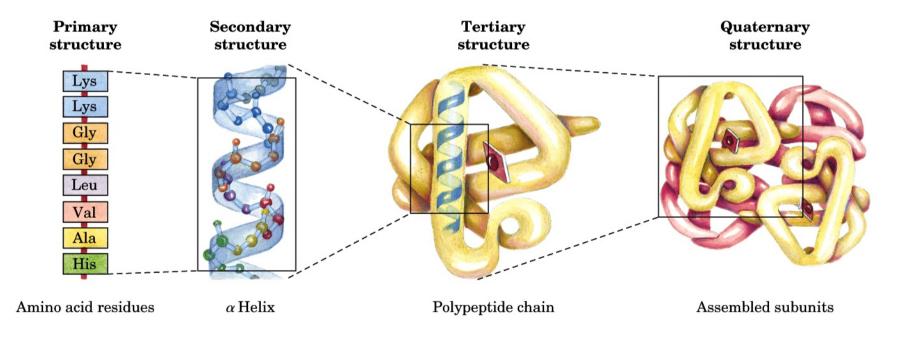
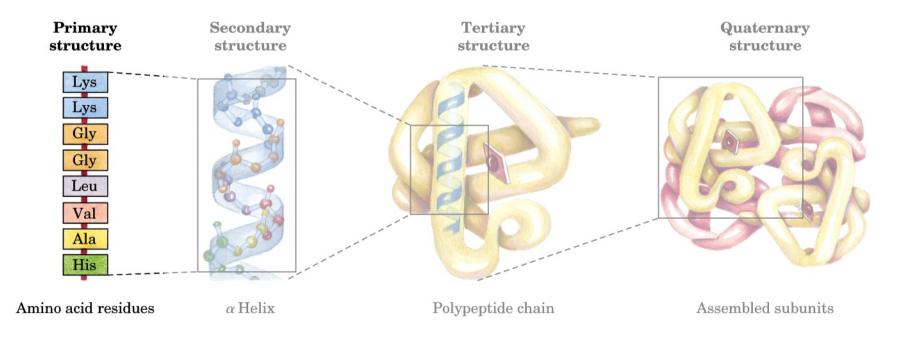
Protein Chemistry & Structure

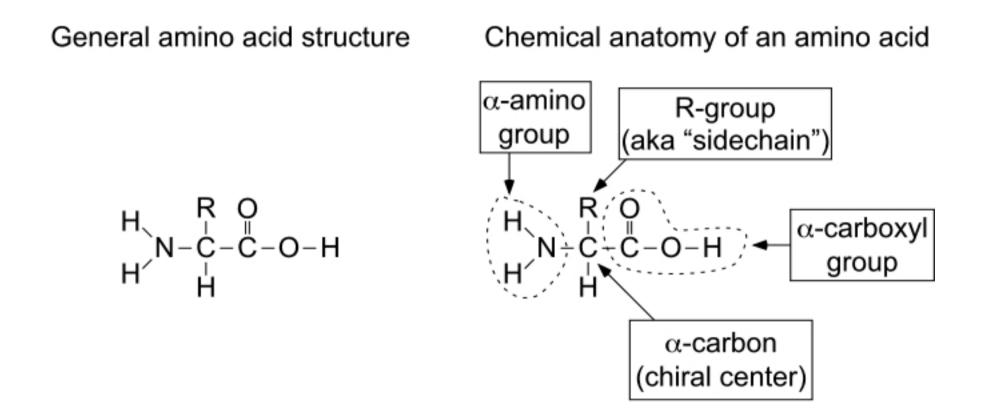
Levels of Protein Structure



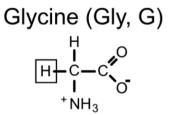
Primary structure = order of amino acids in the protein chain

