Simulations of the membrane proteins in the lipid bilayer with the UNRES coarse-grained force field

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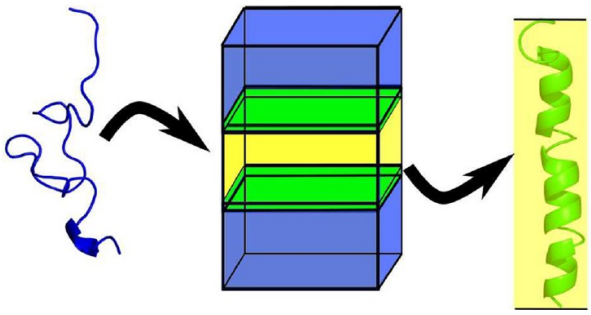

UNRES is a physics-based force field, which is a tool for a protein modeling, can be used for structure prediction and study of the protein pathway folding [1]. This model is especially dedicated to simulate proteins in water environment and, therefore, membrane proteins could not be treated. Membrane proteins are immersed in a lipid bilayer and have only partial contact with the water environment [2]. Because membrane proteins are very important for cell functioning, we recently extended the UNRES model to include the lipid bilayer as a continuous phase, with a transition zone between the lipid and water phase that corresponds to the lipid head groups. We implemented the periodic-box scheme, which is used in UNRES in our earlier work [3]. The lipid bilayer has been modeled by introducing a continuous nonpolar phase with the water-interface region of appropriate thickness. The potentials for average electrostatic and correlation interactions of the peptide groups have been rescaled to account for the reduction of the dielectric permittivity compared to the water phase and new potentials for protein side-chain–side-chain interactions inside and across the lipid phase have been introduced. The model was implemented in the UNRES package for coarse-grained simulations of proteins, and the package with the new functionality was tested for total energy conservation and thermostat behavior in microcanonical and canonical molecular dynamics simulations runs, respectively. The efficiency of the new force field was estimated by using 10 short α-helical membrane proteins with low similarity [4], which were simulated starting from extended structures. The extended UNRES force field was able to predict correctly the overall folds of the membrane proteins studied.

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