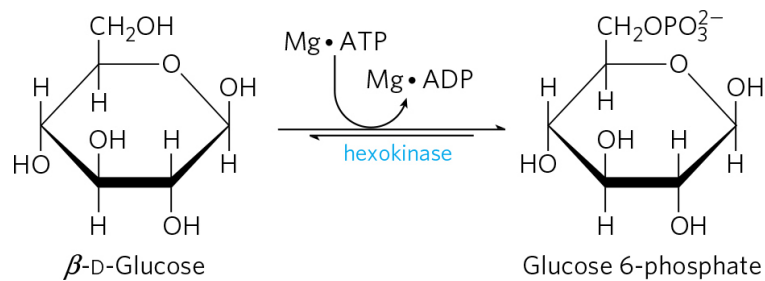


Example 2: Hexokinase



Hexokinase is an enzyme that phosphorylates a six-carbon sugar, a hexose, to a hexose phosphate.

Hexokinase catalyzes the first reaction of glycolysis: the gamma-phosphoryl group of an ATP molecule is transferred to the oxygen at the C-6 of glucose.

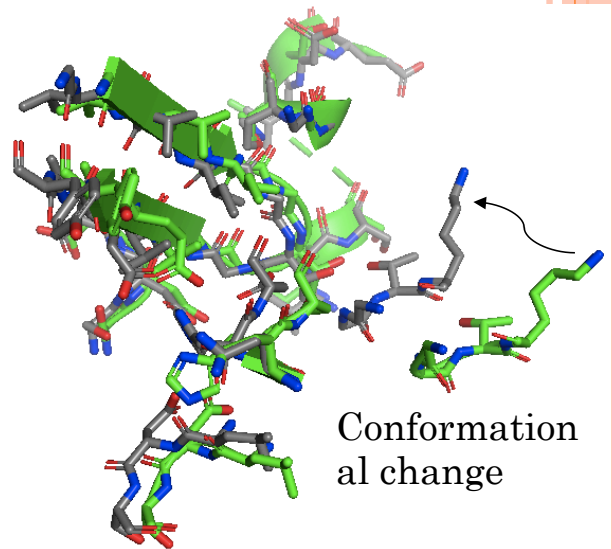
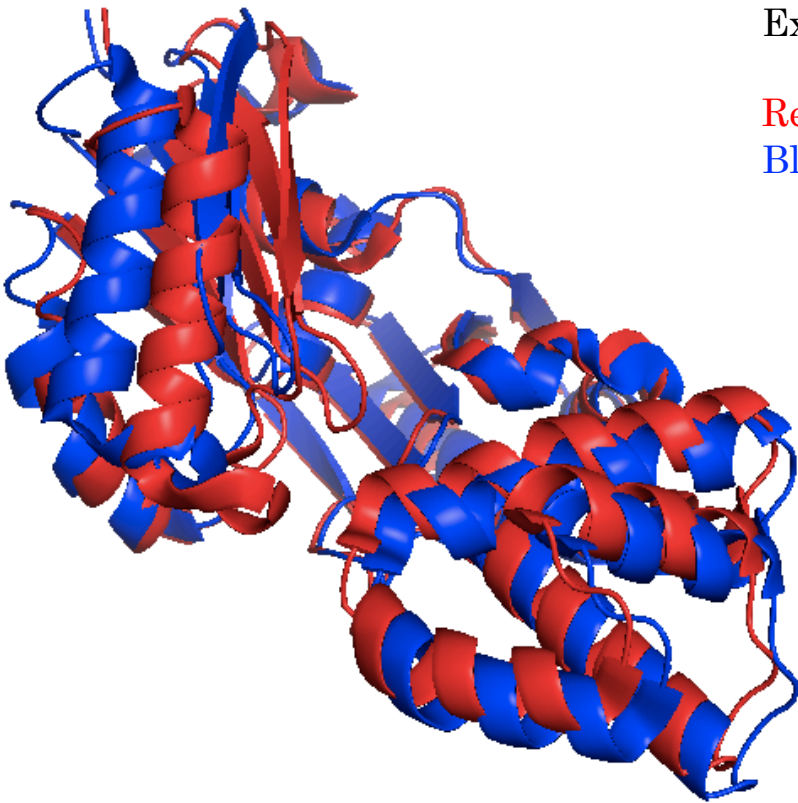


