Public Abstract

First Name: Bahar

Middle Name: Tuba

Last Name: Findik

Adviser's First Name: Linda

Adviser's Last Name: Randall

Co-Adviser's First Name:

Co-Adviser's Last Name:

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Title: INTERACTION OF SECRETORY PROTEIN SECA WITH ITS BINDING PARTNERS: LIPIDS AND SECB

The barrier function of biological membranes, a universal structural feature, is fundamental in all cells from single-celled organisms to multicellular plants and animals. Membranes not only separate the inside of a cell from its environment but also divide the cell into compartments within the cells. Each compartment is unique and has functions that are required specialized proteins. To carry out their function in a specialized compartment, these proteins must be localized to the proper place. Selective localization of proteins from their site of synthesis to their final location is a ubiquitous process performed in all organisms.

In our laboratory, we investigate the export of proteins by the general secretory (Sec) pathway in the Gram-negative bacterium, *Escherichia coli*. The Sec pathway only transports unstructured proteins through a channel, SecYEG, in the membrane. SecB is a chaperone that captures precursor proteins and keeps them in an unstructured state for translocation. SecB with unstructured protein bound interacts with SecA. SecA directs the ternary complex to the channel via specific interaction with both channel and membrane. At the membrane SecA hydrolyses ATP to supply energy to the system.

In this thesis, we investigated the interactions of SecA with its binding partners; SecB, SecYEG and lipids in the membrane using the analytical techniques that are available in our laboratory such as electron paramagnetic resonance spectroscopy, column chromatography with in-line light scattering and titration calorimetry. We found that the N-terminal region of SecA lie parallel to the plane of the membrane with a maximum depth of ~ 7.5 Å penetrations into the bilayer.