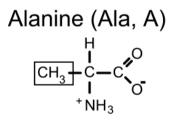


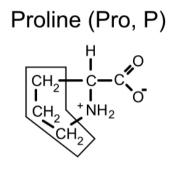
Anatomy of an amino acid



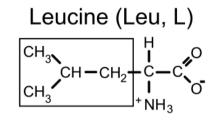
Non-polar amino acids

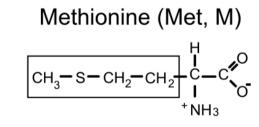


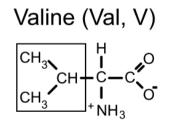


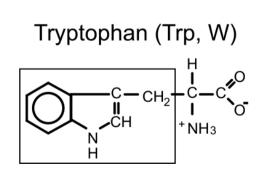


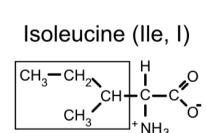
Phenylalanine (Phe, F)



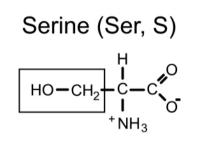


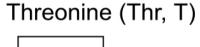


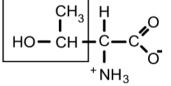




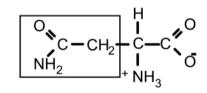
Polar, non-charged amino acids

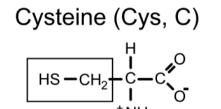


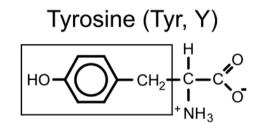


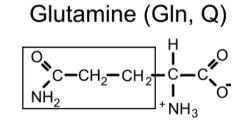


Asparagine (Asn, N)



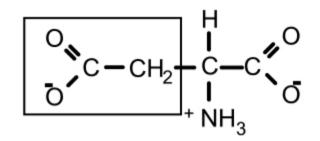




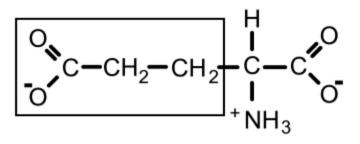


Negatively-charged amino acids

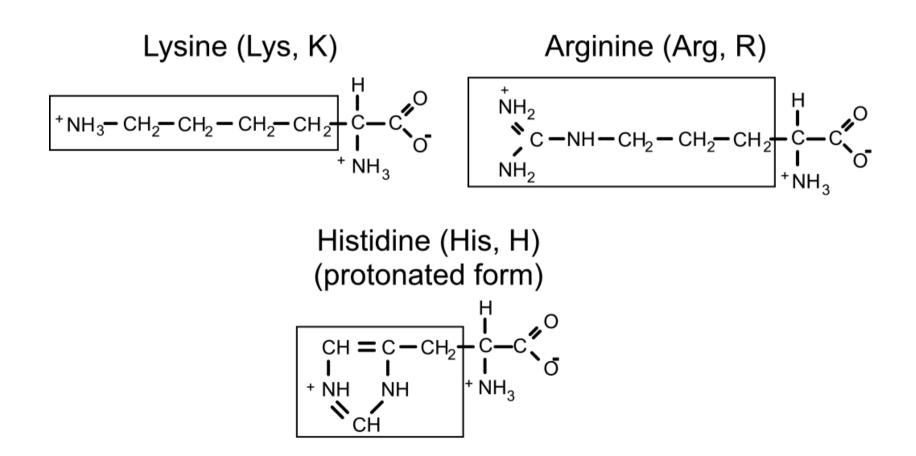
Aspartate (Asp, D)



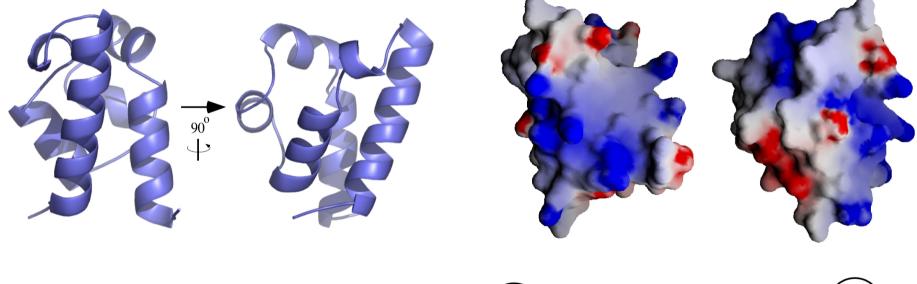
Glutamate (Glu, E)

