Has anyone looked into the *binding site* in *any* of these heterooligomers? How about for PorB? Is PorB homologous to any of the porins I'm looking at?

If the moments are due to heterooligomerization in the porins, then the homoolig site shoudl be high ez-β as well, right? WHat's a heatmap look like?

If the binding is on the side, dosen't that mean that there will be a 1:1 rtaio of POrB to RmpM molecules?

Anything I can't find out about RmpM, I might be able to find out about the PI-PIII association

"Strucutre of TonB in cComplex with FhuA, E. coli Outer Membrane REceptor"

Looks like TonB interacts with periplasmci face, not with membrane-facing surface.

"Trimeric Structure of Major Outer Membrane Proteins Homologous to OmpA in Porphyromonas gingivalis"

Heterotrimer stabilized by S-S bond

"Structure of the OmpA-like domain of RmpM from Neisseria menginitidis":

RmpM associates with porins and TonB dependent transporters, but is not a transmembrane barrel

By analogy with TonB and the peptide associated with Omp32 (Zeth et. al), this association may be on the periplasmic faces of the protein. But maybe not.

"High Resolution Clear Native Electrophoresis (hrCNE) Allows a Detailed Analysis of the Heterotrimeric Structure of Recombinant Neisseria meningitidis Porins Inserted into Liposomes":

Neisserial porins form complexes with RmpM, FetA, and TbpA

According to "A Dynamic Model of the Meningococcal Transferrin Receptor", TbpA is probs a porin-like molecule and is homologous to TBDT's!

Heterooligomerization