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> Summary

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## EDITORS' CHOICE: HIGHLIGHTS OF THE RECENT LITERATURE

For proteins,  $\alpha$ -helices and  $\beta$ -sheets are the two main secondary structural elements to consider when relating amino acid sequence to three-dimensional structure. For RNA, there are stems (double-stranded regions) and pseudoknots--where bases within the loop of a stem-loop region are paired with those outside of the stem.

Isambert and Siggia offer a computationally feasible approach to predicting the energetics of stem-loop and pseudoknot structures and apply it to the folding of a well-studied molecule, the 87-nucleotide human delta virus (HDV) ribozyme. They observe the formation and disappearance of nonnative stem interactions as well as a kinetic bifurcation (if both P1 and P5 stems exist, then correct folding is likely to ensue) that occurs at the time when about 40 nucleotides have been synthesized. They describe two stems as "folding guides" whose transient existence might be assessed experimentally with single-molecule techniques (see Zhuang *et al.*, Reports, this issue, p. [2048](#)). -- **GJC**

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