Biochemistry 404
CRN 10267
Proteins
Course Outline - Fall 2018

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Instructors will announce office hours in class.

This course is aimed at understanding the detailed connection between the *structure* and the *function* of macromolecules. Part 1 (Dr. Boraston) is focused on understanding specific methods of quantifying *function.* Part 2 (Dr. Evans) is focused on understanding methods of determining *structure*, and on protein folding.

Part 1 Dr. Boraston (September 6 October 18)

Molecular Interactions: Theoretical and Practical Aspects

1. Properties and isolation of proteins (~4.5 hours)

   Review of general protein properties
   Amino acid side chain reactivity
   Recombinant protein production
   Methods of protein purification

2. Detecting and quantifying protein-ligand interactions. (~7 hours).

   Overview of protein-ligand interactions.
   What is a ligand and why is their interaction with proteins important?
   Overview of high resolution vs. medium vs. low resolution methods
   Discussion of selected methods.

3. Binding equilibria (~5 hours).

   Symbolic equilibrium expressions: representing simple and complex equilibria.
   Mathematical modeling of binding equilibria and analysis of binding data.
   Thermodynamics for biochemists.

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Part 2 - Dr. Evans (October 22 December 3)

1. Review of protein and peptide structure (1.5 hours)

   Secondary structures as a structural biologist looks at them. STRUCTURE = FUNCTION, peptide bonds & Ramachandran plots, complementarity and the -helix: 4-helix bundle, globin fold, -sheets, -bulges, -turns, antibody fold, Rossmann fold, jellyroll, TIM barrels, etc.

2. Structure determination by protein crystallography (9 hours)

   Crystal symmetry: What are crystals? Why use crystals?
   X- law.
   Crystal quality & data resolution.
   What information can be obtained from each determination?
   The phase problem: Heavy atoms, MAD & molecular replacement.
   Electron density maps.
   Data collection & structure fitting.
   Refinement of protein structures & indicators of

3. Structure determination by NMR (1.5 hours)

   Larmour frequency & proton coupling.
   Comparison of NMR of small molecules and proteins.
   Fourier Transform methods for data collection.
   NOE and multi-dimensional NMR.
   Comparison of X-ray and NMR methods.

4. Concepts of protein folding (3.0 hours)

   Levinthal paradox & the protein folding problem.
   Methods to characterize protein folding: UV-Vis; NMR; X-ray scattering, enzyme activity.
   Isomerization of peptide bonds as a rate-limiting step in protein folding.
   Disulfide bond formation as a rate-limiting step in protein folding.
   Cellular strategies: enzymes, chaperones & chaperonins.
   Simple concepts of proteins folding,

DEPARTMENT INFORMATION AND POLICIES

1. The Departme