



IIT Guwahati

Lecture 13

Course BT 631

Protein Structure function and Crystallography

Prof. Arun Goyal

Dept. of Biosciences and Bioengineering



B) Sheet super-secondary structures

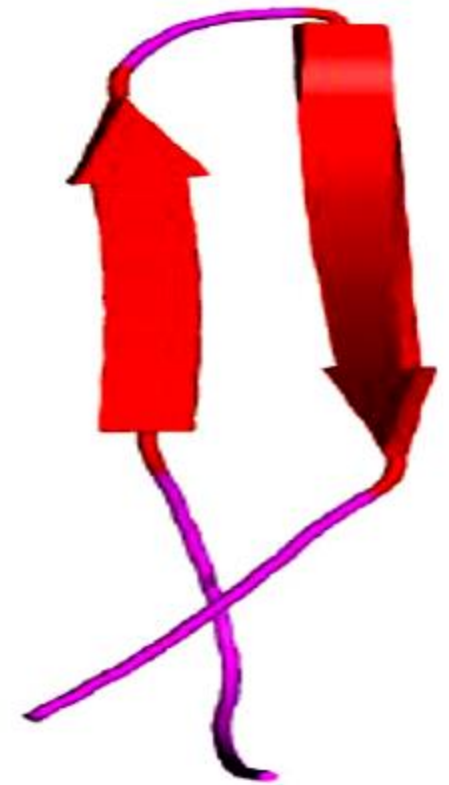
B) Sheet super-secondary structures

1. Beta corner (β - β corner)
2. Greek key motif
3. Beta Jelly Roll

1. Beta corner (β - β corner)

A β - β -corner can be represented as a long β - β -hairpin folded orthogonally on itself so that the strands, when passing from one layer to the other, rotate in a *right-handed direction* about an imaginary axis.

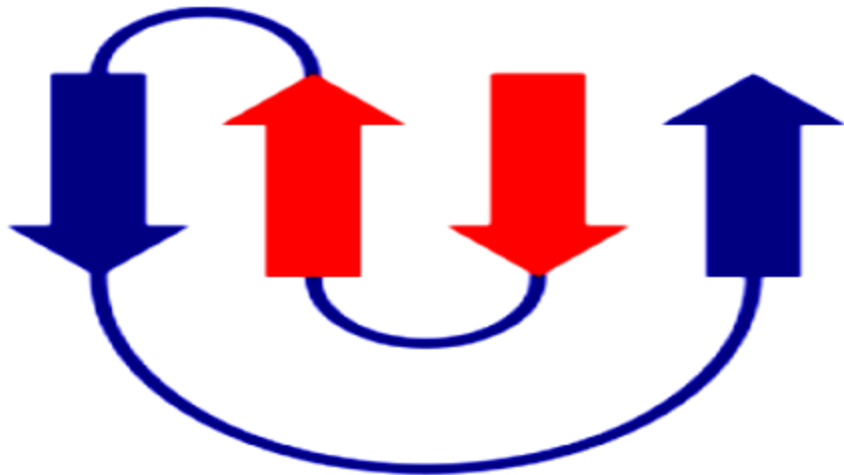
Anti-parallel beta strands forming a beta-hairpin can accommodate a 90° change in direction known as beta corner.



