MS8-P2 Structural Analysis of a Soluble Fragment of the Membrane Fusion Protein HlyD in a Type I Secretion System of Escherichia coli.

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The protein toxin HlyA of Escherichia coli is exported without a periplasmic intermediate by the type I secretion system (T1SS). The T1SS is composed of an inner membrane ABC transporter HlyB, an outer-membrane channel protein TolC, and a membrane fusion protein HlyD. However, the assembly of the T1SS remains to be elucidated. In this study, we determine the crystal structure of a part of the C-terminal periplasmic domain of HlyD. The long α-helical domain consisting of three α helices and a lipoyl domain was identified in the crystal structure. Based on the HlyD structure, we modeled the hexameric assembly of HlyD with a long α-helical barrel, which formed a complex with TolC in an intermeshing cogwheel-to-cogwheel manner, as observed in tripartite RND-type drug efflux pumps. These observations provide a structural blueprint for understanding the type I secretion system in pathogenic Gram-negative bacteria.

Keywords: HlyD, T1SS, Hexamer, Toxin secretion, E. coli

MS8-P3 Structure of complete rotary ATP synthase and its role as new drug target against tuberculosis

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F_1F_o-ATP synthases are paradigmatic molecular machines, which use the transmembrane electrochemical ion gradient to power ATP synthesis. The enzymes belong to the class of rotary ATPases, which all share a common architecture principle, consisting of a rotor and stator entity. While ions are shuttled through the F_o complex of the enzyme, torque is generated at the rotor/stator and transferred to the F_1-catalytic subunits for ATP synthesis. In the opposite direction, ATP hydrolysis can be used to drive ion pumping. I am going to present the structure of complete ATP synthase taking advantage of the combined approach of X-ray crystallography and cryo-electron microscopy. I will also focus on biochemical and structural investigations of the ATP synthase with respect to the development of new antibiotics in the fight against infectious diseases such as tuberculosis.

Keywords: Bioenergetics, X-ray crystallography, electron microscopy