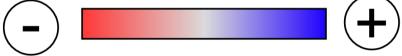


Positively-charged amino acids

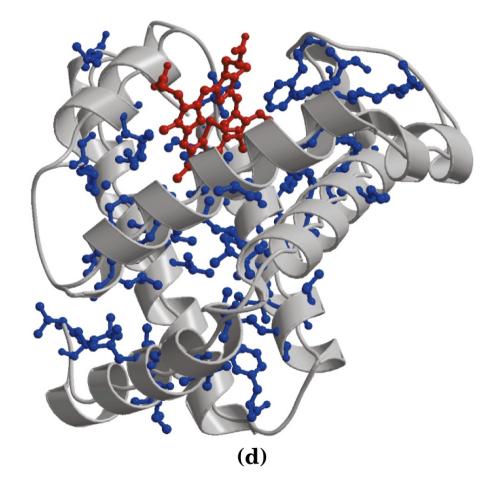


Charged and polar R-groups tend to map to protein surfaces





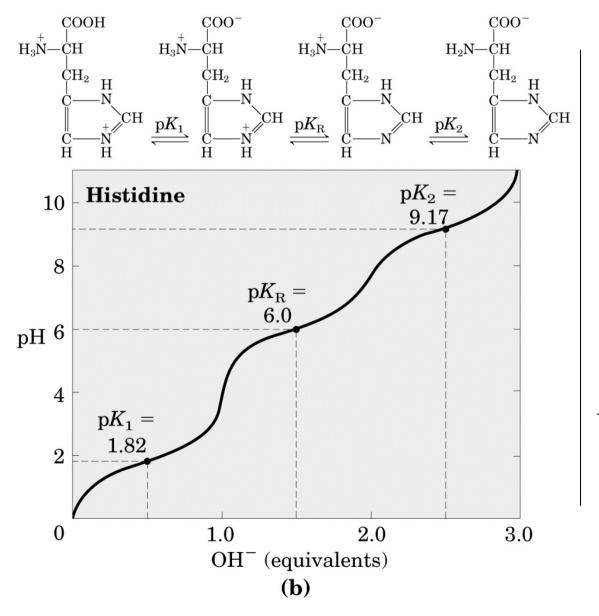
Non-polar R-groups tend to be buried in the cores of proteins



<u>Myoglobin</u> Blue = non-polar R-group

Red = Heme

Some R-groups can be ionized



The Henderson-Hasselbalch equation allows calculation of the ratio of a weak acid and its conjugate base at any pH

 $\frac{\text{Henderson-Hasselbalch}}{\text{pH} = \text{pK'} - \log \frac{[\text{HB}]}{[\text{B}^-]}}$

General protein pK' values

	Approximate pK'
Group	In a "Typical" Protein
α -carboxyl (free)	3 (C-terminal only)
β-carboxyl (Asp)	4
γ-carboxyl (Glu)	4
imidazole (His)	6
sulfhydryl (Cys)	8
$1^{\circ}\alpha$ -amino (free)	8 (N-terminal only)
ε-amino (Lys)	10
hydroxyl (Tyr)	10
2°α-amino (Pro)(fi	ree) 9 (N-terminal only)
guanido (Arg)	12