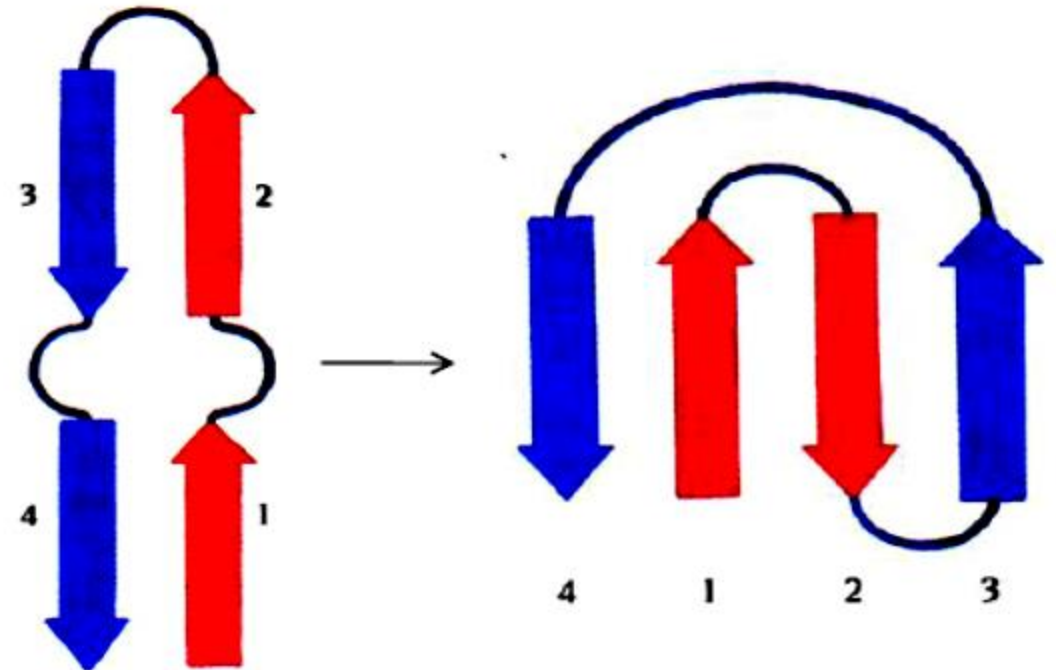
B) Sheet super-secondary structures

2. Greek key motif

- The Greek key motif is found in anti-parallel sheets with 4 adjacent β -strands.
- The motif occurs in many β -sheets, such as enzyme *Staphylococcus* nuclease.
- This type of structure forms easily during the protein folding process.



- Suggested folding pathway is from a hairpin-like structure to the Greek key motif (Fig. below).
- β -strands 2 and 3 fold over such that strand 2 is aligned adjacent and antiparallel to strand 1.

