184. Reconstruction of Protein Translocation in *Escherichia coli* Allows For Bottom-Up Predictions of Compartmentalization Properties

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Project goal: Reconstruct protein translocation in a genome-scale metabolic and gene- expression model of *Escherichia coli* to serve as an accessible tool that represents a consolidation of research and permits studying the effects compartmentalization has on bacterial metabolism

Compartmentalization is essential for life, and bacteria have evolved pathways to translocate proteins from one compartment to another. Although the individual pathways have been studied in detail, the cumulative effects the pathways have on the whole cell, and vice versa, has yet to be studied. A recent and novel genome-scale model of metabolism and gene-expression of *Escherichia coli* allows us to now study the effects of compartmentalization on a systems-level. To enable such analysis, the model was significantly expanded to include a comprehensive reconstruction of protein translocation pathways. Other improvements to the model include the incorporation of five distinct protein compartments (cytoplasm, periplasm, the inner and the outer membrane, and the extracellular space), published enzymatic rates of the translocases, and a membrane constraint based on cell morphology. The metabolic and phenotypic demands of the improved model allow for the de novo prediction of enzyme abundances. Comparison against experimental data reveals that we are capable of estimating accurate protein expression levels (Pearson correlation of 0.998 for translocase pathways). Furthermore, the model can be used to examine optimal energy generation and growth states and how they differ from an observed measured state in vivo. For example, one observation was that the model predicted more resources can be diverted to oxidative phosphorylation instead of unnecessary ABC transporters not needed in a given condition. This model reveals that the consolidation of current scientific knowledge enables calculation of protein abundances based on enzymatic activities and compartmental demands.