**I glossed over the SAXS analysis because I don't think it's the strongest data. However, I’ve come to agree that a more nuanced analysis is necessary.**

**However, even given the noise, I think our data supports compaction in Eco80 and nothing crazy happening, like dimerization between solution conditions. Other than that, I don't want to over interpret ambiguous data.**

**Conversation topics**

1.) The signal is not that high above background. See the scatter in the Kratkey plots (SI figure 7A)

**Neela:** The quality of the DENSS reconstructions indicate that the data is fine.

**Phil:** It doesn’t look that much worse than Kate’s data

2.) I think the high scatter means that p(r) plots (which are models) could be ambiguous. In fact, The Dmax is not well defined. See how the p(r) plot shoots straight down to the x-axis. It should reach a x = 0 limit instead.

**Neela:** Try adjusting the p(r) plot parameters

This leads to weird results. I think the thing to say is that the Dmax is undefined.

3.) The bead models could look different because the RNA was different in solution, or they could look different because many different bead models could explain our data. Thus, we got a sampling of random bead models that appear different. This is reflected by the high AMBITER score (SI table 9).

**Phil and Neela: Don’t use the bead models.**

Are the ambiguous bead models symptomatic of ambiguous DENSS reconstructions?

**Neela:** No, DENSS seems to handle noisy data better

**SI Figure 7 changes**

I threw out the bead model reconstructions.

7A:

**Phil:** **try connecting points with lines to make Kratky plots look better..**

I tried. It looks like a seismometer trace. I faceted the data by condition and it looks a lot better.

-I added a line at y = 0

-I ordered the conditions to match the rest of the manuscript

-I added a black line representing data calculated using the crystal structure.

7B:

-I ordered the conditions to match the rest of the manuscript

-I added a black line representing data calculated using the crystal structure.

Add: Modeled curve

**SI Table 6**

-Delete columns associated with bead model reconstructions

-Use Porod volume from the density distribution **(Neela suggested)**

-Add in Rg, p(r), Dmax, Porod volume for simulated data

-Add in DENSS resolution

**SI Table 9**

-Delete this table because it is associated with bead model reconstructions

**Points to make in Results**

**Paragraph 1**

* SAXS data indicates that the guanine aptamer adopts a similar structure but with more dynamics
* Bell shaped Kratkey plots (SI Figure 7A) indicate that the RNA adopts a folded structure-probing
* We modeled data using WAXSiS in order to understand differences between the solution state and the crystal structure
* Larger radius of gyration in all conditions in comparison to the crystal structure-probing (Table
* Increased radius of gyration is consistent across methods
* Distance distribution indicates a sampling of expanded states in comparison to the crystal structure data (SI Figure 7B)
* Likewise, *ab-initio* electron density reconstructions are consistent with an expanded version of the crystal structure in solution (SI Table 6)

**Paragraph 2**

* A more detailed comparison of SAXS data between conditions is confounded by three factors:
  + (1) The low signal to scatter ratio in our data
  + (2) Ambiguous determination of Dmax (SI Figure 7B, note that the data does not reach a limit at Dmax)
  + (3) Inability to deconvolute differences in structure from changes in the composition of the solvent layer
* However, there is consistent support for structural compaction in Eco80
  + Rg goes from 24.6 to 23.9 in comparison to 2 mM free Mg
  + Dmax is ruduced from 69.81 to 65.4 in comparison to 2 mM free Mg
  + And the Porod volume is reduced from 42787 to 33212
* Similar to compaction by crowders observed by Kate and Woodsen