

Structural insight into the biogenesis of beta barrel membrane proteins

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Abstract

β -barrel membrane proteins are essential for nutrient import, signaling, motility, and survival. In Gram-negative bacteria, the β -barrel assembly machinery (BAM) complex is responsible for the biogenesis of β -barrel membrane proteins, with homologous complexes found in mitochondria and chloroplasts. Here we describe the structure of BamA, the central and essential component of the BAM complex, from two species of bacteria: *Neisseria gonorrhoeae* and *Haemophilus ducreyi*. BamA consists of a large periplasmic domain attached to a 16-strand transmembrane β -barrel domain. Three structural features speak to the mechanism by which BamA catalyzes β -barrel assembly. First, the interior cavity is accessible in one BamA structure and conformationally closed in the other. Second, an exterior rim of the β -barrel has a distinctly narrowed hydrophobic surface, locally destabilizing the outer membrane. And third, the β -barrel can undergo lateral opening, evocatively suggesting a route from the interior cavity in BamA into the outer membrane.