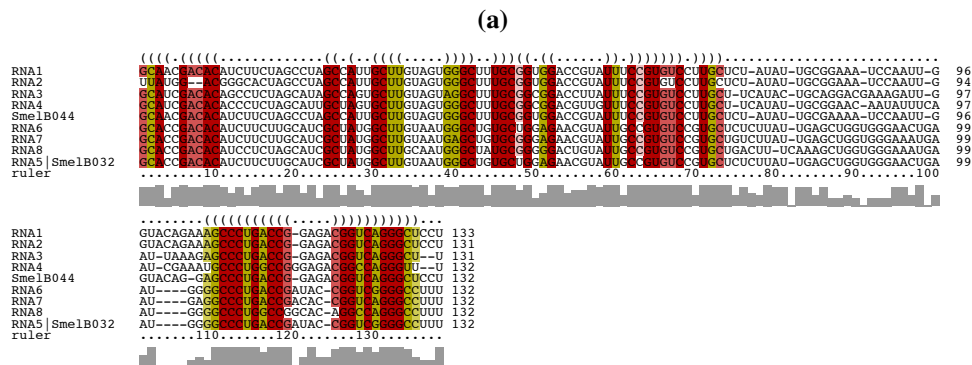
RNA Family Model of SmelB009. (a) Alignment of $RFM_{SmelB009}$ sequences (SCI = 1.02); (b) Consensus secondary structure (minimum free energy -34.61 kcal/mol) for the alignment shown in (a).



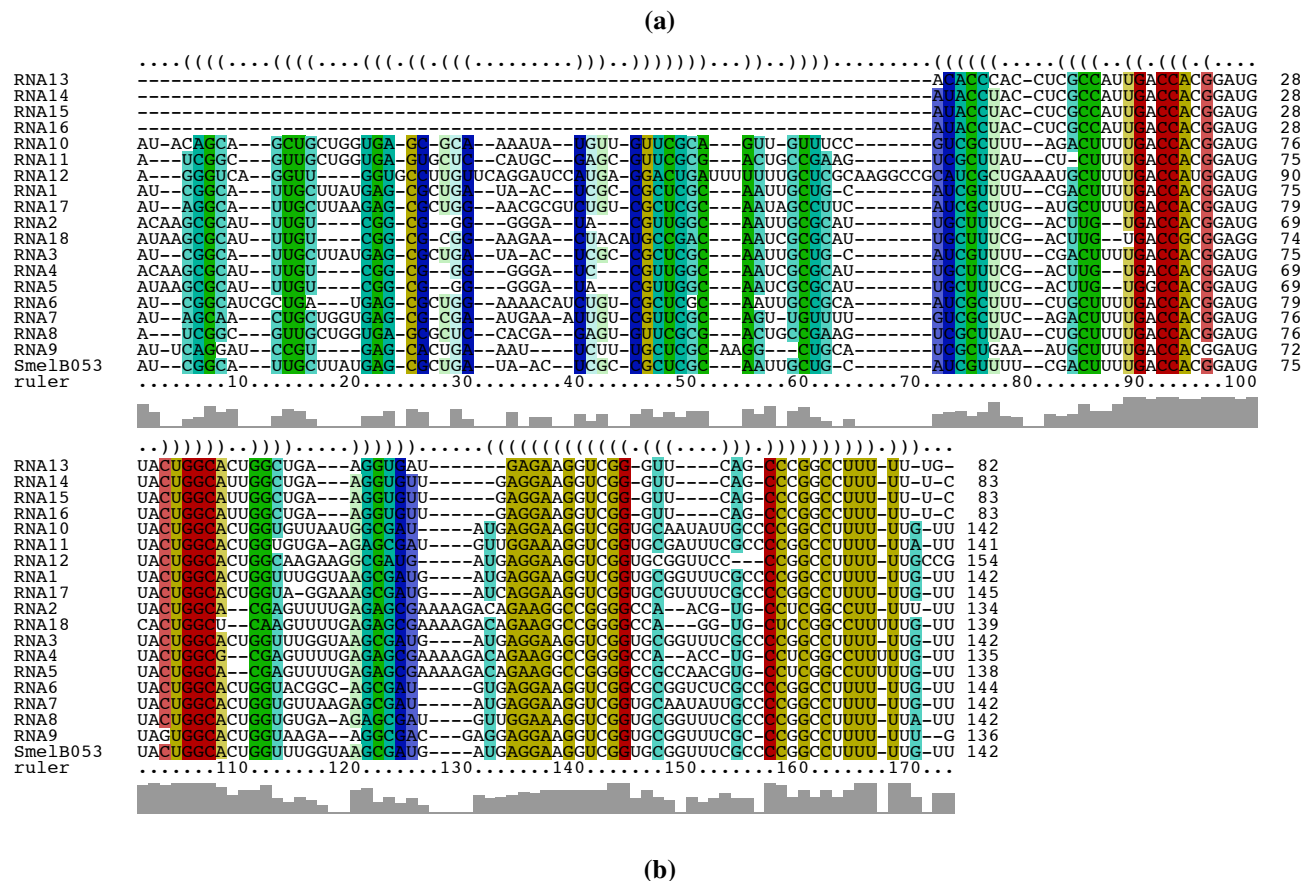
RNA Family Model of SmelB033. (a) Alignment of $RFM_{SmelB033}$ sequences (SCI = 0.67); (b) Consensus secondary structure (minimum free energy -24.07 kcal/mol) for the alignment shown in (a).



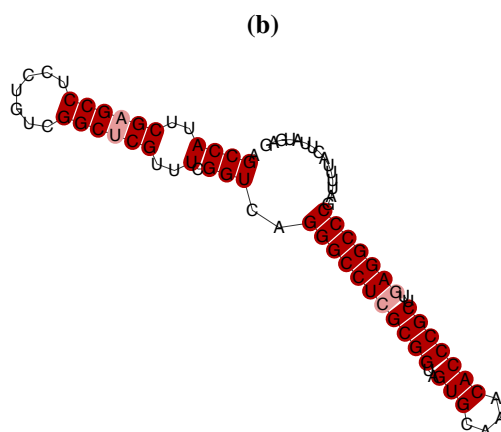
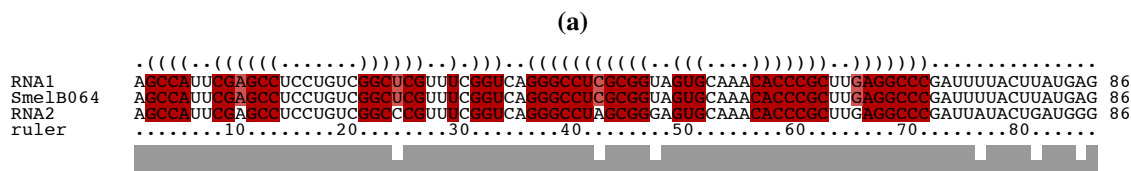
RNA Family Model of SmelB044. (a) Alignment of $RFM_{SmelB044}$ sequences (SCI = 0.76); (b) Consensus secondary structure (minimum free energy -41.37 kcal/mol) for the alignment shown in (a).



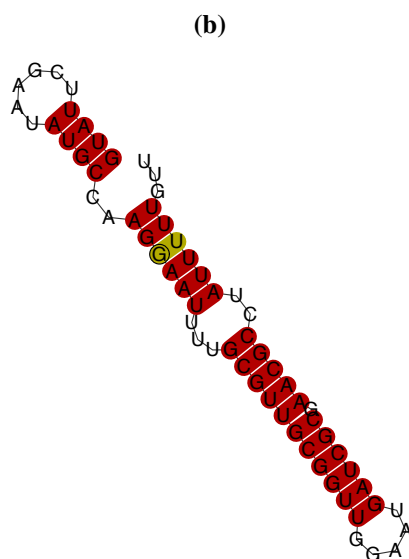
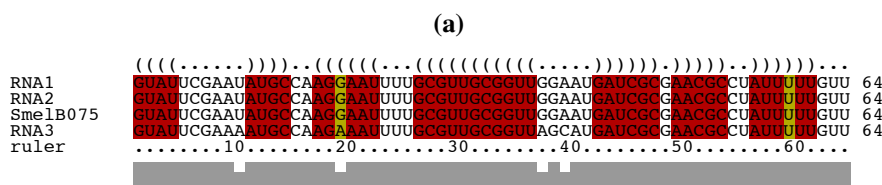
RNA Family Model of SmelB053. (a) Alignment of $RFM_{SmelB053}$ sequences (SCI = 0.32); (b) Consensus secondary structure (minimum free energy -16.88 kcal/mol) for the alignment shown in (a).



