1. How does SHAPE report on RNA structure?

2. How are the authors able to achieve ~1 s resolution of the folding pathway using SHAPE?

3. How do the authors distinguish between interactions involved in initial dimerization versus those involved in structural rearrangements within the dimerized RNA? What factors would influence the rate of initial dimerization?

4. What is the stoichiometry of NC to the RNA and why would it matter?

5. Why is Mg$^{2+}$ unable to function fully as a chaperone in this case? How does Mg function in other folding pathways?

6. Explain the gel-shift method used in Figure S4. How do these data compare to the SHAPE data?

7. How were the secondary structure models in Figures 4G and S3 deduced?

8. Based on the model in Figure 4G, how do you envision the energy landscape of the folding pathway in the absence of a chaperone? How does a chaperone alter this landscape?

9. Why might guanosines be particularly good targets for chaperone activity? What properties of UP1 might allow it to function as a chaperone even though it has no physiological role in viral RNA dimerization?

10. Could you design a nucleic acid-based chaperone based on the conclusions of this paper?