Welcome to the 2010 edition of Binghamton's Biochemistry newsletter!

This newsletter was compiled by the dedicated members of the Biochemistry Advisory Board, or BCAB. I have to thank the contributors and especially the editor, Kalle Yee, for putting this newsletter together. This issue includes some of the latest research being done by professors, research done by Biochemistry majors, career options that the Biochemistry degree can lead to, and alumni profiles.

Under the leadership of Emma Schweizer, the current president, the BCAB has regained its SA charter and is continuing to expand its activities. The members of the BCAB invited a speaker, Daniel Brazeau from the University of Buffalo, to talk about opportunities for graduate study in pharmacy and pharmaceutical science. In addition, they have been fundraising and holding information sessions on getting involved in research, both at Binghamton and at other universities. They have also organized fun activities, including a model-building competition and a soccer match against the Chemistry Club.

We are always trying to enhance the Biochemistry experience for our students. Maura Loew, our Assistant to the Director, has been focusing on improving career advising for students. If you are an alumnus and are willing to talk with us about what path your career has taken, please get in touch with Maura! Her e-mail address is mloew1@binghamton.edu. We could feature your story in our next newsletter, put you in touch with current undergraduate students, or even have you come back to your alma mater and talk about your experiences. Whatever amount of time you're willing to give to us, we will certainly benefit from it!

If you are a current student, we encourage you to take advantage of the resources that the biochemistry program has to offer. Some students don't realize how important it is to get experience in their undergraduate years. Whether your plans after graduation are to go to graduate school, medical school, or to start working, you will only further your prospects by getting hands-on experience. In an internship or research experience, you will get a chance to experience a career field to see if it is something that you enjoy. For more career-related information, visit http://biochem.binghamton.edu/opportunities.html or e-mail Maura at mloew1@binghamton.edu.

As the number of Biochemistry students continues to grow, we try to accommodate the needs and further the interests of students. There were 100 or less Biochemistry majors prior to 2005; but this fall, we had 137! We wish the best to the 42 Biochemistry majors graduating this May on their future endeavors! Congratulations!

I hope you enjoy the newsletter, and thanks for reading!

Susan Bane
Biochemistry Program Director
Chemical synthesis of carbohydrates as ligands for cellular and protein interactions

Carbohydrates are the third major bio-polymers in the nature, after proteins and nucleic acids. While, they are most well known as energy sources (such as starch in food) and structural materials (such as cellulose in wood and cotton), carbohydrates also play many important roles in biological processes that are not well understood. One of the major forms of carbohydrates in living organisms is the glycoconjugates, such as glycoproteins and glycolipids, expressed on the cell or virus surfaces. These surface carbohydrate structures are responsible for the interactions between cells, and play pivotal roles in processes like cell adhesion, cell-cell recognition, signal transduction, antibody-antigen interaction and pathogenesis of bacteria and virus. For example, the influenza virus infects human cells through interactions between the viral surface protein called hemagglutinin and a carbohydrate epitope called sialic acid on human cell surfaces. Similar processes are also found in other disease causing pathogens and tumor metastasis. Understanding the role and function of carbohydrates in these processes will help understand the mechanism of the diseases and develop new therapeutic and diagnostic methods.

High-mannose type oligosaccharides are expressed on the glycoprotein (gp120) of HIV (human immunodeficiency virus). Glycoprotein gp120 is the surface protein of HIV that is responsible for the binding with the CD4 white cells and consequent AIDS (acquired immunodeficiency syndrome) symptoms. Specific binding of these high-mannose type oligosaccharides can inhibit the activity of HIV virus. Study of the interaction of these oligosaccharides (like Man9) is therefore critical for the development of new anti-HIV therapies. However, these oligosaccharide compounds are very difficult to obtain from natural sources due to the low concentration and difficulty of isolation and purification. Chemical synthesis is currently one of the most important ways to obtain homogeneous carbohydrate molecules, but the chemical synthesis of oligosaccharides, especially compounds like the high mannose type oligosaccharides with heavily branched structures, is also very challenging. The objective of our research is to develop highly efficient synthetic methods for the synthesis of branched oligosaccharide like Man9 molecules. The approach we are taking is to synthesize these molecules with minimum protection through regioselective glycosylation reactions. Compared to traditional methods, this new method is much faster, more efficient and less time and labor consuming. We have also established a theoretical model that can help us predict the regioselectivity of the diol acceptors. The Man9 molecule and its derivatives will be synthesized and used for the screening of new anti-HIV proteins and antibodies.

