Heterooligomerization in the outer membrane

The outer membrane of gram-negative bacteria is full of protein complexes. I know this because I've seen it in AFM images: little triangular structures, and outer mebmrane protein is known to be primarily porin, and porin crystallizes, and when you do x-ray scattering on the crystal you see triplets of identicaly β-barrel domains. The weird thing is though that under AFM you see these 10 nm long heighteinings of the needle but the trimer in the crystal is only 6.5 nm across. The tips have a radius of 6-8 nanometers. Assuming data is recorded at the center with a 7 nm tip, then the width of a 6.5 nm object should look like about 20 nm. I have no theory which predicts 10 nm heights.

This kind of homooligomerization is observable in crystal, though sometimes even when something crystaliizes as a monomer there's evidence for oligomerization. Jie Liang thinks that FhuA forms oligomers in vitro but not in vivo. There may bew some proteins that form oligomers when expressed in high concentration but not low concentration. THe function of OMPLA is controlled by oligomerization, and it has been crystallized as a monomer and as a dimer.

But. What may *not* be apparent in crystals is *heterooligomerization*. But I think I heard that porin monomers aren't even really stable. ANd Petra Fromme said of mitochondrial memmbrane proteins involved in photosynthesis that if something was an oligomer, ypou wouldn't be able to crystallize a monomer. But PorB crystallizes without sometimes binding partner RmpM, see PDB structure 4AUI.

Yes there is sometimes heterooligomerization in the outer membrane as well. In the case of TBDTs it is essential to their function, that's why they're called "TonB dependent transporters". This contact is on the periplasmic face of the protein.

RmpM is porbably for anchoring the membrane to the periplasm, and it is linked to PorB, though I'm not sure of even the stoichiometry of the complexes or the evidence that supports their existenec. The PorB/RmpM pair is homologous to the PI/PIII pair ins ome other species, though I don't remebmer which proten is homologous to whcihc. I think PorB is also homologous to OmpF. But in any case RmpM is *not* a transmembrane protein. I don't know *how* it is connected to the membrane. Or where on the porin it interfaces.

Supposedly neisserial porins aslos form complexes with other molecuels: FetA and TbpA. W doner if those have transmembrane domains. I could look it up or maybe I culd just find the seqences and run them through ProfTMB or HHOMP.

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Maybe RmpM binds on the surface. Then, maybe FetA and TbpA are transmembrane proteins. ANd also probably it binds 1-3 at a time to porin complexes, dep[endending only on the concentration. So if at sufficient concentration it still only binds one at a time, then either it binds eweakly so that band shouldn't be that populated, or it's binding to like the center or something. Or it has a big periplasmic domain that crowwds out others from binding also.

But it also binds to TBDTs. How much room even is there for it if TOnB is also attached? So I'm thinking if it binds the periplasmic face then there's some interference between it binding and tonb binding.

Maybe somebody has publiished a theoretical study about either RmpM or PI binding to β barrels.