Undergraduate Research Symposium
ADVANCING RESEARCH AND STEM FIELD ENGAGEMENT
PROJECT 13

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Felician University, Class of 2020
Majors: **Biology/Education**
Minor: **K-12**

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Using Molecular Visualization to Explore Enzyme Structure and Function

Open educational resources (OER) computer-based programs such as Chimera, a protein analysis software, and MarvinSketch, an advanced chemical editor for drawing chemical structures, were used to predict the structure and function of Tyrosinase. With the use of these databases and computational tools, the molecular visualization of the structure was thoroughly investigated. Following the model developed by Terrell and Listenberger (2017), a five-step assignment project was completed to determine if future use of databases and computational tools as substitutes for the laboratory experience, would benefit students in biochemistry courses at Felician University. The object of the original study was to provide evidence to support the hypothesis that through visualization of the structure and function of the Prostaglandin H2 Synthase, students would be able to comprehend the complex structure and function of the enzyme in a virtual setting (Jaswal, *et.al*, 2013). Students should also be able to "propose an active site point mutation that will alter the effectiveness of their inhibitor binding while retaining catalytic activity" (Terrell & Listenberger, pg. 4).

In order to assess the possible implementation of this model at Felician University, Tyrosinase was used as the test enzyme. Tyrosinase is found in the melanocytes, which is a mature melanin-forming cell, found in skin cells (Kumar, *et.al*, 2011). The enzyme also aids in the production of pigment called melanin. Melanin gives skin, hair, and eyes the color shown and is also found in the retina where it has a major role in normal vision. Tyrosine is the building block amino acid to make the compound dopaquinone, which is chemically converted into melanin. After completing this project, which analyzed and studied the structure and function of Tyrosinase, a model active site as well as an inhibitor was tested to investigate catalytic activity or inhibition.

REFERENCES

Terrell, C. R., & Listenberger, L. L. (2017). Using molecular visualization to explore protein structure and function and enhance student facility with computational tools. Biochemistry and Molecular Biology Education, 45(4), 318-328. doi:10.1002/bmb.21040

Jaswal, S. S., O'Hara, P. B., Williamson, P. L., Springer, A. L. (2013). Teaching structure: Student use of software tools for understanding macromolecular structure in an undergraduate biochemistry course. Biochem. Mol. Biol. Educ. 41, 351–359.

Kumar CM, Sathisha UV, Dharmesh S, Rao AG, Singh SA (2011). "Interaction of sesamol (3,4-methylenedioxyphenol) with tyrosinase and its effect on melanin synthesis". *Biochimie*. **93** (3): 562–9. doi:10.1016/j.biochi.2010.11.014

http://www.rbvi.ucsf.edu/chimera

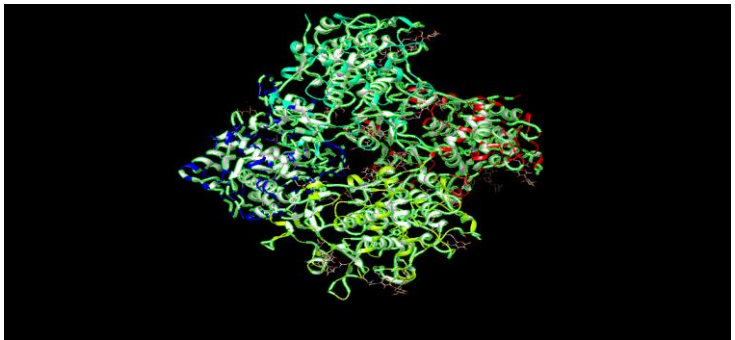
Using Molecular Visualization to Explore Protein Structure and Function with Computational Tools in Biochemistry Courses

By: Stephanie Donah
Professor: Alfredo Castro

Assignment 1: Primary Sequence Analysis

Create a protein sequence and analyze the primary sequence of the protein.

Predicted the regions or residues that are significant to structure and function.



Assignment 2: Review of Protein Structure

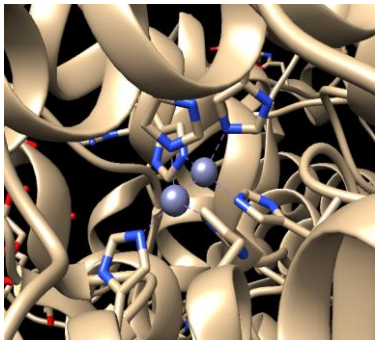
Built off the primary sequence to secondary, tertiary, and quaternary structures. Used simple structure to learn manipulation of molecules in UCSF Chimera. Analyzed the structure: protein structure and noncovalent interactions

Pictured right: The structure of tyrosinase and its four main chains. The parts that appear white are leucine.

Assignment 3

Manipulated a virtual model of TYRP1 to distinguish and interpret the secondary, tertiary, and quaternary structure.

Predicted the location of where an enzyme would associate. Histidine is located around the ZN molecules where a strong bond is holding this “pocket” together.



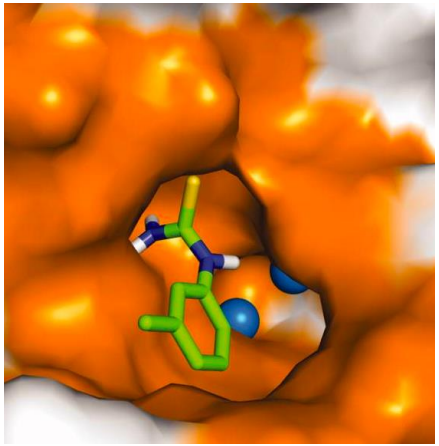
Pictured: Possible location where an enzyme would associate.

Assignment 4

Designed an inhibitor based on prior knowledge.

Prepared the enzyme before “docking” using Dock Prep, then analyzed the “docking” of an enzyme.

Observed the energy for the binding of the substrate.



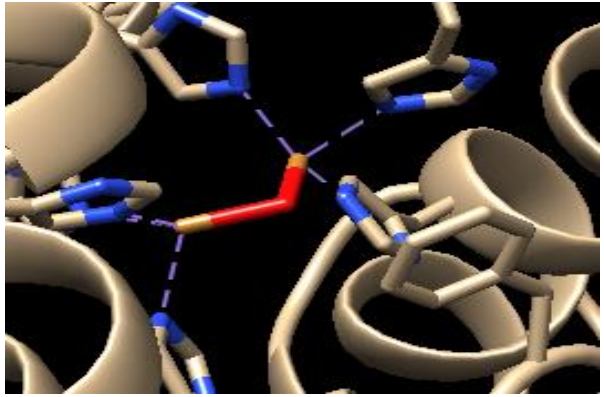
Pictured right: The docking of **Hydroquinone 24d** is shown with the two copper ions (blue spheres) and the binding pocket of tyrosinase.

Assignment 5

Introduced to catechol oxidase, a related enzyme.

Used Chimera for point mutation, propose an active site for new mutation

Pictured below: Catechol oxidase active site.



Conclusion

Tyrosine is the building block amino acid to make the compound dopaquinone, which is chemically converted into melanin.
After completing this project, which analyzed and studied the structure and function of Tyrosinase, a model active site as well as an inhibitor was tested to investigate catalytic activity or inhibition.

Bibliography

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