Okay. I think I'm ready to write an outline for the NaJaLi section.

They've created a classifier. It separates the trimers and the proteins with inplugs/outclamps from the rest. Then, it further separates from these the trimers.

What's special about the trimers? High energy strands IN ONE PART OF THE PROTEIN. Should also be true of proteins with out-clamps. Proteins with in-plugs should have high energy strands that are detected by the melting temperature metric, but not high strand energy *variance* detected by the deviation metric.

What does it mean, that we see this? Well, if the proteins are stable as a trimer, and *not* stable when not a trimer, this is what we'd see. Separate them, and there's instability. There's not much flexibility, so the instability is *local*.