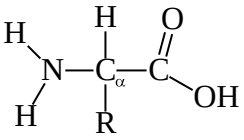
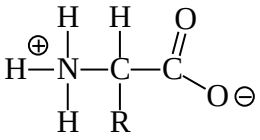
PROTEIN STRUCTURE

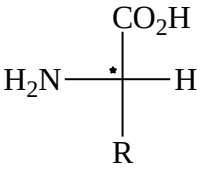
Hydrolysis of proteins with aqueous acid or base yields a mixture of free amino acids. Each type of protein yields a characteristic mixture of the ~ 20 amino acids.

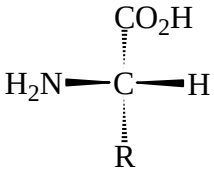
AMINO ACIDS



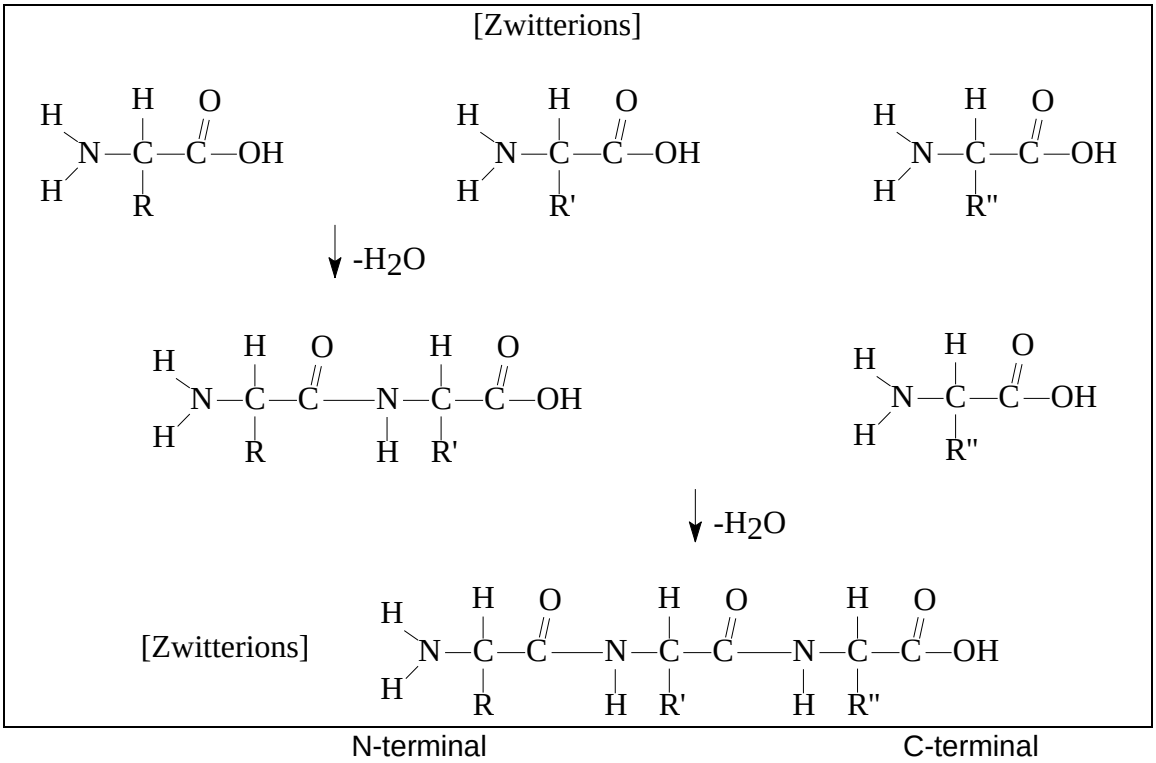


Zwitterion (dipolar ion)





PEPTIDES *Formal reactions showing formation of peptide bond by dehydration:*



"**FROM SEQUENCE TO CONSEQUENCE**"
(D. Ringe, Brandeis Univ.)

Proteins differ from each other in the number and sequence of amino acids in the polypeptide chain. A specific sequence of covalently bonded amino acid residues folds into a unique three-dimensional structure, and it is this structure that determines the function of the protein.

Primary structure is the sequence of amino acids in the protein and includes all the covalent bonds between them, including disulfide bonds.

Secondary structure is defined by the regular, recurring arrangements of adjacent amino acid residues in the polypeptide backbone. The most prominent are the *α-helix* and the *β-pleated sheet*. Less prominent are *coils/loops*, and *turns*. The helix and sheet maintain their conformation through hydrogen-bonding of the C=O and H-N groups of the polypeptide backbone.

Tertiary structure refers to the three-dimensional spatial relationship among all amino acid residues in a polypeptide. The shape arises from the folding of the polypeptide chain. The most important forces stabilizing the three dimensional structure of proteins are non-covalent interactions.

