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Conformational Entropy in Protein Structure Changes; Instrumental and Computational Analysis

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Abstract

Entropy is a thermodynamic quantity representing the unavailability of a system. Proteins also undergo structural changes through various processes such as folding, unfolding, intermolecular interactions, and etc. resulting in changes in the rate of disorder or entropy. Conformational entropy is the entropy associated with the number of conformations of a molecule. A conformational entropy is usually defined for the backbone and the side chain of residues of the protein.

Calculation of the probable states for backbone dihedral angles and side chain rotamers is one of the computational methods for conformational entropy analysis. These properties are used to define the degree of freedom. These variables can express the amount of conformational entropy with the Boltzmann equation. On the other hand, the only empirical method capable of measuring conformational entropy is NMR relaxation.

The amount of conformational entropy associated with a protein structure, such as α-helix, fold or unfold state, depends on the probability of its formation. The entropy of a random coil and denatured structure is significantly greater than the folded state. The side chain conformational entropy appears to play an important role in stabilizing the energy level in the denatured state, thereby inhibiting protein folding. However, recent studies have shown that the side chain conformational entropy is able to stabilize the Native structure of a protein against other folded structures. In this study, in addition to introducing structural entropy and its measurement methods, we discuss the role of this phenomenon in protein structure and dynamics.

Keywords: Conformational entropy, dihedral angle, rotamer, Boltzmann equation, NMR relaxation

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