

PROTEIN

RCSB PDB-101

Introduction

Protein name is derived from a Greek word PROTOS which means "the first or the supreme".

Proteins are extremely complicated and nitrogenous molecule made up of variable number of amino acid residue joined to each other by a specific covalent bond called peptide bond.

20 amino acid which have been found to occur in all proteins, known as standard amino acid.

Why are proteins important to us?

Proteins make up about 15% of the mass of the average person

Enzymes act as a biological catalyst

Storage and transport – Hemoglobin

Defence -Antibodies

Hormones – Insulin

Ligaments and arteries (mainly formed by elastin Protein)

Muscle – Proteins in the muscle respond to nerve impulses by changing the packing of their molecules (Actin and myosin)

Hair, nails and skin: Protein keratin as main component

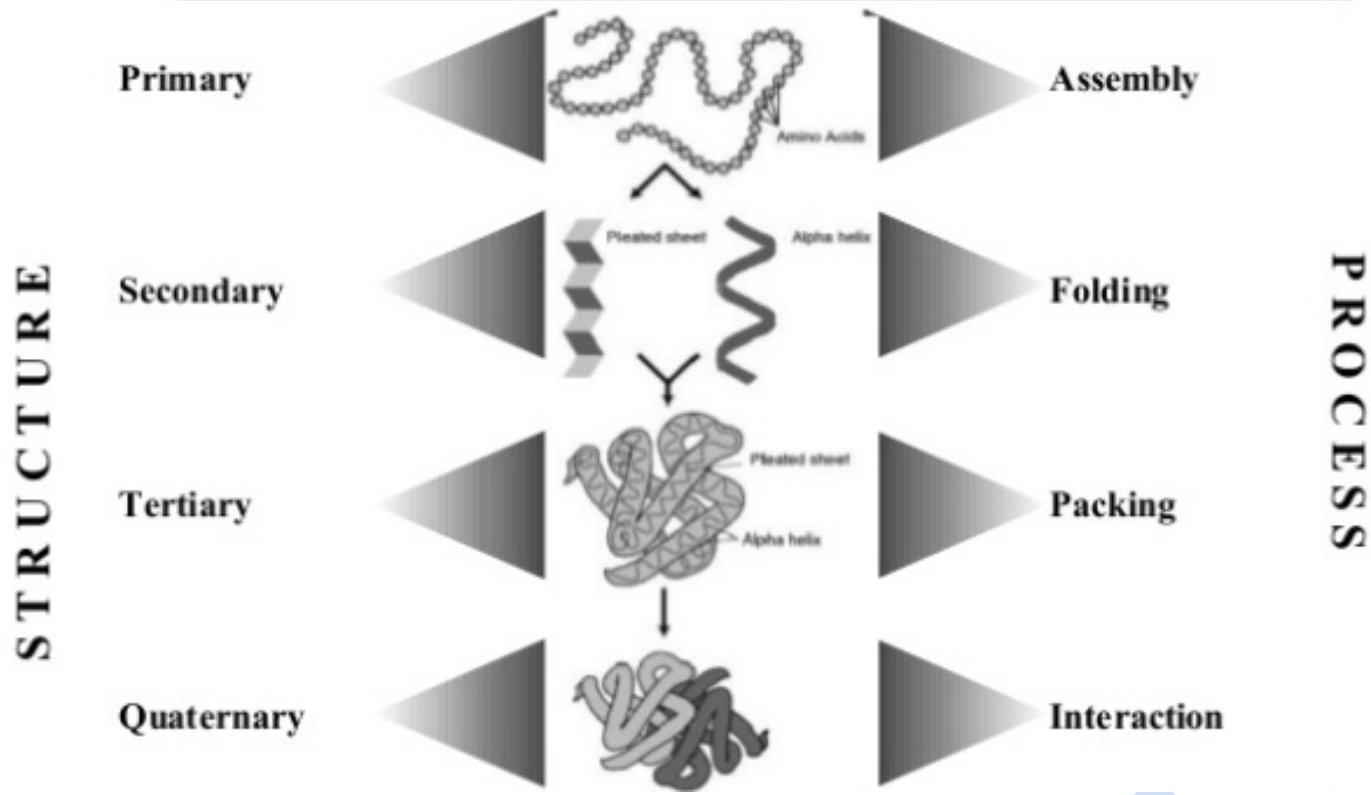
Levels in Protein structure

Majority of protein are compact and highly convoluted molecules.

