CYI101 Common CHEMISTRY(Organic)

Macromolecules: Introduction to peptides and proteins

Amino Acids: Structure & Diversity

20

R = sidechain

α- Amino Acid

Peptides, and Proteins

monomer unit: α -amino acids

Nonpolar

(S)-(-)-Leucine *(Leu, L)*

(S)-(+)-Alanine (Ala, A)

(2S,3S)-(+)-Isoleucine (*IIe, I*)

(S)-(–)-Methionine (Met, M)

(S)-(-)-Proline (*Pro, P*)

(S)-(–)-Phenylalanine (Phe, F)

(S)-(–)-Tryptophan (Trp, W)

(S)-(-)-Tyrosine *(Tyr, Y)* pKa ~ 10.1

$$H_2N$$
 $COO^ O$ $+ NH_3$

(S)-(-)-Asparagine (Asn, N)

Acidic:

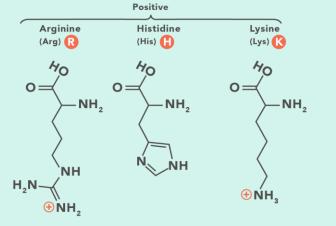
(S)-(+)-Aspartic Acid (Asp, D)
pKa ~ 3.6

Basic:

(S)-(+)-Lysine (Lys, K) pKa ~ 10.5

Amino Acids: Structure & Diversit

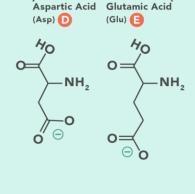
A. Amino Acids with Electrically Charged Side Chains



Asparagine

Glutamine

Leucine



Negative

B. Amino Acids with Polar Uncharged Side Chains

Threonine

Serine

Alanine

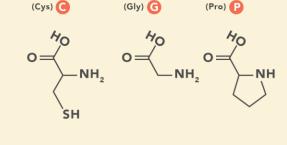
(Ser) (Ser) (Asn) (Gin) (Gin)	
$O = \begin{pmatrix} A_{0} & A_{0} & A_{0} & A_{0} \\ NH_{2} & O = \begin{pmatrix} A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix} = \begin{pmatrix} A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$ $O = \begin{pmatrix} A_{0} & A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$ $O = \begin{pmatrix} A_{0} & A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$ $O = \begin{pmatrix} A_{0} & A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$ $O = \begin{pmatrix} A_{0} & A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$ $O = \begin{pmatrix} A_{0} & A_{0} & A_{0} \\ NH_{2} & O \end{pmatrix}$	·NH

Isoleucine

C. Special Cases

Cysteine

Phenylalanine



Tyrosine

Glycine

Proline

Tryptophan

D. Amino Acids with Hydrophobic Side Chains

Valine

Methionine

Peptide & Protein: Sequences

Proteins and peptides are Biopolymers made up of amino acid units (residues) that are linked together through the formation of amide bonds (peptide bonds) from the aminogroup of one residue and the carboxylate of a second residue

Proteins are large, complex molecules that serve diverse functional and structural roles within cells.

Amino Acids: Zwitterionic Behaviour

Acid-Base Behavior of Amino Acids: Amino acids exist as a zwitterion: a dipolar ion having both a formal positive and formal negative charge (overall charge neutral).

Amino acids are amphoteric: they can react as either an acid or a base. Ammonium ion acts as an acid, the carboxylate as a base.

Isoelectric point (pl): The pH at which the amino acid exists largely in a neutral, zwitterionic form (I nfluenced by the nature of the side chain)

Calculating the Isoelectric Point of Alanine:

Amino Acids: Synthesis

Strecker Synthesis: The Strecker amino acid synthesis, is a method for the synthesis of amino acids by the reaction of an aldehyde with ammonium chloride in the presence of Sodium cyanide.

$$\begin{array}{c|c} O \\ R-C-H \end{array} \longrightarrow \begin{bmatrix} \begin{array}{c} (+) \\ NH_2 \\ R-C-H \end{array} \end{array} \end{array} \longrightarrow \begin{array}{c|c} NAC=N \\ R-C-C=N \end{array} \longrightarrow \begin{array}{c} NH_2 \\ R-C-C=N \end{array} \longrightarrow \begin{array}{c} NH_2 \\ R-C-CO_2H \\ NaOH, H_2O \end{array} \longrightarrow \begin{array}{c} NH_2 \\ R-C-CO_2H \\ H \end{array}$$

Mechanism

Amino Acids: Synthesis

The Strecker Synthesis of Amino Acids From Aldehydes

Notes:

- although "NH₄CN" may sometimes be written, NH₄CN itself is not a stable solid. However NH4CN is made in solution by combining NH₄Cl and KCN, with KCl as a byproduct
- MgSO₄ is sometimes used to assist in imine formation, as it absorbs H₂O and drives the equilibrium towards the imine

· (greatly preferred to using HCN gas!)



