

My Favorite Protein Lesson Plan

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Introduction

Proteins are a diverse class of biological molecules, which play a crucial role in almost every biological process. Proteins, known as enzymes, are responsible for the catalysis of nearly every reaction in the cell; protein receptors are crucial for the communication of nerve impulses & hormonal signals. The cytoskeleton, which gives the cell its shape and mechanical support, is composed entirely of proteins. One of the most impressive examples of protein diversity are the antibodies and T-cell receptors of our adaptive immune system. These proteins must differ enough that they can respond to all the infectious agents our body will encounter in our lifetime, but they must be identical in their overall 3-dimensional shape in order to perform their job properly. A reasonable question to ask about proteins is: How can they function in so many different ways if they are all made of the same 20 amino acids? Indeed, the basic building blocks of every protein are the 20 essential amino acids listed in your textbook. The difference between individual proteins, however, is the exact number and order of these amino acids. A change at even one location in the sequence of amino acids which make up a protein can lead to a loss of function. This may be because that amino acid was important for the protein to fold up into its proper structure, or it may be because the amino acid was important for reacting with other molecules in the protein's active site.

Lesson Goals:

1. To improve students' understanding of the relationship between protein structure and function.
2. To improve student understanding of intermolecular forces which stabilize proteins.
3. To help students understand the importance of proteins and the varied roles they play in cells and organisms.

These lesson goals are assessed using the quality of student reports and models. See the grading rubric and handout for details.

Prior knowledge required:

We developed this lesson as a follow up to the molecular biology unit in college preparatory biology. We implemented the lesson over two years at Danville and Neuqua Valley High Schools in Illinois. The lessons were taught in introductory, honors and AP classes with a total of 7 different teachers, all of whom were novices with respect to VMD in particular and computer-based molecular visualization in general. Students should understand the following prior to beginning this lesson:

1. Proteins are hetero-polymers of amino acids. There are 20 unique amino acids, some positively charged, some negatively charged, some non-polar, and some polar.
2. A protein's sequence refers to the exact type and order of amino acids. A protein's structure refers to its 3-dimensional form.
3. A protein will fold up into a unique, compact structure, depending on what types of amino acids compose it and the order in which these amino acids are arranged.

4. Hydrophobic amino acids are non-polar, oil-like molecules. They will tend to associate with one-another when dissolved in water. This separation of oil-like and water-like parts of a protein is part of what makes it fold. Hydrophobic amino acids will be found on the inside of a folded protein, unless it is a membrane protein, which will have hydrophobic amino acids on the outside.
5. In addition to hydrophobic effects, hydrogen bonds, ionic bonds (salt bridges), and covalent sulfur-sulfur (disulfide) bonds are important for protein stability.
6. Enzymes are proteins that speed up (catalyze) reactions. They all have little pockets inside them called active sites where the reaction takes place.
7. Protein function is usually very sensitive to structural changes, particularly near an active site or binding site.

Materials:

- A computer with VMD installed and an LCD projector for the instructor.
- A computer with VMD installed for each student group.
- The VMD tutorial (“Getting to know RNA Polymerase”).
- A Student handout (“My Favorite Protein”) for each student.
- Data storage is required for saving VMD states or rendered images.

Alternatively, images can be printed, preferably in color.

Software: VMD is freely available at www.ks.uiuc.edu/vmd. The software requires 35 megabytes of disk space on a computer running Microsoft Windows 2000, XP, or Vista, or MacOSX 10.3.5 or later.

Protocol

1-5 Days before:

Prepare students for the activity by going over relevant terms and concepts in the “Prior Knowledge Required” section above.

Day 1

Introduce the activity and distribute the handout to students. Help them navigate to the PDB website and choose an appropriate protein. Allow them to read a little about their protein before writing down its name and PDB ID on their handout. Lead the class in launching VMD and begin the “Getting to know RNA Polymerase” tutorial. If there is a printer, students can print their “Molecule of The Month” protein handout and read it for homework.

Day 2

Complete the “VMD Basics” tutorial and help students get their proteins loaded into VMD. They should spend the rest of the day working on creating a VMD representation for their report that highlights the parts of the protein required for its structure and function. Students must save a VMD state or render an image to save their work by the end of the day.

Day 3

Students continue with their VMD representations and render a final image for their report, which can be saved to a disk, e-mailed or printed if a printer exists. Two to three days are usually sufficient for report writing and building the 3-dimensional model at home.

Note to the instructor:

This lesson can be simplified if the entire class works on the same protein. It may be necessary to warn against plagiarism before report writing begins to ensure protein descriptions aren't lifted directly from the "Molecule of the Month" handouts.

Grading Rubric

CRITERIA	Poor	Good	Excellent
THE VMD MODEL (this is worth 25% of the total grade for this project)	Student made an attempt which was significantly below the standard set by his/her classmates and the instructor.	Student made a great attempt at identifying all the applicable features described to the right. Studnet simply missed one or two features that could've been shown.	This model contained where applicable: -ID of active/binding site including amino acids involved in the active site chemistry -ID of alpha helices and beta sheets -ID of at least one of the following: disulfide bridges, salt bridges, hydrophobic interactions, or hydrogen bonds.
THE 3-DIMENSIONAL MODEL (this is worth 25% of the total grade for this project)	Student made an attempt which was significantly below the standard set by his/her classmates and the instructor.	Student produced a good product, but may have fell short in one of the categories listed below: -ID of essential protein features. -Creativity in use of materials. -Simplification of model down to essential features.	This model contained, where applicable: -ID of all the essential features for this protein listed in the box above. -Creative use of materials. -Was simplified to the point that one could really focus on the important aspects of the protein.
THE REPORT (this is worth 50% of the total grade for this project)	Student made an attempt which was significantly below the standard set by his/her classmates and the instructor.	Student produced a good report, but fell short in one of the categories listed to the right.	The report included: -A concise, clear, and interesting discussion concerning protein function and real-world significance. -A clear and understandable explanation of structural features important for protein stability.

			<ul style="list-style-type: none"> - A clear and understandable explanation of structural features important for protein function. - Specific references to important features of the VMD and physical models. - The report was at least 3 pages and was not copied from any website or textbook.
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