

Research Opportunities

You're probably not in the most fun and rewarding part of science just yet. See, nobody goes into science because they want to sit in a classroom and learn about what other people did; they go into science because they want to do science, which means, research!!

Now, ordinarily, research is reserved for graduate students and a very few select upper level undergraduate seniors, but here at DSU, you have an opportunity to engage in independent research projects before you get into graduate school!

So what's in it for you, you ask? Well, aside from the pure exhilaration of research (believe me, you don't know what an adrenalin rush is until you realize that you are the first one to ever figure something out), there are great benefits (no, not financial, at least not yet) to research. First, it looks FANTASTIC on a resume to speak of your research project. It is amazing how potential employers tend to look past all of the schooling, and instead focus on independent research. Second, there is the real possibility of getting a paper out of it. While at DSU, I've co published an article with one DSU undergraduate so far, and this year I expect my second. Finally, if you are a physical science major, any research you do can be "morphed" into a capstone project, so by your senior year, you are finished with the capstone and only have to write the paper.

Now, having said that, let me clue you in on some of my research interests. If you find you are curious or interested in any of these, please let me know. I'll highlight the type of work any given project could include.

DNA Sequence Specific Binders: A number of years ago I was sitting in a seminar while a biochemist explained his hypothesis on DNA sequence specific binders. He was working with Distamycin, an anti-tumor drug that binds in the minor groove of DNA but only to the sequence AAATT (don't worry if you don't understand some of the details here; if you find you are interested in this project, you will learn). The question becomes; how does the molecule "find" the sequence it binds to? I didn't believe his explanation, so I started to look into it. I believe I found the answer, but the model needs some serious work to "clean it up" before publication.

This project needs either **math modeling** or **computer programming (non-graphical)** work.

Hydrogen Bonding: The reason I didn't believe the explanation on DNA Sequence Specific Binders is because it relied on the concept of the "bifurcated hydrogen bond," which I do not believe can exist. This led me to look into what is known of the incredibly important intermolecular force, only to discover that the nature of the hydrogen bond, as important as it is, is still not well understood. Thus, in this research project I want to run high level quantum mechanical calculations (don't worry, we'll start with just running programs; you can do it if you are interested) in an attempt to elucidate the nature of this intermolecular force.

This project needs **computer application execution** to succeed. The program exists, but it needs to be set up and run a number of times with a number of parameter changes.

Protein Folding Self Avoiding Walk Model: This is an old project that will almost certainly lead to a publication for anybody willing to spend the time and effort on it. The question of protein folding is of critical physiological importance; a protein can be thought of as a long chain. It is a straight molecule, ranging from several hundred to several hundred thousand atoms in length. For the protein to function properly, it must be properly “folded”, so unlike a random chain, every protein is folded in exactly the same manner as every other protein. The question is, how does the protein “know” how to fold? The self-avoiding walk model is a very simplified model to help demonstrate the basic principles of protein folding, but in my last paper on the topic, I showed a fairly important shortcoming in the model. The model can be simply modified to overcome this problem.

This project needs **computer programming (non-graphical)** and time.

Teaching Protein Folding Concepts through the Self Avoiding Walk Model: The self-avoiding walk model is a very simple model conceptually and demonstrates the critical components that leads to a properly folded protein. It struck me that this might be a useful tool in courses such as biochemistry where the concepts of protein folding are often taught, but, a lot of work has to be done to make it user friendly. This means a GUI interface and a graphical output.

This project needs **computer programming (graphical)**.

Pivot Minimization Algorithm, Lennard Jones Clusters: Finding the global minimum of a multiple minima function is of great importance in many fields. We are talking about finding the optimum solution, so there are applications in economy, business, the military and science just to name a few. A brainstorm a few years ago lead to a new approach to finding this global minimum, an approach that seems to be anywhere from two to five times faster than the current methods. This means less computing time on more complicated problems. The initial project on test functions is coming to a close, and we are ready to try our first realistic model, the Lennard Jones clusters. This will almost certainly lead to a publication.

This project requires **some computer programming (non-graphical)** and **computer application execution**.