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Incorporating Engineering in High School Biology

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Incorporating Engineering in High School Biology

by

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Report

Presented to the Faculty of the Graduate School of
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of the Requirements
for the Degree of

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Dedication

This work is dedicated to my family and coworkers. Without their support this would not have been possible.

Acknowledgements

I would like to acknowledge Dr. Pengyu Ren for his support and guidance through this journey. I would also like to thank my mother, UTeach faculty, and UTeach classmates for inspiring me to continue to perfect my craft.

Abstract

Incorporating Engineering in High School Biology

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The University of Texas at Austin, 2014

Supervisor: Pengyu Ren

The purpose of this project was to create a series of lessons that incorporate both Biology and Engineering concepts. The three lessons were intended to increase in complexity as the students progress throughout the year. Using PyMol software allowed students to visually represent complex protein structures while introducing and providing an opportunity to practice programming. Each lesson was followed by a worksheet or activity to aid in students' comprehension and application of practice.

These lessons were designed to maximize students' time learning to program and using PyMol software while enhancing the current curriculum. Lesson one introduced students to the PyMol software while building and representing the four main structures of proteins. With increased programming knowledge, lesson two focused on modeling the DNA double helix. The final lesson introduced students to evolutionary relationships based on a protein's amino acid sequence.

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Chapter 1: Introduction

The educational curriculum in the United States is constantly adapting to meet the needs of the students and society. The 21st century skills required for today's students have had a great influence on education, blending many disciplines into a cohesive curriculum that meets these demands (Singer, 2011). STEM (Science, Technology, Engineering, and Mathematics) education reform has been gaining momentum, and is slowly being adopted by several states and schools.

There are a number of schools however; if changes are not made, may fall behind or not reap the benefits that STEM education can provide. The acronym for STEM is incorrectly used by many professionals. If you do not cover all four disciplines is it still STEM? The "E" in STEM education is one of the hardest components for most teachers to integrate in their lessons (Rockland, 2010). A few reasons why engineering may be hard to incorporate in a classroom are: funding, lack of knowledge in the field, or class time.

There are several schools that may not offer an engineering program. Districts may not be equipped with the staff to offer a standalone engineering program. For students to receive the full benefits of STEM education, integration of all the components must be met.

Integrating engineering concepts into the classroom may be difficult, so why even try? For most educators, the easiest way to integrate engineering concepts is weaving them throughout the physics curriculum, but what if you don't teach engineering?

Teachers may be skeptical that engineering concepts can be incorporated into their scope and sequence.

The project outlined in this report is an example of incorporating engineering concepts into a Biology classroom. Through several lessons on molecular modeling and DNA sequencing with the aid of PyMol software, students use 21st century skills and software designed and used by bioengineers to learn:, how DNA is sequenced, the structure of proteins, and common ancestry. These lessons are intended to be taught throughout the year aiding in students understanding of complex biomolecules. The intent of this project is to provide biology teachers a guide to incorporate engineering into a traditional classroom and challenge all teachers to revamp their existing curriculum by using engineering concepts to increase students' engagement and content retention.

Many challenges are involved when introducing engineering into traditional curriculum, including; determining what information the teacher needs and the budget required for materials. This thesis purposes a solution to these obstacles, through my perspective as a teacher, with the intent of laying the foundation for incorporating engineering concepts within the classroom.

Chapter 2: Review of the Literature

2.1 BUILDING AN ENGINEERING PROFESSIONAL LEARNING COMMUNITY

Teachers are constantly revamping their craft; changing to meet the demands of their students. Once again, education has been challenged to combine science, technology, engineering, and mathematics (STEM) into a cohesive curriculum. Some schools have added engineering courses, others have integrated engineering concepts into current curriculum, and yet many have not addressed how to handle the "E" in STEM.

With this recent change, math and science teachers with the STEM endorsement might be assigned to teach an engineering class, but lack the knowledge within the field of engineering. There are several questions that arise as one tackles engineering curriculum within a campus, district, and state. At what level should engineering concepts be introduced, will this be a standalone curriculum, incorporated into an existing curriculum, or will this idea be ignored.

With the President's support and many states passing legislation to include STEM education in public schools, the idea of engineering education can no longer be ignored. Several curriculums, such as Project Lead the Way and Engineer Your World, have been developed to aid teachers in teaching an introductory engineering class. A well designed curriculum can provide support, but a teacher must have access to background knowledge in the subject area they are to teach. One step that may provide answers to some of these questions and support the instructor is the development of a professional learning community. A professional learning community (PLC) is not a new concept; in fact most teachers probably are unknowingly involved in at least one or more learning communities. According to the book, Professional Learning Communities: An Implementation Guide and Toolkit, the benefits for the teacher participating in a PLC include: “increase student achievement, shape their own professional growth, work effectively with colleagues, become more accountable for results, and develop interdependence with other educators and leaders within their school and district,” (Foord & Haar, 2008).

A professional learning community can be made up of many different individuals. These may include administrators, curriculum directors, and teachers. The field of engineering as a viable high school curriculum is relatively new; as a result, other districts with a successful engineering programs or even post-secondary professors may be included to provide an insight into the field and its multi-faceted disciplines.

Collaboration is important but for a successful PLC there are other attributes that must met: “(a) shared mission, vision, values, and goals; (b) collective inquiry; (c) collaborative teams; (d) action orientation and experimentation; (e) continuous improvement; and (f) results orientation” (Foord & Haar, 2008). Each part is crucial to the next and will result in a positive overall transformation. When these changes have been successfully made the overall student achievement, according to Professional Learning Communities: An Implementation Guide and Tool Kit, will increase (Foord & Haar, 2008).

The first priority for the PLC is to set a goal, which can vary, but should include incorporating engineering within the curriculum. This goal could be providing an engineering class at the high school level or integrating engineering concepts in math and science classes. This goal can be a campus, district, or a state wide goal.

Teachers of the PLC work collaboratively in collective inquiry to investigate and propose solutions to teaching strategies, students' success, curriculum development, and any other questions that may arise. This process is ongoing and as new questions arise the group should evaluate them and make key decisions. Each member may contribute an important piece to the puzzle and bring new insight that may not have been proposed earlier.

Choosing a collaborative team is critical for the success of the PLC. This team should consist of individuals that share a common goal, and are willing to make changes based on the data and needs of the students. The team does not have a specific size, but each member should contribute. For example a curriculum director might be in charge of verifying state standards, a post-secondary instructor could provide insight on what an entering engineering freshman needs to know, an administrator oversees the budget for the class, and the teacher provides insight based on student data. Since the PLC will be focused on STEM education, suggested teachers to include in this group are from the four disciplines of STEM (science, technology, engineering, and mathematics). Although not all the teachers may be assigned an engineering class, they can contribute professional perspectives, and may even try engineering concepts in a non-engineering course (i.e. physics or trigonometry); a true integration of STEM curriculum.

The main focus of the professional learning community is the students. Team members are responsible for collecting data and presenting the information so the group can make new informed decisions. For engineering this data could take several different forms, such as pre- and posttest, projects, or student portfolios. This should provide the team with information on student growth, and can be broken down by grade level and sub population. It is important that if growth is not occurring, the group reflects on what changes were made and develop a plan of action to rectify the situation. This is a constant cycle of gathering data, reflection, and problem solving. There is always room for growth and improvement. This growth may be from individual students, success in other curriculum areas as a result of engineering, or expanding the program to include more engineering practices.

If successful the team may expand to other campus and add new members to the group. This is probably the most tedious task of the PLC and where responsibility of individual team members becomes essential. To alleviate stress on team members, the group may assign each individual with a task. One may collect the data, another disaggregates it, and someone different present the data to the team. This is a team effort and requires time and dedication to achieve student growth

A professional learning community is different from a regular teacher meeting; as a result it can lead to many beneficial changes within the campus. The benefits that may arise from a professional learning community include: “improved collaboration between teachers and leaders through effective PLCs leads to four important results: improved student achievement regardless of demographics, increased teacher proficiency in using research-based practices, increased student sense of belonging and efficacy, and increased sense of belonging and efficacy of teachers,”(Foord & Haar, 2008). The group should meet at the end of each school year and revisit their goal. Have the students met the goal, or should it be altered? Are there any long term benefits from the engineering class? Should the program be expanded? What where the successes and failures that occurred throughout the year? All these questions should be considered by the PLC.

2.2 APPLYING ENGINEERING CONCEPTS IN A TRADITIONAL CLASSROOM

"The education of science and mathematics teachers in different content areas generally does not include courses that promote an understanding of engineering principles and design," (Rockland, 2010). Trying to encompass engineering concepts in a non-engineering class may be difficult, some may even think impossible, but the key to success is support. "Teachers require a certain set of skills and knowledge to begin integrating technology and engineering concepts into their classroom practices," (Rockland, 2010). STEM education is the incorporation of science, technology, engineering, and mathematics into a cohesive curriculum. There are several components to consider when integrating engineering in a traditional (non-engineering) classroom including: "instruction, student learning, time, resources, and training," (Rockland, 2010).