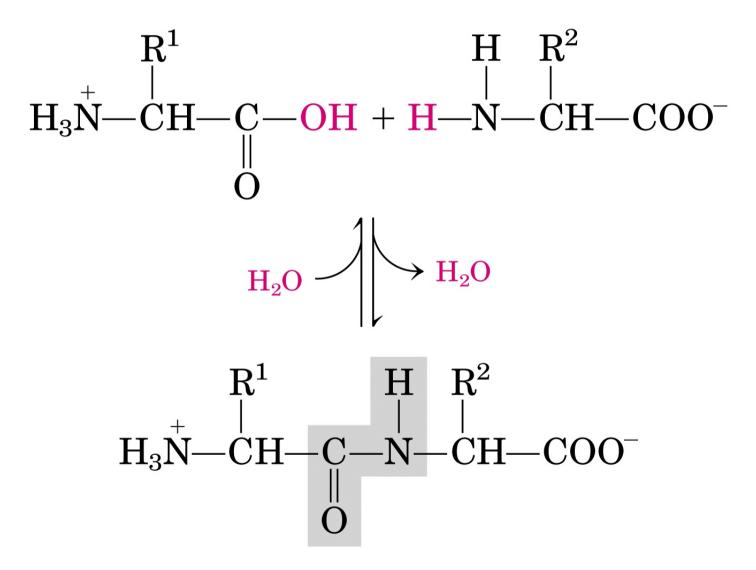
Some R-groups can modified

Modification Phosphorylation R	<u>Chemistry</u> -OH + HPO4 ²⁻ → R-O-PO3 ²⁻ + H20	Common sites of attachment ► Residues with hydroxyl ^O groups (Ser, Thr, Tyr)
N-Glycosylation	R-NH-sugar	Asn
O-Glycosylation	R-O-sugar	Ser, Thr, and modified residues
Hydroxylation Carboxylation	hydroxyl group (OH) added to R g carboxyl group	Glu
	(COOH) added to	r group

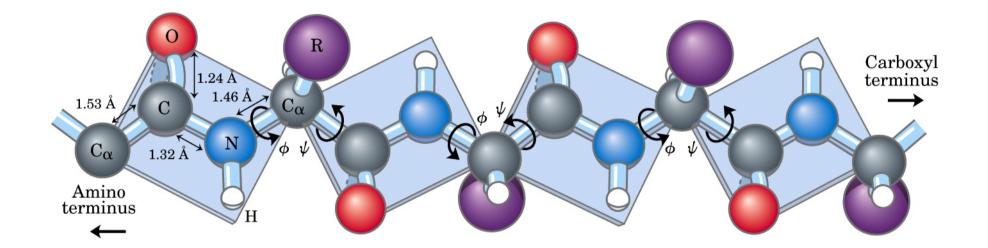
Amino Acids Are Joined By Peptide Bonds In Peptides

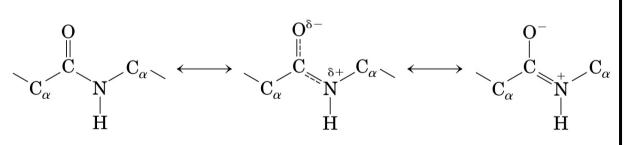
- α-carboxyl of one amino acid is joined to α-amino of a second amino acid (with removal of water)
- only α -carboxyl and α -amino groups are used, not R-group carboxyl or amino groups

Chemistry of peptide bond formation



The peptide bond is planar



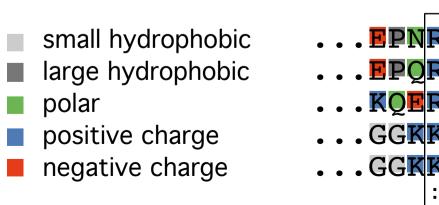


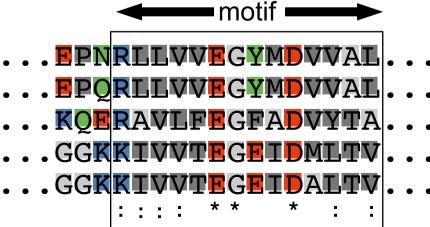
This resonance restricts the number of conformations in proteins -- main chain rotations are restricted to ϕ and ψ .