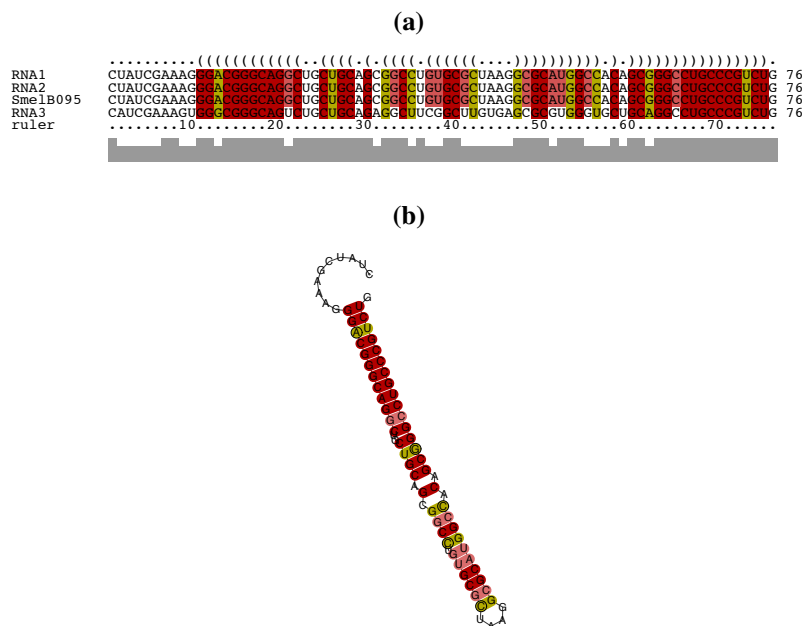
RNA Family Model of SmelB064. (a) Alignment of $RFM_{SmelB064}$ sequences (SCI = 0.91); (b) Consensus secondary structure (minimum free energy -32.97 kcal/mol) for the alignment shown in (a).



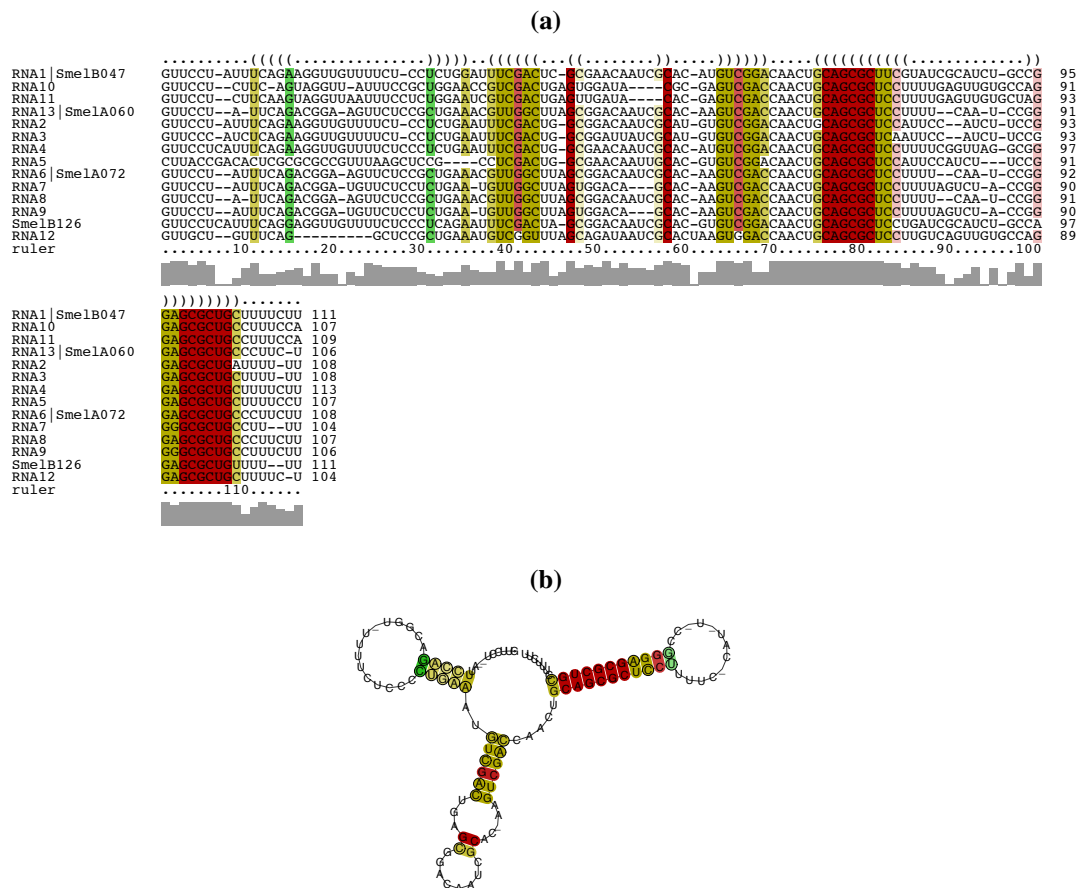
RNA Family Model of SmelB075. (a) Alignment of $RFM_{SmelB075}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -15.81 kcal/mol) for the alignment shown in (a).



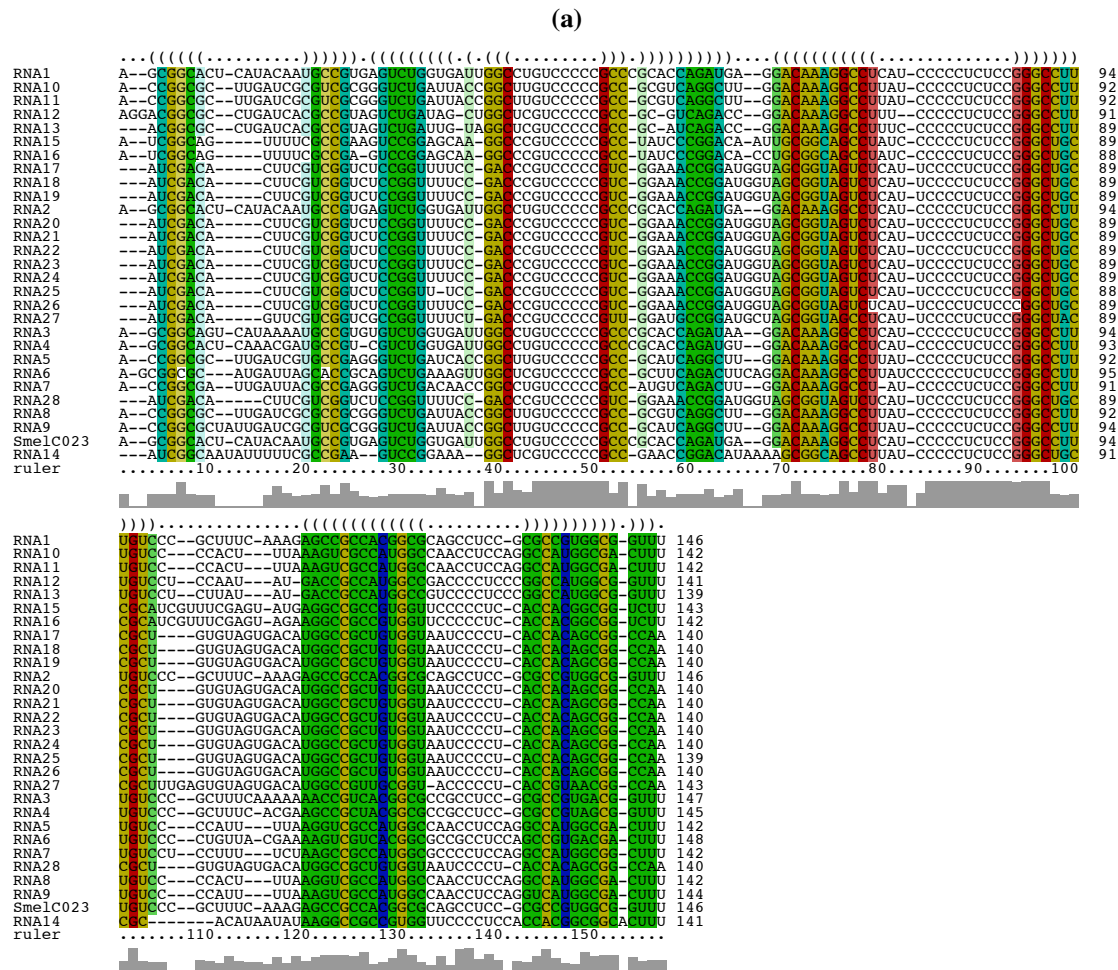
RNA Family Model of SmelB095. (a) Alignment of $RFM_{SmelB095}$ sequences (SCI = 0.89); (b) Consensus secondary structure (minimum free energy -43.39 kcal/mol) for the alignment shown in (a).



