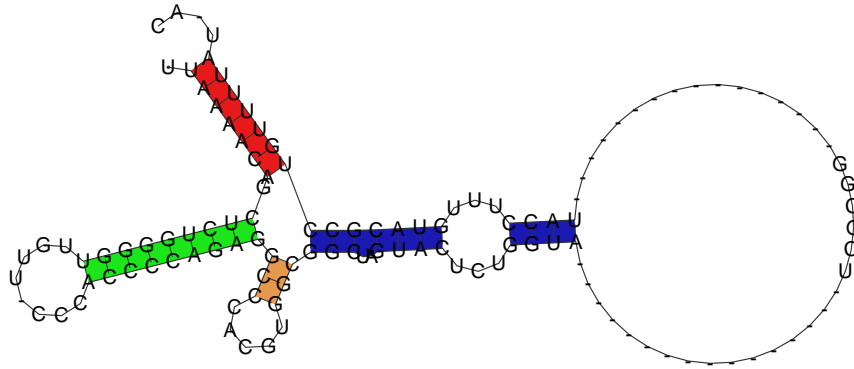


Entero_5_CRE

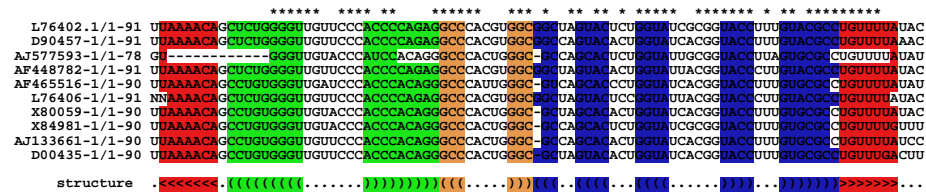


Rfam reference structure of Entero_5_CRE

Positive effect of the RIBOSUM covariance scoring on predictive power – Entero_5_CRE: The closing stem of the Multi loop (red) can not be predicted using hamming distance scoring. About 15 sequences of an alignment of 160 can not form it.

The alignment shows a representative sample of the 160 sequences in the Rfam. The third sequence of the picture is one of the examples where the closing stem can not be formed. Because there is little compensatory mutation, the covariance score is negative in the original RNAalifold.

When the new energy parameters are used, there is a – small – positive effect of not having any mutations, also. In this case, the huge number (more than 140 or about 90%) of sequences that contain no mutations is enough to outweigh the 10 structures that can not form the structure.



Alignment and dot bracket reference structure of Entero_5_CRE.