Each polypeptide assumes at least three levels of structural organization termed as primary, secondary and tertiary structure.

Proteins which possess more than one polypeptide chain in their molecule also possess a fourth structure called quaternary structure.

Chemistry of Protein Structure





Primary structure

The sequence of amino acid residues along the peptide is called primary structure of the peptide.

It also include the determination of the number of amino acid residues in a peptide chain.

Shows whether the peptide chain is open, cyclic or branched.

Primary structure is linear, ordered and 1 dimensional.

Written from amino end to carboxyl end that is N to C.

primary structure of human insulin


CHAIN 1: GIVEQ CCTSI CSLYQ LENYC N

CHAIN 2: FVNQH LCGSH LVEAL YLVCG ERGFF YTPKT



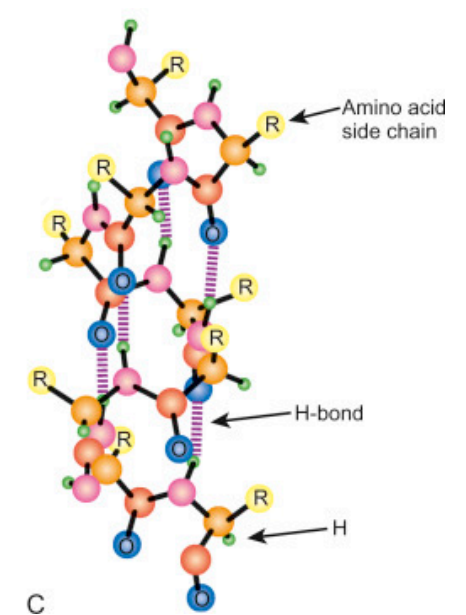
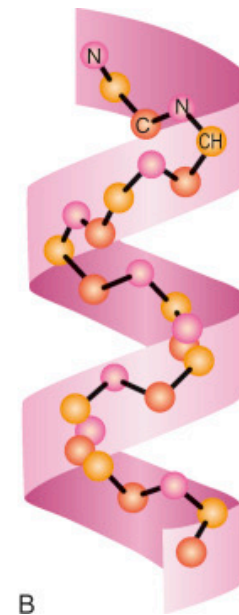


Secondary Structure

- Primary structure shows that peptide are quite straight and extended.
 - X-rays diffraction on protein crystals shows that polypeptide chain tend to twist or coil upon themselves.
 - The folding of the polypeptide chain into specific coiled structure held together by H bonds is called secondary structure of protein.
 - Secondary structure may take one of the following form.
 1. Alpha – Helix
 2. Beta Pleated Sheet
 3. Loop or Coil Conformation
 4. Super secondary motifs
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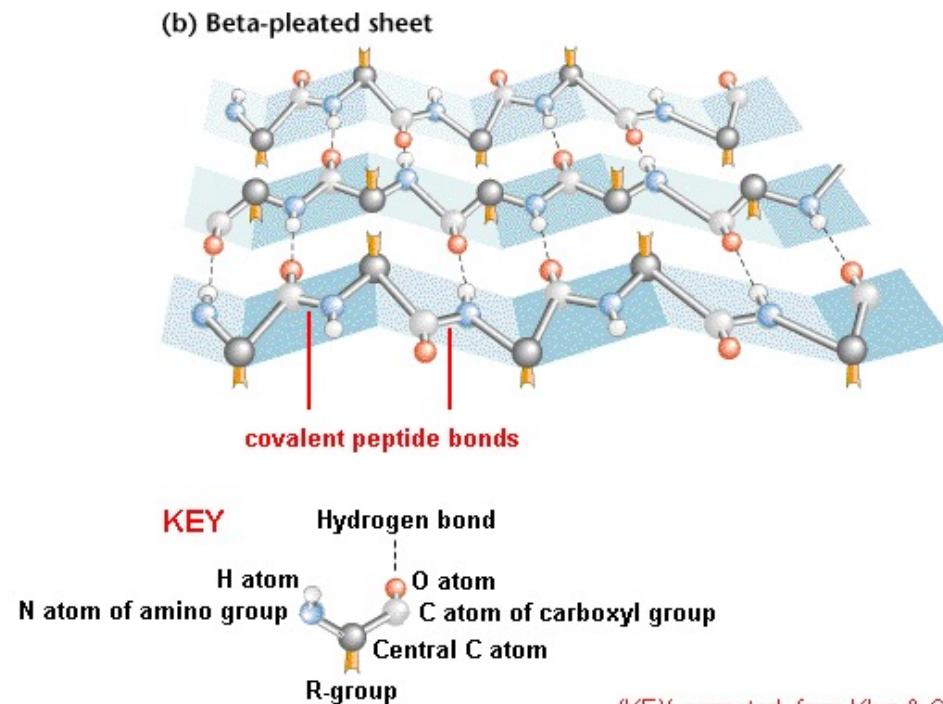
Alpha(α)- Helix

