

Exam 1 Review Guide:**Basic Chemistry**

- Be able to predict from the electronic structure of atoms the number of bonds the atom can form, or the charge on an ion.
- Be able to identify the following functional groups in a molecule, and state the properties of the functional group (non-polar, polar, potentially charged).
 - i) hydrocarbon
 - ii) alcohol
 - iii) carboxylate
 - iv) carbonyl
 - v) benzyl (phenyl)
 - vi) amino
 - vii) amide
- Know the relationship between hybrid orbitals and molecular geometry for sp^2 and sp^3 hybrid orbitals.
- Identify chiral centers on molecules, and discuss implications of chiral centers on drug activity.
- Identify hydrogen bond donors and acceptors.
- Be able to discuss role of pH in drug transport across membranes and binding to targets
- Be able to predict whether a group will be largely protonated or deprotonated, given pKa and pH. State the charge on each species (be able to do this for either carboxyl or amino groups).
- Predict the relative solubility of compounds
- Understand the fundamental molecular basis for:
 - i) electrostatic interactions
 - ii) van der Waals interactions
 - iii) hydrophobic effect.
- Know that the overall energy change depends on both enthalpic and entropic terms
- Predict whether reactants or products will be favored given ΔG° for the reaction.

Protein structure – important characteristics of each level:

1. Primary structure:

- Know how amino acids are linked together by peptide bonds to form proteins, given the structure of two amino acids, could you draw the correct structure after they are joined?
- Nomenclature – sequence begins at the amino terminus.
- Distinguish mainchain from sidechain atoms.
- Know that order (sequence) of amino acids defines folded structure, defines activity.

2. Secondary structure

- conformation of the mainchain
- only two that can be stabilized by hydrogen bonds are α -helix and β -sheet.
- know structural properties (location of H-bonds, sidechains)

3. Tertiary structure

- Relate structure to energetic terms:
 - Folded form destabilized by high entropy of the unfolded form.
 - Folded form stabilized by burial of hydrophobic groups, therefore core is composed of non-polar amino acids.
 - Folded form stabilized by van der Waals interaction in the core – therefore core is well packed.
 - Folded form stabilized by mainchain hydrogen bonds (same one that stabilize secondary structure) and sidechain hydrogen bonds.
- All polar and charged residues are on the surface
- Significant number of non-polar residues are on the surface.

4. Quaternary Structure

- Structure with multiple chains.

Enzymes

- Catalysts – make reactions go faster without being changed by the reaction.
- Active site – part of the enzyme that has amino acid residues that recognize substrate and facilitate chemistry on the substrate, converting it to product.
- Increase in rate occurs because enzyme decrease the energy of the high energy transition state
- Decrease in the energy of the transition state is due to the fact that reactants are pre-ordered in enzymatic reactions, so no unfavorable decrease in entropy
- Rate of product formation as a function of substrate – initially linear, but eventually becomes constant at high substrate because all of the enzymes have substrate bound – saturated.

Competitive inhibitors:

- Similar in structure to the substrate
- Bind at the active site, prevent (compete for substrate binding)
- Therefore, substrate can't bind – no product formed.

Allosteric Inhibitors:

- Bind to the enzyme at a different site than the active site
- Cause a change in the shape or conformation of the enzyme, so that it is no longer active.