

BIOL213 Lecture Notes

Lecture 1 - Amino Acids

Function

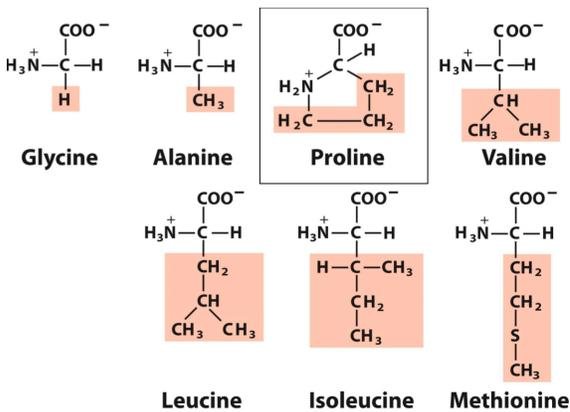
- Free amino acid analogues used as medicines.
 - Glutamate is the most abundant excitatory neurotransmitter in the vertebrate nervous system
 - Derivatives used as drugs/sensors
- Free amino acids used as supplements, food additives, enhancers, preservatives
 - Glutamate in food is responsible for umami.
 - Monosodium glutamate (MSG) easily manufactured for use as flavour enhancer.
 - Joined together to form a polypeptide chain (a polymer)

Structure

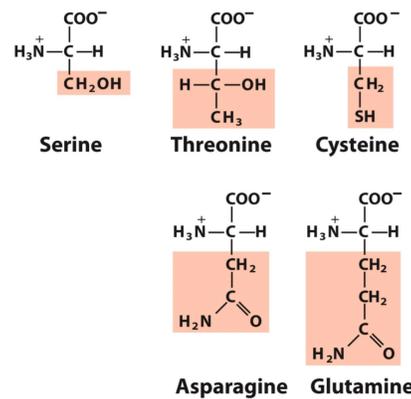
- Constant region: a basic amino group ($-NH_2$), an acidic carboxyl group ($-COOH$), and a hydrogen connected to the Alpha carbon
- Variable region: Side chains affecting how amino acids interact with one another and how a protein interacts with other molecules
- All amino acids are chiral meaning they're asymmetrical (except glycine)
- Peptide bond- A bond formed when the carboxyl group of an amino acid attaches to the amino group of another, with the release of a molecule of water (dehydration reaction).

Classification

Nonpolar side chains; hydrophobic

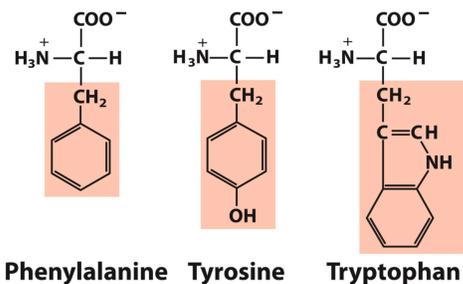


Polar side chains; hydrophilic

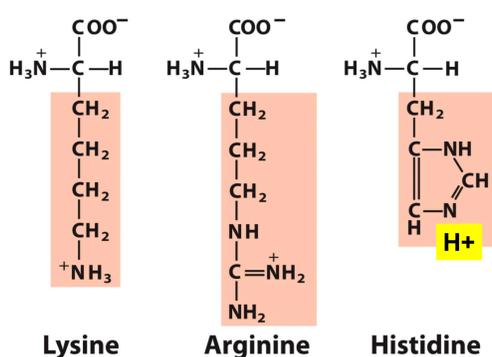


When 2 Cysteine molecules are oxidized a disulfide bond can be reversibly formed. The disulfide linked residues are strongly hydrophobic and stabilize the structures of many proteins.

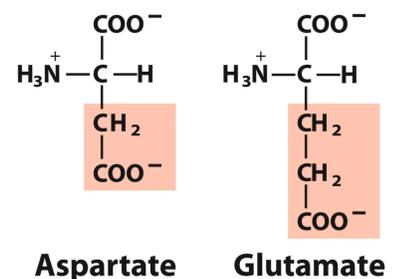
Aromatic R Groups



Positively Charged R Groups Basic



Negatively Charged R Groups Acidic



pH

A weak acid or base is incompletely ionized in solution compared to a strong acid or base.

