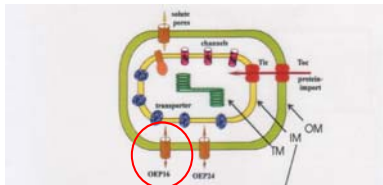


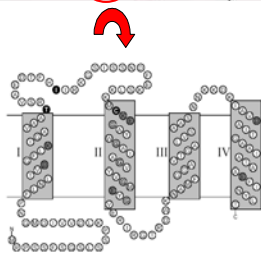
Structure and function of the Amino acid transporter OEP 16

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OEP 16 (outer envelope protein 16) is a new type of membrane pore in the Outer Envelope of Chloroplasts (OEP 16). Structure predictions vary from a mixed alpha-helical-beta-sheet structure to a purely alpha helical protein. We have shown recently that the functional intact protein is alpha helical.



Top: Schematic picture of transporters in chloroplast membranes



Bottom: Predicted Topology of OEP 16

Topology prediction of OEP 16 (from Linke et al 2004)

There is evidence that similar membrane proteins are responsible for the "substance-transport" in all organisms including humans. This protein, which is selective for amino acids, is overexpressed in *E. coli* in the form of inclusion bodies and has to be functionally reconstituted before functional investigations and structural studies are performed. This system is an ideal model for the investigations of other rare membrane proteins involved in the protein import/export machinery as well as in cell recognition.

We have achieved the successful refolding of this membrane protein from inclusion bodies and the reconstitution of the protein functionally intact in liposomes and in detergent micelles. We are presently working in parallel on

- ◆ the crystallization of the protein and
- ◆ the structure determination by Nuclear Magnetic Resonance.

This project is a cooperation with Ronald Nieman, Douglas A. Klewer (ASU) and Juergen Soll (MLU Munich)