The structure of SecA, the *Escherichia coli* preprotein translocase motor

About 25-30% of the bacterial proteins function in the cell envelope or outside the cell. These proteins are secreted primarily as unfolded polypeptide chains by various secretion systems. SecA is the ATPase component of the vital preprotein translocase complex Sec and an RNA helicase that belongs to Superfamily 2 (SF2). We determined the structures of the dimeric SecA from *E. coli* in the apo form as well as in complex with the nucleotides: adenosine-triphosphate (ATP), magnesium adenosine-diphosphate (Mg^{2+}.ADP) and magnesium adenosine-5'-[β,γ-imido]-triphosphate (Mg^{2+}.AMP-PNP) by means of single crystal X-ray diffraction at 2 Å resolution (*1*). Each monomer contains the core of the SF2 helicase/ATPase, i.e. the DEAD-motor (from the characteristic sequence "Asp-Glu-Ala-Asp" or "DEAD" and the derivatives thereof "DExD/H" of the helicase Motif II (Walker Box B)). The DEAD-motor in turn, contains two domains/folds: the Nucleotide Binding Fold 1, NBF1 and the Nucleotide Binding Fold 2, NBF2. The protein monomer contains also the Preprotein Binding Domain, PBD, which is inserted into NBF1 *via* two antiparallel β-strands and, the Carboxy-domain, C-domain, which is linked to the end of NBF2. The two latter domains are called also SecA specificity domains.

The structures of the SecA complexes with nucleotides determine the cleft located at the interface between the two DEAD-motor domains, which defines the critical aminoacyl residues for the catalytic hydrolysis of ATP.

The dimeric protein consists of two essentially identical protomers associated in an anti-parallel fashion. The dimerization is mediated mainly through extensive contacts of the two DEAD-motor domains leaving the C-domains facing outwards from the dimerization core. This dimerization mode (*1*) explains the effect of functionally important mutations and, is completely different from the dimerization models proposed for SecA structures from other biological sources (*2*-*6*). Based on the above mentioned experimental results, the comparison of the SecA structures and taking into account the recently determined structure of the complex SecA:SecYEG (*7*), the description of a probable mode of action of the Sec translocon will be attempted.

References:

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