Hexokinase

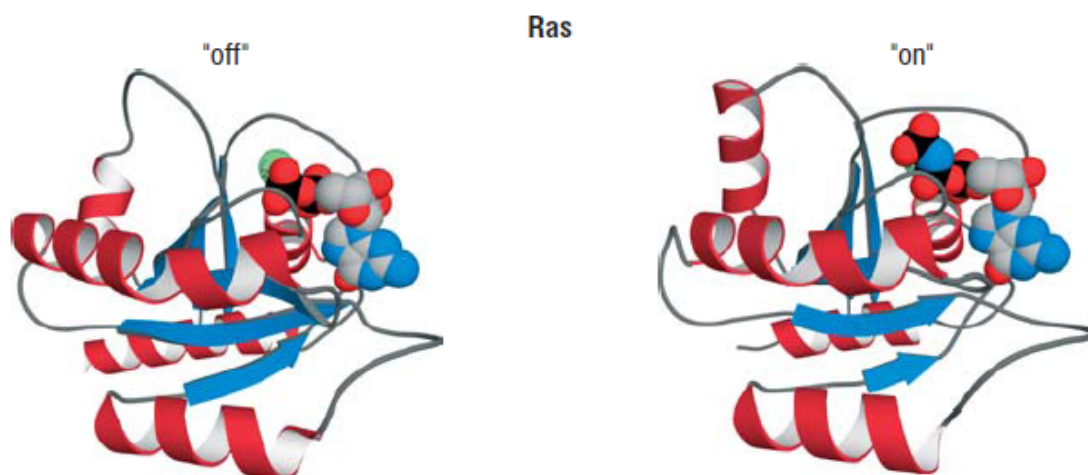
Example for Induced fit

Red: enzyme-substrate

Blue: enzyme without substrate



SWITCHING



The GDP-bound ("off"; PDB 1pll) state of Ras differs significantly from the GTP-bound ("on"; PDB 121p) state. This difference causes the two states to be recognized by different proteins in signal transduction pathways.



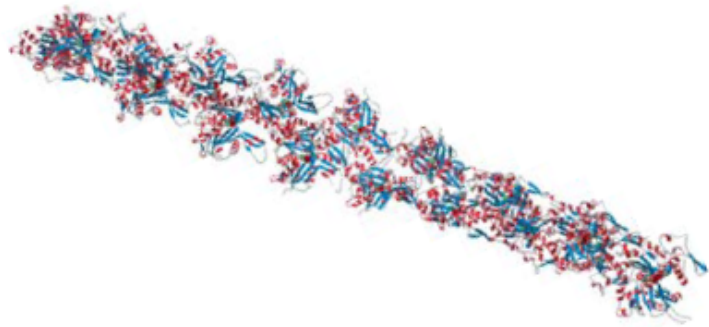
STRUCTURAL PROTEINS

Silk



Silk derives its strength and flexibility from its structure: it is a giant stack of antiparallel beta sheets. Its strength comes from the covalent and hydrogen bonds within each sheet; the flexibility from the van der Waals interactions that hold the sheets together. (PDB 1slk)

