IIT Guwahati

Lecture 16

Course BT 631

Protein Structure, function and Crystallography

Prof. Arun Goyal

Dept. of Biosciences and Bioengineering

Tertiary structure

The organization of proteins into Domains

For proteins larger than 150 amino acid residues the tertiary structure may be organized by more than one structural unit. *Each structural unit is called domain*.

***A rigorous definition of a domain does not exist*.**

One acceptable definition is

the presence of an autonomously folding unit within protein.

The domains of proteins interact together although with fewer interactions than the secondary structure elements within each domain.

Domains are classified into four types

a) α-Domain

b) β-Domain

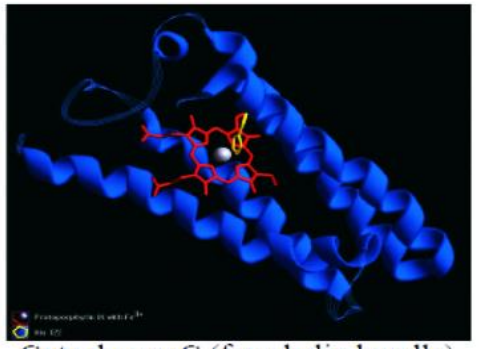
c) α/β Domain

d) α+β Domain

Tertiary structure: The organization of proteins into Domains

a) All-α proteins

is a class of structural domains in which the secondary structure is composed entirely of α-helices, with the possible exception of a few isolated β-sheets on the periphery. Common examples are

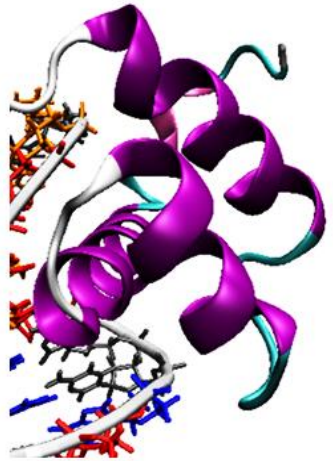


CytochromeC (four-helix bundle)

i) Bromodomain: **The domain itself adopts an all α-protein fold, a bundle of 4 α-helices each separated by loop regions of variable lengths. e.g. Histones, Cytochrome C.**

(Bromodomain)

ii) Homeodomain: **The fold consists of a 60-amino acid helix-turn-helix structure in which 3 α-helices are connected by short loop regions. e.g. Transcription factors.**



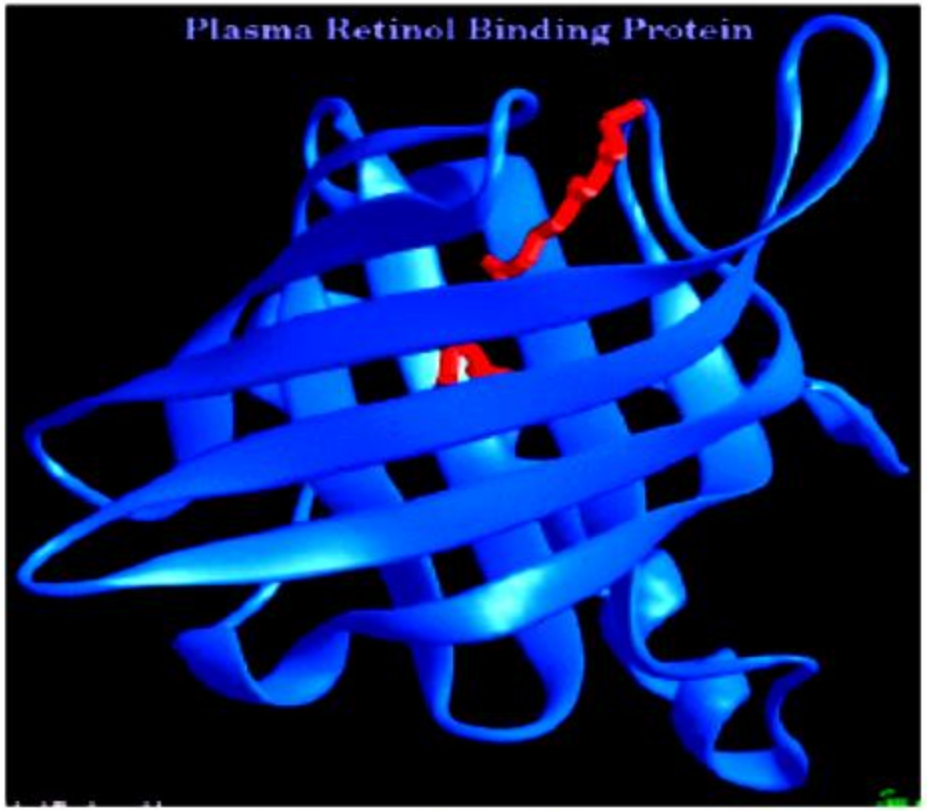
(Homeodomain)

Tertiary structure: The organization of proteins into Domains

b) All-β protein

is a class of structural domain in which the secondary structure is composed entirely of β-sheets, with the possible exception of a few isolated α-helices on the periphery.

e.g. β-propeller domain and B3DNA binding domain.



β sandwich

Tertiary structure: The organization of proteins into Domains

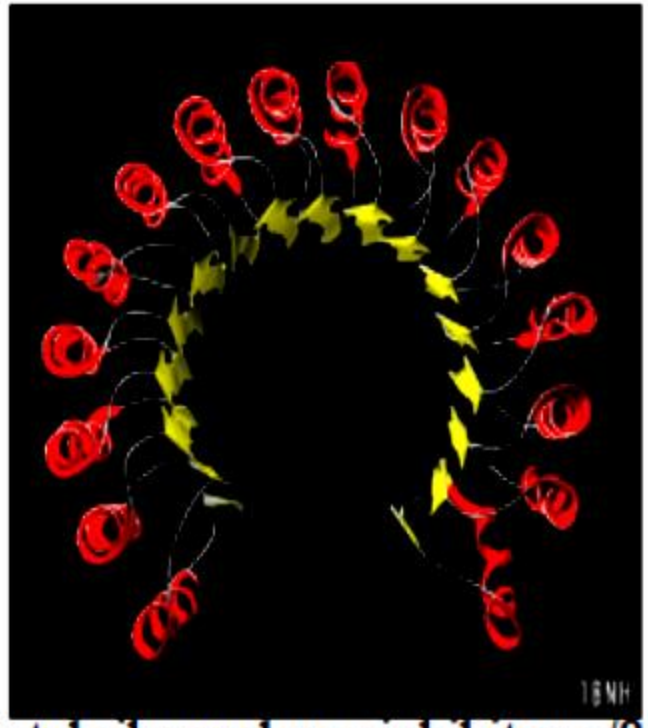
c) α/β protein

the secondary structure is composed of alternating α-helices and β-strands along the backbone.

The β-strands are mostly *parallel*.
e.g. the flavodoxin fold, the TIM barrel and ribonuclease inhibitor.

This is common tertiary fold observed in high resolution protein crystal structures.

10% of all known enzymes have this α/β domain.



Placental ribonuclease inhibitor α/β horseshoe

Tertiary structure: The organization of proteins into Domains

d) α+β proteins

are a class of structural domains in which the secondary structure is composed of α-helices and β-strands that occur separately along the backbone.

The β-strands are therefore mostly *anti-parallel*. e.g. ferredoxin fold and ribonucleaseA.