Primary sequence reveals important clues about a protein

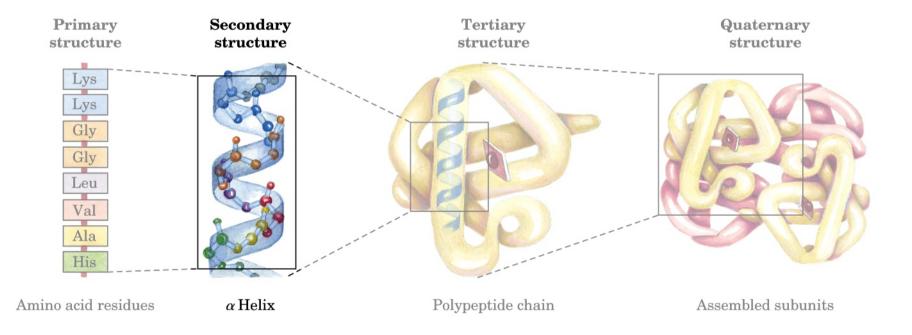
• Evolution conserves amino acids that are important to protein structure and function across species. Sequence comparison of multiple "homologs" of a particular protein reveals highly conserved regions that are important for function.

• Clusters of conserved residues are called "motifs" -- motifs carry out a particular function or form a particular structure that is important for the conserved protein.

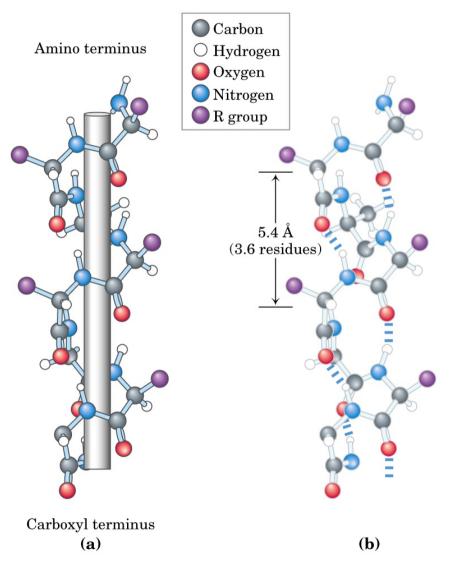




Secondary structure = <u>local</u> folding of residues into regular patterns



The α -helix

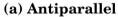


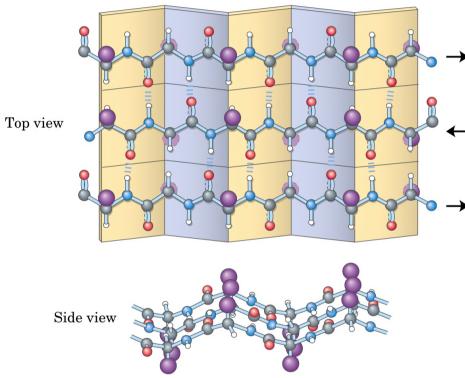
• In the α -helix, the carbonyl oxygen of residue "i" forms a hydrogen bond with the amide of residue "i+4".

 Although each hydrogen bond is relatively weak in isolation, the sum of the hydrogen bonds in a helix makes it quite stable.

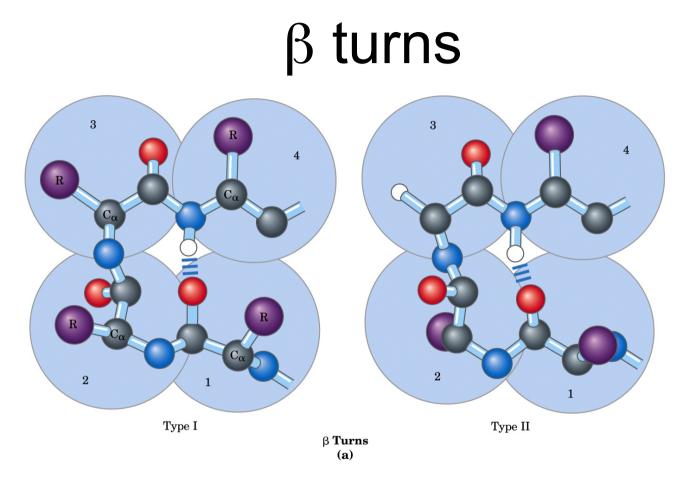
• The propensity of a peptide for forming an α -helix also depends on its sequence.