One of the first classes integrated with engineering is physics, however; just because it is the most obvious doesn't mean it's the only answer. "Boundaries between STEM disciplines are blurring as students and practitioners seek to understand the natural and designed worlds," (Singer, 2011). A first step to integrating engineering in a non-engineering class would be learning about the different disciplines of engineering within the field. For example, mechanical engineering may be incorporated into an auto mechanics class or a physics class, while bioengineering could be introduced in a biology class, and chemical engineering in a chemistry class.

Once familiar with the discipline of interest, talk to a professional or a post-secondary instructor and find a description of what the professional would do within that specialty. “Quality curricular materials in these areas are scarce and teachers have not been trained to incorporate these topics into their curriculum and instruction,” (Rockland, 2010). This instructor may be a useful member in a professional learning community, and can provide insight to lead to student success. For example after talking to a biomedical engineer, the teacher is informed that they use computer technology to sequence proteins. Protein synthesis is a major part of high school biology curriculum, so these concepts would integrate into a stem lesson plan incorporating science, engineering, and technology. “Integration of the physical sciences, computer science, biology, engineering, science education, and mathematics is viewed as a foundational for a deeper understanding of biological systems, (Singer, 2011). The post-secondary resource can be a valuable resource and a wealth of information in creating a lesson for a non-engineering course.

“Like scientist, engineers look at and think about the real world and what counts as knowledge,” (Rockland, 2010). Lessons that may be perceived to the student as abstract now come to life using engineering techniques. Integrated STEM lessons “provide a context and framework for organizing abstract understandings of science and mathematics and encourage students to actively construct contextualized knowledge of science and mathematics, thereby promoting recall and learning transfer,” (Sanders, 2008). With this transfer occurring students are able to recall information, increasing student's achievement, and provide an engaging learning environment.

A factor that may result in teachers not incorporating engineering concepts into their traditional classroom is lack of training. With a push towards the integration of engineering in education (STEM), teacher workshops and trainings are beginning to appear; however they may be overlooked for workshops emphasizing the importance of state testing. Since the integration of engineering into other disciplines can be difficult and workshops training may not be an option, it is important for teachers to form or extend their professional learning communities to provide support.

Teachers complain that they do not have enough time to teach a new concept; however, if the lesson is integrated and increases learning transfer then wouldn't STEM lessons be more beneficial? According to Sanders, "students in integrated curricular programs consistently outperformed students in traditional classes on national standardized tests, in state-wide testing programs, and on program developed assessments," (2008). Furthermore, these programs were "successful for teaching science and mathematics across all grade levels and were especially beneficial for students with below-average achievement levels," (Sanders, 2008). Since time is a crucial in the classroom, a lesson that can build upon each other and incorporate many different yet related topics would take advantage of both integration and lack of time.

Traditional methods of teaching must change to include 21st century skills. "In our increasing technological and knowledge based competitive global society, it is critical to produce more engineers in the United States and to increase awareness about engineering in order to support and use engineering for a more efficient, effective, safe, and secure world community," (Rockland, 2010). The benefits of STEM education are endless and will promote student success in and out of the classroom.

Chapter 3: Background and Developing the Lesson

3.1 BACKGROUND

The 2013-2014 school year started with the Biology teachers at Dumas High School, in Dumas, TX, planning the years scope and sequence. It was important for the teachers to follow the class syllabus, if not, concepts on the STAAR Biology End-of-Course Assessment, may not be covered.

If projects or new ideas are implemented, they have to fit within the time frame, or completed by students outside of class. Along with the scope and sequence time frame, classes are only fifty-six minutes, Monday, Wednesday, and Friday. Tuesdays and Thursdays classes are 50 minutes due to interventions. When writing this lesson, time played a crucial role.

Also during this meeting weak areas were discussed based on data from the 2012-2013 school year. The weak areas found were: biomolecules, DNA sequencing, and evolution. These areas could drive the engineering lesson, and become the starting point for brainstorming. Below is the scope and sequence that the Dumas High School Biology department used and the time allotted for each unit:

Semester 1

Lab Safety	*4 days*
Biochemistry	*10 days*
Cells	*14 days*
Cellular Processes	*33 days*
Genetics and Heredity	*15 days*

Semester 2

Evolution	*15 days*
Classification	*15 days*
Microorganisms	*7 days*
Ecology	*14 days*
Plants	*10 days*
Animals/Body Systems	*17 days*

How can engineering be incorporated into a high school Biology class? I was fortunate to be part of the UTeach Engineering Program, and in January was paired with Dr. Pengyu Ren as my advisor. After many discussions and emails, the premise of my lesson would be using PyMol software, to tackle the task of bridging Biology and Engineering while incorporating technology within the classroom. With input from my professional learning community (Dumas Biology Teachers and Uteach engineering program), these lessons were created to be implemented into a freshman biology class, with no prior knowledge of programming.

3.2 DEVELOPMENT

Using different lesson plans as a template led to the idea of creating a set of instructional PyMol lessons to address and enhance the weak areas, while maximizing the students' time in the classroom. Incorporating these ideas would lead to a successful translation of STEM education. There are several other molecular building softwares, but PyMol is free for educational purposes, which helps when working on a budget.

Not familiar with PyMol, the internet and my advisor guided me through this process. My goal was to find a balance between a challenging lesson, and one that would allow all students to experience success in programming. Some coding was more difficult than others, and after trial and error, a way to represent proteins three dimensionally, and show similarities and differences was reached.

Each lesson was created to enhance teaching a specific unit, while providing an opportunity to learn basic programming commands. As the activities increase from unit to unit, they become more complex and require students to use prior knowledge. These lessons were meant to be taught in sequential order throughout the year, adaptations can be made, but more instruction may be needed if presented out of order.

Introducing students to the PyMol software while modeling the complexity of proteins is the goal of lesson one. This is intended to be taught to introduce students to protein structures, within the biochemistry unit, while exploring characteristics common to all proteins. Depending on the time frame, students can be challenged to find alternative proteins within the data bank, and classify them based on their structure.

Lesson two focuses strictly on modeling. The codes for this lesson were provided by Wu KP (2011). One project that I incorporated in my Biology class is having students build a three-dimensional model of DNA. Students would make models out of common everyday objects. Now with the aid of technology students can build the complex DNA double helix through a sequence of programming codes. It was my intention that this lesson be taught during the protein synthesis unit, when students are exploring the different properties of a DNA molecule. A modification to this lesson for advanced classes is creating a three dimensional model of RNA.

The University of Indiana's lab, Cytochrome C Comparison Lab, inspired the third and final lesson, to be taught using PyMol during the Evolution unit. The third lesson builds on coding from the previous two, while introducing students to more features for comparing the complexity of proteins. A couple of options to make this lesson more advanced is having students follow the same guidelines using a different set of proteins they select from the data bank, or using the color by mutation script when comparing proteins.

