Abstract

This master's thesis provides study of individual helixes from C-terminal pore-forming domain (CTD) of colicin U and their behavior in lipid bilayer on atomic level. For this purpose the all-atom molecular simulation method was used. Later the study was extended an applied on CTD of published structures of other pore-forming colicins. On the base of study extension the ability of disruption of lipid bilayer integrity by helixes H1 and H10 was successfully observed. Helix H1 was synthesized and its activity was experimentally proved on black lipid membranes. The other helixes are often too short to be able to keep position in lipid bilayer and their behavior could be affected by artificial termini, therefore they were not synthesized. The MD simulations of pairs of helixes show that structure stability and their ability to stay in the membrane depends on binding partners. The results of the thesis show the importance of H10 for colicin pore-formation, which has not been observed yet. The results also support the toroidal pore model suggested previously for colicin E1. The results prove that colicins contain specific secondary structures, which are able to disrupt the inner bacterial membrane not only in its native form but also when artificially separated from the rest of the protein.

Klíčová slova: Pore-Forming Colicins, Protein topology, Protein-Membrane Interaction, Molecular dynamics simulation