The β -sheet



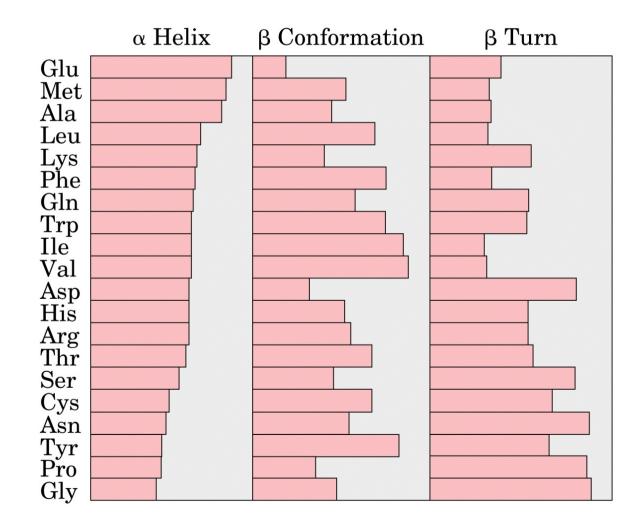


- In a β-sheet, carbonyl oxygens and amides form hydrogen bonds.
- These secondary
 structures can be either
 antiparallel (as shown) or
 parallel and need not be
 planar (as shown) but can be
 twisted.
 - The propensity of a peptide for forming β -sheet also depends on its sequence.

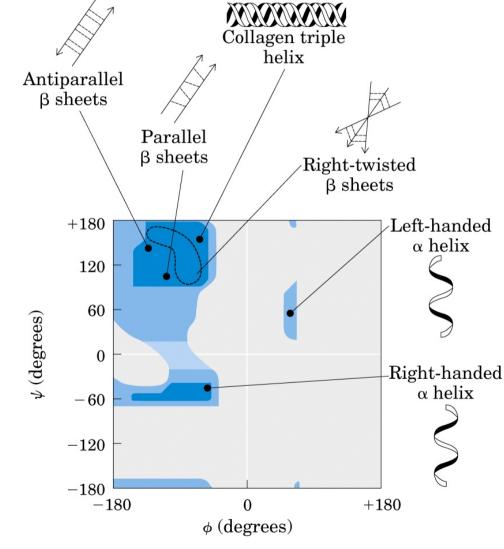


- β -turns allow the protein backbone to make abrupt turns.
- Again, the propensity of a peptide for forming β -turns depends on its sequence.

Which residues are common for α -helix, β -sheet, and β -turn elements?