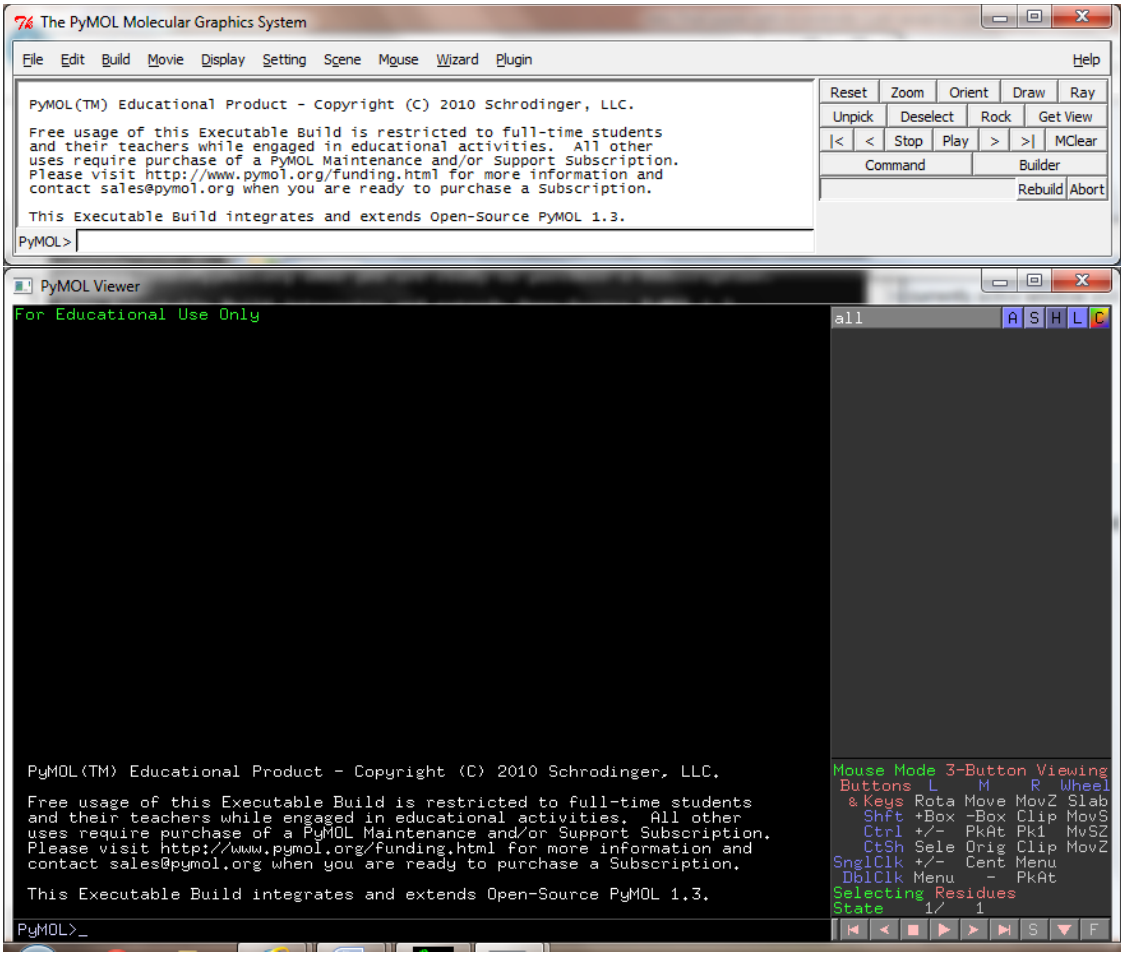
Chapter 4: PyMol Lessons

To prepare for these lessons, download PyMol, and place *PyMol + Tcl-Tk GUI + Console,* as an icon on the students desktop. Before lesson three, the five cytochrome c proteins from the different organisms should also be downloaded onto the students desktop. Print the students a copy of the lessons, and let the students keep the copies for reference. It would be advised that the teacher work through the lessons, to become familiar with the program, and if questions arise, most are searchable, or located within tutorials on the Internet.

4.1 LESSON 1: UNDERSTANDING PROTEINS AND PYMOL

TEKS addressed:
B 9.A: Compare the structures and functions of different types of biomolecules including carbohydrates, lipids, proteins, and nucleic acids.
B. 9.D: Analyze and evaluate the evidence regarding formation of simple organic molescules and their organization into long complex molecules having information such as the DNA molecule for self-replicating life.

1. **Open up PyMol + Tcl-Tk GUI + Console icon on your desktop (the two windows below should pop up on your desktop).**



```
PyMOL(TM) Educational Product - Copyright (C) 2010 Schrodinger, LLC.

Free usage of this Executable Build is restricted to full-time students
and their teachers while engaged in educational activities.  All other
uses require purchase of a PyMOL Maintenance and/or Support Subscription.
Please visit http://www.pymol.org/funding.html for more information and
contact sales@pymol.org when you are ready to purchase a Subscription.

This Executable Build integrates and extends Open-Source PyMOL 1.3.
PyMOL>
```

```
For Educational Use Only

PyMOL(TM) Educational Product - Copyright (C) 2010 Schrodinger, LLC.

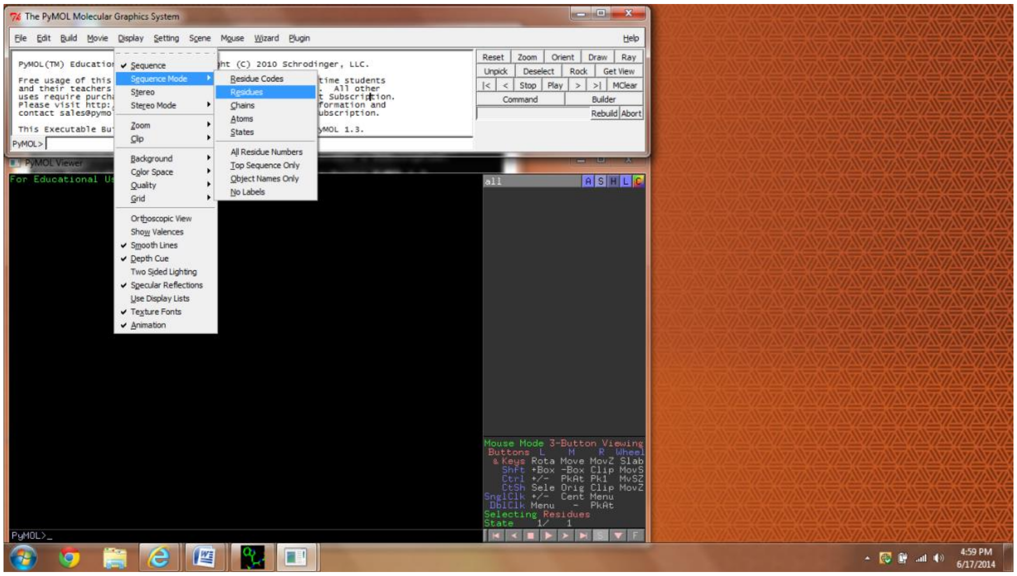
Free usage of this Executable Build is restricted to full-time students
and their teachers while engaged in educational activities.  All other
uses require purchase of a PyMOL Maintenance and/or Support Subscription.
Please visit http://www.pymol.org/funding.html for more information and
contact sales@pymol.org when you are ready to purchase a Subscription.

This Executable Build integrates and extends Open-Source PyMOL 1.3.
PyMOL>_
```

```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
SnglClk +/-  Cent Menu
 DblClk Menu  -   PkAt
Selecting Residues
State    1/   1
```

2. **Left click on Display on the toolbar:**
    a. **click sequence.**

3. **Left click Display again:**
    a. **sequence mode,**
    b. **residues (this will display the amino acid sequence of the proteins).**



```
PyMOL(TM) Educatio                 ght (C) 2010 Schrodinger, LLC.

Free usage of this                              time students
and their teachers                              .  All other
uses require purcha                             t Subscription.
Please visit http:/                             formation and
contact sales@pymo                              ubscription.

This Executable Bu                              yMOL 1.3.
PyMOL>
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For Educational Us
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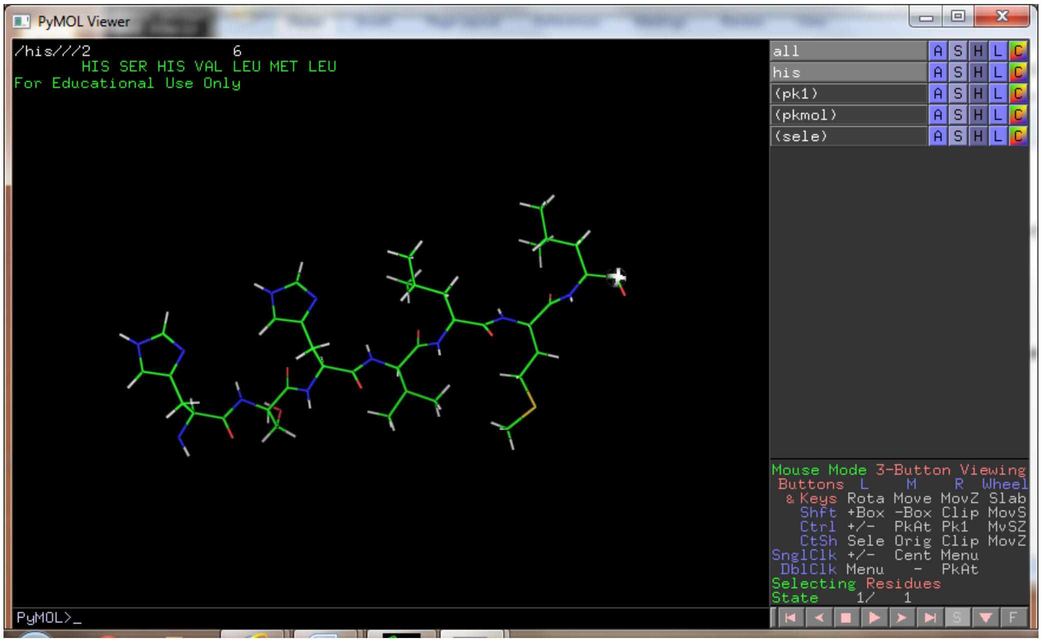
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
 SnglClk +/-  Cent Menu
  DblClk Menu  -   PkAt
Selecting Residues
State    1/   1
PyMOL>_
```

4. **To build the primary structure of the protein, use amino acids (residue codes listed in step 5).**

5. **Each amino acid has a specific letter assigned to it and a three letter code, there are 20 common amino acids:**

   A=Alanine (Ala),
   C=Cysteine (Cys),
   D=Aspartic acid (Asp),
   E=Glutamate (Glu),
   F=Phenylalanine (Phe),
   G=Glycine (Gly),
   H=Histidine (His),
   I=Isoleucine (Ile),
   K=Lysine (Lys),
   L=Leucine (Leu),
   M=Methionine (Met),
   N=Asparagine (Asn),
   P=Proline (Pro),
   Q=Glutamine (Gln),
   R=Arginine (Arg),
   S=Serine (Ser),
   T=Threonine (Thr),
   V=Valine (Val),
   W=Tryptophan (Trp),
   Y=Tyrosine (Tyr).

