

BE 560
BIOMOLECULAR ARCHITECTURE
(Fall 2008)

Instructor: Temple F. Smith
Office hours: By appointment
36 Cummington St., Rm. 313
(617) 353-7123

Text: **Protein: Structures and Molecular Properties**, Creighton (**REQUIRED**)
Hand-outs and web references

This course provides an introduction to the physical-chemical basis of protein structure and function, including signal transduction, enzymatic catalysis, and gene regulation. The physical/chemical, thermodynamics, and kinetics aspects will be covered along with the problems and current approaches to predicting protein structure and function. Sequence patterns, structural motifs and other mathematical approaches will be used to relate protein structure to function. The level of understanding that is expected to be achieved should allow the student to read most of the current protein research literature and extract the key ideas and new developments.

A standard bioscience or engineering background is assumed. This should include two undergraduate semesters of basic biology (or one semester of biochemistry), introductory chemistry and/or physics along with the associated mathematics courses.

Grades will be based on two of three written exams (the lowest grade of the three will be dropped), quizzes, one literature research project, and weekly homework assignments. Graduate students will, in addition, be expected to demonstrate the ability to read critically the related scientific literature (through a written project report and exam questions) for the minimum graduate passing grade of B.

BME 560 - SYLLABUS

- 1) Introduction and review of course outline (1.5 hr lecture)**
 - a) What are proteins?
 - b) What is the function of a protein?

- 2) Information flow(s) in living systems (2 x 1.5 hr lecture)**
 - a) Review of probability, information and thermodynamic entropy
 - b) The "central dogma" of molecular biology and the cellular environment

- 3) Protein basics (7 x 1.5 hr lectures)**
 - a) The building blocks, the amino acids
 - b) The peptide bond and the allowed polypeptide chain geometry in the (Phi and Psi) conformational space
 - c) Secondary structure classification
 - d) The peptide chain conformational "forces"
 - i) Heuristic forces (H₂O, hydrogen bonds, the hydrophobic effect and entropy)
 - ii) Semi-empirical potential energy functions
 - e) Protein architecture classification
 - i) Single domain globular proteins
 - ii) Multidomain proteins
 - iii) Membrane proteins
 - iv) Multiple protein complexes

EXAM I

- 4) Experimental methods for determining structures (3 x 1.5 hr lectures)**
 - a) Genomic sequencing
 - b) Circular dichroism
 - c) X-ray crystallography
 - d) NMR analyses (basic concepts only)

- 5) Structure prediction (3 x 1.5 hr lectures and laboratories)**
 - a) Modeling by homologous extension
 - b) Statistical methods
 - c) HMM modeling
 - d) Minimum free energy modeling

BME 560 outline (cont.)

- 6) Protein function (7 x 1.5 hr lectures)**
 - a) Evolutionary considerations and family recognition
 - b) The enzyme
 - i) Substrate binding
 - ii) Catalysis and cooperativity
 - iii) Kinetics
 - iv) The immune system components
 - c) Protein protein interaction
 - i) Signal transduction cascades
 - ii) Protein-Nucleic acid (DNA) interaction
 - d) Protein motors

EXAM II

- 7) Implications of the current data/knowledge explosion (1.5 hr lecture)**
 - a) Scientific: Predictive system biology
 - b) Technological: Engineering applications and challenges
 - c) Ethical and societal issues

FINAL EXAM