

"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"

Secondary structure prediction of the 150 nt RNA sequence. The structure shows several stem-loops and internal loops. Key features include a 4-6 nt loop at the 5' end, a large stem-loop structure in the middle, and a 4-6 nt loop at the 3' end. The sequence is color-coded to match the base pairing: red for C-G, green for G-C, blue for A-U, and black for U-R. The 5' end is labeled '5'-' and the 3' end is labeled '3'-'.