6. **To build the primary protein structure insert the following command in the PyMol viewer window:**
    a. **hold down the alt key (it is by the space bar),**
    b. **while holding down alt type in the following: HSHLVLML,**
        i. **the program will start to piece the amino acids together using peptide bonds,**
    c. **to view the whole protein right click on the mouse and select zoom (your screen should look like the picture below) Notice the amino acid sequence in green,**
    d. **you can use the mouse to rotate the protein (put the pointer on the protein, hold down the left mouse button, and move the mouse around on your desktop; this will rotate the protein).**



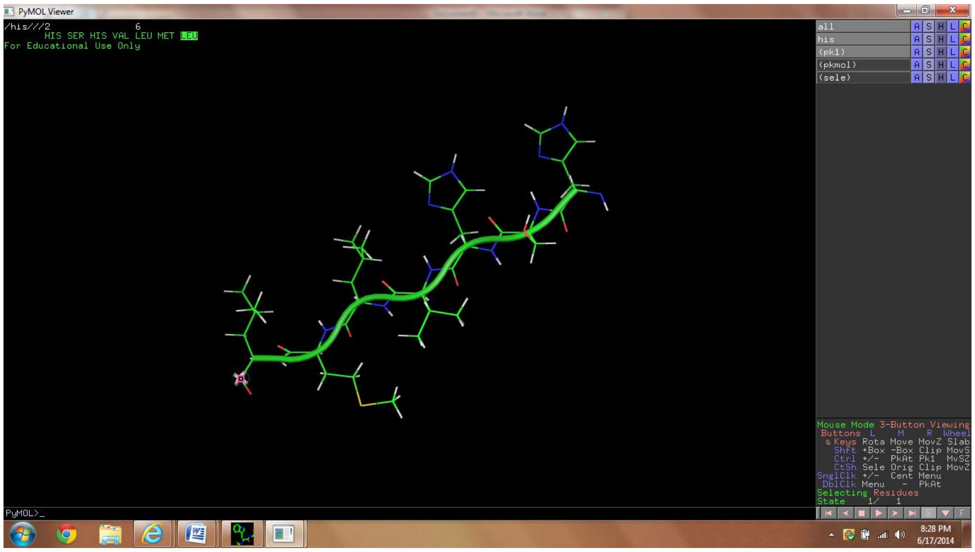
```
/his///2               6
       HIS SER HIS VAL LEU MET LEU
For Educational Use Only
```

```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
SnglClk +/-  Cent Menu
 DblClk Menu   -  PkAt
Selecting Residues
State     1/    1
```

```
PyMOL>_
```

7. **On the right side of the PyMol viewer next to the “all” click the S button and select cartoon.**

8. Next to the all click the C button (rainbow) and select color by chain (different protein chains will be different colors) and select the first option. Your screen should now look like the one below. This is the shape of a primary protein.



```
/his///2                6
      HIS SER HIS VAL LEU MET LEU
For Educational Use Only
```

```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
SnglClk +/-  Cent Menu
 DblClk Menu   -  PkAt
Selecting Residues
State    1/   1
```

```
PyMOL>_
```

9. The next three structures of proteins are large and complex. Instead of building these proteins we are going to download them from the Internet.

10. Open the Internet and go to http://www.rcsb.org/pdb/home/home.do. You are going to search for three different proteins.

11. **In the search tool bar type 2X9K and hit enter. (The picture below should be displayed on your screen).**

STRUCTURE OF A E.COLI PORIN

2X9K

DOI:10.2210/pdb2x9k/pdb

Primary Citation

Correlation between the OmpG secondary structure and its pH-dependent alterations monitored by FTIR.

Korkmaz-Ozkan, F., Koster, S., Kuhlbrandt, W., Mantele, W., Yildiz, O.

Journal: (2010) J.Mol.Biol. **401:** 56-67

PubMed: 20561532
DOI: 10.1016/j.jmb.2010.06.015
Search Related Articles in PubMed

PubMed Abstract:

The channel activity of the outer-membrane protein G (OmpG) from Escherichia coli is pH-dependent. To investigate the role of the histidine pair His231/His261 in triggering channel opening and closing, we mutated both histidines to alanines and cysteines. Fourier transform infrared... [Read More & Search PubMed Abstracts]

Molecular Description Hide

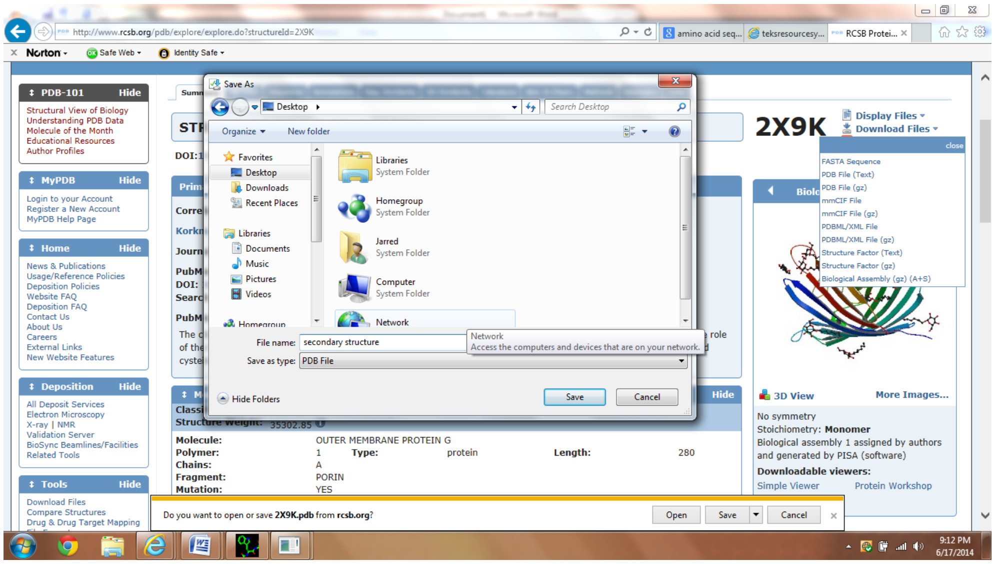
Classification: Transport Protein
Structure Weight: 35302.85

Molecule: OUTER MEMBRANE PROTEIN G
Polymer: 1 **Type:** protein **Length:** 280
Chains: A
Fragment: PORIN
Mutation: YES
Organism Escherichia coli K-12
Gene Names ompG b1319 JW1312
UniProtKB: Protein Feature View | Search PDB | P76045

No symmetry
Stoichiometry: **Monomer**
Biological assembly 1 assigned by authors and generated by PISA (software)
Downloadable viewers:
Simple Viewer Protein Workshop
Kiosk Viewer

12. On the left click download files:

- **a. select PDB file (text) left click,**
- **b. save as,**
- **c. select the desktop,**
- **d. name the file: secondary structure,**
- **e. Click save.**



File name: secondary structure

Save as type: PDB File

Do you want to open or save **2X9K.pdb** from **rcsb.org**?

