

Structural and Thermodynamic Characterization of High Mobility Group Proteins (HMGB1)

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The high mobility group (HMG) B1 protein is a highly abundant protein in the nucleus of all Metazoa, present in about one molecule per 10-20 nucleosomes. The protein contains two copies of homologous DNA-binding motifs named HMG-boxes A and B. Some of these HMG-Box family proteins have a C-terminal acidic tail rich in Asp and Glu residues that might be important for the transient DNA-binding properties of the protein. HMGB1 protein exhibits a remarkably high affinity for distorted DNA conformations such as supercoiled DNA, four-way junction and others. In the previous work, we have studied the thermodynamics aspects of HMGB1 from *Schistosoma mansoni* (SmHMGB1). We observed that SmHMGB1 was totally unfolded at low urea concentrations and its ΔG° (1.54 kcal/mol) was a small value for a monomeric protein, suggesting a metastable stability. We are now studying thermodynamics of full-length rat HMGB1 and rHMGB1 without the acidic tail (Δ acidic tail rHMGB1). Our goal is to compare these results with that obtained for SmHMGB1 and try to understand its DNA-binding properties. We have already purified the full length rat HMGB1 and Δ acidic tail rHMGB1 in our laboratory. Fluorescence spectrum indicates that both proteins are in the native conformation. It was observed a red shift on the Trp emission spectra at 8M urea and a decrease in the center of spectral mass of about 800cm^{-1} . The $[\text{Urea}]_{50\%}$ was 2.5M, which is considerably low. The next step is to compare the thermodynamics behavior of full-length rHMGB1 with the Δ acidic tail rHMGB1, concerning its stability with chaotropic and physical agents.

Keywords: DNA-binding protein, High Mobility Group protein, Protein purification.
Supported by: FAPERJ, CNPq.