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Single molecule studies of the protein export system RAGHAVENDAR REDDY SANGANNA GARI, NATHAN FREY, LINDA RANDALL, GAVIN KING, University of Missouri-Columbia, MEMBRANE GROUP AT UNIVERSITY OF MISSOURI COLLABORATION — Numerous proteins are exported across or into cell membranes to carry out critical cellular functions. In *Escherichia coli,* pathway through the membrane is provided by the translocon SecYEG, which is highly conserved and has homologs across the kingdoms of life. At the cytoplasmic membrane SecA binds SecYEG and provides energy for protein translocation through the cycle of binding and hydrolysis of ATP. SecA makes large surface area contact ($\sim$ 6,800 $\AA^2$) with cytoplasmic loops spanning TM helices 6-7 and 8-9 of SecY. Despite their functional significance, measurements of these flexible and disordered protein regions remain a significant experimental challenge. Major challenges in protein export system include: determining the oligomeric state of SecYEG and SecA during protein export, and elucidating the mechanism of SecA driving precursor through translocon. Structural details at single molecule level in near native conditions can address these major questions. Recently, atomic force microscopy (AFM) has emerged as an important complementary tool to study membrane proteins. In contrast to other techniques AFM can directly monitor conformational changes and dynamics of bio-molecules. In this work we present the structural details of major components of protein export system at single molecule level in native conditions determined via AFM.

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