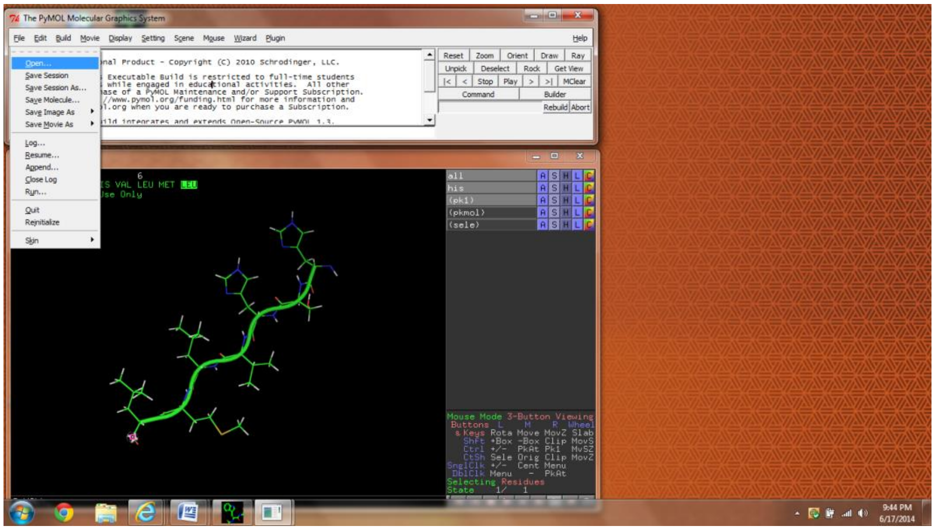
13. In the search tool bar search for 1DV5:

- **a. follow the same steps as in step 12 for downloading the file,**
- **b. name the file: tertiary structure,**
- **c. save to the desktop.**

14. Last protein to search is 1YZI:

- **a. Follow the same steps as in step 12 for downloading the file,**
- **b. Name the file: quaternary structure,**
- **c. save to the desktop.**

15. **To open up these saved files in PyMol:**
    a. **left click file,**
    b. **left click open,**
    c. **select the desktop,**
    d. **select the file to open,**
    e. **and click open.**



```
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 Executable Build is restricted to full-time students
 while engaged in educational activities.  All other
ase of a PyMOL Maintenance and/or Support Subscription.
//www.pymol.org/funding.html for more information and
l.org when you are ready to purchase a Subscription.

ild integrates and extends Open-Source PyMOL 1.3.
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             6
IS VAL LEU MET LEU
se Only
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```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    ShFt +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
 SnglClk +/-  Cent Menu
  DblClk Menu  -   PkAt
Selecting Residues
State    1/   1
```

16. **Repeat this process until all three files have been uploaded into pymol.**

17. **In the command bar type:**
    a. **set grid_mode,1 (this command should separate your proteins)**
    b. **hit "enter" on the keyboard**

18. Repeat steps 7 and 8. (Your screen should look like the one below)

```
   /primary_structure/// 2               6
                         HIS SER HIS VAL LEU MET LEU
 /Secondary_Structure//A/3           6                   11                  16                  21                  26                  31
                         ARG ASN ASP TRP HIS PHE ASN ILE GLY ALA MET TYR GLU ILE GLU ASN VAL GLU GLY TYR GLY GLU ASP MET ASP GLY LEU ALA GLU
  /Tertiary_Structure//A/2               6                   11                  16                  21                  26                  31
                         ALA ASP GLU ALA ILE LYS ASN GLY VAL LEU ASP ILE LEU ALA ASP LEU THR GLY SER ASP ASP VAL LYS LYS ASN LEU ASP LEU ASN
/quaternary_structure//A/1                   6                   11                  16                  21                  26
                         VAL LEU SER PRO ALA ASP LYS THR ASN VAL LYS ALA ALA TRP GLY LYS VAL GLY ALA HIS ALA GLY GLU TYR GLY ALA GLU ALA LEU
For Educational Use Only
PyMOL>_
```

19. To change the name of "his" to primary structure:
  a. **select the "A" by the "his" on the right side of the PyMol viewer,**
  b. **select rename object**
  c. **delete the "his" and type primary structure.**

20. To examine each protein individually:
  a. **deselect all four structures on the right (your screen should be black),**
  b. **select the structure you want to view (that structure should appear on the screen),**
  c. **click the "A" by the structure name,**
  d. **and select zoom,**
  e. **repeat for each structure.**

21. You can also examine the amino acid sequence:
  a. **use the scroll bar on top of the Pymol Viewer to view all the amino acids (residues).**

22. To see what elements are common between all proteins:
  a. **next to "all" select the "L"**
  b. **select element symobol (this displays the elements in your proteins).**

23. To save your work:

  a. **file save session as,**
  b. **select your user file,**
  c. **name the file your firstname_lastname_pymol1.**

24. Complete the protein structure worksheet.

25. Exit the program and log out of the computer

4.2 LESSON 1 WORKSHEET: PROTEIN STRUCTURE WORKSHEET

Answer the following questions in complete sentences.

1. The building blocks of proteins are ____________________?

    ____
    ____

2. What protein structure or structures are made up of only one protein chain?

    ____
    ____

3. What protein structure or structures are made up of more than one protein chain?

    ____
    ____

4. Amino acids are held together by what type of bonds?

    ____
    ____

5. Which four elements are common in all proteins?

    ____
    ____

6. Compare and contrast the four different structures of proteins, using a Venn Diagram, on the back of the worksheet.

4.3 LESSON 2: USING PYMOL TO THREE-DIMENSIONALLY REPRESENT DNA

TEKS addressed:
B 6.A: Identify components of DNA, and describe how information for specifying traits of an organism is carried in DNA.
B 9.A: Compare the structures and functions of different types of biomolecules including carbohydrates, lipids, proteins, and nucleic acids.
B 9.D: Analyze and evaluate the evidence regarding formation of simple organic molecules and their organization into long complex molecules having information such as the DNA molecule for self-replicating life.

1. **Open up PyMol + Tcl-Tk GUI + Console icon on your desktop (the two windows below should pop up on your desktop).**

2. **Open up the internet and go to http://www.rcsb.org/pdb/home/home.do. You are going to search for 2L8Q.**

3. **On the left click download files:**
    a. **select PDB file (text) left click,**
    b. **save as,**
    c. **select the desktop,**
    d. **name the file: DNA,**
    e. **Click save.**

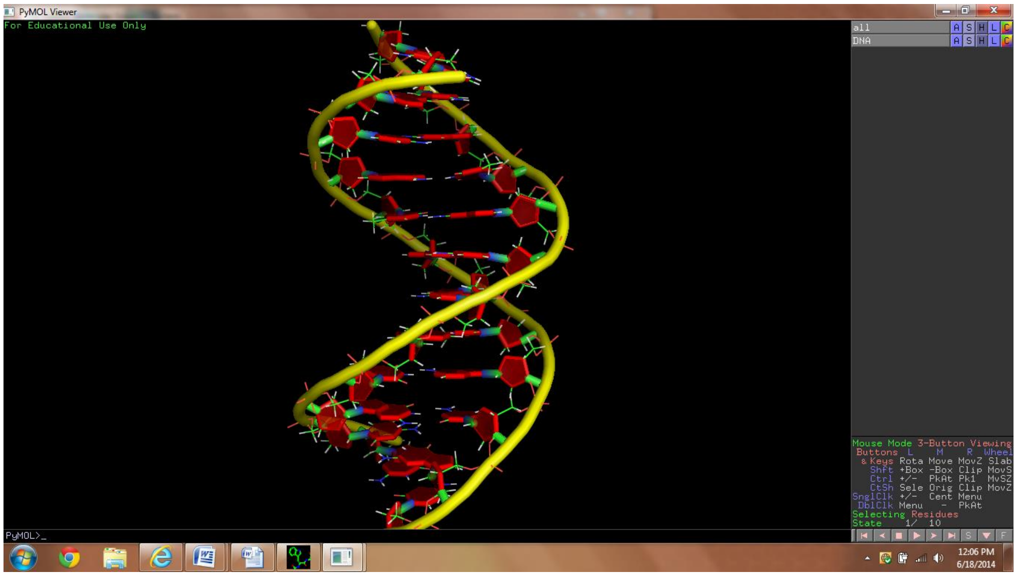
4. **To open up the file in PyMol:**
    a. **left click file,**
    b. **left click open,**
    c. **select the desktop,**
    d. **select the file to open,**
    e. **and click open.**

5. **On the right side next to all left click "S":**
    a. **select cartoon.**

6. **In the command bar (PyMol >) type the following commands (after each command hit "enter" on the keyboard):**
    a. **set cartoon_nucleic_acid_color, yellow**
    b. **set cartoon_ring_mode, 1**
    c. **set cartoon_ring_color, red**

d. set cartoon_ring_transparency, 0.5
e. set cartoon_oval_length, 1.6
f. set cartoon_oval_width, 0.8
g. set cartoon_ring_width, 0.5

7. Your DNA molecule should like the one pictured below:



```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
SnglClk +/-  Cent Menu
 DblClk Menu   -  PkAt
Selecting Residues
State    1/  10
```