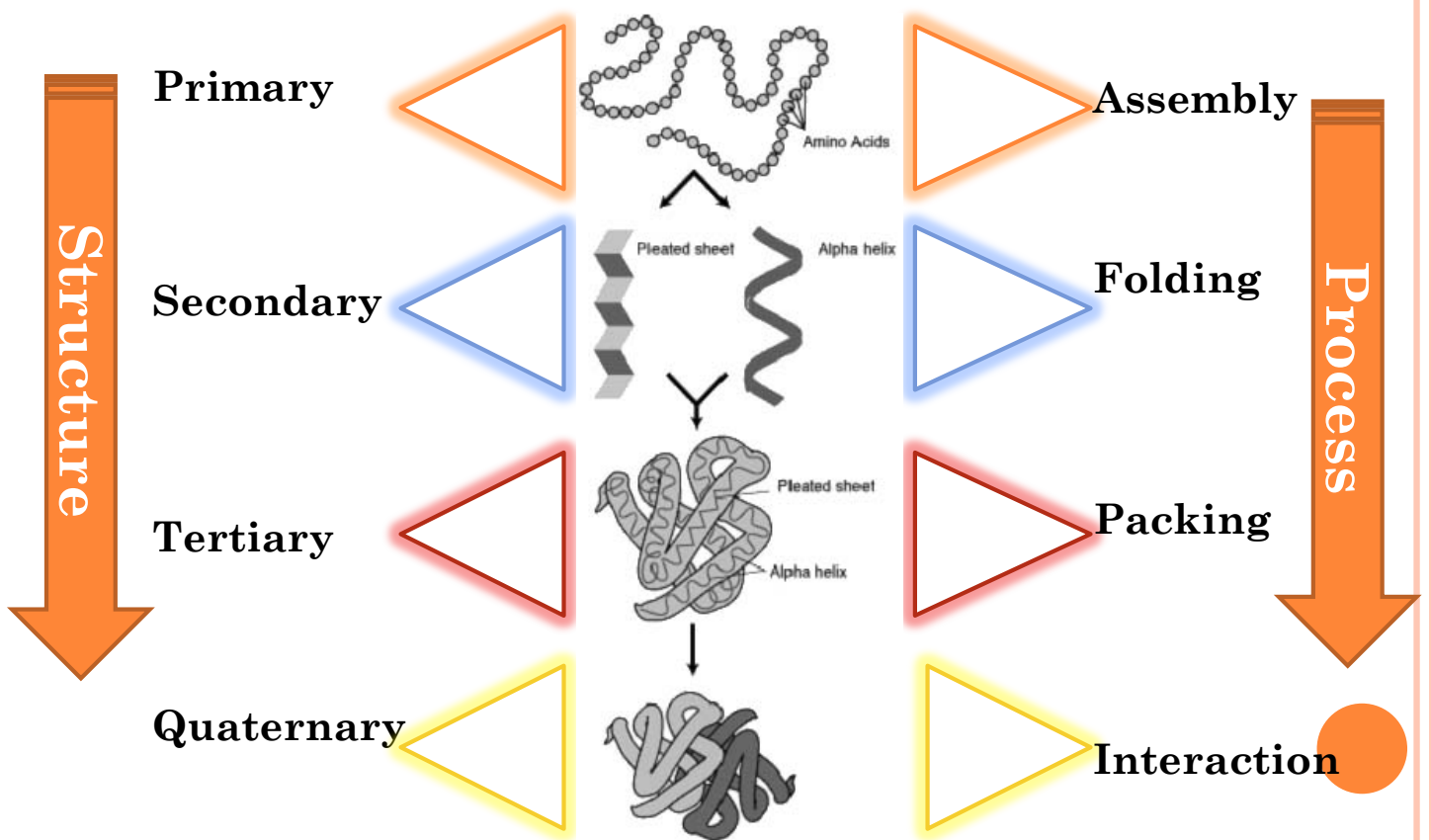
F-actin



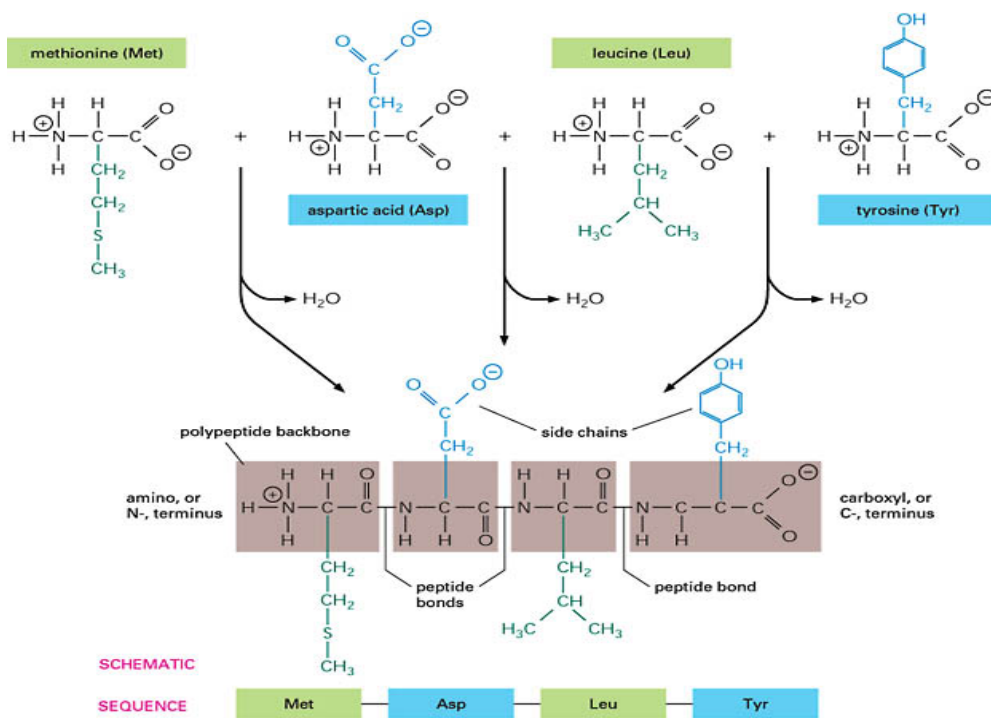
Actin fibers are important for muscle contraction and for the cytoskeleton. They are helical assemblies of actin and actin-associated proteins. (Courtesy of Ken Holmes)



