

Abstract Submitted  
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**Mechanisms of triggering H1 helix in prion proteins unfolding revealed by molecular dynamic simulation**<sup>1</sup> CHIH-YUAN TSENG, Dept. of Physics, National Central University, H.C. LEE, Dept. of Physics and Dept. of Life Science, National Central University — In template-assistance model, normal Prion protein (PrP<sup>C</sup>), the pathogen to cause several prion diseases such as Creutzfeldt-Jakob (CJD) in human, Bovine Spongiform Encephalopathy (BSE) in cow, and scrapie in sheep, converts to infectious prion (PrP<sup>Sc</sup>) through a transient interaction with PrP<sup>Sc</sup>. Furthermore, conventional studies showed S1-H1-S2 region in PrP<sup>C</sup> to be the template of S1-S2  $\beta$ -sheet in PrP<sup>Sc</sup>, and Prion protein's conformational conversion may involve an unfolding of H1 and refolding into  $\beta$ -sheet. Here we prepare several mouse prion peptides that contain S1-H1-S2 region with specific different structures, which are corresponding to specific interactions, to investigate possible mechanisms to trigger H1  $\alpha$ -helix unfolding process via molecular dynamic simulation. Three properties, conformational transition, salt-bridge in H1, and hydrophobic solvent accessible surface (SAS) are analyzed. From these studies, we found the interaction that triggers H1 unfolding to be the one that causes dihedral angle at residue Asn<sup>143</sup> changes. Whereas interactions that cause S1 segment's conformational changes play a minor in this process. These studies offers an additional evidence for template-assistance model.

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