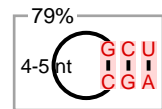


"This automated R2R annotation [of covariation] does not reflect the extent or confidence of covariation. While such information can be useful, we believe that thorough evaluation of covariation evidence ultimately requires analysis of the full sequence alignment. For example, misleading covariation 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 *Drosophila* 28S rRNA gene. The diagram illustrates the predicted RNA fold, showing various stem-loops and internal loops. Key features include:

- 3-5 nt** loop at the top.
- 0-2 nt** loop.
- 11-73 nt** loop at the bottom, labeled "usu. stable, but not conserved".
- Annotations indicating regions where the "stem might not form".
- A potential start codon (SD?) is marked.
- The sequence starts with 5' UACGUGYAGGGU and ends with ACAUG.