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Factors Influencing Recombinant Transmembrane Protein Expression. G. Mazock, V. Madhavan, C. Jeffery, Laboratory for Molecular Biology, Univ. of Illinois at Chicago, Chicago, IL, USA.

Approximately 30% of known proteins are predicted to be transmembrane proteins. These proteins play key roles in important cellular activities, including ion transport, multi-drug resistance, biofilm formation, and host-pathogen interactions. The misfolding or improper activity of transmembrane proteins can lead to genetic diseases. The majority of pharmaceuticals in use target transmembrane proteins. However, there are far fewer structures known for transmembrane proteins than there are of soluble enzymes because the presence of the hydrophobic membrane-embedded domains result in difficulties in protein expression, purification, and crystallization. Our project addresses the first bottleneck in working with these proteins: expressing sufficient levels of protein for structural studies. We selected eighty-seven transmembrane proteins from the opportunistic bacterial pathogen *Pseudomonas aeruginosa*. These proteins featured at least two predicted alpha-helical regions and a wide variety of predicted functions. Relative protein expression levels were determined under a variety of culture growth conditions to address whether transmembrane protein expression levels correlate with physical features of the protein (such as the number of transmembrane helices) and/or growth conditions.