

# Modeling of the OmpE36 porin from *Enterobacter cloacae* in an LPS bilayer

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Porins inserted into the outer membrane (OM) of gram-negative bacteria act as portal for the entry of nutrients and antibiotics into the cell. Lipid and porin interactions play a main role in providing a stable OM to Gram-negative bacteria. The X-ray structure of OmpE36-LPS complex revealed two LPS binding sites on the membrane protein. To test the ability of molecular dynamics (MD) simulations to reproduce the specific binding of LPS lipids, we performed a series of long MD simulations. The results are discussed in the poster.