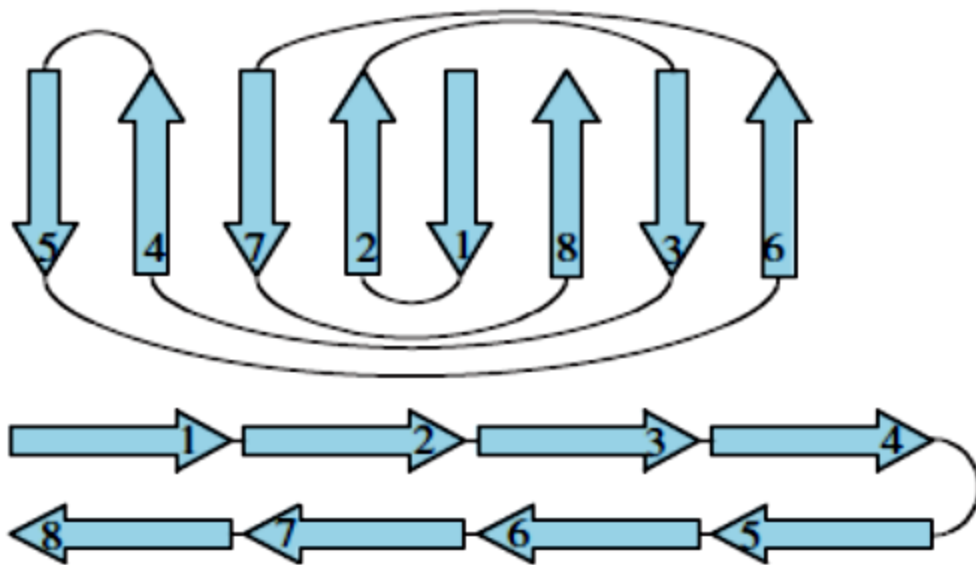


B) Sheet super-secondary structures

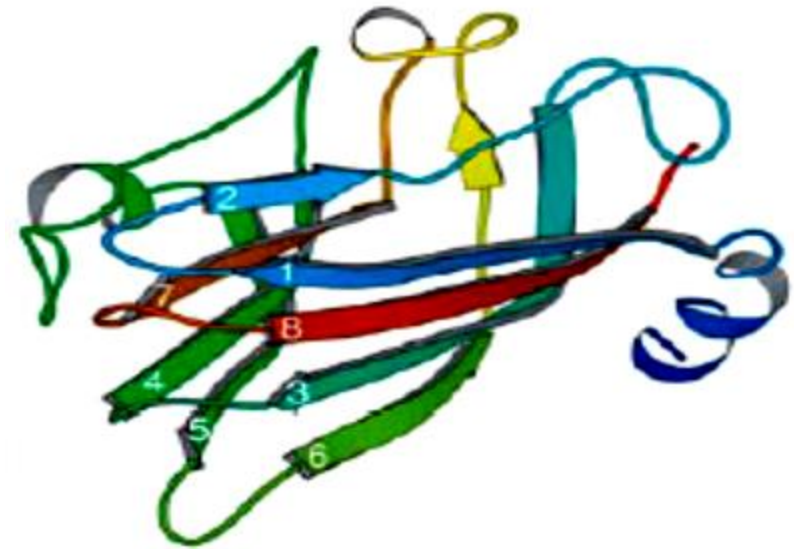
3. β -Jelly Roll

A special type of a Greek key structure is an extended version called *jelly roll*.

This is an **eight-stranded** arrangement that forms a β -sandwich of **two, four-stranded sheets**.



(β -jelly roll topology is formed as a hairpin rolled up)



(Coat protein of plant virus STNV, a β -jelly roll)