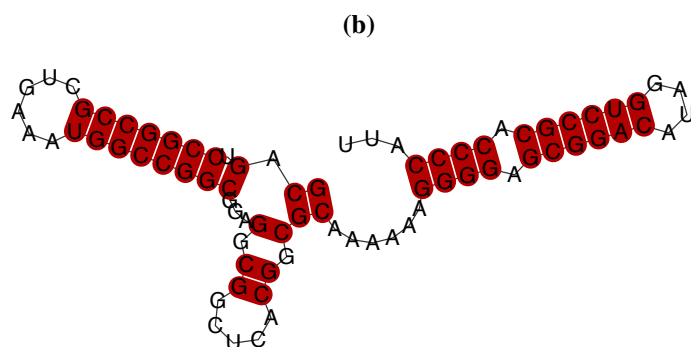
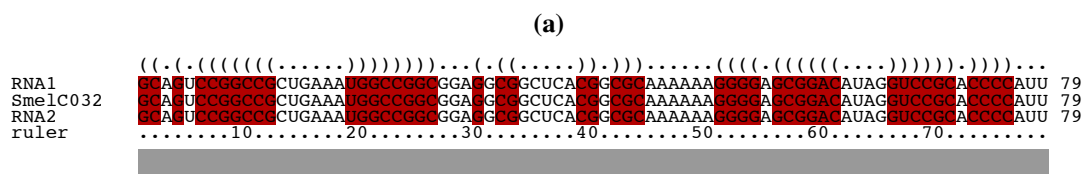
RNA Family Model of SmelB126. (a) Alignment of $RFM_{SmelB126}$ sequences (SCI = 0.7); (b) Consensus secondary structure (minimum free energy -27.44 kcal/mol) for the alignment shown in (a).



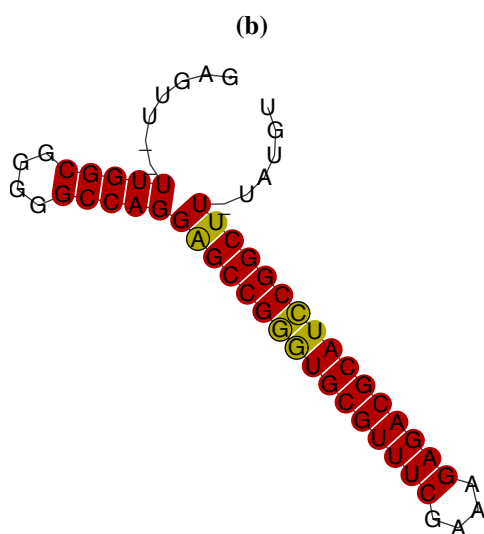
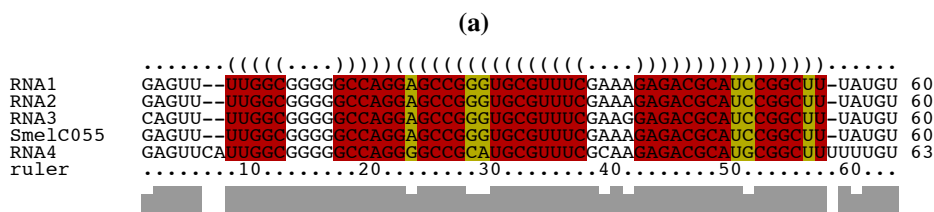
RNA Family Model of SmelC023. (a) Alignment of $RFM_{SmelC023}$ sequences (SCI = 1.11); (b) Consensus secondary structure (minimum free energy -78.06 kcal/mol) for the alignment shown in (a).



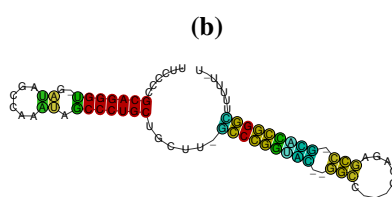
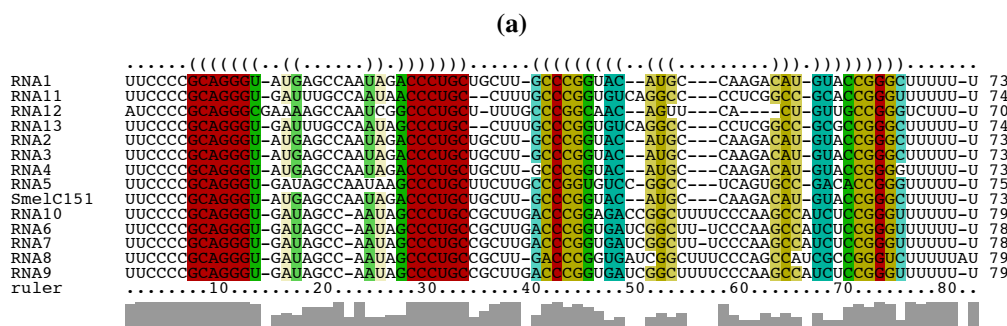
RNA Family Model of SmelC032. (a) Alignment of $RFM_{SmelC032}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -38.80 kcal/mol) for the alignment shown in (a).



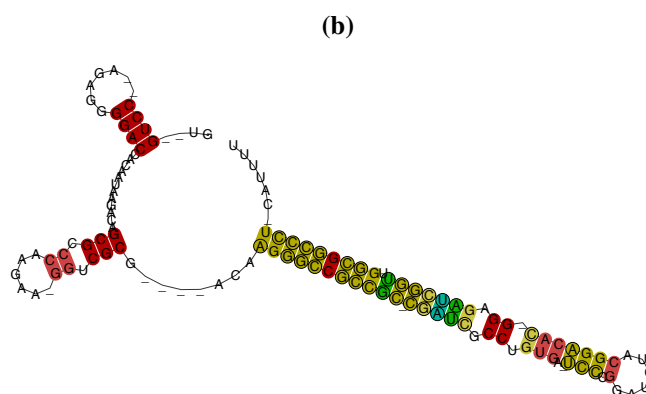
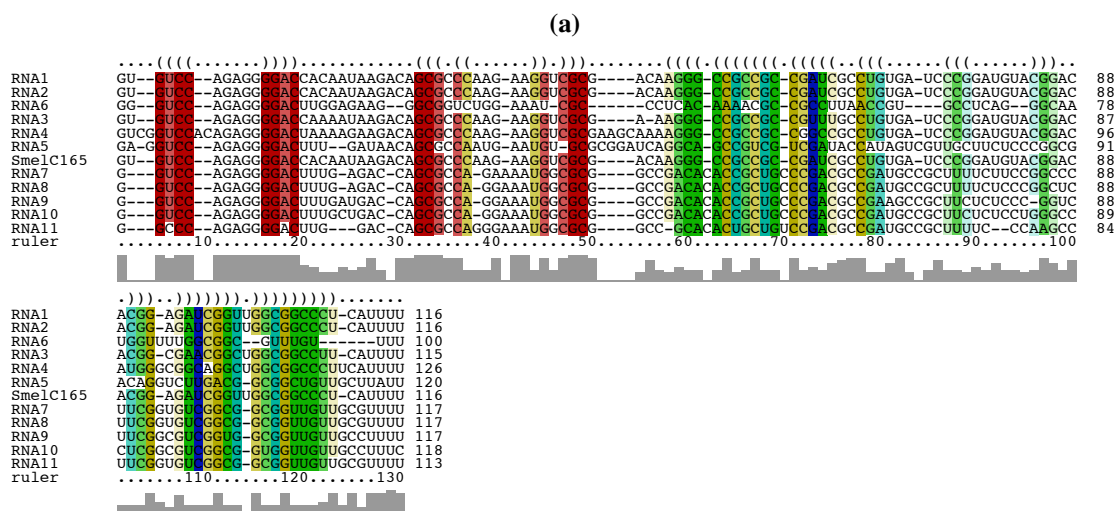
RNA Family Model of SmelC055. (a) Alignment of $RFM_{SmelC055}$ sequences (SCI = 1.04); (b) Consensus secondary structure (minimum free energy -38.96 kcal/mol) for the alignment shown in (a).



