Proteins

Tuesday, December 9, 2014
8:14 PM

PRIMARY STRUCTURE

Amino Acids

1		Gly		flexible	Gly	Gly
2		Pr		5-ring	Pro	Pro
3	**Aliphatic**	Al, Le, V, I		hydrophobic	AlLeVI	Allevi
4	**Aromatic**	Tr, Ph, Ty		hydrophobic 6-ring H-bonds	TrPhTy	Trphty
5	**Acidic**	Glu, Asp		COOH (-)	GluAsp	Gluasp
6	**Basic**	H, Arg, Ly		N (+)	HArgLy	Hargly
7	**Polar**	Asn, Gln, Th, S		hydrophilic H-bonds	AsnGlnThS	Asnglnths
8	**Sulfur**	C, M		S	CM	CM

Gly	flex
Pro	5
Allevi	Ali
Trphty	6
Gluasp	COO^-
Hargly	NH_3^+
Asnglnths	H
CM	S

SECONDARY STRUCTURE

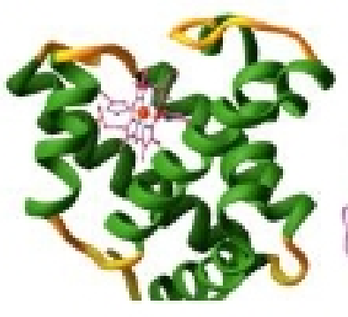
a-Helix
- counter-clockwise (right-handed)
- 3.6 residues/turn
- H-Bond: between n ... n+4, vertical, parallel to helical axis, all except @ terminal
- side chains point toward N-terminus
- Gly/Pro not used

B-Sheet
- extended, *trans* peptide chains
- planar, pleated
- amphipathic (alternatic hydrophilic/hydrophobic)
- H-Bond: between strands, horizontal, perpendicular (antiparallel) to chain direction
- (right-handed)

TERTIARY STRUCTURE

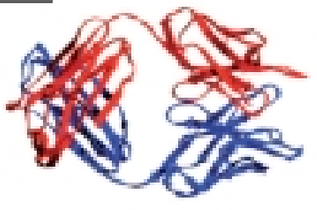
- interior = nonpolar
- exterior = polar
- (a/B/both)

Hb

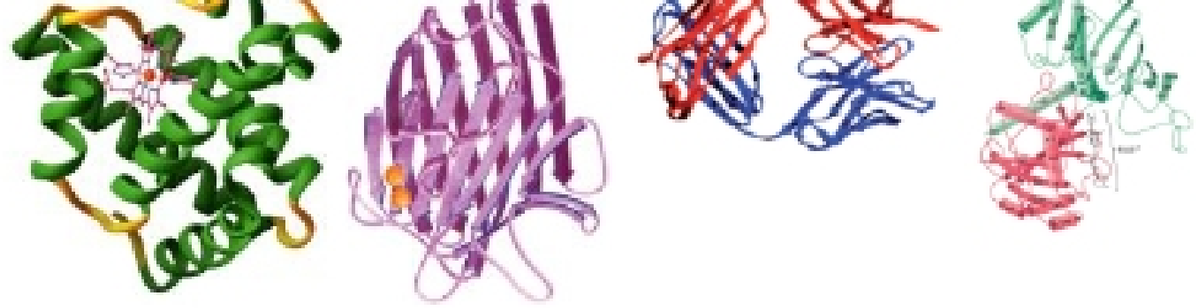


Concanavillin

Fab



G3PD



- loops: flexible/rigid (not random)

HYDROPATHIC INDEX - AA polarity

**Most proteins > 200 AAs*

SUMMARY

- A protein is a linear polymer of a -amino acids that assumes a specific three-dimensional conformation that confers unique functionality.
- All a-amino acids have an **amine**, a **carboxylate** and a side chain **R-group** attached to a central carbon, denoted **Ca**. Amino acids covalently linked through **peptide bonds**.
- Proteins are mainly composed from a group of 20 amino acids divided into 8 **functional groups**. Some amino acids can be pre- and post-translationally modified to meet the structural or functional needs of specific proteins.
- The structure of a polypeptide can be characterized at four levels:
  - **Primary structure** = amino acid sequence
  - **Secondary structure** = local organization of polypeptide backbone into recognizable units stabilized by main chain H-bonding
  - **Tertiary structure** = global folding of a single polypeptide chain
  - **Quaternary structure** = assembly of multiple polypeptide chains
- The 3-D folding of the polypeptide chain is largely governed by three noncovalent bonding interactions (**ionic, hydrogen** and **van der Waals bonding**) and the **hydrophobic effect**.
- There are 2 main **secondary structural** elements in proteins:
  - **-helix** = helical conformation of backbone characterized by a hydrogen bond between the n^{th} and $(n+4)^{th}$ residue; 3.6 residues per turn; side chains point away from the helical axis
  - **-sheet** = parallel or antiparallel assembly of extended polypeptide chains that forms a pleated layer; stabilized by hydrogen bonding between strands
- **Tertiary structure** describes the 3-D conformation of the polypeptide chain, essentially how the secondary structural elements and polypepitde loops are organized in space.
- Generally, for aqueous proteins, nonpolar side chains buried in the interior while polar groups are exposed the protein surface.
- Large proteins are often composed of structurally independent **domains.**

OTHER SUMMARY

- The folding of an amino acid polymer into secondary (local), tertiary (global), and quaternary (assembled) structures involves bonding and nonbonding interactions.
- The main noncovalent bonding interactions include ionic, hydrogen and van der Waals bonding.
- The hydrophobic effect plays an important role by encouraging the burial of hydrophobic side chains in the interior of proteins.
- Disulfide bond formation between the side chains of two Cys residues is important for stabilizing tertiary and quaternary structures.