Quaternary structure consists of an aggregate of two or more polypeptides.

FORCES STABILIZING PROTEIN STRUCTURES – non-covalent interactions

*Electrostatic force*s result from favorable charge-charge (ionic) interactions between oppositely charged amino acid side groups. Most side groups containing charged atoms as well as polar side groups are located on the protein surface at the protein-water interface.

Hydrogen-bonding occurs with side groups containing OH and NH groups. Most of the potential H-bond forming side groups of the protein are near the protein-water interface where they can interact directly with water.

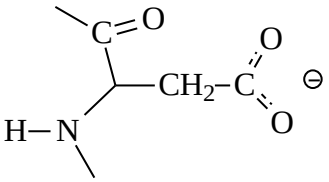
van der Waals forces (induced-dipole/induced-dipole) favor close packing in folded protein structures. Repulsive van der Waals interactions are steric interactions.

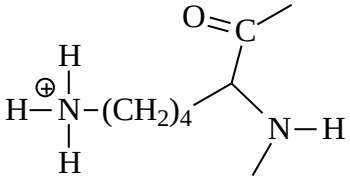
Hydrophobic forces are mainly an entropic factor involving the water solvent. Water molecules are highly ordered by hydrogen-bonding and there is an increase in this order when water is required to solvate non-polar molecules -- a decrease in entropy. Therefore, non-polar molecules cluster together, excluded by the water molecules. Entropic effects strongly favor non- and weakly polar side groups in internal locations where they are free from contacts with water.

EXAMPLES:

