Using Programming to Simulate and Visualize Proteins

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The use of programming to conduct simulations and structure visualizations can help understand the functions of biomolecules at the molecular level. This approach can be used to study structures from any organism. This understanding can lead to advances in medicine, healthcare, and bio-engineering. In this study, Chymotrypsin Inhibitor 2 (CI2) was simulated in order to assess the degree which simulations capture experimental values determined from protein folding. There are two dominant conformational ensembles that exist near the folding temperature, a folded and unfolded ensemble. Connecting these two states is the transitions state, a highly unstable set of conformations with a structure between the folded and unfolded ensembles. In order to find the temperature that maximally populates the transition state, simulations were performed at different temperatures. The optimal folding temperature was confirmed by the observation of an equal population of folded and unfolded states, with frequent flipping back and forth between them. Visualization software (VMD) of the simulations served as an aid to see the actual trajectory of CI2 as it flipped back and forth, and data was collected to compare the structural features of all three conformations. The data was split into two graphs showing what amino acid residues were found to be in close proximity in each structural ensemble. The more contacts that were present, the more of the “native” protein structure exists. When compared with experimental assessments of the transition state structure, the simulated structure gave a slope of +0.25 and correlation coefficient of +0.28. The results provided some predictive value but there is clearly still room for improvement. This method can be applied to different proteins found within other organisms to predict their behavior under different conditions.