



INDIAN INSTITUTE OF TECHNOLOGY GUWAHATI  
SHORT ABSTRACT OF THESIS

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Thesis Title: **Characterization of a putative antimicrobial peptide transporter in Gram-negative bacteria via *in vitro* and computational strategies**

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SHORT ABSTRACT

Humans are always surrounded by dreaded bacterial pathogens and are at risk of getting infected. The shield that protects humans from such pathogens is known as the human immune system, which is a multilayered conglomerate of multiple mechanisms. One of the key components of this system are the antimicrobial peptides (AMPs), which target the bacterial membranes and disrupt their membrane homeostasis, thus leading to the death of the bacterium. To evade the action of the AMPs, Gram-negative bacterial systems have developed multiple resistance mechanisms that neutralize the action of the AMPs. One such crucial strategy is the sensitivity to antimicrobial peptide (Sap) transport system, which is an ABC importer and is suggested to import AMPs into the bacterial cytoplasm, wherein they are proteolytically degraded. The Sap transport system consists of a substrate-binding protein (SBP) SapA, two transmembrane domains (TMDs) SapBC, and two nucleotide-binding domains (NBDs) SapDF. Surprisingly, the *Escherichia coli* Sap (*EcSap*) transport system was reported to stray away from the norm, wherein the membrane components (*EcSapBCDF*) were suggested to function as a putrescine exporter, and further *EcSapA* was banished as a member of the *EcSap* transport system. The peculiar status of the *EcSap* transport system piqued our interest in venturing into this aspect. Moreover, with the aid of computational and biophysical strategies, the outcomes of the study establish *EcSapA* as a part of the *EcSap* transport system and further demonstrate its multifunctional attributes. Hence, indicating the *EcSap* transport system to be crucial for the pathogenesis and sustenance of *E. coli* within the host, therefore, making it a lucrative target for future drug development projects.