Electrostatic forces

asp

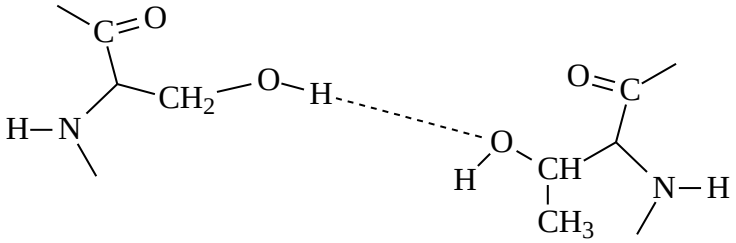




lys

Hydrogen-bonding

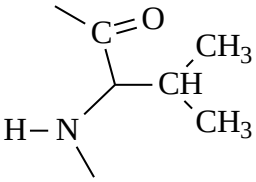
ser

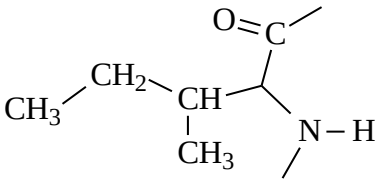


thr

van der Waals forces

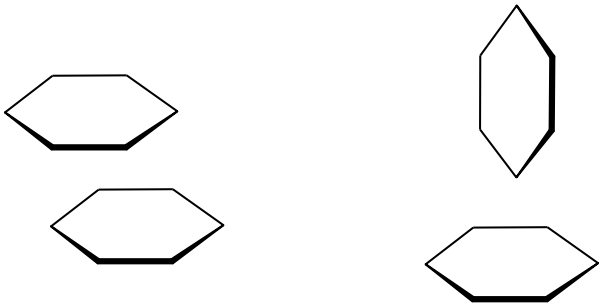
val



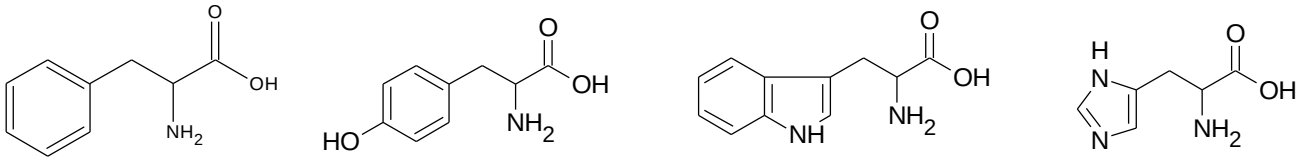


ile

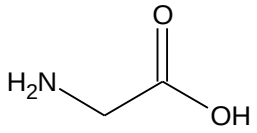
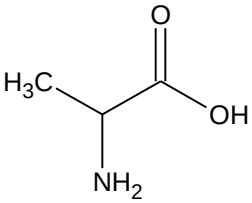
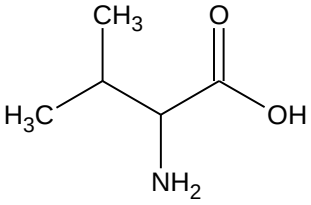
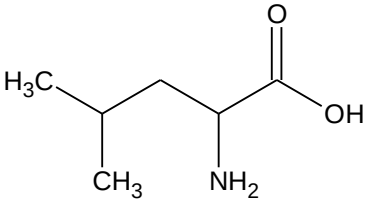
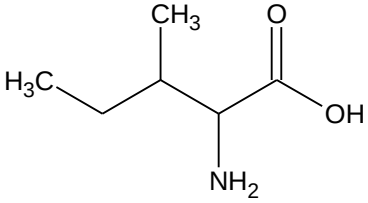
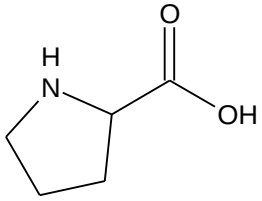
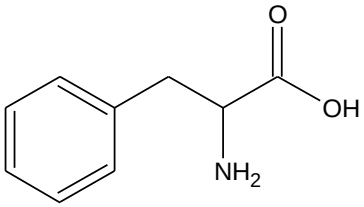
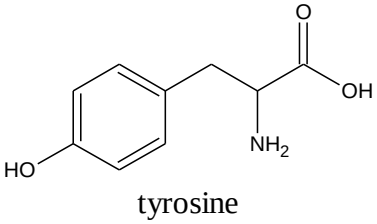
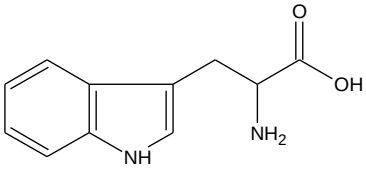
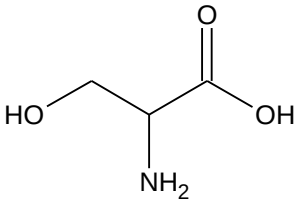
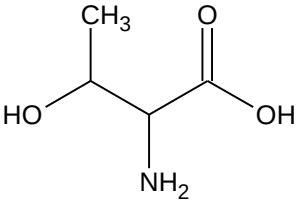
Attractive interactions between aromatic rings are seen in many areas of chemistry, notably in the base-pair stacking of DNA. Although known as **pi-stacking interactions**, there are two, nearly equal energy orientations for the aromatic rings, *off-center stacked* and *T-shaped*, illustrated here for the benzene dimer.

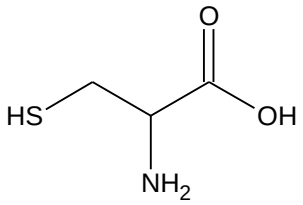
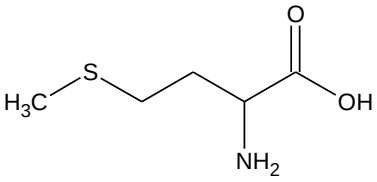
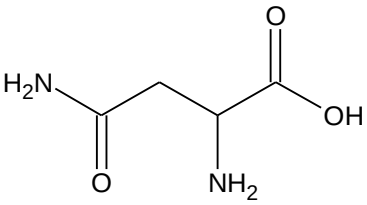
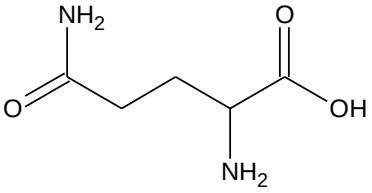
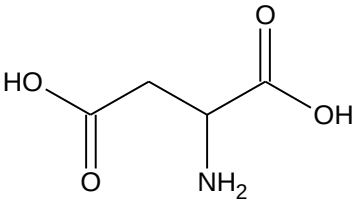
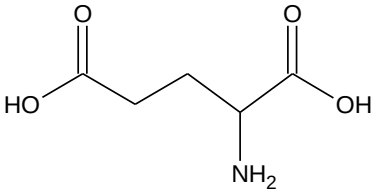
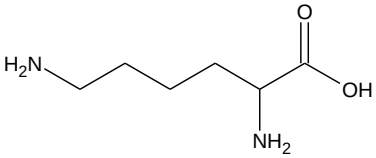
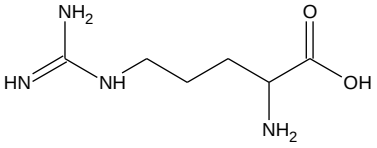
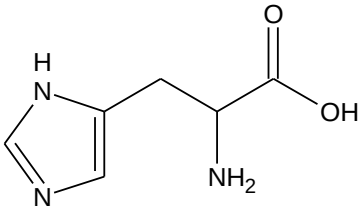


The aromatic amino acids are phenylalanine, tyrosine, tryptophan and histidine.



Classification of Amino Acids by Side Chain

Aliphatic		
 glycine	 alanine	 valine
 leucine	 isoleucine	 proline
Aromatic		
 phenylalanine	 tyrosine	 tryptophan
Alcohols		
 serine	 threonine	

Sulfur-containing		
 cysteine	 methionine	
Amides		
 asparagine	 glutamine	
Carboxylic acids/carboxylate		
 aspartic acid	 glutamic acid	
Bases/aminium ion		
 lysine	 arginine	 histidine