RNA Family Model of SmelC151. (a) Alignment of $RFM_{SmelC151}$ sequences (SCI = 1.02); (b) Consensus secondary structure (minimum free energy -36.37 kcal/mol) for the alignment shown in (a).

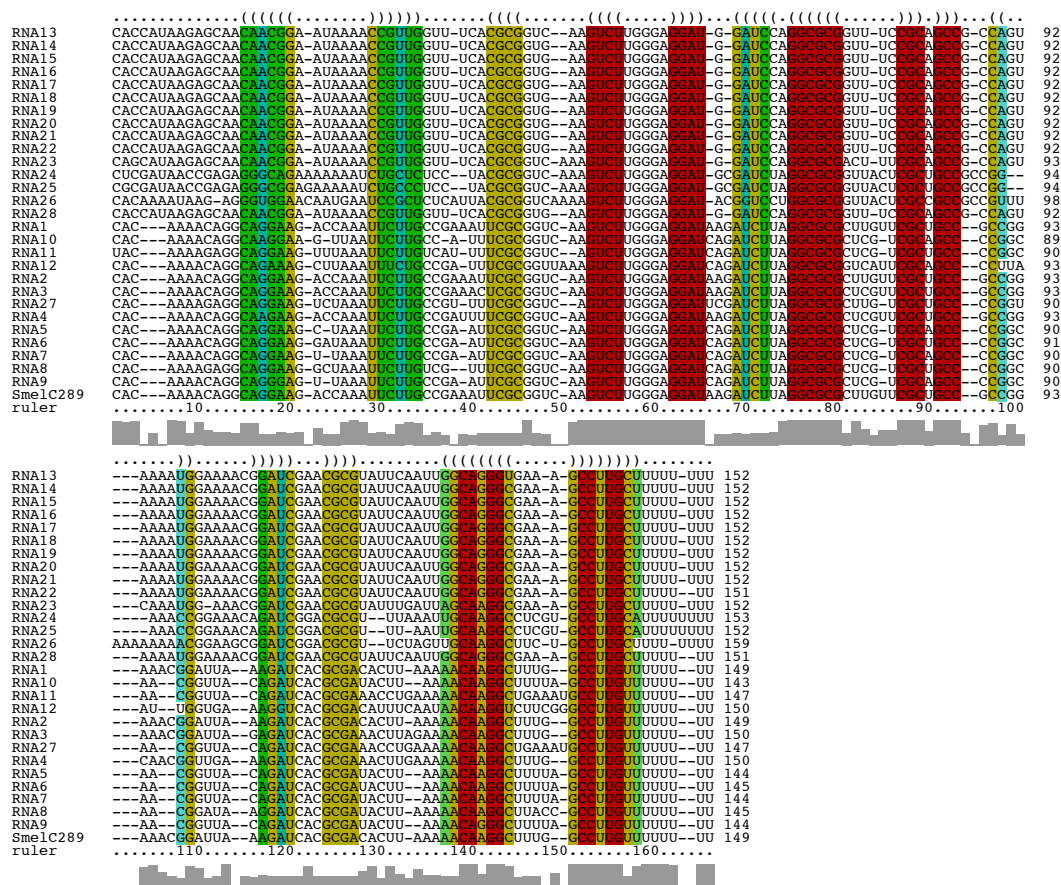


RNA Family Model of SmelC165. (a) Alignment of $RFM_{SmelC165}$ sequences (SCI = 0.71); (b) Consensus secondary structure (minimum free energy -43.24 kcal/mol) for the alignment shown in (a).

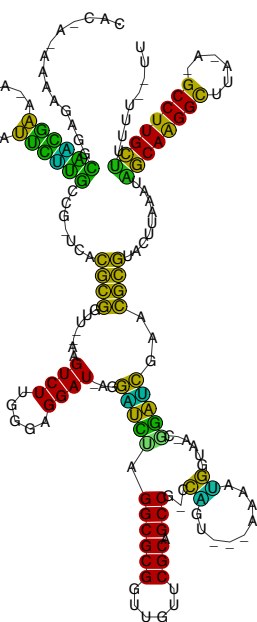


RNA Family Model of SmelC289. (a) Alignment of $RFM_{SmelC289}$ sequences (SCI = 0.9); (b) Consensus secondary structure (minimum free energy -48.93 kcal/mol) for the alignment shown in (a).

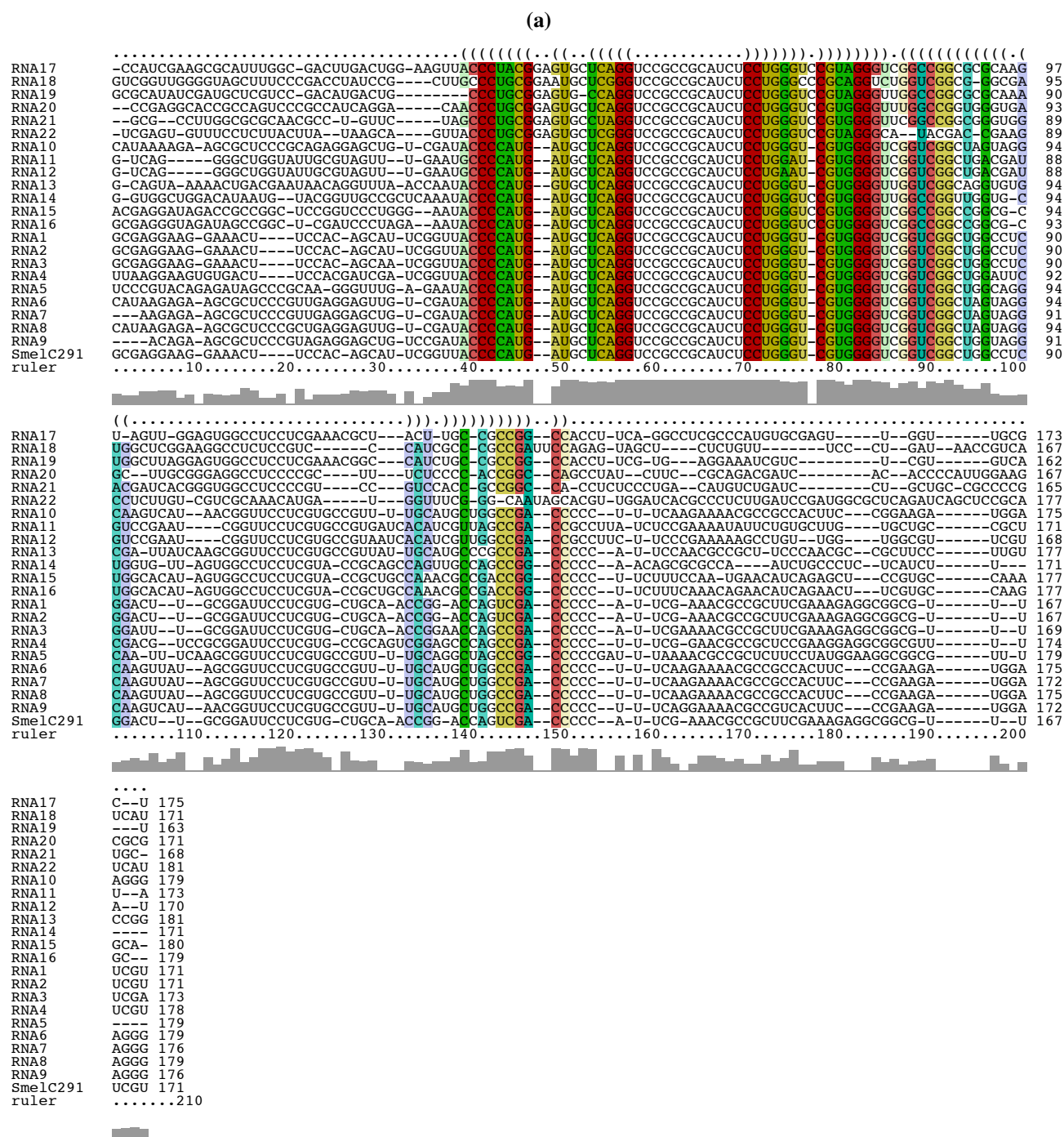
(a)



(b)



