

Preparation for the exam 1

Chem112L, Spring 2009

Exam dates: Monday, May 11, and Tuesday, May 12

This exam focuses on mass spectrometry, enzyme kinetics, and study of protein folding by circular dichroism. I intend to have a mix of knowledge-showing essay-type, problem-solving, and multiple-choice questions. Knowledge of the following helps you in preparing for the exam:

1. Physical principles behind each of the molecular process
 - a. Protein ionization and its relevance to mass spectrometry
 - b. Protein folding, especially role of entropy in it
 - b. Enzyme catalysis and inhibition
2. Physical principles behind each of the observation/detection methods
 - a. Polarimetry and circular dichroism
 - c. Separation of molecules based on m/z values; protein identification
 - d. Measurement of reaction rates by UV-Vis spectrophotometry
3. Theoretical description of conformational equilibria, and chemical reactions
 - a. Estimation of thermodynamic parameters from experimental data
 - b. Dissociation constant in relation to equilibrium concentrations
 - c. Rate constants in relation to equilibrium constant
 - d. Steady state approximation for consecutive reactions
 - e. Transition state stabilization concept in enzyme catalysis
 - f. Description of reactions via intersecting potential energy surfaces
 - g. The energy levels and wave functions of quantum harmonic oscillator
 - h. Kinetic isotope effect and tunneling in chemical reactions
 - i. Enthalpy and heat capacity change in chemical reactions
4. Structural and functions concepts pertaining to kinetics, mass spectrometry and protein folding
 - a. Biological function and catalytic mechanism of lysozyme
 - b. Structure of peptides and proteins
 - c. Chiral and achiral molecules
 - d. Protein folding diseases: prions
 - e. Structure and function of heme-containing proteins
 - f. Chemistry of NAD-dependent dehydrogenases
5. Instrumentation
 - a. Basic design and operation of a spectropolarimeter
 - b. Basic design and operation of a dual-beam UV spectrophotometer
 - c. Ionization/vaporization methods for small molecule MS
 - d. Ionization/vaporization methods for macromolecule MS
 - e. Basic design and operation of a ESI mass spectrometer
 - f. Comparison of different mass analyzers
6. Broader applications of methods covered; other approaches to study these phenomena
 - a. Using circular dichroism to monitor structural changes in protein
 - b. Other methods to study protein folding
 - c. Other methods to study enzyme catalysis

- d. Applications of mass spectrometry in proteomics
7. Practical aspects of each of the experiments
- a. Why such wavelengths and cuvettes
 - b. Why such concentrations, pH, salts, buffers, etc
8. Data analysis.
- a. Understand why we used such model equations for fitting
 - b. Understand the meaning of each of the fitting parameters
 - c. Understand the measures of quality of data and fitting
 - d. Understand the workflow of scientific data analysis programs such as *Mathematica*
9. Miscellaneous
- a. How to estimate fitting parameters: you may need a calculator
 - b. How to make solutions: you may need a calculator
 - c. How to derive one and two-substrate enzyme kinetic equations
 - d. How to derive kinetic equations with one substrate and inhibitor
 - e. How to derive equations for protein unfolding equilibrium
 - f. How to derive equations that describe temperature-dependence of equilibrium constants

Answers to many of the questions require substantial thinking. Memorizing all the material may not be the best way to study for this exam.