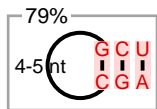


"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation can result from an incorrect alignment of sequences, or from alignments of sequences that do not function as structured RNAs. Unfortunately, there is no accepted method to assign confidence that entirely eliminates the need to analyze the full alignment. To disable this warning, run r2r with --disable-usage-warning"

rne-ll-O2.cons
subfam_weight=0.78706



Secondary structure prediction of the 5' UTR of the 18S rRNA gene from the bacterium 1234567890. The diagram shows a complex RNA fold with multiple stems and loops. Key features include a 3-5 nt loop at the top left, a 0-2 nt loop in the center, and a 11-73 nt loop at the bottom left. The sequence is color-coded by base pairing: red for G-C, green for Y-R, blue for G-C, and black for U-A. Red dots indicate potential start sites. Annotations include 'usu. stable, but not conserved' for the 11-73 nt loop, 'stem might not form' for several regions, and 'SD?' for a Shine-Dalgarno sequence. The sequence ends with 'start' at the 3' end.