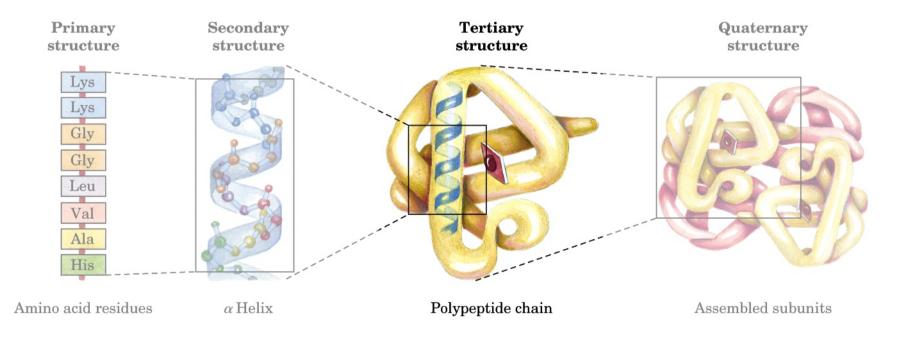


Ramachandran plot -- shows ϕ and ψ angles for secondary structures

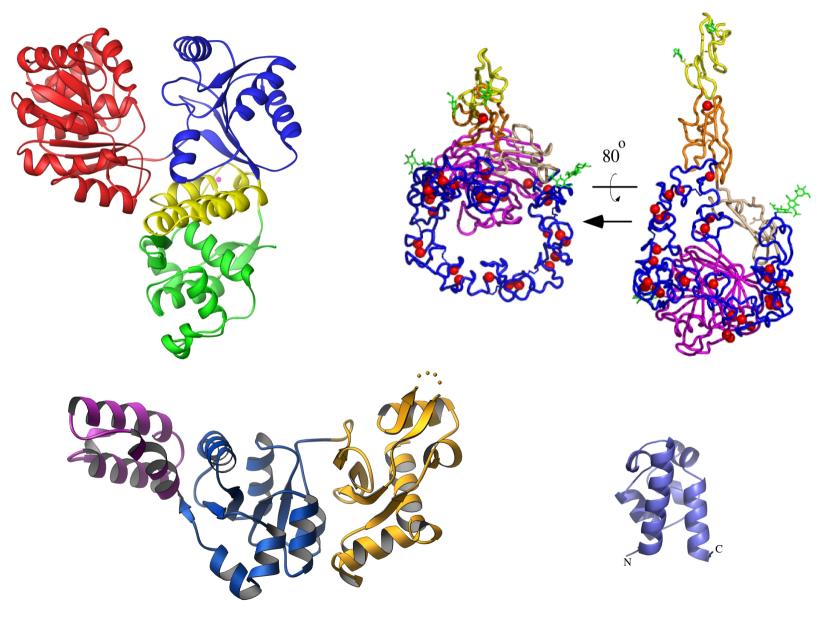


(a)

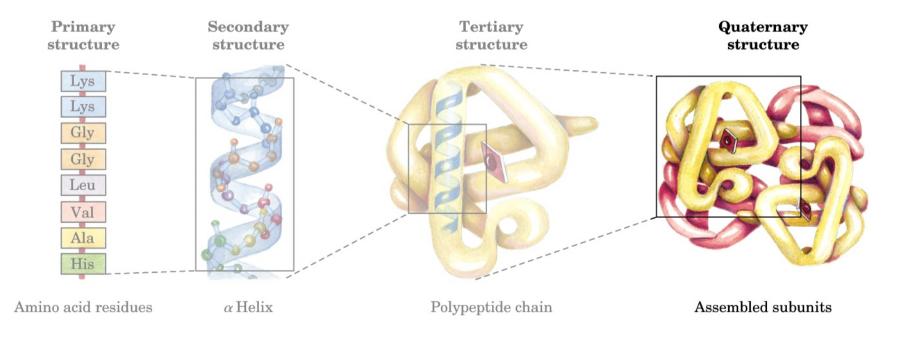
Tertiary structure = <u>global</u> folding of a protein chain



