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The use of bioinformatics to discover the hidden world of the Twin arginine transport (Tat) system's signal peptides

A project in bioinformatics will significantly increase the portfolio of skills in science research on top of an already extensive set of laboratory skills you have achieved until now. The twin arginine transport (Tat) system transports folded proteins across bacterial and thylakoid membranes. In gram-negative organisms, it is encoded by tatABC genes and the system recognizes substrates bearing signal peptides with a conserved twin-arginine motif. Most gram-positive organisms lack a tatB gene, indicating major differences in organisation and/or mechanism. The essential targeting determinants that are recognized by a Bacillus subtilis TatAC-type system, TatAdCd have been characterized. Substitution by lysine of either of the twin-arginine residues in the TorA signal peptide can be tolerated, but the presence of twin-lysine residues blocks export completely. The DmsA signal peptide (sequence SRRGLV) appears to play an equally important role and substitution by alanine or phenylalanine blocks export by both the *B. subtilis* and *E. coli* systems. These data identify three distinct determinants, whose importance varies depending on the signal peptide in question. The data also show that the *B. subtilis* TatAdCd and *E. coli* TatABC systems recognize very similar determinants within their target peptides, and exhibit surprisingly similar responses to mutations within these determinants. In the current project you will use bioinformatics in order to find other signal peptides that can be used by the Tat systems and you will use different prediction methods and compare the results.

Recent Publication

Mendel Williams S, McCarthy A, Barnett J P, Eijlander RT, Nenninger A, Kuipers O P and Robinson C (2008) The *Escherichia coli* TatABC system and a *Bacillus subtilis* TatAC-type system recognize three distinct targeting determinants in twin-arginine signal peptides. J Mol Biol. 375(3):661-72.

Pantelis G Bagos, Elisanthi P Nikolaou, Theodore D Liakopoulos and Konstantinos D Tsirigos (2010) Combined prediction of Tat and Sec signal peptides with hidden Markov models. *Bioinformatics* 6(22):2811–2817.

Biography

Sharon Mendel Williams joined Coventry University as a Lecturer in the School of Life Sciences in the year 2014. She has worked as a Post-doctoral Research Fellow in both departments of Chemistry and Biology, Warwick University. Her research focuses on biophysics and biochemistry of proteins, and understanding the mechanisms of enzymes. She has a wide range of experience in molecular biology, biochemistry, and chemistry. She is a member of the Royal Society of Chemistry and has been awarded a grant from the RSC research fund to accomplish her research work.

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