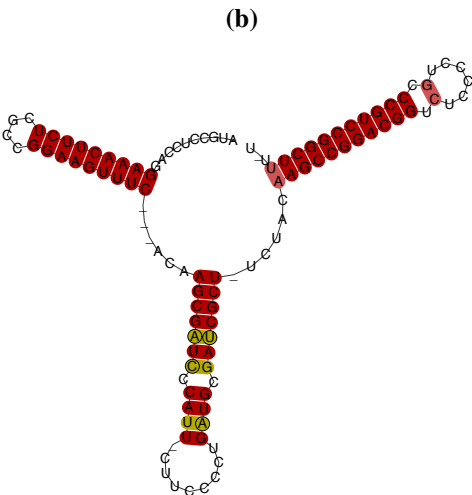
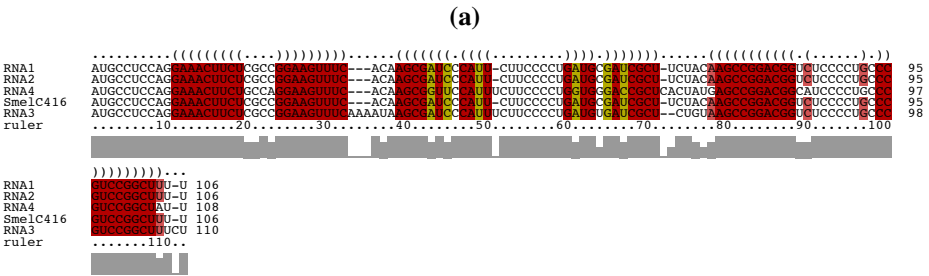
RNA Family Model of SmelC291. (a) Alignment of $RFM_{SmelC291}$ sequences (SCI = 0.55); (b) Consensus secondary structure (minimum free energy -42.63 kcal/mol) for the alignment shown in (a).



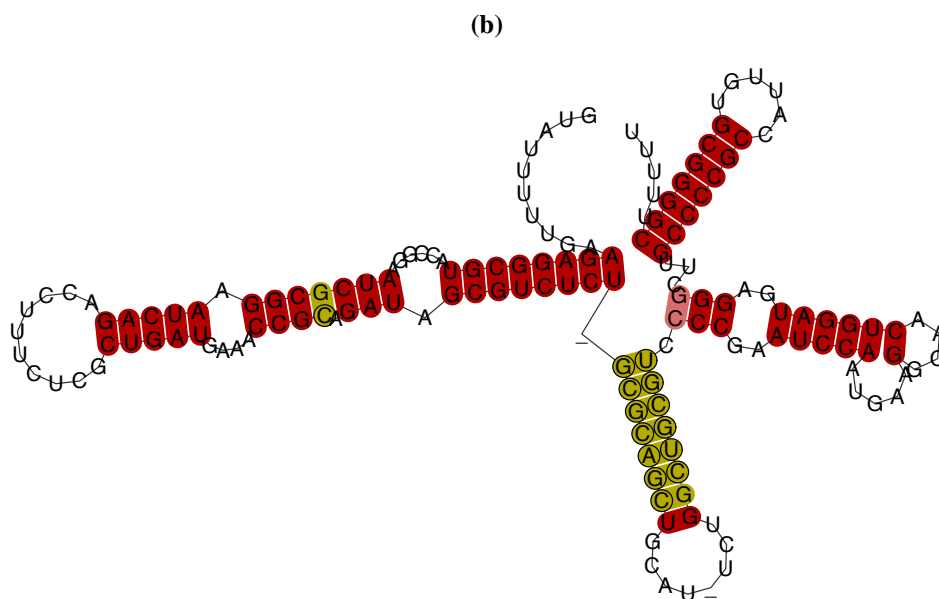
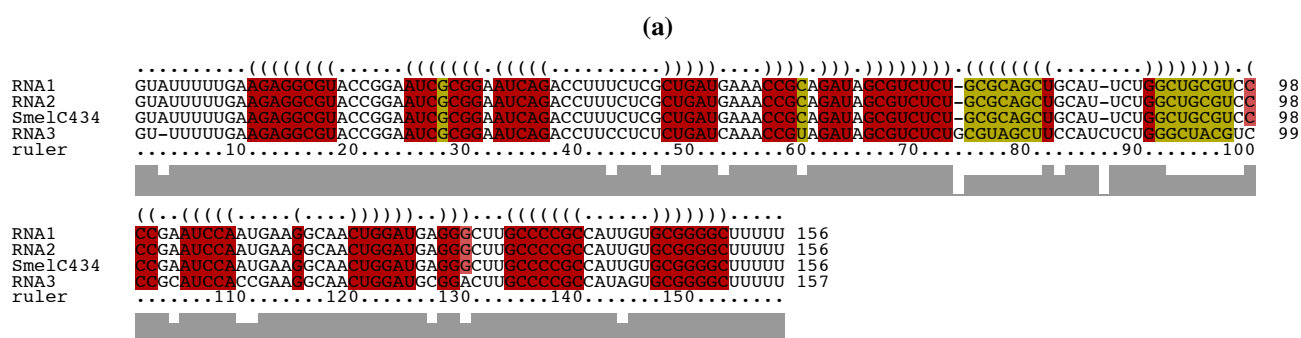
RNA Family Model of SmelC291. *Cont.*



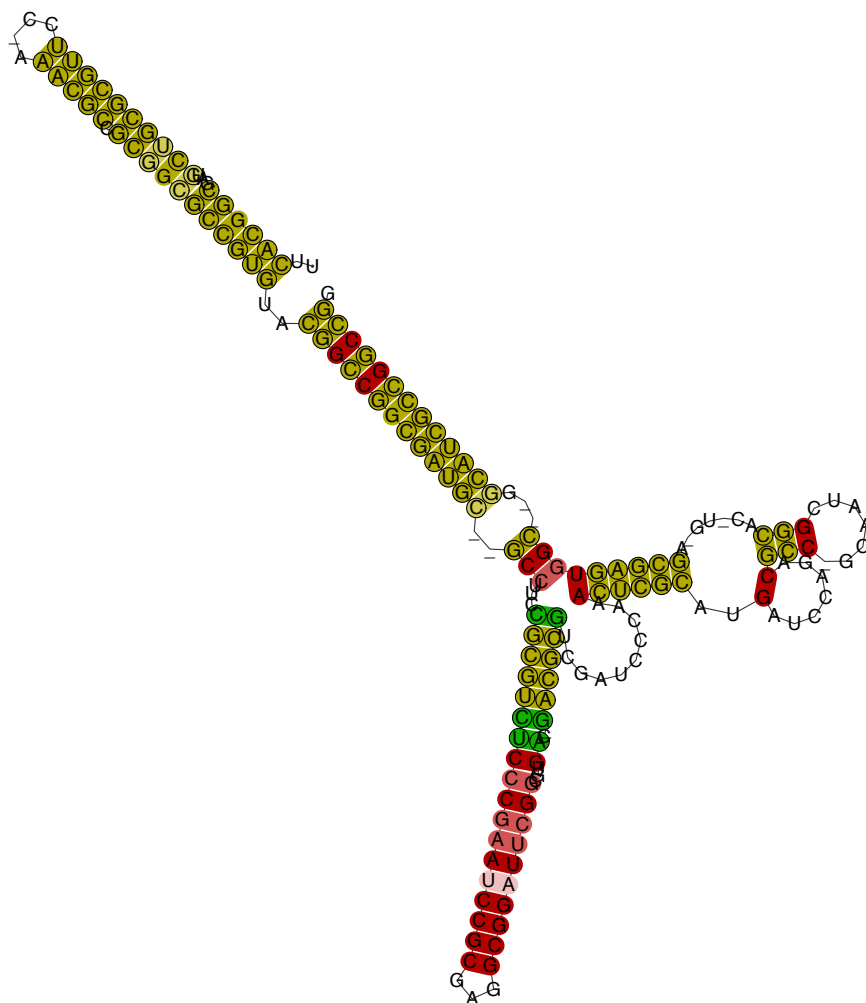
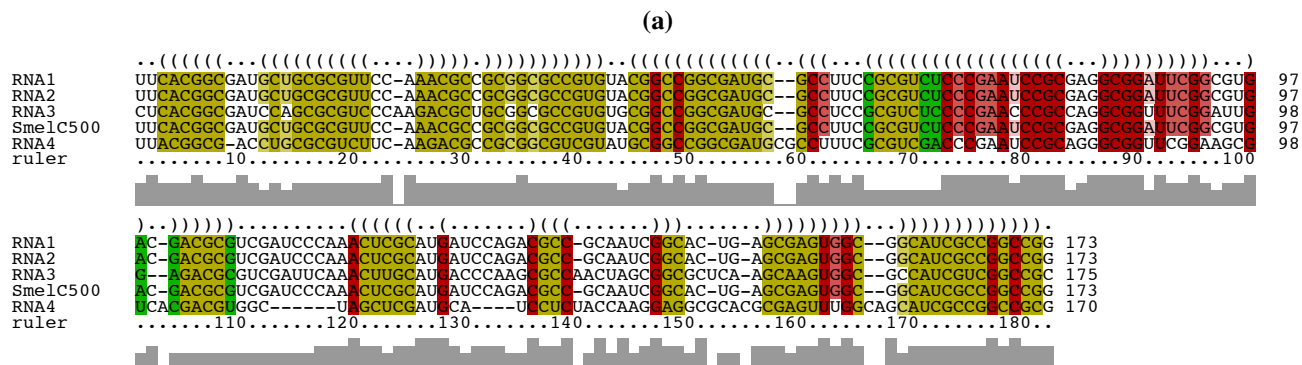
RNA Family Model of SmelC416. (a) Alignment of $RFM_{SmelC416}$ sequences (SCI = 0.98); (b) Consensus secondary structure (minimum free energy -43.52 kcal/mol) for the alignment shown in (a).