8. Hold down the left mouse button while on the DNA molecule:
a. moving the mouse moves the molecule

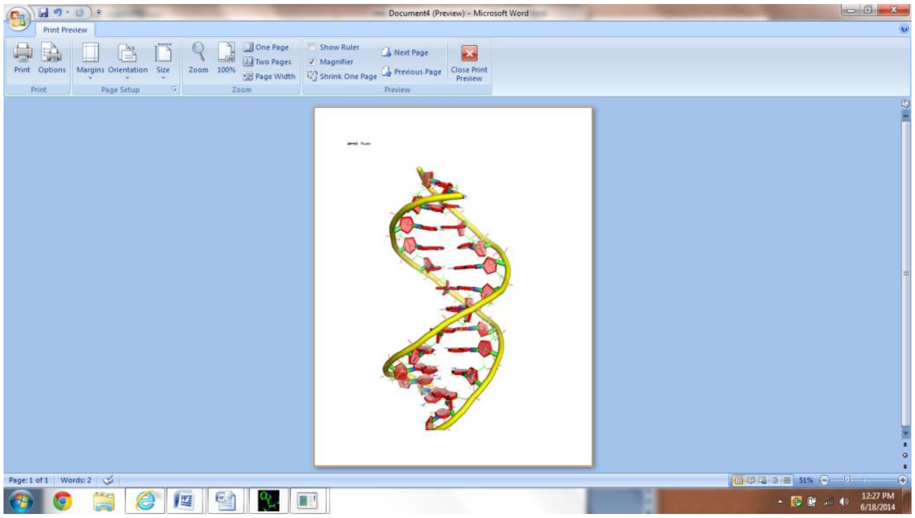
9. Left click "Display":
a. scroll down to background,
b. left click "white".

10. Left click "Edit":
a. left click "Copy Image to Clipboard".

11. Open up Microsoft Word on your desktop:
   - **a. type your name on the page,**
   - **b. hit enter,**
   - **c. right click on the page,**
   - **d. left click “Paste”.**

12. Right click on the DNA molecule in your word document:
   - **a. scroll down to “Text Wrapping”,**
   - **b. left click “Behind Text”.**

13. Select your DNA molecule and resize it using the squares located on the outside. (Make sure not to distort your image, and make sure your DNA fits on one page. Your document should look something like the one down below.)



14. Print your document.

15. Draw arrows to and label on your printed DNA document the following information:
   - **a. Phosphate backbone**
   - **b. Nitrogen Bases**
   - **c. Deoxyribose sugar**
   - **d. Hydrogen bonds**

4.4 LESSON 3: USING PYMOL TO THREE-DIMENSIONALLY REPRESENT DNA

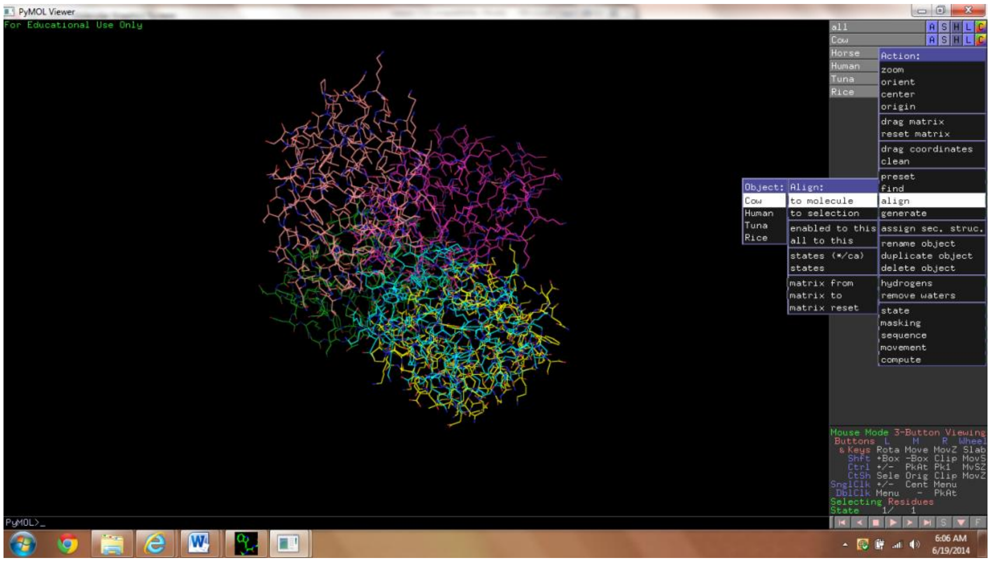
TEKS addressed:
B 6.A: Identify components of DNA, and describe how information for specifying traits of an organism is carried in DNA.
B 6.B: Recognize that components that make up the genetic code are common to all organisms.
B 6.D: Identify and illustrate changes in DNA and evaluate the significance of these changes.
B 6.E: Identify and illustrate changes in DNA and evaluate the significance of these changes.
B 7.A: Analyze and evaluate how evidence of common ancestry among groups is provided by the fossil record, biogeography, and homologies, including anatomical, molecular, and developmental.
B 7.C: Analyze and evaluate scientific explanations concerning any data of sudden appearance, stasis, and sequential nature of groups in the fossil record.
B 7.F: Analyze and evaluate the effects of other evolutionary mechanisms, including genetic drift, gene flow, mutation, and recombination
B 9.A: Compare the structures and functions of different types of biomolecules including carbohydrates, lipids, proteins, and nucleic acids.
B 9.D: Analyze and evaluate the evidence regarding formation of simple organic molecules and their organization into long complex molecules having information such as the DNA molecule for self-replicating life.
Background: Cytochrome C is a protein, located in the mitochondria, and plays a vital role in ATP synthesis. This protein can be found in all eukaryotes; and over time, random mutations in the DNA sequence occur. These mutations resulted in a change in the amino acid sequence.
PURPOSE: To compare the relatedness between organisms by examining the amino acid sequence in the protein, Cytochrome C.

1. **Open up PyMol + Tcl-Tk GUI + Console icon on your desktop (the two windows below should pop up on your desktop).**

2. **Open up 5 proteins loaded on your desktop (preloaded):**
   a. **cow**
   b. **horse**
   c. **human**
   d. **tuna**
   e. **and rice.**

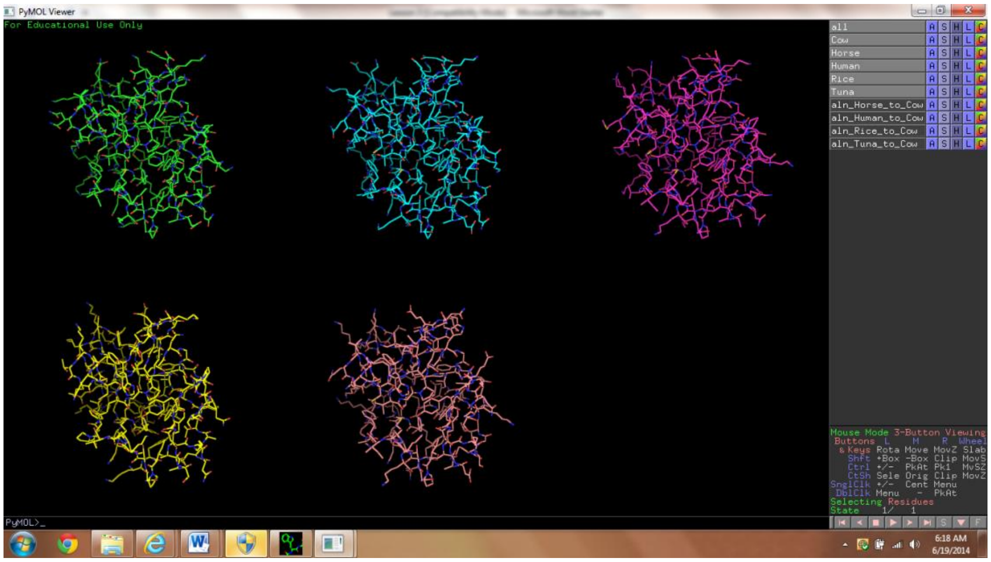
3. **To open up the file in PyMol:**
    1. **left click file,**
    2. **left click open,**
    3. **select the desktop,**
    4. **select the file to open,**
    5. **and click open.**

4. **Align each protein to the cow molecule:**
    1. **by horse click the “A”,**
    2. **scroll down to align,**
    3. **to molecule,**
    4. **and left click cow.**



5. **Repeat the same step for the following proteins:**
    1. **human,**
    2. **tuna,**
    3. **and rice.**