Figure 1. Structure of HIV

Figure 2. Chemical Synthesis of Man9
How cells respond to stress is a fundamental question that underlies many facets in medical science, cell biology and biochemistry. For instance, most of the chemotoxic compounds as well as internal and external radiation approaches to treat cancer kill cancer cells due to the activation of a number of cell stress pathways. In some select cases where mutant cancer cells over-produce cell stress protective mechanisms, the cancer is very difficult if not nearly impossible to treat effectively. Our translational research focuses in two very different areas of fundamental medical importance that rely on understanding and manipulating cell stress pathways.

One area constitutes the general area of cell bioprocessing – the ability to manipulate cells so that they can be used, for instance, to effectively treat disease states. The cell bioprocessing field is now growing at a very fast rate due, in part, to select cell types being used as “factories” to produce monoclonal antibodies now in clinical trials to treat a variety of cancers. Some experts estimate that the cell bioprocessing industry is now valued at $30B+ worldwide. Cell bioprocessing also includes manipulating fragile stem cells so that they can be used in cell therapy and tissue engineering with the latter being the fabrication of lab grown, 3-D tissue facsimiles that might be used as implants. For instance, stem cells can now be harvested from fat tissue through standard liposuction, differentiated in a laboratory cell culture dish to pancreatic islets that secrete insulin, and then re-introduced into the same diabetic patient as an effective treatment regime with the hope that this diabetic patient would be free of insulin injections. In the above cell bioprocessing examples, cells are subjected to a great deal of stress that often culminates in cell death which, in turn, limits the utility and effectiveness of the application. Much of the work that we do is focused on analyzing and investigating these cell stress pathways with the hope that once manipulated, the information gathered will lead to more productive cell bioprocessing. This type of approach demands the use of cell and molecular biology techniques including fluorescence assays, western blots, flow cytometry, and cDNA microarrays as well as standard microscopy techniques such as fluorescence microscopy and confocal imaging.

Our second area that focuses on cell stress is the cryoablation of cancers. In this regard once again, we study the cell stress pathways activated in freezing tumors so that we can develop “cryoadjuvants” - agents that increase the lethal or killing power of freezing. Over the past several years we have published a variety of papers indicating that standard chemotherapeutic compounds such as cisplatin and 5-FU can serve as effective cryoadjuvants. More recently, however, we have discovered that select, naturally occurring compounds that are not considered chemotherapeutic compounds can have similar effects when combined with freezing. Yet when used alone, these compounds are not toxic to cancer or normal cells. Studies are underway now to understand their molecular mechanisms of action.

In summary, our laboratory focuses on suppressing the cell stress pathways so that once these molecular cascades are controlled, a variety of cell bioprocessing procedures can be optimized. On the other hand, we also try to understand how to best activate the same cell stress pathways so that more effective cryoablation paradigms can be developed for treating cancer. Our research is supported primarily by the National Institutes of Health and to some extent biotechnology contracts related to both of these areas.
Most of my work thus far has focused on the mobilization of storage proteins during seed germination. My approach has been to 1) characterize the products of the proteolysis seed proteins in these plants, and 2) to characterize the enzymes responsible for these degradative steps. An example of this approach is our work on the degradation of the major storage proteins of the soybean (*Glycine max*), glycinin and β-conglycinin (βCG), as well as to the proteases involved. βCG is a trimeric protein containing three possible subunits, α’, α, and β. While the larger α’ and α subunits are rapidly degraded during germination, the smaller β subunit is unaffected until day 6 of growth.

We have found that the enzyme that initially degrades the α’ and α subunits, protease C1, is a serine protease. It cleaves at sequences with multiple Glu residues - in the α’ and α subunits in their N-terminal regions, producing products approximately the size of the β subunit. Protease C1 does not effect the β subunit, which lacks the N-terminal extensions of the α’ and α subunits. The further degradation of the truncated α’ and α subunits, as well as the β subunit, is carried out by a cysteine protease, protease C2. Protease C2 can cleave a wide range of peptide bonds *in vitro*, but its action on the βCG subunits is restricted to cutting them approximately in half. This specificity is forced by the 3-D structure of the substrate - cleavage occurring only in an exposed flexible loop on the substrate's surface.