PROTEIN STRUCTURES



PROTEIN ASSEMBLY



- occurs at the ribosome
- involves dehydration synthesis and polymerization of amino acids attached to tRNA
- yields primary structure

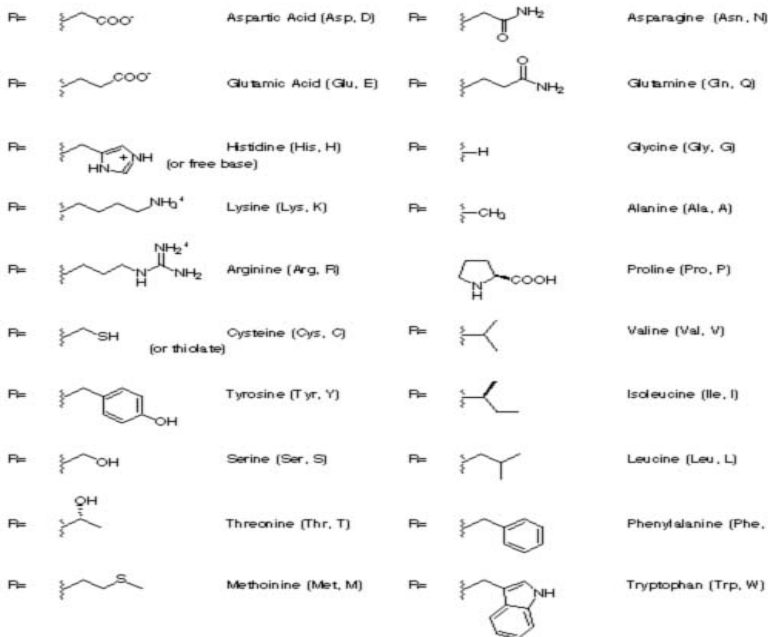
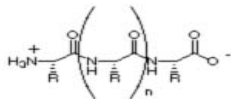