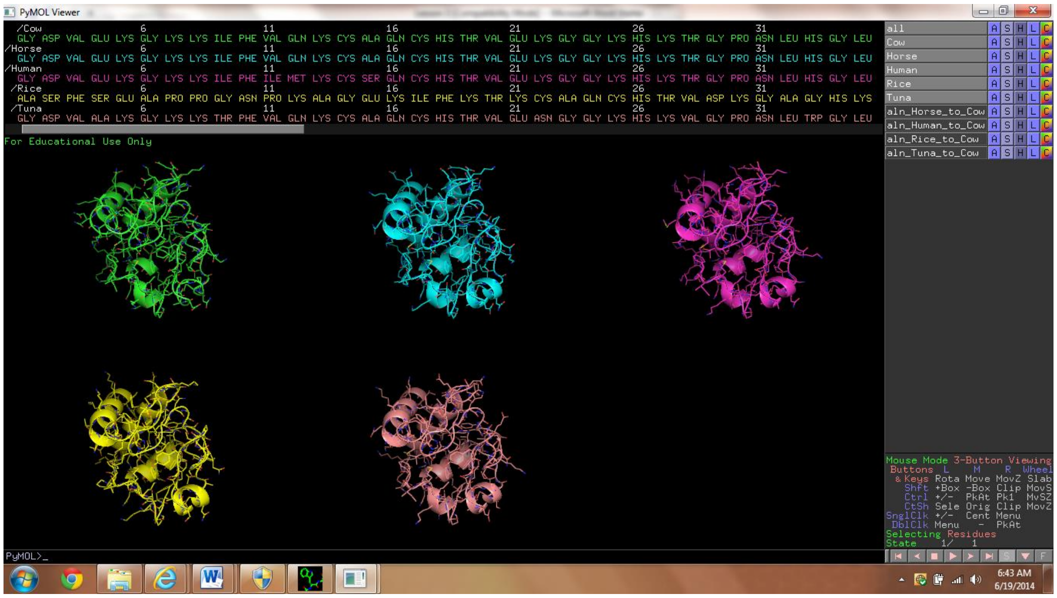
6. **All proteins should be aligned (notice the very similar structure):**
    a. **enter the command: set grid_mode, 1(hit the "enter" key on the keyboard). (This will keep the proteins aligned, but moves them off of each other, see picture below).**



7. **Next to "all" left click "S":**
    a. **scroll down to cartoon and left click.**

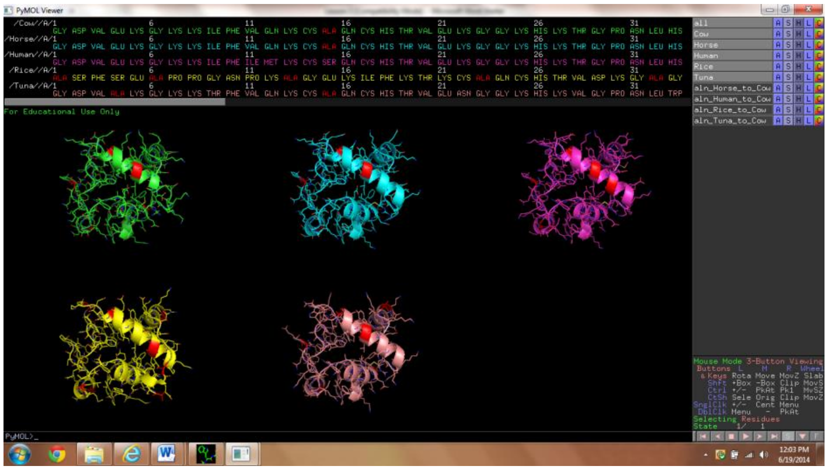
8. **Select Display:**
    a. **scroll down to sequence mode,**
    b. **select residue code.**

9. **Select Display again:**
    a. **left click sequence (this displays the amino acid sequence for each protein along the top of the PyMol Viewer). You may need to use the horizontal scroll bar to see all the amino acids. See picture below.**



```
 /Cow                6                   11                  16                  21                  26                  31
 GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS GLY LEU
/Horse               6                   11                  16                  21                  26                  31
 GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS GLY LEU
/Human               6                   11                  16                  21                  26                  31
 GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE ILE MET LYS CYS SER GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS GLY LEU
 /Rice               6                   11                  16                  21                  26                  31
 ALA SER PHE SER GLU ALA PRO PRO GLY ASN PRO LYS ALA GLY GLU LYS ILE PHE LYS THR LYS CYS ALA GLN CYS HIS THR VAL ASP LYS GLY ALA GLY HIS LYS
 /Tuna               6                   11                  16                  21                  26                  31
 GLY ASP VAL ALA LYS GLY LYS LYS THR PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU ASN GLY GLY LYS HIS LYS VAL GLY PRO ASN LEU TRP GLY LEU
For Educational Use Only
```

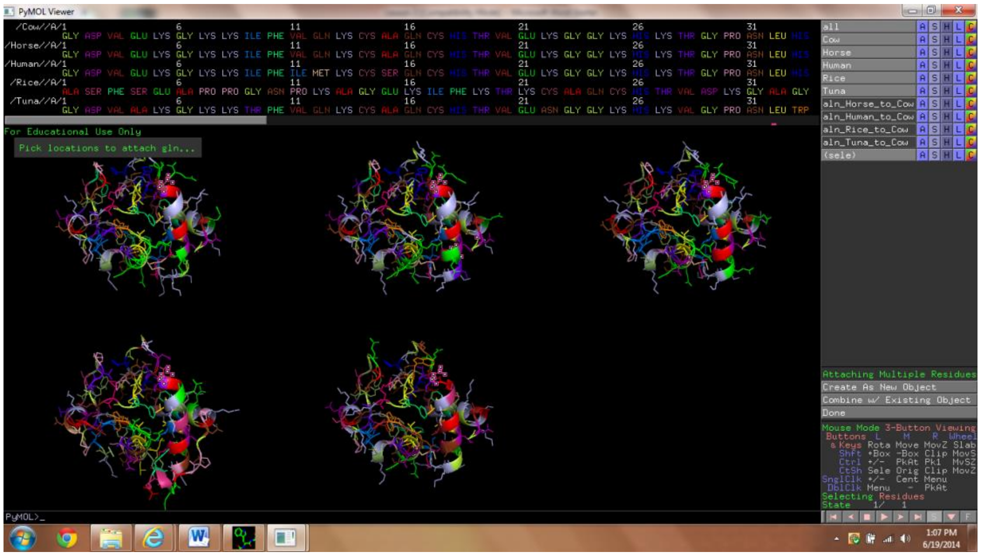
10. **Next color different amino acids (residues) different colors:**
    a. **type the command:**
        i. **color red,////Ala (hit the "enter" key on the keyboard. Notice how all the alanine amino acids are colored in each protein and colored above in the amino acid chain, see picture below).**



```
 /Cow//A/1           6                   11                  16                  21                  26                  31
     GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
/Horse//A/1          6                   11                  16                  21                  26                  31
     GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
/Human//A/1          6                   11                  16                  21                  26                  31
     GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE ILE MET LYS CYS SER GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
 /Rice//A/1          6                   11                  16                  21                  26                  31
     ALA SER PHE SER GLU ALA PRO PRO GLY ASN PRO LYS ALA GLY GLU LYS ILE PHE LYS THR LYS CYS ALA GLN CYS HIS THR VAL ASP LYS GLY ALA GLY
 /Tuna//A/1          6                   11                  16                  21                  26                  31
     GLY ASP VAL ALA LYS GLY LYS LYS THR PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU ASN GLY GLY LYS HIS LYS VAL GLY PRO ASN LEU TRP
For Educational Use Only
```

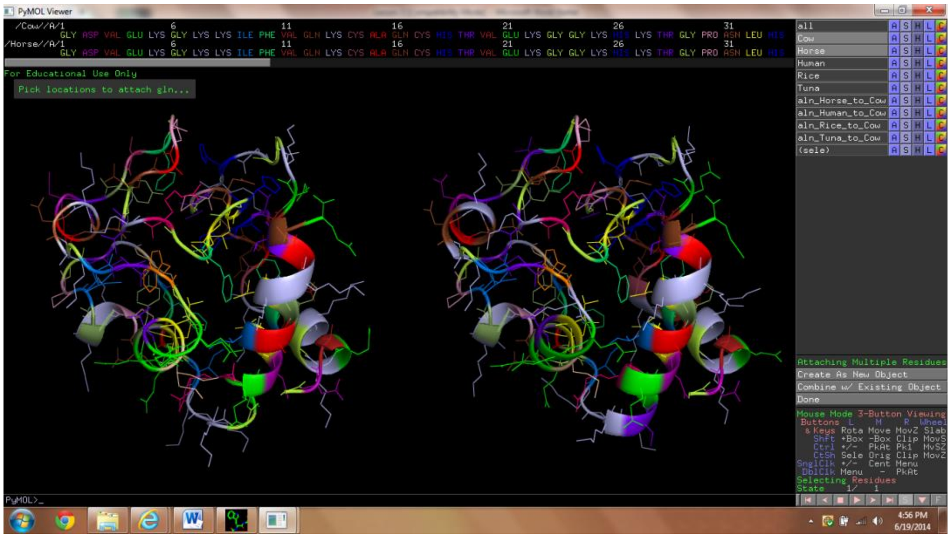
11. Finish coloring the rest of the amino acids:

