

## “OPEN” STRUCTURE OF SecA PROTEIN OF *ESCHERICHIA COLI* IN SOLUTION

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SecA protein which has a pivotal role in the preprotein translocation across the inner membrane of *Escherichia coli* is a water-soluble protein with an unusual property of penetrating the membrane readily. An interesting and important question is what structural characteristics of SecA enables its ready penetration of lipid bilayer. The conformational properties of SecA in solution at 30 °C, pH 7.5 were observed by hydrogen-tritium (HT) exchange, and denaturant-induced denaturation/renaturation and thermal unfolding. HT exchange suggests that approximately 60% of peptide backbone is located in disordered or flexible secondary structure and proximity to water. GdnHCl-induced denaturation/renaturation was followed by three-state model, and a stable intermediate which has molten-globule conformational characteristics was observed. Free energy change ( $\Delta G$ ) as conformational stability was calculated. The  $C_m$  and  $\Delta G$  of the first transition without Mg-ATP are 0.22 M and 1.49 kcal/mol, respectively. Only the first transition of three-state unfolding was changed by Mg-ATP. In the thermal unfolding, SecA has molten-globule characteristics at physiological temperature. These results suggest that SecA has more loose structure in the aqueous conditions than other proteins which may explain its spontaneous penetration into membranes.