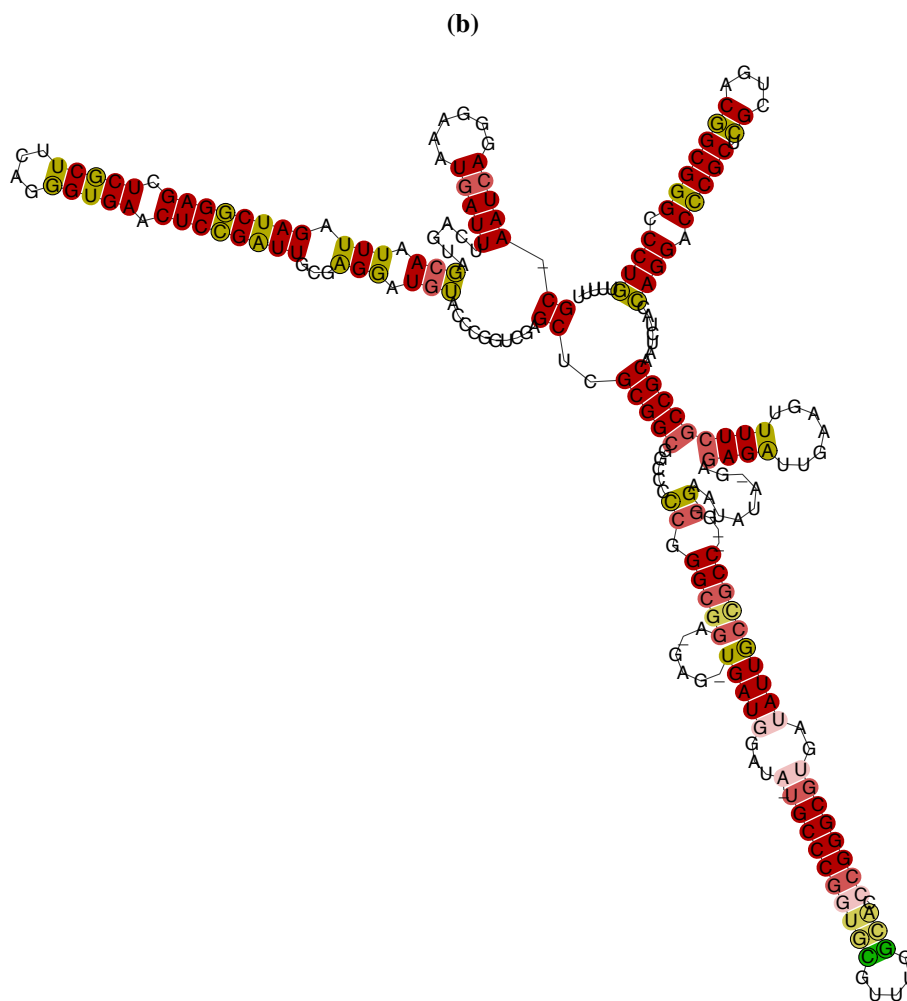
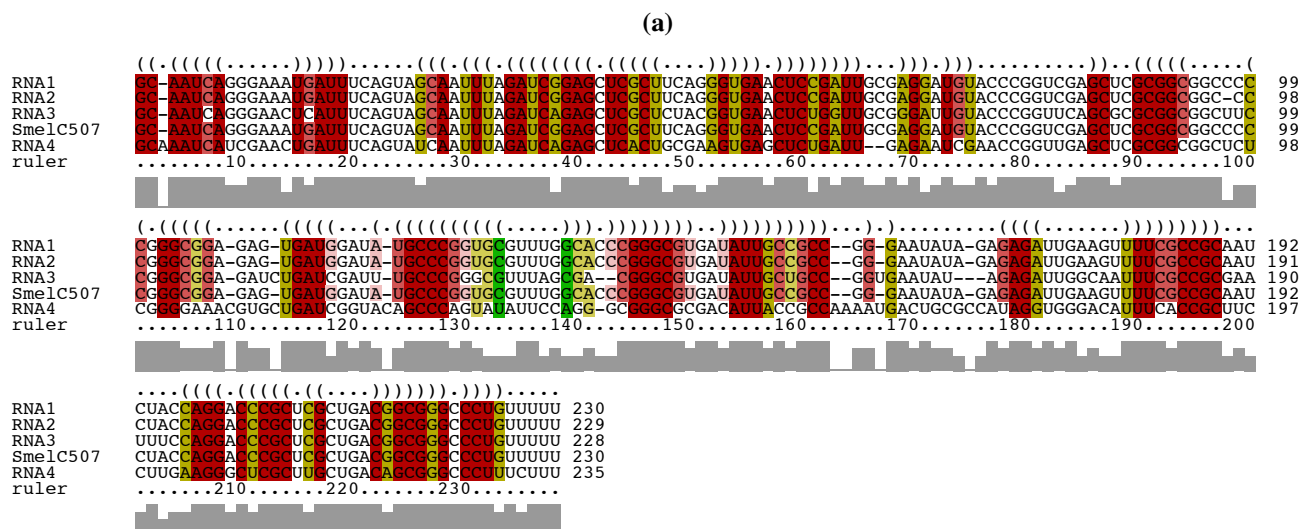
RNA Family Model of SmelC434. (a) Alignment of $RFM_{SmelC434}$ sequences (SCI = 0.99); (b) Consensus secondary structure (minimum free energy -59.35 kcal/mol) for the alignment shown in (a).



RNA Family Model of SmelC500. (a) Alignment of $RFM_{SmelC500}$ sequences (SCI = 1.01); (b) Consensus secondary structure (minimum free energy -101.60 kcal/mol) for the alignment shown in (a).

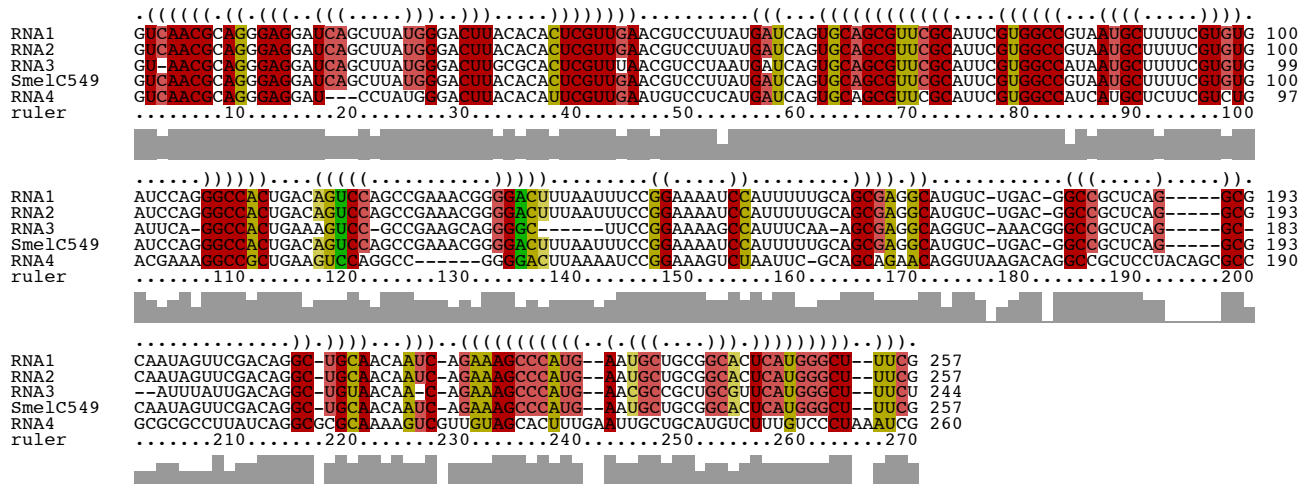


RNA Family Model of SmelC507. (a) Alignment of $RFM_{SmelC507}$ sequences (SCI = 0.79); (b) Consensus secondary structure (minimum free energy -72.08 kcal/mol) for the alignment shown in (a).