I have extended my studies to other legumes in collaboration with Dr. Andrei Shutov of Moldova State University, Moldova. Our combined labs have compared the action of the major legumain-like and papain-like cysteine proteases from the common garden bean, *Phaseolus vulgaris*, either alone or combined, on the endogenous bean storage protein, phaseolin. While LLP quantitatively modifies phaseolin, cleaving it in half, it cannot extensively cleave the phaseolin to short peptides. CPPh has a similar effect. In contrast, treatment of phaseolin with LLP followed by CPPh leads to extensive phaseolin hydrolysis.

Current projects in my lab are examining the degradation of the other major soybean storage protein, glycinin, as well as the degradation of storage proteins in the maturing pea (*Pisum sativum*) seed and during its germination.

For additional information see my website: [http://bingweb.binghamton.edu/~biochem/KarlWilson/Default.htm](http://bingweb.binghamton.edu/~biochem/KarlWilson/Default.htm)
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**Biochemistry Book Swap**

Each Semester, the Biochemistry Advisory Board will loan out textbooks for Biochemistry courses, prerequisites and electives (including select courses in Biology and Chemistry). In exchange, the student will be asked to put down a deposit at the beginning of the semester, most of which they will be refunded upon returning each book to the Biochemistry Advisory Board. **We reserve the right to keep your deposit if you do not return the book.** Books should be returned during finals week of the semester they are borrowed, the exception being the textbooks borrowed for year-long courses (such as Organic Chemistry).

**How to borrow:** Keep an eye on your inbox at the beginning of next semester for more details about how to get involved

**How to donate:** If you have an old copy of any Biochemistry, Biology or Chemistry textbook, and are willing to donate it to the Book Swap, please send an email to Maura Loew (mloew1@binghamton.edu).

**Example:** The used 7th Edition of Organic Chemistry (Carey)
You pay $135
You get back $125 upon returning the book

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Are you an **alum** with experience working in the pharmaceutical or biotechnology industries? We would **love** to hear from you!

**Students involved in research:**
We would like to include your work in our next issue. *Contact us if you are interested!*

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**Find out the most recent Biochemistry information at:**

[biochem.binghamton.edu](http://biochem.binghamton.edu)
Cancer is the second leading cause of death in the USA, claiming nearly 600,000 lives every year. Furthermore, 1 in 2 men and 1 in 3 women will be diagnosed with cancer at some point in their life, meaning virtually everyone is a stakeholder in its treatment. Since the FDA approval of paclitaxel in 1992, tubulin, the main component of cytoskeletal microtubules, has been one of the most successful and widely used chemotherapeutic targets. However, as with most chemotherapeutics, tubulin-targeting molecules are associated with significant adverse effects because of their interactions with healthy cells.

Microtubules are monumentally important to eukaryotic life, and are found in virtually every cell. They are now considered to be the main contributor to the biophysical properties of the cell, and are also involved in nearly everything relating to cellular transport. They provide a dynamic network of "molecular highways" on which the cell moves proteins, nucleic acids, and other structures important to cellular function. Thus, in a very real sense, microtubules provide the cell with structure and infrastructure necessary for survival.

Because microtubules are so essential to eukaryotic life, the observation that tubulin is highly conserved comes as no surprise. Typically, tubulin from higher order eukaryotes contains only 2-8% sequence divergence. Although it is highly conserved, it is also known that tubulin exists as several microvariants called isotypes which selectively localize to different tissues in the body. By studying the drug binding properties of these variants, it may be possible to improve current treatments.

A binding site of particular interest to our lab is that of colchicine. Colchicine is a small molecule isolated from *Colchicum autumnale*, whose medicinal use dates back over two-thousand years. It is known to bind ubiquitously and specifically to its binding site on β-tubulin. Once bound, colchicine acts as a microtubule poison, destabilizing the microtubule network in cells. Because microtubules form the mitotic spindle, which is necessary for cell division, colchicine can act as a "spindle poison," hurdling cells about to divide into apoptosis. Because of this effect, it seems that colchicine should be an effective cancer treatment due to the increased rate of mitosis found in cancer cells. However, its toxicity is so high in normal cells that it has virtually no use as an anti-neoplastic agent.

