

19aTC-8 Biophysical approaches for understanding the folding and stability of proteins

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During the process of protein folding, the amino acid residues along the polypeptide chain interact with each other in a cooperative manner to form the stable native structure. Protein structures are stabilized with various non-covalent interactions, such as, hydrophobic, electrostatic, hydrogen bonding, van der Waals etc. and are collectively termed as “inter-residue interactions”. The knowledge about inter-residue interactions in protein structures is very helpful to understand the mechanism of protein folding and stability. In this presentation, I introduce the classification of inter-residue interactions into short, medium and long range based on a simple geometric approach, the location of amino acid residues in protein sequence and structure (Figure 1).

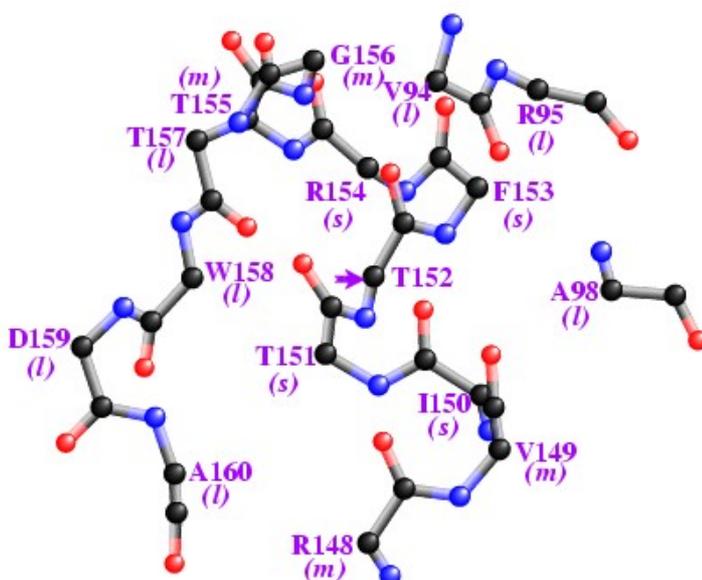


Figure 1: Representation of short, medium and long-range contacts in protein structures (1). A typical example of

surrounding residues around T152 of T4 lysozyme within 8Å is shown: s: short-range contacts, m: medium-range contacts and l: long-range contacts.

The features of these interactions in different structural classes of globular and membrane proteins, membrane protein-ligand interactions and their applications to protein secondary structure prediction and discriminate β -barrel membrane proteins will be presented (2,3). Further, the relationship between inter-residue contacts and protein folding rates will be highlighted (4,5). We have developed the novel parameter, long-range order (LRO) based on the long-range contacts in protein structures, which can be used to understand and predict the folding rates of two-state proteins. Moreover, the importance of inter-residue interactions in protein folding kinetics and for understanding the stability of proteins including the development of protein thermodynamic database will be discussed (6-8). In essence, the information gained from the studies on inter-residue interactions provides valuable insights for understanding protein folding and *de novo* protein design.

References:

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