

CHEM 645 - Protein Structure and Function

Fall 2013, Wednesday 7-10 pm, 221 Brown Lab

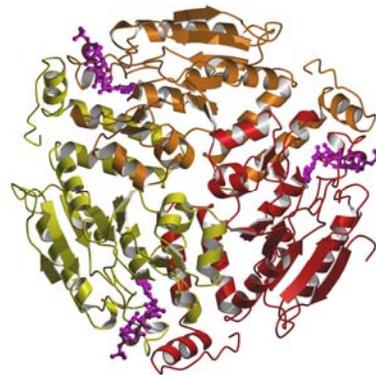
Prof. Brian Bahnson, 312 Drake Hall, phone: 831-0786

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Course web page:

<http://www.udel.edu/chem/bahnson/chem645/>

Office hours: by appointment



Outline of course: The course will begin with an overview of structural biology, including how X-ray crystallography, NMR spectroscopy, homology modeling and other techniques are used to solve structures and develop models of macromolecules. Then representative classes of proteins will be discussed in terms of how the protein's structure relates to its function. This class is meant for both people directly interested in structural biology, as well as those that plan to collaborate with structural biologists.

X-ray crystallography vs. NMR spectroscopy - Each method has advantages and disadvantages. Also each technique supplies different information. Topics that will be covered include: crystal growth and sample preparation, data collection and instrumentation, methods to obtain phases or obtain NMR distance restraints, model building and model refinement. Next we'll go through a homology modeling assignment. Your in class presentations and final projects will bring other related topics into our discussion. Examples of information about structure and dynamics from other methods include: CD, UV/VIS, raman, FT-IR, mass spec, fluorescence, genomics, structure prediction, protein folding, can structure be predicted *ab initio*? Modeling the dynamics of protein motion - molecular dynamics, potential energy functions, energy minimization, functional role of proteins in biological systems- enzymes, transporters, ion channels, energy transducers, signal transduction, molecular motors, structural scaffolds, gene expression, etc...

Required texts:

"Crystallography Made Crystal Clear, A Guide for User's of Macromolecular Models" by Gale Rhodes, Third Edition, Academic Press (2006) ISBN 0-12-587073-6

You should have and refer to a decent biochemistry textbook.

Review articles and primary literature will be used extensively.

Many other useful texts - available to borrow short term from my office.

Grade breakdown for Fall 2013

Midterm exam - 20% - in class

Homology modeling assignment - 20% - will be problem set based and will utilize the primary literature, the www, your laptops and classroom linux computers (in 221 BRL).

You will be encouraged and instructed in how to load much of the software (freeware) on your own computers.

Research Paper Discussions - 20% - our 2nd half of the semester will be devoted to in depth discussion of primary literature on selected topics of your choosing. You will each be assigned a portion of the topic to lead the discussion on.

Final Exam - 20% - take home

Class participation - 20%

Course prerequisites

Introductory biochemistry class, such as CHEM 527 or 641

Course objectives

The course presents a theoretical and practical overview of structural biology, including how X-ray crystallography, NMR spectroscopy, homology modeling and other techniques are used to solve or model structure of macromolecules. Representative proteins discussed in terms of how each protein's structure relates to its function. This class is meant for both people directly interested in structural biology, as well as those that plan to collaborate with structural biologists. Students will improve their abilities to read, understand and critically discuss primary literature related to structural biology.

Students will likewise improve presentation skills, working with fellow students on joint tasks, and develop skills using computers to aid in structural biology pursuits.

Departmental learning objectives

This course meets departmental [learning objectives](#) 1, 3, 4, 5, 8, 9 and 10.