

Streszczenie pracy w języku angielskim:

Proteins are primary chemical compounds building all living organisms. Knowledge of their structure, properties, and dynamics plays a significant role in the diagnosis of the causes of many diseases (e.g. Parkinson's disease, Alzheimer's disease) and during drug design. Experimental research on protein structure is a very difficult and time-consuming task, therefore computer simulation methods, especially with coarse-grained force fields, are very helpful as they significantly simplify protein representation and allow quick and effective determination of protein spatial structure and dynamics.

The structure of proteins depends on the environment and is stabilized by many factors including local and hydrophobic interactions. To research these interactions in proteins I used the UNRES coarse-grained force field for which I parametrized local interactions with five types of amino acid residues and I expanded the scope of UNRES application from the water phase to the lipid environment including lipid bilayer. To predict the structure of proteins I also used the hybrid method combining the UNRES force field with homology modeling and information from sequence and structural databases. UNRES force field extended to the lipid environment allowed for the correct definition of alpha-helical membrane protein structures. Extending the parametrization of the local interactions in the UNRES force field to five types of amino acid residues resulted in only a slight improvement in predictive ability for a set of proteins that I tested. Protein structures predicted using the hybrid approach were highly evaluated in the 13th edition of the CASP experiment and their accuracy depends on the quality of the input server models and the coverage of their common consensus fragments.

To understand the molecular basis of the hydrophobic effect and the hydrophobic interactions I simulated small model systems consisting of one and two nonpolar particles described using Lennard-Jones and Mie pseudo-hard-spheres potentials in explicit SPC/E, TIP3P-Ew, and TIP4P-2005 water models over a wide temperature range from 237 to 373 K. With increasing temperature, the hydration of small particles with a diameter of less than 8.8 Å exhibits an increase in the Gibbs free energy ΔG , the enthalpy ΔH , and the entropy term $T\Delta S$. For larger particles, hydration ΔG decreases with temperature, and ΔH and $T\Delta S$ increase. The results of the simulations I obtained are in agreement with the experimental data from the hydration process of ethane, cyclohexane, and 2,2,4-trimethylpentane. The association of nonpolar particles at the contact minimum distance was accompanied by an increase of $T\Delta S$ value and a decrease in average strength potential $\Delta G [r]$ and enthalpy ΔH . The best compatibility with the theoretical iceberg model of the Frank and Evans was characterized in a system composed of pseudo hard-spheres with the diameter of the atom Xe described using Mie potential and a 4-site water model TIP4P-2005.