P047 The structure of the kink-turn motif in RNA depends on metal ions and L7Ae protein binding

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The kink-turn (K-turn) is a common motif in RNA structure, first identified in the ribosome. In free solution, the K-turn RNA exists in a dynamic equilibrium between a tightly-kinked conformation, and a more open structure similar to a simple bulge bend. The highly-kinked form is stabilised by the binding of divalent metal ions, but a significant population of the less-kinked form is present even in the presence of relatively high concentrations of metal ions. The conformation of the tightly kinked population is in excellent agreement with that of the K-turn structures observed in the ribosome by crystallography. This conformation is highly dependent on the presence of A·G mismatched basepairs, and is intolerant of any changes of sequence in that region. K-turns are common protein binding elements. The ribosomal L7Ae protein binds a K-turn in the large ribosomal subunit, but is also required to bind K-turns that form in the box C/D and H/ACA guide RNAs. The related human 15.5 kDa protein also binds a K-turn in U4 snRNA. Using steady-state and time-resolved FRET measurements, we have shown that the binding of the L7Ae protein from *Archeoglobus fulgidus* induces the formation of the tightly-kinked conformation of the ribosomal K-turn 7.

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