- **a. type the following commands and hit “enter” on the keyboard after each line; notice the PyMol Viewer when the codes are entered):**
    - **i. color raspberry,////Cys**
    - **ii. color brown,////Asn**
    - **iii. color green,////Glu**
    - **iv. color limegreen,////Phe**
    - **v. color limon,////Gly**
    - **vi. color blue,////His**
    - **vii. color marine,////Ile**
    - **viii. color lightblue,////Lys**
    - **ix. color yellow,////Leu**
    - **x. color wheat,////Met**
    - **xi. color purple,////Asp**
    - **xii. color pink,////Pro**
    - **xiii. color hotpink,////Arg**
    - **xiv. color warmpink,////Ser**
    - **xv. color purpleblue,////Thr**
    - **xvi. color firebrick,////Val**
    - **xvii. color orange,////Trp**
    - **xviii. color chocolate,////Gln**
    - **xix. color smudge,////Tyr.**
- **b. Your screen should now have each type of amino acid a different color like the image below.**



```
 /Cow//A/1          6                   11                  16                  21                  26                  31
          GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
/Horse//A/1         6                   11                  16                  21                  26                  31
          GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
/Human//A/1         6                   11                  16                  21                  26                  31
          GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE ILE MET LYS CYS SER GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
 /Rice//A/1         6                   11                  16                  21                  26                  31
          ALA SER PHE SER GLU ALA PRO PRO GLY ASN PRO LYS ALA GLY GLU LYS ILE PHE LYS THR LYS CYS ALA GLN CYS HIS THR VAL ASP LYS GLY ALA GLY
 /Tuna//A/1         6                   11                  16                  21                  26                  31
          GLY ASP VAL ALA LYS GLY LYS LYS THR PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU ASN GLY GLY LYS HIS LYS VAL GLY PRO ASN LEU TRP
For Educational Use Only
  Pick locations to attach gln...
PyMOL>_
```

12. **To compare proteins side by side:**
    a. **left click all until everything on the screen turns black,**
    b. **left click the two proteins you want to compare,**
    c. **repeat steps a and b to compare all proteins side by side and see the similarities and differences of the same protein in different organisms (see picture below).**



```
 /Cow//A/1                    6                   11                  16                  21                  26                  31
          GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
/Horse//A/1                   6                   11                  16                  21                  26                  31
          GLY ASP VAL GLU LYS GLY LYS LYS ILE PHE VAL GLN LYS CYS ALA GLN CYS HIS THR VAL GLU LYS GLY GLY LYS HIS LYS THR GLY PRO ASN LEU HIS
For Educational Use Only
  Pick locations to attach gln...
```

```
Mouse Mode 3-Button Viewing
 Buttons  L    M    R  Wheel
  & Keys Rota Move MovZ Slab
    Shft +Box -Box Clip MovS
    Ctrl +/-  PkAt Pk1  MvSZ
    CtSh Sele Orig Clip MovZ
SnglClk +/-  Cent Menu
 DblClk Menu  -   PkAt
Selecting Residues
State    1/   1
```

```
PyMOL>_
```

13. **To move the proteins and compare the entire structure:**
    a. **place the mouse pointer on a protein,**
    b. **hold down the left mouse button,**
    c. **move the mouse (this rotates both proteins, remember they are aligned).**

14. **Look at the entire amino acid sequence on the top of the viewer:**
    a. **use the color coding (vertically) to identify the differences between the amino acid sequence within the proteins**

15. **Complete the following worksheet.**

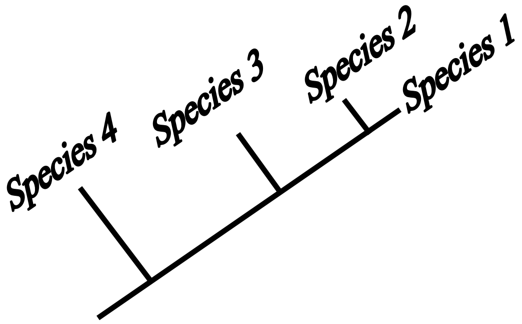
4.5 LESSON 3 WORKSHEET: CYTOCHROME C COMPARISON WORKSHEET

1. **Complete the table by listing the total number of differences between the amino acid sequence in Cytochrome C for five species.**

	Cow	**Horse**	**Human**	**Rice**	**Tuna**
Cow	**0**				
Horse	■	**0**			
Human	■	■	**0**		
Rice	■	■	■	**0**	
Tuna	■	■	■	■	**0**

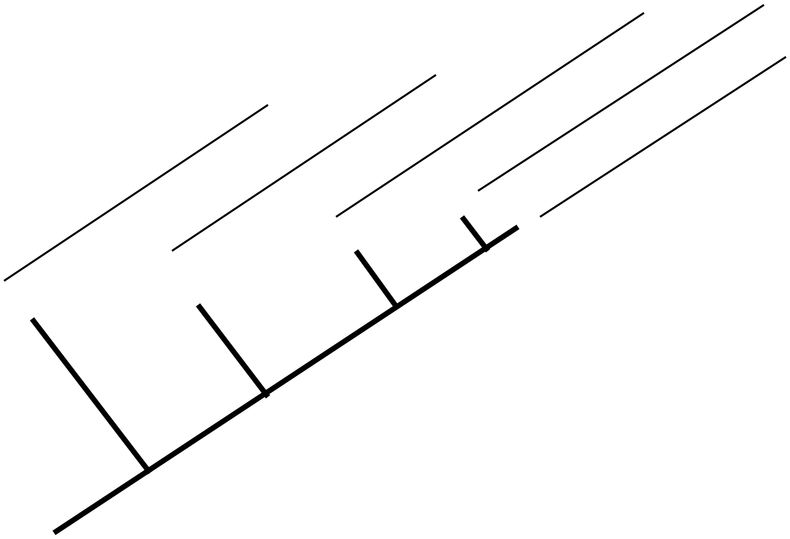
2. **Fill in the cladogram using the data in the table and the following directions (a-c):**
    a. **The two most closely related species have the fewest differences in their amino acid sequence. Place the two most closely related species on the two shortest branches of the tree.**

    b. **Place the next to closest species on the next shortest branches.**



    c. **Continue until all the species have been placed on the cladogram.**

d. Now fill in the blank cladogram with your following species.



3. **If two organisms have similar amino acid sequences, do you think they will have similar DNA? Explain your answer in complete sentences.**

4. **Other proteins can be used to determine the relatedness of two organisms. Would you expect to find around the same number of differences in the amino acid sequences when comparing these organisms? Explain your answer in complete sentences.**

Chapter 5: Conclusion

This report pays tribute to my time within the UTeach Engineering program. I entered the program with no knowledge of Engineering Education, but within two years and support of staff and students, I have grown within my profession. I have championed the benefits of a high school engineering program, but because of budget cuts and lack of personnel this class has not yet been possible.

Being a part of Cohort four has been a highlight in my educational career. We might not always see eye to eye on some issues, but always respected and valued each other's opinions and viewpoints. I have learned as much from my classmates, as I have the instructors. The summers spent in Austin have led to the development of lasting friendships and a professional learning community with the same passion for engineering education as me.

Along with building a PLC with my classmates, I have also established a strong working connection with instructors at the University of Texas in Austin, who will always be there to answer questions and provide guidance as I promote engineering education. They have provided evidence to support the benefits of engineering education for primary and secondary students. Each instructor has contributed to the shaping, inspiring, and developing of my teaching career.

I came into the program believing that engineering concepts cannot be taught without an engineering class, but through this process have learned that engineering can be incorporate in any class. Using engineering concepts keeps students engaged and increases student's retention of content. Through writing this report, I realize that planning is the most important aspect to when including engineering concepts in the classroom. Although I am not teaching Biology this upcoming school year, I am looking forward to brainstorming ways to incorporate engineering concepts into my chemistry classroom, while promoting engineering education.

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The PyMOL Molecular Graphics System, Version 1.2r3pre, Schrödinger, LLC.

Vita

Jarred Nusz is the son of Lorree Nusz. He currently lives in Amarillo, Texas and teaches in Dumas, Texas. He has been teaching chemistry for six years and in the 2013-2014 school year added biology to his repertoire. He was awarded a Bachelors of Science in Biology, graduating Magna Cum Laude, from Oklahoma Panhandle State University in 2005. He will complete his Masters of Arts in STEM Education at the University of Texas at Austin in the summer of 2014.

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This report was typed by Jarred Nusz.