C) Mix super-secondary structures

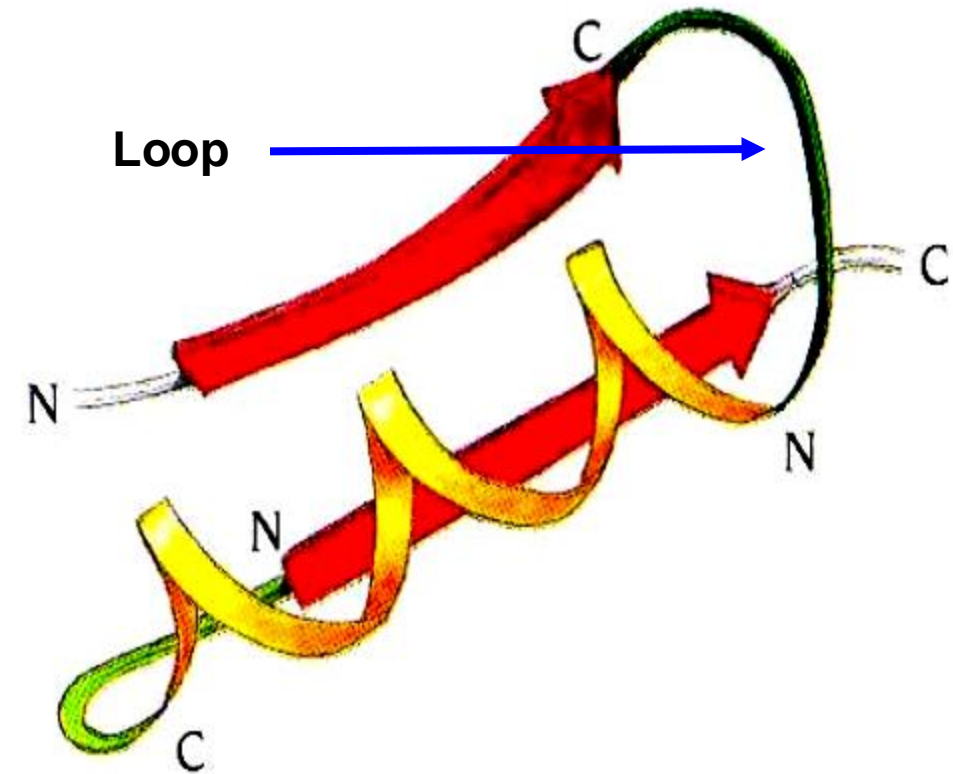
C) Mix super-secondary structures

1. Beta-alpha-beta (β - α - β)
2. Rossmann fold
3. Zinc Finger Motif

C) Mix super-secondary structures

1. Beta-alpha-beta (β - α - β)

- If two adjacent β -strands are joined to form **parallel strands** of a sheet and the connection between the two ends is made by an α -helix is called **$\beta\alpha\beta$ motif**.
- The motif that is formed is thus a β -strand followed by a loop, an α -helix, another loop and, finally, the second β -strand.
- The **loop connecting the Carboxyl end of the β -strand with the Amino end of the α -helix** often have conserved amino acid sequences in homologous proteins and are involved in forming the **active site** of these structures.



C) Mix super-secondary structures

1. Beta-alpha-beta (β - α - β)

Handedness of the $\beta\alpha\beta$ motif

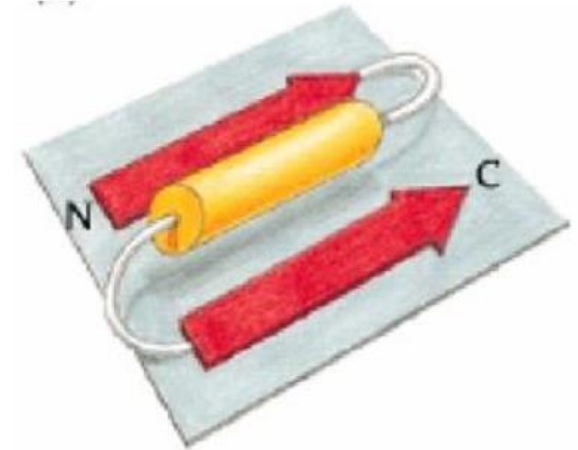
The motif can in principle occur in two different "enantiomeric forms", with α -helix either above or below the plane of the β -sheet.

α -Helix above the plane is called right handed.

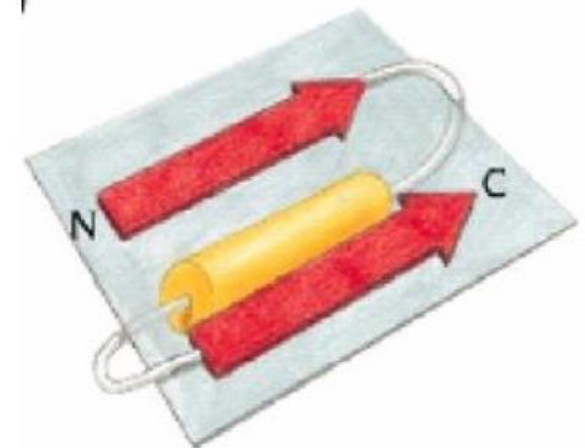
α -Helix below the plane is called left handed.

Essentially, every β - α - β motif in the known protein structures has been found to be right-handed. No convincing explanation has been found for this regularity.

This handedness has important structural and functional consequences when several of these motifs are linked into a domain structure.