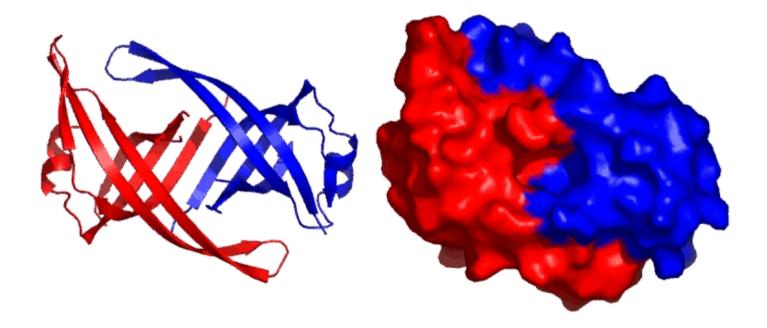
Tertiary structures are quite varied



Quaternary structure = Higher-order assembly of proteins

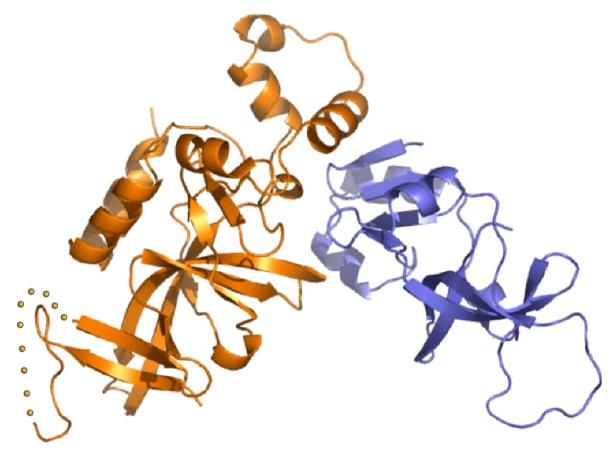


Example of tertiary and quaternary structure - PriB homodimer

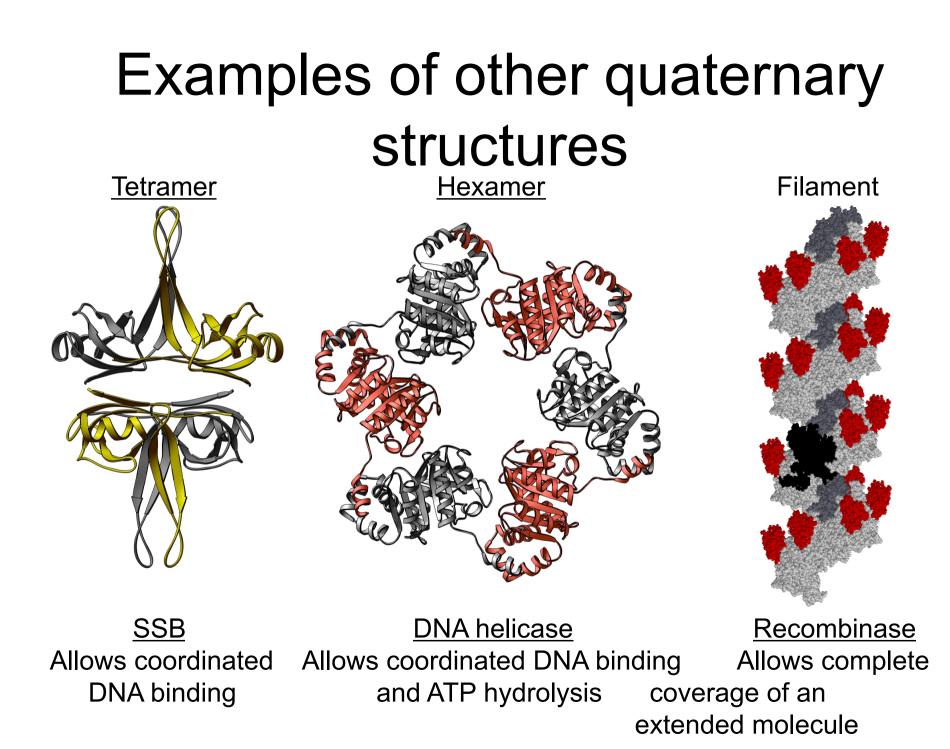


Example is PriB replication protein solved at UW: Lopper, Holton, and Keck (2004) *Structure* **12**, 1967-75.

Example of tertiary and quaternary structure - Sir1/Orc1 heterodimer



Example is Sir1/Orc1 complex solved at UW: Hou, Bernstein, Fox, and Keck (2005) *Proc. Natl. Acad. Sci.* **102**, 8489-94.



Classes of proteins

Functional definition:

Enzymes:	Accelerate biochemical reactions
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- Structural: Form biological structures
- Transport: Carry biochemically important substances
- Defense: Protect the body from foreign invaders

Structural definition:

Globular: Complex folds, irregularly shaped tertiary structures

Fibrous: Extended, simple folds -- generally structural proteins

Cellular localization definition:

Membrane: In direct physical contact with a membrane; generally water insoluble.

Soluble: Water soluble; can be anywhere in the cell.