

Folding and inserting outer-membrane porins

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Gram-negative bacteria are distinguished by having two membranes surrounding them instead of just one. This second, outer membrane (OM) is a specialized region that is quite distinct from the inner membrane; for example, it possesses an outer, extracellular-facing leaflet composed not of phospholipids but rather of a bulky amphiphilic molecule known as a lipopolysaccharide. Additionally, OM proteins, such as the ubiquitous porins, are almost uniformly β -barrels, indicating a unique sorting and folding process going on to place them there. Nearly all of these OM proteins are inserted using the so-called BAM complex, which is made up of five proteins including the core component, BamA. In this talk, I will discuss our recent simulation work aimed at determining (1) the unique protein-membrane interactions that occur in the OM environment and (2) how BamA catalyzes insertion. In particular, I will present evidence supporting a lateral gate in BamA as the exit point for nascent OM proteins. The behavior of this opening will be discussed in the context of recent crystal structures as well as simulations of the entire BAM complex.