Helix above the plane, right handed



Helix below the plane, left handed

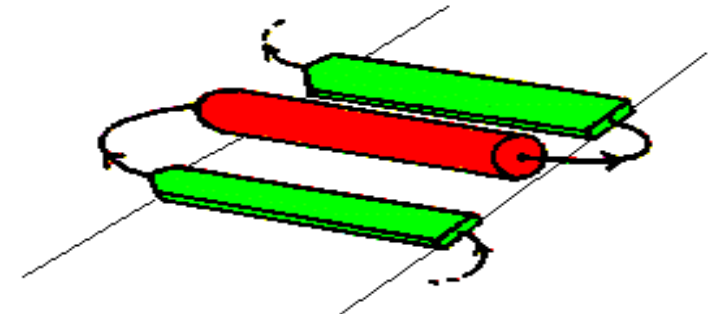
C) Mix super-secondary structures

2. Rossmann fold

The Rossmann fold is a super-secondary structure that is characterized by an alternating motif of **beta-strand-alpha helix-beta strand** secondary structures. Hence this fold is also called a $\beta\alpha\beta$ fold. The β -strands participate in the formation of a β -sheet.

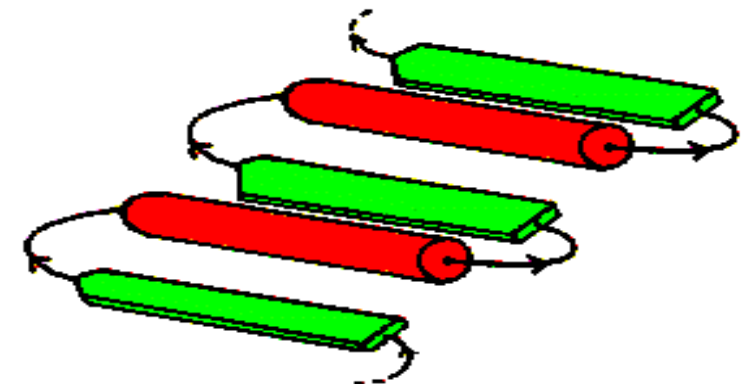
The $\beta\alpha\beta$ fold structure is commonly observed in enzymes that have dinucleotide coenzymes, such as FAD, NAD and NADP.

Simple $\beta\alpha\beta$ motifs can combine to generate more complex structures such as Rossmann fold ($\beta\alpha\beta\alpha\beta$) motif with the **middle β -strand** shared between the two units. Involved in binding FAD, NAD.



The right-handed beta-alpha-beta unit. The helix lies above the plane of the strands.

The Rossman fold



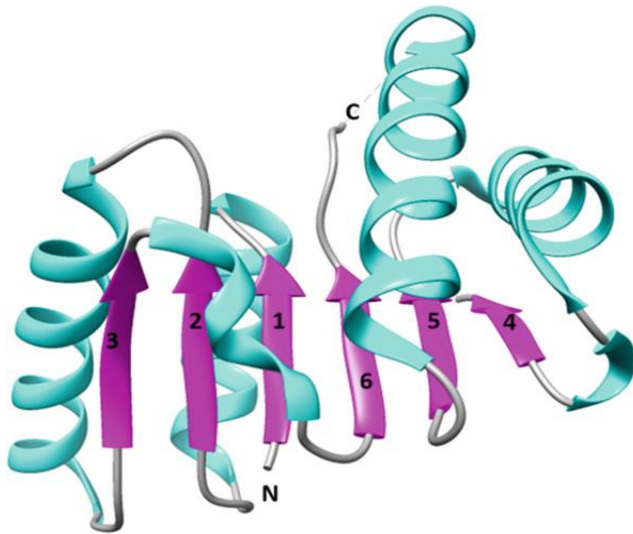
($\beta\alpha\beta\alpha\beta$, dehydrogenases)