$$K_a = \frac{[\text{products}]}{[\text{reactants}]}$$

- Strong acids have a high K_a value and thus a lower pK_a value
- The weaker the acid, the stronger its conjugate base
- The bigger the K_a ; more products, more hydronium, more acidic

$$pK_a = -\log K_a$$

$$pH = -\log [H_3O^+]$$

$$pOH = -\log [OH^-]$$

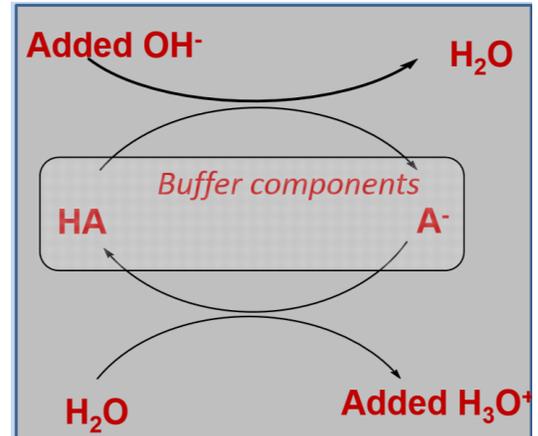
$$pH + pOH = 14$$

Buffer

- Buffer is a solution of weak acid and its conjugate base
- Resistant to sharp changes in pH
- Result is weak acid and weak base remaining but no H_3O^+ or OH^- remains.

$$pH = pK_a + \log \frac{[\text{base}]}{[\text{acid}]}$$

When $[\text{base}] = [\text{acid}]$ then $pH = pK$ (inflection point)



Ionization of Amino Acids

At acidic pH, the carboxyl group is protonated and the amino acid is in the cationic (positive) form

At neutral pH, the carboxyl group is deprotonated but the amino group is protonated.

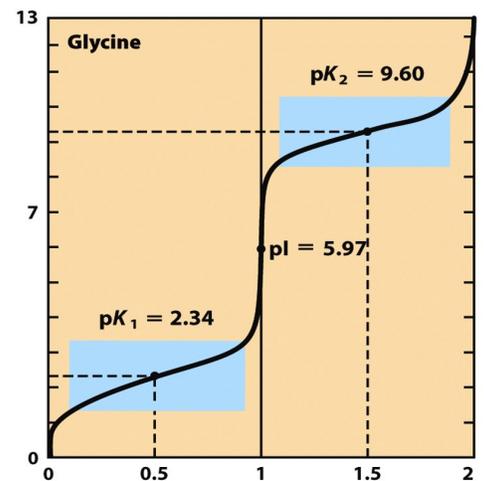
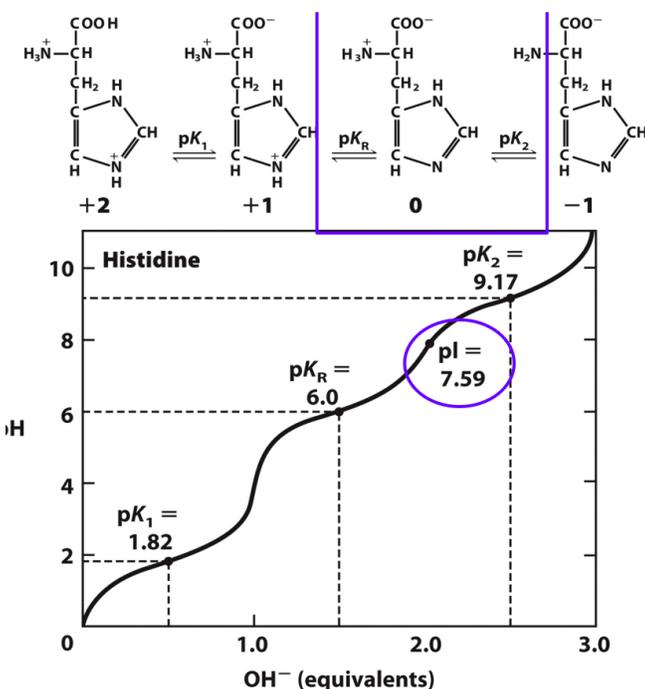
At alkaline pH, the amino group is neutral and the amino acid is in the anionic (negative) form.

- For amino acid without ionizable side chains, the Isoelectric Point (equivalence point, pI) is the pH at which the net electric charge is zero.

When a side chain is ionizable there will be 3 pK_a values on a graph, to find the correct pI value:

Use structure of the amino acid to find when the net charge is 0

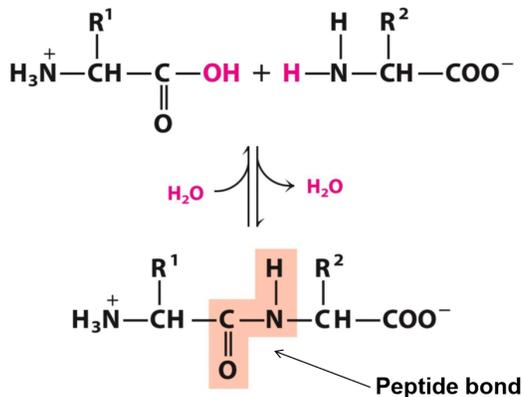
Then use the 2 pK_a values closest to this structure. See below



