Poster Presentation

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Engineering of the tat pathway and chaperons

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The Tat pathway is unique as compared to other export pathways such as the Sec pathway because it is able to export mature, folded proteins instead of only the protein in its primary structure. The main components of the Tat pathway are TatA/E, TatB, TatC and Tat Chaperons. The quality-control mechanism for substrates transported by the Tat machinery is taken care of by chaperones. These chaperones mask the twin-arginine signal and ensure proper folding and substrate maturation with appropriate cofactor loading. This machinery if properly tweaked can be used as a universal expression system for expression of properly folded functional protein. One such chaperon is DmsD which helps in the transport of Dimethylsulfoxide reductase complex (DmsABC). DmsD binds to the Tat signal sequence of DmsA in the complex but the exact interaction i.e. the binding site and the structure of bound DmsD on DmsA remains unknown. A fusion construct containing the TAT signal sequence in DmsA (residues 1-53) and DmsD was expressed to study the interaction between the two. As interaction between DmsD and the Tat signal sequence in DmsA has already been confirmed, it was assumed that the expressed DD fusion protein molecules would interact with each other. It was hypothesized that the molecules would form dimer which could be crystallized to further study the interaction between DmsD and DmsA. Additionally, DD fusion monomers could also be crystallized. Form this study the ideal Tat signal can be developed to make a much improved expression system.

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