How about, to keep myself entertained, I write everything I know about prediction of protein-protein interfaces in outer membrane proteins?  
  
I don't know why membrane proteins oligomerize. But I do know a little physics.  
If all the protein units in the membrane are oligomers, then membrane protein oligomerization is a spontaneous reaction, and membrane protein dissociation is not a spontaneous reaction.

Halving the area of the membrane causes reaction to move forward: crowding drives oligomerization.

Not as many LamB molecules (not as much LamB) will oligomerize (which has a corresponding property of LamB substance as well as LamB molecules) in the absence of SurA ("SurA assists in the folding of Escherichia coli outer membrane proteins", Lazar and Kolter, Journal of Bacteriology, 1996). I don't know why this is though.

Dimerization of OMPLA is calcium-dependent and substrate (some molecule with a long hydrocarbon chain) dependent (from intro to Energetics of OMPLA Dimerization). This dependence is funcitonal, since the dimer form is an enzyme, and uncontrolled activity would kill the bacterium.

The extreme thermostability of OmpF is due to a salt bridge. The salt bridge is on a loop rather than a strand. So electrostatics can reduce the ΔG of oligomerization.