

## **BSE prion fragment (90-231): pH-induced conformational changes and binding with potential inhibitors by molecular dynamics**

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The prion protein PrP<sup>c</sup> is a glycosylated component of the extracellular surface of neurons, which appears to have an active role in signal transduction. Its misfolded isoform, PrP<sup>Sc</sup>, is a  $\beta$ -sheet-rich, protease-resistant protein that causes fatal neurodegenerative disorders in humans and in other mammals, which can exhibit sporadic, inherited or infectious presentations. Despite remarkable differences in phenotypic expressions, these disorders share a similar pathogenic mechanism: a post-translational modification of the prion from the normal cellular isoform PrP<sup>c</sup> to disease-specific species PrP<sup>Sc</sup>. The PrP<sup>c</sup>  $\rightarrow$  PrP<sup>Sc</sup> transition involves a profound conformational change with a decrease in  $\alpha$ -helical secondary structure (from approximately 40% to 30%) and a consequent, remarkable increase in  $\beta$ -sheet content (from  $\sim$  3% to 40%). This, in turn, is accompanied by the exhibition of abnormal physicochemical properties, including insolubility in typical non-denaturing detergents and partial resistance to proteinase K digestion.

In recent studies it has been found that residues 90-120 are antigenically accessible in PrP<sup>c</sup> but are encrypted in PrP<sup>Sc</sup>. Further, experiments on mini-prions containing only residues 89-140 and 177-231 showed that one of these two regions is critical to the conformational changes but, since a peptide containing residues 90-144 carrying the P101L mutation folds into a  $\beta$ -rich structure that can cause a prion disease in transgenic mice and PrP(121-231) is not scrapie competent, residues 90-120 must be of paramount importance.

In this paper we present the results obtained from a detailed molecular modeling and dynamic simulation studies of the entire PrP<sup>c</sup> fragment (90-231) of the Syrian hamster above and below a pH that triggers conformational changes. Further, we report the evidence of possible binding sites of PrP<sup>c</sup> with several potential inhibitors, such as tetracyclines, Congo red and doxorubicin.