PRIMARY STRUCTURE

primary structure of human insulin

CHAIN 1: GIVEQ CCTSI CSLYQ LENYC N

CHAIN 2: FVNQH LCGSH LVEAL YLVCG ERGFF YTPKT

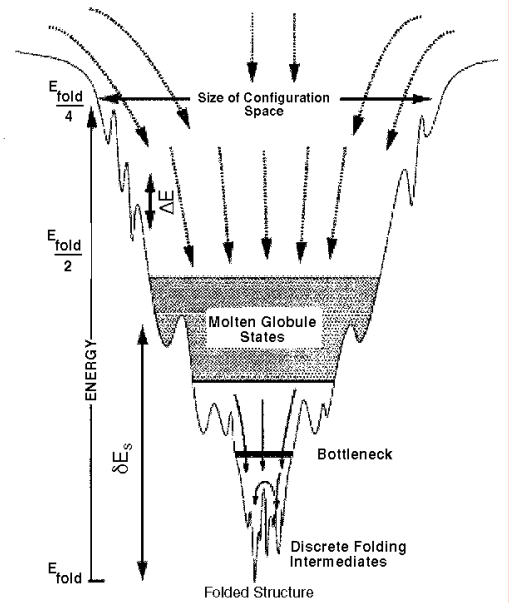
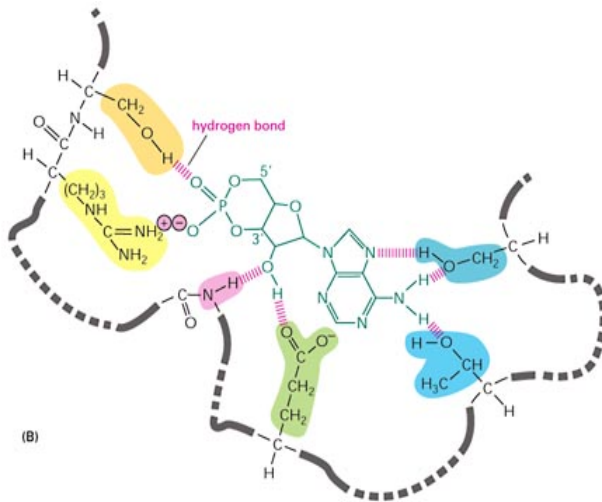
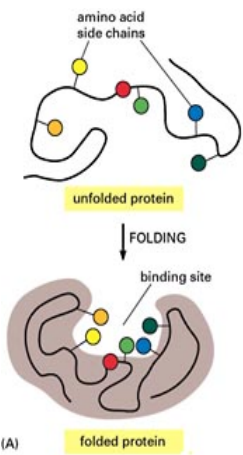


- linear
- ordered
- 1 dimensional
- sequence of amino acid polymer
- by convention, written from amino end to carboxyl end
- a perfectly linear amino acid polymer is neither functional nor energetically favorable → folding!

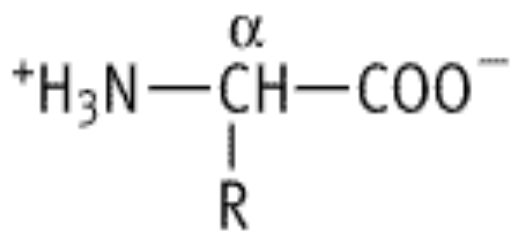


PROTEIN FOLDING

- occurs in the cytosol
- involves localized spatial interaction among primary structure elements, i.e. the amino acids
- may or may not involve chaperone proteins
- tumbles towards conformations that reduce ΔE (this process is thermo-dynamically favorable)
- yields secondary structure



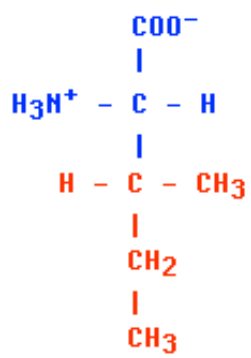
AMINO ACIDS



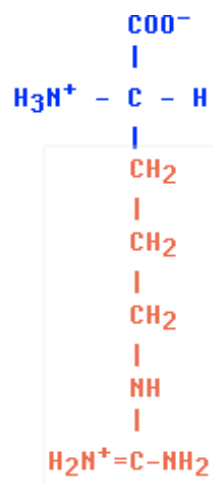
- 20 amino acids make up protein
- 8 essential amino acids
 - 9 in infant (histidine)
- Dipolar
 - +ve end (NH_3^+)
 - -ve end (COO^-)



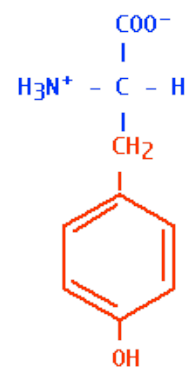
Isoleucine



Arginine

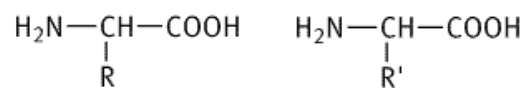


Tyrosine

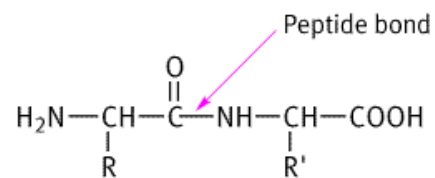


PEPTIDE BOND

- Peptide bond joins amino acids
- Bond at both ends
 - Increases range of possible proteins
 - 2 peptides can result from bonding of 2 amino acids
 - 1.0×10^{26} peptides can be formed from 20 amino acids