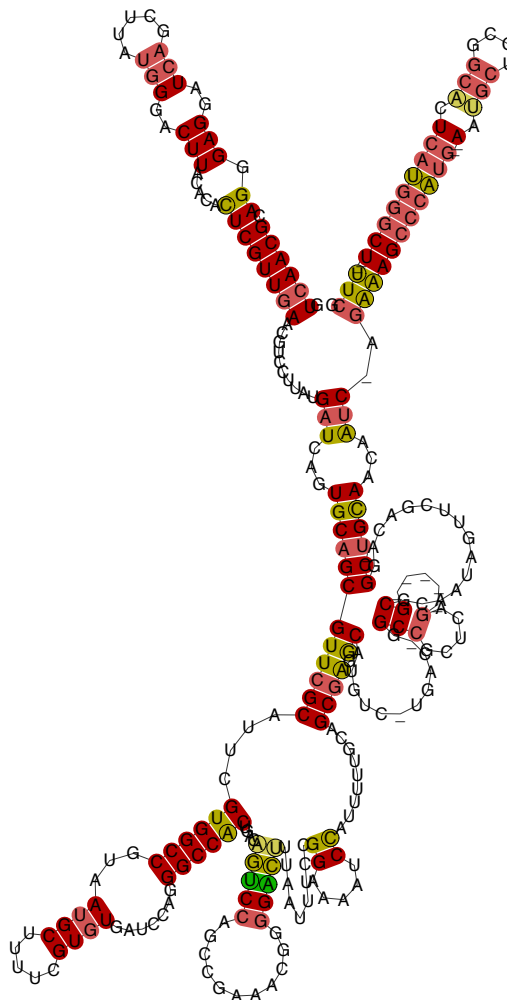


RNA Family Model of SmelC549. (a) Alignment of $RFM_{SmelC549}$ sequences (SCI = 0.69); (b) Consensus secondary structure (minimum free energy -61.88 kcal/mol) for the alignment shown in (a).

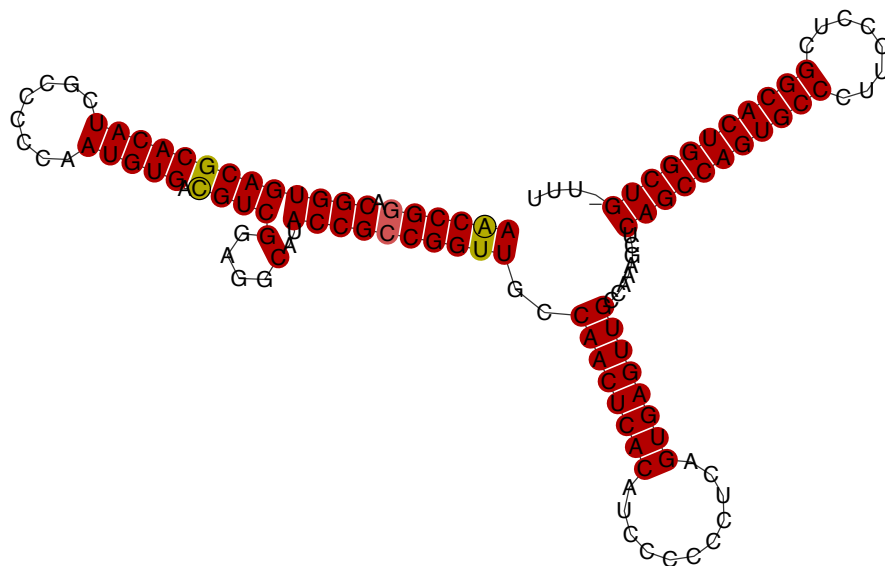
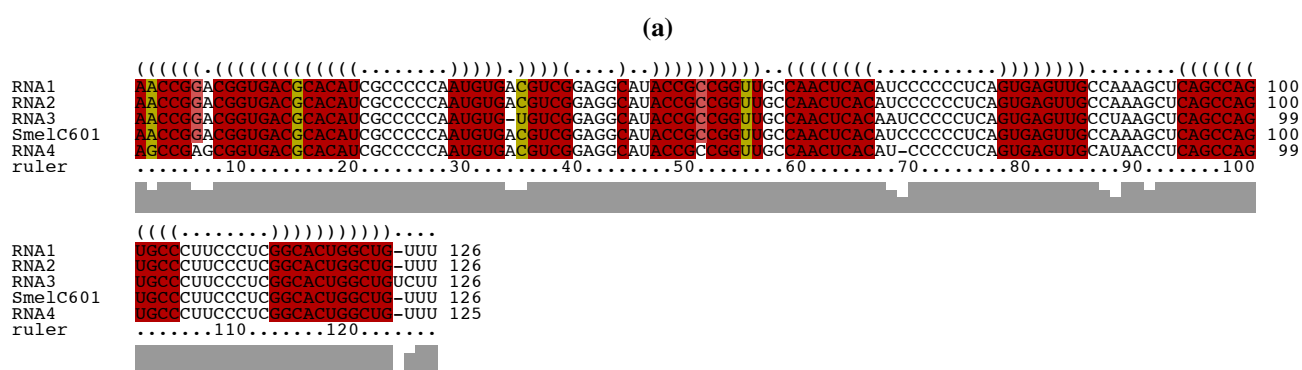
(a)



(b)