However, in our lab we are currently investigating a particular isotype of β-tubulin for which we find no evidence of colchicine binding. This tubulin is called avian βVI, which is isolated from the marginal band of avian erythrocytes. This is particularly exciting in the world of tubulin research because colchicine binding was thought to be a nearly universally conserved property of the protein.

Avian βVI is an outlier, resisting the observation that tubulin is conserved among higher order eukaryotes. It has a relatively high degree of sequence divergence (~17% from other tubulins), is found almost exclusively in hematopoietic tissue, and, as our results indicate, contains a different colchicine binding site. However, our results with other colchicine-site ligands indicate that although it is divergent, the site has not lost function. This considered, it may be possible to find ligands which bind to the divergent on avian βVI specifically.

Although interesting, there must be a human tubulin equivalent to make these findings medically relevant. Through molecular modeling and sequence alignments, we have indications that the human hematopoietic tubulin, human β1, contains a nearly identical colchicine-site to avian βVI. It stands to reason that human β1 tubulin may exhibit the same divergent colchicine binding activity seen in avian βVI. Furthermore, if we are able to find small molecules that target this isotype, it may lead to an *in vivo* targeting mechanism for hematopoietic tissue. In essence, for cancers of cells which contain this isotype, we could globally administer our small molecule, and it would only affect cells of a similar type to the cancer and leave the rest of the body unscathed, thereby reducing the toxic side effects common to tubulin drugs.

We are currently investigating the similarity in drug binding properties at the colchicine site of avian βVI and human β1 predicted by our molecular modeling results. Hopefully, this will evolve into a viable treatment option for hematopoietic cancers in years to come.
Characterization of Rice Seedling Leaf Proteases

Proteolytic enzymes hydrolyze peptide bonds in proteins via proteolysis. These proteolytic enzymes are noteworthy, contributing to many significant bodily functions, including gene regulation, amino acid storage, and enzymatic action. Whole genome sequencing has shown that plant genomes encode a large number of proteases, but beyond recognition by sequence relatedness to large multigene families including those in bacteria and animals, little is known about most of these.

For instance, the rice (*Oryza sativa*) genome encodes 628 proteases. Only a few proteases have been characterized. Those that have been studied show significant roles in determining plant morphology and contributing to development and defense. Proteomic studies are beginning to note the more abundant proteases in plants, but there is no indication whether these are active or not. Understanding the function of each protease requires information not only on quantitative levels of gene expression at both the mRNA and protein levels, but also quantitative levels of proteolytic activity and eventually information on endogenous protein substrate and products along with their physiological significance.

The goal of this project is to detect general-acting proteases in rice, that are not so specific with regard to protein substrates, and are able to cleave a heterologous protein substrate such as gelatin. Characterization of the proteases in rice seedling leaf tissues was conducted using non-reducing SDS-PAGE gelatin-zymography to analyze protein extracts. Zymography, an electrophoretic technique in which a protein substrate is co-polymerized with the acrylamide, allows for detection of protease activity. The use of gelatin provides a substrate for the proteolytic enzymes to break down, generating smaller peptides that will diffuse out of the matrix. Upon protein staining, clear bands on a dark blue background, due to a lack of substrate, indicate the presence of proteolytic enzymes able to hydrolyze gelatin.

My focus is on the 14-day developing stage *Oryza Sativa*, where leaves are rapidly expanding. These proteases are characterized according to molecular weight, pH optimum, and mechanistic class. Fractionation by anion-exchange spin column chromatography has proven useful in separating numerous proteases in the extract, and further characterizing them according to their binding affinity to quaternary ammonium compounds on the resin. Moreover, it has allowed for separation of proteases similar in size and/or pH optima into different fractions.

