A Molecular Dynamics Investigation of Outer Membrane Phospholipase A and Two Polar Mutations

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ABSTRACT

Outer Membrane Phospholipase A (OMPLA) is a 31kDa monomer, 45KDa dimer, beta-barrel protein that has implications in a variety of diseases including Meningitis and Gonorrhea. Over the past decade and a half many mutations have been made to OMPLA in order to study their effects on stability, energetic, and structure. A majority of diseases caused by outer membrane proteins are due to polar mutations.[11] However, little work has been done to study polar mutations in OMPLA. In this work we perform molecular dynamics simulations on wild-type OMPLA and two polar mutations, A210E and A210R in a D10PC lipid environment.

Substituting arginine or glutamic acid for the alanine at position 210 leads to a slight disturbance in the lipid bilayer and a decrease in the movement of the protein at that specific location. In the A210R mutant the phosphorous and oxygen head group of the lipid is brought close to the arginine to balance out the slight positive charge introduced into the system. In the A210E analogue two lipid $N(CH_3)_3$ groups are pulled into the bilayer to balance out the negative effect of the glutamic acid.