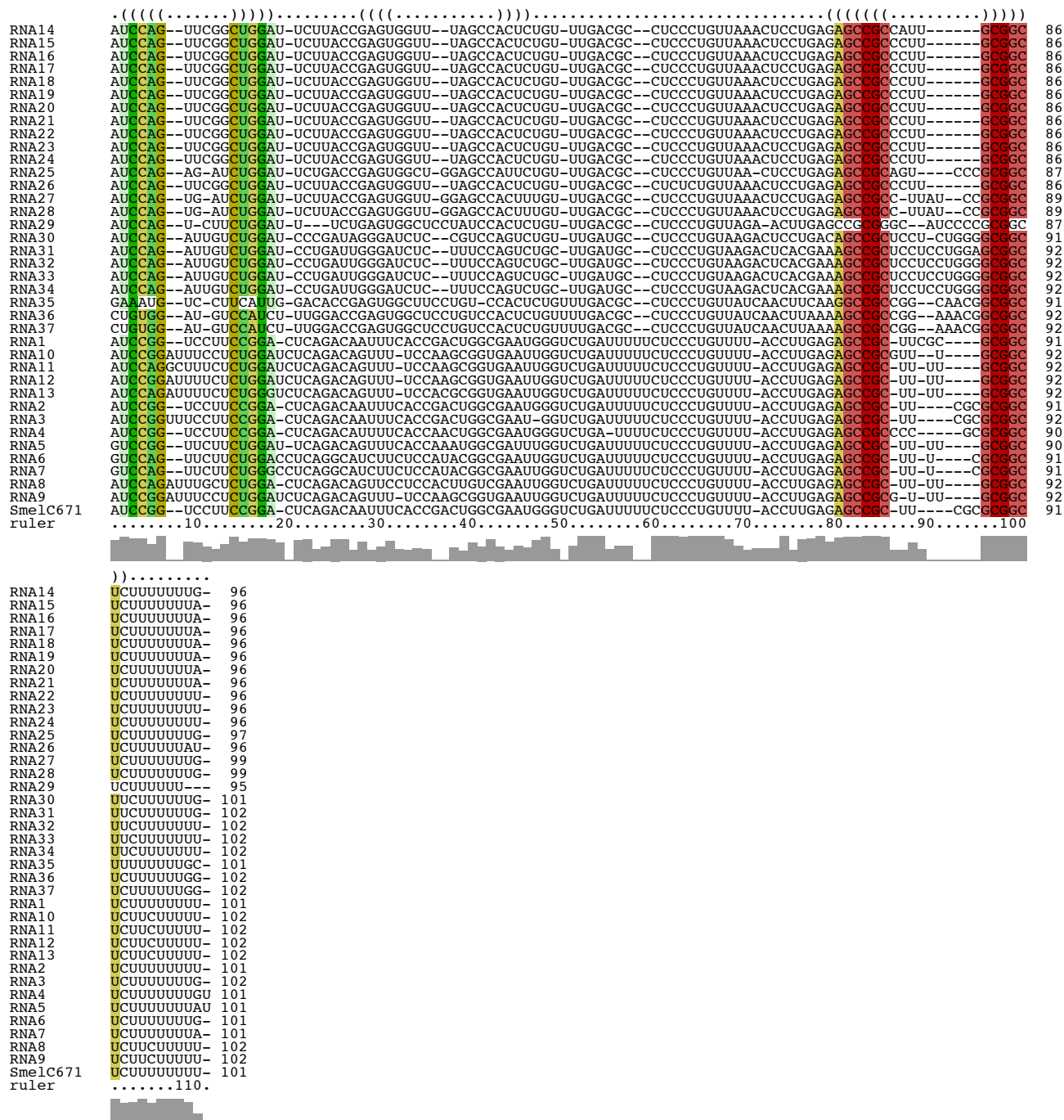


RNA Family Model of SmelC601. (a) Alignment of $RFM_{SmelC601}$ sequences (SCI = 0.98); (b) Consensus secondary structure (minimum free energy -54.68 kcal/mol) for the alignment shown in (a).

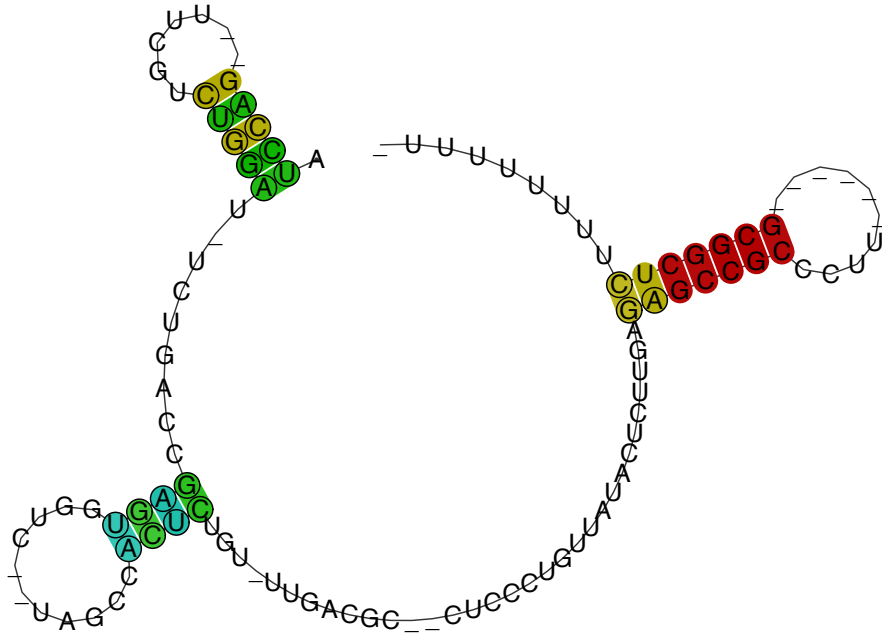


RNA Family Model of SmelC671. (a) Alignment of $RFM_{SmelC671}$ sequences (SCI = 0.55);
 (b) Consensus secondary structure (minimum free energy -20.30 kcal/mol) for the alignment
 shown in (a).

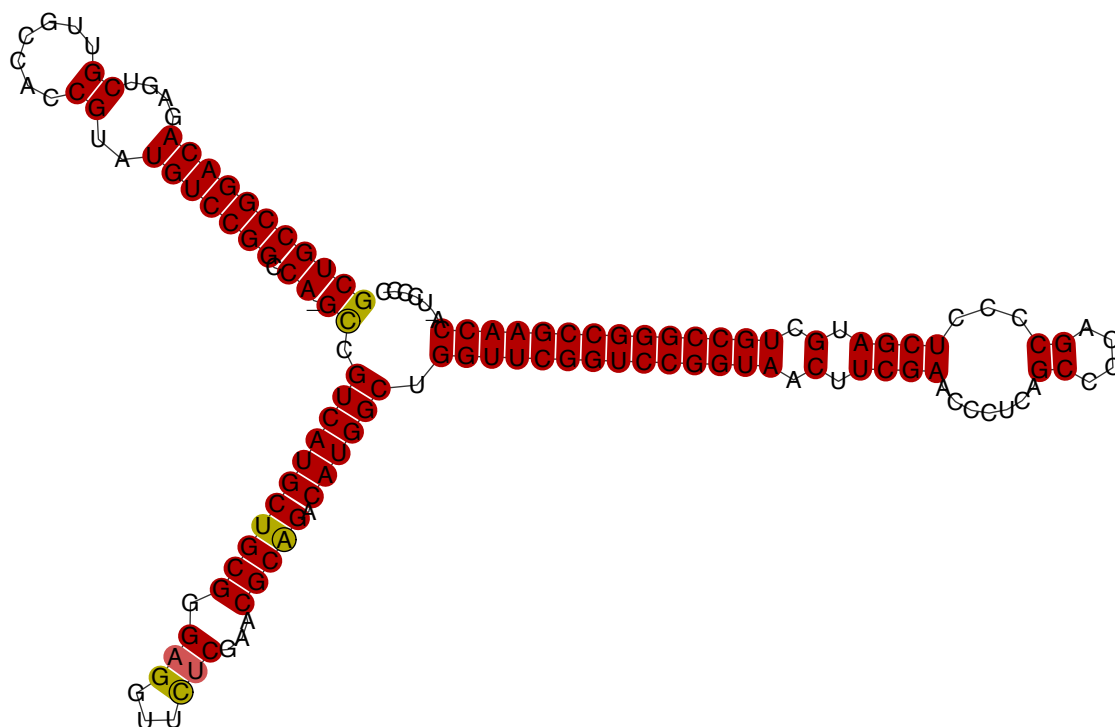
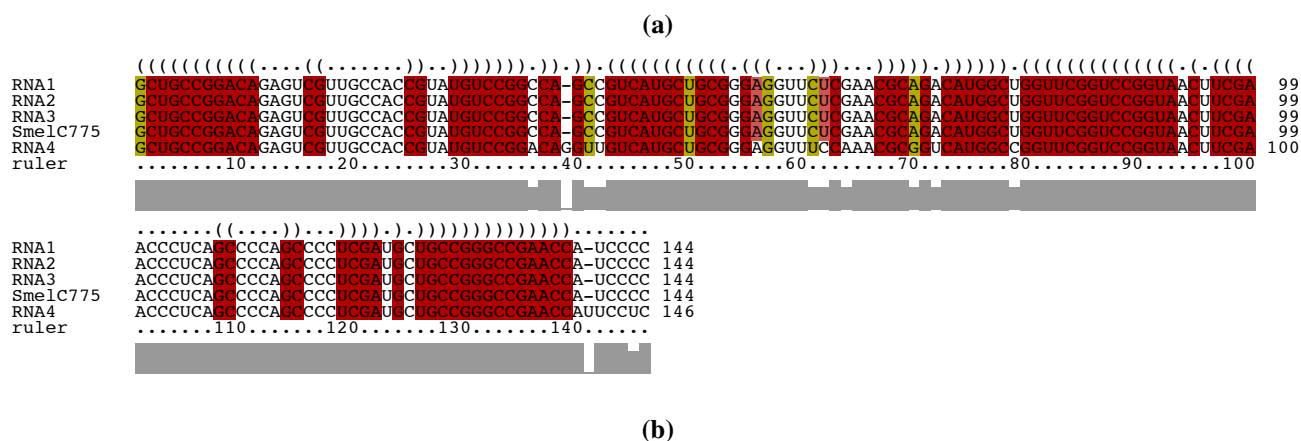
(a)



(b)



RNA Family Model of SmelC775. (a) Alignment of $RFM_{SmelC775}$ sequences (SCI = 1.00); (b) Consensus secondary structure (minimum free energy -66.30 kcal/mol) for the alignment shown in (a).



RNA Family Model of SmelC776. (a) Alignment of $RFM_{SmelC776}$ sequences (SCI = 0.95); (b) Consensus secondary structure (minimum free energy -45.14 kcal/mol) for the alignment shown in (a).