Gelatin-zymography has proven to be a very useful technique in detecting protease activity. Protease activities were identified as eight bands between 30-118 kD, most of which had a pH optimum of 5.5, 7.5 or 8.5. In addition, these proteases have revealed different binding affinities to the anion exchange chromatography column. Proteases in the broad band 70-80 kD and 80-90 kD bands (Figure 1) constituted a heterogeneous group as these were distributed among the fractions. Some separation among them was achieved, manifesting as two distinct bands in some fractions. Additional bands of mass 25, 30, 34, and 40 kD that have shown activities with pH optimum of 5.5 were eluted only with 0.3-0.5 M NaCl in the eluting buffer. Interestingly, there appears to be two 80 kD proteolytic enzymes with pH optima of 8.5; one eluting at very low NaCl concentrations indicating that the protease does not bind tightly to the column, while the other eluting with 0.3-1.0 M NaCl in the buffer. In comparison, work with *Arabidopsis thaliana* seedling tissues were also profiled for protease activity directed against the exogenous substrate, gelatin. As with *Oryza Sativa*, a broad band around 75 kD was seen at pH 5.5 and 6.0.

In my senior year, I intend to use small molecule inhibitors to characterize each protease as a serine, cysteine, aspartic or metalloprotease. Identification of these active proteases will be achieved through mass spectrometric analysis of trypsin digests.
Fluorescence microscopy has led to many impacting discoveries in the field of biology. One common method of fluorescence is immunofluorescence in which fluorescently labeled antibodies are used to probe cellular structures. Green fluorescent protein (GFP) labeling is another fluorescent microscopy method for which the gene for the production of GFP is spliced into the genome of the organism in the region of the DNA which codes for the target proteins. Upon the synthesis of the target protein, the cell intrinsically conjugates GFP, allowing fluorescence imaging of the target protein. Although these techniques have historically provided fantastic images of the cell, their size limits their effectiveness when using super resolution microscopic techniques.

Sub-diffraction limit fluorescence microscopic techniques (STORM, PALM, etc.) have increased the resolution of fluorescence micrographs down the range of tens of nanometers. In these super-resolution microscopy experiments, the effective resolution of an image is dependent on the intrinsic resolution of the technique and the size of the probe. The smaller the probe, the closer the fluorophore is to the target site; thus a higher resolution image is produced.

To address this problem, our lab has designed a chemical linker which can bioorthogonally label intracellular structures. The concept behind bioorthogonal labeling is to use non-native, site-specific probes which are small enough to label intracellular structures of live cells without perturbing cellular activity. This way, fluorescent experiments can develop images of the labeled target as the cell performs its functions. Since the linker is on the order of 1 nanometer in length, the fluorophore will be very close to the protein allowing a higher effective resolution image to be gathered from super-resolution microscopic techniques.

To have the linker site-specifically react with a protein, our group developed a system which takes advantage of artificial amino-acid hybridization and the hydrazone linkage. The linker is bound to a commercially available fluorophore while the target protein is hybridized with the artificial amino acid, 3-formyl tyrosine. 3-formyl tyrosine is unique because aldehydes are rare functionalities in cells, which gives us a site-specific, non-native handle with which to attach our fluorophores. Since the linker’s hydrazine moiety seeks out to react with aldehydes, the linker will readily and specifically react wherever the 3-formyl tyrosine is found in the target protein.

Working in organic synthesis, I was given the task to synthesize the linker. The synthetic schematics can be observed in Fig 2. (1): Via catalytic hydrogenation, trans p-nitrocinamic acid is saturated simultaneously at both the alpha carbon double bond and the para-positioned aromatic nitro group. (2): The product is then submitted to a lithium aluminum hydride reduction which reduces the carboxylic acid into a primary alcohol. (3): The aniline is then diazotized to form the hydrazine functional group that will bind the hybridized protein. Once this step is completed our raw linker, 3-(4-hydrazinyl phenyl)propanol, has been synthesized. (4): Protecting groups are then covalently bonded to the hydrazine for the chemoselectivity of the linker’s hydroxy end to react with the fluorophore (5). Once the linker-fluorophore complex is formed, only a simple acid hydrolysis (6), is needed to reactivate the hydrazine for hydrazone linkage to the modified protein.

