* How to detect oligomerization?
  + Weakly stable surface
    - **\*** Two ways I can think of to explain the theoretical basis, of why this is worth trying
      1. It has been observed in other proteins that there is a stabilization upon binding. For example, many intrinsically disordered proteins fold upon binding
         * **\*** though this may be obvious if I understood more, why does folding upon binding imply stabiliziation upon binding?
      2. If the oligomerization reaction is in equilibrium, and the native form is for example a trimer, then we expect the trimer to have lower energy than the three proteins separated. If the monomer is a barrel in the trimer, and we look at the structure of the barrel individually (no change of shape), the high energy should be local to the interface, where the native bonds have been severed. If a protein exists in the membrane as mixed monomer and oligomer, then we won't be able to detect it in this way, since that suggests that the monomeric form is of comparable energy to the oligomeric form (the concentration of the protein within the membrane is a factor too and other stuff that I don't know about), but if it exists in a membrane primarily as an oligomer, if the monomeric form is of two high energy for it to have much of a frequency, then this is worth trying
    - Naveed Jackups Liang (NaJaLi) have tried it
      * Used a knowledge-based potential to predict weakly stable regions, and successfully predict interfacial sites
      * Their method works almost as well from sequence as it does from structure, which makes it usable
        + It does this by considering only the transmembrane strands, which can be predicted fairly well from sequence

**\*** How do they make sure they have the strand registry right, in the paper on predicting oligomeric interfaces? Do they use TMSIP for that? Certainly by the time they publish that structure prediction paper they can do this with TMSIP

* + - * Contiguous above-average energy strands are predicted interfacial site
      * A complication:
        + Explain what in-plugs and outclamps are
        + Since they're only looking at the strands, there are *two* disturbances to native structure in their model: separation of the complex, and removal of inplugs/outclamps
        + When they look at just predicted stability (specifically, predicted melting temperature), the high energy barrels are those in oligomers, as well as those with inplugs and outclamps
        + So, the TMSIP energy function predicts that removing these inplugs is a disturbance to the native state on par with separating the oligomer

\*While I feel like I can explain why we'd expect oligomeric interfaces to have high energy, this isn't something I'd necessarily expect. Thermodynamic hypothesis means that the native structure, with the inplug inside the protein, is the lowest energy structure that *contains the inplug*It doesn't necessarily say anything about the stability if it were possible for the inplug to be removed, that is, if the inplug was not covalently linked. As far as I understand, it's possible for a protein to have an inplug inside of it that is destabilizing (compared to if the inplug was cleaved off), but the inplug would be *more* destabilizing if it went anywhere else.  
So, I'm prepared to just say that the energy function gives high energy to the proteins with inplugs

* + - * + Maltoporin and similar proteins have both an interface and an inplug (specifically, a pore constriction loop) , which are on *opposite sides of the barrel*
        + But, the prediction of interfacial site is still correct in almost all of these proteins.