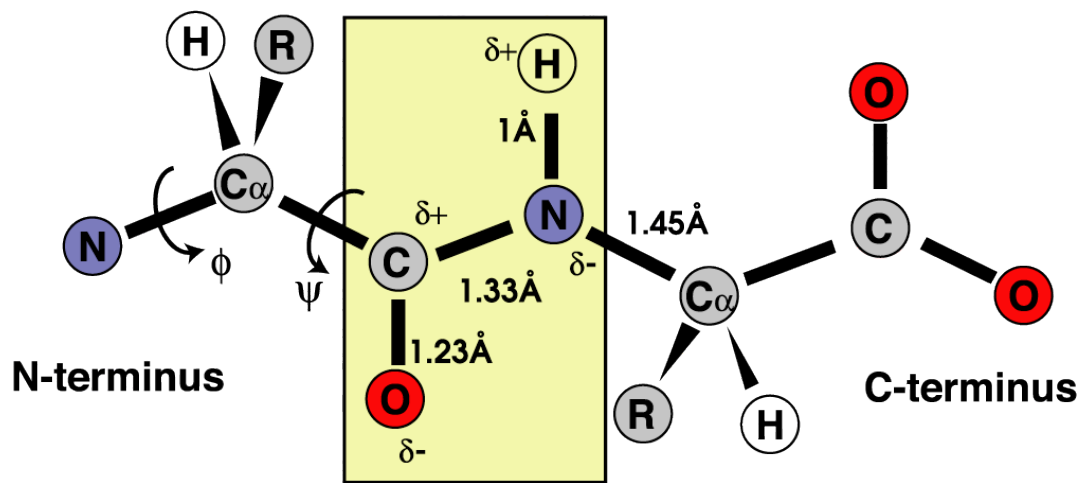
Two amino acids



A dipeptide



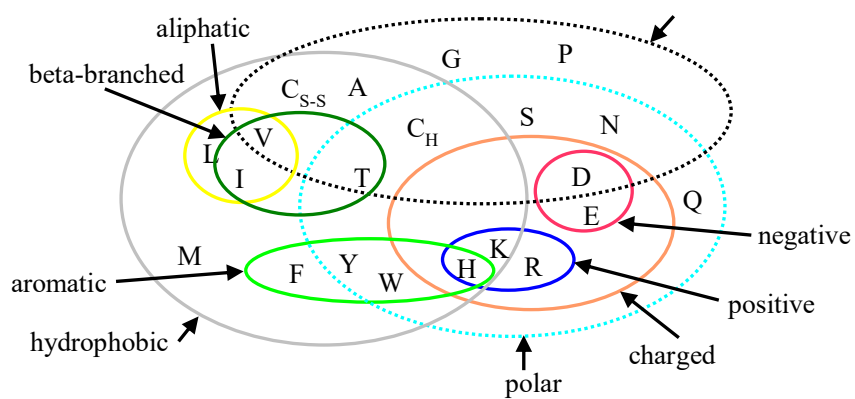
PEPTIDE BOND



- The peptide bond influences all aspects of protein structure and function.
- Key features:
 - 1. Planar
 - 2. Fairly rigid, due to partial double bond character.
 - 3. Almost always in trans configuration.
 - 4. Polar. Can form at least two hydrogen bonds.
 - 5. Places restrictions on the conformation of the polypeptide chain.



AMINO ACID CLASSIFICATION



Bioinformatics Methods II, Spring 2003

A Venn diagram showing the relationship of the 20 naturally occurring amino acids to a selection of physio-chemical properties thought to be important in the determination of protein structure.



PRIMARY PROTEIN STRUCTURE

- Linear sequence of amino acids forms primary structure
- Sequence essential for proper physiological function

Primary structure of insulin