Being able to choose from a library of commercially available fluorophores in conjunction with bioorthogonal labeling, the linker provides endless combinations of fluorescent labels for a variety of different kinds of cells. With the introduction of the linker, the Bane lab will be able to, in theory, develop extremely high-resolution images of intracellular structures, expanding our knowledge of the cellular environment one fluorescent image at a time.
Eric Loesch  
Alum of ‘07  
Currently a Neurology Clinical Research Coordinator at Mass General Hospital

I am currently working as a Neurology Clinical Research Coordinator at Massachusetts General Hospital in Boston, having graduated from Binghamton University in 2007 with a degree in Biochemistry. The Biochemistry program at Binghamton prepares students for excellent careers in medicine, biotechnical, pharmaceutical and environmental related businesses or even governmental agencies. I firmly believe that the strong foundation that Binghamton provided me was a key reason that I was selected for my current position. I am in charge of an NIH funded clinical trial concerning stroke patients. My study utilizes results based on a number of proteomic techniques, including mass spectrometry, ELISA, and western blotting, all of which I was first introduced to in my studies at Binghamton. My job at the hospital involves translational research which means that I work with patients in the clinic, perform laboratory research on their specimens, and eventually participate in expressing our results via publication. It is our hope that sharing our results with others will ultimately produce targeted therapies that can contribute to the evolving branch of “personalized medicine.”

I think that this exchange of information is one of the most gratifying things about being a researcher. The information and insight that you possess makes you not only a valuable scientist, but also a valuable person. The desire to discover truths about nature and provide products that can improve the quality of peoples’ lives is what has driven me in my work. This knowledge can be used towards fighting illness and improving the quality of life, making the field interesting, challenging, rewarding, and full of opportunity. Ultimately, this is why I pursued a career in medicine.

Jonathan Sarker  
Alum of ‘09  
Currently a Biophysics graduate student at UC Davis

I chose to major in Biochemistry because the subject seemed to give more depth, rigor, and understanding to the life sciences. The core classes/electives have given me a well-rounded “sampler” of science, whetting my appetite for the interdisciplinary research I now pursue in Biophysics. In retrospect, considering all that I’ve learned, the dedicated instructors I’ve had, and of course, the wonderful friends I’ve made through this major, I couldn’t have chosen better.

Like everyone else in the major, I had to take two semesters of Biology, Chemistry, Calculus and Physics. As interesting as they were, I was amazed at how they all intersected in Biophysical Chemistry. Who knew that something as abstract as Thermodynamics could apply to biological processes or that Calculus would be seen in Biology? Even Organic Chemistry shared some topics with Quantum Chemistry and Physics. By taking the wide spectrum of courses that the Biochemistry major required, I could see connections between what before seemed like distinct subjects. From this, I gained a new appreciation for Mathematics and the Physical Sciences. They gave more dimensions and detail to Biology, making the study of life all the more exciting.
You may know that your biochemistry degree can lead to a career in the pharmaceutical industry. Did you also know there is a burgeoning industry that is highly related to biochemistry? It is called the biotechnology, or “biotech,” industry. This industry uses biological macromolecules, such as proteins, RNA, or DNA, to treat diseases. An example of a biotech drug is an antibody that binds to cancer cells specifically, triggering the patient's immune system to attack the cancer.

The book *Career Opportunities in Biotechnology and Drug Development*, by Toby Freedman, can be a valuable resource for those of you considering working in industry. This book is available at the Science Library. The route to drug discovery and FDA approval is similar for biotech drugs and traditional ones, so the information below applies both to biotech and traditional pharmaceutical careers. There are specialized careers for each step along the way. The BS in biochemistry can make you a candidate for any of the fields below, but your opportunity for advancement may be limited if you only have a bachelor's degree.

**Drug Discovery**

The scientists who discover or develop potential drugs work in “Drug Discovery” research. This initial step requires scientists to identify a potential target for a given disease. This target could be a receptor, enzyme, or other protein which is thought to be responsible for the disease's effect. After a drug target is identified, an assay must be developed to measure whether a potential drug binds to the target. For small-molecule drugs (traditional drugs), the assay will usually be used to screen thousands of molecules called a “library.” For biotech drugs, a more deliberate, rational approach is usually used. The “lead” compound that is found from these efforts is then modified for potency, solubility, toxicity and other properties.

If this sounds like a field you would be interested in, you should try to get research experience ([http://biochem.binghamton.edu/honors.html](http://biochem.binghamton.edu/honors.html)) and/or an internship ([http://biochem.binghamton.edu/internships.html](http://biochem.binghamton.edu/internships.html)) during your undergrad years. You would also be wise to take biology electives that are lab-based and will teach you experimental techniques, such as microbiology or cell biology lab.

