

Study Guide, Exam 1, Chemistry 5700

I recommend the following strategies for preparing for Exam 1

- (1) Look over your lecture overheads and class notes. I never ask questions that are not directly relevant to material presented in class.
- (2) Read the assigned chapters, emphasizing concepts we discussed in class.
- (3) Work the problems at the end of each text chapter that are relevant to material covered in class.
- (4) Work the previous years exams
- (5) Review your webCT quizzes, and the iclicker questions. Concepts from these will reappear on the exam.
- (6) Study hard
- (7) *Confused? Overwhelmed?* Don't be bashful or shy; visit Professor Ensign during office hours or make an appointment.
- (8) Take advantage of your supplemental instructor, Jon Gardner. He holds weekly recitations, and will have a preexam help session.

Concepts checklist:

1. meaning of G, H, S
2. know your organic functional groups
3. features of water that make it suitable for supporting life
4. thermodynamics of the dissolving process
5. the hydrophobic effect
6. acid/base properties of water and weak acids/bases; meaning of and relation between K_a and pK_a
7. composition of a buffer, interpretation of a titration curve, meaning of equivalence point, polyprotic acids
8. buffer problems: calculate values of $[HA]$, $[A^-]$, pH, etc. given the necessary data for a buffer problem; be able to predict/calculate outcome of titration of a buffer solution with a weak acid or base.
9. Properties of α -amino acids: chirality, numbering/lettering; acid/base properties; isoelectric point; know the names and structures of the 20 standard amino acids; reactivity of side chains; classify amino acids on the basis of "R" group
10. peptide bond, nomenclature for naming polypeptides, disulfide bonds
11. Protein composition: subunits, homo and hetero
12. Protein purification: principles of ion exchange, size exclusion, affinity chromatography, nondenaturing and SDS-PAGE and the information they provide
13. Specific activity, enzyme recovery, fold purification, estimate % of total protein based on fold purification
14. 1°, 2°, 3°, 4° structure
15. the nature of the peptide bond; cis vs. trans
16. phi and psi angles and polypeptide conformation; Ramachandran plot
17. Secondary structure: properties of the α -helix, β -sheet, β -turn, random coil
18. fibrous proteins: α -keratin and collagen: structural features; use of nonnatural amino acids and why

19. common structural motifs: globin fold, 4-helix bundle, α/β motifs (e.g. α/β barrel and saddle)
20. motif vs. domain
21. principles of ligand binding to proteins
22. cooperativity vs. noncooperativity; hyperbola vs. sigmoidal binding curve
23. oxygen binding properties of Mb and Hb; distal and proximal His
24. Allostery of hemoglobin; CO_2 , H^+ , and 2,3-BPG effects and physiological significance
25. Basis for transition from T to S hemoglobin; importance of salt bridges (DON'T memorize specific ones!), O_2 binding, N-terminal carbamylation, protonation. Understand how nearby groups can perturb the pKa of another functional group and how this is important in hemoglobin
26. Molecular explanation for sickle cell anemia
27. Homology between proteins: conserved vs. nonconserved residues; identical, similar, radical amino acid substitutions and possible consequences (think sickle cell anemia)
28. Enzymes: features, cofactors vs coenzymes vs prosthetic groups
29. Reaction coordinate diagram, activation energy, transition state, G, H, S
30. Principles of enzyme catalysis: proximity, orientation, general acid/base, metal ion catalysis, covalent catalysis
31. binding energy and transition state theory
32. Enzyme kinetics: kinetic mechanism, reaction order, elementary steps, rate constant, Michaelis-Menten kinetics
33. steady state assumptions, pre-steady state, post-steady state
34. Michaelis-Menten equation; V_{max} , K_m , k_{cat} , K_D , catalytic efficiency. v vs. S plot and double-reciprocal plots
35. Reversible inhibitors: competitive, noncompetitive, and uncompetitive. How they work and determining inhibitor type from kinetic data
36. Is that enough or do you want more???