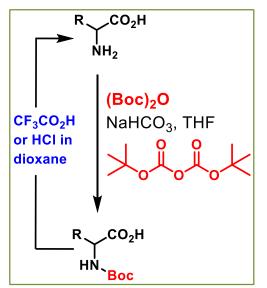
An application of the Strecker: synthesis of important non-proteinogenic amino acids

Peptide Synthesis: Amide Bond

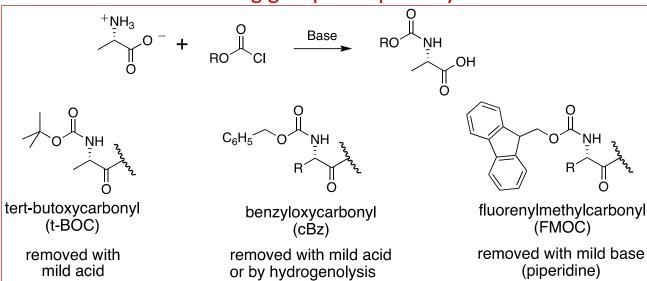
Peptide Bond Formation. Amide formation from the reaction of an amine with a carboxylic acid is slow. Amide bond formation (peptide coupling) can be accelerated if the carboxylic acid is activated. *Reagent: dicyclohexylcarbodiimide (DCC)*

Peptide Synthesis: Phe-Ala-Val

(F - A - V)
Common Protecting group in Peptide Synthesis



Phe (F)



The amide (peptide) bond has C=N double bond character due to resonance resulting in a planar geometry

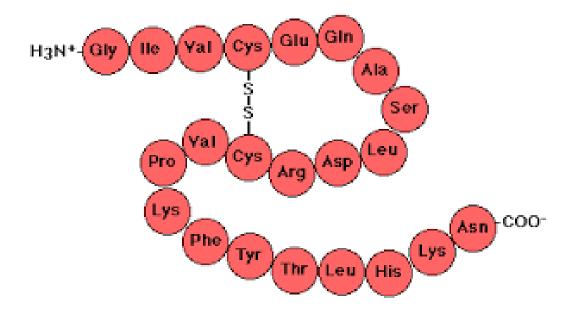
The N-H bond of one amide linkage can form a hydrogen bond with the C=0 of another.

Disulfide bonds: the thiol groups of cysteine can be oxidized to form disulfides (Cys S-S-Cys)

Protein: *Primary structure*

The primary structure is the sequence of amino acids.

Protein primary structure is the linear sequence of amino acids in a peptide or protein. By convention, the primary structure of a protein is reported starting from the amino-terminal (N) end to the carboxyl-terminal (C) end. The amino acids in the primary structure are held together by covalent bonds, which are made during the process of protein synthesis.



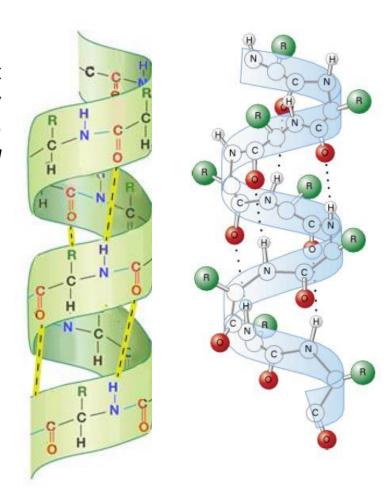
The secondary structure is primarily composed of alpha helices and betasheets.

Protein: Secondary structure

Secondary structure of proteins is formally defined by the *pattern of hydrogen bonds* between the *amino hydrogen* and *carboxyl oxygen* atoms in the peptide backbone. The most common secondary structures are *alpha helices* and *beta sheets*.

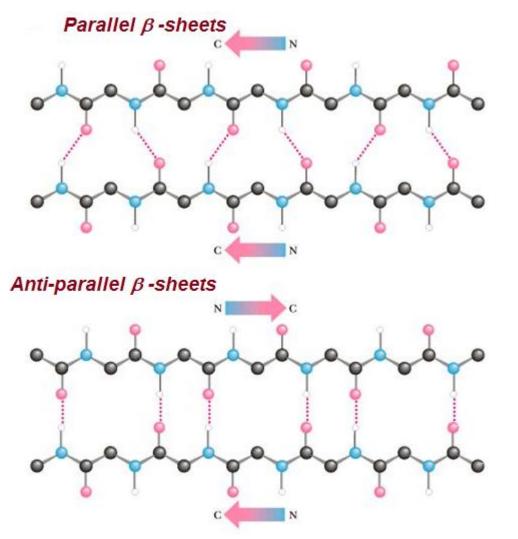
The alpha helix (α -helix) is a common motif in the secondary structure of proteins and is a right hand-helix conformation in which every backbone N-H group hydrogen bonds to the backbone C=O group of the amino acid located three or four residues earlier along the protein sequence.

Alpha helix (α-helix)



Protein: Secondary structure

The β -sheet is a common motif of regular secondary structure in proteins. Beta sheets consist of so β -strand connected laterally by at least two or three backbone hydrogen bonds, forming a generally twisted, pleated sheet.



- β-sheets formed from multiple side-by-side betastrands.
- ➤ Can be parallel or antiparallel configuration.
- Anti-parallel beta-sheets are more stable.

The supramolecular association of 6-sheets has been implicated in formation of the protein aggregates and fibrils observed in many human diseases, notably the amyloidosis such as Alzheimer's disease.