

**Table 1.** Sequence of the 35-nt accessory domain of clones obtained at the start of continuous evolution (transfer 0) and after transfers 15, 50, 80, and 100

**Type I Sequence Motif**

**cons** CAGAG-UCUCAACCAAG-AGCAGCGCGAUGAACUCUC  
**0-1** -..C.A..C..-G....C....AGU.--.U...AGCACA  
**0-2** .....A.....  
**0-8** .....U.....  
**0-10** .....  
**0-11** .....C.

**cons** GCCA-AUUAGGCCAACAG-AGCAGACGACAAA-GUGUA  
**15-1** .....  
**15-2** .....  
**15-3** .AGUG...UUUGAG.A.UC...GC...-.G..C.-CC  
**15-5** .....  
**15-6\*** .....  
**15-9** .....  
**15-11** .....  
**15-12** .....  
**15-16** .....U.....  
**15-17** .....A.....  
**15-19** .....  
**15-21** .....

**50-1** .....-----.....U.....  
**50-2** .....A..U.....U.....  
**50-3** .....-----.....U.....U  
**50-4** .....A..U.....U.....  
**50-5** .....G.....U.....  
**50-6** .....U..U.....U.....  
**50-7** .....-.....U.....  
**50-8** .....A.....U..A.....  
**50-9** .....AG.U.....U.....  
**50-10** .....G.....U.....U

**90**                                  **100**                                  **110**  
**5'** ...|------|.....-.....|.....-.....|.....**3'**  
**80-1\*** .....-----.....U.....U  
**80-2** .....-----.....U.....U  
**80-3** .....-----.....U.....U  
**80-4** .....-----.....U.....U  
**80-5** .....-----.....U.....U  
**80-7** .....-----.....U.....U  
**80-8** .....-----.....U.....U  
**80-9** .....-----.....U.....U  
**80-10** .....-----.....U.....U

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          90                100                110
5' ... |-----|.....|.....|..... 3'
100-1* .....-----U.....U.....U
100-2 .....-----U.....U.....U
100-3 .....-----U.....U.....U
100-4 .....-----U.....U.....U
100-5 .....-----U.....U.....U
100-6 .....-----U.....U.....U
100-7 ...U.....-----U.....U.....U
100-8 .....-----U.....U.....U
100-9 .....-----U.....U.....U
100-10 .....-----U.....U.....U

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### Type II Sequence Motif

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cons ---AUGAUAAGAG--UAGCAUGCGUUGAUGUCGUACAUA
0-3 .....U.....
0-4 .....A.....
0-5 .....A.....
0-6 .....
0-7 .....
0-9 .....A.....U...
0-12 AGU..UGC.....CU.C.....-..G.CA.-.U.-----

cons ' AUG---UUAAGAGUAGCAUGCGUUGAU---GUCGU---ACAUA
15-4 .....A.....
15-7 .....A.....AU..CGU.....
15-8* .....
15-10 C.....
15-13 ...AAA.GGC...C...CCAACAA.AGAAG.....-----
15-14 .....
15-15 .....A.....
15-18 .....A.A.....
15-20 .....A.....

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Clones conforming to the type I and II sequence motifs are listed separately. Residues identical to the consensus sequence are indicated by a dot; deletions are indicated by a dash. Asterisks indicate representative clones that were chosen for more detailed analysis. Numbering of residues is based on the T80-1 ribozyme (see Fig. 2B).