1. It is a clockwise rodlike spiral shape.
2. Formed by intrachain Hydrogen bonding between C=O group of each amino acid and NH₂ group that is present 4 residue ahead.
3. Proteins have great strength and elasticity.
4. Can easily be stretched due to tight coiling.



β - Pleated Sheath

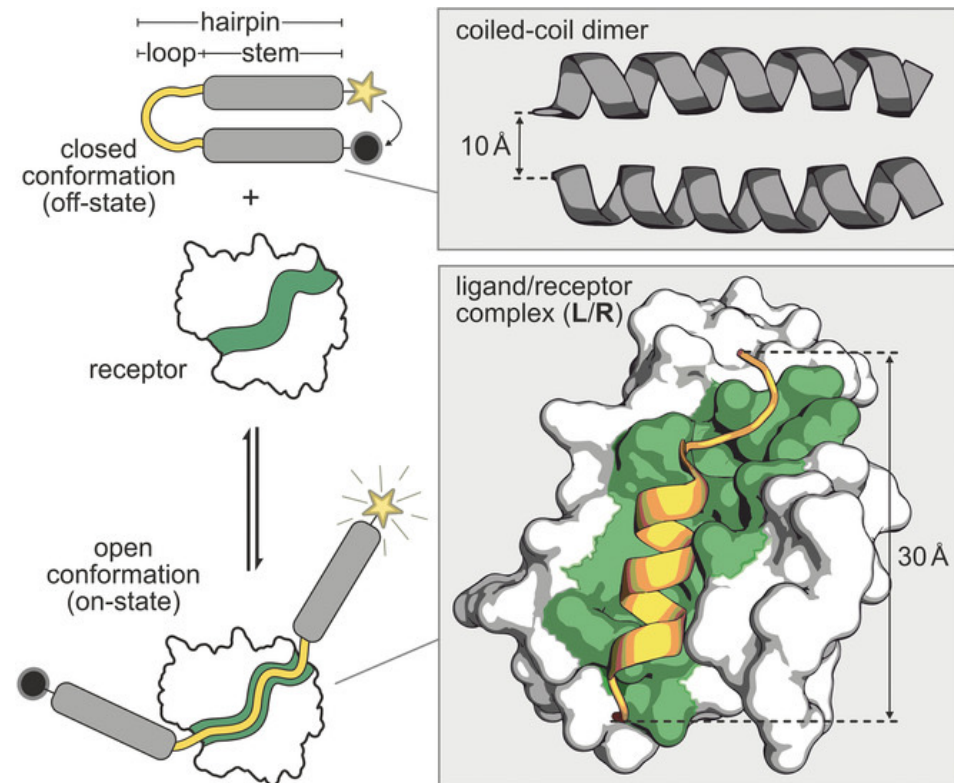
1. 5 to 10 amino acid in this structure line up side by side just like a sheath of cloth can be folded again and again
2. Hydrogen bond present between the peptide strands that is interstrand.
3. This form is fully expended and can't be further stretched and they are inelastic



(KEY corrected, from Klug & Cummings 1997)

Loop or Coil Conformation

1. Present mainly in globular protein.
2. Connect two Alpha helix or Beta sheath.
3. Present in those area where bend is required.



Super secondary Motifs


1. Present in Globular protein.
2. This structure form when two beta pleated sheath are connected to each other by an alpha helix.
3. For example β - α - β supersecondary motif

SUPER SECONDARY STRUCTURE

- ✓ Super-secondary structure comprises localized motifs of secondary structures.
- ✓ Motifs give proteins unique structural features that enable their unique function.
- ✓ Super-secondary structures:
 - ALPHA HELIX MOTIFS**
 - ✓ Helix-turn-helix
 - ✓ Helix-loop-helix
 - ✓ Coiled-coil
 - BETA MOTIFS**
 - ✓ β -hairpin
 - ✓ Greek key
 - ✓ β -barrel
 - ALPHA + BETA MOTIFS**
 - ✓ β - α - β
 - ✓ Zinc finger


ALPHA HELIX MOTIFS

Helix-turn-helix (HTH)




- ✓ Turn ~ 4 amino acids
- ✓ HTH motif binds DNA

Helix-loop-helix (bHLH)



- ✓ HLH is a DNA-binding motif commonly found in transcription factors.