**Pre-Clinical Research**

Clinical trials evaluate the safety and efficacy of a drug candidate in humans. Because this is very expensive, and potentially dangerous, drugs are tested as much as possible in animals and cultured humans cells before clinical trials begin. Pre-clinical researchers will study the “ADMET,” or pharmacokinetic, properties. ADMET stands for absorption, distribution, metabolism, excretion and toxicity.

A major function of the pre-clinical research division is to file an application with the FDA to get approval to begin trials in humans. Efficacy and safety must be demonstrated before any human can take the drug. Employees in preclinical research can hold bachelors, masters, PhD, MD or DVM.

**Clinical Research**

Once a drug is approved for testing in humans, it is tested in humans. It is tested first for safety, then for efficacy. These clinical trials take several years. Every step of clinical trials in humans requires regulatory paperwork to be filed with the FDA. This stage of drug discovery has many positions that do not require lab work. Some careers require travel to monitor clinical trials which are being held all over the country. Most of the positions in clinical research go to employees with medical degrees (MD, PharmD, MPH, RN) but there are also careers for those who hold a PhD, MS or BS. A medical doctor will find higher-paying, but higher-responsibility positions.

The field of drug discovery is one that many biochemistry majors would enjoy. Due to the state of the economy, many pharmaceutical companies are laying off workers, but conditions are expected to improve. Consider pursuing an advanced degree to increase your marketability. Students with an MS or PhD in pharmaceutical science are highly sought. If you want to take a break from science, an MBA would also improve your prospects. You can read much more about careers in drug discovery in Toby Freedman’s book. He provides snapshots on a wide variety of careers, including ones that might not be obvious from this article—writing, marketing, business, law, and computer science-related careers. Now is the time to learn about careers that your biochemistry degree will prepare you for.

Written by: Maura Loew
A note from the Newsletter Coordinator...

To the dedicated BCAB Executive Board, faculty, student, alumni, and YOU,

THANK YOU!!!!

To Dr. Zhitao Li, Dr. Robert Van Buskirk, and Dr. Karl Wilson, thank you so much for contributing and sharing your work with Binghamton University. With all the exciting research that each of you do, I believe that students will be inspired by your work and become interested in research.

To Dan Pan, Adam, Anthony, and Stefano, thank you guys for your contributions and bearing with my annoying e-mails. You are all role models for current and future Biochemistry students, so I hope many will follow in your steps!

Thank you Maura for always being so on top of everything and helping BCAB become a great success. The newsletter wouldn’t be complete without your assistance. A huge thank you to Dr. Bane, Emma, everyone on E-board, and BCAB members.

On behalf of the Biochemistry Advisory Board, thank you so much for reading this year’s newsletter. I hope that you enjoyed it!

Kalle Yee
Newsletter Coordinator 2009-2010

A note from the President...

Binghamton Students, Faculty and Alumni:

I’m proud to say that the Biochemistry Advisory Board has led a number of events this year. Last semester, we held an informational event on how to apply for summer research and early this semester we held an event advising students on how to pursue research positions here on campus. In late March, we were happy to join the Biochemistry and Chemistry departments in hosting Dr. Brazeau from the University of Buffalo, who spoke about UB’s Pharmaceutical program, giving our students another path to consider after their studies here at Binghamton University. We also held a bake sale and a “Molecular Model Building” event with Late Nite to get the word out about our club and our mission. In April, we held a soccer game against the Chemistry club and other events to show our versatile approach toward supporting and advising undergraduate Biochemistry students and those who are interested in this field.

Many thanks to those who made this possible, including: Dr. Susan Bane, Maura Loew, Dr. Karl Wilson, Dr. Robert Van Buskirk, Dr. Zhitao Li, Dr. Eriks Rozners, Adam Blanden, Jacky Chow, Solomon Dawson, Emily Greene, Anthony Kashou, Stefano Quarta, and last but not least Kalle Yee, who single-handedly coordinated the production of this newsletter. Thank you!

Emma Schweizer
Biochemistry Advisory Board President 2009-2010
The Biochemistry Advisory Board is seeking new members! If you are interested in meeting people with similar interests, taking on leadership roles in creating next year's newsletter and peer advising, or just chatting about life as a Biochemistry major, this is the club for you! Contact us if you would like to join!

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