Course Co-ordinator
Dr. Gary Shaw
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Lecturers (Office)
Dr. Gary Shaw (MSB 306) gshaw1@uwo.ca
Dr. Greg Gloor (MBL 8) ggloor@uwo.ca
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Teaching Assistants
Matthew Berg
Karen Dunkerley
Christina Chung

Lectures and Labs/Tutorials
Monday, Wednesday – 12:30-1:30 pm, DSB-2016
Thursday 10:30-11:30 pm, SH-1310

Computers
Lectures and labs will utilize online databases and programs. Students may find it advantageous to bring their laptop to class and lab/tutorials. Computers will be provided in SH-1310.

Course Overview
This course will explore the chemical and physical underpinnings of biochemical phenomena. Students will learn the background and basic theory for important biochemical techniques and apply this knowledge to solve quantitative problems. The first portion of the course will introduce tools to determine, visualize and assess three-dimensional protein structures. Students will learn about different techniques to examine and assess protein-protein interactions. The second module of the course will introduce students to some basic molecular biology methods. In the third section students will be introduced to some principles of bioinformatics and biochemical database mining.

Assessment for this course will be from problem-based assignments. There are no midterm or final exams.

Outline
A. Protein Structures and Interactions (8 lectures, 2 labs) - Shaw

Lectures – January 8, 10, 15, 17, 22, 24. February 5, 7
Lab/Tutorial – January 11, 18, 25

Objectives
In this section of the course, students will acquire skills to critically analyze three-dimensional structures of proteins and nucleic acids. Students will learn how to describe structures in terms of secondary structure, surface area, motifs and energetics. Skills will be developed to assess experiments that describe secondary structure, three-dimensional structure, size and shape. Students will also learn how to quantitatively assess protein-protein and protein-nucleic acid interactions in biochemistry. Students will acquire skills to assess and measure strengths of interactions using different techniques and critically analyze data.

Details of Protein Structure (helices, sheets, Ramachandran Plots)
Secondary Structure Analysis (Circular Dichroism Spectropolarimetry)
Protein Size and Shape (gel filtration, sedimentation equilibrium)
Methods to Determine Protein Structure (X-ray crystallography, NMR spectroscopy)
Visualizing Protein Structures (PyMol, SwissPDB Viewer)
Analyzing Structures (Contact maps, Surface area)
Modelling a Protein Structure (Prediction, Online Tools)
Protein Interactions using Affinity Methods (Pull-down, Gel Shift)
Determining Interactions using Mass Spectrometry
Dissociation constants (Kd), Dynamic Range, Sensitivity and Protein Concentrations
Optical Methods to Measure Protein Interactions (Fluorescence, FRET)
Direct Methods for Affinity and Thermodynamics (Isothermal Titration Calorimetry)
Kinetics of Ligand Binding (on/off rates, Surface Plasmon Resonance)

B. Molecular Biology Methods (8 lectures, 3 labs) - Berg

Lectures – January 29, 31; February 12, 14, 26, 28, March 5, 7
Lab/Tutorial – February 14, 26, 28

Objectives
This section of the course will provide students with an introduction to the steps necessary for cloning, expression and mutational analyses of a protein of interest. Students will learn the skills necessary to navigate the NCBI sequence database using the NCBI tool kit, and how to retrieve linked records from various NCBI databases. Concepts such as optimization of codon usage, strategies for site-directed or random mutagenesis, and evolutionary sequence analysis to guide mutagenesis will be introduced. Students will be required to analyze DNA and amino acid sequence data.

Introduction to sequence and record retrieval from NCBI.
Retrieving linked records using NCBI utilities.
Codon usage and codon optimization.
Site-directed and random mutagenesis studies.
Evolutionary analyses of protein sequence to guide mutagenesis.
Sequence logos – concept and calculation of information content.

C. Bioinformatics (8 lectures, 3 labs) - Gloor

Lectures – March 12, 14, 19, 21, 26, 28, April 2, 4
Lab/Tutorial – March 15, 22, 29

Objectives
This section of the course will introduce students to the basics of bioinformatics.

Basics of protein sequence alignment
BLAST and similar tools
Structure-guided sequence alignment

Grading

Assignments - There will be 9 assignments in this class, three in each section. Assignments will be worth between 8-15% of your final mark. The assignments will be given out during each lab/tutorial class.

Late Policy - Assignments are due at the time and date marked on each assignment. Late assignments will not be accepted and will be given a mark or zero.

Grades - Final grades in this course, irrespective of the number of decimal places used in marking individual assignments and tests, will be calculated to one decimal place and rounded to the nearest integer (e.g., 74.4 becomes 74, while 74.5 becomes 75). Marks WILL NOT be bumped to the next grade or GPA level (e.g., an 84 will NOT be bumped up to an 85). The mark attained is the mark you achieved and the mark assigned; requests for mark bumping will be denied, in accordance with Bachelor of Medical Science Undergraduate Education policy.

Plagiarism

“Students must write their essays and assignments in their own words. Whenever students take an idea, or a passage from another author, they must acknowledge their debt both by using quotation marks where appropriate and by proper referencing such as footnotes or citations. Plagiarism is a major academic offense (see Scholastic Offense Policy in the Western Academic Calendar - http://www.uwo.ca/univsec/handbook/appeals/scholoff.pdf).”