

Structural and conformational characterization of Sticholysin II

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Sticholysin II (StnII) is a pore-forming protein that belongs to the actinoporin family of toxins. These molecules are known to present hemolytic activity (HA), for which two regions were shown to be functionally important: the N-terminal segment and the phosphocholine-binding-site. Additionally, specific solution conditions are capable to influence StnII pore formation. In this context, the current work intends to analyze the solution and crystallographic data of actinoporins, as well as the influence of physicochemical factors on its pore-formation activity in order to get further insights into the structural and conformational requirements for HA of actinoporins. The proteins conformations in different solution conditions were evaluated through molecular dynamics (MD) employing the GROMACS package and GROMOS96 force field. The evolution of secondary structure content in the simulations, as well as its dependence on surrounding environment were analyzed. Based on the so obtained data, the increased flexibility observed for the phosphocholine-binding-site in high ionic strength appears to be related to an increased recognition of its molecular target, so promoting HA. Increased flexibilities in other regions of the protein correlates to the decrease in its HA at high pH, while urea promoted a lowering in protein dynamics, which in opposition may reflects its loss of HA. Further studies are being developed in order to associate such environment conformational modification to the membrane-pore oligomeric organization. Supported by CNPq Universal (472174/2007-0) and CAPES.