Coiled-coil



- ✓ Coiled coil domains also bind DNA
- ✓ Individual helices have heptad repeats.

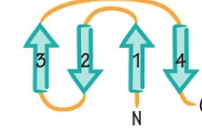
BETA MOTIFS

β -hairpin




- ✓ Proline and glycine residues favored for sharp angle of turn.

Greek key




β -barrel



- ✓ A complex beta sheet structure.
- ✓ β -barrels are commonly found in proteins that transport ions across cell membranes.


ALPHA + BETA MOTIFS

β - α - β



- ✓ Often found in parallel sections of beta sheets
- ✓ β - α - β motifs are almost always right-handed

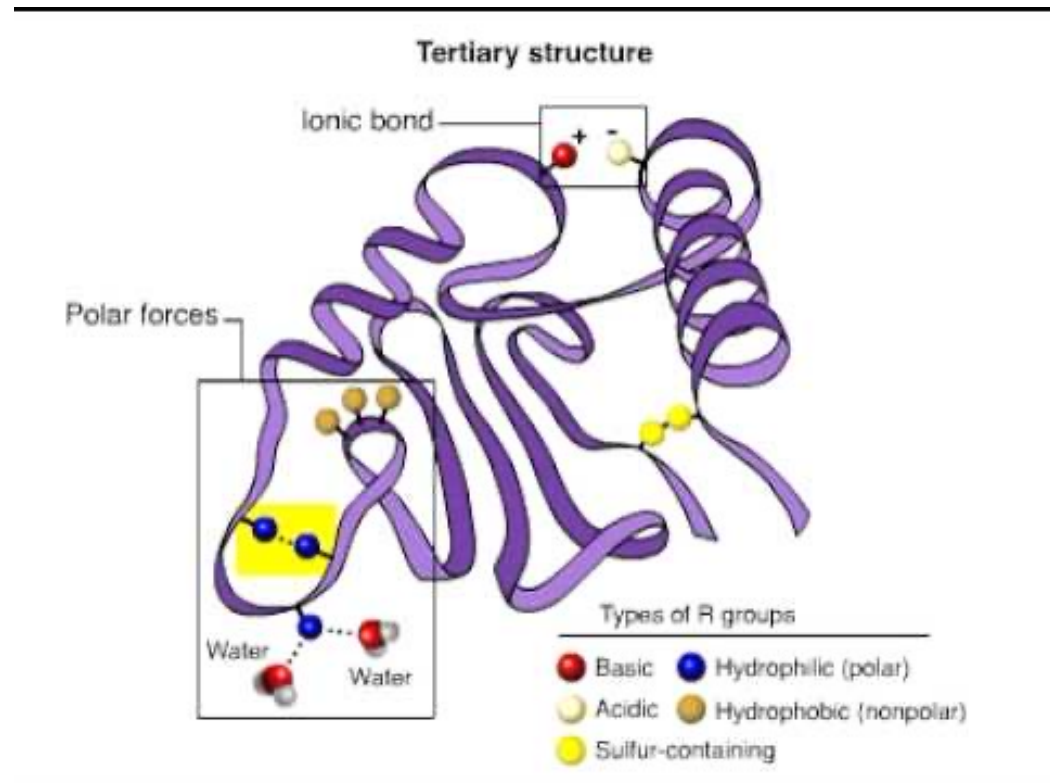
Zinc finger



- ✓ Cys2His2 zinc finger motif
- ✓ Zinc fingers have a variety of shapes and structures
- ✓ Zinc fingers also bind DNA

