BioC 4351/5351 Protein Engineering  
Fall 2014

Instructor:  
Dr. Romas Kazlauskas  
Department of Biochemistry, Molecular Biology & Biophysics  
174A Gortner Labs (walk through the lab to find my office)  
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office hours: before & after class or by appointment

Class Schedule:  
Mon, Wed 11:15 am to 12:30 pm

Text: assigned papers and reviews

Prerequisite:  
BioC 4331 (Biochemistry I) or instructors consent

Description:  
Key properties of enzymes and their molecular basis, computer modeling strategies, mutagenesis strategies to create protein variants, expression and screening of protein variants. Students critically evaluate research papers, identify unsolved practical and theoretical problems in protein engineering and plan a protein engineering experiment.

Learning Outcomes:

Foundational Knowledge: Be able to explain and discuss key ideas regarding the role of biocatalysis in sustainable development, key enzyme properties and their molecular basis, computer modeling strategies, mutagenesis strategies to create protein variants, expression and screening of protein variants.

Application Goals: Be able to critically evaluate a research paper in protein engineering. How important is the paper? What hypothesis did they test? How does it simplify future protein engineering? Be able to identify unsolved practical and theoretical problems in protein engineering and to plan a protein engineering experiment.

Integration: Be able to identify where proteins, enzymes and biocatalysis affect our daily life, current society issues involving protein engineering, where advances in protein engineering have created business opportunities and ethical issues created by protein engineering.

Assignments & grading:
1. Readings of original papers & in-class discussion 15%
2. Weekly homework assignments 15%
3. Critical review of a protein engineering paper (paper & oral presentation) 20%
4. Protein engineering project planning (paper & oral presentation) 20%
5. Midterm & Final Exams 30%

Work Load: ~6 hr reading and critical analysis of current research papers each week, in class discussion of current research papers, midterm and final exam, weekly homework projects (~3 hr per week) culminating in an oral presentation on a student-designed protein engineering project.

Course Web Site: public site: https://wiki.umn.edu/ProtEngInfo/WebHome; registered student site (Moodle) will be also available once the course starts
Course administration

- You should adhere to the University of Minnesota Student Conduct Code found at http://regents.umn.edu/sites/default/files/policies/Code_of_Conduct.pdf
- Class attendance is required. You are responsible for all information announced in class.
- Course information will occasionally be emailed to your umn.edu mailbox and also posted to the course Moodle site. Any important information e-mailed or posted to the web will also be announced in class.
- Late work: loss of 10% of max score per 24 h or part thereof including weekends and holidays. Example: Five points will be deducted from an assignment worth 50 points that is 12 h late.
- Changes of grade: If your work is graded incorrectly, please write down what is wrong (e-mail OK) within two weeks. I will answer in writing within two days.
- Extra work: Students are not permitted to submit extra work to raise their grade.
- See the U of M website link below for information on Scholastic Dishonesty, Makeup Work for Legitimate Absences, Appropriate Student Use of Class Notes and Course Materials, Grading and Transcripts, Sexual Harassment, Equity, Diversity, Equal Opportunity, and Affirmative Action, Disability Accommodations, Mental Health and Stress Management, Academic Freedom and Responsibility.
  http://policy.umn.edu/Policies/Education/Education/SYLLABUSREQUIREMENTS_APPA.html
- Grades of incomplete are rare. See criteria at http://www.cbs.umn.edu/students/grades-and-grading-options

Topics - each topic represents ~2 lecture hours
1. Biocatalysis, green chemistry, why proteins need to be engineered
2. Protein structures & folding (PyMOL)
3. Measuring protein stability
4. Strategies to engineer more stable proteins
5. Molecular mechanics approach to modeling
6. Strategies to engineer more stable proteins
7. Measuring reaction rates (MM kinetics)
8. Strategies to increase reaction rates
9. Measuring enzyme selectivity
10. Strategies to increase selectivity
11. Modeling selectivity (conformations & molecular dynamics)
12. Survey of directed evolution: screening, random mutagenesis
13. Single amino acid substitutions – error prone PCR
15. Multiple amino acid substitutions – stepwise combinations
16. Multiple amino acid substitutions – simultaneous changes
17. Recombination methods – limitations, homology
18. Adding multiple mutations simultaneously
19. Other mutagenesis approaches
20. Screening & selections strategies
21. Protein expression
22. Metabolic engineering
23. Student presentations

revisions history:
17 Dec 2013 initial draft
20 May 2014 updated course number, meeting times, website information