Simple cell, complex envelope: modelling the heterogeneous membrane of E. coli

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Gram-negative bacteria such as *E. coli* are typically regarded as "simple" model organisms, yet their cell envelopes are surprisingly complex. Recent experimental and theoretical studies have revealed that contrary to the traditional view of the cell membrane as a passive bystander in membrane protein function, it plays a key role in protein folding, assembly, and function. To study the influence of the bacterial membrane on the dynamics of embedded proteins, we have performed atomistic molecular dynamics simulations of members of the TonB-dependent transporter family of proteins from *E. coli*. In particular, our aim has been to capture the details of lipid composition; we have modeled the outer membrane as an asymmetric bilayer containing an asymmetric distribution of lipopolysaccharide (LPS) and heterogeneous phospholipid mixtures. Our simulations enable us to explore the dynamics of the extracellular loops with a level of detail that is not possible using more traditional, simpler model membranes. By extending the simulation timescales out to hundreds of nanoseconds we are gaining new insights into the influence of "realistic" membrane environments on the structure and dynamics of membrane proteins.