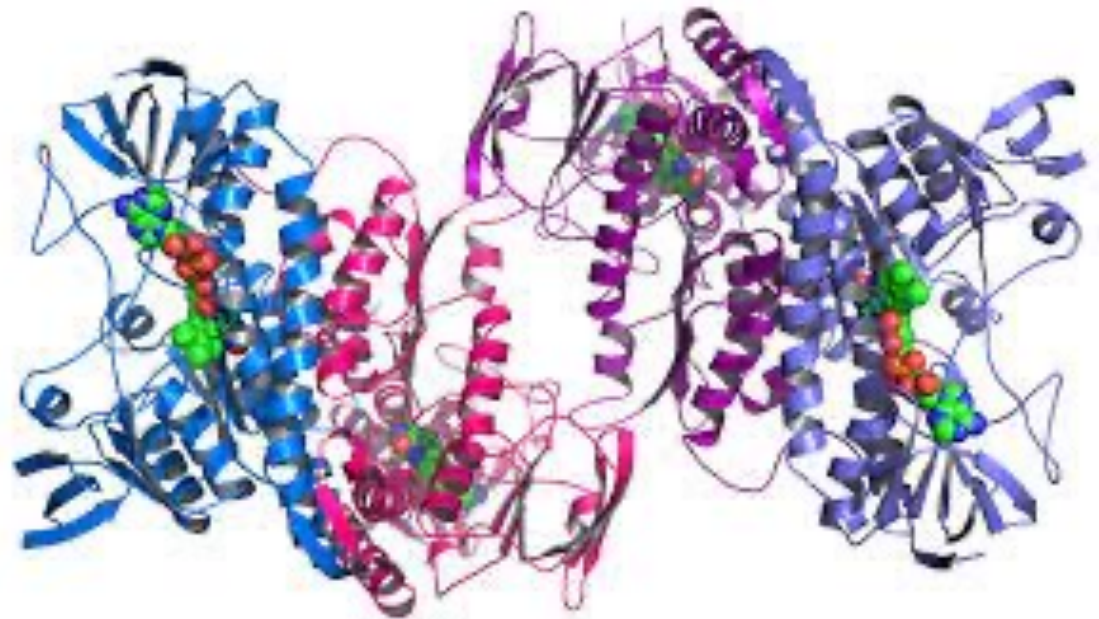
Tertiary structure

1. The tertiary structure mean the overall conformation of a polypeptide.
2. Myoglobin chain is when fully extended its length is 20 time than is width.
3. X-rays diffraction show that its structure is just like a foot ball i.e. globular.
4. The globular structure is due to folding and refolding

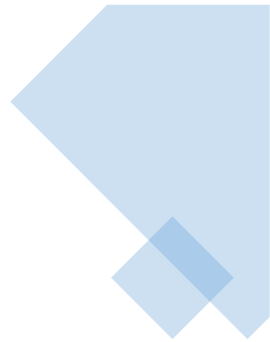
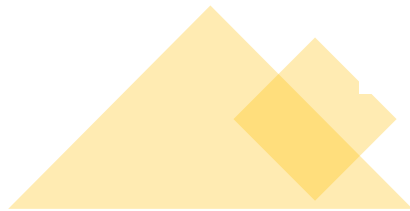
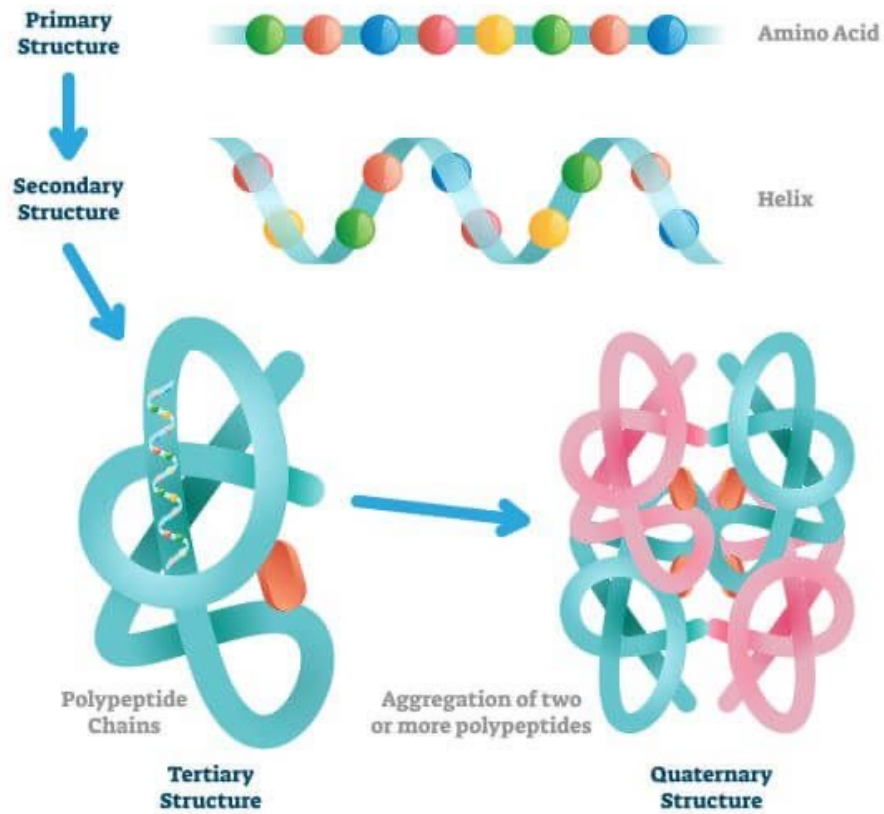


