**Initial recognition steps of a Type 1 secretion system**

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The paradigm of Type I secretion is the Haemolysin (Hly) A secretion system of *E. coli*. A central element of the secretion complex is the ABC transporter HlyB that acts in concert with the membrane fusion protein HlyD and the outer membrane protein TolC to translocate the 110 kDa toxin HlyA in one step from the cytoplasm to the exterior. HlyB consists of a nucleotide binding domain (NBD) and a transmembrane domain (TMD) and is suggested to be functional upon dimerization. Like all bacteriocin ABC transporter, HlyB contains an extra N-terminal domain of about 150 amino acids, which shows high homology to C39 peptidase domains. In HlyB, however, the catalytic site for proteolysis is degenerated, and therefore we called it C39 peptidase-like domain (CLD). Of course, the question arises why an inactive C39 domain is preserved in HlyB and what role this CLD plays in the transport process.

In this study we were able to 1.) show that the CLD is crucial for the transport process, 2.) describe a new interaction between the CLD and the substrate HlyA, 3.) solve the structure of the CLD in solution using NMR spectroscopy, and 4.) mapping the binding pocket for HlyA on the CLD by chemical shift perturbation experiments. Taken together we provide strong evidence for a distinct role in the transport process of the degenerated CLD, which was preserved during evolution in HlyB. Moreover we assign a receptor function to it enabling binding of HlyA as the initial step by its cognate T1SS.