Hong et al. 2010:

How does the assay work? From what I understand, it fluoresces when it is a monomer, but quenches when it is a dimer. Why would the same molecule be able to quench itself?

A random question I though about while reading this paper that might be good for me to discuss with you: We kind of already have a guess at what sidechain packing impacts association is from literature on Bacteriorhodopsin and others, however, these are just in single systems and not applied to the general field of membrane proteins. What should I expect me research to tell me when I compare to those results? If the correlation is higher than those, what does that suggest about sidechain packing? If it’s the same, what does that suggest about packing and the methods currently used in the field? If it’s less, what does that suggest about packing?

Chadda et al. 2016

I think I need some help on figure 1. From what I understand, these liposomes are assumed to be distributed in this way every time for their simulated model. Thus, protein has to get to a concentration that fills many of these liposomes individually before any of the proteins are found together to interact. Once it reaches that point, these proteins are more likely to be found in the same liposome, and depending on size of the liposomes, they are more or less likely to be found in the same liposome. So by simulating the sizes of the liposomes and the number of liposomes, then change the protein concentration while following those distributions, they were able to get potential mole fractions for the protein to be found as a monomer, dimer, or trimer?

Also, I will likely need to have a discussion on the math as to why they assumed that half of the protein signal was lost, and how to explain why this is the case