Predicting structures of small non-amyloid and amyloid proteins using molecular dynamics simulation in implicit water

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It is still a grand challenge to predict protein structures using physics-based models given the sequence information. Yet, more and more successful examples start to emerge as a result of significant improvements in Molecular Mechanics force field and conformation sampling technique (e.g. Replica Exchange Molecular Dynamics/REMD). In the first part of this talk, I will talk about our recent work (JCTC, in press) on assessing performance of popular Quantum Mechanics and Molecular Mechanics methods using MP2/ccPVTZ results of 100 tetrapeptide structural models. In the second part, I will present our recent successful modeling of several small non-amyloid and amyloid proteins by using AMBER force field (ff96) plus an implicit solvent model (iGB=5) and Replica Exchange Molecular Dynamics (REMD). The examples include an alpha/beta fold protein and two amyloid peptides (a prion fragment and amylin). The predicted results are verified by experimental techniques (Ion Mobility Mass Spectroscopy, CD and others).