Outer membrane protein folding by the BAM-complex

Michael Zahn[1], Leonor Morgado[1], Irena Burmann[1], Jean-Baptiste Hartmann[1], Timm Maier[1], Sebastian Hiller[1]

[1]Biozentrum, University of Basel, Switzerland

β-barrel outer membrane proteins (Omps) are key functional components of the outer membranes (OM) of Gram-negative bacteria, mitochondria and plastids. For example, they mediate transport across the membrane, act as receptors or are involved in bacterial pathogenicity. The biogenesis of Omps requires a protein from the Omp85 family of proteins to mediate the insertion and translocation into the OM. In Gram-negative bacteria, this role is fulfilled by the Omp85 protein BamA, the central protein of the BAM complex. BamA comprises five substrate-interacting N-terminal POTRA domains and a C-terminal 16-stranded transmembrane β-barrel domain [1]. Despite the recent elucidations of crystal structures of the BAM complex [2-4], the translocation and insertion mechanism of chaperone-bound unfolded Omps into the OM remains still elusive. NMR spectroscopy allows studying highly dynamic systems at atomic resolution and it is thus a method of choice for the elucidation of the BamA functional mechanism. Here, we show initial results for the preparation of BamA samples in detergent micelles, bicelles and lipid bilayer nanodiscs and our progress towards sequence-specific resonance assignments for the BamA β-barrel domain.

[1] Noinaj et al. (**2013**), Structural insight into the biogenesis of β-barrel membrane proteins. *Nature*, 501 (7467): 385-90.

[2] Gu et al. (**2016**), Structural basis of outer membrane protein insertion by the BAM complex. *Nature*, 531 (7592): 64-9.

[3] Han et al. (**2016**). Structure of the BAM complex and its implications for biogenesis of outer-membrane proteins. *Nat Struct Mol Biol.,* 23 (3): 192-6.

[4] Bakelat et al. (**2016**), The structure of the β-barrel assembly machinery complex. *Science*, 351 (6269): 180-6.