

Exploring Protein Folding Using Gromacs Simulation Software

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Chymotrypsin inhibitor 2 (2ci2) is a serine proteinase found in barley seed, that is of interest in many protein transition state studies due to its two-state model where no intermediate state is found between the unfolded and folded state (Mcphalen & James, 1987; Jackson & Fersht, 1991). This study explored the parameters that enabled chymotrypsin inhibitor 2 to be found between the folded state and the unfolded state. This further allowed for the analysis of the protein's structure and phi value when found within the transition state. When at 115K the protein was found to be in a folded state, while at 150K the protein was found to be in an unfolded state. It is between these temperatures, at 138K, that the protein was found existing in both a folded and an unfolded state allowing us to explore the transition state further. Using the temperature of 138K and gromacs software, the chymotrypsin inhibitor ran through a longer simulation than prior allowing for the protein to flip between the folded and unfolded state multiple times. Using gromacs software and its program "xmgrace," a contact graph was made to compare contacts within the crystal structure, folded state, transition state, and unfolded state. The unfolded state had the least amount of contacts, however the protein was not completely unravelled. Xmgrace then allowed for the plotting of phi values, with the y-axis showing the phi values within the simulation and the x-axis plotting the experimental phi values known. The correlation between the simulation and the experimental values was found to be 0.28, with a slope of 0.25. This showed that the simulated protein is not a perfect model to the experimental structure of chymotrypsin inhibitor 2, although with the use of gromacs software, the simulated protein did allow for the ability to analyze contacts and the structure of the protein within the transition state.

Mcphalen & James. 1987. Crystal and molecular structure of serine proteinase inhibitor CI-2 from barley seeds. 26(1):261-9. doi: 10.1021/bi00375a036. Retrieved from:
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Jackson & Fersht. 1991. Folding of chymotrypsin inhibitor 2. 1. Evidence for a two-state transition. Biochemistry. 30(43):10428-35. doi: 10.1021/bi00107a010. Retrieved from:
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