Structures of YidC and Oxa1 bound to translating ribosomes: Dimeric pores for membrane protein insertion

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The insertion of proteins into membranes is an essential process in the cell as membrane proteins have key roles in energy transduction, nutrient and ion transport. Two different systems exist for the insertion of membrane proteins, the Sec translocase system and the YidC/Oxa1/Alb3 family of membrane proteins. The YidC/Oxa1/Alb3 proteins facilitate the co-translational insertion and assembly of membrane proteins in bacteria, mitochondria and chloroplasts. In bacteria, YidC can function on its own or together with the SecYEG translocon depending on the substrate protein. Cryo-electron microscopy offers the unique possibility to study these protein insertases in action bound to a newly synthesized protein on the ribosome.

Here, we present the structures of both *Escherichia coli* YidC and *Saccharomyces cerevisiae* Oxa1 bound to *E. coli* ribosome nascent chain complexes determined by cryoelectron microscopy [1] (Fig. 1). Dimers of YidC and Oxa1 are localized above the exit of the ribosomal tunnel. Crosslinking experiments show that the ribosome specifically stabilizes the dimeric state. Functionally important and conserved transmembrane helices of YidC and Oxa1 were localized at the dimer interface by cysteine crosslinking. Both Oxa1 and YidC dimers contact the ribosome at ribosomal protein L23 and conserved rRNA helices 59 and 24 similarly to what was observed for the non-homologous SecYEG translocon [2, 3]. We suggest that dimers of the YidC and Oxa1 proteins form insertion pores and share a common overall architecture with the SecY monomer. We provide first insight into the mechanism of these insertases and the Sec system.

- 1. Kohler et al., Mol. Cell (2009) in press
- 2. Mitra et al., Nature **438** (2005) p318
- 3. Menetret et al., Mol. Cell **28** (2007) p1083
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Figure 1. Cryo-electron microscopy structure of *E. coli* YidC bound to a translating ribosome. YidC is bound at the tunnel exit of the ribosome nascent chain complex. The small ribosomal subunit is shown in yellow, the large ribosomal subunit in blue and the YidC density in red.