Lecture 2 - Proteins

Peptide bonds

- Condensation reaction between two AA, the amine end of one and the carboxyl end of another
- The carbonyl oxygen has a slight negative charge and the amide nitrogen has a partial positive → forms a resonance (sharing 2 pairs of electrons) → forming a dipole moment
- Causes them to be less reactive and to be **quite rigid and nearly planar** (cannot rotate)



- When naming a protein start from the N-terminus and move toward the carboxyl terminus.
- Using the three-letter code abbreviation – Ser-Gly-Tyr-Ala-Leu
- For longer peptides (like proteins) the one letter code can be used – SGYAL

Structure

- Protein molecules adopt a unique three dimensional conformation by folding called native fold
- The native fold (conformation) has a large number of favorable interactions within the protein –

Weak (non-covalent)

1. Hydrogen bonds – Interaction of N-H and C=O of the peptide bond leads to local regular structures such as α -helices and β -sheets
2. Electrostatic (ionic) interactions – Long-range strong interactions between permanently charged groups – Salt-bridges, esp. buried in the hydrophobic environment strongly stabilize the protein
3. Hydrophobic effect – Forces that hold the nonpolar regions of the molecule together, presents the smallest hydrophobic area to the aqueous solvent (generally in the center of protein away from water)
4. Van der Waals – Medium-range weak attraction between all atoms contributes significantly to the stability in the interior of the protein

Non-peptide, covalent (eg disulfide)

4 Levels of Protein Structure

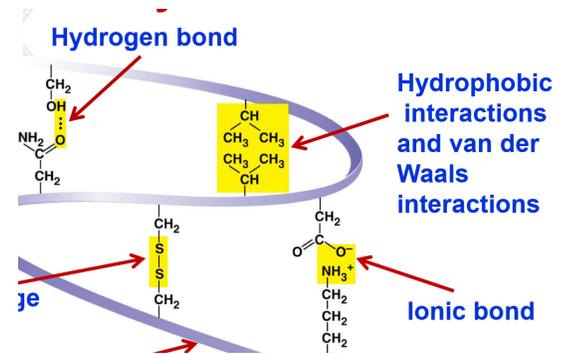
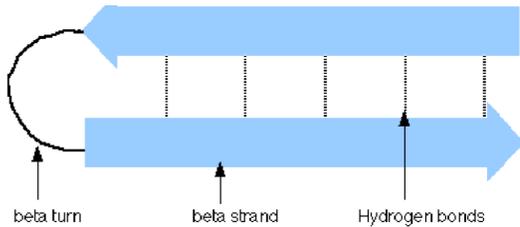
Primary (1°)

- The linear sequence of amino acids in the polypeptide is called its primary structure.

Secondary (2°)

- Secondary structure refers to a local spatial arrangement of the polypeptide **backbone**
- The α -helix – stabilized by hydrogen bonds between nearby residues
 - Polypeptide backbone winds tightly around a longitudinal axis.
 - The R groups stick out from the helical backbone
 - formed and stabilised by H bonding between C=O and N-H groups of peptide bonds 4 amino acid residues apart in the backbone
 - Not all polypeptide sequences adopt helical structures
 - Interactions between R groups can stabilise or destabilise the helix.
 - Bulky amino acids won't fit if close together in the chain (steric hindrance)

- The β -sheet – stabilized by hydrogen bonds between adjacent segments that may not be nearby
 - β -sheets are composed of several strands that run alongside each other
 - Can also occur between different polypeptide chains.
 - In parallel sheets the H-bonded strands run in the same direction \rightarrow bent H-bonds (weaker)
 - Same amino-to-carboxyl terminal orientation
 - In antiparallel sheets the H-bonded strands run in opposite directions \rightarrow linear (stronger)
 - Opposite amino-to-carboxyl orientation
 - B-turns occur whenever strands in sheets change the direction
 - Can also link α -helices to sheets or to each other



Tertiary (3°)

- final, folded 3D shape of a protein, determined by interactions between R groups, rather than interactions between backbone constituents

Quaternary (4°)

- Refers to proteins with 2 or more separate polypeptide chains
- Stabilized by numerous weak interactions between amino acid side chains and disulfide bonds

Major classes of proteins

Fibrous proteins

- Polypeptide chains arranged in long strands or sheets
- Made from a single type of secondary structure
- Provide support, shape, external protection
- Tough, rigid, hard - α -helixes -keratin (hair, nails, horns)
- Soft, flexible Non-covalently held- β -sheets non-stretchy numerous weak interactions

Globular proteins

- Often contain several types of secondary structure
- Tend to be enzymes and regulatory proteins
- More compact shape