Quaternary Structure

1. Formed by those protein having more than one peptide chain subunit.
2. Each peptide have its own primary, secondary, and tertiary structure.
3. The number and arrangement of the over all structure of the peptide subunit is called quaternary structure.
4. For example structure of Hemoglobin.



PROTEIN STRUCTURE



Phyre²

Protein Homology/analogY Recognition Engine V 2.0

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Position opening

If you are interested in joining the Phyre development team, please contact [Prof. Michael Sternberg](#) for further information.




Other Resources

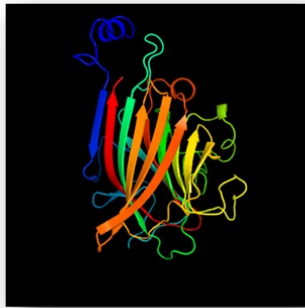
[Missense3D](#): Analyse structural impact of missense variants

[PhyreRisk](#): A dynamic database to view human sequences and structures and map genetic variants

[Cambridge 2019 Workshop](#) | [Older Workshops](#) | [Phyre2 paper](#)

- <http://www.sbg.bio.ic.ac.uk/phyre2/html/page.cgi?id=index>

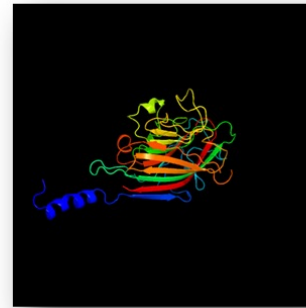
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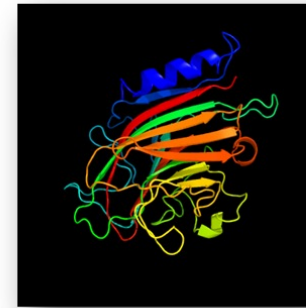
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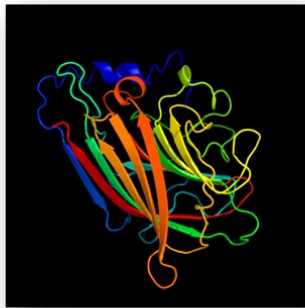
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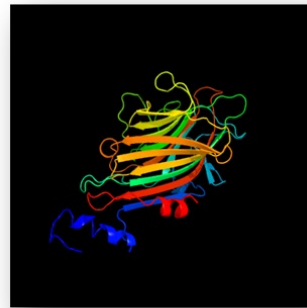
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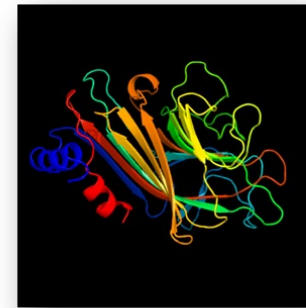
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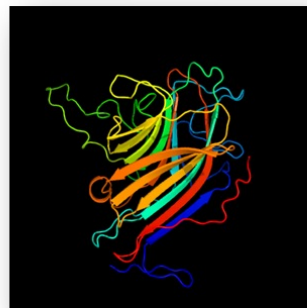
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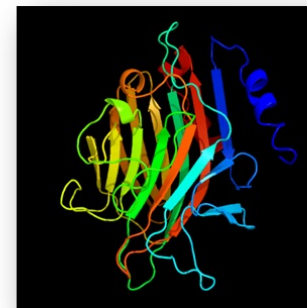
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PvuI-BLEC-13



PvuI-BLEC-14



PvuI-BLEC-17