C) Mix super-secondary structures

2. Rossmann fold

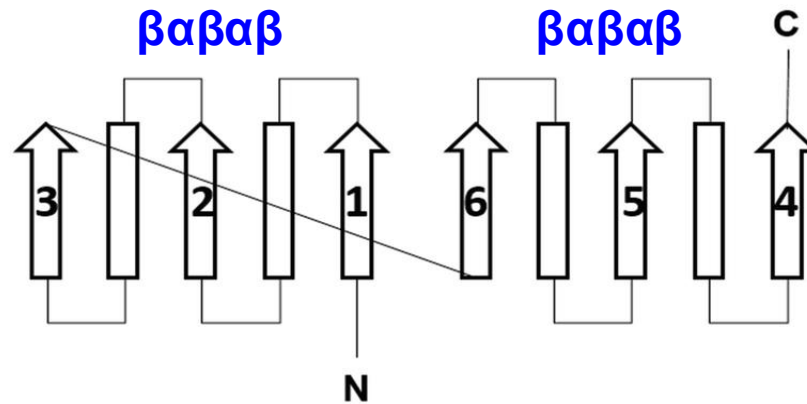
The $\beta\alpha\beta\alpha\beta$ motif can also combine to generate more complex structures, such as Rossmann fold (= 2 x $\beta\alpha\beta\alpha\beta$) with the **two middle β -strands** shared between the two units).

(a)



(a) Rossmann fold (PDB ID: 2D4A) in Malate dehydrogenase.
Helices are in Cyan and Strands are in Magenta.

(b)



(b) 2-Dimensional model of Rossmann fold.
Arrows are β -strands and squares are α -helices.
Numbering on β -strands starts from N-terminus of protein

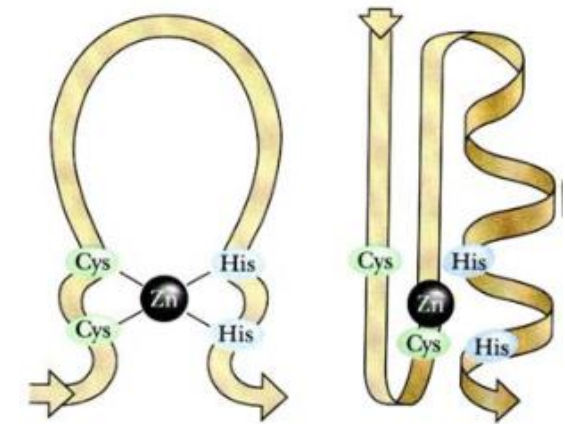
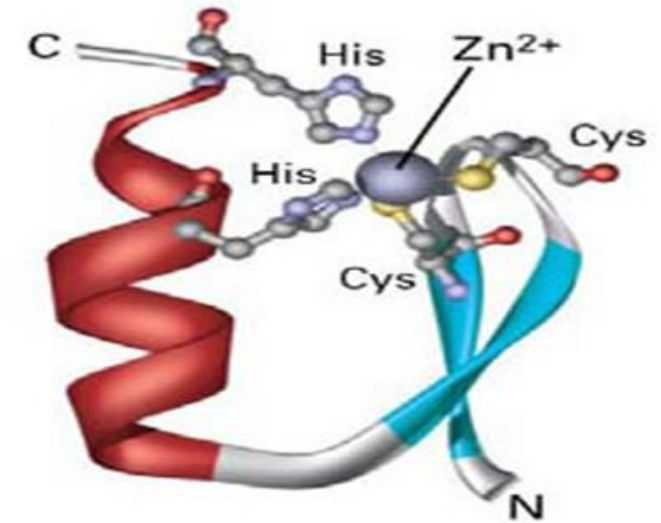
C) Mix super-secondary structures

3. Zinc Finger Motif

- Zinc Finger Motif (ZnF) consists of a segment of α -helix bound to a loop by a Zinc ion (Zn^{2+}).
- The Zinc ion is held in place by two Cysteine from loop and two Histidine side chains from α -helix.
- The α -helix lies in the major groove of DNA double helix.
- DNA-binding proteins with ZnF motifs are involved in gene transcription.
- Proteins carrying RNA-binding ZnF motifs include are HIV nucleocapsid, reovirus sigma3 and Plant nuclear protein.

Database of Structural motifs in Proteins

<http://www.203.200.217.185/DSMPO/>



Zinc Finger Motif